Spatial transcriptomics using combinatorial fluorescence spectral and lifetime encoding, imaging and analysis

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Abstract:

Multiplexed mRNA profiling in the spatial context provides important new information enabling basic research and clinical applications. Unfortunately, most existing spatial transcriptomics methods are limited due to either low multiplexing or assay complexity. Here, we introduce a new spatialomics technology, termed Multi Omic Single-scan Assay with Integrated Combinatorial Analysis (MOSAICA), that integrates *in situ* labeling of mRNA markers in cells or tissues with combinatorial fluorescence spectral and lifetime encoded probes, spectral and time-resolved fluorescence imaging, and machine learning-based target decoding. This technology is the first application combining the biophotonic techniques; Spectral and Fluorescence Lifetime Imaging and Microscopy (FLIM), to the field of spatial transcriptomics. By integrating the time dimension with conventional spectrum-based measurements, MOSAICA enables direct, highly-multiplexed, *in situ* spatial biomarker profiling in a single round of staining and imaging while providing error correction removal of background autofluorescence. We demonstrate mRNA encoding using combinatorial spectral and lifetime labeling and target decoding and quantification using a phasor-based image segmentation and machine learning clustering technique. We then showcase MOSAICA's multiplexing scalability in detecting 10-plex targets in fixed colorectal cancer cells using combinatorial labeling of only five fluorophores with facile error-correction and removal of autofluorescent moieties. MOSAICA's analysis is strongly correlated with sequencing data (Pearson's r = 0.9) and was further benchmarked using RNAscope™ and LGC Stellaris™. We further apply MOSAICA for multiplexed analysis of clinical melanoma Formalin-Fixed Paraffin-Embedded (FFPE) tissues that have a high degree of tissue scattering and intrinsic autofluorescence, demonstrating the robustness of the approach. MOSAICA represents a simple, versatile, and scalable tool for targeted spatial transcriptomics analysis that can find broad utility in constructing human cell atlases, elucidating biological and disease processes in the spatial context, and serving as companion diagnostics for stratified patient care.

Introduction

Cell fate and cell-cell, cell-niche interactions are tightly regulated in space at both genetic and tissue and system level to mediate organ development, tissue homeostasis and repair, and disease appearance and progression. Therefore, spatial transcriptomics that profile gene expression landscape at the single-cell level in tissues in a 3D spatial context as shown in this work represents a new frontier in biological research and precision medicine[1-8]. For instance, spatial transcriptomics techniques can (a) help realize the vision of the human cell atlas in generating "high-resolution and comprehensive, three-dimensional reference maps of all human cells in the body", (b) determine molecular mechanisms that govern cell fate, state, lineage and cell cooperation in tissue formation in developmental biology and regenerative medicine, (c) investigate the biological changes associated with different diseases in a spatial-dynamic fashion and to uncover disease molecular mechanisms and discover disease biomarkers, and (d) characterize the complexities of tissue biopsy (e.g. tumor) in clinical pathology to inform personalized disease diagnosis and therapeutic intervention in the era of precision medicine. Spatial transcriptomics tools need to be able to assess multiple transcripts within the same cell and sample in a highly multiplexed fashion due to the heterogeneous gene expression and many different cell identities/states exist in a particular tissue. Furthermore, patient derived materials are often available in limited quantity and generating many sections to test for different markers separately is tedious and non-feasible.

A major bottleneck in spatial transcriptomics is the lack of tools that can be both easy-of-use and highly multiplexing[7-11]. Conventional tools for in situ analysis including fluorescence in situ hybridization (FISH) (e.g., LGC Stellaris™) can only detect 3-4 targets at a time because of the limited number of spectral channels in fluorescence microscopes[12-14]. Conventional methods for *in situ* profiling of transcripts are further confounded by the autofluorescent moieties in tissue preparations including clinical biopsies. Recent single-cell RNA sequencing (scRNAseq) methods provide information on the presence and identity of transcripts in single cells but lack the critical spatial context needed to understand complex heterogeneous tissue [15-17]. Spatial transcriptomic methods that are based on sequential labeling, stripping, and imaging (e.g. seqFISH, MERFISH), branched amplification (e.g. RNAscope™, SABER), or in situ sequencing (e.g. GeoMx™, Slide-seq) are often too complicated, error-prone, time-consuming, laborious and costly to scale up, limiting their broad usage [18-23]. Furthermore, repeated processing of the same sample can damage tissue structural integrity and target molecules and are often not feasible for precious samples such as clinical biopsies.

In this work we report a new spatial-omics technology termed MOSAICA (Multi Omic Single-scan Assay with Integrated Combinatorial Analysis) that enables direct, highly multiplexed biomarker profiling in the 3D spatial context in a single round of staining and imaging. MOSAICA employs *in situ* staining with combinatorial fluorescence spectral and lifetime encoded probes, spectral- and time-resolved fluorescence imaging, and AI-based target decoding pipeline (Fig. 1). Fluorescence lifetime is a measure of the time a fluorophore spends in the excited state before returning to the ground state and is an inherent characteristic of the fluorophore and its surrounding environment[24]. By utilizing both time and intensity domains for labeling and imaging, we were

able to discriminate a large repertoire of spectral and lifetime components simultaneously within the same sample to enable increased multiplexing capabilities with standard optical systems.

In this study, we described the MOSAICA pipeline including automated probe design algorithm, probe hybridization optimization and validation, combinatorial spectral and lifetime labeling and analysis for target encoding and decoding. Particularly, we developed an automated machine learning-powered spectral and lifetime phasor segmentation software that has been developed to spatially reveal and visualize the presence, identity, expression level, location, distribution, and heterogeneity of each target mRNA in the 3D context. We showcased MOSAICA in analyzing a 10-plex gene panel in colorectal SW480 cells based on combinatorial spectral and lifetime barcoding of only five generic commercial fluorophores. Using this model, we illustrated the multiplexing scalability and MOSAICA's ability to correct for stochastic nonbinding artifacts present within the sample. We further demonstrated MOSAICA's utility in improved multiplexing, error-correction, and autofluorescence removal in highly scattering and autofluorescent clinical melanoma FFPE tissues, demonstrating its potential use in tissue for cancer diagnosis and prognosis. The MOSAICA is rapid, cost-effective, and easy-to-use and can fill a critical gap between conventional FISH and sequential- and sequencing-based techniques for targeted and multiplexed spatial transcriptomics.

Results

MOSAICA Workflow

In a typical MOSAICA workflow (Figure 1), primary oligonucleotide probes designed to specifically bind to mRNA targets with a complementary target region (25 to 30 base long) are incubated with fixed cell or tissue samples (Fig. 1A,B). These primary probes also contain an adjacent adaptor region consisting of two readout sequences for modular secondary probe binding. In this study, double ended secondary probes with fluorophores on each end are hybridized to the readout region on the primary probes (Fig. 1C). Through combinatorial labeling, each target is encoded with a dye with a distinct spectrum and lifetime signature. The labeled samples are then imaged using a confocal microscope (Fig. 1D) that is equipped with both spectral and lifetime imaging capabilities. Both spectral and fluorescence lifetime data will be captured and visualized using phasor plots (Fig. 1E). Our automated machine learning algorithm and a codebook then reveals the locations, identities, counts, and distributions of the present mRNA targets in a 3D context (Fig. 1F).

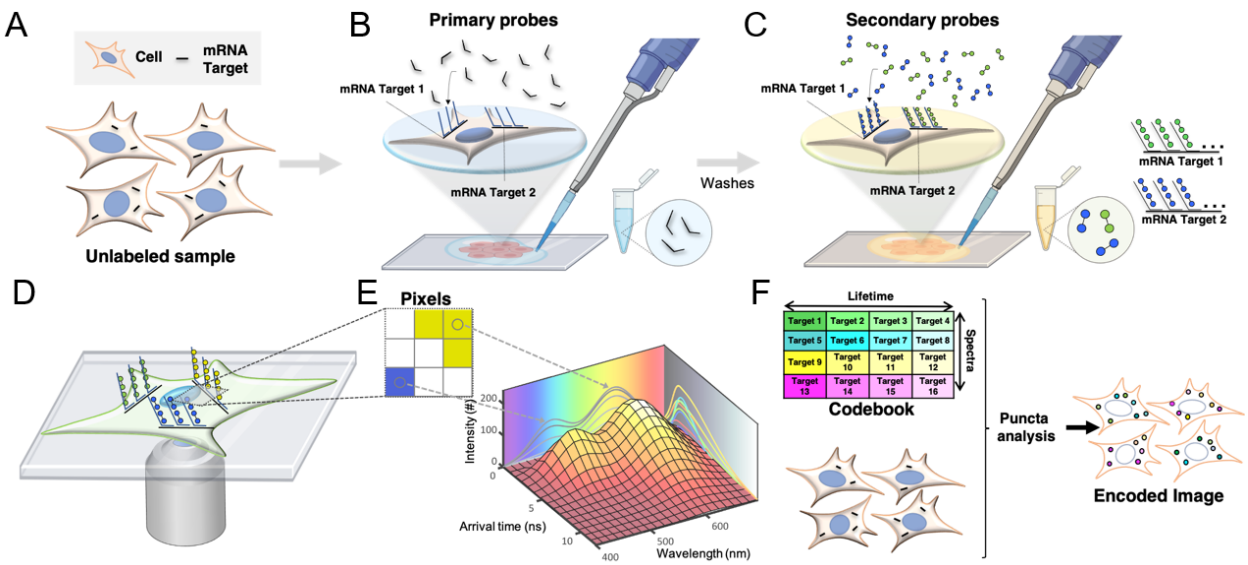

Figure 1. Schematic of the MOSAICA approach for labeling and analysis of spectral and time-resolved components. ***A)*** *Sample(s) can be fixed cells or tissues. RNA transcripts from genes of interest are targeted for detection.* ***B)*** *Primary labeling probes are designed to include two functional regions: a target region which is complementary and can bind to the mRNA target and an adjacent readout region which can subsequently bind to fluorescently labeled oligonucleotides.* ***C)*** *Secondary fluorescent probes are added to bind to the primary probes to form different combinations (combinatorial labeling) through a "readout" domain.* ***D)*** *Labeled targets are measured under a fluorescent microscope to interrogate the spectral and lifetime characteristics of the labeled moieties.* ***E)*** *Phasor analysis is used to identify which fluorophore labels are present in each pixel and puncta.* ***F)*** *Labeled targets eliciting the encoded intensity-based or time-based signature are decoded to reveal the locations, identities, counts, and distributions of the present mRNA targets in a multiplexed fashion.*

Probe design pipeline

To rapidly design oligonucleotide probes for each gene, we modified the python platform, OligoMiner[25], a validated pipeline for rapid design of oligonucleotide FISH probes. Briefly, as shown in Supplementary Figure 1A, using the mRNA or coding sequence (CDS) file of the target gene, the blockParse.py script will screen the input sequence and output a file with candidate probes while allowing us to maintain consistent and customized length, GC, melting temperature, spacing, and prohibited sequences. Using Bowtie2, the candidate probes are rapidly aligned to the genome to provide specificity information that is used by the outputClean.py script to generate a file of unique candidates only. The primary probes comprise complementary sequence of typically 27-30 nucleotides (nt) and are designed mostly within the CDS region, which has fewer variation than the untranslated region (UTR)[20]. We wrote a script, seqAnalyzer.py, to automate the alignment of primary probes to sequencing data (Fig. S1B) so that probes that aligned to regions of lower read counts would be discarded. Furthermore, primary probe "read-out" domains and secondary probes (typically 15 to 20 nt long) are designed to be orthogonal to each other to avoid off-target binding. Libraries and databases of over 200,000 orthogonal sequences are available online and we have simply used those that have been previously validated[26]. Fluorophores exhibiting distinct spectrum (typically with excitation/emission spectra in the 400-700 nm range) and lifetimes (typically in the 0.3-10 ns range) can be conjugated to oligos which were obtained through commercial vendors (see Methods).

Probe labeling validation and optimization

We first investigated the specificity of our labeling condition using a simple cell mixture model comprising wild-type HEK293T-X cells and HEK293T-X cells engineered with mNeonGreen (Fig. S2A) by detecting mNeonGreen mRNA as the target gene. Since only fluorescent mNeonGreen positive cells can express the corresponding mRNA transcripts, this cell mixture model provides a straightforward tool to assess specificity and nonspecific binding. Using a Nikon epifluorescence microscope to image the samples following staining with primary and secondary probes (all probe sequences used in this study are provided in Table S3), we detected on average 43.5 puncta per mNeonGreen positive cell (n = 76 cells) and 0.25 puncta per wild-type cell (n = 164) (Fig. S2B,C), indicating minimal nonspecific binding with our probe labeling strategy. To further validate the baseline level of nonspecific binding, we included a negative control with the primary probe designed towards dopachrome tautomerase (DCT), a gene in the mouse genome that is not expressed in our HEK293T-X model system, along with a condition with secondary probes only. Similarly, an average of 43.5 puncta per cell was detected for the mNeonGreen cells while the wild type and negative controls a mean of 2.5 puncta per cell was detected with a lower signal to noise (Fig. S2B,C). We next optimized labeling efficiency by testing the number of primary probes and incubation times of primary probes and secondary probes (summarized in Fig. S3). We determined our optimal condition to comprise a minimal of least 12 primary probes for each target mRNA (Fig. S3A,B) (in practice, we always maximize the number of primary probes per mRNA depending on the size of mRNA. Indeed, 40 primary probes per channel per mRNA were subsequently used in this study) with incubation time of 16 hours for primary probe hybridization and 1 hour for secondary probe hybridization, respectively (Fig. S3C,D), which were used in subsequent experiments.

