Detailed analysis of public RNAseq data and long non-coding RNA: a proposed enhancement to mesenchymal stem cell characterisation

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Abstract

The development of RNA sequencing (RNAseq) and corresponding emergence of public datasets have created new avenues of transcriptional marker search. The long non-coding RNAs (lncRNAs) constitute an emerging class of transcripts with a potential for high tissue specificity and function. Using a dedicated bioinformatics pipeline, we propose to construct a cell-specific catalogue of unannotated lncRNAs and to identify the strongest cell markers. This pipeline uses *ab initio* transcript identification, pseudoalignment and new methodologies such as a specific k-mer approach for naive quantification of expression in numerous RNAseq data.

For an application model, we focused on Mesenchymal Stem Cells (MSCs), a type of adult multipotent stem-cells of diverse tissue origins. Frequently used in clinics, these cells lack extensive characterisation. Our pipeline was able to highlight different lncRNAs with high specificity for MSCs. *In silico* methodologies for functional prediction demonstrated that each candidate represents one specific state of MSCs biology. Together, these results suggest an approach that can be employed to harness lncRNA as cell marker, showing different candidates as potential actors in MSCs biology, while suggesting promising directions for future experimental investigations.

1 Introduction

[1]

The increasing popularity of RNAseq and the ensuing aggregation of this data-type into public databases enable the search for new biomarkers across large cohorts of donors or cell types for the purpose pathological conditions or cellular lineages identification. As such, RNAseq has paved the way for the discovery of novel transcriptional biomarkers such as long noncoding RNAs (lncRNAs), that have emerged as a fundamental molecular class. A growing number of lncRNAs have been identified in the last decades, with their number approaching that of coding RNAs (17910 annotated human lncRNAs in the latest v32 version of the GENCODE versus 19 965 coding genes).

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An increasing body of evidence has highlighted characteristics that define lncRNAs as therapeutic targets as well as potential tissue-specific markers [1]. Indeed, despite their non-coding nature, a large spectrum of functional mechanisms have been associated to lncRNAs [2, 3]. These include: endogenous competition (miRNA sponging for example), protein complex scaffolding and guides for active proteins with RNA-DNA homology interactions. These mechanisms occur in various physiological or pathological processes such as development, cancer and immunity [4, 5, 6]. To date, there is no finite list of long non-coding isoforms, making it difficult to construct a complete lncRNA catalogue due to the high number of transcripts and their tissue-specific expression [7, 8]. The absence of a complete catalogue makes it difficult to establish a comprehensive lncRNA expression profile.Thus, currently, the best strategy for the study of lncRNAs consists in the prediction of transcripts from a selection of RNAseq data in a tissue-specific condition. This strategy was successful in novel lncRNA biomarker discovery in pathological conditions [9, 10], but was poorly explored for cell lineage characterisation. Taking into account their functional importance and specificity, these RNAs should therefore not be ignored in establishing the molecular identity of a cell type.

Cell characterisation by specific markers bring different challenges such as the importance of probing the specificity of the marker and its limits in an extended number of various cell types, rather than using a control/patient experimental model. Moreover, the cells are not in a fixed state and display a variable transcriptional activity depending on cell status, environment, culture conditions and other parameters [1]. Furthermore, the lncRNAs' function is generally poorly assessed, except in the case of recurrent known transcripts (HOTAIR, H19). Thus, the *in silico* elaboration of a lncRNA catalogue that document the functional domains where the candidates could act, will be beneficial in the identification of lncRNAs' role and thus, in future experiments.

To this end, we have developed an integrated four-step procedure consisting of: i) an *ab initio* transcript reconstruction from RNAseq data and characterisation of novel transcripts, ii) a differential analysis using pseudoalignment coupled with a machine learning solution in order to extract the most cell-specific candidates, iii) an original step of tissue-expression validation with specific k-mers search in large and diversified transcriptomic datasets iv) an in-depth analysis to predict lncRNAs' functional potential from *in silico* prediction approaches. The notable advantage of introducing an *in silico* verification using k-mers is to allow a precise and in-depth determination of lncRNAs expression profile and to quickly interrogate their lineage specificity. In addition to that, validation of newly identified lncRNAs has been undertaken using RT-qPCR and long read sequencing (with Oxford Nanopore technology).

Mesenchymal Stem Cells (MSCs) are defined as multipotent adult stem cells, harvested from various tissues, including Bone Marrow (BM), Umbilical Cord (UC), and Adipose tissue (Ad). MSCs are an interesting cell type to explore since these cells lack the extended transcriptional characterisation that could highlight their lineage belonging and/or the possibility of distinguishing them from other mesodermal cell types such as fibroblasts and pericytes [11, 12]. The commonly admitted surface markers for MSCs, proposed by the International Society for Cellular Therapy (ISCT), and required to identify MSCs since 2006 are THY1 (CD90), NT5E (CD73), ENG (CD105) concerning the positive markers, and CD45, CD34, CD14 or CD11b, CD79alpha or CD19 and HLA-DR concerning the negative markers [13]. These markers are not distinctive and

may therefore not be sufficient for the definition of cellular or biological properties. Considering their different therapeutic properties (chondro and osteo differentiation potential, immunomodulation and production of trophic factors) [14] and given the increasing usage of these cells for academic and preclinical research [15], a detailed molecular characterisation of MSCs and predictive marker of functionality will constitute an important tool in regenerative medicine. lncRNAs have emerged as a class of transcripts with tissue-specific expression and important functions, such as the regulation of MSCs function [16, 17, 18], and remain largely unexplored in these cells.

To address this need, we performed a broad transcriptomic analysis of novel lncRNAs on human Mesenchymal Stem Cells (MSCs). We started from publicly available MSCs RNAseq, selecting ribodepleted datasets in order to enhance lncRNAs discovery and to explore the poly-(A)+ as poly(A)- lncRNAs. We restricted the differential expression analysis to a bone-marrow MSCs source compared to "nonMSC" cell counterparts. Once achieved, in depth *in silico* analysis was performed to check the lncRNA cell specific profiles with more and extensive datasets. To validate our approach, RNAseq data from eight publicly available libraries of normal MSCs containing a large diversity of noncancerous cell types were used for novel lncRNAs detection and tissue expression comparison. We initially reconstructed more than 70000 unannotated lncRNAs present in human bone-marrow MSCs. These lncRNAs were assigned depending on their position relative to annotated genes: MSC-related Long Intergenic Non Coding trancripts" named "Mlinc", and MSC-related Long Overlapping Antisense transcripts called "Mloanc". Among them, 35 Mlincs were specifically enriched in the cell lineage compared to the "non-MSC" counterpart group. Finally, after a further selection of the three most specific Mlincs, detailed *in vitro* and *in silico* functional exploration were performed.

2 Material and methods

2.1 Data collection and basic processing

The public RNAseq datasets (in fastq format) have been assessed using the ENCODE, EBI ArrayExpress service or SRA database at each step of the pipeline:

i) lncRNAs prediction and first differential analysis (Table S1), ii) k-mer search in ENCODE data to refine lncRNAs' specificity (Table S2), iii) k-mer search in FANTOM6 CAGE dataset and single cell analysis (scRNAseq) from Adipose MSCs by X. Liu et al raw data [19] for functional investigations (Table S3), iv) k-mer search in MSCs in different conditions (Table S4).

The reads quality were assessed with FastQC (https://www.bioinformatics.babraham.ac.uk /projects/fastqc/) to avoid the implementation of poor quality data in the analysis. Data from Peffers et al. [20], added to ENCODEs BM-MSCs RNAseq data, were selected for the MSClinc and Mloanc characterisation and the differential step analysis considering the above-mentioned features: Ribo-zero technology, stranded and paired-ends RNAseq. Peffers data had a forward-reverse library orientation instead of a reverse-forward orientation of a classic Illumina sequencing, thereby the order of paired files was manually reversed. The fastq files used for lncRNAs prediction, referred as "MSC" group, were used for the differential analysis against the other cell types as "non-MSC" group, (Table S1) were mapped using CRAC v2.5.0 software [21] on the indexed GRCh38 human genome, including mitochondria, with stranded, -k 22 and rf options.

2.2 *Ab initio* assembly for transcripts prediction or unannotated transcripts prediction

The aligned reads of the "MSC" group were put through *ab initio* transcript assembly. Unannotated transcripts were predicted with the following procedure: i/an *ab initio* reconstruction was performed on individual RNAseq with the StringTie [22] version 1.3.3b, with -c 5 -j 5 rf -f 0.1 (5 spliced reads are necessary to predict a junction and 5 reads at minimum are required to predict an expressed locus), ii/ the output individual gtf files obtained with the RNAseq of "MSC" group were then merged with the StringTie version 1.3.3b with -f 0.01 -m 200 and with a minimum TPM of 0.5, with the Ensembl human annotation (hg38) v90 used as guide for StringTie. The GTF was parsed with BEDTools [23] to dissociate new intergenic lncRNAs (lincRNAs) from annotated RNAs (coding or annotated lncRNAs), by applying filter criteria classically used in lncRNAs prediction [24], excluding transcript models overlapping (by 1 bp or more) any annotated coordinates. The resulting GTF of unannotated lincRNA from MSCs is referred as "Mlinc".

In parallel, the GTF was parsed with BEDTools to dissociate overlapping-antisens lncRNAs (named Mloanc), by applying filter criteria classically used in lncRNAs prediction, keeping transcript overlapping any annotated coordinates, then excluding transcript models overlapping these annotated coordinates on the same strand. The resulting GTF of MSCs overlapping-antisens lncRNAs is referred as "Mloanc" (Figure 1).

2.3 Long-read sequencing

The library was generated with 250 ng polyA+ mRNA purified from 50 μg of human BM-MSCs total RNA. The polyA+ mRNA were treated according to the cDNA-PCR sequencing kit protocol (ref SQK-PCS108) as recommended by Oxford Nanopore. 3 254 396 sequences were obtained on the Oxford Nanopore Minion sequencer. The base calling was done with albacore version 2.2.7. 2 720 928 long-reads were successfully mapped using Minimap2 [25] version 2.10-r764 on GRCh38 human genome with default options used for Oxford Nanopore technology.

2.4 Quantification with pseudoalignment and feature selection

Kallisto v0.43.1 [26] was used directly on RNAseq raw fastq from the "MSC" and "non-MSC" groups. This pseudoalignment was performed with a number of bootstraps (-b) of 100, using a Kallisto index containing the sequences of all transcripts: the Ensembl coding and non-coding transcripts (v90) plus the predicted lincRNA and lncoaRNAs. Sleuth version 0.29.0 [27] was used with R for differential expression statistical analysis using the Walt test method, to compare the "MSC" group against the "non-MSC" group (including Lymphocytes, Macrophages, Hepatocytes, IPS, ESCs, HUVECs, Neurons, chondrocytes). Analysis was performed at the gene level for the annotated genes and at the transcript level for the predicted lincRNA and lncoaRNAs. Genes or lncRNAs having a log2 fold-change between "MSC" and others greater than 0.5 and a p-value lower than or equal to 0.05 were selected. Finally, only transcripts/genes overexpressed in MSCs were selected. Each category (annotated transcripts, lincRNAs and lncoaRNAs) of potential candidates passing the first differentiation expression filter were separated for feature selection analysis. Boruta 6.0 [28] was used with 10000 maximum runs and a pvalue of 0.01 on each category, with multiple comparisons adjustment using the Bonferroni method (mcAdj = TRUE). Candidates passing the boruta test as "Confirmed" for each category were selected as reliable biomarkers.

2.5 Quantification by k-mers search

To quantify the expression of a transcript or a gene in available RNAseq with a rapid procedure, specific k-mers of 31nt length were extracted from the candidate sequence. A specific k-mer of an annotated candidate corresponds to a 31nt sequence that maps once on the genome and once on the reference transcriptome (Ensembl v90). In case of unannotated transcript (Mlinc, Mloanc) a specific k-mer maps once on the genome and is absent from reference transcriptome. The automated selection of specific k-mers is ensured by the Kmerator tool (in preparation) (https://github.com/Transipedia/kmerator). The k-mers were then quantified directly in raw fastq files using countTags (https://github.com/Transipedia/countTags). The quantification is expressed by the average count of all k-mers for one transcript, normalised by million of total k-mers in the raw file.

In FANTOM6 Dataset (https://doi.org/10.1101/700864, article not peer-reviewed) containing CAGE Analysis, to approach a "Transcript Per Millions" normalisation, the number of k-mers quantified was normalised by the total number of reads in million.

2.6 Genomic intervals assessment

DNase-seq intervals of enrichment were directly downloaded from ENCODE in bed format for BM-mesenchymal cells (ENCFF832FHZ) and hematopoietic progenitors (ENCFF378FCS). The H3K27ac (GSM3564514) and H3K4me3 (GSM3564510) ChIP results from undifferentiated BM-MSCs of the Agrawal Singh S. et al. study [29] were downloaded from GEO database in wig format, and remapped to the hg38 genome with CrossMap (http://crossmap.sourceforge.net/).

2.7 *in silico* functional prediction

We used LncADeep [30] to identify particular correlations between candidates and proteins. Beginning with our selection of 3 candidates, we filtered shared predicted proteins and selected protein uniquely predicted as interacting uniquely with the concerned candidate. The pathways concerned with these unique protein were identified with reactome.

Tarpmir was used to identify possible target site of human miRNA from miRbase ($p = 0.5$) [31] and FEELnc [32] to decipher the coding potential of candidates, using the coding and non-coding par of Ensembl annotation sequences as model.

2.8 Single-cell analysis

Single-cell data were pseudoaligned with Kallisto, with the same index used for the initial bulk RNAseq analysis. Pseudoalignment of 10X genomics data, correction, sorting and counting was made by Kallisto "bus" functions. Count matrices were processed with Seurat R package [33, 34]. Empty droplets were estimated by barcode ranking knee and inflection points, only droplet with a minimal count of 10000 were kept. In the end, 26071 droplets remain.

After normalisation, Inter-donor batch effect was corrected with ComBat method in sva R package [35] (Combat function, prior.plots=FALSE, par.prior=TRUE). Cell cycle scoring was made by CellCycleScoring Seurat function, using gene set used by the initial authors [19]. Finally, other sources of unnecessary variability as percent of mitochondrial genes, cell cycle and number of UMIs were regressed using ScaleData Seurat function.

To decipher genes enriched in cells positive for our markers, cells with a scaled expression superior or equal to 0.1 were labelled as positives, whereas cells with an expression inferior to the level were labelled as negatives. Then, markers of these cell were deciphered using FindAllMarkers Seurat function with a minimum FC threshold of 0.15. Expression of our markers in the Ad-MSCs population was made by FeaturePlot Seurat function after UMAP dimensional reduction, the gene enrichments were represented with VlnPlot function.

2.9 Data visualisation

Genome browser-like figures were generated with Gviz R package [36]. Bam tracks were generated from merged BAMs used for transcript prediction. Heatmaps were generated using superHeat R package (https://github.com/rlbarter/superheat).

2.10 Ethics approval and consents

Human primary MSCs was obtained from patients who had granted the authors written informed consent with approval of the General Direction for Research and Innovation, the department in responsible for questions of ethics within the French Ministry of Higher Education and Research (registration number: DC-2009-1052). Human primary myoblasts were collected from patients of the CHU of Montpellier, France (the Montpellier University Hospital) who had provided informed consent. All experiments were performed in accordance with the Declaration of Helsinki and approved by the ethical committee of the CHU of Montpellier (France). Samples were approved for storage by the French "Ministre de l'Enseignement et de la Recherche" (NDC-2008-594). Liver samples were obtained from the Biological Resource Center of Montpellier CHU (CRB-CHUM; http://www.chu-montpellier.fr; Biobank ID: BB-0033-00031). The procedure was approved by the French Ethics Committee and written or oral consent was obtained from the patients.

2.11 Cell preparation and culture conditions

MSCs were isolated from bone marrow aspirates of patients undergoing hip replacement surgery, as previously described [37]. Cell suspensions were plated in α-MEM supplemented with 10 % FCS, 1 ng/mL FGF2 (R&D Systems), 2 mM L-glutamine, 100 U/mL penicillin and 100 μg/mL streptomycin. These were shown to be positive for CD44, CD73, CD90 and CD105 and negative for CD14, CD34 and CD45 and used at the third or fourth passage. Human skin fibroblasts were cultured in DMEM high glucose supplemented with 10 % FCS. For Ad-MSCs isolation, adipose tissue was digested with 250 U/mL collagenase type II for 1 h at 37 °C and centrifuged (300 g for 10 min) using routine laboratory practices. The stroma vascular fraction was collected and cells filtered successively through a 100 μm, 70 μm and 40 μm porous membrane (Cell Strainer, BD-Biosciences, Le-Pont-de-Claix, France). Single cells were seeded at the initial density of 4000 cell/cm2 in αMEM supplemented with 100 U/mL penicillin/streptomycin (PS), 2 mmol/mL glutamine (Glu) and 10% fetal calf serum (FCS). After 24 h, cultures were washed twice with PBS. After 1 week, cells were trypsinised and expanded at 2000 cells/cm2 till day 14 (end of passage 1), where Ad-MSCs preparations were used.

Human umbilical vein endothelial cells (HUVEC) obtained from Clonetics (Lonza, Levallois Perret, France) were cultured in complete EGM-2MV (Lonza) supplemented with 3 % FCS (HyClone; Perbio Science, Brebires, France)

Primary human myoblasts were isolated and purified from skeletal muscles of donors, as described by Kitzmann et al [38]. Purified myoblasts were plated in Petri dishes and cultured in growth medium containing Dulbecco's Modified Eagle's Medium (Gibco) supplemented with 20 % foetal bovine serum (FBS) (GE Healthcare, PAA), 0.5 % Ultroser G serum substitute (PALL life sciences) and 50 μg/ml Gentamicin (Thermo Scientific, France) at 37°C in humidified atmosphere with 5 % CO_2. All experiments were carried out between passage 4 (P4) and P8 to avoid cell senescence.

IPSCs were maintained in mTeSR-1TM medium (STEMCELL Technologies), in Petri dishes with matrigel (Corning, France). For the passages, cells were incubated in Gentle Cell Dissociation Reagent (STEMCELL Technologies) at room temperature, dissociation medium was discarded and cells incubated in mTeSR medium. All cell cultures were performed at 37°C with 5% of O_2 and 10% of CO_2.

Primary human hepatocytes (PHHs) were isolated, as described previously [39], from liver resections performed in adult patients.

NSC derived from H9 or directly bought (StemPro) have been cultivated on laminine with StemPro NSC SFM medium.

H9 embryonic stem cells were cultivated in ESICO medium in a coculture H9/MEF (Mouse Embryonic Fibroblasts) at 37 °C with 5% of O_2 and 5% CO_2.

2.12 RNA preparation and reverse transcription

Total RNA was isolated using TRIzol reagent (invitrogen) or RNeasy Mini Kit (Qiagen, France) according to the manufacturer protocol. RNA was quantified using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific, France). RNA quality and quantity were further assessed using the 2100-Bioanalyzer (Agilent Technologies, Waldronn, Germany). Only preparations with RNA integrity number (RIN) values above 7 were considered. Reverse-transcription was performed either with random hexamers using the GeneAmp Gold RNA PCR Core kit (Applied Biosystems) or with oligo(dT) using SuperScriptTM First-Strand Synthesis System for RT-qPCR (invitrogen, France).

2.13 Real-time quantitative PCR

Primer pairs were designed with primer3 online software (http://bioinfo.ut.ee/primer3-0.4.0/) from the transcripts' sequences. Primer pairs with a perfect and unique match on the human genome were validated with ucsc blat software (https://genome.ucsc.edu). As a final verification, primers were visualised in parallel with the bam alignment using IGV (http://software.broadinstitute.org/softw to verify that the primers overlap zones with read coverage. If possible, primer-pairs were designed to span an intron when present in the genomic sequence. Primers were designed for a mean Tm of 60°C. Quantitative PCR (qPCR) were performed using LightCycler 480 SYBR Green I Master mix and real-time PCR instrument (Roche). PCR conditions were 95 °C for 5 min followed by 45 cycles of 15 s at 95 °C, 10 s at 60 °C and 20 s at 72 °C. For each reaction, a single amplicon with the expected melting temperature was obtained.

The gene encoding ribosomal protein S9 (RPS9) was used as house-keeping gene for normalisation. The threshold cycle (Ct) of each amplification curve was calculated by Roche's LightCycler 480 software using the second derivative maximum method. The relative amount of transcripts were calculated using the ddCt method [40].

Results

For the purpose of generating a catalogue of all transcripts in any particular cell type, we developed a pipeline for the characterisation of all RNAs and their expression profile in a large collection of RNAseq data. The procedure includes four steps: i) an *ab initio* transcripts reconstruction from RNAseq data and identification of unannotated transcripts, ii) a differential analysis using pseudoalignment coupled with a machine learning solution in order to extract the most cell-specific candidates, iii) an original step of tissue- expression validation with a kmer approach (comparing large transcriptomic datasets), iv) an in-depth analysis to predict lncRNAs functional potential from *in silico* prediction approaches (Figure 1). To illustrate the procedure, we produced a RNA catalogue from bone-marrow MSCs ("MSC" group).

2.14 General features of the predicted MSC catalogue of lncRNAs

As mentioned above, we started with the *ab initio* reconstruction of any transcript from bone-marrow RNAseq with Stringtie assembler after mapping the reads with the CRAC software (see Materials and Methods for parameters). New isoforms of annotated transcripts were ignored. Of the 200 243 transcripts present in Ensembl annotation (version 90), 105 511 (52.6%) were detected in MSCs (TPM >0.1 in pseudoalignment quantification).

73 463 new lncRNAs were reconstructed. This fraction of unannotated transcripts represent 41% of detected transcripts, so in our case the *ab initio* reconstruction made it possible to almost double the inventory of detectable signatures in MSCs (Figure 2A). Of these, 34 712 were found to be intergenic and were thus referred to as "Mlinc" RNAs (MSC-related long intergenic non-coding RNAs), and 38 751 were found to be overlapping coding regions but in anti-sense orientation and thus referred to as "Mloanc" RNAs (MSC-related long overlapping antisense non-coding RNAs, with criteria as described in materials and methods and Figure 2A).

The *ab initio* method by itself is not sufficient to efficiently determine the lncRNAs' full length sequences. Moreover, this step does not preclude the possibility of false positives and at this point of the analysis, all the different rebuilt transcripts are considered to be windows of RNA expression or possible artefacts. These candidates are filtered and, for most interesting candidates, their true form is to be refined through experimental methods. We also assessed the general characteristics of predicted *de novo* lncRNAs in MSCs. Globally, Mlincs and Mloancs are shorter transcripts with longer exons compared to coding genes and annotated lncRNAs. The large majority of predicted lncRNAs are mono exonic (99% for Mlincs, 79% for Mloancs), with a length close to 200nt (Figure 2B-C). A consequence of the abundance of mono-exonic lncRNAs is an infinitesimally small number of variant forms. Only 0.15% and 0.82% of Mlincs and Mloancs are not mono isoforms, respectively.

The GC content of reconstructed lncRNAs is lower than that of coding or non-coding annotated genes (Figure 2D). This low GC proportion of around 40% is a common feature in *ab initio* transcript prediction, observed in a majority of studies of different species, from mammals, insects, plants or prokaryotes [41, 42, 43, 44].

2.15 Enrichment of a restricted set of Mlincs and Mloancs

In this second step, our objective was to obtain a restricted set of potential transcripts, using successive filtering approaches that would reveal their cell specificity. We quantified annotated transcripts, Mlincs and Mloancs with kallisto pseudoalignment [26] in a cohort constituted of two groups : the "MSC" group contained the BM-MSCs initially used for *ab intio* reconstruction,

and the "non-MSC" group used for comparison, composed of a large panel of different cell types including hESC, hematopoietic precursors and stem cells, primary chondrocytes, IPS, hepatocytes, neurons, lymphocytes and macrophages (Table S1).

Only over-expressed transcripts in "MSC" group versus "nonMSC" group were selected. Differential statistical tests were made with Sleuth, a tool specially dedicated to Kallisto results [27] (see all selective parameters in Materials and Methods). We performed two differential expression analyses: one at the gene level for Ensembl annotation, and the other at the transcript level for unannotated transcripts, to give the most likely variant form of the predicted lncRNAs. After this differential analysis, 2801 annotated genes, 655 Mlincs and 3032 Mloancs are significantly overexpressed in BM-MSCs (Figure 2 E-F).

The lncRNAs are commonly known to be less expressed than coding genes and this was observed in our selected annotated genes and new lncRNAs (Figure 2G). As a validation of our procedure, we found the 3 positive MSCs markers of ISCT among the selected annotated genes: THY1 (CD90), ENG (CD105), and NT5E (CD73). We also retrieved some influencers of MSCs activity, for example WNT5A [45, 46], Lamin A/C [47], FAP [48] and others. The complete list of selected genes is provided in Table S5.

2.16 Feature selection for the most discriminating coding and non-coding markers

In an attempt to select the best candidates, we retained lncRNAs with the most discriminative profile between "MSC" and "non-MSC" groups. In our case, the limitation with a classical "top" ranking by Fold Change (FC) or p-value is the presence of subgroups of different types of cells inside the negative "non-MSC" group. The FC, estimated by the Beta value in Figure 2C, appears to be a biased indicator of differential expression as it can select strong but localised expressed lncRNAs in cells poorly represented in our negative group, leading to potential false positive results.

To avoid this problem, we used the Boruta feature selection (see material and method section), for selection of discriminating features based on "random forest" machine learning methodology. Boruta was used separately on each group of candidates (annotated genes, Mlincs and Mloancs) to extract a restricted representation of the most relevant MSCs signatures. The top 35 importance scores were selected for genes, Mlincs and Mloancs. We arbitrary chose to select the first 35 transcripts for each group based on our observation of a drop in the importance score in coding the gene series. Considering the expression profile of the top 35 coding genes and predicted Mlincs, BM-MSCs clusterised independently from other cells types (Figure 3A).

In contrast, the selection of Mloancs did not provide a satisfying clustering as they had similar expression profiles in MSCs and other closely related cell types, in particular in primary chondrocytes (Figure S1). For this reason, Mloancs were not retained for further analysis. Selected annotated genes showed a poor specificity, with only few candidates showing a clear difference of expression between MSC and others: APCDD1L, HOTAIR, KRTAP1-5 and SMILR. The 3 positive MSCs markers from the ISCT were absent in this selection. The novel top 35 Mlincs showed less expression overall but with a more distinctive profile and a higher number of possible MSCs markers with clear contrast of expression. The characteristics, genomic intervals and sequences of the 35 candidates are presented in Table S7.

To assess the potential of genes already proposed as potential MSCs biomarkers by ISCT (Figure S2) or other potential MSCs markers proposed by different authors [14] (Figure S3), we

made a separated expression heatmap, without filter. Among these previously proposed markers, THY1 (CD90) presented the most specific profile. However, each gene presented expression in distinct non-MSC types.

2.17 Validation of selected Mlincs with long reads sequencing

As mentioned above, classical annotation of lncRNAs with *ab initio* short read methods suffers from inaccuracies and biases. The Oxford Nanopore long read technology (ONT) can sequence entire cDNA, which constitutes a clear technological advantage, not only in confirming the existence of the transcripts but also as it makes it possible to precisely identify the genomic intervals of lncRNA candidates. We performed long-read sequencing of a poly(A) RNA library obtained from a BM-MSCs sample. Among the top 35 selected Mlincs, with around 3 million total reads, 4 transcripts are covered with the ONT sequencing.

These intergenic lncRNAs are named as Stringtie output (SetName. TranscriptNumber. VariantNumber): Mlinc.28428.2, MlincV4.128022.2, MlincV4.89912.1 and MlincV4.64225.1. To support the above transcriptional units, we compared them with our short read data and searched for epigenetic status at the locus of the Mlincs in bone-marrow stromal mesenchymal cells. We looked at DNase sensitive site, H3K27 acetylation, H3K4 trimethylation that commonly corresponds to active regulatory regions (Figure 3B). We globally observed a DNA accessibility enrichment and acetylation of Histone 3 at the promotor region of our candidates, correlating with DNAse sensitivity hotspots in BM mesenchymal cells that reinforce the prediction of the expression windows. In particular, for Mlinc.28428.2, the transcript observed with long reads sequencing corresponded to the prediction made with short reads. It was also supported by Mlinc.28428.1, a variant that differ by the absence of the second exon. Similar characteristics were observed for Mlinc.128022, which also produced two variants with a different organisation of 5 exons. The two other candidates, Mlinc.89912.1 and Mlinc.64225.1 are mono-exonic. Mlinc.89912.1 occurs at the close proximity of FGF5 3' end, in reverse orientation at this locus. For this reason, the different epigenomic features could not be attributed with certainty to the Mlinc. For Mlinc.64225.1, the sequence is longer than the *ab initio* short read prediction. KRTAP1-5, HOTAIR and SMILR, selected for their good expression profile, were also covered by long reads (Data not shown).

2.18 High-throughput investigation of a marker's specificity by specific k-mers search

A marker can only be considered specific within the limits of the diversity of samples used for its study. Considering the growing number of cell/tissues and transcriptional profiles, it is essential to probe the limits of a chosen biomarker against these various cell types. Most of published analyses highlighting new potential biomarkers of MSCs or fibroblasts have been restricted to a comparison between only few cell types and, as discussed, commonly described markers are not strictly distinctive. In order to assess the expression of Mlincs candidates in a large number of samples, we extracted specific 31nt k-mers from each of their sequences, as previously described [49]. These simplified but candidate-specific (oligonucleotide-like) probes allow a simple and fast presence/absence search to be made on large-scale cohorts and a direct quantification in raw fastq data. The k-mers were quantified in ENCODE human RNAseq database, including "primary cells" and "*in vitro* differentiated cell" categories (Table S2). Particularly, as the bibliography suggests that MSCs can also express phenotypic characteristics of endothelial, neural, smooth

muscle cells, skeletal myoblasts and cardiac myocytes, RNAseq samples from this mesodermal origin were tested.

With ISCT positive markers, we observed an expected expression profile that recapitulate previous biological studies, particularly the high expression of Endoglin (ENG, CD105) in endothelial cells (Figure S4) and the overexpression of NT5E (CD73) in epithelial and endothelial cells (Figure S5). Interestingly, their expression varied among MSCs cell sources : NT5E (CD73) was strongly enriched in adipose and BM derived MSCs, and THY1 (CD90) in umbilical cord derived MSCs (UC-MSCs) (Figure S6). We next analysed the expression profile using our candidate annotated genes Mlinc specific k-mers (Figure 4). The specific k-mers search supported the stated expression profile of Mlincs previously shown : our Mlinc candidates were positive in MSCs and displayed weak or absent expression in cells of ectodermal lineage, hematopoietic or endothelial origins.

However the high throughput and naive quantification in the ENCODE cohort made it possible to extend the observation of this absence of expression into cell types not previously studied. Moreover, this diversity showed that the expression of most of the candidates, contrarily to positive markers of the ISCT, were exclusive of cells with mesodermal origin. All candidates were expressed in at least one type of fibroblasts and differentially present in other mesodermal cell types. For the 4 selected Mlincs, they shared: (i) a systematic and strong expression in cell types like skin fibroblasts, and cells derived from reservoir of mesenchymal progenitors (muscle satellite cells or dermis papilla cells), (ii) a regular over-expression in regular cardiac myocytes, (iii) a significant and irregular expression in smooth muscle cells. The ENCODE cohort containing MSCs of different origins, we can therefore observe that the Mlincs show differences of expression depending of the tissular origin, these candidates being mainly expressed in two MSCs types. The results permitted the classification of our Mlincs according to observed specificity, from the most promising to the least restricted profile : Mlinc.28428.2 is expressed in Ad and BM derived MSCs. It is the candidate with the clearest absence of expression in non-mesodermal cells, and with the poorest relative expression in Smooth Muscle Cells (SMC). Mlinc.128022.2 is expressed in Adipose and Bone Marrow MSCs, and particularly in preadipocytes and muscle cells : (myoblasts, myocytes and myotubes). Mlinc.89912.1 is principally expressed BM-MSCs and less in UC-MSCs and AD-MSCs, but shows expression in epithelial and endothelial cell. Finally, Mlinc.64225.1 differs from other Mlincs as it is also strongly expressed in keratinocytes, HSC, and epithelial cells (Figure S7). Its expression in critical non-MSC types has led us to retain the three other Mlincs for further investigations.

2.19 RT-qPCR mimics the *in silico* prediction and deciphers multiple transcript variants

To confirm the specificity of selected Mlincs' expression experimentally, we performed RT-qPCR on a set of 80 RNA preparations from different primary cell (Figure 4C). These includes MSCs from Bone Marrow (BM), Adipose (Ad) and Umbillical Cord (UC), fibroblasts of different tissue origins, IPS cells, neural stem cells, myoblasts, HUVECs and hepatocytes (Table S6). RT-qPCR and amplicon sequencing using sets of specific primers (Table S7) confirmed different predicted forms of the Mlincs candidates in BM-MSCs (Figure S8). We designed two primer pairs for both Mlinc.128022 variants to validate the existence of first splice, and two pairs for Mlinc.28428 variants, one overlapping the second exon and another corresponding to a splice between first and third exon. All variations captured by the primer designs were quantified, suggesting that all these different variations predicted *in silico* exist biologically in MSCs. We confirmed most of the

expression profiles obtained by k-mers quantification using RT-qPCR, notably the specificity of expression dependency on the MSCs tissular origin: over expression of Mlinc.28428 and 128022 in BM- and Ad-MSCs. Nevertheless, few exceptions, such as Mlinc.89912.1, present an enrichment in UC-MSCs not found in k-mers quantification. Moreover, the restricted expression to cells of mesodermal origin is replicated in our RT-qPCR results. We obtained similar observations with annotated candidates : overexpression of KRTAP1-5 and SMILR in BM-MSCs specifically, and of HOTAIR in UC- and BM-MSCs.

2.20 *In silico* prediction of lncRNAs interactions and functions

The relative specificity of selected Mlincs for mesenchymal cells could be an indication of their roles in MSCs function. The prediction of their possible function could therefore suggest their suitability as markers of MSCs' function potential. To this end, we explored assumptions on the function of Mlinc.28428.2, Mlinc.128022.2 and Mlinc.89912.1 candidates using different published methods. We first used bioinformatic tools based on machine learning and deep learning to decipher general characteristics of our candidates : FEELnc to assess coding potential, tarpMir to decipher "miRNA sponge" function, and LncADeep to analyse potential interactions with proteins.Only two of the 35 selected Mlincs and none of the 3 selected Mlincs with validated specificity were revealed as potentially coding RNAs with the majority being predicted as non-coding by FEELnc (33/35). None candidate had more than five target sites for a given miRNA, indicating a low probability of a "miRNA sponge" activity (Table S7). For the 3 retained Mlincs, predicted interacting proteins by LncADeep were submitted to Reactome (Table S8).

We noted a predicted interaction between Mlinc.28428.2 and Betacatenin (CTNNB1) as part of apoptosis-linked modules, 5'-3' Exoribonuclease 1, component of the CCR4-NOT complex, mRNA Decapping Enzyme 1B as part of the mRNA decapping and decay pathways. The interaction was also predicted with different mediators of RNA polymerase II transcription subunits (MED), ATP Binding Cassette Subfamily B Members as part of the PPARA activity linked to ER-stress [50], and Proteasome subunits for intracellular transport, response to hypoxia and cell cycle modules. Mlinc.128022 could interact with important genes like THY1 (CD90), NRF1 (mitochondria metabolism) with no module clearly highlighted. Mlinc.89912 could interact with tubulins, UBB (ubiquitin B), SMG6 nonsense mediated mRNA decay factor and ribosomes subunits (RPSX) proteins, (RPL24) for nonsense Mediated Decay (NMD), PINK1 (mitophagy) and finally MGMT, as part of the MGMT mediated DNA damage reversal module.

We further quantified expresssion of candidates by counting their specific k-mers in the entire FANTOM6 set of 154 Known-Downed (KD) annotated lncRNAs in human dermal fibroblasts (https://doi.org/10.1101/700864, not peer-reviewed). We selected the KD experiments where expression of the Mlincs was statistically differential when compared with controls. Particular attention was paid to KD lncRNAs with reported function(s) in bibliography, and to KD lncRNAs overlapping a gene with reported functions. Mlinc.28428.2 is down-regulated when JPX, SERTAD4-AS1, BOLA3-AS1, and SNRPD3 are KD, and over-expressed with the KD of PTCHD3P1, ERVK3.1, MEG3, among other lncRNAs without reported function (Figure 5A). Interestingly, interactions between p53 pathway and JPX [51], SNRPD3 [52] and MEG3 [53, 54]) respectively, have been previously reported. All these features converge on the hypothesis of a link between the function of Mlinc.28428, stress response, senescence and cellular maintenance. The implications of BOLA3 [55, 56]) and PTCHD3P1 [57] in mitochondria homeostasis and glycolysis, the role of BOLA3 in stress response [58], the status of SERTAD4 as target of the YAP/TAZ pathway [59], vital pathway of stress response [60], and the role of MEG3 in aging [61], all reinforce

this hypothesis.

Mlinc.128022.2 is down-regulated with the KD of FOXN3-AS1, A1BG-AS1, CD27-AS1, and FLVCR1-AS1 (Figure 5B). FOXN3 seems to be more than a regulator of cell cycle, it is also described as a regulator of osteogenesis in different cases of defective craniofacial development [62, 63]. Moreover, the reported over-expression of FOXN3 during the early stages of MSCs osteodifferentiation [64], and downregulation of CD27-AS1 in MSCs of donors with bone fracture [65], allow us to hypothesise a possible function of Mlinc.128022 in bone remodelling and osteogenesis. In addition, both A1BG-AS1 and FLVCR1-AS have an influence in osteogenesis and cell differentiation. A recent study showed that A1BG-AS1 interacts with miR-216a and SMAD7 in suppressing hepatocellular carcinoma proliferation [66], both partners having an important role in the positive regulation of osteoblastic differentiation in mice [67] [68]. FLVR1 participates to resistance of oxydative stress by heme exportation in mouse MSCs [69], iron metabolism being closely linked with bone homeostasis, formation [70] and cell differentiation [71].

Finally, Mlinc.89912.1 is down-regulated after the KD of NEAT1-1 and PCAT6, and over-expressed when MFI2.AS1, CDKN2B.AS1 (or ANRIL) and MKLN1.AS2 are KD (Figure 5C). The manifest relations between cell proliferation and CDKN2B-AS1 [72, 73], MFI2 [74], MFI.AS1 [75], PCAT6 [76] and NEAT1 [77, 78], an combination with the between ones and DNA damage repair response, [79, 80] reinforces the prediction of a role of Mlinc.89912 in these mechanisms. Moreover, we explored RNAseq from chromatin, nucleus and cytoplasm subcellular compartments of fibroblastic cells in the FANTOM6 Dataset. Mlinc.28428 and Mlinc.128022 are enriched in at least cytoplasm, whereas Mlinc.89912 is enriched in free nucleus fraction suggesting interaction with nuclear component (Figure 5C).

2.21 The single cell RNAseq: an emergent level of completion in marker search

We analysed the single cell RNAseq data from 26 071 adipose MSCs (Ad-MSCs) to assess the heterogeneity of the 3 Mlincs and to explore their expression at the single-cell level. No clear correlation between cell cycle and expression of our Mlincs was identified (Figure S9). We observed a high variability of the number of cells expressing the markers (Threshold ≥ 0.1). 11 927/26 071 were Mlinc.28428-positives, 4944 were Mlinc.128022-positives, and 404 were Mlinc.89912-positives. For each Mlinc, we performed a differential test to decipher genes differentially expressed in Ad-MSCs Mlinc-positive and Mlinc-negative cells.

We found that Mlinc.28428-positive cells under-expressed H19 and PI16 (Figure 5A). These genes, that present a diversity of functions, are involved in stress mechanisms (oxydative response and shear stress), inflammation in fibroblasts and MSCs, and senescence pathways [81, 82, 83, 84]. Despite the low number of differentially expressed genes in Mlinc.28428-positive cells, their functional behaviour and their known targets suggest a pathway linked to stress response and senescence establishment that reinforce our previous assumptions on Mlinc.28428 function.

Mlinc.128022-positive cells are enriched in FTH1, TPM2, FTL and CD24 and present a lower expression in HMGN2, HMGB1, ODC1, PTTG1, BIRC5, EIF5A, MKI67, UBE2S, FGF5, HAS2-AS1 (Figure 5B). A significant portion of these genes are linked to osteogenic properties of MSCs as previously observed with FANTOM analysis. The Mlinc.128022-positive cells have an increased expression of ferritin (light and heavy chains), major actor in iron metabolism in osteoblastic cell line [85], that is also involved in osteogenic differentiation [86] and osteogenic calcification [87]. Two genes, enriched in Mlinc.128022-positive cells are positively linked to the osteogenic

differentiation potential of MSCs : the tropomyosin 2 (TPM2), downregulated when hMSCs were cultured in OS medium for the induction of osteoblasts at the calcification phase [88], and CD24 a membrane antigen recently proposed as a new marker for the sub-fraction of notochordal cells with increased differentiation capabilities [89]. In addition ODC1, under-represented in Mlinc.128022-positive cells, inhibited the MSCs osteogenic differentiation [90, 91]. Finally, the decrease of FGF5, MKI67, BIRC5 (Survivin) and PTTG1 (securin) expressions, all linked to proliferation active phases of cell cycle, tend to show cell with arrested cell cycle. These data suggest that the expression profile of Mlinc.128022 positive cells indicate a subpopulation of undifferentiated osteogenic progenitors, probably in senescence or quiescence.

Mlinc.89912-positive cells are enriched in FGF5 and HIST1H4C (Figure 5C). FGF5 is a protein with mitogenic properties, identified as an oncogene, that facilitates cell proliferation in both autocrine [92] and paracrine manner [93]. HIST1H4C, the Histone Core number 4, is a cell cycle-related gene. Modification of histone H4 (post-transcriptional or mutation) has been highlighted as important for Non-Homologous End-Joining (NHEJ) in yeast [94]. Its mutation cause genomic instability, resulting in increased apoptosis and cell cycle progression anomalies in zebrafish development. It reinforces our assumptions that Mlinc.89912 has a role in cell proliferation and DNA damage repair. In conclusion, the single cell RNAseq analysis enabled the observation of different features that characterise the phenotype of Mlincs positive cells and reinforced hypotheses on their functions previously observed through k-mers quantification.

2.22 K-mers analysis of markers in functional cell situation

Previously, we have presented a number of strategies to formulate hypotheses on the functions of an unannotated lncRNAs, suggesting directions of future experimental investigations. To evaluate the relevance of these strategies, we sought to quantifiy with specific k-mers search the expression of our Mlincs in MSCs in different conditions, linked to above mentioned findings: stress and senescence for Mlinc.28428.2, osteodifferentiation for Mlinc.128022.2 and cell cycle/proliferation for Mlinc.89912. We downloaded RNAseq data corresponding to the above-mentioned focus, described in Table S4.

As shown in Figure 6, we observed a statistically relevant increase of Mlinc.28428 expression in MSCs under replicative stress and in MSCs with CrisprCas9 depletion of genes with important role against senescence. In the Wang et al. study [95], MSCs senescence was observed with the KO of ATF6 and the stress induced with tunicamycin (endoplasmic reticulum stress) and late passage (replicative stress). Mlinc.28428 expression increased with tunicamycin treatment, late passage and ATF6 KO. The highest increase is observed in ATF6 KO MSCs associated with late passage condition.

In Fu et al. study [96], YAP, but not TAZ, was found to safeguard MSCs from cellular senescence as shown by KO experiments. Interestingly, YAP KO, but not TAZ, significantly increases the expression of Mlinc.28428.2. This would lead us to conclude that Mlinc.28428 is overexpressed in senescence and stress conditions, suggesting a role in one or both of these phenomena.

The change in Mlinc.128022 expression is strictly linked to osteodifferentiation conditions. Mlinc.128022 expression shows a relevant increase in MSCs exposed to fungal metabolite Cytochalasin D (CytoD). The cytoD is reported as a osteogenic stimulant in the concerned study [97]. Moreover, no expression variation was observed between MSCs and MSC-derived adipocytes from Wang et al. study, implying a role in adipodifferentiation. Agrawal Singh et al. have studied osteogenic MSCs differentiation [29], with a similar increase of Mlinc.128022 being observed after ten days.

We then quantified the expression of Mlinc.89912 in a study that compare proliferating MSCs versus confluent MSCs [98, 99]. Our candidate was clearly over-expressed in proliferating cells, validating its capacity to mark the MSCs in proliferation. Moreover, its expression was not statistically modified when MSCs were exposed to EGF with pro-mitotic capabilities [100]. However Mlinc.89912 expression was reduced when IWR-1, an inhibitor of Beta-catenin nuclear translocation, that reduced the proliferation of MSCs, was added to the medium. The functional domains of these genes is summarised in table 1 and confirm the potential functional role suggested from FANTOM data: stress-related pathways for Mlinc.28428, MSCs differentiation with a presumed orientation in osteo-progenitors for Mlinc.128022 and a more restricted role in proliferation and DNA repair for Mlinc.89912.

3 Discussion

With recent evolution of omics analysis, the landscape of biomarkers has been extended beyond known genes to the exploration of the unexplored transcriptome. This potential has been assessed in pathological conditions but to a lesser extent in cell-specific conditions, where this new pool of potential markers could be used to identify less well-characterised cells and hence predict their function. In this article, we propose an integrated procedure and strategies to identify the best markers (annotated or not) in a cell-specific condition, and predict their potential functions, primarily from RNA sequencing data (Figure 1). RNAseq facilitates the creation of large lncRNA catalogues [8, 101] through the total catalogue of lncRNAs remains incomplete given the diversity of biological entities and lncRNAs specific expression in non-pathological, cell-specific conditions. The creation of a "home-made" catalogue associated with a specific condition remains the best way to assess the full diversity of potential biomarkers in a cell, rather than resorting to a global catalogue made from diverse samples. To give an idea of the completeness of such a focused lncRNA catalogue when compared to a global one, Jiang et al. recently published "an expanded landscape of human long non-coding RNA" with 25 000 new lncRNAs from normal and tumor tissues, whereas in our focused analysis only 50% of our 35 selected MSClinc can be found in this collection [101].