Imaging and phasor analysis

Lifetime imaging is a tool that measures the spatial distribution of probes with different fluorescence lifetime. Samples are stimulated with modulated or pulsed lasers at a particular frequency, typically around the 40 to 80 MHz, which allows the fluorescence to decay within the stimulated period, typically in the ns range. After acquiring for sufficient time, i.e., after enough laser pulses or periods, one can construct a histogram of photon arrival times at each pixel. The shape of this histogram has a rapid rise, followed by a faster or slower decay which is characteristic of the fluorescent molecule(s) present in the pixel. To model this decay data, an exponential decay model can be fitted or alternatively one can make use of the fit-free phasor approach[27,28]. We used this second approach because it requires no a priori knowledge of an underlying model (i.e. number of fluorescent species at the pixel) and it is computationally inexpensive in virtue of the Fast Fourier Transform algorithm. The phasor transform extracts two values from the decay curve that characterize the shape (and importantly not the size, so that the transform is independent of the amount of photons) and these two values, namely S and G, correspond to the two coordinates of the pixel on the phasor plot (see equations in the supplemental material). The values are obtained by an integral of the product of the decay of the two trigonometric functions, sine and cosine, fit in the stimulation period, and they correspond to the first order terms of the Fourier Series decomposition of the decay curve.

Similarly, if one uses a spectral detector, i.e., a separate detector for different spectral bands, then for each pixel, one can obtain another histogram, in this case with the number of photons arriving in each channel, i.e., at each wavelength. This curve can also be transformed to an analogous spectral phasor space to map the recorded spectra at each pixel onto the 2D spectral phasor space[29]. Combining the lifetime measurement with a spectral detector, one effectively has a 5-dimensional space in which to characterize each pixel. On top of the spatio-temporal coordinates (x,y,z,t), each pixel now carries information in 5 additional coordinates: its intensity value (however many photons arrived at that pixel), the two phasor coordinates for the lifetime phasor transform, and the two phasor coordinates for the spectral phasor transform. A typical image, on the order of 10^6 pixels, obtained with this method provides 10^6 points in this 5D space[30]. If the sample presents different populations of fluorescent molecules at different locations, the pixel phasor data at these different locations map to different positions in this phasor space and a clustering technique can be used to resolve each population.

Figure 2 depicts the spectral/lifetime analogy for fluorescence microscopy using the phasor approach. As an example, it uses a hypothetical experiment where 4 different target genes are targeted with 4 fluorescent species. Of the 4 species, we construct the example so that two fluorescent species emit in one color and the other two in another color. At the same time, within each color, one has a short lifetime and the other has a long lifetime. This hypothetical sample is excited, and the individual photons are detected at each pixel (Fig. 2A). In each pixel, we accumulate enough photons to build a spectral histogram and a lifetime histogram (Fig. 2B). These curves are phasor-transformed to reveal two distinct populations in the phasor space, corresponding to the two colors and the two lifetimes. By means of our previously published automatic clustering using machine learning[31], we identify these populations and return to the image space to label each pixel depending on the group it belongs to in the phasor space (Fig. 2C). By combining the spectral and lifetime information, we have automatically segmented the image into regions, i.e., identified the pixels that belong to the different species (Fig. 2D). Again, note that in this example in Figure 2, we have chosen the probes to be the most convoluted case possible; one couple shares a similar spectrum and the other couple shares another spectrum. At the same time, one of the members of either couple share a similar lifetime and the other two members of either couple share another lifetime. This is the reason why even if there are four distinct fluorescent probes, only two spectral populations are detected both in the spectral and lifetime phasor space, and the combinations of these two populations yield to the four distinct groups. The four probes cannot be resolved unless both the lifetime and spectral information are accessed.

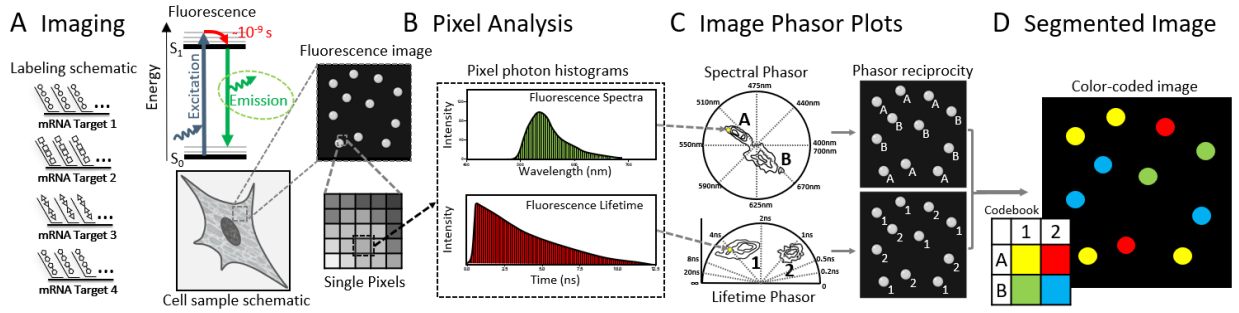

***Figure 2. Image and phasor analysis with spectrum and lifetime analysis in MOSAICA**. **A)** As an example, four different probes are used to target four different genes. The fluorescence is collected using the spectral and FLIM instrument to form images where each pixel carries information of the spectra and lifetime. **B)** At each pixel we compute the photon distribution in the spectral and temporal dimension. The phasor transform maps these distributions in each pixel to a position on the phasor space. **C)** The phasor plots reveal the presence of different populations. These populations are identified and then mapped back to the original image. **D)** We color code the pixels based on the combination of the two properties. This allows us to separate by lifetime probes that were emitting with similar spectra and vice-versa, separate by spectra probes that fluoresce with similar lifetimes.*

Combinatorial target spectral and lifetime encoding and decoding

In the previous section, we showed how by combining the time dimension with the spectral dimension, we can increase the number of possibilities and therefore enhance the multiplexing capabilities squaring the number of targets that can be resolved. To further increase multiplexing and improve detection efficiency, we employ combinatorial labeling, a method in which targets are labeled with two or more unique fluorophores, to greatly increase the base number of targets we can label with a given number of fluorophores/probes. To illustrate this concept, here we demonstrate a minimal exemplary working example of combinatorial labeling where two probes are used to label three targets. In this situation, each probe labels one target and the third target is labeled with both probes simultaneously. Figure 3 shows a real case with such configuration, both for spectra and for lifetime. In Figure 3A, the cartoon represents the case of using two probes with distinct spectra. When imaging this sample, we can use two spectral channels, Figure 3B/C, where some targets appear in only one channel, other targets appear in only the other channel and the target that is labeled with both probes appears in both channels. All targets are then detected and color-coded depending on their presence in one channel, the other or the two simultaneously (Fig. 3D) and the overall counts of each combination in the field of view can be provided (Fig. 3E).

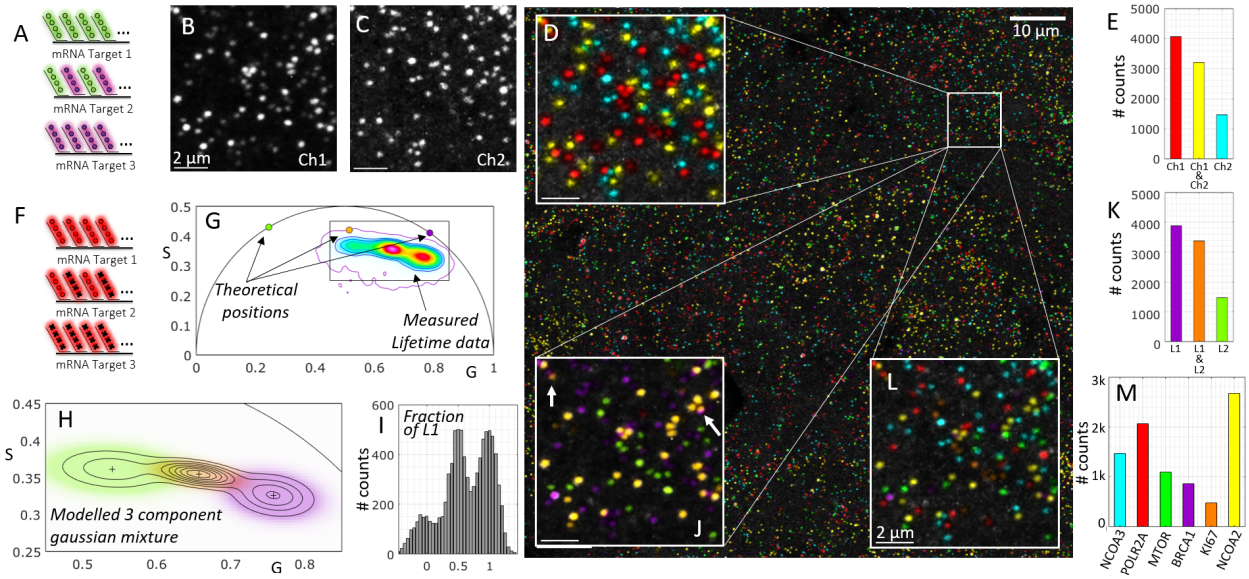

Figure 3. Working example of combinatorial labelling of three mRNA targets with two probes. A) *Three different target genes are tagged using two probes with different spectra. Targets 1 and 3 are tagged each with one probe, Target 2 is tagged with both simultaneously.* ***B,C)*** *The fluorescence is collected in the two expected spectral channels for the known emission of the two probes.* ***D)*** *The maximum projection of the two channels is shown and pseudocolored depending on the presence in the respective channels (as an inset within the whole field of view.* ***E)*** *The actual counts of each target within the whole field of view.* ***F)*** *As a parallel example, three different target genes are tagged using two probes with different lifetime. Targets 1 and 3 are tagged each with one probe, Target 2 is tagged with both simultaneously.* ***G)*** *The phasor plot presents three populations, corresponding to the pixels with the three combinations; the two components by themselves plus the linear combination falling in the middle.* ***H)*** *Machine learning clustering technique is used to identify the groups (Gaussian mixture model).* ***I)*** *The multicomponent method is used to extract the fraction of one of the components in each detected puncta.* ***J)*** *The same inset is shown with the pseudocoloring now depending on the lifetime clustering.* ***K)*** *The counts for each lifetime cluster in the whole field of view.* ***L)*** *The combination of the information in both the spectral and the lifetime dimension yields a final 6-plex.* ***M)*** *The overall counts for the 6-plex detection including POLR2A (Alexa647 & ATTO565), MTOR (ATTO647 & ATTO565), KI67 (Alexa647 & ATTO647), BRCA1 (Alexa647), NCOA2 (ATTO647), NCOA3 (ATTO565) with the appropriate genes that correspond to each combination. Experiments were conducted with cultures of mNeon green cells.*

Similarly, we show a case in which the targets are now labeled with two probes that have similar spectra but different lifetimes (Fig. 3F). In this case, we also introduce the use of the phasor approach to reveal the three expected populations, the pixels that contain both probes appear in the midpoint between the phasor positions of the pixels that contain only one of the probes. Figure 3G shows the phasor distribution obtained from the same field of view as in the spectral example, in which we also show the theoretical locations of the probes (corresponding to Alexa647 and ATTO647 with respective lifetimes of 1 ns and 3.5 ns). As is expected in real experimental conditions, there are additional fluorescent components in the sample. We broadly refer to the bulk of these additional components as autofluorescence, which pulls the data away from the expected positions and converges to the mean phasor position of the autofluorescent components. We have previously shown that the Gaussian Mixture Models is the most optimal machine learning clustering algorithm to model phasor data[31], and we use this machine learning technique to infer the phasor locations of the probe combinations (Fig. 3H). We can now successfully classify each pixel of the original image into one of the clusters and obtain a probability of belonging to each, i.e., the posterior probability of the model. This allows us to

color-code the transcripts depending on their assignment to one of the 3 clusters (Fig. 3J) and obtain the counts of the three lifetime components (Fig. 3K). Additionally, we apply our lifetime multicomponent analysis technique[32] in which for each detected puncta, we estimate the presence of one of the lifetime components, in this case lifetime1 (Alexa647, purple in the figure), to obtain the expected result; that there are clearly three populations with respective fractions centered around [0, ½ and 1] (Fig. 3I).