Futhermore, providing new candidates of good quality to improve lncRNA collection remains a complex task. As could be expected, the raw catalogue in our study contains predictions of disparate quality observed with a large number of mono-exonic transcripts. Without any filter, *ab initio* methods are insufficient to adequately reconstruct full length transcripts. The usage of long-read sequencing has been particularly effective in helping to validate our predictions. Given the benefits of full-length RNA sequence, long-read RNAseq should become the standard for lncRNA validation. A specific lncRNA can be the one presenting the most relevant properties after *in silico* analysis. The first task remain the identification of the more specific markers for a given cell type, task that present differences from classic comparative analysis. The MSCs markers proposed in the past were determined through a simple comparison between MSCs of a certain origin with negative cell whose types are either unique or few in number.

Historically, MSCs have been compared to bone marrow haematopoietic stem cells. However, our initial RNAseq analysis revealed that all potential MSCs markers proposed in the past are expressed in at least one other non-mesenchymatous cells type, and so do not constitute exclusive MSCs markers at the transcriptome level. Even if all cell types cannot be investigated, the diversity of the negative cell set is a critical criterion in selecting the most specific transcripts. In keeping with this idea, we then restricted the list of potential biomarkers with an enrichment step based

Table 1: Summary of functional investigation results

Mlinc	Predicted RNA-Protein interactions (lncADeep)	subcompartment enrichment	FANTOM6 expr. changes	Diff. genes in positive cells	K-mers investigations
Mlinc.28428	apoptosis, mRNA decay, PPARA activity, intracellular transport, response to hypoxia and cell cycle	Chromatin, cytoplasm	BOLA3-AS1, JPX, SERTAD4-AS1, PTCHD3P1, ERVK3.1, SNRPD3, MEG3	H19 - PI16 -	Stress, senescence
Mlinc.128022	THY1, NRF1	Chromatin, cytoplasm	FOXN3-AS1, A1BG-AS1, CD27-AS1, FLVCR1-AS1	FTH1, TPM2, FTL, CD24, HMGN2, HMGB1, ODC1, PTTG1, BIRC5, EIF5A, MKI67, UBE2S, FGF5, HAS2-AS1	Osteodiff., stress
Mlinc.89912	MGMT-mediated DNA damage reversal, Nonsense Mediated Decay, Tubulin metabolism	nucleus (free), cytoplasm	NEAT1_1, PCAT6, MFI2.AS1, MKLN1.AS2, CDKN2B.AS1	FGF5 and HIST1H4C	Proliferation

on a differential expression comparing BM-MSCs to other cells including mainly stem cells, as well as differentiated cells of various lineages (lymphocytes, macrophages, primary chondrocytes, hepatocytes and neurons). In the enriched list, the overexpressed annotated genes contained members of MSC-related pathways as well as the ISCT markers. This result supported the MSCs characterisation made by the original authors [13], thus validating the identity of MSCs used for this RNAseq analysis with the currently defined criteria. The problem with classical differential

analysis used on diverse "non-MSC" group is that all the "non-MSC" group is considered to be homogeneous. As a result, candidates with positive expression in small cell groups could pass statistical test, creating false positives. For this kind of differential analysis, we propose to select the most discriminating transcripts by feature selection, a machine learning methodology, that reduces the number of non-discriminating candidates after selection. We used feature selection through Boruta, a method based on random forest, to retain the top 35 of the most relevant MSCs signature for annotated genes, Mlincs and Mloancs separately. Putting aside our initial focus on unannotated lncRNAs, different annotated lncRNAs or coding genes with interesting profiles were also selected by feature selection : among them, KRTAP1-5 have been exclusively studied in BM-MSCs [102], where its preferential expression was validated by our results. These discoveries can bring new features concerning these genes and suggest directions for future investigations concerning their impact on the MSCs.

However, a marker is classically considered as specific on condition that its positive expression cannot be observed in any other cell type. Therefore, the expression of these potential markers should be explored in an entire RNAseq database to further validate its specificity. The exploration of a wide set of RNAseq data as proposed by ENCODE including a diversified set of primary and stem cells could support or invalidate the specificity of potential markers. In order to assess the expression of Mlincs candidates in a large number of samples, we used a signature for each candidate, extracting specific 31nt k-mers from their sequences. The specific k-mers extraction was made using Kmerator software. These k-mers were then quantified in the ENCODE human RNAseq databaseThe new and simplified procedure based on k-mers counting and large scale RNAseq exploration has the following advantages: i) a direct textual search that requires less time and CPU resources than classical methods, ii) a restricted set of lncRNAs supported by different results in the biological (wet) and *in silico* level (RNAseq data). The counterpart of the extensive vision of marker expression is that we observe a limit of specificity among our best candidates. We observed expression in fibroblasts, in close primary cells of common embryonic origin like smooth muscle cells (SMC) and other tissue-specific fibroblastic cells. Other tissue resident fibroblastic cells like skeletal muscle satellite cells, pre-adipocytes, and fibroblasts from different sources, especially dermis, express our selected MSClincs markers. The question of the differences between MSCs and related cell types is crucial to the issue. Specifically, the differences between MSCs and fibroblasts remain a subject of debate [103, 12]. According to the ISCT statement, no phenotypical differences have been reported between fibroblasts of different sources and adult MSCs [104], suggesting a hypothesis of a uniform cell type that show functional variation depending on the tissue source. Our results support this idea: distinguishing MSCs from fibroblast with only few positive markers remains a complicated task.

Moreover we observe low to medium expression of our candidates in close cell type from the same embryonic origin such as muscular cells and smooth muscle cells (SMC). This could be due to a shared phenotype between cells with close embryonic origin. Common markers between MSCs and SMCs have already been described. Notably, MSCs can express similar levels of SMC markers such as alpha-actin [105, 106]. Moreover Kumar et al. [107] determined that MSCs, pericytes, and SMCs could have the same mesenchymo-angioblast progenitor and that SMCs share a certain plasticity with MSCs as they can be differentiated in chondrocyte-like and beige adipocytes or myo-fibroblasts. However, a lot of cell types in ENCODE have not been actively sorted by expression of their respective surface markers, and fibroblast contamination is a classical feature in primary cell culture. We should not therefore exclude the possibility of fibroblast contamination when investigating marker for MSCs by bulk omics technology. Given this, single-cell RNAseq could be the best solution to identify the source of marker expression in counterpart cells.

To conclude, our extensive cell type comparison shows that the discovery of a marker of MSCs as distinct cell type is not plausible. After deepening our own research on MSCs biomarkers at the annotated and unannotated level, we were unable to find a marker that could simultaneously i) distinguish MSCs to close or homologuous cell types (fibroblasts, satellite cells, SMCs) ii) be present in all MSCs types iii) distinguish MSCs from more characterised cell types (Hematopoietic lineage, neurones etc). Our results suggest, like other studies, a strong proximity between MSCs, fibroblast and mesodermal cell types.

More than a marker of MSCs, candidates extracted by our method could be used to explore important features in MSCs biology and therefore warrant investigation into their function, assuming that the specificity of RNA for a cell type can highlight its importance in cell activity. Even if the functional invalidation stands as the principal method to efficiently determine the function of a lncRNA, its expression and co-expression with known genes can potentially characterise a function or an intrinsic state of a cell type, particularly for MSCs with reported diversity of states and function (ex : differentiation, immunomodulation, senescence, proliferation...). In our opinion, it is vital that during the creation of a catalogue of lncRNAs, a restricted set of selected biomarkers should be studied more intensively, both in term of specificity and functions. Assumptions on functional domains, where lncRNAs could act, could increase the relevance and visibility of discovered lncRNAs, and far from the bioinformatics implications, encourage future biological investigations. We decided to investigate the three selected MSClincs, validated by k-mers search, RT-qPCR and long-read sequencing, in term of biological impact with complementary *in silico* experimental approaches. We propose to use different *in silico* strategies, depending on the amount and diversity of the available data. The analysis confirms the non-coding potential of candidates and indicates a low probability of "miRNA sponge" activity. However, protein potential interaction results give interesting paths that were then investigated by complementary exploration. The k-mers quantification permits a naive high throughput exploration of numerous RNAseq data, simultaneously exploring potential functions and specificity to assess their potential. Instead of different cells, each candidate's expression was quantified in MSCs in different experimental conditions. FANTOM6 data recently offered a pilot about lncRNAs functional investigation, with a high-throughput invalidation of 154 lncRNAs and coding genes in fibroblasts and their RNAseq counterpart added to phenotypical observations. The utilisation of co-expressions between knock-out genes and candidates lncRNAs remains an efficient way to decipher lncRNAs function, provided number of KD genes is high. Moreover, the availability of recent single cell data of MSCs have been a good complement to lncRNAs functional investigation.

Using scRNAseq from Ad-MSCs [19], we observed that our markers are not expressed in all cells but constitute different subpopulations with different levels of rarity in Ad-MSCs. FANTOM6 and single-cell analysis could permit tracing three components of these states : stress inducible cells, lineage commited osteogenic progenitors and proliferating cells. Globally, we observed a global concordance of the results between the different strategies used for functional prediction. Mlinc.28428 has concomitant expression with genes related to the stress response pathway. Mlinc.28428 could be a good target for treatment to study the senescence process, age pathologies or stress response. Mlinc.128022 potentially interacts with THY1 (CD90) and has co-occurences with genes linked to osteoprogenitors and cell differentiation. The k-mers search highlights its participation in MSCs' osteo-differentiation. Finally, Mlinc.89912 potentially interacts with damage repair and RNA decay, and tubulin metabolism, all linked to cell proliferation and cell cycle. Moreover, the subcompartment enrichment corresponds to this prediction: Mlinc.89912.1 is the only candidate to have possible interactions with DNA-repair system, a hypothesis corresponding to his observed enrichment in the nucleus. A final selection of bulk RNAseq of MSCs in specific biological con-

ditions allowed confirmation of our initial assumptions, showing that the different strategies we propose could be used to give relevant indication of the lncRNAs' functions. These results show that a lncRNA selected by its expression specificity has a high probability of being part of a functional mechanism.

In conclusion, we have predicted genes and lncRNAs enriched in MSCs and proposed several selection steps including feature selection (machine learning), large scale signature search, RT-qPCR validation, *in silico* tools and single cell analysis. We present the application of a new way of quantification in RNAseq : The specific k-mers search could be used as a naive information in lncRNA catalogue creation. The strategies presented here are transferable to other cell types and different studies while the specificity and functional assumption present a significant potential in long non-coding transcriptome exploration. We present three lncRNAs markers of bone marrow and adipose MSCs that passed all selection steps and present interesting features: Mlinc.28428.2, Mlinc.128022.2 and Mlinc.89912.1. These markers could be used by the scientific community as potential targets for functional biological experiments on MSCs, with pre-indications of potential functions to orientate the experiments, and finally initiate the objective of transition between informatical problematics and cell biology.

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4.0.1 Conflict of interest statement.

The authors declare that they have no competing interests.

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5 Figure Legends

5.1 Figure 1: Flowchart representation of the Pipeline used for this in the study.

The 4 steps of the flowchart are described A) Ab initio reconstruction of transcrit expressed in MSC from SRA dataset and creation of a reference (gtf+fasta) for quantification of Ensembl annotated genes, unannotated intergenic (Mlincs) and unannotated overlapping antisens (Mloanc). The results are shown in Fig2.
B) Differential Analysis for the selection of MSC markers (restrained candidate set) with i/ kallisto pseudoalignement and Sleuth differential test followed by feature selection by random forest with Boruta package. Long read sequencing and active transcription in MSC by epigenetic marks information completed the selection step (see figures 2 and 3).
C) Validation of cell expression specificity of candidates by kmer quantification in ENCODE RNAseq datasets (see table S2 for list of data) and qPCR validation. The results are presented in figure 4.
D) Functional investigations were performed with in silico prediction methods from the sequence of candidates, followed by k-mer quantification with FANTOM6 data set, single cell RNAseq and selected MSC conditions. Kmer quantification phases are shown by corresponding icons (figures 5 and 6).

5.2 Figure 2: Overview of annotated genes and unannotated transcripts enriched in BM-MSC.

A) Left pannels represented: i/EnsemblV90 transcript categories and distribution, ii/ transcripts distribution expressed in MSCs, showing unnatotated transcripts obtained with Ab initio reconstruction by StringTie vs annotated transcripts (expression $>$ 0.1 TPM) iii/ Predicted long non-coding RNA(lncRNA) from unnanotated reconstructed transcripts include new long non coding RNA with intergenic (Mlinc) and antisens (Mlncoa) RNA categories.
B-C-D) Distribution of transcript length, exon length and GC percentage across different categories respectively with the same colors as in A pannel : coding transcripts (blue), annotated lincRNA (pink), annotated overlapping antisens lncRNA (purple), novel lincRNA (Mlincs, yellow), novel overlapping antisens RNA (Mloanc, red).
E) Representation of annotated genes (top pannel) and unannotated transcripts (bottom pannel) overexpresed in MSC versus non-MSC types (log2FC $>$0.5 and padj $<$ 0.05), separately showed in MA plot.
F) Total number of transcripts transcript by category. The colored bar indicated the number of differential expression of annotated genes (Ensemblv90) and unannotated transcripts (Mlinc and Mloanc).
G) Global expression in BM-MSC (with Sleuth normalization) of the same categories as in F for annotated genes and unannotated transcripts.

5.3 Figure 3: Selection of a refined set of best candidates by random forest (top35), long read sequencing and epigenetic features.

A) Expression of the best MSC-specific candidates selected by boruta machine learning along MSC group and not MSC cohorts. Left pannel : top35 most relevant annotated genes (non-coding included); Right pannel: unannotated intergenic lncRNAs (Mlincs) and their average importance scores determined by Boruta method displayed in upside line plot.
B) Genomic visualisation of Mlincs predictions 28428, 128022, 89912, and 64225 (MSClinc orange) from short reads alignement of all MSC group files (blue/magenta and bam visualisation), compared with long read alignements (long reads grey). Additional epigenomic features are shown to reveal active transcriptional activity from trimethylation of Histone H3 (H3K4me3), acetylation of Histone H3 H3K27 in MSCs (H3K4me3 and H3K27ac, green), and Dnase sensibitity hotspots of MSC (MSC DNAse, red).

5.4 Figure 4: High throughput exploration of selected candidate across strong variety of samples by k-mer quantification in RNAseq and biological validation by RT-qPCR.

A : List of tissues for the cell specific expression exploration (samples with ID numbers are listed in table S1)
B: Relative expression of Mlinc.28428.2, Mlinc.128022.2, and Mlinc.89912.1 across ENCODEs ribodepleted RNAseq datas, made by k-mer quantification, normalized by k-mer by million.
C: qPCR relative quantification was performed on the selected 3 Mlincs in MSC of different origins (BM-MSC, Ad-MSC, Umbilical cord msc) and other indicated cell types. Relative quantification (Log induction) was quantified by ddCt method using non MSC types types as calibrator (mean of triplicates). Student tests have been made between triplicates, each test use BM-MSCs as reference group (ns : $P > 0.05$, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$, ****: $P \leq 0.0001$).

5.5 Figure 5: Prediction of potential functions of candidates with k-mer quantification and single-cell.

For each Mlinc (Mlinc.28428 (A), Mlinc.128022 (B) and Mlinc.89912 (C) respectively) 3 steps of prediction were performed. a. Enrichment in the different subcompartments of fibroblasts from FANTOM6 dataset: Free nuclear fraction (Nuc), chromatin (Chr) and cytoplasm (Cyt); b. Expression of marker in FANTOM6 data depending of the KnockDown (KD) of an annotated lncRNA. Normalised count of all specific k-mers is averaged by sample (zeros vlues deleted) and t-tests are made between control and KD fibroblasts. c. General expression of Mlincs inside Ad-MSC population, dimensionnal reduction made with UMAP method, made from batch corrected counts. Expression of differentially expressed annotated genes between positive and negative cells for Mlinc.28428, Mlinc.128022 and Mlinc.89912 respectively.

5.6 Figure 6:Expression of markers in different datasets from SRA in cell conditions related to previous findings

A) Expression of Mlinc.28428.1 in the context of oxydative, replicative, or KO-driven, stress and senescence (PRJNA396193, PRJNA433339). Relevant changes of expressions are showed with t-test results (ns : $P > 0.05$, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$, ****: $P \leq 0.0001$).
B) Expression of Mlinc.128022 in osteodifferentiation conditions (PRJNA515466) or osteodifferentiation potential (PRJNA379707). Relevant changes of expressions are showed with t-test results (ns : $P > 0.05$, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$, ****: $P \leq 0.0001$).
C)Expression of Mlinc.89912 in the context of proliferation (PRJNA328824 and PRJNA498109). Relevant changes of expressions are showed with t-test results (ns : $P > 0.05$, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$, ****: $P \leq 0.0001$). The detailed list of datasets is provided in table S4.

Figure 1

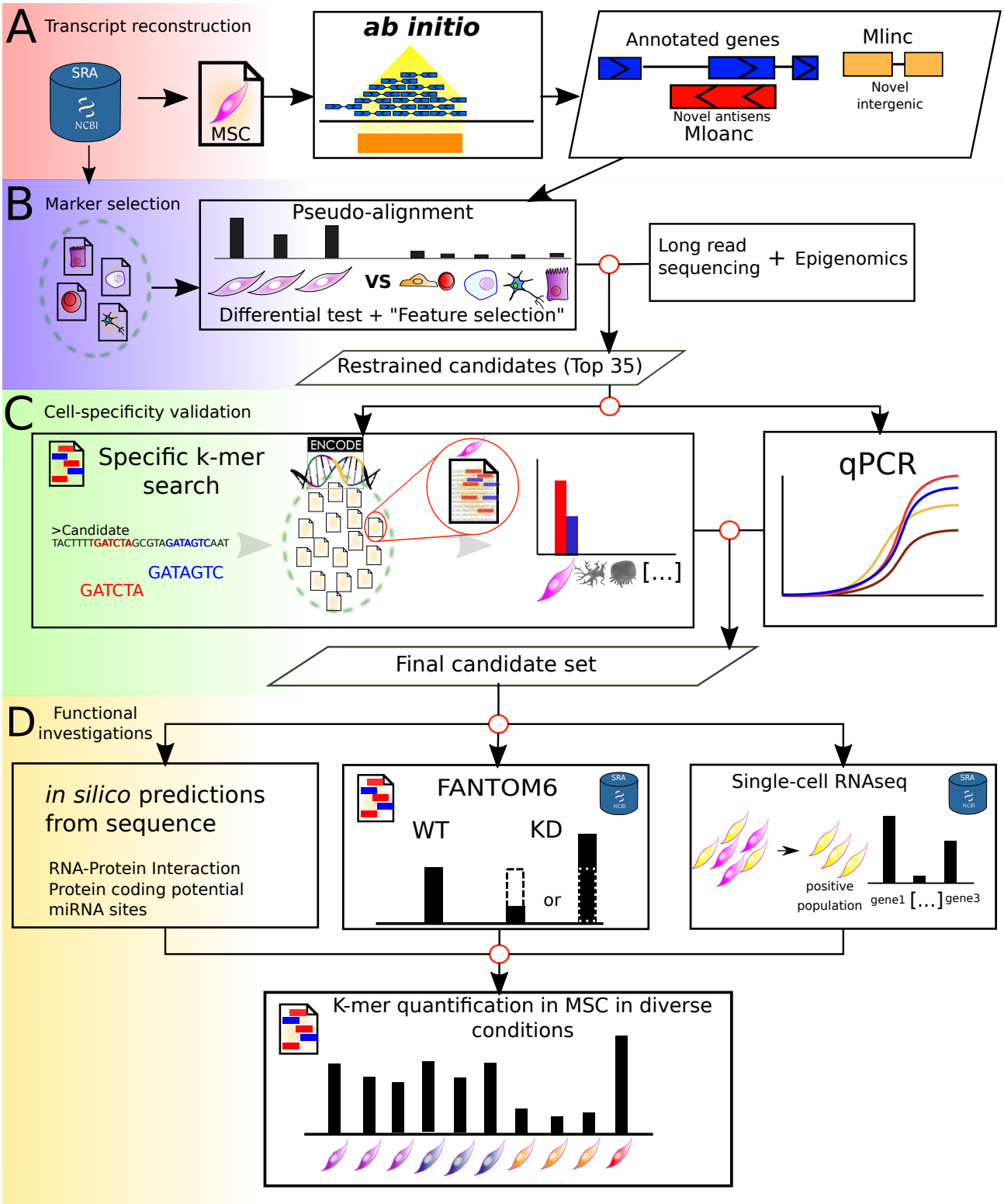


Figure 2

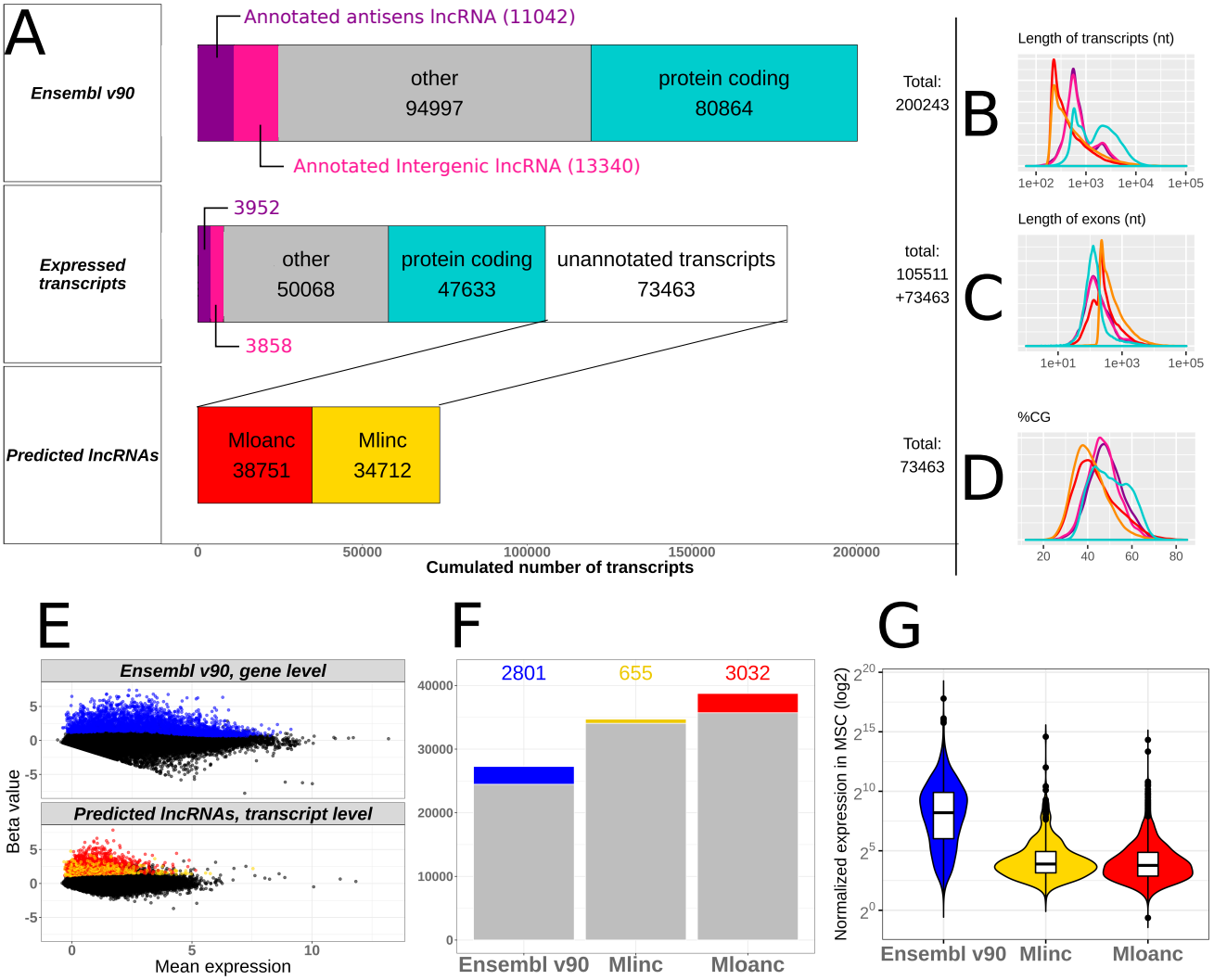


Figure 3

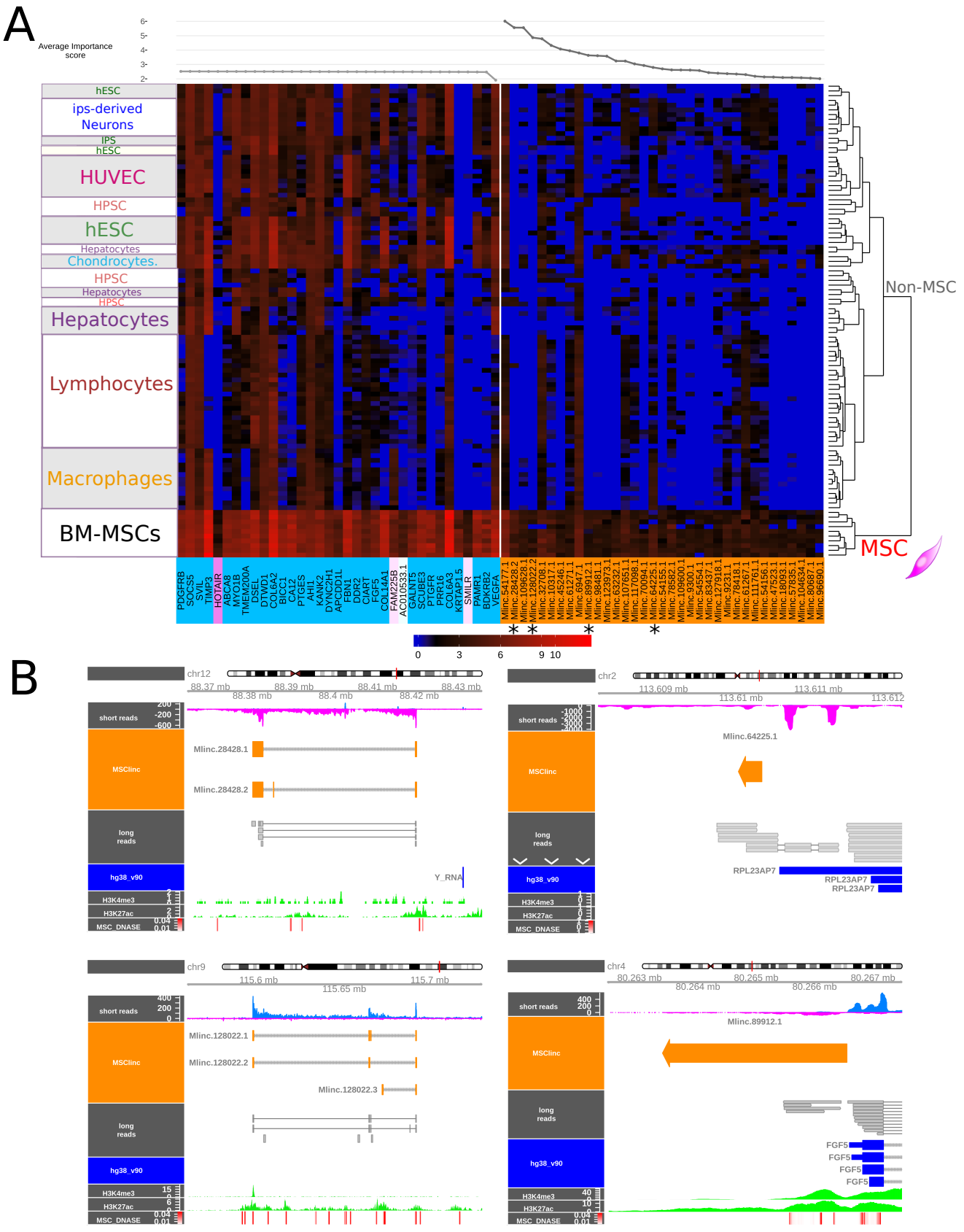
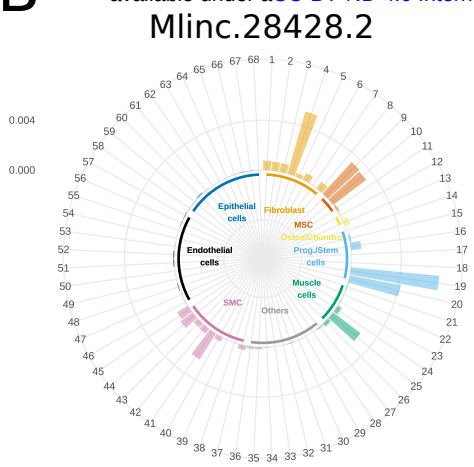


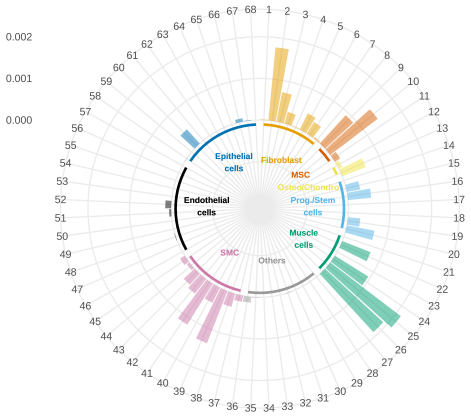
Figure 4

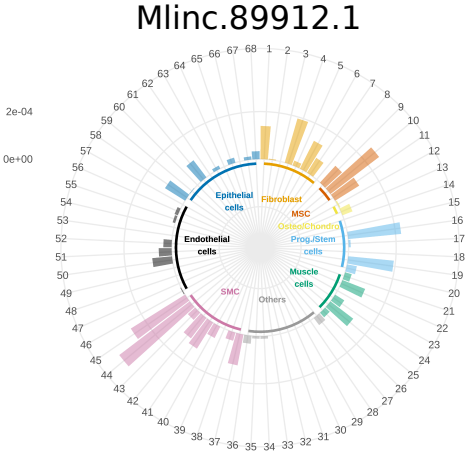
A

id	variable	n
1	bronchus fibroblast of lung	2
2	cardiac atrium fibroblast	2
3	cardiac ventricle fibroblast	2
4	fibroblast of dermis	2
5	fibroblast of lung	2
6	fibroblast of the aortic adventitia	2
7	fibroblast of villous mesenchyme	2
8	pericardium fibroblast	2
9	MSC of adipose	2
10	MSC of the bone marrow	2
11	MSC of Wharton's jelly	2
12	articular chondrocyte	2
13	osteoblast	2
14	H1-hESC	5
15	H7-hESC	2
16	hair follicle dermal papilla cell	2
17	hematopoietic multipotent progenitor cell	1
18	neural progenitor cell	2
19	skeletal muscle satellite cell	2
20	subcutaneous preadipocyte	2
21	cardiac muscle cell	2
22	myocyte	2
23	myometrial cell	2
24	myotube	2
25	regular cardiac myocyte	2
26	skeletal muscle myoblast	2
27	astrocyte	2
28	bipolar neuron	2
29	dendritic cell	20
30	foreskin keratinocyte	6
31	hair follicular keratinocyte	2
32	hepatocyte	2
33	melanocyte of skin	4
34	mesangial cell	2
35	mononuclear cell	1
36	placental pericyte	2
37	aortic SMC	2
38	bronchial smooth muscle cell	2
39	smooth muscle cell	2
40	smooth muscle cell of bladder	2
41	smooth muscle cell of the coronary artery	2
42	smooth muscle cell of the pulmonary artery	2
43	smooth muscle cell of the umbilical artery	2
44	smooth muscle cell of trachea	2
45	uterine smooth muscle cell	2
46	bladder microvascular endothelial cell	2
47	dermis blood vessel endothelial cell	2
48	dermis lymphatic vessel endothelial cell	2
49	dermis microvascular lymphatic vessel endothelial cell	2
50	endometrial microvascular endothelial cells	2
51	endothelial cell of coronary artery	2
52	glomerular endothelial cell	2
53	lung microvascular endothelial cell	2
54	mammary microvascular endothelial cell	2
55	pulmonary artery endothelial cell	2
56	thoracic aorta endothelial cell	2
57	vein endothelial cell	2
58	airway epithelial cell	2
59	bronchial epithelial cell	2
60	epithelial cell of alveolus of lung	2
61	epithelial cell of proximal tubule	2
62	epithelial cell of umbilical artery	2
63	kidney epithelial cell	2
64	mammary epithelial cell	1
65	epithelial cell of viscerocranial mucosa	2
66	placental epithelial cell	2
67	renal cortical epithelial cell	2
68	tracheal epithelial cell	2

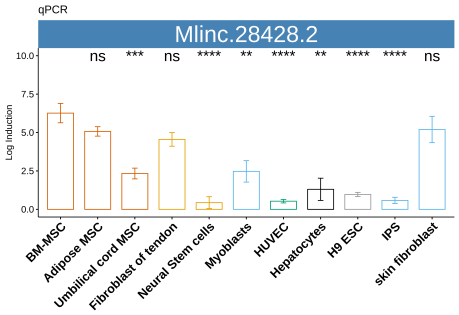
B

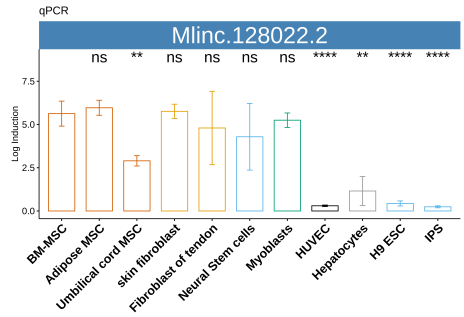






C





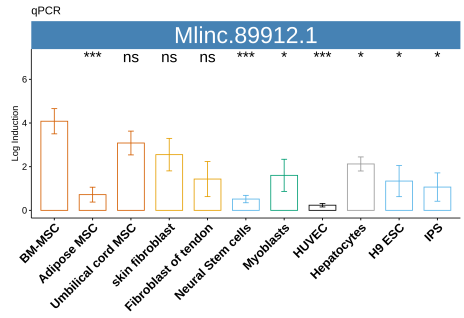
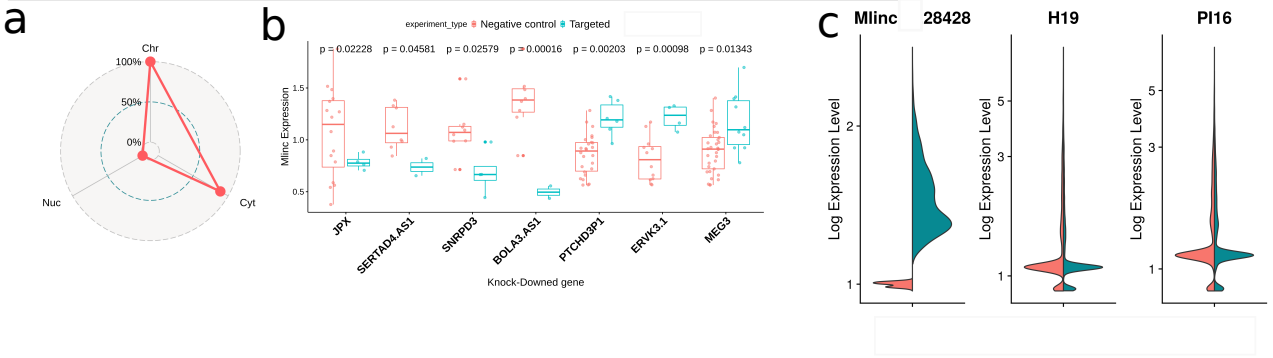
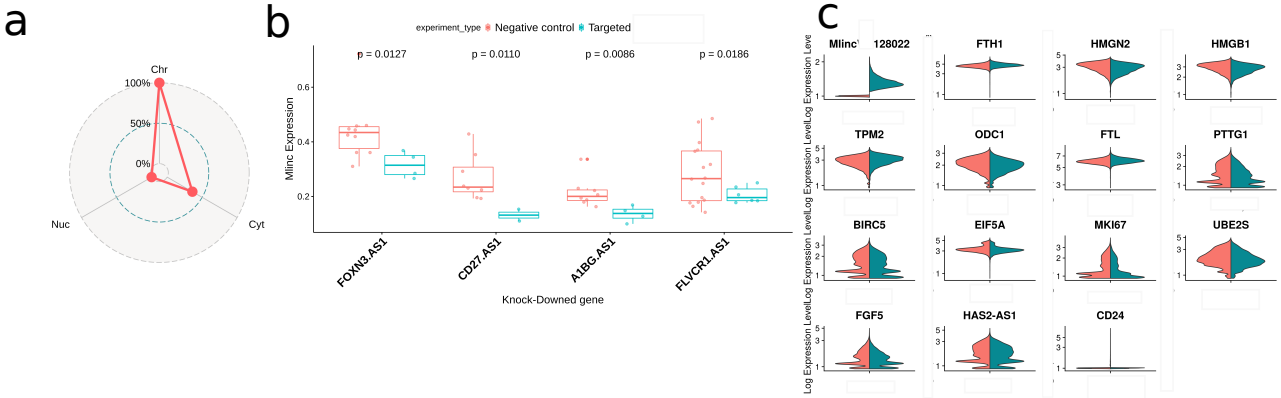


Figure 5

A: Mlinc.28428



B: Mlinc.128022



C : Mlinc.89912

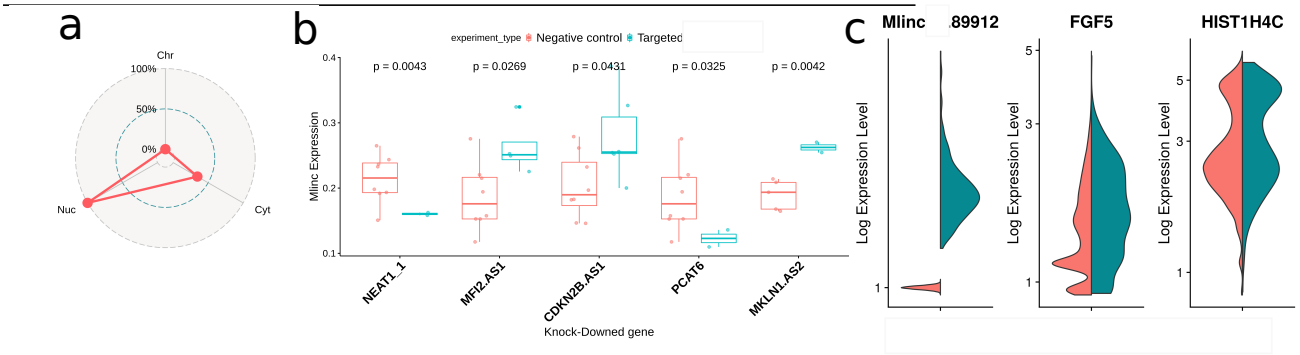
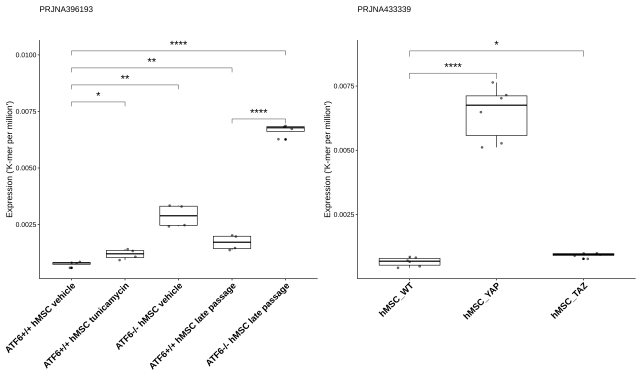
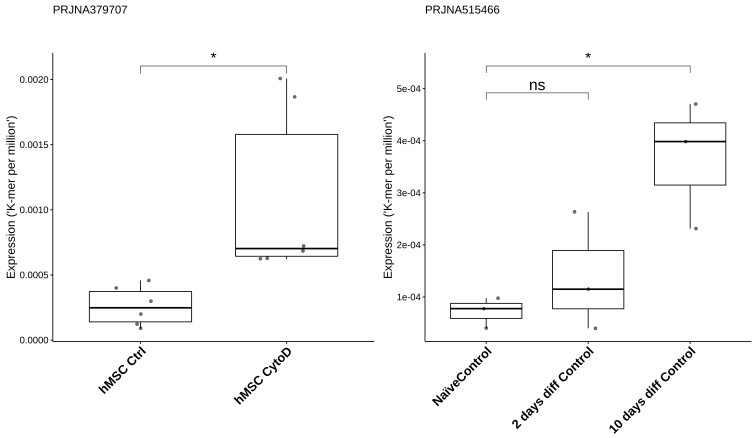


Figure 6

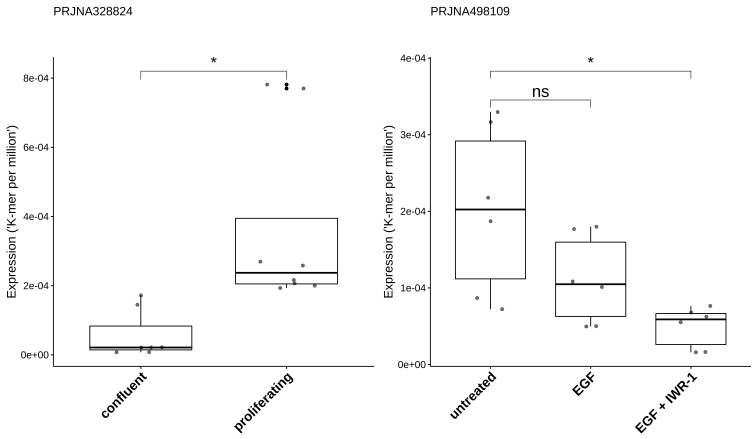
A: Mlinc.28428



B: Mlinc.128022



C : Mlinc.89912



Supplementary figures

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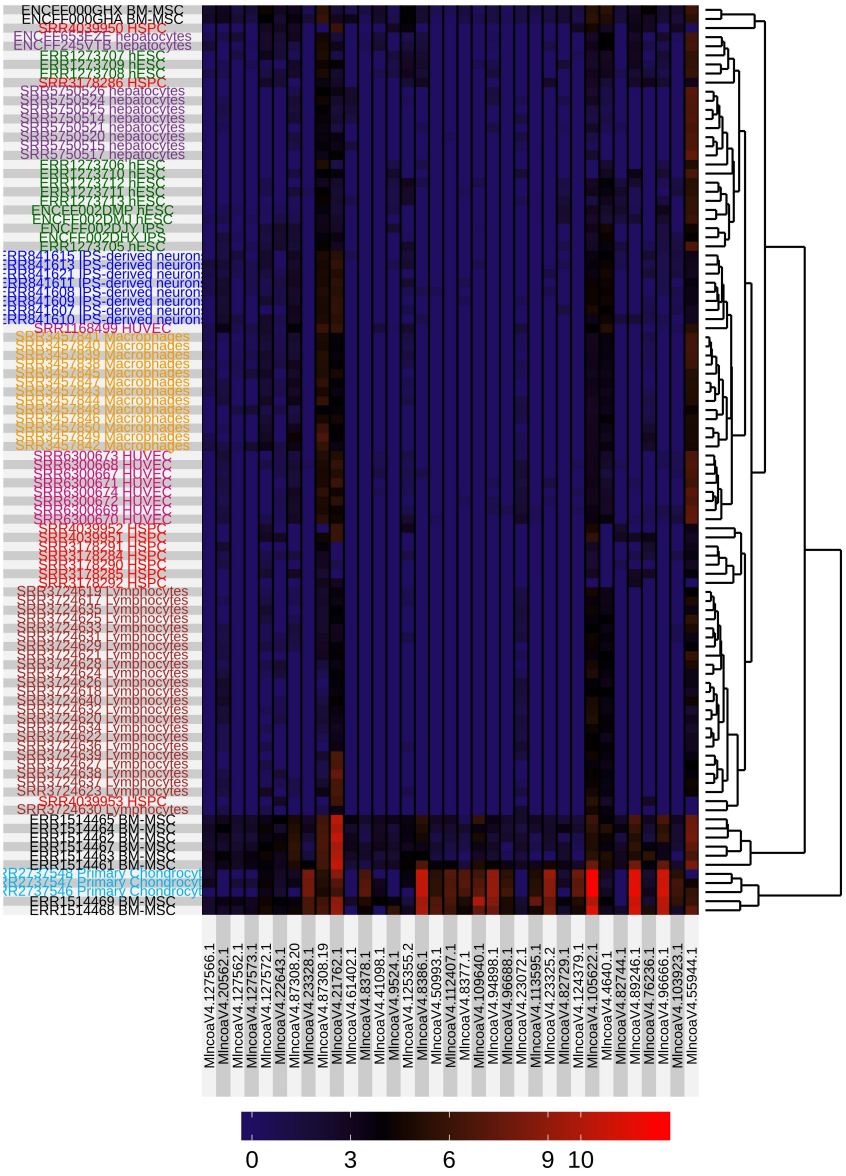
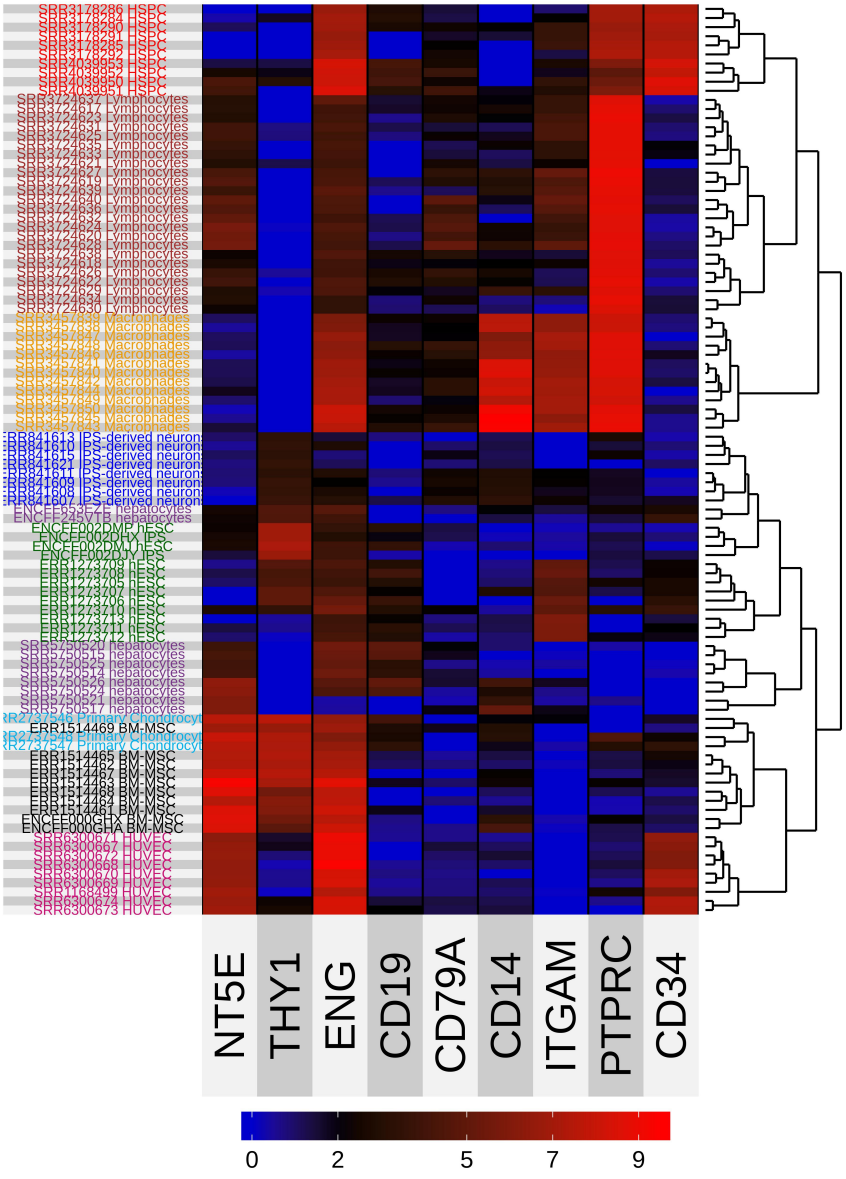
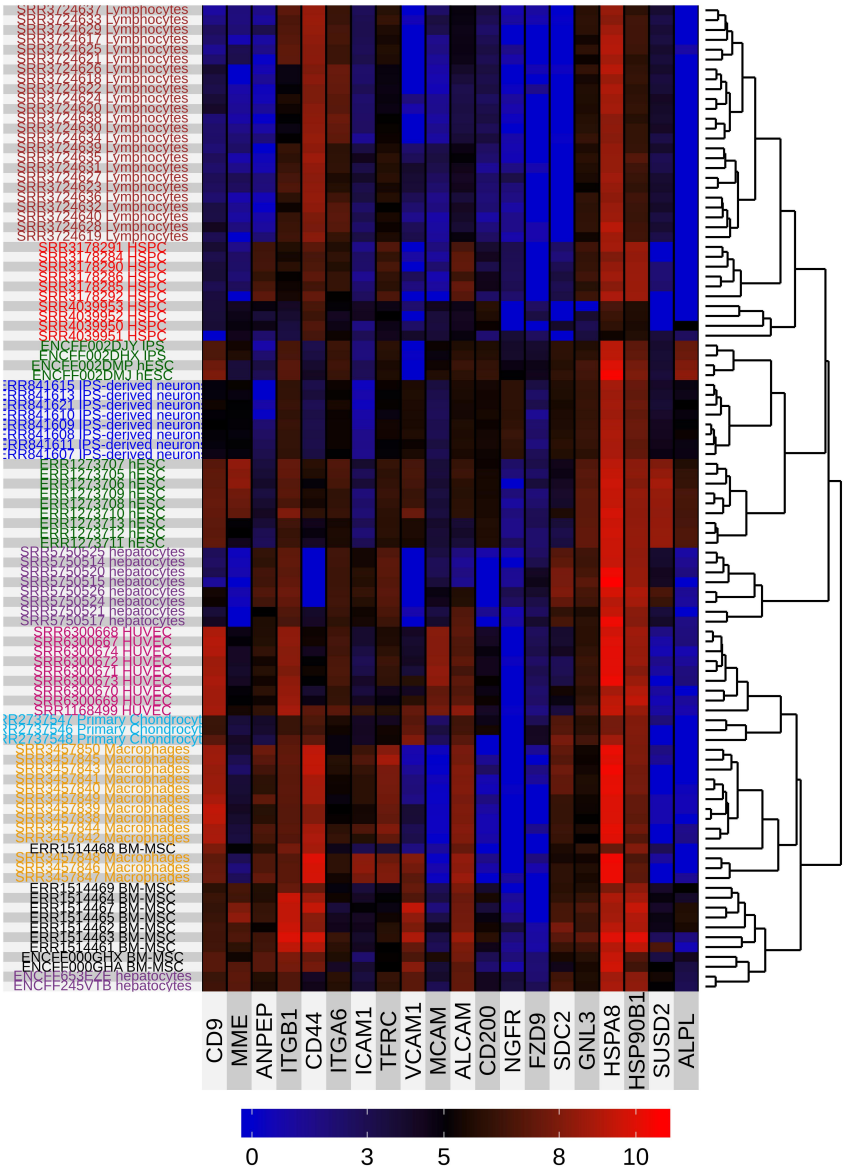
January 2020