In the general case, we combine the lifetime and spectral dimensions, and we perform the clustering of the data in a 4D spectral/lifetime phasor space. The clustering technique has the power to not only identify which puncta belong to each cluster but also to assign a probability of belonging to that cluster, which can be used to quantify the certainty of the labeling. For example, in the inset in Figure 3J, we show two cases of puncta that have relatively low confidence in the cluster assignment; they are depicted with blended colors because they fall in the regions of the phasor space where the two clusters are merging.

In this combinatorial example in Figure 3, the three clusters in the lifetime domain multiplexed with the channel-based in the spectral domain yield a 6-plex image using only 3 probes (Fig. 3L,M). The specific genes targeted for this experiment with the combined probes were POLR2A (Alexa647 & ATTO565), MTOR (ATTO647 & ATTO565), KI67 (Alexa647 & ATTO 647), BRCA1 (Alexa647), NCOA2 (ATTO647), NCOA3 (ATTO565). In the general combinatorial experiment using couples of N probes the total number of possible target genes grows quadratically:

$$\binom{N}{2} = \frac{N!}{2(N-2)!} = \frac{N^2 - N}{2} \tag{1}$$

Simultaneous 10-plex mRNA detection in fixed colorectal cancer SW480 cells using MOSAICA

We next applied MOSAICA to a 10-plex panel of mRNA targets in colorectal cancer SW480 cell culture samples. This cell line was chosen because its xenograft model exhibits spatial patterns of heterogeneity in WNT signaling[33], which will allow us to study tumorigenesis in the spatial context and potentially identify cancer stem cell populations in colorectal cancer in future. Here, we selected this model as a validation platform to demonstrate the multiplexing scalability and error correction capabilities of our approach. We began by first identifying a set of 10 genes with known expression levels from our bulk sequencing data. Using the aforementioned probe design pipeline, we designed 80 probes (two pairs of 40 probes) for each gene: BRCA1, BRCA2, CENPF, CKAP5, KI67, MTOR, NCOA1, NCOA2, and NCOA3. These genes were chosen due to their housekeeping status or involvement in tumorigenesis in colorectal cancer. By encoding each gene with a distinct combination of two fluorophores, we generated a codebook of 10 labelling combinations from only five fluorophores following Equation 1: $\binom{5}{2} = 10$ (Fig. 4A) (see Table S2 for the probes used for each target). To assess the baseline nonspecific binding events of our assay, we included a negative probe control sample which was labelled with primary probes not targeting any specific sequence in the human genome or transcriptome but still containing readout regions for secondary fluorescent probes hybridization (Fig. 4A right). Matching numbers

and concentrations of primary and secondary probes that were used in the 10-plex panel were used in this sample.

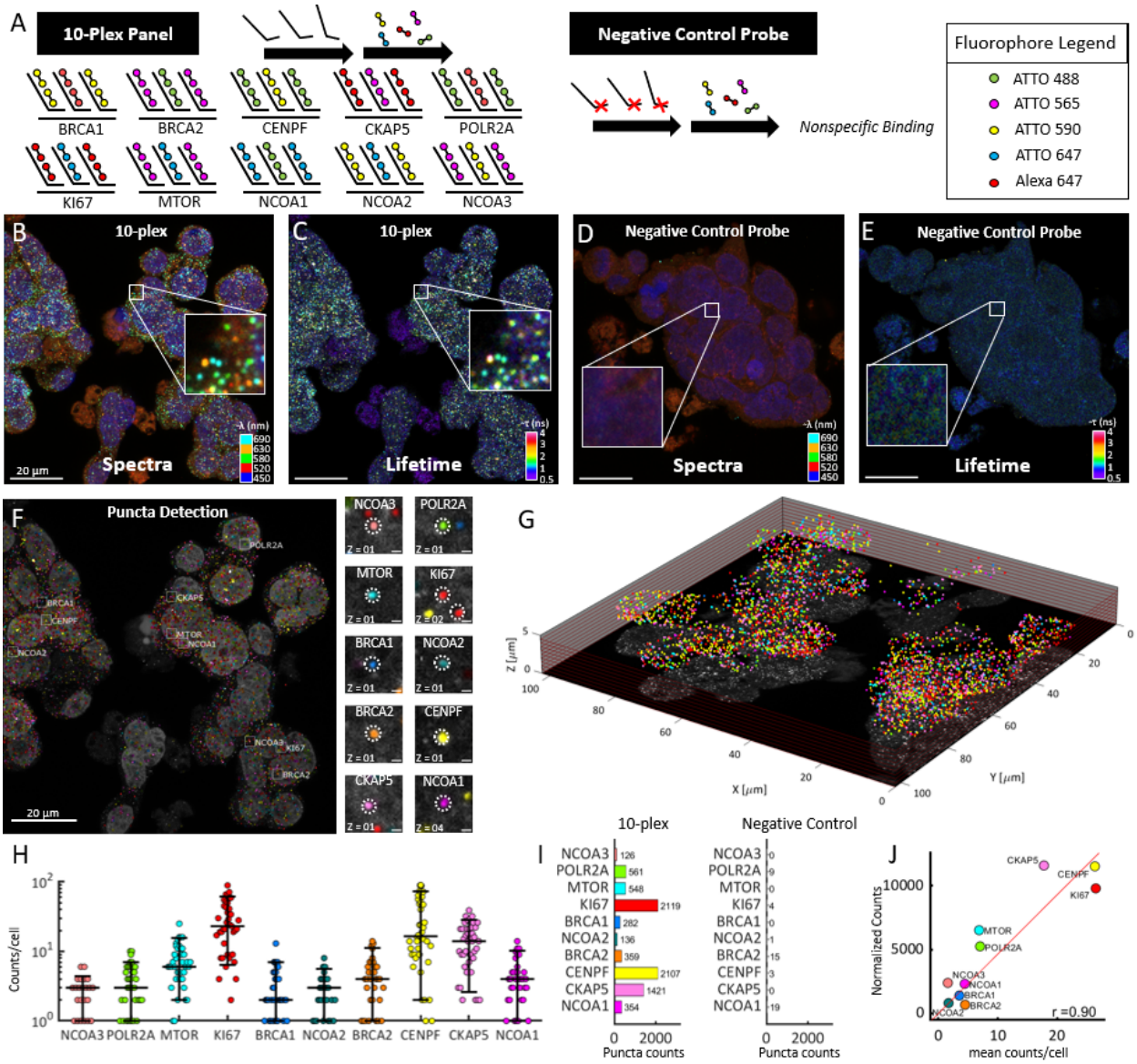

Figure 4. Simultaneous 10-plex detection of genes in colorectal cancer SW480 cells in a single round of labeling and imaging. A) *10 different types of gene transcripts are labeled with primary probes followed by respective and complementary fluorescent secondary probes. Each gene is labeled with a combination of 2 different fluorophores for 10 combinations. Negative control probes (mNeonGreen, DCT, TYRP1, and PAX3) targeting transcripts not present in the sample were used with their respective secondary fluorophore probes.* ***B)*** *Spectral image (max-projection in z) of a field of view of the labeled 10-plex sample (5-channel pseudo coloring).* ***C)*** *Lifetime image (max-projection in z) of a field of view of the labeled 10-plex sample (phasor projection on universal circle pseudo coloring).* ***D)*** *Spectral image of the labeled negative control probe sample.* ***E)*** *Lifetime image of the labeled negative control probe sample.* ***F)*** *Final puncta detection after being processed in our analysis software showing highlighted example puncta of each target (insets, right). Scale bar 20 µm in main image and 1 µm in insets.* ***G)*** *3D representation of the field of view for the 10-plex sample.* ***H)*** *Number of puncta detected for each gene expression target in each cell for the labeled 10-plex sample (N=80 cells).* ***I)*** *Overall puncta count of each transcript in the 10-plex sample (left) and negative control*

probe sample (right). ***J)*** *Correlation of detected puncta (mRNA puncta count) vs. RNA-bulk sequencing (normalized counts) is shown for each target with Pearson r of 0.9.*

Figure 4B depicts a spectral image overlay (five fluorescent channels including DAPI) of the labeled 10-plex SW480 sample. Additionally, in the same measurement, the orthogonal lifetime information attained by interrogating each pixel for their lifetime components. These pixels were phasor-transformed and pseudo-colored based on their projected phasor coordinates on the universal circle, creating the image depicted in Figure 4C. In doing so, both dimensions of data can now be simultaneously accessed to determine which cluster of pixels meet the appropriate and stringent criteria for puncta classification. Similarly, Figure 4D/E depict the merged composite spectral and lifetime images of the corresponding negative control probe sample. Figure 4F depicts the now detected pseudo-colored clusters which were successfully classified as one of the RNA markers. A representative inset image for each marker and its targeted detection is provided on the right. With 40 Z-stack images, we generated a 3D spatial distribution of the field of view to visualize the spatial analysis in a 3D context (Fig. 4G).

MOSAICA employs an error-correction strategy by gating for specific and pre-encoded fluorophore combinations and rejecting any fluorescent signature which do not meet these criteria. Specifically, in addition to the population of pixels that represents the decodified puncta as mentioned above, there was a population of pixels of various shapes and sizes which did not fit the criteria. Simulations to look into overlapping and inconsistent signals were run (Fig S4A,B). Plotted in Supplementary Figure 4C are the total detected puncta in this experiment, separated into populations depending on our classification criteria. Of the total detected puncta (n = 13,521), a considerable fraction n = 4,488 (33%), were observed emitting fluorescence only in a single channel and was indicative of nonspecific binding events and/or autofluorescence moieties. As previously characterized by several groups, nonspecific binding events is an inherent issue with smFISH which arises from the stochastic binding of cDNA probes towards cellular components such as proteins, lipids, or nonspecific regions of RNA and follow a random distribution[14]. When combined with native autofluorescence moieties which can also exists as diffraction-limited structures that emits a strong fluorescent signal in any single channel, this group represents a confounding problem for standard intensity-based measurements and analysis because they share similar SNR and intensities to real labeled puncta and cannot be differentiated. This is the main benefit of implementing the combinatorial encoded criteria which rejects this large amount (around 33%) of stochastic and nonspecific binding labeling events as well as any event eliciting a lifetime signature that deviated from the utilized commercial fluorophores. Finally, we also observed a relatively small group of puncta emitting fluorescent signal across more than two spectral channels but still eliciting the same spectral and lifetime signatures as the utilized fluorophores, n = 880. To characterize this population, we performed a simulation running 20,000 iterations of various puncta densities and fitted the corresponding exponential model that characterizes the probability of puncta overlap (described in Methods section and Supplementary Figure 4A and B). We attained an interval for the fraction of lost puncta due to optical crowding ranging from 2.1% to 6.6% which accounts for the 880 puncta or 6% of the total detected puncta. We name this group the overlapped in Supplementary Figure 4C.

The number of puncta detected for each target gene in each cell for the labeled 10-plex sample was plotted (Fig. 4H). Figure 4I plots the total number of detected puncta for the labeled 10-plex sample split into the different genes classified using MOSAICA phasor analysis with combinatorial labeling. In comparison, we also show the MOSAICA pipeline results with the negative control sample obtaining counts of less than five per thousand mainly due to noise in the images. To validate these puncta count, we compared them to matching RNA-seq data from the same cell type. Shown in Figure 4J is a scatter plot of the average mRNA puncta count for each cell plotted against the normalized counts from DESeq2 of our bulk RNA-sequencing data for each gene. When fitting with a straight line we obtained a Pearson correlation of $r = 0.904$, indicating a significant positive association between the two methods. The number of counts per cell was obtained by simply dividing the total number of detected genes into the number of cells obtained by 3D segmentation of the individual nuclei stained with DAPI. The individual cell edges were estimated by growing the edges of the nuclei until convergence (see Methods section). A total of 80 cells were analyzed for this experiment.

To further evaluate the detection efficiency, we performed benchmarking tests with our method against LGC Stellaris™ and RNAscope™ which are commercial gold standard FISH methods (Fig. S5). Using the housekeeping gene, POLR2A, as an exemplary target, we found a significant association between the number of detected puncta by our method and LGC Stellaris™ (t-test p-value = 0.4). When compared to RNASCOPE™, we observed that for this cell type and target, both our assays and LGC Stellaris™ did not correlate significantly ($p = 7.8\times10^{-4}$ and $p = 3.4\times10^{-4}$), indicating a discrepancy in detection efficiency between the two methods. We attribute this difference to MOSAICA and LGC Stellaris™ utilizing a direct labeling and amplification-free method while RNASCOPE™ utilizes a tyramide signal amplification reaction which generates thousands of fluorophore substrate per transcript and can lead to overlapping puncta or undercounting of detected puncta. Together, these data show MOSAICA can robustly detect target mRNAs of broad dynamic range of expression levels from single digit to hundreds of copies per cell.

Multiplexed mRNA analysis in clinical melanoma skin FFPE tissues

We next investigated whether MOSAICA can provide multiplexed mRNA detection and phasor-based error-correction to clinically relevant and challenging sample matrices. Assaying biomarkers *in situ* in tissue biopsies has great clinical values in disease diagnosis, prognosis and stratification including in oncology[34-36]. Specifically, we applied a mRNA panel consisting of KI67 (indicative of cell proliferation), POLR2A, BRCA1, MTOR, NCOA2, and NCOA3 to highly scattering and autofluorescent human melanoma skin biopsy FFPE tissues obtained from and characterized by the UCI Dermatopathology Center. Using the same probe design pipeline, primary probes were encoded with a combination of two fluorophores for each gene to exhibit a unique fluorescent signature (Fig. 5A left).

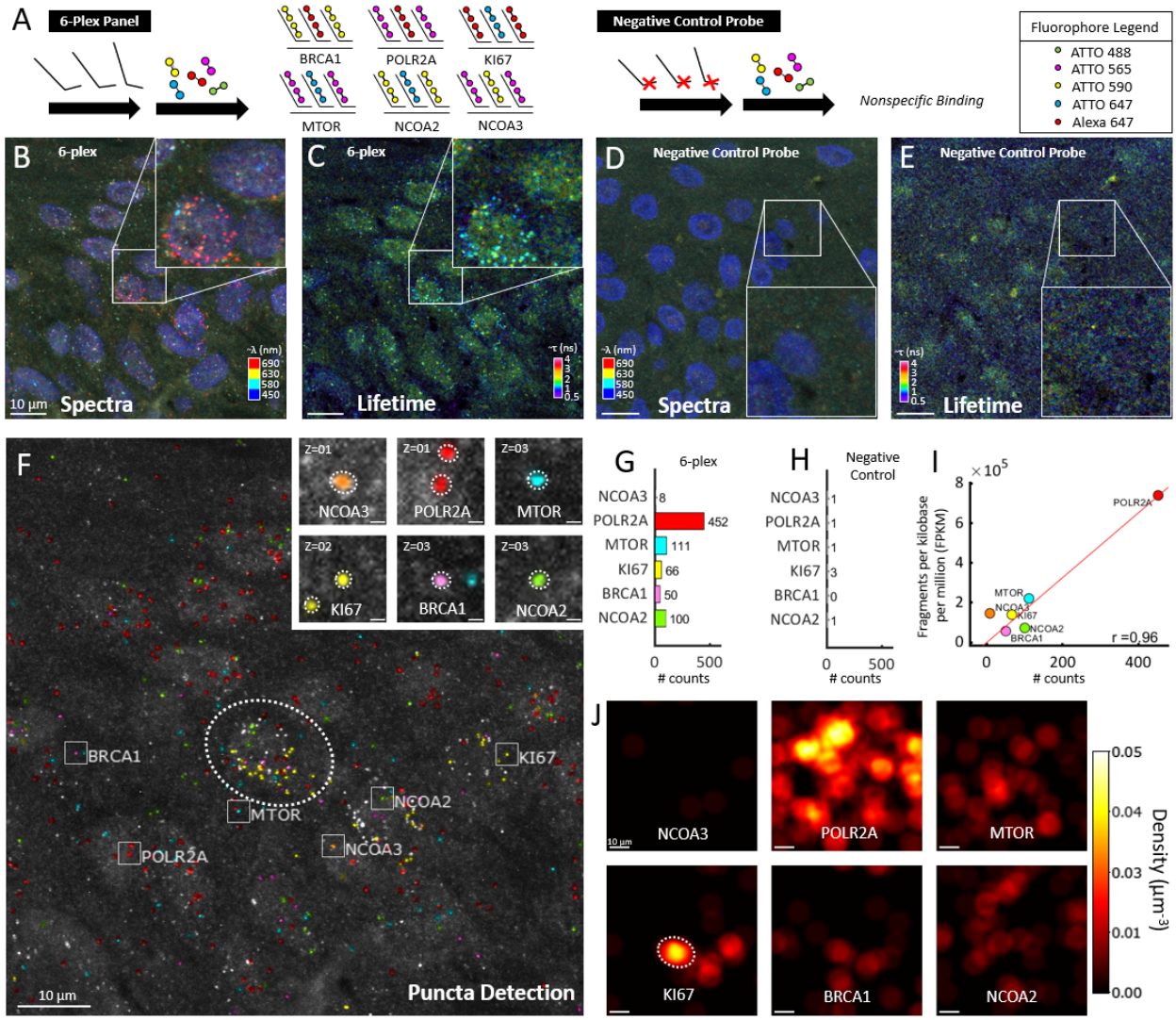

Figure 5. Multiplexed mRNA detection in epidermis region of human skin melanoma FFPE tissue. A) *6 different types of gene transcripts were labeled with primary probes followed by respective and complementary fluorescent secondary probes. Each gene was labeled with a combination of 2 different fluorophores for 10 combinations. Negative control probes targeting transcripts not present in the sample were used with their respective secondary fluorophore probes.* ***B)*** *Spectral image (max-projection in z) of a field of view of the labeled 10-plex sample (3 channel pseudo coloring).* ***C)*** *Lifetime image (max-projection in z) of a field of view of the labeled 10-plex sample (phasor projection on universal circle pseudo coloring).* ***D)*** *Spectral image of the labeled negative control probe sample is depicted.* ***E)*** *Lifetime image of the labeled negative control probe sample.* ***F)*** *Final puncta detection of the 6-plex field of view after being processed in our analysis software showing highlighted example puncta of each target (insets, right). Scale bar is 10 µm in the main image and 1 µm in insets.* ***G)*** *Overall puncta count of each transcript in the 6-plex sample.* ***H)*** *Puncta count for the negative control probe sample.* ***I)*** *Correlation of detected puncta (mRNA puncta count) vs. bulk sequencing (fragments per kilobase per million (FPKM)) is shown for each target.* ***J)*** *Transcript density in the field of view for each of the genes reveals clustering of specific genes, as an example KI67 appears highly expressed in three cells, one of them marked with a dotted ellipse that corresponds to location in F.*

Figure 5B depicts a spectral image overlay (four fluorescent channels including DAPI) of the epidermis region of a labeled 6-plex skin tissue sample. Similarly, as in the previous section, the orthogonal lifetime image was attained after using phasor analysis to create the image depicted

in Figure 5C. Figure 5D/E depict the merged composite spectral and lifetime images of the corresponding negative probe sample also in the epidermis region. Figure 5F depicts the pseudo-colored puncta which were successfully classified and identified as their assigned mRNA markers. A representative inset image for each marker and its targeted detection is provided on the right. Using this approach, we observed that a population of puncta consisting of nonspecific, autofluorescent, or unknown sample artifacts were rejected from analysis, (n = 438) or 29% of total detected clusters (Fig. S4D). In addition to this group, we observed MOSAICA rejecting a small group of puncta that emitted fluorescence in multiple spectral channels (n = 168). Since, this fraction (11%) exceeded the optical crowding range (2.1% to 6.6%) our simulations and model permits, we attribute this discrepancy to autofluorescence moieties which had fluorescent signatures that spans a broad emission spectrum and elicits a multispectral response. With conventional intensity-based measurements and analysis, both contaminating groups are inherent image artifacts that compromise the integrity of puncta detection unless complicated quenching steps or additional rounds of stripping, hybridization, and imaging are utilized[14,37]. With MOSAICA, these contaminating artifacts can be accounted for with the integration of spectral, lifetime, and shape-fitting algorithms.

Figure 5G/H plots the total number of detected puncta for the labeled 6-plex sample and the negative control probe sample to highlight the final counts obtained using MOSAICA. We observed MOSAICA platform results with the negative control sample obtaining counts of less than five per thousand. To validate these puncta counts and their relative expressions, we examined the relationship between the decodified puncta with matching bulk RNA-sequencing obtained from The Cancer Genome Atlas (TCGA) database (see Methods section). Shown in Figure 5I is a scatter plot of mRNA puncta count for each cell plotted against fragments per kilobase per million (FPKM). We observed a Pearson correlation of r = 0.959 for this 6-plex sample, indicating a significant positive association between the two methods and the capability for MOSAICA to capture a wide range of differentially expressing markers. Lastly, as shown in Figure 5J, the density map of the detected transcripts provides a visual method to identify spatial localization of clusters of genes, such as KI67 (indicative of proliferating tumor cells) being more prevalent in the dermis region while POLR2A is dispersed throughout the region. Overall, *in situ* profiling biomarkers such as KI67 and their spatial clustering can have diagnostic and prognostic values in malignant diseases and MOSAICA provides a robust platform to profile these markers[38].

Discussion

MOSAICA provides a new solution that fills a major gap in the spatialomics field (Fig. S6) by simultaneously achieving both simplicity and multiplexing by enabling direct *in situ* spatial profiling of many biomarkers in a single round of staining and imaging. This solution contrasts existing approaches such as conventional direct labeling approaches (e.g., LGC Stellaris™, RNAscope™, etc.) which can only analyze 3 - 4 targets due to limited spectral channels as well as recent spatial transcriptomic approaches (e.g., seqFISH) which can provide greater multiplexing capabilities but at the expense of many iterations of sample re-labeling, imaging, indexing, and error-prone image registration. MOASICA accomplishes this by uniquely integrating the lifetime dimension with the conventional spectral dimension, employing combinatorial fluorescence

spectral and lifetime target encoding, and exploiting machine learning- and phasor-based deconvolution algorithms to enable high-plex analysis and error-correction. This enables MOSAICA to simultaneously access both spectral and lifetime dimensions to achieve higher plex detection without sacrificing assay throughput as well as correcting for autofluorescent moieties and stochastic nonspecific binding artifacts, which are inherent challenges associated with existing intensity-based measurements.

Compared to existing sequential hybridization and imaging approaches, MOSAICA significantly reduces the number of hybridization and imaging rounds required to profile larger multiplexed panels of RNA biomarkers. By imaging every fluorophore and labeled transcript simultaneously rather than sequentially, the need to relabel probes or reimaging samples is precluded which is often the bottleneck for these complex and lengthy assays. For a 10-plex panel, this drastically shortens assay time by at least of factor of 4 – 5x and scales up even more as the panel becomes more multiplexed, making these assays more practical, effective, and affordable for routine laboratory or clinical usage. This is particularly important in clinical settings, where biopsy samples are limited in quantity and the need to avoid repetitive stripping, rehybridization, and image registration to preclude damage to the tissue structure integrity and target molecules is highly critical. In terms of cost, compared to existing commercial platforms where assay ranges from several hundred dollars to thousand dollars per batch of samples, MOSAICA utilizes inexpensive DNA primary probes which can be purchased in batch or as microarrays for a minimal price. Fluorescently conjugated secondary probes can also be used and shared as a common set among many different genes, scaling down costs to several dollars per assay or 10 – 20x less than commercial vendors. Compared to indirect spatial transcriptomic methods that analyze barcoded regions of interest (ROIs) using downstream sequencing (e.g., GeoMx® Digital Spatial Profiler, 10x Genomics Visium), the direct, imaging-based MOSAICA would be advantageous for targeted mRNA profiling with higher spatial resolution (subcellular features or single molecules), simpler workflow, lower cost, and potentially higher throughput (number of tissue sections analyzed per day) with a camera-based system (below). Moreover, the MOSAICA platform utilizes standard fluorescent probes and fluorescence microscopy (several commercial instruments capable of acquiring both spectral and lifetime information are available, e.g., Leica SP8 FALCON, PicoQuant rapidFLIM, ISS FastFLIM, etc., and already exist in many shared core facilities in academia and industry). Fluorescence imaging remains the most familiar and widely used technique in biological research and its minimal requirements of MOSAICA will permit quick and broad adoption in the scientific community.

As a complementary tool to existing spatial-omics methods, MOSAICA broadly enables scientists and clinicians to better study biology, health, and disease and to develop precision diagnostics and treatments. Gene expression is heterogeneous and many different cell identities/states exist in a particular tissue. To fully characterize cells *in situ,* we need to be able to assess multiplexed panels of genes within the same cell, which can be readily addressed by MOSAICA. As such, MOSAICA can help accelerate spatiotemporal mapping experiments to construct 3D tissue cell atlas maps. Additionally, MOSAICA represents a powerful tool for targeted *in situ* validation of RNA sequencing data. scRNAseq returns cell identities in the form of “differentially expressed gene lists” that “define” cell types. However, the clustering process is subjective, variable and

error-prone. Multiplex spatial transcriptomics using MOSAICA can validate whether a pattern of gene expression really defines a cell type or conflates multiple cell types. Furthermore, we are currently developing MOSAICA to serve as a clinical companion diagnostic tool for stratified care. Of particular interest is the spatial profiling of the organization and interactions between tumor cells, immune cells and stromal components in tumor tissues that can inform cancer diagnosis, prognosis, and patient stratification[39,40]. With MOSAICA's ability to analyze numerous markers in a single round, we believe this feature will be particularly attractive for clinicians or researchers working with precious patient derived materials.