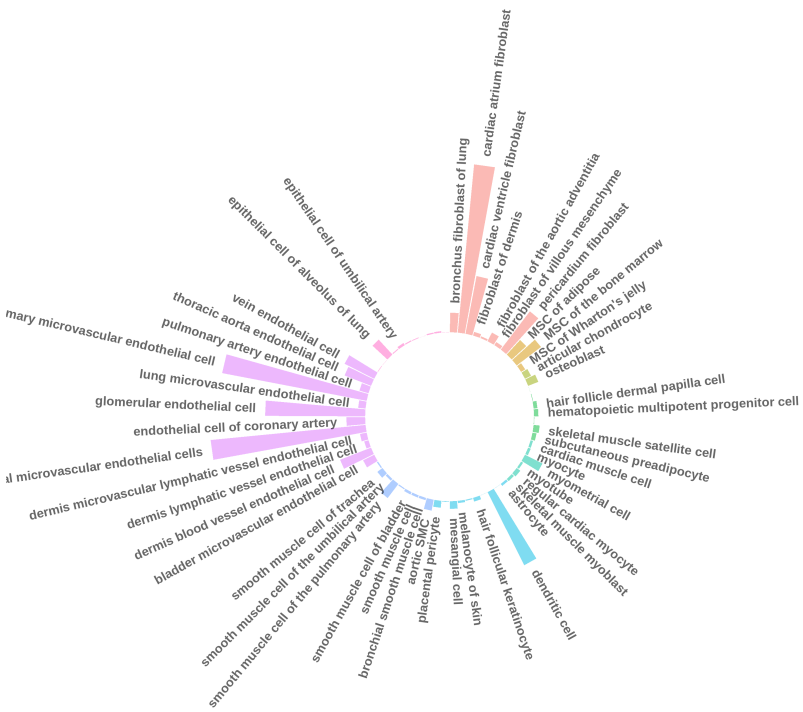
Supplementary Figure 1: Expression of Mloanc (Antisens unannotated RNA) selected after feature selection in the differential analysis cohort



Supplementary Figure 2: Expression of ISCT's MSC markers in the differential analysis cohort THY1 = CD90, NT5E = CD73, ENG = CD105, ITGAM = CD11B, PTPRC = CD45

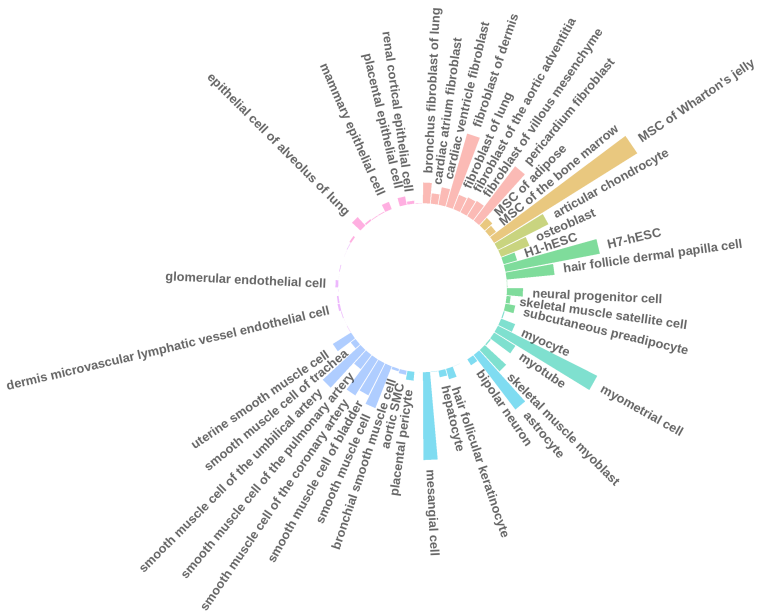


Supplementary Figure 3: Heatmap present positive markers for MSC proposed in the bibliography



Supplementary Figure 4: Relative expression of 3 positive markers of ENG (CD105) across ENCODE's ribodepleted RNAseq datas, made by K-mer quantification, normalized in kmer by million

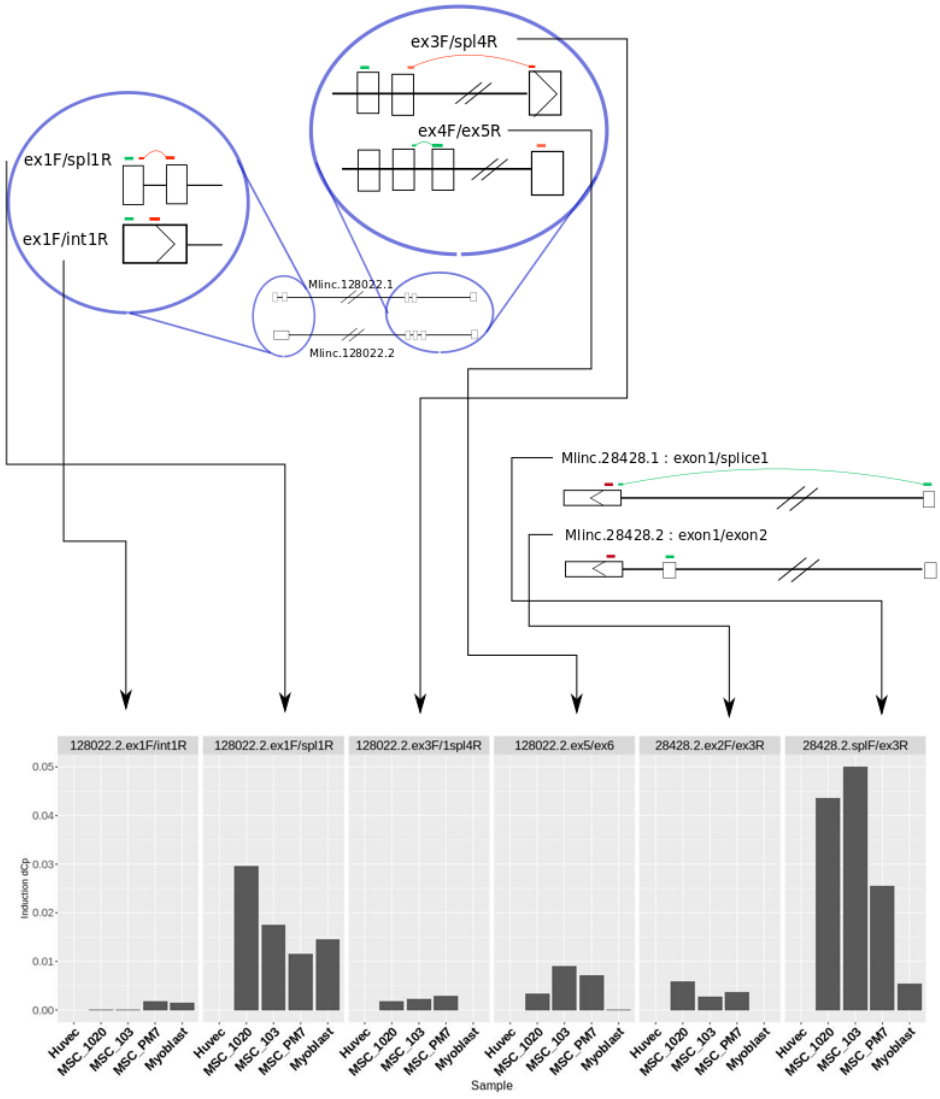
Supplementary Figure 5: Relative expression of 3 positive markers of NT5E (CD73) across ENCODE's ribodepleted RNAseq datas, made by K-mer quantification, normalized in kmer by million



Supplementary Figure 6: Relative expression of 3 positive markers of THY1 (CD90) across ENCODE ribodepleted RNAseq datas, made by K-mer quantification, normalized in kmer by million

MlincV4.64225.1

Supplementary Figure 7: Relative expression of 3 positive markers of Mlinc.64225.1 across ENCODE's ribodepleted RNAseq datas, made by K-mer quantification, normalized in kmer by million



Supplementary Figure 8: Primer position on selected Mlinc candidates and corresponding expression in MSCs, HUVECs and Myoblasts

Supplementary Figure 9: cell cycle and single cell.

Table_S1 Metadata for differential analysis

sample ID	Group	Type	SRX ID	external ID	sra sample title	specie	project title	project ID	nb total reads	length reads	detail	
ENCFF000GHA	MSC	BM-MSC			total RNA-seqof mesenchymal stem cell of the bone marrow	Homo sapiens	ENCODE					
ENCFF000GHX	MSC	BM-MSC			total RNA-seqof mesenchymal stem cell of the bone marrow	Homo sapiens	ENCODE					
ENCFF002DHX	Not	IPS			total RNA-seqof GM23338	Homo sapiens	ENCODE					
ENCFF002DJY	Not	IPS			total RNA-seqof GM23338	Homo sapiens	ENCODE					
ENCFF002DMJ	Not	hESC			total RNA-seqof H7	Homo sapiens	ENCODE					
ENCFF002DMP	Not	hESC			total RNA-seqof H7	Homo sapiens	ENCODE					
ERR1273705	Not	hESC	ERX1345312		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	67286349	125		
ERR1273706	Not	hESC	ERX1345313		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	18924239	125		
ERR1273707	Not	hESC	ERX1345314		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	55745935	125		
ERR1273708	Not	hESC	ERX1345315		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	28988509	125		
ERR1273709	Not	hESC	ERX1345316		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	NA	NA		
ERR1273710	Not	hESC	ERX1345317		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	NA	NA		
ERR1273711	Not	hESC	ERX1345318		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	NA	NA		
ERR1273712	Not	hESC	ERX1345319		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	NA	NA		
ERR1273713	Not	hESC	ERX1345320		Transcriptional profiling of human naive embryonic stem cells	Homo sapiens	Transcriptional profiling of human naive embryonic stem cells	PRJEB12748	NA	NA		
ERR1514461	MSC	BM-MSC	ERX1585480		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	32467641	96.41		
ERR1514462	MSC	BM-MSC	ERX1585481		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	34192962	96.30		
ERR1514463	MSC	BM-MSC	ERX1585482		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	28164147	95.51		
ERR1514464	MSC	BM-MSC	ERX1585483		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	28633110	96.97		
ERR1514465	MSC	BM-MSC	ERX1585484		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	25135660	96.96		
ERR1514467	MSC	BM-MSC	ERX1585486		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	28240410	96.79		
ERR1514468	MSC	BM-MSC	ERX1585487		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	29410953	96.97		
ERR1514469	MSC	BM-MSC	ERX1585488		RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	Homo sapiens	RNASeq of musculoskeletal ageing using human mesenchymal stem cells and their tissue constructs	PRJEB14688	28966083	97.22		
ERR841607	Not	IPS-derived neurons	ERX921697		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	14282989	101	KCl	
ERR841608	Not	IPS-derived neurons	ERX921709		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	22188866	101	KCl	
ERR841609	Not	IPS-derived neurons	ERX921694		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	22616373	101	KCl	
ERR841610	Not	IPS-derived neurons	ERX921708		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	13192833	101	NA	
ERR841611	Not	IPS-derived neurons	ERX921705		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	15290840	101	KCl	
ERR841613	Not	IPS-derived neurons	ERX921699		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	15686003	101	NA	
ERR841615	Not	IPS-derived neurons	ERX921702		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	14182869	101	NA	
ERR841621	Not	IPS-derived neurons	ERX921696		Illumina HiSeq 2500 paired end sequencing; RNA-seq of NEAT1 knockdown in neuronal excitability	Homo sapiens	RNA-seq of NEAT1 knockdown in neuronal excitability	PRJEB9006	15232542	101	NA	
SRR2737546	Not	Primary Chondrocytes	SRX1358410		GSM1914777: Control 1; Homo sapiens; RNA-Seq	Homo sapiens	Transcriptome response to 4h IL-1b stimulation of primary chondrocytes	PRJNA299568	34300359	97.39	No stimulation	
SRR2737547	Not	Primary Chondrocytes	SRX1358411		GSM1914778: Control 2; Homo sapiens; RNA-Seq	Homo sapiens	Transcriptome response to 4h IL-1b stimulation of primary chondrocytes	PRJNA299568	37284758	96.91	No stimulation	
SRR2737548	Not	Primary Chondrocytes	SRX1358412		GSM1914779: Control 3; Homo sapiens; RNA-Seq	Homo sapiens	Transcriptome response to 4h IL-1b stimulation of primary chondrocytes	PRJNA299568	33144961	96.89	No stimulation	
SRR4039950	Not	HSPC	SRX2031066		GSM2284651: HSPC day 0 rep1; Homo sapiens; RNA-Seq	Homo sapiens	Hematopoietic Stem/Progenitor Cell Expansion Without Differentiation is Achieved in Zwitterionic Hydrogels	PRJNA339416	17369972	50		
SRR4039951	Not	HSPC	SRX2031067		GSM2284652: HSPC day 0 rep2; Homo sapiens; RNA-Seq	Homo sapiens	Hematopoietic Stem/Progenitor Cell Expansion Without Differentiation is Achieved in Zwitterionic Hydrogels	PRJNA339416	18053125	50		
SRR4039952	Not	HSPC	SRX2031068		GSM2284653: HSPC day 24 rep1; Homo sapiens; RNA-Seq	Homo sapiens	Hematopoietic Stem/Progenitor Cell Expansion Without Differentiation is Achieved in Zwitterionic Hydrogels	PRJNA339416	20682268	50		
SRR4039953	Not	HSPC	SRX2031069		GSM2284654: HSPC day 24 rep2; Homo sapiens; RNA-Seq	Homo sapiens	Hematopoietic Stem/Progenitor Cell Expansion Without Differentiation is Achieved in Zwitterionic Hydrogels	PRJNA339416	19282208	50		
SRR3178284	Not	HSPC	SRX1592574		GSM2066393: huCB stem ctrl_rep1; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	25398470	100.79	huCB stem ctrl	
SRR3178285	Not	HSPC	SRX1592575		GSM2066394: huCB stem ctrl_rep2; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	5926147	100.77	huCB stem ctrl	
SRR3178286	Not	HSPC	SRX1592576		GSM2066395: huCB stem ctrl_rep3; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	7615479	100.78	huCB stem ctrl	
SRR3178290	Not	HSPC	SRX1592580		GSM2066399: huCB progenitors ctrl_rep1; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	36341406	100.77	huCB progenitors ctrl	
SRR3178291	Not	HSPC	SRX1592581		GSM2066400: huCB progenitors ctrl_rep2; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	6431588	100.78	huCB progenitors ctrl	
SRR3178292	Not	HSPC	SRX1592582		GSM2066401: huCB progenitors ctrl_rep3; Homo sapiens; RNA-Seq	Homo sapiens	miR-126 Orchestrates an Oncogenic Program in B-Cell Precursor Acute Lymphoblastic Leukemia	PRJNA312538	3602619	100.77	huCB progenitors ctrl	
ENCFF245VTB	Not	hepatocytes			total RNA-seqof hepatocyte	Homo sapiens	ENCODE					
ENCFF653EZE	Not	hepatocytes			total RNA-seqof hepatocyte	Homo sapiens	ENCODE					
SRR1168499	Not	HUVEC	SRX470246		GSM1327344: HUVEC; Homo sapiens; RNA-Seq	Homo sapiens	Transcriptomic analysis reveals novel long non-coding RNAs critical for vertebrate development [RNA-Seq]	PRJNA238180	97606136	90		
SRR3457838	Not	Macrophages	SRX1733620		GSM2135456: 140421_S2_CNT_A__; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	62681472	50	CNT	NA
SRR3457839	Not	Macrophages	SRX1733621		GSM2135457: 140421_S2_CNT_B__; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	66405838	50	CNT	NA
SRR3457840	Not	Macrophages	SRX1733622		GSM2135458: 140421_S2_IL10_A__; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	70016991	50	IL10	NA
SRR3457841	Not	Macrophages	SRX1733623		GSM2135459: 140421_S2_IL10_B__; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	80257003	50	IL10	NA
SRR3457842	Not	Macrophages	SRX1733624		GSM2135460: 140825_S3_CNT__; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	37671849	75	CNT	NA

Table_S1 Metadata for differential analysis

SRR3457843	Not	Macrophages	SRX1733625		GSM2135461: 140825_S3_IL10___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	40575802		75	IL10	NA
SRR3457844	Not	Macrophages	SRX1733626		GSM2135462: 140825_S1_CNT___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	28548046		75	CNT	NA
SRR3457845	Not	Macrophages	SRX1733627		GSM2135463: 140825_S1_IL10___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	44848576		75	IL10	NA
SRR3457846	Not	Macrophages	SRX1733628		GSM2135464: 140825_S1_IFNgTNFa___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	33920601		75	IFNgTNFa	NA
SRR3457847	Not	Macrophages	SRX1733629		GSM2135465: 140825_S2_IFNgTNFa___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	26580763		75	IFNgTNFa	NA
SRR3457848	Not	Macrophages	SRX1733630		GSM2135466: 140825_S3_IFNgTNFa___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	28565135		75	IFNgTNFa	NA
SRR3457849	Not	Macrophages	SRX1733631		GSM2135467: 140825_S2_CNT___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	41595399		75	CNT	NA
SRR3457850	Not	Macrophages	SRX1733632		GSM2135468: 140825_S2_IL10___; Homo sapiens; RNA-Seq	Homo sapiens	Single-cell qPCR, and bulk-level transcriptomics and epigenomics of treated macrophages	PRJNA315538	38443748		75	IL10	NA
SRR5750514	Not	hepatocytes	SRX2950738		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	62983452	99.38		Infected with Plasmodium berghei	NA
SRR5750515	Not	hepatocytes	SRX2950737		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	46318597	99.38		NA	NA
SRR5750517	Not	hepatocytes	SRX2950735		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	63391464	99.29		NA	NA
SRR5750520	Not	hepatocytes	SRX2950732		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	57010988	99.33		NA	NA
SRR5750521	Not	hepatocytes	SRX2950731		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	47651456	99.41		Infected with Plasmodium berghei	NA
SRR5750524	Not	hepatocytes	SRX2950728		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	47486674	99.53		NA	NA
SRR5750525	Not	hepatocytes	SRX2950727		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	52736152	99.44		Infected with Plasmodium berghei	NA
SRR5750526	Not	hepatocytes	SRX2950726		Dual RNAseq: Human hepatocytes and Plasmodium berghei	Homo sapiens	Dual RNAseq - Human hepatocytes infected with Plasmodium berghei	PRJNA390648	49216420	99.16		NA	NA
SRR6300667	Not	HUVEC	SRX3401581		GSM2859866: hyp_12h_n1_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	39712730		94	Hypoxia 0.2% O2, 5% CO2 humidified atmosphere	
SRR6300668	Not	HUVEC	SRX3401582		GSM2859867: hyp_12h_n2_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	43357452		94	Hypoxia 0.2% O2, 5% CO2 humidified atmosphere	
SRR6300669	Not	HUVEC	SRX3401583		GSM2859868: hyp_24h_n1_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	41045511		94	Hypoxia 0.2% O2, 5% CO2 humidified atmosphere	
SRR6300670	Not	HUVEC	SRX3401584		GSM2859869: hyp_24h_n2_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	44557122		94	Hypoxia 0.2% O2, 5% CO2 humidified atmosphere	
SRR6300671	Not	HUVEC	SRX3401585		GSM2859870: norm_12h_n1_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	42304183		94	Normoxia 20% O2, 5% CO2 humidified atmosphere	
SRR6300672	Not	HUVEC	SRX3401586		GSM2859871: norm_12h_n2_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	42748680		94	Normoxia 20% O2, 5% CO2 humidified atmosphere	
SRR6300673	Not	HUVEC	SRX3401587		GSM2859872: norm_24h_n1_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	42771271		94	Normoxia 20% O2, 5% CO2 humidified atmosphere	
SRR6300674	Not	HUVEC	SRX3401588		GSM2859873: norm_24h_n2_1; Homo sapiens; RNA-Seq	Homo sapiens	Total RNA deep sequencing (ribosomal depleted) of human umbilical vein endothelial cells exposed to hypoxia (0.2%) for 12h and 24h or kept under normoxic conditions.	PRJNA418883	42131852		94	Normoxia 20% O2, 5% CO2 humidified atmosphere	
SRR3724617	Not	Lymphocytes	SRX1881712		GSM2218995: Healthy1-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	29296358		100	healthy	
SRR3724618	Not	Lymphocytes	SRX1881713		GSM2218996: Healthy1-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	27598581		100	healthy	
SRR3724619	Not	Lymphocytes	SRX1881714		GSM2218997: Healthy1-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	26351498		100	healthy	
SRR3724620	Not	Lymphocytes	SRX1881715		GSM2218998: Healthy1-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	29464342		100	healthy	
SRR3724621	Not	Lymphocytes	SRX1881716		GSM2218999: Healthy2-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	48167581		100	healthy	
SRR3724622	Not	Lymphocytes	SRX1881717		GSM2219000: Healthy2-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	42220340		100	healthy	
SRR3724623	Not	Lymphocytes	SRX1881718		GSM2219001: Healthy2-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	38563382		100	healthy	
SRR3724624	Not	Lymphocytes	SRX1881719		GSM2219002: Healthy2-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	45267949		100	healthy	
SRR3724625	Not	Lymphocytes	SRX1881720		GSM2219003: Healthy3-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	45930063		100	healthy	
SRR3724626	Not	Lymphocytes	SRX1881721		GSM2219004: Healthy3-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	40731526		100	healthy	
SRR3724627	Not	Lymphocytes	SRX1881722		GSM2219005: Healthy3-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	47542258		100	healthy	
SRR3724628	Not	Lymphocytes	SRX1881723		GSM2219006: Healthy3-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	53718245		100	healthy	
SRR3724629	Not	Lymphocytes	SRX1881724		GSM2219007: PNH1-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	30025375		100	paroxysmal nocturnal hemoglobinuria (PNH)	
SRR3724630	Not	Lymphocytes	SRX1881725		GSM2219008: PNH1-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	29638535		100	paroxysmal nocturnal hemoglobinuria (PNH)	
SRR3724631	Not	Lymphocytes	SRX1881726		GSM2219009: PNH1-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	30553368		100	paroxysmal nocturnal hemoglobinuria (PNH)	
SRR3724632	Not	Lymphocytes	SRX1881727		GSM2219010: PNH1-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	34722293		100	paroxysmal nocturnal hemoglobinuria (PNH)	

Table_S1 Metadata for differential analysis

SRR3724633	Not	Lymphocytes	SRX1881728		GSM2219011: PNH2-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	32466930	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724634	Not	Lymphocytes	SRX1881729		GSM2219012: PNH2-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	29139809	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724635	Not	Lymphocytes	SRX1881730		GSM2219013: PNH2-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	28506728	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724636	Not	Lymphocytes	SRX1881731		GSM2219014: PNH2-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	30666327	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724637	Not	Lymphocytes	SRX1881732		GSM2219015: PNH3-CD4Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	49485440	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724638	Not	Lymphocytes	SRX1881733		GSM2219016: PNH3-CD4Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	43428307	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724639	Not	Lymphocytes	SRX1881734		GSM2219017: PNH3-CD8Memory; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	41998683	100	paroxysmal nocturnal hemoglobinuria (PNH)
SRR3724640	Not	Lymphocytes	SRX1881735		GSM2219018: PNH3-CD8Naive; Homo sapiens; RNA-Seq	Homo sapiens	T cells from paroxysmal nocturnal hemoglobinuria patients show an altered TNFR signaling pathway	PRJNA327044	52622177	100	paroxysmal nocturnal hemoglobinuria (PNH)

Table_S2 Metadata for ENCODE kmer research

Original.files	label	group	Accession	Assay.Nickname	Biosample.summary	Lab	Project	Species	Life.stage	Age	Age.Units	Treatment
ENCFF371KWE	dendritic cell	6: Others	ENCSR892ZUK	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 2 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF534HFO	dendritic cell	6: Others	ENCSR519NFO	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 1 hour	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF126HPJ	endometrial microvascular endothelial cells	8: Endothelial cells	ENCSR919MZM	total RNA-seq	endometrial microvascular endothelial cells female adult (34 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	34	year	
ENCFF502JCS	endometrial microvascular endothelial cells	8: Endothelial cells	ENCSR919MZM	total RNA-seq	endometrial microvascular endothelial cells female adult (34 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	34	year	
ENCFF001QZS	smooth muscle cell of bladder	7: SMC	ENCSR000AAC	total RNA-seq	smooth muscle cell of bladder female adult (53 years) and male adult (62 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53,62	year	
ENCFF001RAO	smooth muscle cell of bladder	7: SMC	ENCSR000AAC	total RNA-seq	smooth muscle cell of bladder female adult (53 years) and male adult (62 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53,62	year	
ENCFF001QZC	renal cortical epithelial cell	9: Epithelial cells	ENCSR000AAQ	total RNA-seq	renal cortical epithelial cell female adult (69 years) and male adult (84 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	69,84	year	
ENCFF001RAU	renal cortical epithelial cell	9: Epithelial cells	ENCSR000AAQ	total RNA-seq	renal cortical epithelial cell female adult (69 years) and male adult (84 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	69,84	year	
ENCFF001QZK	bladder microvascular endothelial cell	8: Endothelial cells	ENCSR000AAB	total RNA-seq	bladder microvascular endothelial cell male adult (46 years) and male adult (60 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	46,6	year	
ENCFF001RAI	bladder microvascular endothelial cell	8: Endothelial cells	ENCSR000AAB	total RNA-seq	bladder microvascular endothelial cell male adult (46 years) and male adult (60 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	46,6	year	
ENCFF001QZG	dermis blood vessel endothelial cell	8: Endothelial cells	ENCSR000AAI	total RNA-seq	dermis blood vessel endothelial cell female child (16 years) and male child (13 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	13,16	year	
ENCFF001RAQ	dermis blood vessel endothelial cell	8: Endothelial cells	ENCSR000AAI	total RNA-seq	dermis blood vessel endothelial cell female child (16 years) and male child (13 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	13,16	year	
ENCFF000ILE	skeletal muscle satellite cell	4: Progenitor or Stem cell	ENCSR000CUI	total RNA-seq	skeletal muscle satellite cell female adult (64 years) and male adult (21 year)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	21,64	year	
ENCFF000ILQ	skeletal muscle satellite cell	4: Progenitor or Stem cell	ENCSR000CUI	total RNA-seq	skeletal muscle satellite cell female adult (64 years) and male adult (21 year)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	21,64	year	
ENCFF000GFS	mononuclear cell	6: Others	ENCSR000CUT	total RNA-seq	mononuclear cell female adult (52 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	52	year	
ENCFF810KXA	dendritic cell	6: Others	ENCSR682CFV	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 2 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF928LQX	dendritic cell	6: Others	ENCSR652RSO	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 6 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF816SSU	dendritic cell	6: Others	ENCSR536GUD	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF720QTK	dendritic cell	6: Others	ENCSR870DRE	total RNA-seq	dendritic cell treated with 0 ng/mL Lipopolysaccharide for 0 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF816QOY	H1-hESC	4: Progenitor or Stem cell	ENCSR537BCG	total RNA-seq	H1-hESC	Joe Ecker, Salk	Roadmap	Homo sapiens	embryonic	unknown		
ENCFF476PHC	H1-hESC	4: Progenitor or Stem cell	ENCSR537BCG	total RNA-seq	H1-hESC	Joe Ecker, Salk	Roadmap	Homo sapiens	embryonic	unknown		
ENCFF821YWS	H1-hESC	4: Progenitor or Stem cell	ENCSR537BCG	total RNA-seq	H1-hESC	Joe Ecker, Salk	Roadmap	Homo sapiens	embryonic	unknown		
ENCFF712SHP	H1-hESC	4: Progenitor or Stem cell	ENCSR537BCG	total RNA-seq	H1-hESC	Joe Ecker, Salk	Roadmap	Homo sapiens	embryonic	unknown		
ENCFF793PLC	H1-hESC	4: Progenitor or Stem cell	ENCSR537BCG	total RNA-seq	H1-hESC	Joe Ecker, Salk	Roadmap	Homo sapiens	embryonic	unknown		
ENCFF000FKR	thoracic aorta endothelial cell	8: Endothelial cells	ENCSR000CUK	total RNA-seq	thoracic aorta endothelial cell female adult (22 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,22	year	
ENCFF000FLI	thoracic aorta endothelial cell	8: Endothelial cells	ENCSR000CUK	total RNA-seq	thoracic aorta endothelial cell female adult (22 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,22	year	
ENCFF000GBQ	hair follicle dermal papilla cell	4: Progenitor or Stem cell	ENCSR000CUB	total RNA-seq	hair follicle dermal papilla cell female adult (47 years) and female adult (70 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	70,47	year	
ENCFF000GBT	hair follicle dermal papilla cell	4: Progenitor or Stem cell	ENCSR000CUB	total RNA-seq	hair follicle dermal papilla cell female adult (47 years) and female adult (70 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	70,47	year	
ENCFF656QHH	myometrial cell	5: Muscle cells	ENCSR371VGV	total RNA-seq	myometrial cell female adult (34 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	34	year	
ENCFF212TDB	myometrial cell	5: Muscle cells	ENCSR371VGV	total RNA-seq	myometrial cell female adult (34 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	34	year	
ENCFF995TMT	dendritic cell	6: Others	ENCSR332SRS	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF605VBT	glomerular endothelial cell	8: Endothelial cells	ENCSR878EUT	total RNA-seq	glomerular endothelial cell female embryo (22 weeks) and male embryo (22 weeks)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	22	week	
ENCFF509JLH	glomerular endothelial cell	8: Endothelial cells	ENCSR878EUT	total RNA-seq	glomerular endothelial cell female embryo (22 weeks) and male embryo (22 weeks)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	22	week	
ENCFF000FLO	articular chondrocyte	character(0)	ENCSR000CUE	total RNA-seq	articular chondrocyte of knee joint female adult (56 years) and male adult (64 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	64,56	year	
ENCFF000FMM	articular chondrocyte	character(0)	ENCSR000CUE	total RNA-seq	articular chondrocyte of knee joint female adult (56 years) and male adult (64 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	64,56	year	
ENCFF875NIU	dendritic cell	6: Others	ENCSR178SNP	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 1 hour	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF000GXC	fibroblast of villous mesenchyme	1: Fibroblast	ENCSR000CUL	total RNA-seq	fibroblast of villous mesenchyme female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000GXV	fibroblast of villous mesenchyme	1: Fibroblast	ENCSR000CUL	total RNA-seq	fibroblast of villous mesenchyme female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF236EYN	hair follicular keratinocyte	6: Others	ENCSR680USE	total RNA-seq	hair follicular keratinocyte male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55	year	
ENCFF917MHA	hair follicular keratinocyte	6: Others	ENCSR680USE	total RNA-seq	hair follicular keratinocyte male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55	year	
ENCFF142YQX	mesangial cell	6: Others	ENCSR198TKA	total RNA-seq	mesangial cell NONE and female embryo (21 week)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown,embry	unknown,21	week	
ENCFF644UKX	mesangial cell	6: Others	ENCSR198TKA	total RNA-seq	mesangial cell NONE and female embryo (21 week)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown,embry	unknown,21	week	
ENCFF927MXX	myotube	5: Muscle cells	ENCSR828TEI	total RNA-seq	myotube originated from skeletal muscle myoblast	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF999QZD	myotube	5: Muscle cells	ENCSR828TEI	total RNA-seq	myotube originated from skeletal muscle myoblast	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF911ELB	foreskin keratinocyte	6: Others	ENCSR034RPU	total RNA-seq	foreskin keratinocyte male newborn (2-4 days)	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	
ENCFF578CTE	foreskin keratinocyte	6: Others	ENCSR034RPU	total RNA-seq	foreskin keratinocyte male newborn (2-4 days)	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	
ENCFF000GNB	vein endothelial cell	8: Endothelial cells	ENCSR000CUG	total RNA-seq	vein endothelial cell male adult (48 years) and male adult (52 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	52,48	year	

ENCFF000GNC	vein endothelial cell	8: Endothelial cells	ENCSR000CUG	total RNA-seq	vein endothelial cell male adult (48 years) and male adult (52 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	52,48	year	
ENCFF001QZM	smooth muscle cell of trachea	7: SMC	ENCSR000AAS	total RNA-seq	smooth muscle cell of trachea male adult (28 years) and male adult (56 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	56,28	year	
ENCFF001RDQ	smooth muscle cell of trachea	7: SMC	ENCSR000AAS	total RNA-seq	smooth muscle cell of trachea male adult (28 years) and male adult (56 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	56,28	year	
ENCFF001RCA	smooth muscle cell of the pulmonary artery	7: SMC	ENCSR000AAN	total RNA-seq	smooth muscle cell of the pulmonary artery male adult (26 years) and male adult (28 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	28,26	year	
ENCFF001RDO	smooth muscle cell of the pulmonary artery	7: SMC	ENCSR000AAN	total RNA-seq	smooth muscle cell of the pulmonary artery male adult (26 years) and male adult (28 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	28,26	year	
ENCFF000GKX	placental pericyte	6: Others	ENCSR000CTX	total RNA-seq	placental pericyte female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000GKZ	placental pericyte	6: Others	ENCSR000CTX	total RNA-seq	placental pericyte female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000HWI	fibroblast of dermis	1: Fibroblast	ENCSR000CUH	total RNA-seq	fibroblast of dermis female adult (44 years) and female adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,44	year	
ENCFF000HXB	fibroblast of dermis	1: Fibroblast	ENCSR000CUH	total RNA-seq	fibroblast of dermis female adult (44 years) and female adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,44	year	
ENCFF644CJJ	bipolar neuron	6: Others	ENCSR968WKR	total RNA-seq	bipolar neuron originated from GM23338 treated with 0.5 µg/mL doxycycline hyclate for 4 days	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53	year	doxycycline hyclate
ENCFF040TFC	bipolar neuron	6: Others	ENCSR968WKR	total RNA-seq	bipolar neuron originated from GM23338 treated with 0.5 µg/mL doxycycline hyclate for 4 days	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53	year	doxycycline hyclate
ENCFF000GFU	MSC of adipose	character(0)	ENCSR000CTZ	total RNA-seq	mesenchymal stem cell of adipose	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	42,37	year	
ENCFF000GGR	MSC of adipose	character(0)	ENCSR000CTZ	total RNA-seq	mesenchymal stem cell of adipose	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	42,37	year	
ENCFF001RBG	lung microvascular endothelial cell	8: Endothelial cells	ENCSR000AAP	total RNA-seq	lung microvascular endothelial cell female adult (55 years) and male adult (63 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	63,55	year	
ENCFF001RBW	lung microvascular endothelial cell	8: Endothelial cells	ENCSR000AAP	total RNA-seq	lung microvascular endothelial cell female adult (55 years) and male adult (63 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	63,55	year	
ENCFF840QXH	bronchus fibroblast of lung	1: Fibroblast	ENCSR620NSN	total RNA-seq	bronchus fibroblast of lung	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF480YLH	bronchus fibroblast of lung	1: Fibroblast	ENCSR620NSN	total RNA-seq	bronchus fibroblast of lung	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF001RAK	tracheal epithelial cell	9: Epithelial cells	ENCSR000AAR	total RNA-seq	tracheal epithelial cell male adult (21 year) and male adult (68 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	21,68	year	
ENCFF001RBS	tracheal epithelial cell	9: Epithelial cells	ENCSR000AAR	total RNA-seq	tracheal epithelial cell male adult (21 year) and male adult (68 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	21,68	year	
ENCFF001QZE	epithelial cell of viscerocranial mucosa	character(0)	ENCSR000AAL	total RNA-seq	nasal cavity respiratory epithelium epithelial cell of viscerocranial mucosa female adult (70 years) and male adult (46 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	46,7	year	
ENCFF001QZI	epithelial cell of viscerocranial mucosa	character(0)	ENCSR000AAL	total RNA-seq	nasal cavity respiratory epithelium epithelial cell of viscerocranial mucosa female adult (70 years) and male adult (46 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	46,7	year	
ENCFF001RBA	uterine smooth muscle cell	7: SMC	ENCSR000AAV	total RNA-seq	uterine smooth muscle cell female adult (48 years) and female adult (50 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	48,5	year	
ENCFF001RCC	uterine smooth muscle cell	7: SMC	ENCSR000AAV	total RNA-seq	uterine smooth muscle cell female adult (48 years) and female adult (50 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	48,5	year	
ENCFF001QZQ	aortic SMC	character(0)	ENCSR000AAA	total RNA-seq	aortic smooth muscle cell male adult (21 year) and male adult (54 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	54,21	year	
ENCFF001RAM	aortic SMC	character(0)	ENCSR000AAA	total RNA-seq	aortic smooth muscle cell male adult (21 year) and male adult (54 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	54,21	year	
ENCFF000IGA	melanocyte of skin	6: Others	ENCSR000CUQ	total RNA-seq	melanocyte of skin male child (1 year) and male child (3 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	3,1	year	
ENCFF000IGU	melanocyte of skin	6: Others	ENCSR000CUQ	total RNA-seq	melanocyte of skin male child (1 year) and male child (3 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	3,1	year	
ENCFF446LHV	dendritic cell	6: Others	ENCSR022BYE	total RNA-seq	dendritic cell treated with 0 ng/mL Lipopolysaccharide for 0 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF817RIH	dendritic cell	6: Others	ENCSR227MWL	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 2 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF662HMZ	dendritic cell	6: Others	ENCSR975YGW	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 2 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF001RAG	bronchial smooth muscle cell	7: SMC	ENCSR000AAE	total RNA-seq	bronchial smooth muscle cell male adult (52 years) and male adult (59 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	52,59	year	
ENCFF001RAS	bronchial smooth muscle cell	7: SMC	ENCSR000AAE	total RNA-seq	bronchial smooth muscle cell male adult (52 years) and male adult (59 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	52,59	year	
ENCFF001RAA	endothelial cell of coronary artery	8: Endothelial cells	ENCSR000AAF	total RNA-seq	endothelial cell of coronary artery female adult (41 year) and male adult (77 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	41,77	year	
ENCFF001RBK	endothelial cell of coronary artery	8: Endothelial cells	ENCSR000AAF	total RNA-seq	endothelial cell of coronary artery female adult (41 year) and male adult (77 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	41,77	year	
ENCFF001QZY	smooth muscle cell of the coronary artery	7: SMC	ENCSR000AAG	total RNA-seq	smooth muscle cell of the coronary artery female adult (53 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53,55	year	
ENCFF001RCG	smooth muscle cell of the coronary artery	7: SMC	ENCSR000AAG	total RNA-seq	smooth muscle cell of the coronary artery female adult (53 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	53,55	year	
ENCFF001QZU	pulmonary artery endothelial cell	8: Endothelial cells	ENCSR000AAM	total RNA-seq	pulmonary artery endothelial cell male adult (23 years) and male adult (52 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	23,52	year	
ENCFF001RCE	pulmonary artery endothelial cell	8: Endothelial cells	ENCSR000AAM	total RNA-seq	pulmonary artery endothelial cell male adult (23 years) and male adult (52 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	23,52	year	
ENCFF071TOB	dendritic cell	6: Others	ENCSR084JIA	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 1 hour	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF001RAE	regular cardiac myocyte	5: Muscle cells	ENCSR000AAH	total RNA-seq	regular cardiac myocyte female adult (51 year) and male adult (48 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	48,51	year	
ENCFF001RBM	regular cardiac myocyte	5: Muscle cells	ENCSR000AAH	total RNA-seq	regular cardiac myocyte female adult (51 year) and male adult (48 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	48,51	year	
ENCFF001RAY	dermis lymphatic vessel endothelial cell	8: Endothelial cells	ENCSR000AAJ	total RNA-seq	dermis lymphatic vessel endothelial cell female adult (45 years) and male child (6 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child,adult	6,45	year	