Further ongoing work for this platform includes improving multiplexing by scaling up the number of fluorophores and their combinations using our combinatorial-based labeling approach. For instance, Equation A and our simulation (Fig. S4) predict that with different combinations of 10 fluorophores using triple labeling strategy, MOSAICA can barcode and detect 120 mRNA targets. Our immediate next step is to scale our multiplexing capability to about 60-plex, which will bridge the gap between conventional FISH and sequential- and sequencing-based methods and can be rapidly employed to numerous applications in targeted spatial transcriptomic analysis in basic and translational research. In the future, we will further expand our codebook by implementing a Förster resonance energy transfer (FRET)-based barcoding method[41] by using different FRET fluorophore pairs and tuning the distance between fluorophore donor and acceptor. We can utilize the FRET phenomena as an additional error correction mechanism at the nanometer level to resolve multiple transcripts in the same voxel. Moreover, we will improve imaging throughput with our recently developed camera-based light-sheet imaging [42] and hyperspectral imaging[30]. Indeed, MOSAICA is versatile and can be further integrated with other imaging modalities such as super-resolution, expansion microscope and multi-photon imaging techniques [43-45] to increase subcellular resolution and enable imaging large highly scattering tissues.

Additionally, we will further develop our image analysis software with a user interface which enables classification and visualization of single-cell phenotypes, spatial organization and neighborhood relationship. Our current software platform's puncta detection and puncta classifier algorithm can also be improved using modern image processing techniques such as convolutional neural networks with clinical training sets to optimize true and false positive detection of biomarkers. We anticipate on benchmarking these sets with experimental data with stripping methods to determine fidelity of labeled targets Lastly, we will implement multi-omics analysis enabling codetection of mRNA, protein and other omics markers. In particular, simultaneous detection of protein and transcript levels within the same sample can reveal the genotypic and phenotypic heterogeneity and provide enriched information for biology and disease diagnosis.

Methods

Primary probe design

A set of primary probes were designed for each gene. A python code was used to rapidly design the primary probes while controlling various aspects of the probes such as GC content, length, spacing, melting temp, and prohibited sequences. To begin, probes are designed using exons

within the CDS region. However, if that region does not provide over 40 probes, the exons from the CDS and UTR regions are used. The candidate probes are then aligned to the genome using Bowtie2, an NGS aligner, to determine if these probes are specific. Probes that are determined specific are then aligned to the RNA sequencing data on the UCSC Genome Browser, further eliminating probes that do not align to regions with an adequate number of reads. While mapping the probes to the genome on the UCSC Genome Browser, the probes are aligned with BLAT (BLAST-like alignment tool). A local BLAST query was run on the probes for the genes in the panel to eliminate off-target hits. For this experiment, each gene had the maximum number of probes that could be designed with our pipeline and requirements. The final primary probe design included 2 assigned readout sequences of secondary probe with a "TTT" connector in between, another connector, then one of the probes specific for the gene. The primary probes were ordered from Sigma Aldrich and pooled together for each gene. The sequences of all probes used in this study are listed in Table S3.

Secondary probe design

Secondary probe structures were based on the design from the Zhuang group[46]. In short, the 20-nt, three-letter readout sequences were designed by generating a random set of sequences with the per-base probability of 25% for A, 25% for T, and 50% for G. Sequences generated in this fashion can vary in their nucleotide content. To eliminate outlier sequences, only sequences with a GC content between 40% and 50% were kept. In addition, sequences with internal stretches of G longer than 3 nt were removed to eliminate the presence of G-quadruplets, which can form secondary structures that inhibit synthesis and binding. To remove the possibility of significant cross-binding between these readout sequences, algorithms from previous reports were used to identify a subset of these sequences with no cross-homology regions longer than 11 contiguous bases[46]. Probes were then checked with BLAST to identify and eliminate sequences with contiguous homology regions longer than 11 nt to the human transcriptome. From the readout sequences satisfying the above requirements, 16 were selected.

Cell culture

Human embryonic kidney (HEK293T) cells (632180; Takara) were cultured in DMEM (10-013-CV; Corning) supplemented with 10% FBS (1500-500; Seradigm) and 1% penicillin (25-512; GenClone). Human colorectal adenocarcinoma (SW480) cells were cultured in DMEM with high glucose (SH30081.02; HyClone) supplemented with 10% FBS (1500-500; Seradigm), 1x L-Glutamine (25-509; GenClone), and 1% penicillin (25-512; GenClone). The cells were plated into 8-well chambers and then fixed. The 8-well plates (155409; Thermo Scientific) for HEK293-T and SW480 cells were coated with fibronectin bovine plasma (F1141-2MG; Sigma Aldrich) before seeding cells onto the 8-well plates. All cultures were grown at 37°C with 5% CO_2.

mNeonGreen cell engineering

A mNeonGreen construct was transfected into HEK293T-X cells with FuGENE HD Transfection Reagent (E2311; Promega). The cells were then selected with puromycin (NC9138068; Invivogen) and Zeocin (AAJ67140XF; Alfa Aesar) 3 days after transfection.

Preparation of fixed cells in cell chambers

When the cells reached 70% confluency, cells were fixed for 30 minutes using 4% paraformaldehyde (15710; Electron Microscopy Science), then washed with PBS 3 times. The cells were then incubated with sodium borohydride (102894; MP Biomedicals) for 5 minutes and washed with PBS 3 times. 0.5% Triton X-100 (T8787-100ML; Sigma-Aldrich) in PBS was incubated in each well for 5 minutes and cells were washed with 2x SSCT (2x SSC with 0.1% TWEEN® 20 (P9416-100ML; Sigma-Aldrich). For storage, cells were left in 70% ethanol at 4℃.

Preparation of FFPE tissues

The University of California Irvine IRB approved this study for IRB exemption under protocol number HS# 2019-5054. All human melanoma cases were de-identified samples to the research team at all points and therefore considered exempt for participation consent by the IRB. Fully characterized human patient skin melanoma FFPE tissues with an immune cell score of brisk were obtained from the UCI dermatopathology center then sectioned to 5 µm slices using a rotary microtome, collected in a water bath at 35°C, and mounted to positively charged Fisher super frost coated slides. The tissue sections were then baked at 60°C for 1 hour. For antigen unmasking, slides were deparaffinized, rehydrated then followed by target retrieval (with citrate buffer).

Primary probe hybridization

Blocking buffer containing 100 mg/ml Dextran sulfate sodium salt (D8906-100G; Sigma-Aldrich), 1 mg/ml Deoxyribonucleic acid from herring sperm (D3159-100G; Sigma-Aldrich), 0.01% Sodium Azide (S2002-100G; Sigma-Aldrich), 0.01% tween, and 15% ethylene carbonate (AC118410010; Fisher Scientific) in 2x sodium saline citrate (SSC) was added to the fixed cells or tissues and incubated at 60℃ for 8 minutes and then at 37℃ for 7 minutes. Following this pre-block step, primary probes with 5nM of each probe in blocking buffer were added to the samples and incubated at 60℃ for 30 minutes and then overnight at 37℃.

Secondary probe hybridization

Once the primary probe solution is removed, the sample is washed with 2x Saline-Sodium Citrate Tween (SSCT) twice. Wash buffer (2xSSCT with 10% ethylene carbonate (EC)) is used for 3 washes and incubated in 60℃ for 5 minutes each time. Blocking buffer is added and incubated at room temperature for 5 minutes. The sample is then incubated in a solution with 5 nM of the secondary probes in blocking buffer at 37℃ for an hour. The sample is washed with 2x SSCT twice before using wash buffer to wash 3 times and incubated in 42℃ for 5 minutes each time. For the first wash, 10 mg/mL Hoechst (H3570; Invitrogen) is diluted 1:1000 in PBS and added to cells. Later, the wash buffer is then removed and replaced with glycerol mounting media and ready for imaging.

LGC Stellaris™

LGC Stellaris™ RNA FISH probes (Biosearch Technologies, CA, USA) were used, with 48 × 20 mer fluorophore conjugated oligos tiling the length of the target transcript. The POLR2A probe set

were supplied as predesigned controls conjugated to Quasar 570 fluorophores. Labeling/staining was carried out as described in the LGC Stellaris™ protocol for adherent mammalian cells. The POLR2A probe sets were used at 50 nM.

RNAscope™

The FFPE tissue sections were deparaffinized before endogenous peroxidase activity was quenched with hydrogen peroxide. Target retrieval was then performed, followed by protease plus treatment. The fixed cells pretreatment included treatment with hydrogen peroxide and protease 3. The RNAscope™ assay was then performed using the RNAscope™ Multiplex Fluorescent V2 kit and Akoya Cy5 TSA fluorophore. The positive control (POLR2A) and negative control (dapB) were in C1.

Microscopy Imaging

Our samples can be imaged with any instrument provided that it has spectral and lifetime acquisition capabilities. Our measurements were taken on two separate instruments; a generic FLIM instrument is depicted in Supplementary Figure 7. For validation of fluorophores and their spectral and lifetime signatures, measurements were taken on a 2-channel ISS Alba5 STED platform. This system is equipped with a pulsed white laser (NKT SuperK EXTREME) system where the excitation wavelength(s) can be selected with an acousto-optic tunable filter (NKT SuperK SELECT). Single photons were detected with avalanche photodiode detectors (Excelitas Technologies) and their arrival times with respect to the stimulating frequency (78MHz) were measured with a FPGA-based electronic board (ISS FastFLIM). Imaging was achieved by fast beam scanning with galvo mirrors and 3D stacks of images were acquired with a z-piezo mount on the objective.

For measurements of multiplexed/combinatorial labeling and detection experiments (Figures 4 and 5), we utilized a Leica SP8 with the Falcon module. This platform employs a white light laser and an acoustic optic beam splitter dichroic, and the Leica hybrid detectors with excitation band selectable by means of a prism. 3D measurements of cells and tissue samples were taken with a 100x plan apochromat oil objective with a numerical aperture of 1.40, yielding images with an x-y resolution of 100 nm and z-spacing of 500 nm.

For epifluorescence measurements (Supplementary Figures 2 and 3), images of labeled mRNA transcripts were taken on an inverted Ti-E using a 100× plan apochromat oil objective with a numerical aperture of 1.40. Samples were illuminated with a Spectra-X (Lumencor) LED light source at the 395 nm, 470 nm, 555 nm and/or 640 nm excitation wavelengths. Images were acquired with an Andor Zyla 4.2 sCMOS camera at 4K resolution with 6.5 µm pixels.

Image Processing

A custom set of scripts were written in MATLAB to process the acquired image stacks, identify individual transcripts and assign each of them to each gene. After reconstructing the images out of the digital list of photons, the analysis runs in parallel a 3D blob detection pipeline on the intensity image stacks to identify each transcript and on the other a clustering pipeline on the

phasor-transformed lifetime/spectral phasor data to detect distinct spectral/lifetime populations. A classifier then assigns pixels as belonging to a particular gene. The whole pipeline is depicted in Supplementary Figure 8.

Briefly, the intensity 3D stacks are run through a blob detection algorithm that was developed in order to identify each transcript. The images can be seen as a 3D space where the transcripts appear as spherically symmetric locations with a radial increase in intensity, namely puncta. The algorithm first computes the low frequency background noise by means of a median filter with a kernel 10 times the size of the expected puncta (the diffraction limit of the instrument, in our case around 250 nm). This low frequency background is subtracted from the high-pass filtered data obtained by convolving by a gaussian filter of the expected size of the puncta. This on one hand enhances the puncta in the image by giving a prominence value at each pixel with respect to the surrounding regions and on the other suppresses noise in the images. A search for local maxima is performed by finding the locations where the gradient goes to zero and the divergence of the gradient is negative. Once the centers in the 3D coordinate space are obtained the size, absolute brightness and prominence of each puncta is measured.

In parallel, the raw photon counts are used to construct the photon arrival time histogram and photon spectral histogram at each pixel. Phasor transforms are applied to each pixel in each image of the 3D stack in order to construct the stacks' phasor plot. This phasor data is in general a 4-dimensional, each pixel in the intensity image has four additional coordinates; two for the spectral phasor transform plus two for the lifetime phasor transform. The phasor coordinates are clustered using Gaussian Mixture Models[47]. We used an initial experiment tagging house-keeping genes in order to guarantee that all expected populations were present and we trained the Gaussian Mixture Model using this initial experiment. This pretrained model is then applied to the new sets of data in order to classify each pixel into one of the clusters allowing for the presence of empty clusters. The number of clusters N intuitively should be the number of distinct fluorescent probes or different combinations of probes used to tag the sample, but one must allow for additional populations in the sample, e.g., autofluorescent species. For this reason, in the training of the Gaussian Mixture Models we allowed for one additional cluster to account for autofluorescence and noise.