ENCFF001RBQ	dermis lymphatic vessel endothelial cell	8: Endothelial cells	ENCSR000AAJ	total RNA-seq	dermis lymphatic vessel endothelial cell female adult (45 years) and male child (6 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child,adult	6,45	year	
ENCFF001RAW	dermis microvascular lymphatic vessel endothelial cell	8: Endothelial cells	ENCSR000AAK	total RNA-seq	dermis microvascular lymphatic vessel endothelial cell female adult (38 years) and female adult (64 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	38,64	year	
ENCFF001RBE	dermis microvascular lymphatic vessel endothelial cell	8: Endothelial cells	ENCSR000AAK	total RNA-seq	dermis microvascular lymphatic vessel endothelial cell female adult (38 years) and female adult (64 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	38,64	year	
ENCFF365NAH	foreskin keratinocyte	6: Others	ENCSR527SSD	total RNA-seq	foreskin keratinocyte male newborn (2-4 days) treated with 1.2 mM calcium for 5.5 days	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	calcium
ENCFF668JVG	foreskin keratinocyte	6: Others	ENCSR527SSD	total RNA-seq	foreskin keratinocyte male newborn (2-4 days) treated with 1.2 mM calcium for 5.5 days	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	calcium
ENCFF649ASL	dendritic cell	6: Others	ENCSR571IUZ	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF123JND	dendritic cell	6: Others	ENCSR760INS	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 6 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF945OFS	dendritic cell	6: Others	ENCSR670MXT	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 2 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF124RBL	dendritic cell	6: Others	ENCSR476TKU	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF365UNT	dendritic cell	6: Others	ENCSR475TVN	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 6 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF658PGS	dendritic cell	6: Others	ENCSR707JVU	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF609HPU	dendritic cell	6: Others	ENCSR916YUR	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 6 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF000GLZ	placental epithelial cell	9: Epithelial cells	ENCSR000CUP	total RNA-seq	placental epithelial cell female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000GMA	placental epithelial cell	9: Epithelial cells	ENCSR000CUP	total RNA-seq	placental epithelial cell female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000GYE	subcutaneous preadipocyte	4: Progenitor or Stem cell	ENCSR000CUM	total RNA-seq	subcutaneous preadipocyte female adult (62 years) and male adult (65 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	65,62	year	
ENCFF000GZD	subcutaneous preadipocyte	4: Progenitor or Stem cell	ENCSR000CUM	total RNA-seq	subcutaneous preadipocyte female adult (62 years) and male adult (65 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	65,62	year	
ENCFF947BAG	dendritic cell	6: Others	ENCSR146PLL	total RNA-seq	dendritic cell treated with 100 ng/mL Lipopolysaccharide for 4 hours	Manuel Garber, UMass	GGR	Homo sapiens	unknown	unknown		Lipopolysaccharide
ENCFF659EDN	mammary microvascular endothelial cell	8: Endothelial cells	ENCSR815UVL	total RNA-seq	mammary microvascular endothelial cell female adult (26 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	26	year	
ENCFF143UMB	mammary microvascular endothelial cell	8: Endothelial cells	ENCSR815UVL	total RNA-seq	mammary microvascular endothelial cell female adult (26 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	26	year	
ENCFF001QZW	epithelial cell of umbilical artery	9: Epithelial cells	ENCSR000AAT	total RNA-seq	epithelial cell of umbilical artery female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF001RBC	epithelial cell of umbilical artery	9: Epithelial cells	ENCSR000AAT	total RNA-seq	epithelial cell of umbilical artery female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF001RBU	smooth muscle cell of the umbilical artery	7: SMC	ENCSR000AAU	total RNA-seq	smooth muscle cell of the umbilical artery female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF001RBY	smooth muscle cell of the umbilical artery	7: SMC	ENCSR000AAU	total RNA-seq	smooth muscle cell of the umbilical artery female newborn and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF002DMJ	H7-hESC	4: Progenitor or Stem cell	ENCSR490SQH	total RNA-seq	H7-hESC	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	unknown		
ENCFF002DMP	H7-hESC	4: Progenitor or Stem cell	ENCSR490SQH	total RNA-seq	H7-hESC	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	unknown		
ENCFF000IHC	melanocyte of skin	6: Others	ENCSR000CUR	total RNA-seq	melanocyte of skin female adult (52 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,52	year	
ENCFF000IHY	melanocyte of skin	6: Others	ENCSR000CUR	total RNA-seq	melanocyte of skin female adult (52 years) and male adult (55 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	55,52	year	
ENCFF575SLU	cardiac ventricle fibroblast	1: Fibroblast	ENCSR369RVN	total RNA-seq	cardiac ventricle fibroblast NONE and male adult (18 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult,unknown	18,unknown	year	
ENCFF157UXG	cardiac ventricle fibroblast	1: Fibroblast	ENCSR369RVN	total RNA-seq	cardiac ventricle fibroblast NONE and male adult (18 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult,unknown	18,unknown	year	
ENCFF689YVG	pericardium fibroblast	1: Fibroblast	ENCSR362HMX	total RNA-seq	pericardium fibroblast NONE and female embryo (20 weeks)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic,unkn	20,unknown	week	
ENCFF005EEW	pericardium fibroblast	1: Fibroblast	ENCSR362HMX	total RNA-seq	pericardium fibroblast NONE and female embryo (20 weeks)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic,unkn	20,unknown	week	
ENCFF746KSI	epithelial cell of alveolus of lung	9: Epithelial cells	ENCSR897KTO	total RNA-seq	epithelial cell of alveolus of lung NONE and female embryo (21 week)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown,embry	unknown,21	week	
ENCFF408FWI	epithelial cell of alveolus of lung	9: Epithelial cells	ENCSR897KTO	total RNA-seq	epithelial cell of alveolus of lung NONE and female embryo (21 week)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown,embry	unknown,21	week	
ENCFF109IUU	kidney epithelial cell	9: Epithelial cells	ENCSR373BDG	total RNA-seq	kidney epithelial cell male embryo (22 weeks) and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic,newb	22,unknown	week	
ENCFF999ZER	kidney epithelial cell	9: Epithelial cells	ENCSR373BDG	total RNA-seq	kidney epithelial cell male embryo (22 weeks) and male newborn	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic,newb	22,unknown	week	
ENCFF353STY	cardiac atrium fibroblast	1: Fibroblast	ENCSR110BDY	total RNA-seq	cardiac atrium fibroblast male child (2 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	2	year	
ENCFF753GPU	cardiac atrium fibroblast	1: Fibroblast	ENCSR110BDY	total RNA-seq	cardiac atrium fibroblast male child (2 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	child	2	year	
ENCFF000GJC	osteoblast	3: Osteo/Chondro lineage	ENCSR000CUF	total RNA-seq	osteoblast female adult (56 years) and male adult (62 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	56,62	year	
ENCFF000GKC	osteoblast	3: Osteo/Chondro lineage	ENCSR000CUF	total RNA-seq	osteoblast female adult (56 years) and male adult (62 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	56,62	year	
ENCFF000GET	mammary epithelial cell	9: Epithelial cells	ENCSR000CUN	total RNA-seq	mammary epithelial cell female adult (23 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	23	year	
ENCFF353SPR	cardiac muscle cell	5: Muscle cells	ENCSR379YAE	total RNA-seq	cardiac muscle cell originated from RUES2	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	unknown		
ENCFF030WXU	cardiac muscle cell	5: Muscle cells	ENCSR379YAE	total RNA-seq	cardiac muscle cell originated from RUES2	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	unknown		
ENCFF472QXK	foreskin keratinocyte	6: Others	ENCSR959LTT	total RNA-seq	foreskin keratinocyte male newborn (2-4 days) treated with 1.2 mM calcium for 2.5 days	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	calcium
ENCFF218VQQ	foreskin keratinocyte	6: Others	ENCSR959LTT	total RNA-seq	foreskin keratinocyte male newborn (2-4 days) treated with 1.2 mM calcium for 2.5 days	Michael Snyder, Stanford	GGR	Homo sapiens	newborn	2-4	day	calcium

Table_S2 Metadata for ENCODE kmer research

ENCFF000GIC	MSC of Wharton's jelly	character(0)	ENCSR000CUO	total RNA-seq	mesenchymal stem cell of Wharton's jelly	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF000GIV	MSC of Wharton's jelly	character(0)	ENCSR000CUO	total RNA-seq	mesenchymal stem cell of Wharton's jelly	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	newborn	unknown		
ENCFF548JWS	smooth muscle cell	7: SMC	ENCSR052FJA	total RNA-seq	smooth muscle cell originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF199QMY	smooth muscle cell	7: SMC	ENCSR052FJA	total RNA-seq	smooth muscle cell originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF001RAC	bronchial epithelial cell	9: Epithelial cells	ENCSR000AAD	total RNA-seq	bronchial epithelial cell female adult (40 years) and male adult (68 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	68,4	year	
ENCFF001RBO	bronchial epithelial cell	9: Epithelial cells	ENCSR000AAD	total RNA-seq	bronchial epithelial cell female adult (40 years) and male adult (68 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	68,4	year	
ENCFF653EZE	hepatocyte	6: Others	ENCSR908ZAS	total RNA-seq	hepatocyte originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF245VTB	hepatocyte	6: Others	ENCSR908ZAS	total RNA-seq	hepatocyte originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF996KMK	neural progenitor cell	4: Progenitor or Stem cell	ENCSR244ISQ	total RNA-seq	neural progenitor cell originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF939FVE	neural progenitor cell	4: Progenitor or Stem cell	ENCSR244ISQ	total RNA-seq	neural progenitor cell originated from H9	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	embryonic	5	day	
ENCFF002DMH	skeletal muscle myoblast	5: Muscle cells	ENCSR444WHQ	total RNA-seq	skeletal muscle myoblast	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF002DML	skeletal muscle myoblast	5: Muscle cells	ENCSR444WHQ	total RNA-seq	skeletal muscle myoblast	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF119TIN	myocyte	5: Muscle cells	ENCSR894WMQ	total RNA-seq	myocyte originated from LHCN-M2	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	41	year	
ENCFF700EUG	myocyte	5: Muscle cells	ENCSR894WMQ	total RNA-seq	myocyte originated from LHCN-M2	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	41	year	
ENCFF000GHA	MSC of the bone marrow	character(0)	ENCSR000CUD	total RNA-seq	mesenchymal stem cell of the bone marrow	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	57,6	year	
ENCFF000GHX	MSC of the bone marrow	character(0)	ENCSR000CUD	total RNA-seq	mesenchymal stem cell of the bone marrow	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	57,6	year	
ENCFF464PFE	airway epithelial cell	9: Epithelial cells	ENCSR822SUG	total RNA-seq	airway epithelial cell	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF846YCY	airway epithelial cell	9: Epithelial cells	ENCSR822SUG	total RNA-seq	airway epithelial cell	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF541NUM	epithelial cell of proximal tubule	9: Epithelial cells	ENCSR118TVR	total RNA-seq	epithelial cell of proximal tubule	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF479JTM	epithelial cell of proximal tubule	9: Epithelial cells	ENCSR118TVR	total RNA-seq	epithelial cell of proximal tubule	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF000FJX	fibroblast of the aortic adventitia	1: Fibroblast	ENCSR000CUJ	total RNA-seq	fibroblast of the aortic adventitia female adult (24 years) and male adult (47 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	47,24	year	
ENCFF000FKI	fibroblast of the aortic adventitia	1: Fibroblast	ENCSR000CUJ	total RNA-seq	fibroblast of the aortic adventitia female adult (24 years) and male adult (47 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	47,24	year	
ENCFF000EUS	hematopoietic multipotent progenitor cell	4: Progenitor or Stem cell	ENCSR000CUA	total RNA-seq	hematopoietic multipotent progenitor cell	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF393GQZ	astrocyte	6: Others	ENCSR233IJT	total RNA-seq	astrocyte	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF424DEO	astrocyte	6: Others	ENCSR233IJT	total RNA-seq	astrocyte	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	unknown	unknown		
ENCFF001QZO	fibroblast of lung	1: Fibroblast	ENCSR000AAO	total RNA-seq	fibroblast of lung female adult (83 years) and male adult (23 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	83,23	year	
ENCFF001RBI	fibroblast of lung	1: Fibroblast	ENCSR000AAO	total RNA-seq	fibroblast of lung female adult (83 years) and male adult (23 years)	Thomas Gingeras, CSHL	ENCODE	Homo sapiens	adult	83,23	year	

Table_S3 Meatadata for single cell analysis and FANTOM6 kmer research

Run ID	titles	experiment_type	fraction	run_no	target_gene_symbol	specie	study_title	Study ID	nreads	read_length	library_selection	perturb_id	cell_type_alias
SRR7294023	single-cell RNA-seq of human adipose-derived mesenchymal stem cells	10X genomics sequencing	NA	NA	NA	Homo sapiens	single-cell transcriptomic sequencing of 24,370 adipose-derived mesenchymal stem cells	PRJNA472816	176545104	149.75	PolyA	NA	Ad-MSCs
SRR7253635	single-cell RNA-seq of human adipose-derived mesenchymal stem cells	10X genomics sequencing	NA	NA	NA	Homo sapiens	single-cell transcriptomic sequencing of 24,370 adipose-derived mesenchymal stem cells	PRJNA472816	265719530	149.99	PolyA	NA	Ad-MSCs
SRR7363187	single-cell RNA-seq of human adipose-derived mesenchymal stem cells	10X genomics sequencing	NA	NA	NA	Homo sapiens	single-cell transcriptomic sequencing of 24,370 adipose-derived mesenchymal stem cells	PRJNA472816	352873537	149.98	PolyA	NA	Ad-MSCs
Run ID	titles	experiment_type	fraction	run_no	target_gene_symbol	specie	study_title	Study ID	nreads	read_length	library_selection	perturb_id	cell_type_alias
DRR177156	RDhi10602_ATCACG.experiment	Reference	cytoplasmic	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	33503637	51	Inverse rRNA	NA	HDF (neonatal)
DRR177155	RDhi10602_ACTTGA.experiment	Reference	cytoplasmic	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	30096528	51	Inverse rRNA	NA	HDF (neonatal)
DRR177154	RDhi10601_TTAGGC.experiment	Reference	nuclear	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	35912547	51	Inverse rRNA	NA	HDF (neonatal)
DRR177153	RDhi10601_GATCAG.experiment	Reference	nuclear	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	35267146	51	Inverse rRNA	NA	HDF (neonatal)
DRR177152	RDhi10600_ATCACG.experiment	Reference	chromatin	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	33268855	51	Inverse rRNA	NA	HDF (neonatal)
DRR177151	RDhi10600_ACTTGA.experiment	Reference	chromatin	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	34620706	51	Inverse rRNA	NA	HDF (neonatal)
DRR176801	CNhi10765_ACC.experiment	Targeted	NA	14	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	17143511	47	CAGE	ASO_G0257219_AD_05	HDF (neonatal)
DRR176800	CNhi10764_TAC.experiment	Targeted	NA	13	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	22288472	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176799	CNhi10764_GCT.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16779827	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176798	CNhi10764_GCG.experiment	Targeted	NA	14	RP5-886K2.3	Homo sapiens	FANTOM6 project	PRJDB7993	13412787	47	CAGE	ASO_G0236810_AD_02	HDF (neonatal)
DRR176797	CNhi10764_CAC.experiment	Targeted	NA	14	RP5-886K2.3	Homo sapiens	FANTOM6 project	PRJDB7993	13768161	47	CAGE	ASO_G0236810_AD_02	HDF (neonatal)
DRR176796	CNhi10764_ATG.experiment	Experiment control	NA	13	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	18335819	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176731	CNhi10640_ACG.experiment	Targeted	NA	12	DNM3OS	Homo sapiens	FANTOM6 project	PRJDB7993	14547994	47	CAGE	ASO_G0230630_AD_04	HDF (neonatal)
DRR176730	CNhi10640_ACC.experiment	Targeted	NA	12	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	16086917	47	CAGE	ASO_G0229847_AD_04	HDF (neonatal)
DRR176729	CNhi10639_TAC.experiment	Experiment control	NA	12	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14896166	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176728	CNhi10639_GCT.experiment	Targeted	NA	12	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	14574794	47	CAGE	ASO_G0253352_AD_08	HDF (neonatal)
DRR176727	CNhi10639_GCG.experiment	Targeted	NA	12	C11orf95	Homo sapiens	FANTOM6 project	PRJDB7993	12726968	47	CAGE	ASO_G0188070_AD_05	HDF (neonatal)
DRR176726	CNhi10639_CAC.experiment	Targeted	NA	12	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	13664802	47	CAGE	ASO_G0218510_AD_03	HDF (neonatal)
DRR176725	CNhi10639_ATG.experiment	Targeted	NA	12	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	12597402	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176724	CNhi10639_AGT.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11157330	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176659	CNhi10630_TAC.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14568347	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176658	CNhi10630_GCT.experiment	Targeted	NA	12	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	14061748	47	CAGE	ASO_G0218510_AD_06	HDF (neonatal)
DRR176657	CNhi10630_GCG.experiment	Targeted	NA	12	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	12365942	47	CAGE	ASO_G0223485_AD_06	HDF (neonatal)
DRR176656	CNhi10630_CAC.experiment	Targeted	NA	12	C11orf95	Homo sapiens	FANTOM6 project	PRJDB7993	13926089	47	CAGE	ASO_G0188070_AD_05	HDF (neonatal)
DRR176655	CNhi10630_ATG.experiment	Targeted	NA	12	ERVK13-1	Homo sapiens	FANTOM6 project	PRJDB7993	15897264	47	CAGE	ASO_G0260565_AD_06	HDF (neonatal)
DRR176654	CNhi10630_AGT.experiment	Targeted	NA	12	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	11413198	47	CAGE	ASO_G0223485_AD_04	HDF (neonatal)
DRR176653	CNhi10630_ACG.experiment	Targeted	NA	12	RP6-99M1.2	Homo sapiens	FANTOM6 project	PRJDB7993	14016329	47	CAGE	ASO_G0270069_AD_07	HDF (neonatal)
DRR176652	CNhi10630_ACC.experiment	Targeted	NA	12	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	20414932	47	CAGE	ASO_G0250742_AD_04	HDF (neonatal)
DRR176587	CNhi10605_GCT.experiment	Targeted	NA	10	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	535389	47	CAGE	ASO_G0237187_01	HDF (neonatal)
DRR176586	CNhi10605_GCG.experiment	Targeted	NA	10	RP6-109B7.3	Homo sapiens	FANTOM6 project	PRJDB7993	10382541	47	CAGE	ASO_G0241990_07	HDF (neonatal)
DRR176585	CNhi10605_CAC.experiment	Targeted	NA	10	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	13123013	47	CAGE	ASO_G0237854_05	HDF (neonatal)
DRR176584	CNhi10605_ATG.experiment	Experiment control	NA	10	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14008394	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176583	CNhi10605_AGT.experiment	Targeted	NA	10	CKMT2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16349504	47	CAGE	ASO_G0247572_09	HDF (neonatal)
DRR176582	CNhi10605_ACG.experiment	Targeted	NA	11	LINC00883	Homo sapiens	FANTOM6 project	PRJDB7993	14714634	47	CAGE	ASO_G0243701_01	HDF (neonatal)
DRR176581	CNhi10605_ACC.experiment	Targeted	NA	11	TP53TG1	Homo sapiens	FANTOM6 project	PRJDB7993	16141896	47	CAGE	ASO_G0182165_AD_10	HDF (neonatal)
DRR176580	CNhi10604_TAC.experiment	Targeted	NA	10	LINC00707	Homo sapiens	FANTOM6 project	PRJDB7993	12703583	47	CAGE	ASO_G0238266_03	HDF (neonatal)
DRR176515	CNhi10584_ATG.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	11169949	47	CAGE	ASO_G0262468_07	HDF (neonatal)
DRR176514	CNhi10584_AGT.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	13068899	47	CAGE	ASO_G0262468_04	HDF (neonatal)
DRR176513	CNhi10584_ACG.experiment	Targeted	NA	9	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	11886738	47	CAGE	ASO_G0263753_01	HDF (neonatal)
DRR176512	CNhi10584_ACC.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	19111059	47	CAGE	ASO_G0262468_02	HDF (neonatal)
DRR176511	CNhi10583_TAC.experiment	Targeted	NA	9	RP11-333E1.1	Homo sapiens	FANTOM6 project	PRJDB7993	11345714	47	CAGE	ASO_G0261879_05	HDF (neonatal)
DRR176510	CNhi10583_GCT.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	10783975	47	CAGE	ASO_G0262468_02	HDF (neonatal)
DRR176509	CNhi10583_GCG.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	12579190	47	CAGE	ASO_G0261573_03	HDF (neonatal)
DRR176508	CNhi10583_CAC.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	13226029	47	CAGE	ASO_G0261573_02	HDF (neonatal)
DRR176443	CNhi10543_AGT.experiment	Targeted	NA	5	CATG00000016989.1	Homo sapiens	FANTOM6 project	PRJDB7993	13134737	47	CAGE	ASO_C0020443_06	HDF (neonatal)
DRR176442	CNhi10543_ACG.experiment	Targeted	NA	5	CATG00000079799.1	Homo sapiens	FANTOM6 project	PRJDB7993	11721046	47	CAGE	ASO_C0008586_03	HDF (neonatal)
DRR176441	CNhi10543_ACC.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12082179	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176440	CNhi10542_TAC.experiment	Reference	NA	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11753926	47	CAGE	NA	HDF (neonatal)
DRR176439	CNhi10542_GCT.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15072508	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176438	CNhi10542_CAC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12572386	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176437	CNhi10542_ATG.experiment	Targeted	NA	6	CTC-338M12.4	Homo sapiens	FANTOM6 project	PRJDB7993	10514355	47	CAGE	ASO_G0233937_05	HDF (neonatal)
DRR176436	CNhi10542_AGT.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	11847706	47	CAGE	ASO_G0233137_04	HDF (neonatal)
DRR176371	CNhi10534_ACC.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	11750669	47	CAGE	ASO_G0233527_07	HDF (neonatal)
DRR176370	CNhi10533_TAC.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10753751	47	CAGE	ASO_G0186615_03	HDF (neonatal)
DRR176369	CNhi10533_GCT.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	10343841	47	CAGE	ASO_G0233527_02	HDF (neonatal)
DRR176368	CNhi10533_GCG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9051548	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176367	CNhi10533_CAC.experiment	Targeted	NA	5	RP11-296O14.3	Homo sapiens	FANTOM6 project	PRJDB7993	10389408	47	CAGE	ASO_G0203739_10	HDF (neonatal)
DRR176366	CNhi10533_ATG.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	10291057	47	CAGE	ASO_G0233527_07	HDF (neonatal)
DRR176365	CNhi10533_AGT.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9027563	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176364	CNhi10533_ACG.experiment	Targeted	NA	6	U52111.14	Homo sapiens	FANTOM6 project	PRJDB7993	11119652	47	CAGE	ASO_G0232725_05	HDF (neonatal)
DRR176299	CNhi10524_TAC.experiment	Targeted	NA	5	CATG00000020700.1	Homo sapiens	FANTOM6 project	PRJDB7993	19711422	47	CAGE	ASO_C0020984_09	HDF (neonatal)
DRR176298	CNhi10524_GCT.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	16834564	47	CAGE	ASO_G0223773_05	HDF (neonatal)
DRR176297	CNhi10524_GCG.experiment	Targeted	NA	4	RP11-395B7.4	Homo sapiens	FANTOM6 project	PRJDB7993	12730668	47	CAGE	ASO_G0227053_03	HDF (neonatal)
DRR176296	CNhi10524_CAC.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16433061	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176295	CNhi10524_AGT.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	17651165	47	CAGE	ASO_G0223773_06	HDF (neonatal)

DRR176294	CNhi10524_ACG.experiment	Targeted	NA	4	MFI2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15835443	47	CAGE	ASO_G0228109_06	HDF (neonatal)
DRR176293	CNhi10524_ACC.experiment	Targeted	NA	5	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	21374168	47	CAGE	ASO_C0012015_07	HDF (neonatal)
DRR176292	CNhi10523_TAC.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	19989870	47	CAGE	ASO_G0224086_03	HDF (neonatal)
DRR176227	CNhi10492_GCG.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	11544811	47	CAGE	ASO_G0234171_01	HDF (neonatal)
DRR176226	CNhi10492_CAC.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	12142331	47	CAGE	ASO_G0240875_10	HDF (neonatal)
DRR176225	CNhi10492_ATG.experiment	Targeted	NA	3	AC007246.3	Homo sapiens	FANTOM6 project	PRJDB7993	16768824	47	CAGE	ASO_G0231312_04	HDF (neonatal)
DRR176224	CNhi10492_AGT.experiment	Targeted	NA	3	ZNF131	Homo sapiens	FANTOM6 project	PRJDB7993	15842962	47	CAGE	ASO_C0008543_05	HDF (neonatal)
DRR176223	CNhi10492_ACG.experiment	Targeted	NA	3	AC007246.3	Homo sapiens	FANTOM6 project	PRJDB7993	14941536	47	CAGE	ASO_G0231312_04	HDF (neonatal)
DRR176222	CNhi10492_ACC.experiment	Targeted	NA	3	RP11-38L15.3	Homo sapiens	FANTOM6 project	PRJDB7993	14492220	47	CAGE	ASO_G0231187_02	HDF (neonatal)
DRR176221	CNhi10491_TAC.experiment	Targeted	NA	3	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	17880185	47	CAGE	ASO_G0203721_05	HDF (neonatal)
DRR176220	CNhi10491_GCT.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	16449157	47	CAGE	ASO_G0240875_04	HDF (neonatal)
DRR176155	CNhi10475_ATG.experiment	Targeted	NA	2	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	19637512	47	CAGE	ASO_G0229852_03	HDF (neonatal)
DRR176154	CNhi10475_AGT.experiment	Targeted	NA	2	LINC00654	Homo sapiens	FANTOM6 project	PRJDB7993	16462388	47	CAGE	ASO_G0205181_01	HDF (neonatal)
DRR176153	CNhi10475_ACG.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	19290770	47	CAGE	ASO_G0263072_06	HDF (neonatal)
DRR176152	CNhi10475_ACC.experiment	Targeted	NA	2	LINC00654	Homo sapiens	FANTOM6 project	PRJDB7993	18870242	47	CAGE	ASO_G0205181_01	HDF (neonatal)
DRR176151	CNhi10474_TAC.experiment	Targeted	NA	2	RP11-115C21.2	Homo sapiens	FANTOM6 project	PRJDB7993	18498643	47	CAGE	ASO_G0246089_02	HDF (neonatal)
DRR176150	CNhi10474_GCT.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16385749	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176149	CNhi10474_GCG.experiment	Targeted	NA	2	NEAT1_2	Homo sapiens	FANTOM6 project	PRJDB7993	13959063	47	CAGE	ASO_NEAT1_2	HDF (neonatal)
DRR176148	CNhi10474_CAC.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	13658057	47	CAGE	ASO_G0212978_04	HDF (neonatal)
DRR176083	CNhi10466_AGT.experiment	Targeted	NA	2	AC005592.2	Homo sapiens	FANTOM6 project	PRJDB7993	16326963	47	CAGE	ASO_G0231185_03	HDF (neonatal)
DRR176082	CNhi10466_ACG.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	14489974	47	CAGE	ASO_G0212978_01	HDF (neonatal)
DRR176081	CNhi10466_ACC.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	22044906	47	CAGE	ASO_G0212978_03	HDF (neonatal)
DRR176080	CNhi10463_TAC.experiment	Targeted	NA	1	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17735123	47	CAGE	ASO_G0225733_04	HDF (neonatal)
DRR176079	CNhi10463_GCT.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13264659	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176078	CNhi10463_GCG.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	10978064	47	CAGE	ASO_G0253352_06	HDF (neonatal)
DRR176077	CNhi10463_CAC.experiment	Targeted	NA	1	LINC00938	Homo sapiens	FANTOM6 project	PRJDB7993	14501783	47	CAGE	ASO_G0273015_05	HDF (neonatal)
DRR176076	CNhi10463_ATG.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	15873018	47	CAGE	ASO_G0226950_05	HDF (neonatal)
DRR177150	CNhi10867_CAC.experiment	Targeted	NA	23	XRN2	Homo sapiens	FANTOM6 project	PRJDB7993	16021989	47	CAGE	siRNA_siXRN-2	HDF (neonatal)
DRR176180	CNhi10486_GCG.experiment	Targeted	NA	3	AC009948.5	Homo sapiens	FANTOM6 project	PRJDB7993	17124016	47	CAGE	ASO_G0223960_08	HDF (neonatal)
DRR176115	CNhi10470_ATG.experiment	Targeted	NA	2	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	21992801	47	CAGE	ASO_G0223546_01	HDF (neonatal)
DRR176114	CNhi10470_AGT.experiment	Targeted	NA	2	RP11-611E13.2	Homo sapiens	FANTOM6 project	PRJDB7993	15920027	47	CAGE	ASO_G0257815_01	HDF (neonatal)
DRR176113	CNhi10470_ACG.experiment	Targeted	NA	2	BX322557.10	Homo sapiens	FANTOM6 project	PRJDB7993	15010004	47	CAGE	ASO_G0215447_03	HDF (neonatal)
DRR176112	CNhi10470_ACC.experiment	Targeted	NA	2	SERTAD4-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	23248785	47	CAGE	ASO_G0203706_01	HDF (neonatal)
DRR176111	CNhi10469_TAC.experiment	Targeted	NA	2	AC007879.7	Homo sapiens	FANTOM6 project	PRJDB7993	22846956	47	CAGE	ASO_G0229647_06	HDF (neonatal)
DRR176110	CNhi10469_GCT.experiment	Targeted	NA	2	RP11-458D21.1	Homo sapiens	FANTOM6 project	PRJDB7993	18718993	47	CAGE	ASO_G0233396_02	HDF (neonatal)
DRR176109	CNhi10469_GCG.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13142632	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176108	CNhi10469_CAC.experiment	Targeted	NA	2	TRAM2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17294751	47	CAGE	ASO_G0225791_05	HDF (neonatal)
DRR177115	CNhi10836_ACG.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13655505	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177114	CNhi10836_ACC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23739059	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177113	CNhi10835_TAC.experiment	Targeted	NA	19	RP11-539L10.3	Homo sapiens	FANTOM6 project	PRJDB7993	25798059	47	CAGE	ASO_G0251580_AD_05	HDF (neonatal)
DRR177112	CNhi10835_GCT.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	11567592	47	CAGE	ASO_C0012015_AD_05	HDF (neonatal)
DRR177111	CNhi10835_GCG.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13020861	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177110	CNhi10835_CAC.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	15861574	47	CAGE	ASO_C0012015_AD_05	HDF (neonatal)
DRR177109	CNhi10835_ATG.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14637155	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177108	CNhi10835_AGT.experiment	Targeted	NA	21	JPX	Homo sapiens	FANTOM6 project	PRJDB7993	12147528	47	CAGE	ASO_G0225470_AD_04	HDF (neonatal)
DRR177043	CNhi10819_ACC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15427139	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR177042	CNhi10818_TAC.experiment	Targeted	NA	20	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	12929433	47	CAGE	siRNA_n504056	HDF (neonatal)
DRR177041	CNhi10818_GCT.experiment	Targeted	NA	21	LINC00959	Homo sapiens	FANTOM6 project	PRJDB7993	14818614	47	CAGE	ASO_G0237489_AD_01	HDF (neonatal)
DRR177040	CNhi10818_GCG.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14556123	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR177039	CNhi10818_CAC.experiment	Targeted	NA	20	PRRX1	Homo sapiens	FANTOM6 project	PRJDB7993	10261513	47	CAGE	ASO_G0116132_POS_09	HDF (neonatal)
DRR177038	CNhi10818_ATG.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18746690	47	CAGE	ASO_G0240498_POS_04	HDF (neonatal)
DRR177037	CNhi10818_AGT.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18459646	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR177036	CNhi10818_ACG.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	17427449	47	CAGE	ASO_G0228630_POS_06	HDF (neonatal)
DRR176035	CNhi10458_ACC.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	18272029	47	CAGE	ASO_G0224577_02	HDF (neonatal)
DRR176034	CNhi10457_TAC.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	20936701	47	CAGE	ASO_G0253352_06	HDF (neonatal)
DRR176033	CNhi10457_GCT.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15933999	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176032	CNhi10457_GCG.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	13039795	47	CAGE	ASO_G0226950_05	HDF (neonatal)
DRR176031	CNhi10457_CAC.experiment	Targeted	NA	1	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	13879212	47	CAGE	ASO_G0163364_04	HDF (neonatal)
DRR176030	CNhi10457_ATG.experiment	Targeted	NA	1	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16115160	47	CAGE	ASO_G0246067_05	HDF (neonatal)
DRR176029	CNhi10457_AGT.experiment	Targeted	NA	1	LINC00702	Homo sapiens	FANTOM6 project	PRJDB7993	19006359	47	CAGE	ASO_G0233117_04	HDF (neonatal)
DRR176028	CNhi10457_ACG.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	17398562	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176971	CNhi10809_GCT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15919384	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176970	CNhi10809_GCG.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	11576336	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176969	CNhi10809_CAC.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	9961711	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176968	CNhi10809_ATG.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	17618203	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176967	CNhi10809_AGT.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	12091730	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176966	CNhi10809_ACG.experiment	Experiment control	NA	20	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	24391514	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176965	CNhi10809_ACC.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	18278971	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176964	CNhi10808_TAC.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17737395	47	CAGE	sgRNA_blast5_control	HDF (neonatal)
DRR176899	CNhi10791_GCG.experiment	Targeted	NA	15	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	15151803	47	CAGE	ASO_G0244625_AD_09	HDF (neonatal)
DRR176898	CNhi10791_CAC.experiment	Targeted	NA	15	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	14391634	47	CAGE	ASO_G0219665_AD_04	HDF (neonatal)
DRR176897	CNhi10791_AGT.experiment	Targeted	NA	16	RP11-6N17.4	Homo sapiens	FANTOM6 project	PRJDB7993	15366854	47	CAGE	ASO_G0264920_AD_02	HDF (neonatal)
DRR176896	CNhi10791_ACG.experiment	Experiment control	NA	16	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	20746443	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176895	CNhi10791_ACC.experiment	Targeted	NA	16	RP11-6N17.4	Homo sapiens	FANTOM6 project	PRJDB7993	22523908	47	CAGE	ASO_G0264920_AD_02	HDF (neonatal)
DRR176894	CNhi10790_TAC.experiment	Targeted	NA	16	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	22614587	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176893	CNhi10790_GCT.experiment	Experiment control	NA	15	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15270427	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176892	CNhi10790_GCG.experiment	Targeted	NA	15	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	12986643	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176827	CNhi10782_ATG.experiment	Targeted	NA	16	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	20781459	47	CAGE	ASO_G0263753_AD_06	HDF (neonatal)
DRR176826	CNhi10782_AGT.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19734742	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176825	CNhi10782_ACG.experiment	Targeted	NA	17	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	17599975	47	CAGE	ASO_G0269834_AD_06	HDF (neonatal)

DRR176824	CNhi10782_ACC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23277079	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176823	CNhi10767_TAC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21972404	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176822	CNhi10767_GCT.experiment	Targeted	NA	13	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	11757678	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176821	CNhi10767_GCG.experiment	Targeted	NA	14	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	10872425	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176820	CNhi10767_CAC.experiment	Targeted	NA	17	RP11-611E13.2	Homo sapiens	FANTOM6 project	PRJDB7993	16922148	47	CAGE	ASO_G0257815_AD_03	HDF (neonatal)
DRR176755	CNhi10759_ACG.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	19769317	47	CAGE	ASO_G0261105_AD_10	HDF (neonatal)
DRR176754	CNhi10759_ACC.experiment	Targeted	NA	13	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18228975	47	CAGE	ASO_G0234608_AD_01	HDF (neonatal)
DRR176753	CNhi10758_TAC.experiment	Targeted	NA	13	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	22627200	47	CAGE	ASO_G0225554_AD_04	HDF (neonatal)
DRR176752	CNhi10758_GCT.experiment	Targeted	NA	13	RP11-139H15.1	Homo sapiens	FANTOM6 project	PRJDB7993	16023407	47	CAGE	ASO_G0225973_AD_01	HDF (neonatal)
DRR176751	CNhi10758_GCG.experiment	Targeted	NA	14	LINC00517	Homo sapiens	FANTOM6 project	PRJDB7993	13517430	47	CAGE	ASO_G0259091_AD_04	HDF (neonatal)
DRR176750	CNhi10758_CAC.experiment	Experiment control	NA	14	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14146389	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176749	CNhi10758_ATG.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	8205374	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176748	CNhi10758_AGT.experiment	Targeted	NA	13	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18799556	47	CAGE	ASO_G0234608_AD_01	HDF (neonatal)
DRR176683	CNhi10634_ACC.experiment	Targeted	NA	12	ERVK13-1	Homo sapiens	FANTOM6 project	PRJDB7993	16750405	47	CAGE	ASO_G0260565_AD_06	HDF (neonatal)
DRR176682	CNhi10633_TAC.experiment	Targeted	NA	12	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	13894549	47	CAGE	ASO_G0230590_AD_03	HDF (neonatal)
DRR176681	CNhi10633_GCT.experiment	Targeted	NA	12	ERVK3-1	Homo sapiens	FANTOM6 project	PRJDB7993	14931286	47	CAGE	ASO_G0142396_AD_01	HDF (neonatal)
DRR176680	CNhi10633_GCG.experiment	Targeted	NA	12	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	13046523	47	CAGE	ASO_G0218510_AD_06	HDF (neonatal)
DRR176679	CNhi10633_CAC.experiment	Targeted	NA	12	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	15656972	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176678	CNhi10633_ATG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13781324	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176677	CNhi10633_AGT.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13191782	47	CAGE	ASO_G0246067_AD_09	HDF (neonatal)
DRR176676	CNhi10633_ACG.experiment	Targeted	NA	12	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	14220102	47	CAGE	ASO_G0226950_AD_07	HDF (neonatal)
DRR176611	CNhi10608_GCT.experiment	Targeted	NA	10	LINC00959	Homo sapiens	FANTOM6 project	PRJDB7993	13215357	47	CAGE	ASO_G0237489_09	HDF (neonatal)
DRR176610	CNhi10608_GCG.experiment	Targeted	NA	10	ZSCAN16-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	7948507	47	CAGE	ASO_G0269293_01	HDF (neonatal)
DRR176609	CNhi10608_CAC.experiment	Targeted	NA	10	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	14389504	47	CAGE	ASO_G0267886_03	HDF (neonatal)
DRR176608	CNhi10608_ATG.experiment	Targeted	NA	11	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9486804	47	CAGE	ASO_G0246067_01	HDF (neonatal)
DRR176607	CNhi10608_AGT.experiment	Targeted	NA	11	LINC00883	Homo sapiens	FANTOM6 project	PRJDB7993	11275756	47	CAGE	ASO_G0243701_AD_09	HDF (neonatal)
DRR176606	CNhi10608_ACG.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	10956232	47	CAGE	ASO_G0255121_02	HDF (neonatal)
DRR176605	CNhi10608_ACC.experiment	Experiment control	NA	10	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	10630460	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176604	CNhi10607_TAC.experiment	Experiment control	NA	10	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12814570	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176539	CNhi10587_CAC.experiment	Targeted	NA	9	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	11728992	47	CAGE	ASO_G0267419_02	HDF (neonatal)
DRR176538	CNhi10587_ATG.experiment	Experiment control	NA	9	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12599727	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176537	CNhi10587_AGT.experiment	Targeted	NA	9	AC009005.2	Homo sapiens	FANTOM6 project	PRJDB7993	8446828	47	CAGE	ASO_G0267751_07	HDF (neonatal)
DRR176536	CNhi10587_ACG.experiment	Experiment control	NA	9	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	11244674	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176535	CNhi10587_ACC.experiment	Targeted	NA	9	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	17399755	47	CAGE	ASO_G0267419_02	HDF (neonatal)
DRR176534	CNhi10586_TAC.experiment	Targeted	NA	9	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	12397936	47	CAGE	ASO_G0267248_02	HDF (neonatal)
DRR176533	CNhi10586_GCT.experiment	Targeted	NA	9	CTD-2162K18.5	Homo sapiens	FANTOM6 project	PRJDB7993	13818504	47	CAGE	ASO_G0267254_07	HDF (neonatal)
DRR176532	CNhi10586_CAC.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	11299449	47	CAGE	ASO_G0267213_10	HDF (neonatal)
DRR176467	CNhi10578_AGT.experiment	Targeted	NA	6	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15144036	47	CAGE	ASO_G0236618_07	HDF (neonatal)
DRR176466	CNhi10578_ACG.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12075213	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176465	CNhi10578_ACC.experiment	Targeted	NA	6	LINC00263	Homo sapiens	FANTOM6 project	PRJDB7993	14625012	47	CAGE	ASO_G0235823_03	HDF (neonatal)
DRR176464	CNhi10577_TAC.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	16395136	47	CAGE	ASO_G0235437_09	HDF (neonatal)
DRR176463	CNhi10577_GCT.experiment	Targeted	NA	6	RP11-693N9.2	Homo sapiens	FANTOM6 project	PRJDB7993	13356982	47	CAGE	ASO_G0235505_01	HDF (neonatal)
DRR176462	CNhi10577_GCG.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	15790272	47	CAGE	ASO_G0235437_06	HDF (neonatal)
DRR176461	CNhi10577_CAC.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	15628154	47	CAGE	ASO_G0235437_05	HDF (neonatal)
DRR176460	CNhi10577_ATG.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	13198192	47	CAGE	ASO_G0235437_09	HDF (neonatal)
DRR176395	CNhi10537_ACG.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13858935	47	CAGE	ASO_G0198468_03	HDF (neonatal)
DRR176394	CNhi10537_ACC.experiment	Targeted	NA	6	CTC-338M12.4	Homo sapiens	FANTOM6 project	PRJDB7993	13596462	47	CAGE	ASO_G0233937_05	HDF (neonatal)
DRR176393	CNhi10536_TAC.experiment	Targeted	NA	6	MAGI2-AS3	Homo sapiens	FANTOM6 project	PRJDB7993	14464102	47	CAGE	ASO_G0234456_04	HDF (neonatal)
DRR176392	CNhi10536_GCT.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17180713	47	CAGE	ASO_G0198468_01	HDF (neonatal)
DRR176391	CNhi10536_GCG.experiment	Targeted	NA	5	CATG00000079799.1	Homo sapiens	FANTOM6 project	PRJDB7993	9728130	47	CAGE	ASO_C0008586_03	HDF (neonatal)
DRR176390	CNhi10536_CAC.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11749411	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176389	CNhi10536_AGT.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11365544	47	CAGE	ASO_G0198468_03	HDF (neonatal)
DRR176388	CNhi10536_ACG.experiment	Targeted	NA	5	CATG00000016989.1	Homo sapiens	FANTOM6 project	PRJDB7993	11449770	47	CAGE	ASO_C0020443_03	HDF (neonatal)
DRR176323	CNhi10527_TAC.experiment	Targeted	NA	4	SUGT1P	Homo sapiens	FANTOM6 project	PRJDB7993	19369060	47	CAGE	ASO_G0226823_08	HDF (neonatal)
DRR176322	CNhi10527_GCT.experiment	Targeted	NA	5	CDKN2C	Homo sapiens	FANTOM6 project	PRJDB7993	17776122	47	CAGE	ASO_C0000830_02	HDF (neonatal)
DRR176321	CNhi10527_GCG.experiment	Targeted	NA	4	RP11-395B7.4	Homo sapiens	FANTOM6 project	PRJDB7993	13714212	47	CAGE	ASO_G0227053_04	HDF (neonatal)
DRR176320	CNhi10527_CAC.experiment	Targeted	NA	4	RP4-773A18.4	Homo sapiens	FANTOM6 project	PRJDB7993	18580280	47	CAGE	ASO_G0227811_06	HDF (neonatal)
DRR176319	CNhi10527_ATG.experiment	Targeted	NA	5	CATG00000020700.1	Homo sapiens	FANTOM6 project	PRJDB7993	15653322	47	CAGE	ASO_C0020984_09	HDF (neonatal)
DRR176318	CNhi10527_AGT.experiment	Targeted	NA	4	PCAT6	Homo sapiens	FANTOM6 project	PRJDB7993	18372099	47	CAGE	ASO_G0228288_01	HDF (neonatal)
DRR176317	CNhi10527_ACG.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18247767	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176316	CNhi10527_ACC.experiment	Targeted	NA	5	CDKN2C	Homo sapiens	FANTOM6 project	PRJDB7993	18047930	47	CAGE	ASO_C0000830_08	HDF (neonatal)
DRR176251	CNhi10495_GCT.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	12730601	47	CAGE	ASO_G0240875_04	HDF (neonatal)
DRR176250	CNhi10495_CAC.experiment	Targeted	NA	3	AC004980.7	Homo sapiens	FANTOM6 project	PRJDB7993	8280181	47	CAGE	ASO_G0205485_03	HDF (neonatal)
DRR176249	CNhi10495_ATG.experiment	Targeted	NA	3	AC007246.3	Homo sapiens	FANTOM6 project	PRJDB7993	10763090	47	CAGE	ASO_G0231312_02	HDF (neonatal)
DRR176248	CNhi10495_AGT.experiment	Targeted	NA	3	PRRT3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11403597	47	CAGE	ASO_G0230082_01	HDF (neonatal)
DRR176247	CNhi10495_ACG.experiment	Targeted	NA	3	CTD-2587H24.5	Homo sapiens	FANTOM6 project	PRJDB7993	10939951	47	CAGE	ASO_G0267577_03	HDF (neonatal)
DRR176246	CNhi10495_ACC.experiment	Targeted	NA	3	LINC00856	Homo sapiens	FANTOM6 project	PRJDB7993	12788498	47	CAGE	ASO_G0230417_02	HDF (neonatal)
DRR176245	CNhi10494_TAC.experiment	Targeted	NA	3	AC004980.7	Homo sapiens	FANTOM6 project	PRJDB7993	13771619	47	CAGE	ASO_G0205485_01	HDF (neonatal)
DRR176244	CNhi10494_GCT.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12477515	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176179	CNhi10486_CAC.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	15328070	47	CAGE	ASO_C0020672_07	HDF (neonatal)
DRR176178	CNhi10486_ATG.experiment	Targeted	NA	3	ZNF674-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14830624	47	CAGE	ASO_G0230844_01	HDF (neonatal)
DRR176177	CNhi10486_AGT.experiment	Targeted	NA	3	FBXL19-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15900573	47	CAGE	ASO_G0260852_02	HDF (neonatal)
DRR176176	CNhi10486_ACG.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11850730	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176175	CNhi10486_ACC.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	17017772	47	CAGE	ASO_G0240875_01	HDF (neonatal)
DRR176174	CNhi10477_TAC.experiment	Targeted	NA	2	RP11-150O12.1	Homo sapiens	FANTOM6 project	PRJDB7993	17106848	47	CAGE	ASO_C013368_01	HDF (neonatal)
DRR176173	CNhi10477_GCT.experiment	Targeted	NA	2	CATG00000108369.1	Homo sapiens	FANTOM6 project	PRJDB7993	17651172	47	CAGE	ASO_C014559_06	HDF (neonatal)
DRR176172	CNhi10477_GCG.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	15182075	47	CAGE	ASO_G0233901_02	HDF (neonatal)
DRR176107	CNhi10469_AGT.experiment	Targeted	NA	2	LINC00968	Homo sapiens	FANTOM6 project	PRJDB7993	13482789	47	CAGE	ASO_G0246430_03	HDF (neonatal)