Finally, by computing the mean phasor coordinates of the pixels within each detected puncta, we can compute the phasor position of each puncta and assign a gene label to it by a priori knowing the expected positions of each combination of probes depending on the spectra and lifetime of the probes.

DAPI image stacks are segmented by means of simple thresholding, estimating the threshold value by hard splitting of the histogram of photon counts in the channel. The 3D segmented nuclei are then iteratively grown by convolution by a minimal 3x3x3 kernel. This convolution is applied at each pixel of the edge of the segmented volume until no available space is left in between the segmented volumes. This yields a division of the imaged volume into a number of polyhedra where each face is exactly in the plane bisecting the two closest nuclei edges. This process is analogous to a Voronoi tessellation using the surface of the nuclei instead of points.

Simulations

In order to test the detection and classification pipeline, we wrote a set of scripts to simulate spectral/lifetime data which provided a ground truth towards detection and accurate classification debugging. This data generation script allows randomly distributing N diffraction-limited transcripts in an arbitrarily big 3-dimensional space, each with a gaussian intensity profile. We simulated our transcript gaussian profile with a X-Y standard deviation of 200 nm and a Z standard deviation of 500 nm, a peak intensity of 1 ± 0.3 (the intensity becomes relevant when simulating background noise). In the simulation run that we used to test the crowding limitations of the system we simulated tagging genes with couples out of a total of 12 fluorescent probes; 4 distinct spectral probes and 3 distinct lifetimes in each, yielding a total of $\binom{12}{2} = 66$ possible genes.

We generated the simulated images in a cubic space of 10x10x10 µm, discretized as an image stack of 33 images of 1000 x 1000 pixels (yielding a voxel resolution of 100x100x300 nm). This volume was generated containing increasing densities of transcripts, ranging from a single transcript of each gene (66 transcripts) up to 2,000 transcripts of each gene (132k transcripts) and for each possible value of density a total of 10 iterations each time. These 20k simulated image stack sets were individually processed by our image processing pipeline and the transcript position and labelling obtained by the pipeline was compared to the known ground truth of the generated data. This simulation provided a benchmark of the density limitations of the method but at the same time giving an idea of the underestimation of the number of transcripts as a function of local density. The simulations allowed us to model the estimated number of overlapping transcripts as a function of density.

A similar set of simulations was run by emulating the conditions in the 10-plex experiment (Figure 4) where the genes are tagged with combinations of 2 out of 5 probes. The 20k iterations for different densities allowed to plot the density of the classification obtained after detection compared to the real number of transcripts in the simulations. This simulation was fit to the probabilistic model obtained from calculating the number of transcripts that are not overlapped in space (see next section), from which the true number of puncta was extracted (see Supplementary Figure 4).

Overlapping Probability

The fraction of puncta that do not overlap with any other puncta depends on the total number of puncta present in the volume of study and the relative proportion between said total volume and the volume of each individual puncta. The following expression is obtained as the product of N-1 times the fraction of available space having removed the volume occupied by one transcript:

$$\frac{n}{N} = \left(1 - \frac{v_i}{V_T}\right)^{N-1} \tag{2}$$

where n is the number of isolated puncta, N is the total number of puncta, v_i is the volume of each puncta and V_T is the total volume (simulated or scanned). The real number of transcripts N cannot be analytically isolated from the previous equation, but one can graphically obtain it. Due to the fact that the transcripts are sub-diffraction limit, the value of v_i depends on the point spread function of the instrument. Using the detected number of counts n=13.5k and the estimated cellular volume 68 kμm^3, both obtained from the two image stacks shown in Figure 4, we proceeded to estimate the real number of transcripts present in the sample using the previous expression. Assuming an interval of possible volumes for the transcripts between 0.1 and 0.3 μm^3 we obtained an estimated percentage of overlapping puncta in the interval [2, 6.6]%, which accounts for the number of puncta detected in more than 2 channels in the 10-plex experiment (6%). See Supplementary Figure 4.

Sequencing Data

Colorectal cancer SW480 cell bulk RNA sequencing (unpublished data) was analyzed with DESeq2. Average expression is then obtained for comparison to the MOSAICA puncta count for each gene. For the human skin melanoma FFPE tissue, the patient sample did not have corresponding sequencing data. RNA sequencing data was obtained from The Cancer Genome Atlas (TCGA), available on the National Cancer Institute (NCI) Genomic Data Commons (GDC) data portal, from 5 human skin melanoma FFPE biopsy thigh punch samples [Entity ID: TCGA-EE-A2GO-06A-11R-A18S-07, TCGA-EE-A20C-06A-11R-A18S-07, TCGA-YG-AA3N-01A-11R-A38C-07, TCGA-DA-A95Z-06A-11R-A37K-07, TCGA-GN-A26C-01A-11R-A18T-07]. The sequencing data were analyzed with HTseq and normalized for sequencing depth and gene length using Fragments Per Kilobase Million (FPKM). The average of the 5 patient samples for each transcript were used for correlation graphs with Spectral-FILM puncta count.

Statistical Analysis

When comparing distributions of puncta counts, signal-to-noise ratios, and intensity values, Student t-tests were performed for against the probability that the measured distributions belong to distributions with equal means. The reported probability values in the figures are symbolized with (* for $p<0.05$, ** for $p<0.01$, *** for $p<10^{-3}$ and **** for $p<10^{-4}$). Pearson correlation coefficient was computed to determine the correlation between the average expression level to the puncta count of each transcript.

Author Contribution

T.V., A.V. and J.G. designed, conducted and analyzed the experiments. T.V., A.V., J.G. and W.Z. wrote the manuscript. K.L., Q.X., J.F., J.Z. and C.D. conducted experiments. J.S., L.H., J.W., M.W., A.G., P.H. and E.G. provided technical support and consulted on the study. E.G. and W.Z. designed and directed the project.

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Conflict of interest

T.V and J.G are shareholders of Arvetas Biosciences Inc. A.V. and K.L recently joined Arvetas Biosciences Inc as employees. W.Z. is a cofounder of Velox Biosystems Inc., Amberstone Biosciences Inc, and Arvetas Biosciences Inc.

Data Availability

Scripts and algorithms used for the image manipulation, puncta detection and gene classification are available at request. Raw images and data used for figures 3, 4 and 5 are also available at request. Probe sequences used for labeling are included in the supplementary material section.

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Supplementary Material:

Table S1. List of Fluorophores Used

Fluorophore	Detection Channel	Excitation Max (nm)	Emission Max (nm)	Extinction Coefficient (M-1cm-1)	Quantum Yield	Brightness	Lifetime (ns)
ALEXA 647	1	650	668	270,000	0.33	89,100	1.04
ATTO 647N	1	646	664	150,000	0.65	97,500	3.5
ATTO 590	2	593	622	120,000	0.8	96,000	3.7
ATTO 565	3	564	590	120000	0.9	108,000	4
ATTO 488	4	500	520	90,000	0.8	72,000	4.1

Table S2. List of Genes Used and their Assigned Fluorophore Combination

Gene	Fluorophore 1	Fluorophore 2	No. of Probes per Gene	Present in Channel(s)	Used in Figure(s)
NCOA3	ATTO 565	ATTO 590	80	2, 3	4
POLR2A	ATTO 488	ALEXA 647	80	1, 4	4
MTOR	ATTO 565	ATTO 647	80	1, 3	4
MKI67	ATTO 647	ALEXA 647	80	1	4
BRCA1	ATTO 590	ALEXA 647	80	1, 2	4
NCOA2	ATTO 590	ATTO 647	80	1, 2	4
BRCA2	ATTO 488	ATTO 565	80	3, 4	4, 5
CENPF	ATTO 488	ATTO 590	80	2, 4	4, 5
CKAP5	ATTO 565	ALEXA 647	80	1, 3	4, 5
NCOA1	ATTO 488	ATTO 647	80	1, 4	4, 5