DRR176106	CNhi10469_ACG.experiment	Targeted	NA	2	CTD-3131K8.2	Homo sapiens	FANTOM6 project	PRJDB7993	17628008	47	CAGE	ASO_G0269439_09	HDF (neonatal)
DRR176105	CNhi10469_ACC.experiment	Targeted	NA	2	BX322557.10	Homo sapiens	FANTOM6 project	PRJDB7993	20027503	47	CAGE	ASO_G0215447_01	HDF (neonatal)
DRR176104	CNhi10468_TAC.experiment	Targeted	NA	2	CATG00000089639.1	Homo sapiens	FANTOM6 project	PRJDB7993	24217388	47	CAGE	ASO_G0223811_06	HDF (neonatal)
DRR176103	CNhi10468_GCT.experiment	Targeted	NA	2	RP11-150O12.1	Homo sapiens	FANTOM6 project	PRJDB7993	18033165	47	CAGE	ASO_C013368_02	HDF (neonatal)
DRR176102	CNhi10468_GCG.experiment	Experiment control	NA	2	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	13340172	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176101	CNhi10468_CAC.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	15962914	47	CAGE	ASO_G0263072_05	HDF (neonatal)
DRR176100	CNhi10468_ATG.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	18863550	47	CAGE	ASO_G0233901_04	HDF (neonatal)
DRR177107	CNhi10835_ACG.experiment	Targeted	NA	18	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	17297127	47	CAGE	ASO_C0011632_AD_03	HDF (neonatal)
DRR177106	CNhi10835_ACC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	22721284	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR177105	CNhi10834_TAC.experiment	Targeted	NA	19	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	23083302	47	CAGE	ASO_G0237187_AD_08	HDF (neonatal)
DRR177104	CNhi10834_GCT.experiment	Targeted	NA	21	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	9506419	47	CAGE	ASO_G0180769_AD_03	HDF (neonatal)
DRR177103	CNhi10834_GCG.experiment	Targeted	NA	21	TMCC1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10323399	47	CAGE	ASO_G0271270_AD_10	HDF (neonatal)
DRR177102	CNhi10834_CAC.experiment	Targeted	NA	19	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	16179425	47	CAGE	ASO_G0245937_AD_02	HDF (neonatal)
DRR177101	CNhi10834_ATG.experiment	Targeted	NA	19	LINC00968	Homo sapiens	FANTOM6 project	PRJDB7993	22688373	47	CAGE	ASO_G0246430_AD_03	HDF (neonatal)
DRR177100	CNhi10834_AGT.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	11682214	47	CAGE	ASO_C0012015_AD_04	HDF (neonatal)
DRR177035	CNhi10818_ACC.experiment	Targeted	NA	20	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	4723849	47	CAGE	siRNA_n504056	HDF (neonatal)
DRR177034	CNhi10817_TAC.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	21757196	47	CAGE	siRNA_s32293	HDF (neonatal)
DRR177033	CNhi10817_GCT.experiment	Targeted	NA	20	PRRX1	Homo sapiens	FANTOM6 project	PRJDB7993	10102944	47	CAGE	siRNA_s10745	HDF (neonatal)
DRR177032	CNhi10817_GCG.experiment	Targeted	NA	17	FOXN3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12083637	47	CAGE	ASO_G0258920_AD_07	HDF (neonatal)
DRR177031	CNhi10817_CAC.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	19844065	47	CAGE	ASO_G0134153_POS_05	HDF (neonatal)
DRR177030	CNhi10817_ATG.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14060457	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177029	CNhi10817_AGT.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	12355057	47	CAGE	ASO_G0228630_POS_07	HDF (neonatal)
DRR177028	CNhi10817_ACG.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20891062	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176027	CNhi10457_ACC.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	20007183	47	CAGE	ASO_G0224577_01	HDF (neonatal)
DRR176026	CNhi10456_TAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23294421	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176025	CNhi10456_GCT.experiment	Targeted	NA	1	LINC00883	Homo sapiens	FANTOM6 project	PRJDB7993	37440	47	CAGE	ASO_G0243701_01	HDF (neonatal)
DRR176024	CNhi10456_GCG.experiment	Targeted	NA	1	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	17935999	47	CAGE	ASO_G0230590_05	HDF (neonatal)
DRR176023	CNhi10456_CAC.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	16500362	47	CAGE	ASO_G0226950_02	HDF (neonatal)
DRR176022	CNhi10456_ATG.experiment	Targeted	NA	1	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	22841354	47	CAGE	ASO_G0230590_06	HDF (neonatal)
DRR176021	CNhi10456_AGT.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	22896867	47	CAGE	ASO_G0253352_02	HDF (neonatal)
DRR176020	CNhi10456_ACG.experiment	Targeted	NA	1	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	19122181	47	CAGE	ASO_G0270141_05	HDF (neonatal)
DRR176963	CNhi10808_GCT.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16040232	47	CAGE	sgRNA_NC_gRNA2	HDF (neonatal)
DRR176962	CNhi10808_GCG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10798557	47	CAGE	sgRNA_NC	HDF (neonatal)
DRR176961	CNhi10808_CAC.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	10951182	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176960	CNhi10808_ATG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18657388	47	CAGE	sgRNA_dCas9	HDF (neonatal)
DRR176959	CNhi10808_AGT.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	18296607	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176958	CNhi10808_ACG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16340984	47	CAGE	sgRNA_NC_gRNA1	HDF (neonatal)
DRR176957	CNhi10808_ACC.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	14710450	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176956	CNhi10807_TAC.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	22091564	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176891	CNhi10790_CAC.experiment	Targeted	NA	16	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	17435624	47	CAGE	ASO_G0267248_AD_03	HDF (neonatal)
DRR176890	CNhi10790_ATG.experiment	Targeted	NA	16	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	18138614	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176889	CNhi10790_AGT.experiment	Targeted	NA	16	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	11112769	47	CAGE	ASO_G0267248_AD_03	HDF (neonatal)
DRR176888	CNhi10790_ACG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18258451	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176887	CNhi10790_ACC.experiment	Targeted	NA	15	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	24549007	47	CAGE	ASO_G0236618_AD_09	HDF (neonatal)
DRR176886	CNhi10789_TAC.experiment	Negative control	NA	17	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19085840	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176885	CNhi10789_GCT.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17965221	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176884	CNhi10789_GCG.experiment	Targeted	NA	15	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	15445531	47	CAGE	ASO_G0244625_AD_09	HDF (neonatal)
DRR176819	CNhi10767_AGT.experiment	Targeted	NA	14	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	12316424	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176818	CNhi10767_ACG.experiment	Negative control	NA	17	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15284019	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176817	CNhi10767_ACC.experiment	Targeted	NA	14	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	17597100	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176816	CNhi10766_TAC.experiment	Targeted	NA	14	RAD51-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	20107651	47	CAGE	ASO_G0245849_AD_07	HDF (neonatal)
DRR176815	CNhi10766_GCT.experiment	Targeted	NA	14	LINC00517	Homo sapiens	FANTOM6 project	PRJDB7993	14788123	47	CAGE	ASO_G0259091_AD_10	HDF (neonatal)
DRR176814	CNhi10766_GCG.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14774541	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176813	CNhi10766_CAC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14704305	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176812	CNhi10766_ATG.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18819813	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176747	CNhi10758_ACG.experiment	Targeted	NA	13	RP11-295G20.2	Homo sapiens	FANTOM6 project	PRJDB7993	19693852	47	CAGE	ASO_G0233461_AD_03	HDF (neonatal)
DRR176746	CNhi10758_ACC.experiment	Targeted	NA	13	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	20424485	47	CAGE	ASO_G0234608_AD_04	HDF (neonatal)
DRR176745	CNhi10757_TAC.experiment	Targeted	NA	14	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	20703281	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176744	CNhi10757_GCT.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	14477585	47	CAGE	ASO_G0261105_AD_06	HDF (neonatal)
DRR176743	CNhi10757_GCG.experiment	Experiment control	NA	13	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	10319149	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176742	CNhi10757_CAC.experiment	Targeted	NA	13	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	14472240	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176741	CNhi10757_ATG.experiment	Targeted	NA	13	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	21528387	47	CAGE	ASO_G0234608_AD_04	HDF (neonatal)
DRR176740	CNhi10757_AGT.experiment	Targeted	NA	13	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	16450408	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176675	CNhi10633_ACC.experiment	Targeted	NA	12	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18575231	47	CAGE	ASO_G0225733_AD_06	HDF (neonatal)
DRR176674	CNhi10632_TAC.experiment	Targeted	NA	12	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	16270762	47	CAGE	ASO_G0214548_AD_09	HDF (neonatal)
DRR176673	CNhi10632_GCT.experiment	Targeted	NA	12	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	12692593	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176672	CNhi10632_GCG.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	11500230	47	CAGE	ASO_G0256268_AD_07	HDF (neonatal)
DRR176671	CNhi10632_CAC.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14255046	47	CAGE	ASO_G0246067_AD_06	HDF (neonatal)
DRR176670	CNhi10632_AGT.experiment	Targeted	NA	12	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	13725236	47	CAGE	ASO_G0230590_AD_03	HDF (neonatal)
DRR176669	CNhi10632_ACG.experiment	Targeted	NA	12	ERVK13-1	Homo sapiens	FANTOM6 project	PRJDB7993	13073268	47	CAGE	ASO_G0260565_AD_08	HDF (neonatal)
DRR176668	CNhi10632_ACC.experiment	Targeted	NA	12	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	16724551	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176603	CNhi10607_GCT.experiment	Targeted	NA	10	RP13-463N16.6	Homo sapiens	FANTOM6 project	PRJDB7993	11747961	47	CAGE	ASO_G0242147_07	HDF (neonatal)
DRR176602	CNhi10607_GCG.experiment	Targeted	NA	10	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10310715	47	CAGE	ASO_G0237187_03	HDF (neonatal)
DRR176601	CNhi10607_CAC.experiment	Targeted	NA	10	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	12440397	47	CAGE	ASO_G0244625_04	HDF (neonatal)
DRR176600	CNhi10607_ATG.experiment	Experiment control	NA	10	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	10650016	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176599	CNhi10607_AGT.experiment	Negative control	NA	11	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12455292	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176598	CNhi10607_ACG.experiment	Targeted	NA	10	RP11-660L16.2	Homo sapiens	FANTOM6 project	PRJDB7993	13784084	47	CAGE	ASO_G0254682_06	HDF (neonatal)
DRR176597	CNhi10607_ACC.experiment	Negative control	NA	11	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13823738	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176596	CNhi10606_TAC.experiment	Targeted	NA	10	RP11-660L16.2	Homo sapiens	FANTOM6 project	PRJDB7993	9365743	47	CAGE	ASO_G0254682_02	HDF (neonatal)
DRR176531	CNhi10586_ATG.experiment	Targeted	NA	9	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	11254646	47	CAGE	ASO_G0267248_02	HDF (neonatal)

DRR176530	CNhi10586_AGT.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	10734435	47	CAGE	ASO_G0267213_10	HDF (neonatal)
DRR176529	CNhi10586_ACG.experiment	Targeted	NA	9	CTD-2162K18.5	Homo sapiens	FANTOM6 project	PRJDB7993	16065686	47	CAGE	ASO_G0267254_07	HDF (neonatal)
DRR176528	CNhi10586_ACC.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	11328455	47	CAGE	ASO_G0267213_06	HDF (neonatal)
DRR176527	CNhi10585_TAC.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	13886267	47	CAGE	ASO_G0267213_03	HDF (neonatal)
DRR176526	CNhi10585_GCT.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	11443613	47	CAGE	ASO_G0267213_06	HDF (neonatal)
DRR176525	CNhi10585_GCG.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	14293304	47	CAGE	ASO_G0267213_01	HDF (neonatal)
DRR176524	CNhi10585_CAC.experiment	Targeted	NA	9	RP13-20L14.6	Homo sapiens	FANTOM6 project	PRJDB7993	13906214	47	CAGE	ASO_G0265458_10	HDF (neonatal)
DRR176459	CNhi10577_AGT.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	12766602	47	CAGE	ASO_G0235437_06	HDF (neonatal)
DRR176458	CNhi10577_ACG.experiment	Targeted	NA	6	RP11-693N9.2	Homo sapiens	FANTOM6 project	PRJDB7993	12342944	47	CAGE	ASO_G0235505_01	HDF (neonatal)
DRR176457	CNhi10577_ACC.experiment	Targeted	NA	6	RP11-357C3.3	Homo sapiens	FANTOM6 project	PRJDB7993	10234217	47	CAGE	ASO_G0235437_05	HDF (neonatal)
DRR176456	CNhi10544_TAC.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14941621	47	CAGE	ASO_G0198468_07	HDF (neonatal)
DRR176455	CNhi10544_GCT.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	7716218	47	CAGE	ASO_G0233137_02	HDF (neonatal)
DRR176454	CNhi10544_GCG.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	10388734	47	CAGE	ASO_G0233137_02	HDF (neonatal)
DRR176453	CNhi10544_CAC.experiment	Targeted	NA	6	AC012146.7	Homo sapiens	FANTOM6 project	PRJDB7993	12177645	47	CAGE	ASO_G0234327_07	HDF (neonatal)
DRR176452	CNhi10544_ATG.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	12219152	47	CAGE	ASO_C0008202_04	HDF (neonatal)
DRR176387	CNhi10536_ACC.experiment	Targeted	NA	6	RP11-422J8.1	Homo sapiens	FANTOM6 project	PRJDB7993	10945743	47	CAGE	ASO_G0233621_05	HDF (neonatal)
DRR176386	CNhi10535_TAC.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	18809659	47	CAGE	ASO_G0233137_04	HDF (neonatal)
DRR176385	CNhi10535_GCT.experiment	Targeted	NA	5	RP11-296O14.3	Homo sapiens	FANTOM6 project	PRJDB7993	18022018	47	CAGE	ASO_G0203739_10	HDF (neonatal)
DRR176384	CNhi10535_GCG.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	12697575	47	CAGE	ASO_C0008202_04	HDF (neonatal)
DRR176383	CNhi10535_CAC.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	14539897	47	CAGE	ASO_G0233137_05	HDF (neonatal)
DRR176382	CNhi10535_ATG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12941415	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176381	CNhi10535_AGT.experiment	Targeted	NA	6	MAGI2-AS3	Homo sapiens	FANTOM6 project	PRJDB7993	13764596	47	CAGE	ASO_G0234456_01	HDF (neonatal)
DRR176380	CNhi10535_ACG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14618235	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176315	CNhi10526_TAC.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17536993	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176314	CNhi10526_GCT.experiment	Targeted	NA	4	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	20919134	47	CAGE	ASO_G0225554_02	HDF (neonatal)
DRR176313	CNhi10526_GCG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11868128	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176312	CNhi10526_CAC.experiment	Targeted	NA	4	RP1-152L7.5	Homo sapiens	FANTOM6 project	PRJDB7993	16181406	47	CAGE	ASO_G0216775_03	HDF (neonatal)
DRR176311	CNhi10526_ATG.experiment	Targeted	NA	4	BOLA3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17261984	47	CAGE	ASO_G0225439_06	HDF (neonatal)
DRR176310	CNhi10526_AGT.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18234464	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176309	CNhi10526_ACG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15439481	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176308	CNhi10526_ACC.experiment	Targeted	NA	4	RP11-139H15.1	Homo sapiens	FANTOM6 project	PRJDB7993	15294128	47	CAGE	ASO_G0225973_10	HDF (neonatal)
DRR176243	CNhi10494_GCG.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	11684910	47	CAGE	ASO_G0204054_10	HDF (neonatal)
DRR176242	CNhi10494_CAC.experiment	Targeted	NA	3	ZNF131	Homo sapiens	FANTOM6 project	PRJDB7993	11424694	47	CAGE	ASO_C0008543_05	HDF (neonatal)
DRR176241	CNhi10494_ATG.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	16564637	47	CAGE	ASO_G0240875_02	HDF (neonatal)
DRR176240	CNhi10494_AGT.experiment	Targeted	NA	3	AC091729.9	Homo sapiens	FANTOM6 project	PRJDB7993	14372407	47	CAGE	ASO_G0229043_07	HDF (neonatal)
DRR176239	CNhi10494_ACG.experiment	Targeted	NA	3	FBXL19-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13696451	47	CAGE	ASO_G0260852_02	HDF (neonatal)
DRR176238	CNhi10494_ACC.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	11262911	47	CAGE	ASO_G0234171_09	HDF (neonatal)
DRR176237	CNhi10493_TAC.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	16623164	47	CAGE	ASO_G0204054_01	HDF (neonatal)
DRR176236	CNhi10493_GCT.experiment	Targeted	NA	3	TTN-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15248522	47	CAGE	ASO_G0237298_01	HDF (neonatal)
DRR176171	CNhi10477_CAC.experiment	Targeted	NA	2	CATG00000108369.1	Homo sapiens	FANTOM6 project	PRJDB7993	19517145	47	CAGE	ASO_C014559_06	HDF (neonatal)
DRR176170	CNhi10477_ATG.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	18814708	47	CAGE	ASO_G0263072_02	HDF (neonatal)
DRR176169	CNhi10477_AGT.experiment	Targeted	NA	2	A1BG-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16139368	47	CAGE	ASO_G0268895_01	HDF (neonatal)
DRR176168	CNhi10477_ACG.experiment	Targeted	NA	2	TRAM2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14223437	47	CAGE	ASO_G0225791_05	HDF (neonatal)
DRR176167	CNhi10477_ACC.experiment	Targeted	NA	2	RP11-458D21.1	Homo sapiens	FANTOM6 project	PRJDB7993	19592447	47	CAGE	ASO_G0233396_02	HDF (neonatal)
DRR176166	CNhi10476_TAC.experiment	Targeted	NA	2	RP11-195F19.9	Homo sapiens	FANTOM6 project	PRJDB7993	19249934	47	CAGE	ASO_G0230074_05	HDF (neonatal)
DRR176165	CNhi10476_GCT.experiment	Targeted	NA	2	CATG00000089639.1	Homo sapiens	FANTOM6 project	PRJDB7993	18054700	47	CAGE	ASO_G0223811_06	HDF (neonatal)
DRR176164	CNhi10476_GCG.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13897619	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176099	CNhi10468_AGT.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	20087658	47	CAGE	ASO_G0263072_01	HDF (neonatal)
DRR176098	CNhi10468_ACG.experiment	Targeted	NA	2	AC005592.2	Homo sapiens	FANTOM6 project	PRJDB7993	17257014	47	CAGE	ASO_G0231185_02	HDF (neonatal)
DRR176097	CNhi10468_ACC.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	19886678	47	CAGE	ASO_G0233901_05	HDF (neonatal)
DRR176096	CNhi10467_TAC.experiment	Targeted	NA	2	AC005592.2	Homo sapiens	FANTOM6 project	PRJDB7993	26105456	47	CAGE	ASO_G0231185_02	HDF (neonatal)
DRR177123	CNhi10837_ACG.experiment	Targeted	NA	21	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	15907282	47	CAGE	ASO_G0229852_AD_01	HDF (neonatal)
DRR177122	CNhi10837_ACC.experiment	Targeted	NA	18	ZNF131	Homo sapiens	FANTOM6 project	PRJDB7993	14641374	47	CAGE	ASO_C0008543_AD_10	HDF (neonatal)
DRR177121	CNhi10836_TAC.experiment	Targeted	NA	19	NNT-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	19425777	47	CAGE	ASO_G0248092_AD_10	HDF (neonatal)
DRR177120	CNhi10836_GCT.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13591010	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR177119	CNhi10836_GCG.experiment	Targeted	NA	21	AC091729.9	Homo sapiens	FANTOM6 project	PRJDB7993	13478630	47	CAGE	ASO_G0229043_AD_04	HDF (neonatal)
DRR177118	CNhi10836_CAC.experiment	Targeted	NA	19	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13208980	47	CAGE	ASO_G0237187_AD_01	HDF (neonatal)
DRR177117	CNhi10836_ATG.experiment	Experiment control	NA	18	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17019114	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR177116	CNhi10836_AGT.experiment	Targeted	NA	19	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	16072090	47	CAGE	ASO_G0245213_AD_04	HDF (neonatal)
DRR177051	CNhi10820_ACC.experiment	Targeted	NA	20	SNRPD3	Homo sapiens	FANTOM6 project	PRJDB7993	18018036	47	CAGE	siRNA_s13234	HDF (neonatal)
DRR177050	CNhi10819_TAC.experiment	Targeted	NA	20	EXOSC10	Homo sapiens	FANTOM6 project	PRJDB7993	21196719	47	CAGE	siRNA_s10737	HDF (neonatal)
DRR177049	CNhi10819_GCT.experiment	Targeted	NA	20	EXOSC10	Homo sapiens	FANTOM6 project	PRJDB7993	11648131	47	CAGE	siRNA_s10738	HDF (neonatal)
DRR177048	CNhi10819_GCG.experiment	Targeted	NA	21	CHAF1B	Homo sapiens	FANTOM6 project	PRJDB7993	12223552	47	CAGE	siRNA_s15706	HDF (neonatal)
DRR177047	CNhi10819_CAC.experiment	Targeted	NA	21	CHAF1A	Homo sapiens	FANTOM6 project	PRJDB7993	12620612	47	CAGE	siRNA_s19500	HDF (neonatal)
DRR177046	CNhi10819_ATG.experiment	Targeted	NA	21	CHAF1B	Homo sapiens	FANTOM6 project	PRJDB7993	25113885	47	CAGE	siRNA_s15705	HDF (neonatal)
DRR177045	CNhi10819_AGT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15330368	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR177044	CNhi10819_ACG.experiment	Targeted	NA	20	EXOSC3	Homo sapiens	FANTOM6 project	PRJDB7993	17316875	47	CAGE	siRNA_s27231	HDF (neonatal)
DRR176043	CNhi10459_ACC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13965430	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176042	CNhi10458_TAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16122752	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176041	CNhi10458_GCT.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	19033915	47	CAGE	ASO_G0234546_02	HDF (neonatal)
DRR176040	CNhi10458_GCG.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12105500	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176039	CNhi10458_CAC.experiment	Targeted	NA	1	LINC00702	Homo sapiens	FANTOM6 project	PRJDB7993	14141968	47	CAGE	ASO_G0233117_02	HDF (neonatal)
DRR176038	CNhi10458_ATG.experiment	Targeted	NA	1	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	16795461	47	CAGE	ASO_G0163364_06	HDF (neonatal)
DRR176037	CNhi10458_AGT.experiment	Targeted	NA	1	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	19406130	47	CAGE	ASO_G0224597_06	HDF (neonatal)
DRR176036	CNhi10458_ACG.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	22110185	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176979	CNhi10810_TAC.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	23995884	47	CAGE	ASO_G0228630_POS_06	HDF (neonatal)
DRR176978	CNhi10810_GCT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12677649	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176977	CNhi10810_CAC.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11160269	47	CAGE	siRNA_n509345	HDF (neonatal)
DRR176976	CNhi10810_ATG.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21539518	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176975	CNhi10810_AGT.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12667815	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR176974	CNhi10810_ACG.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	21106543	47	CAGE	ASO_G0228630_POS_07	HDF (neonatal)

DRR176973	CNhi10810_ACC.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	19852143	47	CAGE	siRNA_ADAAYU4	HDF (neonatal)
DRR176972	CNhi10809_TAC.experiment	Targeted	NA	22	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	18042294	47	CAGE	sgRNA_blast5_LINC00862	HDF (neonatal)
DRR176095	CNhi10467_GCT.experiment	Targeted	NA	2	CATG00000089639.1	Homo sapiens	FANTOM6 project	PRJDB7993	14925711	47	CAGE	ASO_G0223811_04	HDF (neonatal)
DRR176094	CNhi10467_GCG.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13869436	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176093	CNhi10467_CAC.experiment	Targeted	NA	2	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	16493655	47	CAGE	ASO_G0229852_05	HDF (neonatal)
DRR176092	CNhi10467_ATG.experiment	Targeted	NA	2	NEAT1_1	Homo sapiens	FANTOM6 project	PRJDB7993	17532467	47	CAGE	ASO_NEAT1_1	HDF (neonatal)
DRR177099	CNhi10834_ACG.experiment	Targeted	NA	19	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	17620895	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR177098	CNhi10834_ACC.experiment	Targeted	NA	18	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	19749552	47	CAGE	ASO_C0011632_AD_01	HDF (neonatal)
DRR177097	CNhi10833_TAC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	24301622	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR177096	CNhi10833_GCT.experiment	Targeted	NA	19	MKLN1-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	12627254	47	CAGE	ASO_G0236753_AD_01	HDF (neonatal)
DRR177095	CNhi10833_CAC.experiment	Targeted	NA	19	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	14096731	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR177094	CNhi10833_ATG.experiment	Targeted	NA	19	U52111.14	Homo sapiens	FANTOM6 project	PRJDB7993	20193999	47	CAGE	ASO_G0232725_AD_10	HDF (neonatal)
DRR177093	CNhi10833_AGT.experiment	Targeted	NA	19	RP11-539L10.3	Homo sapiens	FANTOM6 project	PRJDB7993	13729631	47	CAGE	ASO_G0251580_AD_01	HDF (neonatal)
DRR177092	CNhi10833_ACG.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	20012008	47	CAGE	ASO_C0012015_AD_02	HDF (neonatal)
DRR177027	CNhi10817_ACC.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	19349468	47	CAGE	ASO_G0240498_POS_04	HDF (neonatal)
DRR177026	CNhi10816_TAC.experiment	Targeted	NA	20	PRRX1	Homo sapiens	FANTOM6 project	PRJDB7993	16908584	47	CAGE	ASO_G0116132_POS_09	HDF (neonatal)
DRR177025	CNhi10816_GCT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14536073	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177024	CNhi10816_GCG.experiment	Targeted	NA	21	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11668511	47	CAGE	ASO_G0246985_AD_04	HDF (neonatal)
DRR177023	CNhi10816_CAC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13698916	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177022	CNhi10816_AGT.experiment	Targeted	NA	21	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	15472147	47	CAGE	ASO_G0225554_AD_06	HDF (neonatal)
DRR177021	CNhi10816_ACG.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	17175331	47	CAGE	siRNA_s32293	HDF (neonatal)
DRR177020	CNhi10816_ACC.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19313579	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR176019	CNhi10456_ACC.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	18721025	47	CAGE	ASO_G0253352_01	HDF (neonatal)
DRR176018	CNhi10455_TAC.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	20519020	47	CAGE	ASO_G0224577_05	HDF (neonatal)
DRR176017	CNhi10455_GCT.experiment	Targeted	NA	1	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	15467122	47	CAGE	ASO_G0250742_01	HDF (neonatal)
DRR176016	CNhi10455_GCG.experiment	Targeted	NA	1	LINC00938	Homo sapiens	FANTOM6 project	PRJDB7993	13337520	47	CAGE	ASO_G0273015_05	HDF (neonatal)
DRR176015	CNhi10455_CAC.experiment	Targeted	NA	1	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	13079333	47	CAGE	ASO_G0230590_02	HDF (neonatal)
DRR176014	CNhi10455_AGT.experiment	Targeted	NA	1	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	18755851	47	CAGE	ASO_G0229847_03	HDF (neonatal)
DRR176013	CNhi10455_ACG.experiment	Targeted	NA	1	SNHG18	Homo sapiens	FANTOM6 project	PRJDB7993	14574960	47	CAGE	ASO_G0250786_04	HDF (neonatal)
DRR176012	CNhi10455_ACC.experiment	Targeted	NA	1	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14714264	47	CAGE	ASO_G0225733_04	HDF (neonatal)
DRR176955	CNhi10807_GCT.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	11433567	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176954	CNhi10807_GCG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11670939	47	CAGE	sgRNA_NC_gRNA1	HDF (neonatal)
DRR176953	CNhi10807_CAC.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15710645	47	CAGE	sgRNA_dCas9	HDF (neonatal)
DRR176952	CNhi10807_ATG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11254028	47	CAGE	sgRNA_NC_gRNA2	HDF (neonatal)
DRR176951	CNhi10807_AGT.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17996960	47	CAGE	sgRNA_blast5_control	HDF (neonatal)
DRR176950	CNhi10807_ACG.experiment	Targeted	NA	22	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	15088601	47	CAGE	sgRNA_blast5_LINC00630	HDF (neonatal)
DRR176949	CNhi10807_ACC.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17414905	47	CAGE	sgRNA_NC	HDF (neonatal)
DRR176948	CNhi10805_TAC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18654719	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176883	CNhi10789_CAC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14216151	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176882	CNhi10789_ATG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23355688	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176881	CNhi10789_AGT.experiment	Targeted	NA	16	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	15157624	47	CAGE	ASO_G0267248_AD_07	HDF (neonatal)
DRR176880	CNhi10789_ACG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20850749	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176879	CNhi10789_ACC.experiment	Targeted	NA	15	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	20924093	47	CAGE	ASO_G0237854_AD_02	HDF (neonatal)
DRR176878	CNhi10788_TAC.experiment	Targeted	NA	15	LINC00511	Homo sapiens	FANTOM6 project	PRJDB7993	17561858	47	CAGE	ASO_G0227036_AD_07	HDF (neonatal)
DRR176877	CNhi10788_GCT.experiment	Targeted	NA	15	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	15564975	47	CAGE	ASO_G0219665_AD_04	HDF (neonatal)
DRR176876	CNhi10788_GCG.experiment	Targeted	NA	15	AC007879.7	Homo sapiens	FANTOM6 project	PRJDB7993	15281196	47	CAGE	ASO_G0229647_AD_09	HDF (neonatal)
DRR176811	CNhi10766_AGT.experiment	Targeted	NA	14	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	16942489	47	CAGE	ASO_G0261573_AD_04	HDF (neonatal)
DRR176810	CNhi10766_ACG.experiment	Targeted	NA	14	CTD-2651B20.3	Homo sapiens	FANTOM6 project	PRJDB7993	16584690	47	CAGE	ASO_G0259520_AD_04	HDF (neonatal)
DRR176809	CNhi10766_ACC.experiment	Targeted	NA	13	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	20060022	47	CAGE	ASO_G0214548_AD_06	HDF (neonatal)
DRR176808	CNhi10765_TAC.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21301310	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176807	CNhi10765_GCT.experiment	Targeted	NA	14	CTD-2651B20.3	Homo sapiens	FANTOM6 project	PRJDB7993	14792847	47	CAGE	ASO_G0259520_AD_04	HDF (neonatal)
DRR176806	CNhi10765_GCG.experiment	Targeted	NA	13	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	11939892	47	CAGE	ASO_G0225554_AD_06	HDF (neonatal)
DRR176805	CNhi10765_CAC.experiment	Negative control	NA	17	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13794124	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176804	CNhi10765_ATG.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20044117	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176739	CNhi10757_ACG.experiment	Targeted	NA	17	RP11-611E13.2	Homo sapiens	FANTOM6 project	PRJDB7993	19425424	47	CAGE	ASO_G0257815_AD_03	HDF (neonatal)
DRR176738	CNhi10757_ACC.experiment	Targeted	NA	14	RP5-886K2.3	Homo sapiens	FANTOM6 project	PRJDB7993	16394804	47	CAGE	ASO_G0236810_AD_06	HDF (neonatal)
DRR176737	CNhi10640_TAC.experiment	Experiment control	NA	12	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15512261	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176736	CNhi10640_GCT.experiment	Targeted	NA	12	ERVK13-1	Homo sapiens	FANTOM6 project	PRJDB7993	14044030	47	CAGE	ASO_G0260565_AD_08	HDF (neonatal)
DRR176735	CNhi10640_GCG.experiment	Targeted	NA	12	TP53TG1	Homo sapiens	FANTOM6 project	PRJDB7993	12132651	47	CAGE	ASO_G0182165_AD_04	HDF (neonatal)
DRR176734	CNhi10640_CAC.experiment	Targeted	NA	12	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	14718914	47	CAGE	ASO_G0253352_AD_08	HDF (neonatal)
DRR176733	CNhi10640_ATG.experiment	Targeted	NA	12	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	11278052	47	CAGE	ASO_G0214548_AD_09	HDF (neonatal)
DRR176732	CNhi10640_AGT.experiment	Targeted	NA	12	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	11112329	47	CAGE	ASO_G0230590_AD_02	HDF (neonatal)
DRR176667	CNhi10631_TAC.experiment	Targeted	NA	12	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	15599940	47	CAGE	ASO_G0224577_AD_05	HDF (neonatal)
DRR176666	CNhi10631_GCT.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	12547637	47	CAGE	ASO_G0256268_AD_07	HDF (neonatal)
DRR176665	CNhi10631_GCG.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11841344	47	CAGE	ASO_G0246067_AD_04	HDF (neonatal)
DRR176664	CNhi10631_CAC.experiment	Targeted	NA	12	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	15838681	47	CAGE	ASO_G0224597_AD_04	HDF (neonatal)
DRR176663	CNhi10631_ATG.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15802577	47	CAGE	ASO_G0246067_AD_06	HDF (neonatal)
DRR176662	CNhi10631_AGT.experiment	Targeted	NA	12	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11566342	47	CAGE	ASO_G0225733_AD_06	HDF (neonatal)
DRR176661	CNhi10631_ACG.experiment	Targeted	NA	12	DNM3OS	Homo sapiens	FANTOM6 project	PRJDB7993	13164199	47	CAGE	ASO_G0230630_AD_10	HDF (neonatal)
DRR176660	CNhi10631_ACC.experiment	Targeted	NA	12	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	16237062	47	CAGE	ASO_G0250742_AD_05	HDF (neonatal)
DRR176595	CNhi10606_GCT.experiment	Targeted	NA	10	SBF2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14311399	47	CAGE	ASO_G0246273_02	HDF (neonatal)
DRR176594	CNhi10606_GCG.experiment	Targeted	NA	10	RP11-660L16.2	Homo sapiens	FANTOM6 project	PRJDB7993	10244953	47	CAGE	ASO_G0254682_02	HDF (neonatal)
DRR176593	CNhi10606_CAC.experiment	Targeted	NA	10	SRP14-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9740852	47	CAGE	ASO_G0248508_10	HDF (neonatal)
DRR176592	CNhi10606_ATG.experiment	Targeted	NA	11	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9542937	47	CAGE	ASO_G0246067_AD_04	HDF (neonatal)
DRR176591	CNhi10606_AGT.experiment	Targeted	NA	10	CKMT2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13409484	47	CAGE	ASO_G0247572_09	HDF (neonatal)
DRR176590	CNhi10606_ACG.experiment	Targeted	NA	10	RP11-660L16.2	Homo sapiens	FANTOM6 project	PRJDB7993	13362869	47	CAGE	ASO_G0254682_06	HDF (neonatal)
DRR176589	CNhi10606_ACC.experiment	Targeted	NA	10	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	10561558	47	CAGE	ASO_G0269834_02	HDF (neonatal)
DRR176588	CNhi10605_TAC.experiment	Targeted	NA	11	LINC00938	Homo sapiens	FANTOM6 project	PRJDB7993	16070602	47	CAGE	ASO_G0273015_AD_10	HDF (neonatal)
DRR176523	CNhi10585_ATG.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	11458291	47	CAGE	ASO_G0267213_01	HDF (neonatal)
DRR176522	CNhi10585_AGT.experiment	Targeted	NA	9	RP13-20L14.6	Homo sapiens	FANTOM6 project	PRJDB7993	12008346	47	CAGE	ASO_G0265458_10	HDF (neonatal)
DRR176521	CNhi10585_ACG.experiment	Targeted	NA	9	AC007773.2	Homo sapiens	FANTOM6 project	PRJDB7993	12340199	47	CAGE	ASO_G0267213_03	HDF (neonatal)
DRR176520	CNhi10585_ACC.experiment	Targeted	NA	9	RP11-6N17.4	Homo sapiens	FANTOM6 project	PRJDB7993	14121901	47	CAGE	ASO_G0264920_06	HDF (neonatal)

DRR176519	CNhi10584_TAC.experiment	Targeted	NA	9	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	13909884	47	CAGE	ASO_G0263753_01	HDF (neonatal)
DRR176518	CNhi10584_GCT.experiment	Targeted	NA	9	RP11-6N17.4	Homo sapiens	FANTOM6 project	PRJDB7993	11566175	47	CAGE	ASO_G0264920_06	HDF (neonatal)
DRR176517	CNhi10584_GCG.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	11983984	47	CAGE	ASO_G0262468_07	HDF (neonatal)
DRR176516	CNhi10584_CAC.experiment	Targeted	NA	9	RP11-95P2.1	Homo sapiens	FANTOM6 project	PRJDB7993	17721134	47	CAGE	ASO_G0262468_04	HDF (neonatal)
DRR176451	CNhi10544_AGT.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12690095	47	CAGE	ASO_G0186615_09	HDF (neonatal)
DRR176450	CNhi10544_ACG.experiment	Targeted	NA	6	RP11-422J8.1	Homo sapiens	FANTOM6 project	PRJDB7993	12876174	47	CAGE	ASO_G0233621_01	HDF (neonatal)
DRR176449	CNhi10544_ACC.experiment	Targeted	NA	5	CATG00000090305.1	Homo sapiens	FANTOM6 project	PRJDB7993	14512776	47	CAGE	ASO_C0011140_02	HDF (neonatal)
DRR176907	CNhi10792_GCG.experiment	Targeted	NA	16	AC009005.2	Homo sapiens	FANTOM6 project	PRJDB7993	15652189	47	CAGE	ASO_G0267751_AD_02	HDF (neonatal)
DRR176906	CNhi10792_CAC.experiment	Targeted	NA	15	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	14684033	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176905	CNhi10792_ATG.experiment	Targeted	NA	16	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	21340913	47	CAGE	ASO_G0267886_AD_04	HDF (neonatal)
DRR176904	CNhi10792_AGT.experiment	Targeted	NA	15	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	19131885	47	CAGE	ASO_G0237854_AD_04	HDF (neonatal)
DRR176903	CNhi10792_ACG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	22084137	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176902	CNhi10792_ACC.experiment	Targeted	NA	16	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	22040064	47	CAGE	ASO_G0267419_AD_06	HDF (neonatal)
DRR176901	CNhi10791_TAC.experiment	Targeted	NA	15	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	20556065	47	CAGE	ASO_G0236618_AD_07	HDF (neonatal)
DRR176900	CNhi10791_GCT.experiment	Targeted	NA	16	RP13-20L14.6	Homo sapiens	FANTOM6 project	PRJDB7993	16491490	47	CAGE	ASO_G0265458_AD_03	HDF (neonatal)
DRR176835	CNhi10783_ATG.experiment	Targeted	NA	16	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	20653423	47	CAGE	ASO_G0267419_AD_04	HDF (neonatal)
DRR176834	CNhi10783_AGT.experiment	Targeted	NA	17	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	16016295	47	CAGE	ASO_G0272888_AD_10	HDF (neonatal)
DRR176833	CNhi10783_ACG.experiment	Targeted	NA	17	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	22688667	47	CAGE	ASO_G0272888_AD_10	HDF (neonatal)
DRR176832	CNhi10783_ACC.experiment	Targeted	NA	16	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	20257377	47	CAGE	ASO_G0267886_AD_04	HDF (neonatal)
DRR176831	CNhi10782_TAC.experiment	Targeted	NA	17	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	26329098	47	CAGE	ASO_G0269834_AD_06	HDF (neonatal)
DRR176830	CNhi10782_GCT.experiment	Targeted	NA	15	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	15740880	47	CAGE	ASO_G0237854_AD_02	HDF (neonatal)
DRR176829	CNhi10782_GCG.experiment	Targeted	NA	16	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	15907737	47	CAGE	ASO_G0263753_AD_01	HDF (neonatal)
DRR176828	CNhi10782_CAC.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15353713	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176763	CNhi10760_ACG.experiment	Targeted	NA	14	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	17101439	47	CAGE	ASO_G0261573_AD_06	HDF (neonatal)
DRR176762	CNhi10760_ACC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20527193	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176761	CNhi10759_TAC.experiment	Targeted	NA	14	LINC00959	Homo sapiens	FANTOM6 project	PRJDB7993	23080464	47	CAGE	ASO_G0237489_AD_01	HDF (neonatal)
DRR176760	CNhi10759_GCT.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	16271857	47	CAGE	ASO_G0261105_AD_05	HDF (neonatal)
DRR176759	CNhi10759_GCG.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	12531909	47	CAGE	ASO_G0261105_AD_05	HDF (neonatal)
DRR176758	CNhi10759_CAC.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16338392	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176757	CNhi10759_ATG.experiment	Targeted	NA	13	RP11-137L10.6	Homo sapiens	FANTOM6 project	PRJDB7993	13426352	47	CAGE	ASO_G0221817_AD_08	HDF (neonatal)
DRR176756	CNhi10759_AGT.experiment	Targeted	NA	14	CTD-2651B20.3	Homo sapiens	FANTOM6 project	PRJDB7993	16115894	47	CAGE	ASO_G0259520_AD_08	HDF (neonatal)
DRR176691	CNhi10635_ACC.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15891026	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176690	CNhi10634_TAC.experiment	Targeted	NA	12	SNHG18	Homo sapiens	FANTOM6 project	PRJDB7993	17051215	47	CAGE	ASO_G0250786_AD_10	HDF (neonatal)
DRR176689	CNhi10634_GCT.experiment	Targeted	NA	12	DNM3OS	Homo sapiens	FANTOM6 project	PRJDB7993	12977795	47	CAGE	ASO_G0230630_AD_10	HDF (neonatal)
DRR176688	CNhi10634_GCG.experiment	Targeted	NA	12	SNHG18	Homo sapiens	FANTOM6 project	PRJDB7993	16568914	47	CAGE	ASO_G0250786_AD_10	HDF (neonatal)
DRR176687	CNhi10634_CAC.experiment	Targeted	NA	12	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	14583182	47	CAGE	ASO_G0250742_AD_05	HDF (neonatal)
DRR176686	CNhi10634_ATG.experiment	Targeted	NA	12	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	14043996	47	CAGE	ASO_G0229847_AD_04	HDF (neonatal)
DRR176685	CNhi10634_AGT.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12568153	47	CAGE	ASO_G0246067_AD_09	HDF (neonatal)
DRR176684	CNhi10634_ACG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13648288	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176619	CNhi10609_GCT.experiment	Targeted	NA	10	LINC00959	Homo sapiens	FANTOM6 project	PRJDB7993	12569837	47	CAGE	ASO_G0237489_09	HDF (neonatal)
DRR176618	CNhi10609_GCG.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	9801806	47	CAGE	ASO_G0255121_02	HDF (neonatal)
DRR176617	CNhi10609_CAC.experiment	Negative control	NA	11	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13965835	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176616	CNhi10609_ATG.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	9490839	47	CAGE	ASO_G0255121_03	HDF (neonatal)
DRR176615	CNhi10609_AGT.experiment	Targeted	NA	10	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	11403080	47	CAGE	ASO_G0267886_03	HDF (neonatal)
DRR176614	CNhi10609_ACG.experiment	Targeted	NA	10	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9651859	47	CAGE	ASO_G0237187_01	HDF (neonatal)
DRR176613	CNhi10609_ACC.experiment	Targeted	NA	10	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	12804293	47	CAGE	ASO_G0245937_01	HDF (neonatal)
DRR176612	CNhi10608_TAC.experiment	Targeted	NA	11	LINC00938	Homo sapiens	FANTOM6 project	PRJDB7993	13123402	47	CAGE	ASO_G0273015_05	HDF (neonatal)
DRR176547	CNhi10588_GCG.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9928893	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176546	CNhi10588_CAC.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12751916	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176545	CNhi10588_ATG.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12309647	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176544	CNhi10588_AGT.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13338104	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176543	CNhi10588_ACG.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11546490	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176542	CNhi10588_ACC.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12921391	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176541	CNhi10587_TAC.experiment	Experiment control	NA	9	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12340215	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176540	CNhi10587_GCG.experiment	Targeted	NA	9	AC009005.2	Homo sapiens	FANTOM6 project	PRJDB7993	13579855	47	CAGE	ASO_G0267751_07	HDF (neonatal)
DRR176475	CNhi10579_AGT.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12686319	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176474	CNhi10579_ACG.experiment	Targeted	NA	6	RP11-245M24.1	Homo sapiens	FANTOM6 project	PRJDB7993	10659729	47	CAGE	ASO_G0229563_04	HDF (neonatal)
DRR176473	CNhi10579_ACC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13086624	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176472	CNhi10578_TAC.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14184428	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176471	CNhi10578_GCT.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13324765	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176470	CNhi10578_GCG.experiment	Targeted	NA	6	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15149146	47	CAGE	ASO_G0236618_07	HDF (neonatal)
DRR176469	CNhi10578_CAC.experiment	Targeted	NA	6	LINC00263	Homo sapiens	FANTOM6 project	PRJDB7993	13753762	47	CAGE	ASO_G0235823_03	HDF (neonatal)
DRR176468	CNhi10578_ATG.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	13082652	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176403	CNhi10538_ACG.experiment	Targeted	NA	6	ZNF37BP	Homo sapiens	FANTOM6 project	PRJDB7993	12459693	47	CAGE	ASO_G0234420_01	HDF (neonatal)
DRR176402	CNhi10538_ACC.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13239878	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176401	CNhi10537_TAC.experiment	Experiment control	NA	5	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15048426	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176400	CNhi10537_GCT.experiment	Targeted	NA	6	RP11-422J8.1	Homo sapiens	FANTOM6 project	PRJDB7993	17333569	47	CAGE	ASO_G0233621_05	HDF (neonatal)
DRR176399	CNhi10537_GCG.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	9629498	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176398	CNhi10537_CAC.experiment	Reference	NA	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9434856	47	CAGE	NA	HDF (neonatal)
DRR176397	CNhi10537_ATG.experiment	Targeted	NA	6	AC012146.7	Homo sapiens	FANTOM6 project	PRJDB7993	13874137	47	CAGE	ASO_G0234327_01	HDF (neonatal)
DRR176396	CNhi10537_AGT.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14349519	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176331	CNhi10528_TAC.experiment	Targeted	NA	5	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	14609095	47	CAGE	ASO_G0180769_03	HDF (neonatal)
DRR176330	CNhi10528_GCT.experiment	Targeted	NA	4	SUGT1P	Homo sapiens	FANTOM6 project	PRJDB7993	14786932	47	CAGE	ASO_G0226823_08	HDF (neonatal)
DRR176329	CNhi10528_GCG.experiment	Targeted	NA	4	MFI2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13247145	47	CAGE	ASO_G0228109_06	HDF (neonatal)
DRR176328	CNhi10528_CAC.experiment	Targeted	NA	4	RP5-1103G7.4	Homo sapiens	FANTOM6 project	PRJDB7993	17624981	47	CAGE	ASO_G0225377_05	HDF (neonatal)
DRR176327	CNhi10528_ATG.experiment	Targeted	NA	4	SUGT1P	Homo sapiens	FANTOM6 project	PRJDB7993	15491267	47	CAGE	ASO_G0226823_03	HDF (neonatal)
DRR176326	CNhi10528_AGT.experiment	Targeted	NA	4	RP11-545E17.3	Homo sapiens	FANTOM6 project	PRJDB7993	13621681	47	CAGE	ASO_G0223478_03	HDF (neonatal)
DRR176325	CNhi10528_ACG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12140679	47	CAGE	ASO_NC_A	HDF (neonatal)

DRR176324	CNhi10528_ACC.experiment	Targeted	NA	4	MFI2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17637147	47	CAGE	ASO_G0228109_07	HDF (neonatal)
DRR176259	CNhi10496_GCT.experiment	Targeted	NA	3	RP11-38L15.3	Homo sapiens	FANTOM6 project	PRJDB7993	13811608	47	CAGE	ASO_G0231187_07	HDF (neonatal)
DRR176258	CNhi10496_GCG.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10080491	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176257	CNhi10496_CAC.experiment	Targeted	NA	3	AC124789.1	Homo sapiens	FANTOM6 project	PRJDB7993	11915783	47	CAGE	ASO_G0260833_06	HDF (neonatal)
DRR176256	CNhi10496_ATG.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	13757483	47	CAGE	ASO_G0204054_06	HDF (neonatal)
DRR176255	CNhi10496_AGT.experiment	Targeted	NA	3	TTN-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15072718	47	CAGE	ASO_G0237298_01	HDF (neonatal)
DRR176254	CNhi10496_ACG.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	12892467	47	CAGE	ASO_G0234171_06	HDF (neonatal)
DRR176253	CNhi10496_ACC.experiment	Targeted	NA	3	CATG00000098831.1	Homo sapiens	FANTOM6 project	PRJDB7993	13083730	47	CAGE	ASO_C0013510_06	HDF (neonatal)
DRR176252	CNhi10495_TAC.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13226545	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176187	CNhi10487_CAC.experiment	Targeted	NA	3	LINC00856	Homo sapiens	FANTOM6 project	PRJDB7993	14765856	47	CAGE	ASO_G0230417_01	HDF (neonatal)
DRR176186	CNhi10487_ATG.experiment	Targeted	NA	3	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	15986904	47	CAGE	ASO_G0203721_05	HDF (neonatal)
DRR176185	CNhi10487_AGT.experiment	Targeted	NA	3	AC009948.5	Homo sapiens	FANTOM6 project	PRJDB7993	17227514	47	CAGE	ASO_G0223960_08	HDF (neonatal)
DRR176184	CNhi10487_ACG.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	14351965	47	CAGE	ASO_G0204054_01	HDF (neonatal)
DRR176183	CNhi10487_ACC.experiment	Targeted	NA	3	CTD-2587H24.5	Homo sapiens	FANTOM6 project	PRJDB7993	14785282	47	CAGE	ASO_G0267577_03	HDF (neonatal)
DRR176182	CNhi10486_TAC.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	16962250	47	CAGE	ASO_G0204054_06	HDF (neonatal)
DRR176181	CNhi10486_GCT.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	17019624	47	CAGE	ASO_G0240875_10	HDF (neonatal)
DRR176345	CNhi10530_GCT.experiment	Targeted	NA	4	RP1-152L7.5	Homo sapiens	FANTOM6 project	PRJDB7993	11260651	47	CAGE	ASO_G0216775_01	HDF (neonatal)
DRR176344	CNhi10530_CAC.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11601665	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176343	CNhi10530_ATG.experiment	Reference	NA	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	8941155	47	CAGE	NA	HDF (neonatal)
DRR176342	CNhi10530_AGT.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	12302771	47	CAGE	ASO_G0224086_03	HDF (neonatal)
DRR176341	CNhi10530_ACG.experiment	Targeted	NA	5	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	10179548	47	CAGE	ASO_G0180769_08	HDF (neonatal)
DRR176340	CNhi10530_ACC.experiment	Targeted	NA	4	BOLA3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11320136	47	CAGE	ASO_G0225439_06	HDF (neonatal)
DRR176275	CNhi10521_GCT.experiment	Targeted	NA	5	CDKN2C	Homo sapiens	FANTOM6 project	PRJDB7993	18498761	47	CAGE	ASO_C0000830_08	HDF (neonatal)
DRR176274	CNhi10521_GCG.experiment	Targeted	NA	4	RP11-139H15.1	Homo sapiens	FANTOM6 project	PRJDB7993	14535781	47	CAGE	ASO_G0225973_10	HDF (neonatal)
DRR176273	CNhi10521_CAC.experiment	Targeted	NA	4	DNAJC27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	20745653	47	CAGE	ASO_G0224165_10	HDF (neonatal)
DRR176272	CNhi10521_ATG.experiment	Reference	NA	0	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11175412	47	CAGE	NA	HDF (neonatal)
DRR176271	CNhi10521_AGT.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18154652	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176270	CNhi10521_ACG.experiment	Targeted	NA	4	RP1-152L7.5	Homo sapiens	FANTOM6 project	PRJDB7993	19076896	47	CAGE	ASO_G0216775_03	HDF (neonatal)
DRR176269	CNhi10521_ACC.experiment	Targeted	NA	5	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	20498112	47	CAGE	ASO_G0180769_03	HDF (neonatal)
DRR176268	CNhi10497_TAC.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12936368	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176203	CNhi10489_GCG.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	12590848	47	CAGE	ASO_C0020672_01	HDF (neonatal)
DRR176202	CNhi10489_CAC.experiment	Targeted	NA	3	LINC00517	Homo sapiens	FANTOM6 project	PRJDB7993	12977176	47	CAGE	ASO_G0259091_01	HDF (neonatal)
DRR176201	CNhi10489_AGT.experiment	Targeted	NA	3	TTN-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14079909	47	CAGE	ASO_G0237298_09	HDF (neonatal)
DRR176200	CNhi10489_ACG.experiment	Targeted	NA	3	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	14969455	47	CAGE	ASO_G0203721_02	HDF (neonatal)
DRR176199	CNhi10489_ACC.experiment	Targeted	NA	3	RP11-500C11.3	Homo sapiens	FANTOM6 project	PRJDB7993	15965980	47	CAGE	ASO_G0272269_06	HDF (neonatal)
DRR176198	CNhi10488_TAC.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	16398204	47	CAGE	ASO_C0020672_02	HDF (neonatal)
DRR176197	CNhi10488_GCT.experiment	Targeted	NA	3	CATG00000098831.1	Homo sapiens	FANTOM6 project	PRJDB7993	13970654	47	CAGE	ASO_C0013510_06	HDF (neonatal)
DRR176196	CNhi10488_GCG.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	11923428	47	CAGE	ASO_G0234171_03	HDF (neonatal)
DRR176131	CNhi10472_ATG.experiment	Targeted	NA	2	RP11-115C21.2	Homo sapiens	FANTOM6 project	PRJDB7993	23900630	47	CAGE	ASO_G0246089_02	HDF (neonatal)
DRR176130	CNhi10472_AGT.experiment	Targeted	NA	2	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	17445786	47	CAGE	ASO_G0223546_02	HDF (neonatal)
DRR176129	CNhi10472_ACG.experiment	Targeted	NA	2	RP11-150O12.1	Homo sapiens	FANTOM6 project	PRJDB7993	15554815	47	CAGE	ASO_C013368_02	HDF (neonatal)
DRR176128	CNhi10472_ACC.experiment	Experiment control	NA	2	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15970345	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176127	CNhi10471_TAC.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	20803423	47	CAGE	ASO_G0212978_02	HDF (neonatal)
DRR176126	CNhi10471_GCT.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	17568005	47	CAGE	ASO_G0212978_03	HDF (neonatal)
DRR176125	CNhi10471_GCG.experiment	Targeted	NA	2	CATG00000089639.1	Homo sapiens	FANTOM6 project	PRJDB7993	15619588	47	CAGE	ASO_G0223811_04	HDF (neonatal)
DRR176124	CNhi10471_CAC.experiment	Experiment control	NA	2	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14874028	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176059	CNhi10461_ACC.experiment	Targeted	NA	1	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	17889338	47	CAGE	ASO_G0163364_06	HDF (neonatal)
DRR176058	CNhi10460_TAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13772480	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176057	CNhi10460_GCT.experiment	Targeted	NA	1	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	16138053	47	CAGE	ASO_G0250742_01	HDF (neonatal)
DRR176056	CNhi10460_GCG.experiment	Targeted	NA	1	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	12429098	47	CAGE	ASO_G0229847_01	HDF (neonatal)
DRR176055	CNhi10460_CAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12640019	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176054	CNhi10460_ATG.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18302823	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176053	CNhi10460_AGT.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	18425767	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176052	CNhi10460_ACG.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14280177	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177131	CNhi10842_GCT.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	10228756	47	CAGE	sgRNA_TERC_gRNA1	HDF (neonatal)
DRR177130	CNhi10842_ACG.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18432436	47	CAGE	sgRNA_NC_gRNA2	HDF (neonatal)
DRR177129	CNhi10837_TAC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17411290	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177128	CNhi10837_GCT.experiment	Targeted	NA	19	RP11-33B1.1	Homo sapiens	FANTOM6 project	PRJDB7993	9047520	47	CAGE	ASO_G0245958_AD_04	HDF (neonatal)
DRR177127	CNhi10837_GCG.experiment	Targeted	NA	19	LINC00968	Homo sapiens	FANTOM6 project	PRJDB7993	10297635	47	CAGE	ASO_G0246430_AD_03	HDF (neonatal)
DRR177126	CNhi10837_CAC.experiment	Targeted	NA	21	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	9926818	47	CAGE	ASO_G0180769_AD_03	HDF (neonatal)
DRR177125	CNhi10837_ATG.experiment	Targeted	NA	19	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	39065738	47	CAGE	ASO_G0237187_AD_08	HDF (neonatal)
DRR177124	CNhi10837_AGT.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14732889	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177059	CNhi10821_ACC.experiment	Targeted	NA	21	CHAF1A	Homo sapiens	FANTOM6 project	PRJDB7993	23488651	47	CAGE	siRNA_s19501	HDF (neonatal)
DRR177058	CNhi10820_TAC.experiment	Targeted	NA	20	SNRPD3	Homo sapiens	FANTOM6 project	PRJDB7993	25840381	47	CAGE	siRNA_s13235	HDF (neonatal)
DRR177057	CNhi10820_GCT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10177958	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR177056	CNhi10820_GCG.experiment	Targeted	NA	20	EXOSC10	Homo sapiens	FANTOM6 project	PRJDB7993	7771202	47	CAGE	siRNA_s10737	HDF (neonatal)
DRR177055	CNhi10820_CAC.experiment	Targeted	NA	20	EXOSC3	Homo sapiens	FANTOM6 project	PRJDB7993	15989823	47	CAGE	siRNA_s27230	HDF (neonatal)
DRR177054	CNhi10820_ATG.experiment	Targeted	NA	21	CHAF1B	Homo sapiens	FANTOM6 project	PRJDB7993	17445604	47	CAGE	siRNA_s15706	HDF (neonatal)
DRR177053	CNhi10820_AGT.experiment	Targeted	NA	21	CHAF1A	Homo sapiens	FANTOM6 project	PRJDB7993	12525882	47	CAGE	siRNA_s19501	HDF (neonatal)
DRR177052	CNhi10820_ACG.experiment	Targeted	NA	21	CHAF1B	Homo sapiens	FANTOM6 project	PRJDB7993	22844032	47	CAGE	siRNA_s15705	HDF (neonatal)
DRR176987	CNhi10811_TAC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18414507	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176986	CNhi10811_GCT.experiment	Targeted	NA	13	RP11-296O14.3	Homo sapiens	FANTOM6 project	PRJDB7993	12763114	47	CAGE	ASO_G0203739_AD_03	HDF (neonatal)
DRR176985	CNhi10811_GCG.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14660145	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176984	CNhi10811_CAC.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11987491	47	CAGE	siRNA_n509345	HDF (neonatal)
DRR176983	CNhi10811_ATG.experiment	Targeted	NA	13	RP11-149I23.3	Homo sapiens	FANTOM6 project	PRJDB7993	21288581	47	CAGE	ASO_G0232110_AD_06	HDF (neonatal)
DRR176982	CNhi10811_AGT.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13297601	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176981	CNhi10811_ACG.experiment	Targeted	NA	13	RP11-296O14.3	Homo sapiens	FANTOM6 project	PRJDB7993	20773733	47	CAGE	ASO_G0203739_AD_03	HDF (neonatal)
DRR176980	CNhi10811_ACC.experiment	Targeted	NA	21	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	19793549	47	CAGE	ASO_G0246985_AD_04	HDF (neonatal)
DRR176915	CNhi10793_GCG.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13770257	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176914	CNhi10793_CAC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15635383	47	CAGE	ASO_NC_A	HDF (neonatal)

Table_S3 Meatadata for single cell analysis and FANTOM6 kmer research

DRR176913	CNhi10793_ATG.experiment	Targeted	NA	15	AC007879.7	Homo sapiens	FANTOM6 project	PRJDB7993	21584387	47	CAGE	ASO_G0229647_AD_09	HDF (neonatal)
DRR176912	CNhi10793_AGT.experiment	Targeted	NA	15	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16916306	47	CAGE	ASO_G0236618_AD_07	HDF (neonatal)
DRR176911	CNhi10793_ACG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21634989	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176910	CNhi10793_ACC.experiment	Targeted	NA	17	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	17851701	47	CAGE	ASO_G0269834_AD_02	HDF (neonatal)
DRR176909	CNhi10792_TAC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17835216	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176908	CNhi10792_GCT.experiment	Targeted	NA	15	LINC00511	Homo sapiens	FANTOM6 project	PRJDB7993	15778895	47	CAGE	ASO_G0227036_AD_07	HDF (neonatal)
DRR176843	CNhi10784_ATG.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21441206	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176842	CNhi10784_AGT.experiment	Targeted	NA	16	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	13201480	47	CAGE	ASO_G0267886_AD_02	HDF (neonatal)
DRR176841	CNhi10784_ACG.experiment	Targeted	NA	15	RP5-1103G7.4	Homo sapiens	FANTOM6 project	PRJDB7993	25845946	47	CAGE	ASO_G0225377_AD_05	HDF (neonatal)
DRR176840	CNhi10784_ACC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23488015	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176839	CNhi10783_TAC.experiment	Targeted	NA	16	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	20737933	47	CAGE	ASO_G0267419_AD_06	HDF (neonatal)
DRR176838	CNhi10783_GCT.experiment	Targeted	NA	15	DNAJC27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14842178	47	CAGE	ASO_G0224165_AD_07	HDF (neonatal)
DRR176837	CNhi10783_GCG.experiment	Experiment control	NA	15	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	13439752	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176836	CNhi10783_CAC.experiment	Targeted	NA	16	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	15853984	47	CAGE	ASO_G0263753_AD_06	HDF (neonatal)
DRR176771	CNhi10761_AGT.experiment	Targeted	NA	14	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	19593326	47	CAGE	ASO_G0257219_AD_10	HDF (neonatal)
DRR176770	CNhi10761_ACG.experiment	Targeted	NA	14	LINC00517	Homo sapiens	FANTOM6 project	PRJDB7993	15489618	47	CAGE	ASO_G0259091_AD_04	HDF (neonatal)
DRR176769	CNhi10761_ACC.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	22978791	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176768	CNhi10760_TAC.experiment	Targeted	NA	14	LINC00707	Homo sapiens	FANTOM6 project	PRJDB7993	21896095	47	CAGE	ASO_G0238266_AD_06	HDF (neonatal)
DRR176767	CNhi10760_GCT.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16147032	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176766	CNhi10760_CAC.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12986162	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176765	CNhi10760_ATG.experiment	Targeted	NA	13	RP11-139H15.1	Homo sapiens	FANTOM6 project	PRJDB7993	22489696	47	CAGE	ASO_G0225973_AD_01	HDF (neonatal)
DRR176764	CNhi10760_AGT.experiment	Targeted	NA	13	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	17040254	47	CAGE	ASO_G0225554_AD_04	HDF (neonatal)
DRR176699	CNhi10636_ACC.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14487498	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177149	CNhi10867_ACC.experiment	Targeted	NA	23	XRN2	Homo sapiens	FANTOM6 project	PRJDB7993	21236619	47	CAGE	siRNA_siXRN-1	HDF (neonatal)
DRR177148	CNhi10866_GCT.experiment	Negative control	NA	23	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12506223	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR177083	CNhi10832_ACC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20204359	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177082	CNhi10831_TAC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20034928	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177081	CNhi10831_GCT.experiment	Targeted	NA	19	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	13540341	47	CAGE	ASO_G0245937_AD_05	HDF (neonatal)
DRR177080	CNhi10831_GCG.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16497346	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR177079	CNhi10831_CAC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11544368	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177078	CNhi10831_ATG.experiment	Targeted	NA	19	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	16233696	47	CAGE	ASO_G0245213_AD_03	HDF (neonatal)
DRR177077	CNhi10831_AGT.experiment	Targeted	NA	19	RP11-33B1.1	Homo sapiens	FANTOM6 project	PRJDB7993	14666472	47	CAGE	ASO_G0245958_AD_04	HDF (neonatal)
DRR177076	CNhi10831_ACG.experiment	Targeted	NA	19	RP11-539L10.3	Homo sapiens	FANTOM6 project	PRJDB7993	18638109	47	CAGE	ASO_G0251580_AD_01	HDF (neonatal)
DRR177011	CNhi10814_TAC.experiment	Targeted	NA	20	PRRX1	Homo sapiens	FANTOM6 project	PRJDB7993	16909072	47	CAGE	siRNA_s10745	HDF (neonatal)
DRR177010	CNhi10814_GCT.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12846265	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR177009	CNhi10814_GCG.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10917296	47	CAGE	ASO_G0240498_POS_01	HDF (neonatal)
DRR177008	CNhi10814_CAC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14295845	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177007	CNhi10814_ATG.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	20915537	47	CAGE	siRNA_AD70LI3	HDF (neonatal)
DRR177006	CNhi10814_AGT.experiment	Targeted	NA	21	LINC00707	Homo sapiens	FANTOM6 project	PRJDB7993	20716626	47	CAGE	ASO_G0238266_AD_06	HDF (neonatal)
DRR177005	CNhi10814_ACG.experiment	Experiment control	NA	21	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17873785	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR177004	CNhi10814_ACC.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	19004766	47	CAGE	siRNA_s32294	HDF (neonatal)
DRR176003	CNhi10453_TAC.experiment	Targeted	NA	1	SNHG18	Homo sapiens	FANTOM6 project	PRJDB7993	21947660	47	CAGE	ASO_G0250786_04	HDF (neonatal)
DRR176002	CNhi10453_GCT.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	14274805	47	CAGE	ASO_G0234546_01	HDF (neonatal)
DRR176001	CNhi10453_GCG.experiment	Targeted	NA	1	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	13981771	47	CAGE	ASO_G0218510_04	HDF (neonatal)
DRR176000	CNhi10453_CAC.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	16892243	47	CAGE	ASO_G0234546_07	HDF (neonatal)
DRR175999	CNhi10453_ATG.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	18947020	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR175998	CNhi10453_AGT.experiment	Targeted	NA	1	RP6-99M1.2	Homo sapiens	FANTOM6 project	PRJDB7993	18888572	47	CAGE	ASO_G0270069_05	HDF (neonatal)
DRR175997	CNhi10453_ACG.experiment	Targeted	NA	1	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	17264261	47	CAGE	ASO_G0270141_05	HDF (neonatal)
DRR175996	CNhi10453_ACC.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17913584	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176939	CNhi10804_GCT.experiment	Targeted	NA	21	TRAM2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10047371	47	CAGE	ASO_G0225791_AD_05	HDF (neonatal)
DRR176938	CNhi10804_GCG.experiment	Targeted	NA	19	MKLN1-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	10397751	47	CAGE	ASO_G0236753_AD_01	HDF (neonatal)
DRR176937	CNhi10804_CAC.experiment	Targeted	NA	19	RP11-33B1.1	Homo sapiens	FANTOM6 project	PRJDB7993	10470512	47	CAGE	ASO_G0245958_AD_07	HDF (neonatal)
DRR176936	CNhi10804_ATG.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17028180	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176935	CNhi10804_AGT.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17775061	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176934	CNhi10804_ACG.experiment	Targeted	NA	19	U52111.14	Homo sapiens	FANTOM6 project	PRJDB7993	15218248	47	CAGE	ASO_G0232725_AD_10	HDF (neonatal)
DRR176933	CNhi10804_ACC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14427754	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176932	CNhi10803_TAC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17236791	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176867	CNhi10787_CAC.experiment	Negative control	NA	17	NA	Homo sapiens	FANTOM6 project	PRJDB7993	8444174	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176866	CNhi10787_ATG.experiment	Targeted	NA	15	UBL7-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	25246450	47	CAGE	ASO_G0247240_AD_05	HDF (neonatal)
DRR176865	CNhi10787_AGT.experiment	Targeted	NA	17	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	14415234	47	CAGE	ASO_G0272888_AD_07	HDF (neonatal)
DRR176864	CNhi10787_ACG.experiment	Targeted	NA	15	AC009948.5	Homo sapiens	FANTOM6 project	PRJDB7993	23470712	47	CAGE	ASO_G0223960_AD_10	HDF (neonatal)
DRR176863	CNhi10787_ACC.experiment	Targeted	NA	16	ZNF730	Homo sapiens	FANTOM6 project	PRJDB7993	23895922	47	CAGE	ASO_G0267886_AD_02	HDF (neonatal)
DRR176862	CNhi10786_TAC.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	25938284	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176861	CNhi10786_GCT.experiment	Targeted	NA	15	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	16489762	47	CAGE	ASO_G0219665_AD_08	HDF (neonatal)
DRR176860	CNhi10786_GCG.experiment	Targeted	NA	15	UBL7-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13278053	47	CAGE	ASO_G0247240_AD_06	HDF (neonatal)
DRR176795	CNhi10764_AGT.experiment	Targeted	NA	13	RP11-137L10.6	Homo sapiens	FANTOM6 project	PRJDB7993	16271822	47	CAGE	ASO_G0221817_AD_08	HDF (neonatal)
DRR176794	CNhi10764_ACG.experiment	Experiment control	NA	14	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17328544	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176793	CNhi10764_ACC.experiment	Targeted	NA	14	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	21349220	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176792	CNhi10763_TAC.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	23834413	47	CAGE	ASO_G0261105_AD_06	HDF (neonatal)
DRR176791	CNhi10763_GCT.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13306242	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176790	CNhi10763_GCG.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13165581	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176789	CNhi10763_CAC.experiment	Targeted	NA	14	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12266873	47	CAGE	ASO_G0246985_AD_04	HDF (neonatal)
DRR176788	CNhi10763_ATG.experiment	Targeted	NA	14	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	18886321	47	CAGE	ASO_G0257219_AD_05	HDF (neonatal)
DRR176723	CNhi10639_ACG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15779885	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176722	CNhi10639_ACC.experiment	Targeted	NA	12	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14930980	47	CAGE	ASO_G0246067_AD_04	HDF (neonatal)
DRR176721	CNhi10638_TAC.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	14550282	47	CAGE	ASO_G0256268_AD_06	HDF (neonatal)
DRR176720	CNhi10638_GCT.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	11922776	47	CAGE	ASO_G0256268_AD_03	HDF (neonatal)
DRR176719	CNhi10638_CAC.experiment	Targeted	NA	12	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	13619034	47	CAGE	ASO_G0253352_AD_07	HDF (neonatal)

DRR176718	CNhi10638_ATG.experiment	Targeted	NA	12	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12265194	47	CAGE	ASO_G0225733_AD_03	HDF (neonatal)
DRR176717	CNhi10638_AGT.experiment	Targeted	NA	12	ERVK3-1	Homo sapiens	FANTOM6 project	PRJDB7993	13640863	47	CAGE	ASO_G0142396_AD_07	HDF (neonatal)
DRR176716	CNhi10638_ACG.experiment	Targeted	NA	12	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14653639	47	CAGE	ASO_G0225733_AD_03	HDF (neonatal)
DRR176651	CNhi10629_TAC.experiment	Targeted	NA	12	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	15227693	47	CAGE	ASO_G0226950_AD_07	HDF (neonatal)
DRR176650	CNhi10629_GCT.experiment	Targeted	NA	12	RP11-834C11.4	Homo sapiens	FANTOM6 project	PRJDB7993	14468082	47	CAGE	ASO_G0250742_AD_04	HDF (neonatal)
DRR176649	CNhi10629_GCG.experiment	Targeted	NA	12	LINC00657	Homo sapiens	FANTOM6 project	PRJDB7993	12055340	47	CAGE	ASO_G0260032_AD_06	HDF (neonatal)
DRR176648	CNhi10629_CAC.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	13868209	47	CAGE	ASO_G0256268_AD_06	HDF (neonatal)
DRR176647	CNhi10629_ATG.experiment	Targeted	NA	12	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	12588648	47	CAGE	ASO_G0223485_AD_06	HDF (neonatal)
DRR176646	CNhi10629_AGT.experiment	Targeted	NA	12	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	9468284	47	CAGE	ASO_G0223485_AD_04	HDF (neonatal)
DRR176645	CNhi10629_ACG.experiment	Targeted	NA	12	RP11-221N13.3	Homo sapiens	FANTOM6 project	PRJDB7993	15161436	47	CAGE	ASO_G0256268_AD_03	HDF (neonatal)
DRR176644	CNhi10629_ACC.experiment	Targeted	NA	12	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	19263473	47	CAGE	ASO_G0218510_AD_03	HDF (neonatal)
DRR176579	CNhi10604_GCT.experiment	Targeted	NA	10	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	16562877	47	CAGE	ASO_G0272888_04	HDF (neonatal)
DRR176578	CNhi10604_GCG.experiment	Targeted	NA	10	RP11-85K15.2	Homo sapiens	FANTOM6 project	PRJDB7993	10355078	47	CAGE	ASO_G0258704_09	HDF (neonatal)
DRR176577	CNhi10604_CAC.experiment	Targeted	NA	10	CKMT2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9509283	47	CAGE	ASO_G0247572_08	HDF (neonatal)
DRR176576	CNhi10604_AGT.experiment	Targeted	NA	11	LINC00938	Homo sapiens	FANTOM6 project	PRJDB7993	15925899	47	CAGE	ASO_G0273015_AD_07	HDF (neonatal)
DRR176575	CNhi10604_ACG.experiment	Targeted	NA	10	RP11-379H18.1	Homo sapiens	FANTOM6 project	PRJDB7993	14404782	47	CAGE	ASO_G0271122_05	HDF (neonatal)
DRR176574	CNhi10604_ACC.experiment	Targeted	NA	10	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	14747677	47	CAGE	ASO_G0237854_05	HDF (neonatal)
DRR176573	CNhi10603_TAC.experiment	Targeted	NA	10	RP13-463N16.6	Homo sapiens	FANTOM6 project	PRJDB7993	14062234	47	CAGE	ASO_G0242147_05	HDF (neonatal)
DRR176572	CNhi10603_GCT.experiment	Targeted	NA	10	RP11-85K15.2	Homo sapiens	FANTOM6 project	PRJDB7993	12774702	47	CAGE	ASO_G0258704_09	HDF (neonatal)
DRR176507	CNhi10583_ATG.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	11310071	47	CAGE	ASO_G0261573_03	HDF (neonatal)
DRR176506	CNhi10583_AGT.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	21480085	47	CAGE	ASO_G0261573_02	HDF (neonatal)
DRR176505	CNhi10583_ACG.experiment	Targeted	NA	9	RP11-333E1.1	Homo sapiens	FANTOM6 project	PRJDB7993	9921275	47	CAGE	ASO_G0261879_05	HDF (neonatal)
DRR176504	CNhi10583_ACC.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	10854719	47	CAGE	ASO_G0261573_01	HDF (neonatal)
DRR176503	CNhi10582_TAC.experiment	Targeted	NA	9	RP11-863P13.3	Homo sapiens	FANTOM6 project	PRJDB7993	12618978	47	CAGE	ASO_G0261327_05	HDF (neonatal)
DRR176502	CNhi10582_GCT.experiment	Targeted	NA	9	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	14053115	47	CAGE	ASO_G0261573_01	HDF (neonatal)
DRR176501	CNhi10582_GCG.experiment	Targeted	NA	9	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	14087403	47	CAGE	ASO_G0261105_02	HDF (neonatal)
DRR176500	CNhi10582_CAC.experiment	Targeted	NA	9	RP11-22P6.3	Homo sapiens	FANTOM6 project	PRJDB7993	14641007	47	CAGE	ASO_G0260442_01	HDF (neonatal)
DRR176435	CNhi10542_ACG.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12904962	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176434	CNhi10542_ACC.experiment	Targeted	NA	5	AMZ2P1	Homo sapiens	FANTOM6 project	PRJDB7993	10584409	47	CAGE	ASO_G0214174_02	HDF (neonatal)
DRR176433	CNhi10541_TAC.experiment	Targeted	NA	6	RP11-422J8.1	Homo sapiens	FANTOM6 project	PRJDB7993	14366808	47	CAGE	ASO_G0233621_01	HDF (neonatal)
DRR176432	CNhi10541_GCT.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13406050	47	CAGE	ASO_G0186615_04	HDF (neonatal)
DRR176431	CNhi10541_GCG.experiment	Targeted	NA	5	RP11-622K12.1	Homo sapiens	FANTOM6 project	PRJDB7993	11654694	47	CAGE	ASO_G0204272_03	HDF (neonatal)
DRR176698	CNhi10635_TAC.experiment	Targeted	NA	12	TP53TG1	Homo sapiens	FANTOM6 project	PRJDB7993	14594893	47	CAGE	ASO_G0182165_AD_04	HDF (neonatal)
DRR176697	CNhi10635_GCT.experiment	Targeted	NA	12	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	13684130	47	CAGE	ASO_G0224597_AD_04	HDF (neonatal)
DRR176696	CNhi10635_GCG.experiment	Targeted	NA	12	ERVK3-1	Homo sapiens	FANTOM6 project	PRJDB7993	14034484	47	CAGE	ASO_G0142396_AD_07	HDF (neonatal)
DRR176695	CNhi10635_CAC.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16460475	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176694	CNhi10635_ATG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12700142	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176693	CNhi10635_AGT.experiment	Experiment control	NA	12	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	9257316	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176692	CNhi10635_ACG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13814300	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176627	CNhi10610_TAC.experiment	Targeted	NA	10	RP11-474B16.1	Homo sapiens	FANTOM6 project	PRJDB7993	12295758	47	CAGE	ASO_G0257642_01	HDF (neonatal)
DRR176626	CNhi10610_GCT.experiment	Targeted	NA	10	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	10577790	47	CAGE	ASO_G0257219_09	HDF (neonatal)
DRR176625	CNhi10610_CAC.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	11929568	47	CAGE	ASO_G0255121_03	HDF (neonatal)
DRR176624	CNhi10610_ATG.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9628720	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176623	CNhi10610_AGT.experiment	Targeted	NA	10	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10912025	47	CAGE	ASO_G0237187_03	HDF (neonatal)
DRR176622	CNhi10610_ACG.experiment	Targeted	NA	11	TP53TG1	Homo sapiens	FANTOM6 project	PRJDB7993	12181142	47	CAGE	ASO_G0182165_AD_04	HDF (neonatal)
DRR176621	CNhi10610_ACC.experiment	Targeted	NA	10	RP11-379H18.1	Homo sapiens	FANTOM6 project	PRJDB7993	11161834	47	CAGE	ASO_G0271122_06	HDF (neonatal)
DRR176620	CNhi10609_TAC.experiment	Targeted	NA	10	RP13-463N16.6	Homo sapiens	FANTOM6 project	PRJDB7993	12565195	47	CAGE	ASO_G0242147_05	HDF (neonatal)
DRR176555	CNhi10601_GCG.experiment	Targeted	NA	10	ZSCAN16-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11898818	47	CAGE	ASO_G0269293_01	HDF (neonatal)
DRR176554	CNhi10601_CAC.experiment	Targeted	NA	10	RP11-474B16.1	Homo sapiens	FANTOM6 project	PRJDB7993	11941654	47	CAGE	ASO_G0257642_01	HDF (neonatal)
DRR176553	CNhi10601_ATG.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10197008	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176552	CNhi10601_AGT.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13723095	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176551	CNhi10601_ACG.experiment	Targeted	NA	10	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	12165238	47	CAGE	ASO_G0257219_09	HDF (neonatal)
DRR176550	CNhi10601_ACC.experiment	Targeted	NA	10	RP6-109B7.3	Homo sapiens	FANTOM6 project	PRJDB7993	11775871	47	CAGE	ASO_G0241990_01	HDF (neonatal)
DRR176549	CNhi10588_TAC.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12656521	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176548	CNhi10588_GCT.experiment	Negative control	NA	9	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12217825	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176483	CNhi10580_AGT.experiment	Targeted	NA	6	RP4-794H19.4	Homo sapiens	FANTOM6 project	PRJDB7993	9888327	47	CAGE	ASO_G0230812_10	HDF (neonatal)
DRR176482	CNhi10580_ACG.experiment	Targeted	NA	6	RP11-295G20.2	Homo sapiens	FANTOM6 project	PRJDB7993	8494242	47	CAGE	ASO_G0233461_03	HDF (neonatal)
DRR176481	CNhi10580_ACC.experiment	Targeted	NA	6	RP4-794H19.4	Homo sapiens	FANTOM6 project	PRJDB7993	11119532	47	CAGE	ASO_G0230812_05	HDF (neonatal)
DRR176480	CNhi10579_TAC.experiment	Targeted	NA	6	RP11-245M24.1	Homo sapiens	FANTOM6 project	PRJDB7993	13945217	47	CAGE	ASO_G0229563_04	HDF (neonatal)
DRR176479	CNhi10579_GCT.experiment	Targeted	NA	6	RP4-794H19.4	Homo sapiens	FANTOM6 project	PRJDB7993	13206079	47	CAGE	ASO_G0230812_05	HDF (neonatal)
DRR176478	CNhi10579_GCG.experiment	Targeted	NA	6	RP11-245M24.1	Homo sapiens	FANTOM6 project	PRJDB7993	10603659	47	CAGE	ASO_G0229563_02	HDF (neonatal)
DRR176477	CNhi10579_CAC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12425824	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176476	CNhi10579_ATG.experiment	Targeted	NA	6	RP11-245M24.1	Homo sapiens	FANTOM6 project	PRJDB7993	14068082	47	CAGE	ASO_G0229563_02	HDF (neonatal)
DRR176411	CNhi10539_ACG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14217009	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176410	CNhi10539_ACC.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	13570676	47	CAGE	ASO_G0233527_03	HDF (neonatal)
DRR176409	CNhi10538_TAC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14148704	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176408	CNhi10538_GCT.experiment	Experiment control	NA	5	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	16082949	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176407	CNhi10538_GCG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11512244	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176406	CNhi10538_CAC.experiment	Targeted	NA	6	U52111.14	Homo sapiens	FANTOM6 project	PRJDB7993	12925340	47	CAGE	ASO_G0232725_05	HDF (neonatal)
DRR176405	CNhi10538_ATG.experiment	Targeted	NA	5	AMZ2P1	Homo sapiens	FANTOM6 project	PRJDB7993	12916722	47	CAGE	ASO_G0214174_02	HDF (neonatal)
DRR176404	CNhi10538_AGT.experiment	Targeted	NA	6	AC012146.7	Homo sapiens	FANTOM6 project	PRJDB7993	13934959	47	CAGE	ASO_G0234327_01	HDF (neonatal)
DRR176339	CNhi10529_TAC.experiment	Targeted	NA	5	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	15419519	47	CAGE	ASO_C0012015_07	HDF (neonatal)
DRR176338	CNhi10529_GCT.experiment	Targeted	NA	4	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	14823645	47	CAGE	ASO_G0219665_08	HDF (neonatal)
DRR176337	CNhi10529_GCG.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12564321	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176336	CNhi10529_CAC.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	17308418	47	CAGE	ASO_G0223773_07	HDF (neonatal)
DRR176335	CNhi10529_ATG.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13666333	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176334	CNhi10529_AGT.experiment	Targeted	NA	4	RP5-1103G7.4	Homo sapiens	FANTOM6 project	PRJDB7993	13367028	47	CAGE	ASO_G0225377_05	HDF (neonatal)
DRR176333	CNhi10529_ACG.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	12764410	47	CAGE	ASO_G0224086_04	HDF (neonatal)
DRR176332	CNhi10529_ACC.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	13734373	47	CAGE	ASO_G0224086_06	HDF (neonatal)
DRR176267	CNhi10497_GCT.experiment	Targeted	NA	3	PRRT3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12433132	47	CAGE	ASO_G0230082_01	HDF (neonatal)

DRR176266	CNhi10497_GCG.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	8784496	47	CAGE	ASO_C0020672_07	HDF (neonatal)
DRR176265	CNhi10497_CAC.experiment	Targeted	NA	3	TMCC1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	8384862	47	CAGE	ASO_G0271270_09	HDF (neonatal)
DRR176264	CNhi10497_ATG.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12774683	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176263	CNhi10497_AGT.experiment	Targeted	NA	3	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	12597844	47	CAGE	ASO_G0245213_04	HDF (neonatal)
DRR176262	CNhi10497_ACG.experiment	Targeted	NA	3	LINC00862	Homo sapiens	FANTOM6 project	PRJDB7993	12308143	47	CAGE	ASO_G0203721_02	HDF (neonatal)
DRR176261	CNhi10497_ACC.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	12643805	47	CAGE	ASO_G0234171_01	HDF (neonatal)
DRR176260	CNhi10496_TAC.experiment	Targeted	NA	3	LINC00963	Homo sapiens	FANTOM6 project	PRJDB7993	14339632	47	CAGE	ASO_G0204054_10	HDF (neonatal)
DRR176195	CNhi10488_CAC.experiment	Targeted	NA	3	AC124789.1	Homo sapiens	FANTOM6 project	PRJDB7993	15707409	47	CAGE	ASO_G0260833_06	HDF (neonatal)
DRR176194	CNhi10488_ATG.experiment	Targeted	NA	3	RP11-38L15.3	Homo sapiens	FANTOM6 project	PRJDB7993	15567838	47	CAGE	ASO_G0231187_07	HDF (neonatal)
DRR176193	CNhi10488_AGT.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	15016238	47	CAGE	ASO_C0020672_02	HDF (neonatal)
DRR176192	CNhi10488_ACG.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11010341	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176191	CNhi10488_ACC.experiment	Targeted	NA	3	AP001258.4	Homo sapiens	FANTOM6 project	PRJDB7993	17115849	47	CAGE	ASO_G0245571_06	HDF (neonatal)
DRR176190	CNhi10487_TAC.experiment	Targeted	NA	3	AC004980.7	Homo sapiens	FANTOM6 project	PRJDB7993	16526913	47	CAGE	ASO_G0205485_03	HDF (neonatal)
DRR176189	CNhi10487_GCT.experiment	Targeted	NA	3	RP11-38L15.3	Homo sapiens	FANTOM6 project	PRJDB7993	14278852	47	CAGE	ASO_G0231187_02	HDF (neonatal)
DRR176188	CNhi10487_GCG.experiment	Targeted	NA	3	LINC00856	Homo sapiens	FANTOM6 project	PRJDB7993	12635829	47	CAGE	ASO_G0230417_02	HDF (neonatal)
DRR176123	CNhi10471_ATG.experiment	Targeted	NA	2	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	21532607	47	CAGE	ASO_G0223546_02	HDF (neonatal)
DRR176122	CNhi10471_AGT.experiment	Targeted	NA	2	NEAT1_1	Homo sapiens	FANTOM6 project	PRJDB7993	22052001	47	CAGE	ASO_NEAT1_1	HDF (neonatal)
DRR176121	CNhi10471_ACG.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13678543	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176120	CNhi10471_ACC.experiment	Targeted	NA	2	LINC00630	Homo sapiens	FANTOM6 project	PRJDB7993	21757538	47	CAGE	ASO_G0223546_01	HDF (neonatal)
DRR176119	CNhi10470_TAC.experiment	Targeted	NA	2	BX322557.10	Homo sapiens	FANTOM6 project	PRJDB7993	19162591	47	CAGE	ASO_G0215447_03	HDF (neonatal)
DRR176118	CNhi10470_GCT.experiment	Targeted	NA	2	AC027612.6	Homo sapiens	FANTOM6 project	PRJDB7993	17431726	47	CAGE	ASO_G0143429_05	HDF (neonatal)
DRR176117	CNhi10470_GCG.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	14484673	47	CAGE	ASO_G0263072_06	HDF (neonatal)
DRR176116	CNhi10470_CAC.experiment	Targeted	NA	2	NEAT1_2	Homo sapiens	FANTOM6 project	PRJDB7993	15860916	47	CAGE	ASO_NEAT1_2	HDF (neonatal)
DRR176051	CNhi10460_ACC.experiment	Targeted	NA	1	RP3-510D11.1	Homo sapiens	FANTOM6 project	PRJDB7993	19029363	47	CAGE	ASO_G0228526_10	HDF (neonatal)
DRR176050	CNhi10459_TAC.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	20241534	47	CAGE	ASO_G0253352_01	HDF (neonatal)
DRR176049	CNhi10459_GCT.experiment	Targeted	NA	1	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17326968	47	CAGE	ASO_G0246067_01	HDF (neonatal)
DRR176048	CNhi10459_GCG.experiment	Targeted	NA	1	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	12758493	47	CAGE	ASO_G0223485_01	HDF (neonatal)
DRR176047	CNhi10459_CAC.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	15198775	47	CAGE	ASO_G0234546_07	HDF (neonatal)
DRR176046	CNhi10459_ATG.experiment	Targeted	NA	1	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18388169	47	CAGE	ASO_G0225733_03	HDF (neonatal)
DRR176045	CNhi10459_AGT.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	19759990	47	CAGE	ASO_G0224577_05	HDF (neonatal)
DRR176044	CNhi10459_ACG.experiment	Targeted	NA	1	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	19370324	47	CAGE	ASO_G0246067_05	HDF (neonatal)
DRR175995	CNhi10452_TAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16181073	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR175994	CNhi10452_GCT.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	14213039	47	CAGE	ASO_G0234546_02	HDF (neonatal)
DRR175993	CNhi10452_GCG.experiment	Targeted	NA	1	LINC00883	Homo sapiens	FANTOM6 project	PRJDB7993	14642295	47	CAGE	ASO_G0243701_01	HDF (neonatal)
DRR175992	CNhi10452_CAC.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	16078076	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR175991	CNhi10452_ATG.experiment	Targeted	NA	1	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	19180073	47	CAGE	ASO_G0253352_02	HDF (neonatal)
DRR175990	CNhi10452_AGT.experiment	Targeted	NA	1	RP3-510D11.1	Homo sapiens	FANTOM6 project	PRJDB7993	17307796	47	CAGE	ASO_G0228526_10	HDF (neonatal)
DRR175989	CNhi10452_ACG.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17370390	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR175988	CNhi10452_ACC.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	21445952	47	CAGE	ASO_G0224577_02	HDF (neonatal)
DRR176430	CNhi10541_CAC.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17645667	47	CAGE	ASO_G0198468_07	HDF (neonatal)
DRR176429	CNhi10541_ATG.experiment	Targeted	NA	5	RP11-622K12.1	Homo sapiens	FANTOM6 project	PRJDB7993	10890480	47	CAGE	ASO_G0204272_03	HDF (neonatal)
DRR176428	CNhi10541_AGT.experiment	Targeted	NA	5	RP11-622K12.1	Homo sapiens	FANTOM6 project	PRJDB7993	12501206	47	CAGE	ASO_G0204272_04	HDF (neonatal)
DRR176363	CNhi10533_ACC.experiment	Targeted	NA	6	MAGI2-AS3	Homo sapiens	FANTOM6 project	PRJDB7993	12214133	47	CAGE	ASO_G0234456_04	HDF (neonatal)
DRR176362	CNhi10532_TAC.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	15248670	47	CAGE	ASO_G0223773_07	HDF (neonatal)
DRR176361	CNhi10532_GCT.experiment	Targeted	NA	4	RP11-137L10.6	Homo sapiens	FANTOM6 project	PRJDB7993	15881157	47	CAGE	ASO_G0221817_04	HDF (neonatal)
DRR176360	CNhi10532_GCG.experiment	Targeted	NA	4	RP11-137L10.6	Homo sapiens	FANTOM6 project	PRJDB7993	11190425	47	CAGE	ASO_G0221817_04	HDF (neonatal)
DRR176359	CNhi10532_CAC.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15386042	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176358	CNhi10532_ATG.experiment	Targeted	NA	4	LINC00511	Homo sapiens	FANTOM6 project	PRJDB7993	10622671	47	CAGE	ASO_G0227036_04	HDF (neonatal)
DRR176357	CNhi10532_AGT.experiment	Targeted	NA	4	RP11-545E17.3	Homo sapiens	FANTOM6 project	PRJDB7993	13329693	47	CAGE	ASO_G0223478_03	HDF (neonatal)
DRR176356	CNhi10532_ACG.experiment	Targeted	NA	5	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	15422223	47	CAGE	ASO_C0011632_10	HDF (neonatal)
DRR176291	CNhi10523_GCT.experiment	Targeted	NA	4	DNAJC27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16830942	47	CAGE	ASO_G0224165_10	HDF (neonatal)
DRR176290	CNhi10523_GCG.experiment	Targeted	NA	4	LINC00511	Homo sapiens	FANTOM6 project	PRJDB7993	14987779	47	CAGE	ASO_G0227036_04	HDF (neonatal)
DRR176289	CNhi10523_CAC.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	23081646	47	CAGE	ASO_G0224086_04	HDF (neonatal)
DRR176288	CNhi10523_ATG.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11890731	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176287	CNhi10523_AGT.experiment	Targeted	NA	5	CATG00000020700.1	Homo sapiens	FANTOM6 project	PRJDB7993	16260918	47	CAGE	ASO_C0020984_02	HDF (neonatal)
DRR176286	CNhi10523_ACG.experiment	Targeted	NA	5	CDKN2C	Homo sapiens	FANTOM6 project	PRJDB7993	14906158	47	CAGE	ASO_C0000830_02	HDF (neonatal)
DRR176285	CNhi10523_ACC.experiment	Targeted	NA	5	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	17903763	47	CAGE	ASO_C0011632_03	HDF (neonatal)
DRR176284	CNhi10522_TAC.experiment	Targeted	NA	4	JPX	Homo sapiens	FANTOM6 project	PRJDB7993	18088273	47	CAGE	ASO_G0225470_05	HDF (neonatal)
DRR176219	CNhi10491_GCG.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	13494529	47	CAGE	ASO_G0240875_01	HDF (neonatal)
DRR176218	CNhi10491_CAC.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	11401092	47	CAGE	ASO_G0234171_02	HDF (neonatal)
DRR176217	CNhi10491_ATG.experiment	Targeted	NA	3	CATG00000017883.1	Homo sapiens	FANTOM6 project	PRJDB7993	14802219	47	CAGE	ASO_C0020672_01	HDF (neonatal)
DRR176216	CNhi10491_AGT.experiment	Targeted	NA	3	TTN-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16412826	47	CAGE	ASO_G0237298_09	HDF (neonatal)
DRR176215	CNhi10491_ACG.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	13623090	47	CAGE	ASO_G0234171_03	HDF (neonatal)
DRR176214	CNhi10491_ACC.experiment	Targeted	NA	3	CTD-2587H24.5	Homo sapiens	FANTOM6 project	PRJDB7993	12080196	47	CAGE	ASO_G0267577_01	HDF (neonatal)
DRR176213	CNhi10490_TAC.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	15497851	47	CAGE	ASO_G0234171_02	HDF (neonatal)
DRR176212	CNhi10490_GCT.experiment	Targeted	NA	3	TMCC1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14145944	47	CAGE	ASO_G0271270_09	HDF (neonatal)
DRR176147	CNhi10474_ATG.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16131578	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176146	CNhi10474_AGT.experiment	Targeted	NA	2	AC005592.2	Homo sapiens	FANTOM6 project	PRJDB7993	13723243	47	CAGE	ASO_G0231185_03	HDF (neonatal)
DRR176145	CNhi10474_ACG.experiment	Targeted	NA	2	LINC00968	Homo sapiens	FANTOM6 project	PRJDB7993	15721364	47	CAGE	ASO_G0246430_03	HDF (neonatal)
DRR176144	CNhi10474_ACC.experiment	Targeted	NA	2	AC007879.7	Homo sapiens	FANTOM6 project	PRJDB7993	13704792	47	CAGE	ASO_G0229647_06	HDF (neonatal)
DRR176143	CNhi10473_TAC.experiment	Targeted	NA	2	A1BG-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	19169257	47	CAGE	ASO_G0268895_01	HDF (neonatal)
DRR176142	CNhi10473_GCT.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	18312725	47	CAGE	ASO_G0263072_02	HDF (neonatal)
DRR176141	CNhi10473_GCG.experiment	Targeted	NA	2	CTD-3131K8.2	Homo sapiens	FANTOM6 project	PRJDB7993	13770608	47	CAGE	ASO_G0269439_09	HDF (neonatal)
DRR176140	CNhi10473_CAC.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15661087	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176075	CNhi10463_AGT.experiment	Targeted	NA	1	LINC00702	Homo sapiens	FANTOM6 project	PRJDB7993	17043508	47	CAGE	ASO_G0233117_04	HDF (neonatal)
DRR176074	CNhi10463_ACG.experiment	Targeted	NA	1	FGD5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15200062	47	CAGE	ASO_G0225733_03	HDF (neonatal)
DRR176073	CNhi10463_ACC.experiment	Targeted	NA	1	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	17492543	47	CAGE	ASO_G0163364_04	HDF (neonatal)
DRR176072	CNhi10462_TAC.experiment	Targeted	NA	1	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	19195486	47	CAGE	ASO_G0214548_01	HDF (neonatal)
DRR176071	CNhi10462_GCT.experiment	Targeted	NA	1	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	14195244	47	CAGE	ASO_G0224597_06	HDF (neonatal)
DRR176070	CNhi10462_CAC.experiment	Targeted	NA	1	LINC00339	Homo sapiens	FANTOM6 project	PRJDB7993	12421822	47	CAGE	ASO_G0218510_04	HDF (neonatal)
DRR176069	CNhi10462_ATG.experiment	Targeted	NA	1	LINC00702	Homo sapiens	FANTOM6 project	PRJDB7993	16219421	47	CAGE	ASO_G0233117_02	HDF (neonatal)

DRR176068	CNhi10462_AGT.experiment	Targeted	NA	1	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	17494989	47	CAGE	ASO_G0230590_05	HDF (neonatal)
DRR177147	CNhi10865_TAC.experiment	Targeted	NA	23	XRN2	Homo sapiens	FANTOM6 project	PRJDB7993	22266081	47	CAGE	siRNA_siXRN-2	HDF (neonatal)
DRR177146	CNhi10865_GCG.experiment	Negative control	NA	23	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9212750	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR177145	CNhi10865_ATG.experiment	Targeted	NA	23	XRN2	Homo sapiens	FANTOM6 project	PRJDB7993	15053272	47	CAGE	siRNA_siXRN-1	HDF (neonatal)
DRR177144	CNhi10844_GCG.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	9995934	47	CAGE	sgRNA_FTX_gRNA3	HDF (neonatal)
DRR177143	CNhi10844_CAC.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	12767490	47	CAGE	sgRNA_TERC_gRNA1 sg	HDF (neonatal)
DRR177142	CNhi10844_ATG.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	20564005	47	CAGE	sgRNA_FTX_gRNA1 sgRN	HDF (neonatal)
DRR177141	CNhi10844_AGT.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	15313293	47	CAGE	sgRNA_FTX_gRNA1	HDF (neonatal)
DRR177140	CNhi10844_ACC.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	16574444	47	CAGE	sgRNA_TERC_gRNA4	HDF (neonatal)
DRR177075	CNhi10831_ACC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	20483490	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177074	CNhi10830_TAC.experiment	Targeted	NA	19	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	27162797	47	CAGE	ASO_G0245937_AD_05	HDF (neonatal)
DRR177073	CNhi10830_GCT.experiment	Targeted	NA	18	ZNF131	Homo sapiens	FANTOM6 project	PRJDB7993	10355362	47	CAGE	ASO_C0008543_AD_10	HDF (neonatal)
DRR177072	CNhi10830_GCG.experiment	Targeted	NA	19	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	11014680	47	CAGE	ASO_G0245937_AD_02	HDF (neonatal)
DRR177071	CNhi10830_CAC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13627469	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177070	CNhi10830_ATG.experiment	Targeted	NA	21	JPX	Homo sapiens	FANTOM6 project	PRJDB7993	17886974	47	CAGE	ASO_G0225470_AD_04	HDF (neonatal)
DRR177069	CNhi10830_AGT.experiment	Targeted	NA	19	ZSCAN16-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10910014	47	CAGE	ASO_G0269293_AD_10	HDF (neonatal)
DRR177068	CNhi10830_ACG.experiment	Targeted	NA	19	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	20803362	47	CAGE	ASO_G0245213_AD_04	HDF (neonatal)
DRR177003	CNhi10813_TAC.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	23272562	47	CAGE	ASO_G0134153_POS_07	HDF (neonatal)
DRR177002	CNhi10813_GCT.experiment	Targeted	NA	20	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	10780354	47	CAGE	siRNA_n269549	HDF (neonatal)
DRR177001	CNhi10813_GCG.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11389369	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR177000	CNhi10813_CAC.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12916594	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR176999	CNhi10813_ATG.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16964472	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR176998	CNhi10813_AGT.experiment	Experiment control	NA	20	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	13265771	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176997	CNhi10813_ACG.experiment	Targeted	NA	21	LINC00959	Homo sapiens	FANTOM6 project	PRJDB7993	17490421	47	CAGE	ASO_G0237489_AD_01	HDF (neonatal)
DRR176996	CNhi10813_ACC.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19831236	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176931	CNhi10803_GCT.experiment	Targeted	NA	21	TMCC1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13589048	47	CAGE	ASO_G0271270_AD_10	HDF (neonatal)
DRR176930	CNhi10803_GCG.experiment	Experiment control	NA	19	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12934259	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176929	CNhi10803_CAC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9884362	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176928	CNhi10803_AGT.experiment	Targeted	NA	21	ZNF674-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15488003	47	CAGE	ASO_G0230844_AD_06	HDF (neonatal)
DRR176927	CNhi10803_ACG.experiment	Targeted	NA	21	TRAM2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	17591760	47	CAGE	ASO_G0225791_AD_05	HDF (neonatal)
DRR176926	CNhi10803_ACC.experiment	Targeted	NA	19	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	22654802	47	CAGE	ASO_G0245213_AD_03	HDF (neonatal)
DRR176925	CNhi10801_TAC.experiment	Targeted	NA	21	ZNF674-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16429002	47	CAGE	ASO_G0230844_AD_06	HDF (neonatal)
DRR176924	CNhi10801_GCT.experiment	Experiment control	NA	19	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12981015	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176859	CNhi10786_CAC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13407050	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176858	CNhi10786_ATG.experiment	Targeted	NA	15	LINC00674	Homo sapiens	FANTOM6 project	PRJDB7993	22500218	47	CAGE	ASO_G0237854_AD_04	HDF (neonatal)
DRR176857	CNhi10786_AGT.experiment	Targeted	NA	16	CTD-2319I12.4	Homo sapiens	FANTOM6 project	PRJDB7993	17499042	47	CAGE	ASO_G0267248_AD_07	HDF (neonatal)
DRR176856	CNhi10786_ACG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	18982157	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176855	CNhi10786_ACC.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	24129021	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176854	CNhi10785_TAC.experiment	Targeted	NA	15	UBL7-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	23995761	47	CAGE	ASO_G0247240_AD_05	HDF (neonatal)
DRR176853	CNhi10785_GCT.experiment	Targeted	NA	15	DNAJC27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14270899	47	CAGE	ASO_G0224165_AD_07	HDF (neonatal)
DRR176852	CNhi10785_CAC.experiment	Targeted	NA	16	AC009005.2	Homo sapiens	FANTOM6 project	PRJDB7993	15040228	47	CAGE	ASO_G0267751_AD_02	HDF (neonatal)
DRR176787	CNhi10763_AGT.experiment	Targeted	NA	14	RP11-54A9.1	Homo sapiens	FANTOM6 project	PRJDB7993	16807513	47	CAGE	ASO_G0257219_AD_10	HDF (neonatal)
DRR176786	CNhi10763_ACG.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12903573	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176785	CNhi10763_ACC.experiment	Experiment control	NA	14	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	18573976	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176784	CNhi10762_TAC.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	22431766	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176783	CNhi10762_GCT.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15133454	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176782	CNhi10762_GCG.experiment	Targeted	NA	14	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	15866689	47	CAGE	ASO_G0261105_AD_10	HDF (neonatal)
DRR176781	CNhi10762_CAC.experiment	Targeted	NA	14	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	10965846	47	CAGE	ASO_G0270141_AD_10	HDF (neonatal)
DRR176780	CNhi10762_ATG.experiment	Targeted	NA	14	CTD-2651B20.3	Homo sapiens	FANTOM6 project	PRJDB7993	23608421	47	CAGE	ASO_G0259520_AD_08	HDF (neonatal)
DRR176715	CNhi10638_ACC.experiment	Targeted	NA	12	RP6-99M1.2	Homo sapiens	FANTOM6 project	PRJDB7993	15226663	47	CAGE	ASO_G0270069_AD_07	HDF (neonatal)
DRR176714	CNhi10637_TAC.experiment	Targeted	NA	12	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	18297779	47	CAGE	ASO_G0224577_AD_05	HDF (neonatal)
DRR176713	CNhi10637_GCT.experiment	Targeted	NA	12	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	14132462	47	CAGE	ASO_G0163364_AD_01	HDF (neonatal)
DRR176712	CNhi10637_GCG.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13491334	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176711	CNhi10637_CAC.experiment	Negative control	NA	12	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12913482	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176710	CNhi10637_ATG.experiment	Targeted	NA	12	TUG1	Homo sapiens	FANTOM6 project	PRJDB7993	13187568	47	CAGE	ASO_G0253352_AD_07	HDF (neonatal)
DRR176709	CNhi10637_AGT.experiment	Targeted	NA	12	LINC00657	Homo sapiens	FANTOM6 project	PRJDB7993	9691434	47	CAGE	ASO_G0260032_AD_01	HDF (neonatal)
DRR176708	CNhi10637_ACG.experiment	Targeted	NA	12	ERVK3-1	Homo sapiens	FANTOM6 project	PRJDB7993	17282502	47	CAGE	ASO_G0142396_AD_01	HDF (neonatal)
DRR176643	CNhi10612_TAC.experiment	Targeted	NA	10	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	12426973	47	CAGE	ASO_G0244625_09	HDF (neonatal)
DRR176642	CNhi10612_GCT.experiment	Targeted	NA	10	RP11-379H18.1	Homo sapiens	FANTOM6 project	PRJDB7993	11312664	47	CAGE	ASO_G0271122_05	HDF (neonatal)
DRR176641	CNhi10612_GCG.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	8554159	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176640	CNhi10612_CAC.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	10598063	47	CAGE	ASO_G0255121_08	HDF (neonatal)
DRR176639	CNhi10612_ATG.experiment	Targeted	NA	10	LINC00707	Homo sapiens	FANTOM6 project	PRJDB7993	10820903	47	CAGE	ASO_G0238266_03	HDF (neonatal)
DRR176638	CNhi10612_AGT.experiment	Targeted	NA	11	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10342208	47	CAGE	ASO_G0246067_AD_09	HDF (neonatal)
DRR176637	CNhi10612_ACG.experiment	Targeted	NA	10	CTC-228N24.3	Homo sapiens	FANTOM6 project	PRJDB7993	11000331	47	CAGE	ASO_G0245937_01	HDF (neonatal)
DRR176636	CNhi10612_ACC.experiment	Targeted	NA	11	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12006165	47	CAGE	ASO_G0246067_AD_06	HDF (neonatal)
DRR176571	CNhi10603_GCG.experiment	Targeted	NA	10	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	9602476	47	CAGE	ASO_G0246985_10	HDF (neonatal)
DRR176570	CNhi10603_CAC.experiment	Targeted	NA	10	RP13-463N16.6	Homo sapiens	FANTOM6 project	PRJDB7993	12878134	47	CAGE	ASO_G0242147_07	HDF (neonatal)
DRR176569	CNhi10603_ATG.experiment	Targeted	NA	10	CKMT2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10217996	47	CAGE	ASO_G0247572_08	HDF (neonatal)
DRR176568	CNhi10603_AGT.experiment	Targeted	NA	11	TP53TG1	Homo sapiens	FANTOM6 project	PRJDB7993	11620780	47	CAGE	ASO_G0182165_AD_08	HDF (neonatal)
DRR176567	CNhi10603_ACG.experiment	Targeted	NA	10	SBF2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10807510	47	CAGE	ASO_G0246273_02	HDF (neonatal)
DRR176566	CNhi10603_ACC.experiment	Targeted	NA	10	SRP14-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14016720	47	CAGE	ASO_G0248508_10	HDF (neonatal)
DRR176565	CNhi10602_TAC.experiment	Negative control	NA	11	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15535241	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176564	CNhi10602_GCT.experiment	Targeted	NA	10	RP6-109B7.3	Homo sapiens	FANTOM6 project	PRJDB7993	15350985	47	CAGE	ASO_G0241990_07	HDF (neonatal)
DRR176499	CNhi10582_ATG.experiment	Targeted	NA	9	RP11-173B14.5	Homo sapiens	FANTOM6 project	PRJDB7993	14226731	47	CAGE	ASO_G0261105_02	HDF (neonatal)
DRR176498	CNhi10582_AGT.experiment	Targeted	NA	9	RP11-22P6.3	Homo sapiens	FANTOM6 project	PRJDB7993	12327209	47	CAGE	ASO_G0260442_01	HDF (neonatal)
DRR176497	CNhi10582_ACG.experiment	Targeted	NA	9	RP11-863P13.3	Homo sapiens	FANTOM6 project	PRJDB7993	12325726	47	CAGE	ASO_G0261327_05	HDF (neonatal)
DRR176496	CNhi10582_ACC.experiment	Targeted	NA	9	RP11-253M7.1	Homo sapiens	FANTOM6 project	PRJDB7993	17087797	47	CAGE	ASO_G0259426_02	HDF (neonatal)
DRR176495	CNhi10581_TAC.experiment	Targeted	NA	9	FOXN3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14675723	47	CAGE	ASO_G0258920_01	HDF (neonatal)
DRR176494	CNhi10581_GCT.experiment	Targeted	NA	9	RP11-253M7.1	Homo sapiens	FANTOM6 project	PRJDB7993	14053872	47	CAGE	ASO_G0259426_02	HDF (neonatal)

DRR176493	CNhi10581_GCG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12106544	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176492	CNhi10581_CAC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13966469	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176427	CNhi10541_ACG.experiment	Targeted	NA	6	RP11-220I1.1	Homo sapiens	FANTOM6 project	PRJDB7993	11123665	47	CAGE	ASO_G0233137_05	HDF (neonatal)
DRR176426	CNhi10541_ACC.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11800868	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176425	CNhi10540_TAC.experiment	Targeted	NA	6	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11799170	47	CAGE	ASO_G0234608_06	HDF (neonatal)
DRR176424	CNhi10540_GCT.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	13984626	47	CAGE	ASO_C0008202_02	HDF (neonatal)
DRR176423	CNhi10540_GCG.experiment	Targeted	NA	5	CATG00000016989.1	Homo sapiens	FANTOM6 project	PRJDB7993	11104412	47	CAGE	ASO_C0020443_03	HDF (neonatal)
DRR176422	CNhi10540_CAC.experiment	Targeted	NA	5	RP11-622K12.1	Homo sapiens	FANTOM6 project	PRJDB7993	10844147	47	CAGE	ASO_G0204272_04	HDF (neonatal)
DRR176421	CNhi10540_ATG.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	12571318	47	CAGE	ASO_C0008202_01	HDF (neonatal)
DRR176420	CNhi10540_AGT.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13238245	47	CAGE	ASO_G0186615_09	HDF (neonatal)
DRR176355	CNhi10532_ACC.experiment	Targeted	NA	4	RP11-395B7.4	Homo sapiens	FANTOM6 project	PRJDB7993	13374543	47	CAGE	ASO_G0227053_04	HDF (neonatal)
DRR176354	CNhi10531_TAC.experiment	Targeted	NA	4	SUGT1P	Homo sapiens	FANTOM6 project	PRJDB7993	12015756	47	CAGE	ASO_G0226823_03	HDF (neonatal)
DRR176353	CNhi10531_GCT.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11820256	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176352	CNhi10531_GCG.experiment	Targeted	NA	5	WDFY3-AS2	Homo sapiens	FANTOM6 project	PRJDB7993	8397642	47	CAGE	ASO_G0180769_08	HDF (neonatal)
DRR176351	CNhi10531_CAC.experiment	Targeted	NA	5	CATG00000020700.1	Homo sapiens	FANTOM6 project	PRJDB7993	11601366	47	CAGE	ASO_C0020984_02	HDF (neonatal)
DRR176350	CNhi10531_ATG.experiment	Targeted	NA	4	RP4-773A18.4	Homo sapiens	FANTOM6 project	PRJDB7993	10808666	47	CAGE	ASO_G0227811_06	HDF (neonatal)
DRR176349	CNhi10531_AGT.experiment	Targeted	NA	4	MFI2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11821692	47	CAGE	ASO_G0228109_07	HDF (neonatal)
DRR176348	CNhi10531_ACG.experiment	Targeted	NA	4	RP11-395B7.4	Homo sapiens	FANTOM6 project	PRJDB7993	11530324	47	CAGE	ASO_G0227053_03	HDF (neonatal)
DRR176283	CNhi10522_GCT.experiment	Targeted	NA	4	PCAT6	Homo sapiens	FANTOM6 project	PRJDB7993	16919426	47	CAGE	ASO_G0228288_01	HDF (neonatal)
DRR176282	CNhi10522_GCG.experiment	Negative control	NA	5	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13824230	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176281	CNhi10522_CAC.experiment	Targeted	NA	4	JPX	Homo sapiens	FANTOM6 project	PRJDB7993	16348095	47	CAGE	ASO_G0225470_05	HDF (neonatal)
DRR176280	CNhi10522_ATG.experiment	Targeted	NA	4	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	6267614	47	CAGE	ASO_G0219665_08	HDF (neonatal)
DRR176279	CNhi10522_AGT.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	18248582	47	CAGE	ASO_G0223773_05	HDF (neonatal)
DRR176278	CNhi10522_ACG.experiment	Targeted	NA	4	CD27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15522154	47	CAGE	ASO_G0215039_01	HDF (neonatal)
DRR176277	CNhi10522_ACC.experiment	Targeted	NA	5	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	19880566	47	CAGE	ASO_C0011632_03	HDF (neonatal)
DRR176276	CNhi10521_TAC.experiment	Targeted	NA	4	CD27-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18366909	47	CAGE	ASO_G0215039_01	HDF (neonatal)
DRR176211	CNhi10490_GCG.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	14460822	47	CAGE	ASO_G0234171_06	HDF (neonatal)
DRR176210	CNhi10490_CAC.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	11307055	47	CAGE	ASO_G0240875_02	HDF (neonatal)
DRR176209	CNhi10490_ATG.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	16000638	47	CAGE	ASO_G0240875_03	HDF (neonatal)
DRR176208	CNhi10490_AGT.experiment	Targeted	NA	3	RP11-10K16.1	Homo sapiens	FANTOM6 project	PRJDB7993	17275626	47	CAGE	ASO_G0245213_04	HDF (neonatal)
DRR176207	CNhi10490_ACG.experiment	Targeted	NA	3	LINC00856	Homo sapiens	FANTOM6 project	PRJDB7993	13652351	47	CAGE	ASO_G0230417_01	HDF (neonatal)
DRR176206	CNhi10490_ACC.experiment	Targeted	NA	3	LINC00517	Homo sapiens	FANTOM6 project	PRJDB7993	14077891	47	CAGE	ASO_G0259091_01	HDF (neonatal)
DRR176205	CNhi10489_TAC.experiment	Targeted	NA	3	RP11-500C11.3	Homo sapiens	FANTOM6 project	PRJDB7993	17142828	47	CAGE	ASO_G0272269_06	HDF (neonatal)
DRR176204	CNhi10489_GCT.experiment	Negative control	NA	3	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15054983	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176139	CNhi10473_ATG.experiment	Targeted	NA	2	RP11-611E13.2	Homo sapiens	FANTOM6 project	PRJDB7993	19341728	47	CAGE	ASO_G0257815_01	HDF (neonatal)
DRR176138	CNhi10473_AGT.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	16812682	47	CAGE	ASO_G0212978_02	HDF (neonatal)
DRR176137	CNhi10473_ACG.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	15343797	47	CAGE	ASO_G0212978_04	HDF (neonatal)
DRR176136	CNhi10473_ACC.experiment	Negative control	NA	2	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19771257	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176135	CNhi10472_TAC.experiment	Targeted	NA	2	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	23158002	47	CAGE	ASO_G0229852_05	HDF (neonatal)
DRR176134	CNhi10472_GCT.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	17414736	47	CAGE	ASO_G0263072_01	HDF (neonatal)
DRR176133	CNhi10472_GCG.experiment	Targeted	NA	2	AC016747.3	Homo sapiens	FANTOM6 project	PRJDB7993	15146085	47	CAGE	ASO_G0212978_01	HDF (neonatal)
DRR176132	CNhi10472_CAC.experiment	Targeted	NA	2	RP11-473M20.14	Homo sapiens	FANTOM6 project	PRJDB7993	15159810	47	CAGE	ASO_G0263072_05	HDF (neonatal)
DRR176067	CNhi10462_ACG.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14049470	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176066	CNhi10462_ACC.experiment	Targeted	NA	1	RP6-99M1.2	Homo sapiens	FANTOM6 project	PRJDB7993	20499075	47	CAGE	ASO_G0270069_05	HDF (neonatal)
DRR176065	CNhi10461_TAC.experiment	Targeted	NA	1	RP3-510D11.2	Homo sapiens	FANTOM6 project	PRJDB7993	17807326	47	CAGE	ASO_G0234546_01	HDF (neonatal)
DRR176064	CNhi10461_GCT.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	17579848	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176063	CNhi10461_CAC.experiment	Targeted	NA	1	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	13483938	47	CAGE	ASO_G0229847_03	HDF (neonatal)
DRR176062	CNhi10461_ATG.experiment	Targeted	NA	1	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	15651015	47	CAGE	ASO_G0226950_02	HDF (neonatal)
DRR176061	CNhi10461_AGT.experiment	Targeted	NA	1	RAB30-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	21575839	47	CAGE	ASO_G0246067_01	HDF (neonatal)
DRR176060	CNhi10461_ACG.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13530144	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177139	CNhi10843_TAC.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23443023	47	CAGE	sgRNA_NC_gRNA1	HDF (neonatal)
DRR177138	CNhi10843_GCT.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	12180047	47	CAGE	sgRNA_TERC_gRNA1	HDF (neonatal)
DRR177137	CNhi10843_GCG.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	12824896	47	CAGE	sgRNA_FTX_gRNA3	HDF (neonatal)
DRR176448	CNhi10543_TAC.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	14503377	47	CAGE	ASO_C0008202_01	HDF (neonatal)
DRR176447	CNhi10543_GCT.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14323258	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176446	CNhi10543_GCG.experiment	Targeted	NA	6	MAPKAPK5-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11940335	47	CAGE	ASO_G0234608_06	HDF (neonatal)
DRR176445	CNhi10543_CAC.experiment	Targeted	NA	6	ZNF37BP	Homo sapiens	FANTOM6 project	PRJDB7993	11394708	47	CAGE	ASO_G0234420_01	HDF (neonatal)
DRR176444	CNhi10543_ATG.experiment	Targeted	NA	5	CATG00000090305.1	Homo sapiens	FANTOM6 project	PRJDB7993	12174880	47	CAGE	ASO_C0011140_06	HDF (neonatal)
DRR176379	CNhi10535_ACC.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	14698908	47	CAGE	ASO_G0233527_03	HDF (neonatal)
DRR176378	CNhi10534_TAC.experiment	Targeted	NA	5	AMZ2P1	Homo sapiens	FANTOM6 project	PRJDB7993	12328135	47	CAGE	ASO_G0214174_06	HDF (neonatal)
DRR176377	CNhi10534_GCT.experiment	Experiment control	NA	5	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15226344	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176376	CNhi10534_GCG.experiment	Targeted	NA	6	AC012146.7	Homo sapiens	FANTOM6 project	PRJDB7993	8922371	47	CAGE	ASO_G0234327_07	HDF (neonatal)
DRR176375	CNhi10534_CAC.experiment	Targeted	NA	5	AMZ2P1	Homo sapiens	FANTOM6 project	PRJDB7993	10882945	47	CAGE	ASO_G0214174_06	HDF (neonatal)
DRR176374	CNhi10534_ATG.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	8214294	47	CAGE	ASO_G0186615_04	HDF (neonatal)
DRR176373	CNhi10534_AGT.experiment	Targeted	NA	5	FLVCR1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12599527	47	CAGE	ASO_G0198468_01	HDF (neonatal)
DRR176372	CNhi10534_ACG.experiment	Targeted	NA	5	KTN1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	11265897	47	CAGE	ASO_G0186615_03	HDF (neonatal)
DRR176307	CNhi10525_TAC.experiment	Targeted	NA	4	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	17486887	47	CAGE	ASO_G0225554_02	HDF (neonatal)
DRR176306	CNhi10525_GCT.experiment	Targeted	NA	5	RP11-474P2.4	Homo sapiens	FANTOM6 project	PRJDB7993	17799195	47	CAGE	ASO_C0019316_01	HDF (neonatal)
DRR176305	CNhi10525_GCG.experiment	Targeted	NA	4	LL22NC03-86G7.1	Homo sapiens	FANTOM6 project	PRJDB7993	14176621	47	CAGE	ASO_G0224086_06	HDF (neonatal)
DRR176304	CNhi10525_CAC.experiment	Targeted	NA	5	RP11-474P2.4	Homo sapiens	FANTOM6 project	PRJDB7993	16902977	47	CAGE	ASO_C0019316_08	HDF (neonatal)
DRR176303	CNhi10525_ATG.experiment	Targeted	NA	5	RP11-474P2.4	Homo sapiens	FANTOM6 project	PRJDB7993	15755654	47	CAGE	ASO_C0019316_08	HDF (neonatal)
DRR176302	CNhi10525_AGT.experiment	Negative control	NA	4	NA	Homo sapiens	FANTOM6 project	PRJDB7993	21533454	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176301	CNhi10525_ACG.experiment	Targeted	NA	4	CD99P1	Homo sapiens	FANTOM6 project	PRJDB7993	15081118	47	CAGE	ASO_G0223773_06	HDF (neonatal)
DRR176300	CNhi10525_ACC.experiment	Targeted	NA	5	RP11-474P2.4	Homo sapiens	FANTOM6 project	PRJDB7993	17074292	47	CAGE	ASO_C0019316_01	HDF (neonatal)
DRR176235	CNhi10493_GCG.experiment	Targeted	NA	3	AC004980.7	Homo sapiens	FANTOM6 project	PRJDB7993	12570418	47	CAGE	ASO_G0205485_01	HDF (neonatal)
DRR176234	CNhi10493_CAC.experiment	Targeted	NA	3	AC108488.3	Homo sapiens	FANTOM6 project	PRJDB7993	10427972	47	CAGE	ASO_G0234171_09	HDF (neonatal)
DRR176233	CNhi10493_ATG.experiment	Targeted	NA	3	AC007246.3	Homo sapiens	FANTOM6 project	PRJDB7993	16394140	47	CAGE	ASO_G0231312_02	HDF (neonatal)
DRR176232	CNhi10493_AGT.experiment	Targeted	NA	3	ZNF674-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14956403	47	CAGE	ASO_G0230844_01	HDF (neonatal)
DRR176231	CNhi10493_ACG.experiment	Targeted	NA	3	AC091729.9	Homo sapiens	FANTOM6 project	PRJDB7993	12494530	47	CAGE	ASO_G0229043_07	HDF (neonatal)
DRR176230	CNhi10493_ACC.experiment	Targeted	NA	3	LINC00886	Homo sapiens	FANTOM6 project	PRJDB7993	12134286	47	CAGE	ASO_G0240875_03	HDF (neonatal)
DRR176229	CNhi10492_TAC.experiment	Targeted	NA	3	AP001258.4	Homo sapiens	FANTOM6 project	PRJDB7993	19456432	47	CAGE	ASO_G0245571_06	HDF (neonatal)
DRR176228	CNhi10492_GCT.experiment	Targeted	NA	3	CTD-2587H24.5	Homo sapiens	FANTOM6 project	PRJDB7993	15912842	47	CAGE	ASO_G0267577_01	HDF (neonatal)

DRR176163	CNhi10476_CAC.experiment	Targeted	NA	2	RP11-195F19.9	Homo sapiens	FANTOM6 project	PRJDB7993	14704089	47	CAGE	ASO_G0230074_07	HDF (neonatal)
DRR176162	CNhi10476_ATG.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	16087204	47	CAGE	ASO_G0233901_04	HDF (neonatal)
DRR176161	CNhi10476_AGT.experiment	Targeted	NA	2	BX322557.10	Homo sapiens	FANTOM6 project	PRJDB7993	18493737	47	CAGE	ASO_G0215447_01	HDF (neonatal)
DRR176160	CNhi10476_ACG.experiment	Targeted	NA	2	A1BG-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14631444	47	CAGE	ASO_G0268895_03	HDF (neonatal)
DRR176159	CNhi10476_ACC.experiment	Targeted	NA	2	RP11-195F19.9	Homo sapiens	FANTOM6 project	PRJDB7993	20736809	47	CAGE	ASO_G0230074_07	HDF (neonatal)
DRR176158	CNhi10475_TAC.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	21935610	47	CAGE	ASO_G0233901_02	HDF (neonatal)
DRR176157	CNhi10475_GCT.experiment	Targeted	NA	2	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	20260394	47	CAGE	ASO_G0229852_03	HDF (neonatal)
DRR176156	CNhi10475_CAC.experiment	Experiment control	NA	2	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	15105188	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176091	CNhi10467_AGT.experiment	Targeted	NA	2	RP11-195F19.9	Homo sapiens	FANTOM6 project	PRJDB7993	18530343	47	CAGE	ASO_G0230074_05	HDF (neonatal)
DRR176090	CNhi10467_ACG.experiment	Targeted	NA	2	SERTAD4-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18647594	47	CAGE	ASO_G0203706_01	HDF (neonatal)
DRR176089	CNhi10467_ACC.experiment	Targeted	NA	2	RP11-458D21.1	Homo sapiens	FANTOM6 project	PRJDB7993	17286834	47	CAGE	ASO_G0233396_07	HDF (neonatal)
DRR176088	CNhi10466_TAC.experiment	Targeted	NA	2	RP11-150O12.1	Homo sapiens	FANTOM6 project	PRJDB7993	24153957	47	CAGE	ASO_C013368_01	HDF (neonatal)
DRR176087	CNhi10466_GCT.experiment	Targeted	NA	2	AC027612.6	Homo sapiens	FANTOM6 project	PRJDB7993	16366089	47	CAGE	ASO_G0143429_05	HDF (neonatal)
DRR176086	CNhi10466_GCG.experiment	Targeted	NA	2	RP11-65J3.1	Homo sapiens	FANTOM6 project	PRJDB7993	13427008	47	CAGE	ASO_G0233901_05	HDF (neonatal)
DRR176085	CNhi10466_CAC.experiment	Targeted	NA	2	A1BG-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	18970912	47	CAGE	ASO_G0268895_03	HDF (neonatal)
DRR176084	CNhi10466_ATG.experiment	Targeted	NA	2	RP11-458D21.1	Homo sapiens	FANTOM6 project	PRJDB7993	18474667	47	CAGE	ASO_G0233396_07	HDF (neonatal)
DRR177091	CNhi10833_ACC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	19134187	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177090	CNhi10832_TAC.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	19516719	47	CAGE	ASO_C0012015_AD_02	HDF (neonatal)
DRR177089	CNhi10832_GCT.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11832532	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR177088	CNhi10832_GCG.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	13300348	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177087	CNhi10832_CAC.experiment	Targeted	NA	18	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	10384372	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR177086	CNhi10832_ATG.experiment	Targeted	NA	19	CTD-2336O2.1	Homo sapiens	FANTOM6 project	PRJDB7993	27721514	47	CAGE	ASO_G0253982_AD_01	HDF (neonatal)
DRR177085	CNhi10832_AGT.experiment	Targeted	NA	19	NR2F1-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13530817	47	CAGE	ASO_G0237187_AD_01	HDF (neonatal)
DRR177084	CNhi10832_ACG.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17993361	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR177019	CNhi10815_TAC.experiment	Targeted	NA	20	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	18537536	47	CAGE	siRNA_n269549	HDF (neonatal)
DRR177018	CNhi10815_GCT.experiment	Targeted	NA	21	LINC00707	Homo sapiens	FANTOM6 project	PRJDB7993	14406830	47	CAGE	ASO_G0238266_AD_06	HDF (neonatal)
DRR177017	CNhi10815_GCG.experiment	Targeted	NA	13	RP11-149I23.3	Homo sapiens	FANTOM6 project	PRJDB7993	13854783	47	CAGE	ASO_G0232110_AD_06	HDF (neonatal)
DRR177016	CNhi10815_CAC.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	13379732	47	CAGE	siRNA_ADAAYU4	HDF (neonatal)
DRR177015	CNhi10815_ATG.experiment	Negative control	NA	13	NA	Homo sapiens	FANTOM6 project	PRJDB7993	17496519	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR177014	CNhi10815_AGT.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	17684190	47	CAGE	ASO_G0134153_POS_07	HDF (neonatal)
DRR177013	CNhi10815_ACG.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	20573720	47	CAGE	ASO_G0134153_POS_05	HDF (neonatal)
DRR177012	CNhi10815_ACC.experiment	Targeted	NA	17	FOXN3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	15320993	47	CAGE	ASO_G0258920_AD_07	HDF (neonatal)
DRR176011	CNhi10454_TAC.experiment	Targeted	NA	1	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	23299491	47	CAGE	ASO_G0229847_01	HDF (neonatal)
DRR176010	CNhi10454_GCT.experiment	Targeted	NA	1	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	17931318	47	CAGE	ASO_G0224597_05	HDF (neonatal)
DRR176009	CNhi10454_GCG.experiment	Targeted	NA	1	RP11-417E7.1	Homo sapiens	FANTOM6 project	PRJDB7993	14015331	47	CAGE	ASO_G0223485_01	HDF (neonatal)
DRR176008	CNhi10454_CAC.experiment	Negative control	NA	1	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12960823	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176007	CNhi10454_ATG.experiment	Experiment control	NA	1	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	16324581	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176006	CNhi10454_AGT.experiment	Targeted	NA	1	MEG3	Homo sapiens	FANTOM6 project	PRJDB7993	18085898	47	CAGE	ASO_G0214548_01	HDF (neonatal)
DRR176005	CNhi10454_ACG.experiment	Targeted	NA	1	PTCHD3P1	Homo sapiens	FANTOM6 project	PRJDB7993	14512452	47	CAGE	ASO_G0224597_05	HDF (neonatal)
DRR176004	CNhi10454_ACC.experiment	Targeted	NA	1	AC017048.4	Homo sapiens	FANTOM6 project	PRJDB7993	17330792	47	CAGE	ASO_G0224577_01	HDF (neonatal)
DRR176947	CNhi10805_GCT.experiment	Targeted	NA	19	CTD-2336O2.1	Homo sapiens	FANTOM6 project	PRJDB7993	12336277	47	CAGE	ASO_G0253982_AD_01	HDF (neonatal)
DRR176946	CNhi10805_GCG.experiment	Targeted	NA	19	ZSCAN16-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10376190	47	CAGE	ASO_G0269293_AD_10	HDF (neonatal)
DRR176945	CNhi10805_CAC.experiment	Targeted	NA	19	RP11-539L10.3	Homo sapiens	FANTOM6 project	PRJDB7993	10497605	47	CAGE	ASO_G0251580_AD_05	HDF (neonatal)
DRR176944	CNhi10805_ATG.experiment	Targeted	NA	21	AC091729.9	Homo sapiens	FANTOM6 project	PRJDB7993	17459941	47	CAGE	ASO_G0229043_AD_04	HDF (neonatal)
DRR176943	CNhi10805_AGT.experiment	Targeted	NA	18	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	13044707	47	CAGE	ASO_C0011632_AD_01	HDF (neonatal)
DRR176942	CNhi10805_ACG.experiment	Targeted	NA	19	RP11-33B1.1	Homo sapiens	FANTOM6 project	PRJDB7993	16466257	47	CAGE	ASO_G0245958_AD_07	HDF (neonatal)
DRR176941	CNhi10805_ACC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16524020	47	CAGE	ASO_Lipo	HDF (neonatal)
DRR176940	CNhi10804_TAC.experiment	Negative control	NA	19	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14869760	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176875	CNhi10788_CAC.experiment	Targeted	NA	16	LINC00667	Homo sapiens	FANTOM6 project	PRJDB7993	13995528	47	CAGE	ASO_G0263753_AD_01	HDF (neonatal)
DRR176874	CNhi10788_ATG.experiment	Experiment control	NA	16	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	17985879	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176873	CNhi10788_AGT.experiment	Targeted	NA	16	RP11-333E1.1	Homo sapiens	FANTOM6 project	PRJDB7993	15933723	47	CAGE	ASO_G0261879_AD_07	HDF (neonatal)
DRR176872	CNhi10788_ACG.experiment	Targeted	NA	17	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	19355784	47	CAGE	ASO_G0272888_AD_07	HDF (neonatal)
DRR176871	CNhi10788_ACC.experiment	Targeted	NA	15	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	28305515	47	CAGE	ASO_G0244625_AD_08	HDF (neonatal)
DRR176870	CNhi10787_TAC.experiment	Targeted	NA	16	RP11-333E1.1	Homo sapiens	FANTOM6 project	PRJDB7993	24399594	47	CAGE	ASO_G0261879_AD_07	HDF (neonatal)
DRR176869	CNhi10787_GCT.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15790649	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176868	CNhi10787_GCG.experiment	Targeted	NA	16	CTC-559E9.6	Homo sapiens	FANTOM6 project	PRJDB7993	14310408	47	CAGE	ASO_G0267419_AD_04	HDF (neonatal)
DRR176803	CNhi10765_AGT.experiment	Experiment control	NA	14	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	18093119	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176802	CNhi10765_ACG.experiment	Targeted	NA	14	RP11-553K8.5	Homo sapiens	FANTOM6 project	PRJDB7993	14779060	47	CAGE	ASO_G0261573_AD_06	HDF (neonatal)
DRR177136	CNhi10843_CAC.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	13639309	47	CAGE	sgRNA_TERC_gRNA1 sg	HDF (neonatal)
DRR177135	CNhi10843_ATG.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	18590338	47	CAGE	sgRNA_FTX_gRNA1 sgRN	HDF (neonatal)
DRR177134	CNhi10843_AGT.experiment	Targeted	NA	22	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	13319765	47	CAGE	sgRNA_FTX_gRNA1	HDF (neonatal)
DRR177133	CNhi10843_ACC.experiment	Targeted	NA	22	TERC	Homo sapiens	FANTOM6 project	PRJDB7993	17349932	47	CAGE	sgRNA_TERC_gRNA4	HDF (neonatal)
DRR177132	CNhi10842_TAC.experiment	Negative control	NA	22	NA	Homo sapiens	FANTOM6 project	PRJDB7993	15548859	47	CAGE	sgRNA_NC_gRNA1	HDF (neonatal)
DRR177067	CNhi10830_ACC.experiment	Targeted	NA	21	RP11-398K22.12	Homo sapiens	FANTOM6 project	PRJDB7993	22569097	47	CAGE	ASO_G0229852_AD_01	HDF (neonatal)
DRR177066	CNhi10821_TAC.experiment	Negative control	NA	21	NA	Homo sapiens	FANTOM6 project	PRJDB7993	24057977	47	CAGE	siRNA_NC_2	HDF (neonatal)
DRR177065	CNhi10821_GCT.experiment	Targeted	NA	20	EXOSC3	Homo sapiens	FANTOM6 project	PRJDB7993	9258485	47	CAGE	siRNA_s27231	HDF (neonatal)
DRR177064	CNhi10821_GCG.experiment	Targeted	NA	20	SNRPD3	Homo sapiens	FANTOM6 project	PRJDB7993	10112718	47	CAGE	siRNA_s13235	HDF (neonatal)
DRR177063	CNhi10821_CAC.experiment	Targeted	NA	20	EXOSC3	Homo sapiens	FANTOM6 project	PRJDB7993	12765518	47	CAGE	siRNA_s27230	HDF (neonatal)
DRR177062	CNhi10821_ATG.experiment	Targeted	NA	20	SNRPD3	Homo sapiens	FANTOM6 project	PRJDB7993	22976540	47	CAGE	siRNA_s13234	HDF (neonatal)
DRR177061	CNhi10821_AGT.experiment	Targeted	NA	20	EXOSC10	Homo sapiens	FANTOM6 project	PRJDB7993	10969453	47	CAGE	siRNA_s10738	HDF (neonatal)
DRR177060	CNhi10821_ACG.experiment	Targeted	NA	21	CHAF1A	Homo sapiens	FANTOM6 project	PRJDB7993	25145503	47	CAGE	siRNA_s19500	HDF (neonatal)
DRR176995	CNhi10812_TAC.experiment	Targeted	NA	14	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	26149167	47	CAGE	ASO_G0246985_AD_01	HDF (neonatal)
DRR176994	CNhi10812_GCT.experiment	Targeted	NA	14	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10923390	47	CAGE	ASO_G0246985_AD_01	HDF (neonatal)
DRR176993	CNhi10812_GCG.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	886737	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176992	CNhi10812_CAC.experiment	Targeted	NA	21	RP11-527D7.1	Homo sapiens	FANTOM6 project	PRJDB7993	13969522	47	CAGE	ASO_G0225554_AD_06	HDF (neonatal)
DRR176991	CNhi10812_ATG.experiment	Targeted	NA	20	CDKN2B-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	16491942	47	CAGE	ASO_G0240498_POS_01	HDF (neonatal)
DRR176990	CNhi10812_AGT.experiment	Targeted	NA	20	EMC7	Homo sapiens	FANTOM6 project	PRJDB7993	11314569	47	CAGE	siRNA_s32294	HDF (neonatal)
DRR176989	CNhi10812_ACG.experiment	Negative control	NA	20	NA	Homo sapiens	FANTOM6 project	PRJDB7993	16628634	47	CAGE	siRNA_NC_1	HDF (neonatal)
DRR176988	CNhi10812_ACC.experiment	Targeted	NA	21	HOTAIR	Homo sapiens	FANTOM6 project	PRJDB7993	17575188	47	CAGE	siRNA_AD70LI3	HDF (neonatal)

DRR176923	CNhi10801_GCG.experiment	Experiment control	NA	21	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	10451398	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176922	CNhi10801_CAC.experiment	Negative control	NA	18	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10331467	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176921	CNhi10801_ATG.experiment	Targeted	NA	18	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	15780598	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176920	CNhi10801_AGT.experiment	Targeted	NA	19	NNT-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	14525791	47	CAGE	ASO_G0248092_AD_10	HDF (neonatal)
DRR176919	CNhi10801_ACG.experiment	Targeted	NA	18	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	17332366	47	CAGE	ASO_C0011632_AD_03	HDF (neonatal)
DRR176918	CNhi10801_ACC.experiment	Targeted	NA	18	CATG00000095991.1	Homo sapiens	FANTOM6 project	PRJDB7993	16265024	47	CAGE	ASO_C0012015_AD_04	HDF (neonatal)
DRR176917	CNhi10793_TAC.experiment	Targeted	NA	15	AC009948.5	Homo sapiens	FANTOM6 project	PRJDB7993	17642958	47	CAGE	ASO_G0223960_AD_10	HDF (neonatal)
DRR176916	CNhi10793_GCT.experiment	Targeted	NA	15	RP5-1103G7.4	Homo sapiens	FANTOM6 project	PRJDB7993	16776427	47	CAGE	ASO_G0225377_AD_05	HDF (neonatal)
DRR176851	CNhi10785_ATG.experiment	Targeted	NA	15	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	23481414	47	CAGE	ASO_G0244625_AD_08	HDF (neonatal)
DRR176850	CNhi10785_AGT.experiment	Targeted	NA	16	RP13-20L14.6	Homo sapiens	FANTOM6 project	PRJDB7993	17464058	47	CAGE	ASO_G0265458_AD_03	HDF (neonatal)
DRR176849	CNhi10785_ACG.experiment	Negative control	NA	16	NA	Homo sapiens	FANTOM6 project	PRJDB7993	23569211	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176848	CNhi10785_ACC.experiment	Targeted	NA	17	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	19110270	47	CAGE	ASO_G0269834_AD_02	HDF (neonatal)
DRR176847	CNhi10784_TAC.experiment	Targeted	NA	15	CTD-2006C1.2	Homo sapiens	FANTOM6 project	PRJDB7993	20959309	47	CAGE	ASO_G0219665_AD_08	HDF (neonatal)
DRR176846	CNhi10784_GCT.experiment	Targeted	NA	15	PITPNA-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13142421	47	CAGE	ASO_G0236618_AD_09	HDF (neonatal)
DRR176845	CNhi10784_GCG.experiment	Negative control	NA	15	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14008049	47	CAGE	ASO_Untreat	HDF (neonatal)
DRR176844	CNhi10784_CAC.experiment	Targeted	NA	15	UBL7-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12253203	47	CAGE	ASO_G0247240_AD_06	HDF (neonatal)
DRR176779	CNhi10762_AGT.experiment	Experiment control	NA	17	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	16038454	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176778	CNhi10762_ACG.experiment	Targeted	NA	14	RP5-886K2.3	Homo sapiens	FANTOM6 project	PRJDB7993	17733373	47	CAGE	ASO_G0236810_AD_06	HDF (neonatal)
DRR176777	CNhi10762_ACC.experiment	Targeted	NA	13	RP11-295G20.2	Homo sapiens	FANTOM6 project	PRJDB7993	15374841	47	CAGE	ASO_G0233461_AD_03	HDF (neonatal)
DRR176776	CNhi10761_TAC.experiment	Experiment control	NA	13	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	21544025	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176775	CNhi10761_GCT.experiment	Targeted	NA	13	RP11-149I23.3	Homo sapiens	FANTOM6 project	PRJDB7993	12309090	47	CAGE	ASO_G0232110_AD_02	HDF (neonatal)
DRR176774	CNhi10761_GCG.experiment	Targeted	NA	13	DANCR	Homo sapiens	FANTOM6 project	PRJDB7993	12748501	47	CAGE	ASO_G0226950_04	HDF (neonatal)
DRR176773	CNhi10761_CAC.experiment	Negative control	NA	14	NA	Homo sapiens	FANTOM6 project	PRJDB7993	12581492	47	CAGE	ASO_NC_B	HDF (neonatal)
DRR176772	CNhi10761_ATG.experiment	Targeted	NA	14	RAD51-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	22472889	47	CAGE	ASO_G0245849_AD_07	HDF (neonatal)
DRR176707	CNhi10637_ACC.experiment	Targeted	NA	12	DNM3OS	Homo sapiens	FANTOM6 project	PRJDB7993	15033770	47	CAGE	ASO_G0230630_AD_04	HDF (neonatal)
DRR176706	CNhi10636_TAC.experiment	Targeted	NA	12	FTX	Homo sapiens	FANTOM6 project	PRJDB7993	16918381	47	CAGE	ASO_G0230590_AD_02	HDF (neonatal)
DRR176705	CNhi10636_GCT.experiment	Targeted	NA	12	AC017048.3	Homo sapiens	FANTOM6 project	PRJDB7993	16509918	47	CAGE	ASO_G0163364_AD_01	HDF (neonatal)
DRR176704	CNhi10636_GCG.experiment	Targeted	NA	12	LINC00657	Homo sapiens	FANTOM6 project	PRJDB7993	13636151	47	CAGE	ASO_G0260032_AD_06	HDF (neonatal)
DRR176703	CNhi10636_CAC.experiment	Targeted	NA	12	LINC00657	Homo sapiens	FANTOM6 project	PRJDB7993	13217433	47	CAGE	ASO_G0260032_AD_01	HDF (neonatal)
DRR176702	CNhi10636_ATG.experiment	Targeted	NA	12	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	16244806	47	CAGE	ASO_G0229847_AD_02	HDF (neonatal)
DRR176701	CNhi10636_AGT.experiment	Targeted	NA	12	EMX2OS	Homo sapiens	FANTOM6 project	PRJDB7993	11824543	47	CAGE	ASO_G0229847_AD_02	HDF (neonatal)
DRR176700	CNhi10636_ACG.experiment	Experiment control	NA	12	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	14694197	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176635	CNhi10611_TAC.experiment	Experiment control	NA	10	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	11501566	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176634	CNhi10611_GCT.experiment	Targeted	NA	10	RP11-110I1.12	Homo sapiens	FANTOM6 project	PRJDB7993	8406979	47	CAGE	ASO_G0255121_08	HDF (neonatal)
DRR176633	CNhi10611_GCG.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	9274218	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176632	CNhi10611_CAC.experiment	Targeted	NA	10	RP6-109B7.3	Homo sapiens	FANTOM6 project	PRJDB7993	10469369	47	CAGE	ASO_G0241990_01	HDF (neonatal)
DRR176631	CNhi10611_ATG.experiment	Targeted	NA	10	AC013394.2	Homo sapiens	FANTOM6 project	PRJDB7993	9125788	47	CAGE	ASO_G0272888_04	HDF (neonatal)
DRR176630	CNhi10611_AGT.experiment	Targeted	NA	10	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	12678086	47	CAGE	ASO_G0244625_09	HDF (neonatal)
DRR176629	CNhi10611_ACG.experiment	Targeted	NA	10	CTA-211A9.5	Homo sapiens	FANTOM6 project	PRJDB7993	11573367	47	CAGE	ASO_G0244625_04	HDF (neonatal)
DRR176628	CNhi10611_ACC.experiment	Targeted	NA	10	SOCS2-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10980967	47	CAGE	ASO_G0246985_10	HDF (neonatal)
DRR176563	CNhi10602_GCG.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10065128	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176562	CNhi10602_CAC.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10476544	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176561	CNhi10602_ATG.experiment	Targeted	NA	10	CTD-3018O17.3	Homo sapiens	FANTOM6 project	PRJDB7993	12001193	47	CAGE	ASO_G0269834_02	HDF (neonatal)
DRR176560	CNhi10602_AGT.experiment	Negative control	NA	10	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10821049	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176559	CNhi10602_ACG.experiment	Targeted	NA	10	RP11-379H18.1	Homo sapiens	FANTOM6 project	PRJDB7993	12325227	47	CAGE	ASO_G0271122_06	HDF (neonatal)
DRR176558	CNhi10602_ACC.experiment	Targeted	NA	10	SRP14-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	12510693	47	CAGE	ASO_G0248508_04	HDF (neonatal)
DRR176557	CNhi10601_TAC.experiment	Targeted	NA	11	LINC00883	Homo sapiens	FANTOM6 project	PRJDB7993	17599940	47	CAGE	ASO_G0243701_AD_08	HDF (neonatal)
DRR176556	CNhi10601_GCT.experiment	Targeted	NA	10	SRP14-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	13194337	47	CAGE	ASO_G0248508_04	HDF (neonatal)
DRR176491	CNhi10581_ATG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	14020684	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176490	CNhi10581_AGT.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	11403096	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176489	CNhi10581_ACG.experiment	Targeted	NA	9	FOXN3-AS1	Homo sapiens	FANTOM6 project	PRJDB7993	10725925	47	CAGE	ASO_G0258920_01	HDF (neonatal)
DRR176488	CNhi10581_ACC.experiment	Experiment control	NA	6	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	12558472	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176487	CNhi10580_TAC.experiment	Targeted	NA	6	RP11-149I23.3	Homo sapiens	FANTOM6 project	PRJDB7993	10467445	47	CAGE	ASO_G0232110_04	HDF (neonatal)
DRR176486	CNhi10580_GCT.experiment	Targeted	NA	6	RP11-295G20.2	Homo sapiens	FANTOM6 project	PRJDB7993	10687172	47	CAGE	ASO_G0233461_03	HDF (neonatal)
DRR176485	CNhi10580_GCG.experiment	Targeted	NA	6	RP11-149I23.3	Homo sapiens	FANTOM6 project	PRJDB7993	9900277	47	CAGE	ASO_G0232110_04	HDF (neonatal)
DRR176484	CNhi10580_CAC.experiment	Targeted	NA	6	RP4-794H19.4	Homo sapiens	FANTOM6 project	PRJDB7993	9965639	47	CAGE	ASO_G0230812_10	HDF (neonatal)
DRR176419	CNhi10540_ACG.experiment	Negative control	NA	6	NA	Homo sapiens	FANTOM6 project	PRJDB7993	10262820	47	CAGE	ASO_NC_A	HDF (neonatal)
DRR176418	CNhi10540_ACC.experiment	Targeted	NA	5	CATG00000016989.1	Homo sapiens	FANTOM6 project	PRJDB7993	11327335	47	CAGE	ASO_C0020443_06	HDF (neonatal)
DRR176417	CNhi10539_TAC.experiment	Targeted	NA	5	CLDN22	Homo sapiens	FANTOM6 project	PRJDB7993	17879932	47	CAGE	ASO_C0008202_02	HDF (neonatal)
DRR176416	CNhi10539_GCT.experiment	Targeted	NA	6	AC092295.7	Homo sapiens	FANTOM6 project	PRJDB7993	15872599	47	CAGE	ASO_G0233527_02	HDF (neonatal)
DRR176415	CNhi10539_GCG.experiment	Targeted	NA	5	CATG00000090305.1	Homo sapiens	FANTOM6 project	PRJDB7993	10645579	47	CAGE	ASO_C0011140_02	HDF (neonatal)
DRR176414	CNhi10539_CAC.experiment	Targeted	NA	5	CATG00000090305.1	Homo sapiens	FANTOM6 project	PRJDB7993	13275292	47	CAGE	ASO_C0011140_06	HDF (neonatal)
DRR176413	CNhi10539_ATG.experiment	Targeted	NA	6	MAGI2-AS3	Homo sapiens	FANTOM6 project	PRJDB7993	13121092	47	CAGE	ASO_G0234456_01	HDF (neonatal)
DRR176412	CNhi10539_AGT.experiment	Experiment control	NA	5	MALAT1	Homo sapiens	FANTOM6 project	PRJDB7993	11547941	47	CAGE	ASO_MALAT1	HDF (neonatal)
DRR176347	CNhi10531_ACC.experiment	Targeted	NA	4	RP1-152L7.5	Homo sapiens	FANTOM6 project	PRJDB7993	11790821	47	CAGE	ASO_G0216775_01	HDF (neonatal)
DRR176346	CNhi10530_TAC.experiment	Targeted	NA	5	AHR	Homo sapiens	FANTOM6 project	PRJDB7993	10482319	47	CAGE	ASO_C0011632_10	HDF (neonatal)

Table_S4 metadata for kmer research in MSC in different conditions

Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	passages	treatment
SRR5878104	GSM2720343: ATF6+/+ hMSC vehicle-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045407	GSM2720343	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	2991402	101	MSC	p5	vehicle
SRR5878103	GSM2720342: ATF6+/+ hMSC vehicle-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045406	GSM2720342	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	2957936	101	MSC	p5	vehicle
SRR5878102	GSM2720341: ATF6+/+ hMSC tunicamycin-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045405	GSM2720341	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	11944303	101	MSC	p5	tunicamycin
SRR5878101	GSM2720340: ATF6+/+ hMSC tunicamycin-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045404	GSM2720340	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	9700764	101	MSC	p5	tunicamycin
SRR5878100	GSM2720339: ATF6-/- hMSC tunicamycin-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045403	GSM2720339	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	11592138	101	MSC	p5	tunicamycin
SRR5878099	GSM2720338: ATF6-/- hMSC tunicamycin-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045402	GSM2720338	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	10540607	101	MSC	p5	tunicamycin
SRR5878098	GSM2720337: ATF6-/- hMSC vehicle-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045401	GSM2720337	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	9985873	101	MSC	p5	vehicle
SRR5878097	GSM2720336: ATF6-/- hMSC vehicle-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045400	GSM2720336	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	9924834	101	MSC	p5	vehicle
SRR5878096	GSM2720335: ATF6+/+ hWAPC vehicle-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045399	GSM2720335	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	32613469	101	WAPC	p5	vehicle
SRR5878095	GSM2720334: ATF6+/+ hWAPC vehicle-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045398	GSM2720334	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	11973184	101	WAPC	p5	vehicle
SRR5878094	GSM2720333: ATF6+/+ hWAPC tunicamycin-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045397	GSM2720333	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	10129610	101	WAPC	p5	tunicamycin
SRR5878093	GSM2720332: ATF6+/+ hWAPC tunicamycin-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045396	GSM2720332	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	12628610	101	WAPC	p5	tunicamycin
SRR5878092	GSM2720331: ATF6-/- hWAPC tunicamycin-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045395	GSM2720331	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	10730944	101	WAPC	p5	tunicamycin
SRR5878091	GSM2720330: ATF6-/- hWAPC tunicamycin-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045394	GSM2720330	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	9530313	101	WAPC	p5	tunicamycin
SRR5878090	GSM2720329: ATF6-/- hWAPC vehicle-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045393	GSM2720329	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	10217050	101	WAPC	p5	vehicle
SRR5878089	GSM2720328: ATF6-/- hWAPC vehicle-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045392	GSM2720328	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	10306775	101	WAPC	p5	vehicle
SRR5878080	GSM2720319: ATF6+/+ hMSC late passage-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045383	GSM2720319	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	8182392	143.61	MSC	p10	NA
SRR5878079	GSM2720318: ATF6+/+ hMSC late passage-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045382	GSM2720318	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	6753082	147.91	MSC	p10	NA
SRR5878078	GSM2720317: ATF6-/- hMSC late passage-2 RNA-seq; Homo sapiens; RNA-Seq	SRX3045381	GSM2720317	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	7782173	147.47	MSC	p10	NA
SRR5878077	GSM2720316: ATF6-/- hMSC late passage-1 RNA-seq; Homo sapiens; RNA-Seq	SRX3045380	GSM2720316	Homo sapiens	ATF6 safeguards organelle homeostasis and cellular aging in human mesenchymal stem cells	PRJNA396193	8331869	145.24	MSC	p10	NA
Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	passages	treatment
SRR6680317	GSM2983811: hMSC_TAZ_3; Homo sapiens; RNA-Seq	SRX3656633	GSM2983811	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	10429618	150	MSC		TAZ KO
SRR6680316	GSM2983810: hMSC_TAZ_2; Homo sapiens; RNA-Seq	SRX3656632	GSM2983810	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	11433785	150	MSC		TAZ KO
SRR6680315	GSM2983809: hMSC_TAZ_1; Homo sapiens; RNA-Seq	SRX3656631	GSM2983809	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	11009653	150	MSC		TAZ KO
SRR6680314	GSM2983808: hMSC_YAP_3; Homo sapiens; RNA-Seq	SRX3656630	GSM2983808	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	11196860	150	MSC		YAP KO
SRR6680313	GSM2983807: hMSC_YAP_2; Homo sapiens; RNA-Seq	SRX3656629	GSM2983807	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	11261647	150	MSC		YAP KO
SRR6680312	GSM2983806: hMSC_YAP_1; Homo sapiens; RNA-Seq	SRX3656628	GSM2983806	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	10926717	150	MSC		YAP KO
SRR6680311	GSM2983805: hMSC_WT_3; Homo sapiens; RNA-Seq	SRX3656627	GSM2983805	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	11048601	150	MSC		WT
SRR6680310	GSM2983804: hMSC_WT_2; Homo sapiens; RNA-Seq	SRX3656626	GSM2983804	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	10156337	150	MSC		WT
SRR6680309	GSM2983803: hMSC_WT_1; Homo sapiens; RNA-Seq	SRX3656625	GSM2983803	Homo sapiens	Upregulation of FOXD1 by YAP alleviates senescence and osteoarthritis	PRJNA433339	10341635	150	MSC		WT
Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	passages	treatment
SRR5357818	GSM2544142: MSC 211 CytoD; Homo sapiens; RNA-Seq	SRX2653659	GSM2544142	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	25484965	51	adipose derived mesenchymal stem cells	5-7	CytoD
SRR5357817	GSM2544141: MSC 211 Ctrl; Homo sapiens; RNA-Seq	SRX2653658	GSM2544141	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	26464456	51	adipose derived mesenchymal stem cells	5-7	Ctrl

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SRR5357816	GSM2544140: MSC 283 CytoD; Homo sapiens; RNA-Seq	SRX2653657	GSM2544140	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	24280737	51	adipose derived mesenchymal stem cells	5-7	CytoD
SRR5357815	GSM2544139: MSC 283 Ctrl; Homo sapiens; RNA-Seq	SRX2653656	GSM2544139	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	21040712	51	adipose derived mesenchymal stem cells	5-7	Ctrl
SRR5357814	GSM2544138: MSC 258 CytoD; Homo sapiens; RNA-Seq	SRX2653655	GSM2544138	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	35139902	51	adipose derived mesenchymal stem cells	5-7	CytoD
SRR5357813	GSM2544137: MSC 258 Ctrl; Homo sapiens; RNA-Seq	SRX2653654	GSM2544137	Homo sapiens	Osteogenic programming of adipose-derived mesenchymal stem cells using a fungal metabolite that suppresses the Polycomb protein EZH2	PRJNA379707	34623656	51	adipose derived mesenchymal stem cells	5-7	Ctrl
Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	passages	treatment
SRR8447838	GSM3564546: 10 days diff Control siRNA-C RNA-seq; Homo sapiens; RNA-Seq	SRX5254873	SAMN10755603	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	17969174	44	human Mesenchymal Stem Cells	p4-p10	10d osteo Diff
SRR8447837	GSM3564545: 10 days diff Control siRNA-B RNA-seq; Homo sapiens; RNA-Seq	SRX5254872	SAMN10755604	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	18943085	44	human Mesenchymal Stem Cells	p4-p10	10d osteo Diff
SRR8447836	GSM3564544: 10 days diff Control siRNA-A RNA-seq; Homo sapiens; RNA-Seq	SRX5254871	SAMN10755605	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	26461685	44	human Mesenchymal Stem Cells	p4-p10	10d osteo Diff
SRR8447835	GSM3564543: 2 days diff Control siRNA-C RNA-seq; Homo sapiens; RNA-Seq	SRX5254870	SAMN10755606	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	27117845	44	human Mesenchymal Stem Cells	p4-p10	2d osteo Diff
SRR8447834	GSM3564542: 2 days diff Control siRNA-B RNA-seq; Homo sapiens; RNA-Seq	SRX5254869	SAMN10755607	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	26162294	44	human Mesenchymal Stem Cells	p4-p10	2d osteo Diff
SRR8447833	GSM3564541: 2 days diff Control siRNA-A RNA-seq; Homo sapiens; RNA-Seq	SRX5254868	SAMN10755608	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	19724867	44	human Mesenchymal Stem Cells	p4-p10	2d osteo Diff
SRR8447832	GSM3564540: NaïveControl siRNA-C RNA-seq; Homo sapiens; RNA-Seq	SRX5254867	SAMN10755609	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	24266576	44	human Mesenchymal Stem Cells	p4-p10	Naive
SRR8447831	GSM3564539: NaïveControl siRNA-B RNA-seq; Homo sapiens; RNA-Seq	SRX5254866	SAMN10755610	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	25910627	44	human Mesenchymal Stem Cells	p4-p10	Naive
SRR8447830	GSM3564538: NaïveControl siRNA-A RNA-seq; Homo sapiens; RNA-Seq	SRX5254865	SAMN10755611	Homo sapiens	PLZF targets developmental enhancers for activation during osteogenic differentiation of human mesenchymal stem cells (RNA-seq)	PRJNA515466	24849706	44	human Mesenchymal Stem Cells	p4-p10	Naive
Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	passages	treatment
SRR3882937	GSM2231443: AMSC_19_proliferating; Homo sapiens; RNA-Seq	SRX1939121	GSM2231443	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	29447967	50			
SRR3882936	GSM2231442: AMSC_19_confluent; Homo sapiens; RNA-Seq	SRX1939120	GSM2231442	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	43754165	51	Adipose-derived Mesenchymal Stromal Cell		
SRR3882935	GSM2231441: AMSC_4_proliferating; Homo sapiens; RNA-Seq	SRX1939119	GSM2231441	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	34428851	50	Adipose-derived Mesenchymal Stromal Cell		
SRR3882934	GSM2231440: AMSC_4_confluent; Homo sapiens; RNA-Seq	SRX1939118	GSM2231440	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	42327600	51	Adipose-derived Mesenchymal Stromal Cell		
SRR3882933	GSM2231439: AMSC_3_proliferating; Homo sapiens; RNA-Seq	SRX1939117	GSM2231439	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	33767562	51	Adipose-derived Mesenchymal Stromal Cell		
SRR3882932	GSM2231438: AMSC_3_confluent; Homo sapiens; RNA-Seq	SRX1939116	GSM2231438	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	44801550	51	Adipose-derived Mesenchymal Stromal Cell		
SRR3882931	GSM2231437: AMSC_1_proliferating; Homo sapiens; RNA-Seq	SRX1939115	GSM2231437	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	37501459	50	Adipose-derived Mesenchymal Stromal Cell		
SRR3882930	GSM2231436: AMSC_1_confluent; Homo sapiens; RNA-Seq	SRX1939114	GSM2231436	Homo sapiens	Transcriptome Sequencing of Adipose-Derived Mesechymal Stromal Cells	PRJNA328824	34863048	51	Adipose-derived Mesenchymal Stromal Cell		
Run ID	Run Title	Experiment ID	EXTERNAL_ID	specie	study_title	project ID	nreads	read_length	cell type	source_name	treatment
SRR8099005	GSM3444217: EGF_IWR1_S03; Homo sapiens; RNA-Seq	SRX4925800	GSM3444217	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	14005865	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF + IWR-1
SRR8099004	GSM3444216: EGF_IWR1_S02; Homo sapiens; RNA-Seq	SRX4925799	GSM3444216	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	11575790	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF + IWR-1
SRR8099003	GSM3444215: EGF_IWR1_S01; Homo sapiens; RNA-Seq	SRX4925798	GSM3444215	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	15666602	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF + IWR-1
SRR8099002	GSM3444214: EGF_S03; Homo sapiens; RNA-Seq	SRX4925797	GSM3444214	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	15786160	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF
SRR8099001	GSM3444213: EGF_S02; Homo sapiens; RNA-Seq	SRX4925796	GSM3444213	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	19843529	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF
SRR8099000	GSM3444212: EGF_S01; Homo sapiens; RNA-Seq	SRX4925795	GSM3444212	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	19132337	151	Mesenchymal stromal cells	femoral heads/knee bone explants	EGF
SRR8098999	GSM3444211: untreated_S03; Homo sapiens; RNA-Seq	SRX4925794	GSM3444211	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	13571062	151	Mesenchymal stromal cells	femoral heads/knee bone explants	untreated
SRR8098998	GSM3444210: untreated_S02; Homo sapiens; RNA-Seq	SRX4925793	GSM3444210	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	16677487	151	Mesenchymal stromal cells	femoral heads/knee bone explants	untreated
SRR8098997	GSM3444209: untreated_S01; Homo sapiens; RNA-Seq	SRX4925792	GSM3444209	Homo sapiens	Epidermal growth factor activates ß-catenin via integrin-linked kinase to control proliferation of mesenchymal stromal cells.	PRJNA498109	17232973	151	Mesenchymal stromal cells	femoral heads/knee bone explants	untreated

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SAMD9
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AC008740.1
C11orf74
PHF11
AF165147.1
C2orf69
TSPYL2

VANGL1
AL162231.2
VIM
AC092376.2
PERP
LRRC43
CCDC191
TSC22D2
DLX6.AS1
CDR2L
SNAI1
ZCWPW2
BMP1
HOXA9
ACAD11
TGFBR2
RRAGC
AF230666.1
KCNQ5
GRIK1
LAMP2
NFKBIZ
ME1
CNIH1
DEPP1
PDGFD
AC090099.1
EIF4G3
PFN2
L3HYPDH
PPP1R3G
SLFN12
AC022336.3
IL6ST
GIHCG
ZBTB20
ACBD3
HECTD2
KCTD3
CD44
SDC2
LYSMD3
RNLS
AL359091.5
AL035681.1
AHNAK
AL096711.2
NPIPP1
DAPK2
FLRT3
EPG5
NUDT12
EFHC2
SAMD9L
TGFB3
DOCK1
STAG2
PNMA8B
CCL2
AC010605.1
AC006249.1
RF00019
EMC4
ANKRD50
PAPSS1
ETFDH
GRB14
PAQR7
GOLGA6L5P
NEK6
NRIP1
PFKM
AC026403.1
IFT140
SMARCE1
NSA2
AL031587.3
SYT7
NOTCH2
PDLIM7
STXBP3
VPS13A
LINC00922

TBC1D12
LINGO2
STK17B
ADPRH
MAMDC2
AL451064.2
LINC00475
LINC00840
CTBP2P8
AC009404.1
AL391840.2
CABYR
SOX6
NFE2L2
ARHGEF10
CHST1
KANSL1L
FGF18
CSNK1A1
AC005722.2
PKD1P5
SLC12A8
TMEM87B
BMT2
PFDN1
TRIP10
RBP4
SPRY1
R3HDM2
MTUS2
ID1
AL356515.1
PGF
ACVR1
DDX5
PTP4A2
LIG4
AL355987.2
BMP3
CSTA
MPV17
KCNA4
NOL8
ECHDC1
PCDHB5
LYPD6
PHYHIP
RRAGB
MDGA1
MEG9
LINC00865
SLC9A7P1
ASAP1
LAMB3
FRS2
SDCBP
KYAT3
NMD3
HR
AC012065.2
SLC30A9
AC074143.1
FIG4

Table_S6 summary of qPCR cohort

Type	Number
Adipose MSC	4
BM-MSC	12
Fibroblast of	3
H9 ESC	8
Hepatocytes	3
HUVEC	4
IPS	2
Myoblasts	3
Neural Stem c	2
skin fibroblast	10
Umbilical cor	3

Table_S7 Description of Mlinc Candidates

target_id	Sleuth qval (adj. Pval)	b (FC estimator)	length (nt)	exons	Chr	Interval	Strand	present in long reads	Genome browser remarks	REFLNC/GTEX	discriminative kmers	expressed in MSCs (kmers)	strong expression in SMCs (kmers)	Notable other expressions	FEELnc_coding_potential
Mlinc.54177.1	5.38147421885392e-10	3.64181797640709	17139	1	18	67485128-67502266	-	FALSE	No annotation (close to predicted lncRNA, overexpression in fibro)	FIBRO	FALSE	Ad/Bm	TRUE	myocytes/osteoblasts	0.336
Mlinc.28428.2	**3.91322165116094e-24**	**4.75090994700694**	**2816**	**3**	**12**	**88380133-88419354**	**-**	**TRUE**	**TUCP/TCONS_00020862**	**FIBRO ONLY**	**TRUE**	**Ad/Bm**	**FALSE**	**dermal papilla/muscle satellites**	**0.18**
Mlinc.109628.1	4.18652552062097e-14	3.55558466039083	3615	2	6	169163268-169168514	+	FALSE	TUCP/TCONS_00012024 (in zone)	FIBRO/ARTERY/ BioMarker survie	FALSE	Ad/Bm/UC	TRUE	myocytes/chondrocytes/ astrocytes/preadipocytes	0.446
Mlinc.128022.2	**2.24440052433889e-15**	**3.19030456476542**	**992**	**5**	**9**	**115596550-115692288**	**+**	**TRUE**	**TUCP/TCONS_00016469 (lot of variants in zone) + numerous chromatin marks**	**FIBRO ONLY**	**TRUE**	**Ad/Bm**	**TRUE**	**Myocytes/myoblastes**	**0.268**
Mlinc.32708.1	0.00166963056755997	2.11405992530657	4346	1	13	75859960-75864305	+	FALSE	In close 3' region of LOM7	BRAIN (Isoform ?)	FALSE	Ad/Bm/UC	TRUE	Chondro (very strong)	0.118
Mlinc.10317.1	8.78516928066226e-11	3.69104237801407	8760	1	1	215239087-215247846	+	FALSE	In close 3' region of KCNK2, very high expression in fibro		TRUE	Ad/Bm	FALSE	osteo/chondro	0.266
Mlinc.45246.1	5.52855779835755e-11	3.12467428011448	3825	1	16	65129303-65133127	+	FALSE	TUCP/TCONS_00024436 (partial overlappig)		FALSE	Ad/Bm/UC	TRUE	SMC (very strong)/osteoblast (very strong)	0.156
Mlinc.61271.1	0.000934727743803686	2.11029387027848	4902	1	2	46810683-46815584	+	FALSE	TUCP/TCONS_00003666, partial overlapping	FIBRO/MUSCLE/ ADIPO/Blood	FALSE	Ad/Bm/UC	TRUE	Osteoblast (very strong), chondrocytes (very strong)	0.126
Mlinc.6947.1	0.0087759651506394	1.79363960044882	1126	1	1	148790080-148791205	-	FALSE	On repeated region		FALSE	no expression			0.348
Mlinc.89912.1	**2.19410912061805e-13**	**3.1608578751305**	**3159**	**1**	**4**	**80263395-80266553**	**-**	**TRUE**	**In close 5' region of FGF5 (very high in fibro)/ Zone of regulation ++**		**TRUE**	**Ad/Bm/UC**	**TRUE**	**muscle satellite/papilla/myocytes**	**0.198**
Mlinc.98481.1	4.00458831141693e-14	3.43441525297039	1532	1	5	120687803-120689334	+	FALSE	In close 3' region of PRR16 (very high in fibro)		FALSE	Ad/Bm	TRUE	myoblast/chondro	0.084
Mlinc.123973.1	1.61744832508345e-09	2.80103674598808	494	1	9	12823414-12823907	+	FALSE	In close 3' region of LURAP1L (high in fibro)		FALSE	Ad/Bm/UC	TRUE	hepatocytes/osteo (very strong)	0.244
Mlinc.63232.1	1.85061125320116e-11	3.24619016103911	232	1	2	92068044-92068275	-	FALSE	repetition		FALSE	Ad/Bm	TRUE	Myocytes/myoblasts/SMC	0.368
Mlinc.107651.1	1.43285225448328e-06	2.90795380207381	8953	1	6	130445023-130453975	+	FALSE	In close 3' region of TMEM200A (high in fibro)	OVERLAP / PARTIAL	FALSE	Ad/Bm/UC	TRUE	hepatocytes	0.328
Mlinc.117098.1	9.01415915005679e-06	2.68354574301863	1359	1	8	299352-300710	-	FALSE	lincRNA AC136777.1 in zone (10Kb)		FALSE	Ad/Bm	FALSE	neuron/muscle/endothelial	0.106
Mlinc.70094.1	5.13172839816861e-10	2.8220665603735	946	1	2	237319841-237320786	-	FALSE	In close 3' region of COL613 (very high in fibro)		TRUE	Ad/Bm	FALSE	muscle satellite/papilla/osteo/chondrot	0.12
Mlinc.64225.1	**0.00206523311314836**	**2.01363639988553**	**302**	**1**	**2**	**113609969-113610270**	**-**	**TRUE**	**LTR close to RPL23AP7 (pseudogene + strong repetition (high in fibro)**		**FALSE**	**Bm**	**TRUE**		**0.368**
Mlinc.54155.1	1.00341251767868e-08	2.8967833165776 8	5908	1	18	67389037-67394944	-	FALSE	In intron of AC091042.1		FALSE	Ad/Bm	TRUE	osteo/hESC/chondro	0.402
Mlinc.78582.1	1.60651558091348e-09	3.32612797663159	3402	1	3	30418752-30422153	-	FALSE	HSMM specfic Chr marks (+ FOXA1 site)		NA	NA	NA	NA	0.178
Mlinc.109600.1	1.23389178444261e-08	2.57894271495465	318	1	6	168932197-168932514	+	FALSE	LINE/LTR repetitions? lncRNA in zone		FALSE	Ad/Bm	TRUE	H1-ESC/osteoblast	0.53
Mlinc.9300.1	1.63418031048994e-08	2.66341118521261	1382	1	1	192488616-192489997	-	FALSE	variant of AL390957.1 (Chr marks ++ and FOXP1 site), lot of predicted lncRNA		FALSE	Ad/Bm/UC	TRUE	SMC (very strong)	0.144
Mlinc.54554.1	**2.57868369698677e-07**	**2.45953847799982**	**2156**	**1**	**18**	**75463916-75466071**	**+**	**FALSE**	**HSMM specfic Chr marks (+FOXA1 Site)**		**FALSE**	**Bm/UC**	**TRUE**	**hepatocyes/SMC (very strong)/muscle cell**	**0.19**
Mlinc.83437.1	3.75186606665131e-11	2.92026510167055	2904	1	3	126213050-126215953	+	FALSE	TUCP/TCONS_00006199, lncRNA, Chr Marks		FALSE	Ad/Bm/UC	FALSE	mesenchlial/neural prog./myocytes/epithelial	0.292
Mlinc.127918.1	8.59549299747758e-05	2.2148444399395	2870	2	9	113624677-113628441	+	FALSE	LincRNA /TUCP in zone, Chr Mark, TF binding site		TRUE	Ad/Bm	FALSE	Chondro/papilla	0.302
Mlinc.9231.1	**2.09587353035184e-06**	**2.77869731979218**	**2415**	**1**	**1**	**186681846-186684260**	**+**	**FALSE**	**close to an AS of PTGS2 antisense NFKB1 complex +++: Numerous Chr mark + TF binding sites**		**FALSE**	**Ad/Bm/UC**	**TRUE**	**Mononuclear cells (very strong)**	**0.152**
Mlinc.78418.1	1.82921400272116e-05	2.52537568052055	2945	1	3	27646119-27649063	+	FALSE	Overlap TUCP/TCONS_I2_00018477 (High in fibro)/HSMM specific ChrMark variant of LINC01128 or TUCP		FALSE	Ad/Bm	FALSE	epithelial/myocytes/chondro	0.232
Mlinc.61267.1	0.00800968729326976	1.85151131179545	8834	1	2	46797931-46806764	+	FALSE	TCONS_00003666, rich zone in lincRNA, Chr mark et TF binding site, close to SOCS5 (high in fibro ++)		TRUE	Ad/Bm	TRUE	osteo/myocytes/papilla	0.162
Mlinc.111761.1	**0.00042960980413464 46**	**2.16878061892736**	**1232**	**1**	**7**	**38054085-38055316**	**+**	**FALSE**	**EGRF1 Binding site/ HSMM Xhr sites**		**FALSE**	**BM**	**TRUE**	**Myocytes/myotubes**	**0.084**
Mlinc.54156.1	2.76421814657461e-05	2.55034529045675	6240	1	18	67395327-67401566	-	FALSE	HSMM Chr Binding Site + FOXA1 Sites		TRUE	Ad/Bm	TRUE	smc of trachea (very strong)	0.334
Mlinc.47523.1	6.05265557244177e-08	2.53923057783646	1558	1	17	13490975-13492532	-	FALSE	In 3' of gene HS3ST3A1 (High in fibro)	FIBRO/ DIFFUSE	FALSE	Ad	TRUE	epithelial/mesanglial	0.342
Mlinc.18093.1	3.3005434599755e-09	2.70413881781352	977	1	11	12085459-12086435	-	FALSE	Close to AC124276.2 variant Chr Mark +++ and TF binding site +++		FALSE	Ad/UC	TRUE	epithalial/keratinocytes	0.236
Mlinc.57835.1	1.15589458808076e-08	2.42525523068851	927	1	19	44737723-44738649	+	FALSE	TUCP/TCONS_00027580		FALSE	FALSE	FALSE	Mononuclear cells (very strong)	0.436
Mlinc.104634.1	7.05793182343196e-12	3.12285461836103	2731	1	6	57260477-57263207	-	FALSE	TUCP/TCONS_00011222 + Chr Mark (HSMM) and TF binding site		FALSE	Ad/Bm/UC	TRUE	SMC (strong)	0.314
Mlinc.80687.1	3.47529931298406e-06	2.15786698401882	537	1	3	65018718-65019254	+	FALSE	In Intron of gene ADAM-AS		FALSE	BM	TRUE	epithelia/chondro/neural prog.	0.464
Mlinc.96690.1	2.09413387964091e-06	2.08136277131835	637	2	5	84491916-84493310	+	FALSE			FALSE	BM/UC	FALSE	myocytes/osteo/chondro	0.332

FEELnc label (1=mRNA)	Closest_gene	Distance	TarpmiR max sites by miRNA	Primer1 (F)	Primer2 (R)
0	AC110597.1	162	6		
0	**Y_RNA**	**-11088**	**4**	GAAGGCCGTGAAGCCATTGT	CATGATTTTGCCCTCGGCTT
0	LINC01615	-344	4		
0	**U2**	**42104**	**4**	TGTTTCTGGGCTGCTTGCT	AGGGGACATTTTCCGACCTCAA
0	LMO7	-90	5		
0	KCNK2	-1994	5		
0	CDH11	-3191	4		
0	LINC01118	1084	5		
0	AC245389.1	-4592	4		
0	**FGF5**	**-46**	**5**	TCGGCGTTGGAAAACCAAAC	TACAGACGGAGAGCTTCCCA
0	PRR16	-471	4		
0	LURAP1L	-1283	4		
0	IGKV1OR2-2	33044	3		
0	TMEM200A	-1960	5		
0	AC136777.1	-10423	4		
0	COL6A3	-3217	4		
0	**RPL23AP7**	**-232**	**4**		
0	AC091042.1	13732	5		
0	LINC01985	-102592	4		
1	AL109924.1	30096	4		
0	AL136987.1	-27642	4		
0	**AC116003.2**	**-26959**	**5**		
0	ALDH1L1-AS2	-2881	5		
0	AL162727.1	-2043	4		
0	**PACERR**	**-400**	**4**		
0	AC098614.4	-7343	5		
0	LINC01118	9904	5		
0	**SFRP4**	**-28390**	**4**		
0	AC091042.1	20022	5		
0	HS3ST3A1	-3157	4		
0	AC124276.2	-456	4		
0	BCL3	9056	5		
0	RAB23	38163	4		
1	ADAMTS9-AS2	-7250	4		
0	AC113383.1	-1151	4		

Table_S8 statistically relevant interraction between Mlinc and proteins

Mlinc.28428.2		Mlinc.128022.2		Mlinc.89912.1	
Uniprot ID	gene ID	Uniprot ID	gene ID	Uniprot ID	gene ID
Q496A3	SPATS1	P31994	FCGR2B	P02760	AMBP
Q9UBM1	PEMT	Q9Y2T5	GPR52	Q92830	KAT2A
Q92911	SLC5A5	P14618	PKM	Q6NUI6	CHADL
P09001	MRPL3	Q9P1W8	SIRPG	Q9Y2K9	STXBP5L
Q96G25	MED8	Q9P0J1	PDP1	Q9NV29	TMEM100
P20700	LMNB1	Q8N9I0	SYT2	Q8N6M3	FITM2
Q5FYB0	ARSJ	Q86X59	C17orf82	O43915	VEGFD
O15066	KIF3B	Q8NCL8	TMEM116	Q9NRD1	FBXO6
O77932	DXO	Q9P2T1	GMPR2	Q9UJH8	METRN
Q9P232	CNTN3	O75581	LRP6	Q9BWW8	APOL6
Q9NRY2	INIP	Q7L591	DOK3	Q15746	MYLK
Q12931	TRAP1	Q6IF99	OR10K2	Q9BQE3	TUBA1C
Q0D2K2	KLHL30	Q9UM11	FZR1	Q96HE7	ERO1A
Q16891	IMMT	Q8WUH6	TMEM263	Q8TCG2	PI4K2B
Q9Y6M4	CSNK1G3	Q9UKN8	GTF3C4	Q99969	RARRES2
Q16706	MAN2A1	Q96A47	ISL2	O43148	RNMT
Q99946	PRRT1	Q9ULJ6	ZMIZ1	Q7Z6V5	ADAT2
Q96JJ6	JPH4	Q99829	CPNE1	Q9UIA9	XPO7
Q8IZH2	XRN1	Q29983	MICA	P08684	CYP3A4
Q8NBF1	GLIS1	Q92783	STAM	Q8N135	LGI4
Q9BXF6	RAB11FIP5	Q8IYX7	SAXO1	Q96A04	TSACC
Q8TDB4	MGARP	P0DN77	OPN1MW2	Q99217	AMELX
Q9H251	CDH23	P0DN78	OPN1MW3	Q8NAE3	LINC01555
Q96RQ3	MCCC1	Q6ZMH5	SLC39A5	O60403	OR10H2
Q9HBR0	SLC38A10	Q5TH69	ARFGEF3	P49908	SELENOP
Q9BTU6	PI4K2A	P04062	GBA	Q9Y4C5	CHST2
Q9Y2P8	RCL1	Q8IVM8	SLC22A9	Q14142	TRIM14
Q15056	EIF4H	Q96T88	UHRF1	P30085	CMPK1
Q9UMZ2	SYNRG	Q5SWL8	PRAMEF19	G3V0H7	SLCO1B7
Q9GZP1	NRSN2	Q8N427	NME8	P60880	SNAP25
P0C645	OR4E1	Q8NBP7	PCSK9	P01767	IGHV3-53
Q6ZVL6	KIAA1549L	Q8TCX1	DYNC2LI1	Q8WUJ1	CYB5D2
O75909	CCNK	Q13072	BAGE	Q6ZQN7	SLCO4C1
Q99574	SERPINI1	Q86Y27	BAGE5	P83731	RPL24
Q9Y5G7	PCDHGA6	Q96KE9	BTBD6	Q5T1H1	EYS
Q1A5X6	IQCJ	Q6UXH8	CCBE1	P05496	ATP5MC1
Q8IWD5	MFSD6L	Q14409	GK3P	P78312	FAM193A
Q99607	ELF4	P56177	DLX1	P27918	CFP
Q8N6T3	ARFGAP1	Q9H190	SDCBP2	Q15834	CCDC85B
O14950	MYL12B	P23759	PAX7	Q11201	ST3GAL1
Q6ZN28	MACC1	O15409	FOXP2	Q9Y6H1	CHCHD2
O95402	MED26	P60520	GABARAPL2	P68363	TUBA1B
A6NIV6	LRRIQ4	P55809	OXCT1	Q494X3	ZNF404
A8MUM7	LGALS16	Q9NVH2	INTS7	Q96LJ7	DHRS1
P59536	TAS2R41	Q8N0Z8	PUSL1	Q86XS8	RNF130
O95900	TRUB2	Q7L4S7	ARMCX6	P48742	LHX1
Q99593	TBX5	Q9Y5J6	TIMM10B	P15880	RPS2
P21439	ABCB4	Q8WUI4	HDAC7	P0DMV0	CT45A7
P20073	ANXA7	P04259	KRT6B	Q8N972	ZNF709
Q8TCC3	MRPL30	Q8IYS8	BOD1L2	Q8IUY3	GRAMD2A
Q6Q788	APOA5	O95455	TGDS	Q9NR96	TLR9
Q13443	ADAM9	Q969P6	TOP1MT	Q8NBT0	POC1A
Q7L311	ARMCX2	Q3MIP1	ITPRIPL2	O14827	RASGRF2
Q969Q6	PPP2R3C	Q86YV6	MYLK4	Q17R55	FAM187B
Q8N1B4	VPS52	P04001	OPN1MW	Q9H0M5	ZNF700
P08243	ASNS	Q8NH49	OR4X1	O43715	TRIAP1
Q05193	DNM1	P55771	PAX9	Q9P0V3	SH3BP4
Q13243	SRSF5	Q16656	NRF1	Q04771	ACVR1
Q8NDV7	TNRC6A	Q5JTZ5	C9orf152	Q6ZRS4	ITPRID1
P15941	MUC1	O95382	MAP3K6	O60337	MARCH6
Q96AN5	TMEM143	Q2QD12	RPEL1	Q13103	SPP2
Q9BXT2	CACNG6	Q92796	DLG3	O75663	TIPRL
Q96EY8	MMAB	P05089	ARG1	Q8NBM4	UBAC2
P11498	PC	Q9Y512	SAMM50	Q8NEG0	FAM71C
Q96GC9	VMP1	P20265	POU3F2	O60656	UGT1A9
Q9HC52	CBX8	P04216	THY1	Q7L5L3	GDPD3
Q6UVK1	CSPG4	Q96RY7	IFT140	Q9H9V4	RNF122
P08397	HMBS	O43187	IRAK2	Q71U36	TUBA1A
P54922	ADPRH	P21397	MAOA	Q9UJL9	ZFP69B
Q96SA4	SERINC2	Q9H2S9	IKZF4	Q6NUJ1	PSAPL1
Q7L945	ZNF627	Q8NI99	ANGPTL6	Q6UXH9	PAMR1
Q8NGB6	OR4M2			P08833	IGFBP1
Q9GZX3	CHST6			O75431	MTX2
P80748	IGLV3-21			Q6UDR6	SPINT4
Q6ZTW0	TPGS1			Q5HYN5	CT45A1
Q8TB05	UBALD1			Q5T0J3	C1orf220
O75947	ATP5PD			Q96T68	SETDB2
O75366	AVIL			Q9UHC3	ASIC3
P32754	HPD			Q96SZ5	ADO
Q92600	CNOT9			Q8NHU0	CT45A3
Q8TAS1	UHMK1			P29320	EPHA3

P22794	EVI2A
A8MTQ0	NOTO
Q9Y6U3	SCIN
Q96IZ0	PAWR
P06733	ENO1
P10114	RAP2A
Q5T4B2	CERCAM
Q9HA82	CERS4
Q8IVT2	MISP
O95427	PIGN
Q9NWB7	IFT57
P0C024	NUDT7
Q9Y241	HIGD1A
P55291	CDH15
Q3I5F7	ACOT6
Q9H467	CUEDC2
Q86XN7	PROSER1
Q07075	ENPEP
Q5JPH6	EARS2
Q6ZU45	CLEC20A
Q9Y263	PLAA
O75309	CDH16
Q8N608	DPP10
P36871	PGM1
Q8WXF5	CRYGN
Q8IYX0	ZNF679
Q8NDC0	MAPK1IP1L
Q68DC2	ANKS6
Q9NRA2	SLC17A5
Q5VZE5	NAA35
P13521	SCG2
Q9BU23	LMF2
P48382	RFX5
P35222	CTNNB1
Q7Z7M9	GALNT5
Q8WXD9	CASKIN1
P04843	RPN1
Q9BYD1	MRPL13
Q9Y573	IPP
O00748	CES2
Q9UK45	LSM7
Q8NFJ9	BBS1
O43525	KCNQ3
Q96T83	SLC9A7
O95104	SCAF4
Q9HBI1	PARVB
Q9P2V4	LRIT1
Q9HCN3	TMEM8A
P11464	PSG1
Q9UNN4	GTF2A1L
O75935	DCTN3
Q6V0L0	CYP26C1
Q9H488	POFUT1
Q9NRM1	ENAM
Q9NYP3	DONSON
O60636	TSPAN2
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Q6P4R8	NFRKB
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