Table S3. List of Sequences Used

Gene	Probe Number	Codebook	Target Region	Readout 1	Readout 2	Full Sequence
MNEONGREEN	1	1	CTCGACCTTTCTCTTCTTCTTGGGGCT	GGGATGTATTGAAGGAGGATT	GGGATGTATTGAAGGAGGATT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCGACCTTTCTCTTCTTCTTGGGGCT
MNEONGREEN	2	1	GAACTCGCTGCCATCGGCTGTTCTCTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAACTCGCTGCCATCGGCTGTTCTCTT
MNEONGREEN	3	1	CTCGCCAGAGCCGGCAGCAGATCCAGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCGCCAGAGCCGGCAGCAGATCCAGC
MNEONGREEN	4	1	GCCCTTGTACAGCTCGTCCATGCCCAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCCCTTGTACAGCTCGTCCATGCCCAT
MNEONGREEN	5	1	GTCGGTGAAGGCTTTCTGCCACTCTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTCGGTGAAGGCTTTCTGCCACTCTTT
MNEONGREEN	6	1	GTTCAGTTCTGTCTTGGAGTGCTTCAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGTTCAGTTCTGTCTTGGAGTGCTTCAG
MNEONGREEN	7	1	GGTCTTGCGGAACACGTACATAGGCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGTCTTGCGGAACACGTACATAGGCTG
MNEONGREEN	8	1	CTTCAGGTAGTTGGCGGCCATGGGTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTCAGGTAGTTGGCGGCCATGGGTTT
MNEONGREEN	9	1	GAAGGTGTAGGTGGTCCGGGCGGTGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAAGGTGTAGGTGGTCCGGGCGGTGCT
MNEONGREEN	10	1	GTACCGCTTGCCATTGCCGGTGGTGTA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTACCGCTTGCCATTGCCGGTGGTGTA
MNEONGREEN	11	1	CTCGACCTTTCTCTTCTTCTTGGGGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCGACCTTTCTCTTCTTCTTGGGGCT
MNEONGREEN	12	1	GAACTCGCTGCCATCGGCTGTTCTCTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAACTCGCTGCCATCGGCTGTTCTCTT
MNEONGREEN	13	1	CTCGCCAGAGCCGGCAGCAGATCCAGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCGCCAGAGCCGGCAGCAGATCCAGC
MNEONGREEN	14	1	GCCCTTGTACAGCTCGTCCATGCCCAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCCCTTGTACAGCTCGTCCATGCCCAT
NCOA3	1	2	TTCAATGTCAAACCAGATAAATGTGCG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTCAATGTCAAACCAGATAAATGTGCG
NCOA3	2	2	GTGGTGAATCGAGACGGAAACATTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTGGTGAATCGAGACGGAAACATTG
NCOA3	3	2	CCATACATTTAATTGCCGTATGTTGATGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTCCATACATTTAATTGCCGTATGTTGATGA
NCOA3	4	2	ACCACATGATATTCTGGAAGACATAAACG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACCACATGATATTCTGGAAGACATAAACG
NCOA3	5	2	TGCAGTGCTTTGCCCTGTCTCAGCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCAGTGCTTTGCCCTGTCTCAGCC
NCOA3	6	2	CTGGCTTTGAAGATATAATCCGAAGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGGCTTTGAAGATATAATCCGAAGGT
NCOA3	7	2	AAAAGCAAACTCTTCCGAAATCCTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAAAAGCAAACTCTTCCGAAATCCTG
NCOA3	8	2	AAATGATCGACATGGCTTTGTCTCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAAATGATCGACATGGCTTTGTCTCA
NCOA3	9	2	GATTAGACCCACTATGGCTGGATGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTGAATGTGAGTAGTAGTGGAGTTTTGATTAGACCACCTATGGCTGGATGC
NCOA3	10	2	GTTCGGTAGGCGGCATGAGTATGTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTCGGTAGGCGGCATGAGTATGTC
NCOA3	11	2	GGCCTATGGCTTGGCAGACCCTAGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGCCTATGGCTTGGCAGACCCTAGC
NCOA3	12	2	CAGGGCAGATGAGTGGAGCTAGGTA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAGGGCAGATGAGTGGAGCTAGGTA
NCOA3	13	2	GGGCCAGGCATGCAATCACCATCTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGGCCAGGCATGCAATCACCATCTT
NCOA3	14	2	CCAGAACAACAACTATGGGCTCAAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCAGAACAACAACTATGGGCTCAAC
NCOA3	15	2	ACCAGCAGAATATCATGATTTCTCCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACCAGCAGAATATCATGATTTCTCCT
NCOA3	16	2	ATCGTGGGAGTCCAAAGATAGCCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTATCGTGGGAGTCCAAAGATAGCCTC
NCOA3	17	2	GCCCTGCAAGCCATCAGTGAAGGTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCCCTGCAAGCCATCAGTGAAGGTG
NCOA3	18	2	CCCAAATTGGATAACTCTCCCAATATG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCAAATTGGATAACTCTCCCAATATG
NCOA3	19	2	TTCCAAGAGTCCTCTGGGCTTTTAT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTCAAGAGTCCTCTGGGCTTTTAT
NCOA3	20	2	ACCAAAATCCAGTGGAGAGTTCAAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACCAAAATCCAGTGGAGAGTTCAAT
NCOA3	21	2	CAAAGAAAGTAAGGAGAGCAGTGTTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTCAAAGAAAGTAAGGAGAGCAGTGTTG
NCOA3	22	2	AATTACTGCAGTTACTTACCTGTTCTTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAATTACTGCAGTTACTTACCTGTTCTTCT
NCOA3	23	2	CTGTTACAAGAGAAGCACCGGATTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTGTTACAAGAGAAGCACCGGATTT
NCOA3	24	2	CAAGTTGCTGCAGAATGGGAATTCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAAGTTGCTGCAGAATGGGAATTCA
NCOA3	25	2	ACTGGGAAAGACACCAGCAGTATAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACTGGGAAAGACACCAGCAGTATAA
NCOA3	26	2	GGGACGGAAATGTTGTCAAGCAGGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGGACGGAAATGTTGTCAAGCAGGA
NCOA3	27	2	CAAGAGAAAGACCCTAAAATTAAGACAGAG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCAAGAGAAAGACCCTAAAATTAAGACAGAG
NCOA3	28	2	ATTCCATATCCTCAAATGGTAGTCATCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTATTCCATATCCTCAAATGGTAGTCATCT
NCOA3	29	2	CCCATGTTACCAAAGCAACCCATGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCCATGTTACCAAAGCAACCCATGT
NCOA3	30	2	TGGAACCTATGAATTCAAACTCCATGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGGAACCTATGAATTCAAACTCCATGG
NCOA3	31	2	CCTGCACTGGGTGGCTCTATTCCCA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCTGCACTGGGTGGCTCTATTCCCA
NCOA3	32	2	GCCTCTTCGGTCTAATAGCATACCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCCTCTTCGGTCTAATAGCATACCA
NCOA3	33	2	GCAACACAGATGCCACAGGCCTGGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCAACACAGATGCCACAGGCCTGGA
NCOA3	34	2	AACAGGATGCTTTCCAAGGCCAAGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAACAGGATGCTTTCCAAGGCCAAGA
NCOA3	35	2	ATATGGACAGACATACCCAGCACAG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATATGGACAGACATACCCAGCACAG
NCOA3	36	2	CTCCAATGCAAGGAGGCTTTCATCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCCAATGCAAGGAGGCTTTCATCT
NCOA3	37	2	AGATGAACCAGCAAGGCAATTTTCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGATGAACCAGCAAGGCAATTTTCC
NCOA3	38	2	CCCAAGCAACTTAGAATGCAGCTTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCAAGCAACTTAGAATGCAGCTTC
NCOA3	39	2	CACAATGCCACAAGCTCCTCCGCAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCACAATGCCACAAGCTCCTCCGCAA
NCOA3	40	2	CAACCAGATCCAGCCTTTGGTCGAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAACCAGATCCAGCCTTTGGTCGAG
NCOA3	41	2	CAACACCCGCAGGCTGCATCCATCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCAACACCCGCAGGCTGCATCCATCT
NCOA3	42	2	GTCCTCAGAAATGAAGGGCTGGCCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTCCTCAGAAATGAAGGGCTGGCCA
NCOA3	43	2	CATGAATGGCAGCAGTGGTCACATG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCATGAATGGCAGCAGTGGTCACATG
NCOA3	44	2	CACCAGGACCTCTTAAGGAAACCAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCACCAGGACCTCTTAAGGAAACCAC
NCOA3	45	2	GAATCATTGTTCCAGGCATCCATCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGAATCATTGTTCCAGGCATCCATCT
NCOA3	46	2	AGAAAGGACCAGCTTTGAGCTCCAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGAAAGGACCAGCTTTGAGCTCCAT
NCOA3	47	2	GATTTTAAGCCGAAGGGCAATATCTAC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGATTTAAGCCGAAGGGCAATATCTAC
NCOA3	48	2	CCCTCCTTCTGCTGTGTATCATGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCTCCTTCTGCTGTGTATCATGGT
NCOA3	49	2	TTCTGGAGACATGGAGTGTTACTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCTGGAGACATGGAGTGTTACTGA
NCOA3	50	2	TTTTCTGCCTTGCTAGCCAAAATCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTTTCTGCCTTGCTAGCCAAAATCT
NCOA3	51	2	AATATCTGGTTTCTCTAGTTGCAGTATTGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAATATCTGGTTTCTCTAGTTGCAGTATTGG
NCOA3	52	2	AGAGCATAGTCCCAGCCTTCAGGTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGAGCATAGTCCCAGCCTTCAGGTG
NCOA3	53	2	TGATTCTGAATTGTCCTTTACTAATGGTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTGATTCTGAATTGTCCTTTACTAATGGTG
NCOA3	54	2	GTTGCTCTGTCCCTATTATTTGCCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTGCTCTGTCCCTATTATTTGCCC
NCOA3	55	2	GTCATGGATGTCCAAATGGCTTTGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTCATGGATGTCCAAATGGCTTTGC
NCOA3	56	2	GTAGCAAACTTTTCACATGCTAATGTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTAGCAAACTTTTCACATGCTAATGTG
NCOA3	57	2	TTTTAAAGTACTGGTGTCACCCTTTGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTTAAAGTACTGGTGTCACCCTTTGC
NCOA3	58	2	AAAATAAACTTCTGAAAACCCAAGGCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAAAATAAACTTCTGAAAACCCAAGGCC
NCOA3	59	2	GGCTACCAGTGGAAGAGACATCCCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGCTACCAGTGGAAGAGACATCCCT
NCOA3	60	2	GGGTAGTGCTCCACAGCTTTTCCTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGGTAGTGCTCCACAGCTTTTCCTT
NCOA3	61	2	AAGAGAATCTTTTGGATTTTAAGCAGTCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAAGAGAATCTTTTGGATTTTAAGCAGTCC
NCOA3	62	2	TAATAGCAATTCATGGGCTGTGTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTAATAGCAATTCATGGGCTGTGTGT
NCOA3	63	2	GCTAAGACCTGAATCCCATATTGAGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTAAGACCTGAATCCCATATTGAGA
NCOA3	64	2	GAGTAGAATCCTTGGTGTGGTTTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGAGTAGAATCCTTGGTGTGGTTTCT
NCOA3	65	2	TTGACACCTGTTTTAGTCAGTTGGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTGACACCTGTTTTAGTCAGTTGGG
NCOA3	66	2	TCCCTTTATCTGGGTTAATTCATTTGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCTTTATCTGGGTTAATTCATTTGGT
NCOA3	67	2	CTGTGAATTTCAGAGGTCTCTGCTA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTGTGAATTTCAGAGGTCTCTGCTA
NCOA3	68	2	TGGTATCATTTTCTAGCAATAACTGAGAGC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGGTATCATTTTCTAGCAATAACTGAGAGC
NCOA3	69	2	TCTTTGATATGCTTACGAGTAAGTGAATCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTTGATATGCTTACGAGTAAGTGAATCC
NCOA3	70	2	TAAATCCGAAAACTTCCATTGTAGTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTAAATCCGAAAACTTCCATTGTAGTGG
NCOA3	71	2	ACAGAGGAAGAACCAGGTCAGTCTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACAGAGGAAGAACCAGGTCAGTCTG
NCOA3	72	2	TTTTCAGCTCAATTGTATCTGACCCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTTTCAGCTCAATTGTATCTGACCCT
NCOA3	73	2	TTTTAGGTAATTCTTTGTACTCCTGCTGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTTTTAGGTAATTCTTTGTACTCCTGCTGT
NCOA3	74	2	TTTTCAAACCTTGGTATCTGTTGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTTTCAAACCTTGGTATCTGTTGGGT
NCOA3	75	2	GGGTAGGGTATTACAGAAGATAATTGGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGGTAGGGTATTACAGAAGATAATTGGC
NCOA3	76	2	TGTCCTAGAAGTTCTTTGATCCAGAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTCCTAGAAGTTCTTTGATCCAGAG
NCOA3	77	2	CCAGTTACATGTATGCCTGCCCAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCAGTTACATGTATGCCTGCCCAGT
NCOA3	78	2	TTTGCAGAAGCTGTGAGTTTTGTTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTGCAGAAGCTGTGAGTTTTGTTC
NCOA3	79	2	TTGATTTATTGTTTTCAACTCCAAGGCAC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTGATTTATTGTTTTCAACTCCAAGGCAC
NCOA3	80	2	TTAATAAACGAGCAGGGTGTTTTCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTAATAAACGAGCAGGGTGTTTTCTC
POLR2A	1	3	ACTGGACTCTCTTGATGGTGCGCAGC	GGGGTGTGTTTGTAAAGGGT	GGGGTGTGTTTGTAAAGGGT	GGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACTGGACTCTCTTGATGGTGCGCAGC
POLR2A	2	3	TTGATGCCACCCTCCGTCACAGACAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTTGATGCCACCCTCCGTCACAGACAT
POLR2A	3	3	AGGAAGCCCACGTGAAACACAGGCTT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTAGGAAGCCCACGTGAAACACAGGCTT
POLR2A	4	3	CACAAGCAGTTTGGAGCAGAAGAAGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCACAAGCAGTTTGGAGCAGAAGAAGC
POLR2A	5	3	GGATATCCTTGATCTTTGGGTTGTTAGA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGGATATCCTTGATCTTTGGGTTGTTAGA
POLR2A	6	3	TTGCAAAGGTCGTAGACATGTGTGAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGCAAAGGTCGTAGACATGTGTGAG
POLR2A	7	3	ACCGAACTTGTTGTCCATCTCCTCCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACCGAACTTGTTGTCCATCTCCTCCC
POLR2A	8	3	CATACAGCTCTAGGCCAGAACGCCGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCATACAGCTCTAGGCCAGAACGCCGG
POLR2A	9	3	AGAGTCCTCATTAACGTGCTTCCATT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTAGAGTCCTCATTAACGTGCTTCCATT
POLR2A	10	3	AGATGCGTTTGAAGATCTCATGCACT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGAGATGCGTTTGAAGATCTCATGCACT
POLR2A	11	3	CATGCCCAGCACAAAACACTCCTCAT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCATGCCCAGCACAAAACACTCCTCAT
POLR2A	12	3	TTCACGATGTCAGCCAGTTTGTGAGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCACGATGTCAGCCAGTTTGTGAGT
POLR2A	13	3	GCTCATTGCGCCGCAGCTGATTGTTG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGG

POLR2A	17	3	TGATGTACTTGGCGCCTGGGTACTGG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTTAGGGTGTGTTTGTAAAGGGTTTTTGATGTACTTGGCGCCTGGGTACTGG
POLR2A	18	3	TAGCCGGTCTGCAGGTGAAGGTCACTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTAGCCGGTCTGCAGGTGAAGGTCACTG
POLR2A	19	3	CTGCCGGTTGAAGATAACAATGTCCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCTGCCGGTTGAAGATAACAATGTCCC
POLR2A	20	3	TAGACCATGGGAGAATGCGGACCCGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGACCATGGGAGAATGCGGACCCGA
POLR2A	21	3	TGGCAGGTGCAAGTTCATCTCATCCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTGGCAGGTGCAAGTTCATCTCATCCC
POLR2A	22	3	CAATACCCATGACAGGCCGATTGCTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCAATACCCATGACAGGCCGATTGCTC
POLR2A	23	3	TTTGCGCACTGCTGTGAGTGTGTCCT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTTGCGCACTGCTGTGAGTGTGTCCT
POLR2A	24	3	GGAACATCAGGAGGTTCATCACTTCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGAACATCAGGAGGTTCATCACTTCA
POLR2A	25	3	ACAATTGATGTGACCAGGTATGATGAG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACAATTGATGTGACCAGGTATGATGAG
POLR2A	26	3	GGAGAGATGTGCTTGTAAGGGCCACT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGAGAGATGTGCTTGTAAGGGCCACT
POLR2A	27	3	CTTACACAGGATGCCCATGATCAGCT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCTTACACAGGATGCCCATGATCAGCT
POLR2A	28	3	GACAGTCTGAATGTTGGAGTAGAAGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGACAGTCTGAATGTTGGAGTAGAAGA
POLR2A	29	3	TGACCCTCGATGAGGAGCCAGTTGTT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTTGGGCTGTGTTTGTAAAGGGTTTTTGACCCTCGATGAGGAGCCAGTTGTT
POLR2A	30	3	GCCTTCTTAATAGTGTTCTGAATGTCCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCCTTCTTAATAGTGTTCTGAATGTCCTG
POLR2A	31	3	TCAAACGTCTGCCGCAGAGTGTTCCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTCAAACGTCTGCCGCAGAGTGTTCCC
POLR2A	32	3	CTGAGCAGAGGAGCCAGTCTTGTCTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTGAGCAGAGGAGCCAGTCTTGTCTC
POLR2A	33	3	ACTTGAAGTTATTGTATTCAGACAGGGA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACTTGAAGTTATTGTATTCAGACAGGGA
POLR2A	34	3	CAAATGGAATCCGCTTGCCCTCGAGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCAAATGGAATCCGCTTGCCCTCGAGG
POLR2A	35	3	GAAGTGAGGCAGAGTCCGGTGCTTGA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGAAGTGAGGCAGAGTCCGGTGCTTGA
POLR2A	36	3	CGGCTAGGTAGGAGTTCTCCACAAAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCGGCTAGGTAGGAGTTCTCCACAAAG
POLR2A	37	3	ACTTCACCATCACTGACTCCATGGAC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACTTCACCATCACTGACTCCATGGAC
POLR2A	38	3	AGGTTCTGGAACTCAACGCTCTCGCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGGTTCTGGAACTCAACGCTCTCGCC
POLR2A	39	3	CCTTCACCAGGTCCTCCTGCACGAGTG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCCTTCACCAGGTCCTCCTGCACGAGTG
POLR2A	40	3	CGCATCCGCTCAAATTCCCGCTCCAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCGCATCCGCTCAAATTCCCGCTCCAA
POLR2A	41	3	AGATGACCCTGAGCACCTCCCGATCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTAGATGACCCTGAGCACCTCCCGATCC
POLR2A	42	3	GTGGGTTGATGTGGAAGATTTTCTGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTGGGTTGATGTGGAAGATTTTCTGA
POLR2A	43	3	TCACAATCACCAGCTTCTTGCTCAAT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTCACAATCACCAGCTTCTTGCTCAAT
POLR2A	44	3	ATGTTGAAGAGCAGCGTGGCATTTTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTATGTTGAAGAGCAGCGTGGCATTTTC
POLR2A	45	3	CCACTGAGCCGAAACTCCTCTGCCAT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCCACTGAGCCGAAACTCCTCTGCCAT
POLR2A	46	3	TCTGGGTGGCAGGTTCTCCAAGGGAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCTGGGTGGCAGGTTCTCCAAGGGAC
POLR2A	47	3	ACCAGCATAGTGGAAGGTATTCAAGG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTACCAGCATAGTGGAAGGTATTCAAGG
POLR2A	48	3	AAATGTTGATGAGCTCCTTAAGTCGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAAATGTTGATGAGCTCCTTAAGTCGG
POLR2A	49	3	AGTAAGCGAAGGAGTCTTTGGCTTCT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTAGTAAGCGAAGGAGTCTTTGGCTTCT
POLR2A	50	3	TATGCTCCAGACGGCACAGAATATCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATGCTCCAGACGGCACAGAATATCC
POLR2A	51	3	TGTGTTGGCAGTCACCTTCCTCAACG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTGTGTTGGCAGTCACCTTCCTCAACG
POLR2A	52	3	CAAAGTCAGGCATTTCATAGTAGACATTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCAAAGTCAGGCATTTCATAGTAGACATTC
POLR2A	53	3	AGTCATGTGCTTCCGATCCAGCTCCA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTAGTCATGTGCTTCCGATCCAGCTCCA
POLR2A	54	3	GCATTGTCATCATTAAAGATGCAGTTCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCATTGTCATCATTAAAGATGCAGTTCA
POLR2A	55	3	TGATGCGAATACGGAGCACCAGCTTC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTGATGCGAATACGGAGCACCAGCTTC
POLR2A	56	3	TCATCCATCTTGTCCACCACCTCTTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCATCCATCTTGTCCACCACCTCTTC
POLR2A	57	3	ATGTTGGACTCGATGCAGCGCAGGAA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTATGTTGGACTCGATGCAGCGCAGGAA
POLR2A	58	3	CCACTCCTGCAGGGCCTTGAATTCCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCACTCCTGCAGGGCCTTGAATTCCC
POLR2A	59	3	CTCACTCAGCACCCGCATCAAGCTCA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCTCACTCAGCACCCGCATCAAGCTCA
POLR2A	60	3	AGATGACGTGGTACAGCTCCCGCTCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGATGACGTGGTACAGCTCCCGCTCC
POLR2A	61	3	TCGGTAATTGACATAGGAGCCATCAA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTTCGGTAATTGACATAGGAGCCATCAA
POLR2A	62	3	TTCATGAGTGGTCCTGTGTCCTGGCG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTTCATGAGTGGTCCTGTGTCCTGGCG
POLR2A	63	3	GCCCAGCATGATATTCTCAGAGACCC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGCCCAGCATGATATTCTCAGAGACCC
POLR2A	64	3	CCCTGGTTCCAAGGTGTCATGGCAGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCCTGGTTCCAAGGTGTCATGGCAGG
POLR2A	65	3	GTGACGTTGGCGAGTAGCTGGGAGAC	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGTGACGTTGGCGAGTAGCTGGGAGAC
POLR2A	66	3	GGGTGATGTGGGACTATAGTTGGGAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGGTGATGTGGGACTATAGTTGGGAC
POLR2A	67	3	GAGTAGCTGGGTGACGTTGGCGAATA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGAGTAGCTGGGTGACGTTGGCGAATA
POLR2A	68	3	CGAGTAGCTGGGAGATGTCGGCGAGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCGAGTAGCTGGGAGATGTCGGCGAGT
POLR2A	69	3	GAAGTGGGAGAATAGCTGGGTGAAGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGAAGTGGGAGAATAGCTGGGTGAAGT
POLR2A	70	3	TAGTTCGGGCTGGTGGGTGAGTAACT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTAGTTCGGGCTGGTGGGTGAGTAACT
POLR2A	71	3	GATGTCGGGCTGTAGCTGGGTGATGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGATGTCGGGCTGTAGCTGGGTGATGT
POLR2A	72	3	TGGGCTGTAGTTAGGGCTGGTAGGTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGGGCTGTAGTTAGGGCTGGTAGGTG
POLR2A	73	3	GGTGATGTTGGAGAGTAGCTTGGAGA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGGTGATGTTGGAGAGTAGCTTGGAGA
POLR2A	74	3	TGGGACTGTAAGAAGGACTGGTTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGGGACTGTAAGAAGGACTGGTTGGG
POLR2A	75	3	GAATAGGTGGGACTGGTAGGCGAGTA	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTGAATAGGTGGGACTGGTAGGCGAGTA
POLR2A	76	3	GATAGCCGGGCTTGTGAGACTGTAGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGATAGCCGGGCTTGTGAGACTGTAGG
POLR2A	77	3	CAGTTCTCCTCGTCACTGTCATCCGG	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGT	AGGGTGTGTTTGTAAAGGGTTTTAGGGTGTGTTTGTAAAGGGTTTTCCTCCTCGTCACTGTCATCCGG
MTOR	1	4	ACTGGCAAACTGCTGCAGGACGCTC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACTGGCAAACTGCTGCAGGACGCTC
MTOR	2	4	TGGTTTCCTCATTCCGGCTCTTTAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGGTTTCCTCATTCCGGCTCTTTAG
MTOR	3	4	CCATGCAACTGGGTCATTGGAGGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCATGACAACTGGGTCATTGGAGGG
MTOR	4	4	GGCAAGACGGCCAATGGCCTTGGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGCAAGACGGCCAATGGCCTTGGAT
MTOR	5	4	TTCCAGGGCTCGCTTCACCTCAAAT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCCAGGGCTCGCTTCACCTCAAAT
MTOR	6	4	TTGCTGGAAGAAGAAGGTAGGGACG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTGCTGGAAGAAGAAGGTAGGGACG
MTOR	7	4	ATCAGACAGGCACGAAGGGCGGCTA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTATCAGACAGGCACGAAGGGCGGCTA
MTOR	8	4	CTCCTTCGGCTCACGCTGGGTTGTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTCCTTCGGCTCACGCTGGGTTGTG
MTOR	9	4	AGGCTCCATGGATCCGATCATCCCG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGGCTCCATGGATCCGATCATCCCG
MTOR	10	4	ATTCGGACCAGCTCGTTAAGGATCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTATTCGGACCAGCTCGTTAAGGATCA
MTOR	11	4	TCTTTGCAGTACTTGTCGTGTACCA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTTGCAGTACTTGTCGTGTACCA
MTOR	12	4	ACGAGGTTTTGTTCCGAAGCCCATG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTACGAGGTTTTGTTCCGAAGCCCATG
MTOR	13	4	TGAGGCCTTGGTGAGAGCTGTACCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTGAGGCCTTGGTGAGAGCTGTACCC
MTOR	14	4	CCAGGGTGGACTTAGCTGGACTGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCCAGGGTGGACTTAGCTGGACTGGG
MTOR	15	4	TCTTGACACAGCTTAGGACATGGTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTGACACAGCTTAGGACATGGTT
MTOR	16	4	ACCTCACAGCCACAGAAAGTAGCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTACCTCACAGCCACAGAAAGTAGCCC
MTOR	17	4	CTTTAGCTGTGGAATCTGACGGCTC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTTGCTGTGGAATCTGACGGCTC
MTOR	18	4	CATTTTCAGTAGCCCATCTTGAATGTC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCATTTTCAGTAGCCCATCTTGAATGTC
MTOR	19	4	ATTCAAAGCTGCCAAGCGTTCGGAG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATTCAAAGCTGCCAAGCGTTCGGAG
MTOR	20	4	GTTCAGGAAATGATCCGCACAGTGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTTCAGGAAATGATCCGCACAGTGG
MTOR	21	4	GAGGTGGATGGAGGGTGTGAGCAGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGAGGTGGATGGAGGGTGTGAGCAGG
MTOR	22	4	GGCTAACCACATGAGCATGGCCACT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTGCTAACCACATGAGCATGGCCACT
MTOR	23	4	GTGCATCAAAGCGCTCGTCCAGGGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTGCATCAAAGCGCTCGTCCAGGGA
MTOR	24	4	CAAGGCCTGCAAGTTCTCCGCCTGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCAAGGCCTGCAAGTTCTCCGCCTGG
MTOR	25	4	CATGCGGGCACTCTGCTCTTTGATT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCATGCGGGCACTCTGCTCTTTGATT
MTOR	26	4	GGGCTCTACTACATAGCCAGTGCTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGGCTCTACTACATAGCCAGTGCTG
MTOR	27	4	TCTGCTCAGTCTTCAGAAAATTCAGTA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTGCTCAGTCTTCAGAAAATTCAGTA
MTOR	28	4	TTGTGCTTGTAAGGATCCAAAGCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGTGCTTGTAAGGATCCAAAGCCC
MTOR	29	4	CTGACAGGCTGACAGCAGAGGCATC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTCTGACAGGCTGACAGCAGAGGCATC
MTOR	30	4	GTTGACCAGCATTTCACTAGTGCTA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTTGACCAGCATTTCACTAGTGCTA
MTOR	31	4	ATCAGGGCCACCATGGACACAGCTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATCAGGGCCACCATGGACACAGCTG
MTOR	32	4	AGAGAGTGACTGGTCTCGGAAGATC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGAGAGTGACTGGTCTCGGAAGATC
MTOR	33	4	AGTCCCAGGGACTTGAAGATGAAGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGTCCCAGGGACTTGAAGATGAAGG
MTOR	34	4	TTAAGGAACGTGGGCATGACCTGGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAAGGAACGTGGGCATGACCTGGG
MTOR	35	4	GCTCAATGAGAAGAATGATCGTGCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTCAATGAGAAGAATGATCGTGCT
MTOR	36	4	GGGCAGGTAGAGCTTAAATTCACCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGGCAGGTAGAGCTTAAATTCACCC
MTOR	37	4	GTCAGGCGGTCCACAGTCTCTAGCG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTCAGGCGGTCCACAGTCTCTAGCG
MTOR	38	4	GGCATAGTCAGTGAAATCCAGGGAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGCATAGTCAGTGAAATCCAGGGAC
MTOR	39	4	TCCATGGCTGTGGAGCGCAGTTCTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCCATGGCTGTGGAGCGCAGTTCTG
MTOR	40	4	TCAAAGGATCCTCCTCTTCATCAGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCAAAGGATCCTCCTCTTCATCAGC
MTOR	41	4	ACTGGTCCACTAGCCAATGCATCCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACTGGTCCACTAGCCAATGCATCCC
MTOR	42	4	GTGCAGTTTCTTCATGGGTCCTGTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTGCAGTTTCTTCATGGGTCCTGTT
MTOR	43	4	GGCTCAGCCGTCTCAGCCATTCCAG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGCTCAGCCGTCTCAGCCATTCCAG
MTOR	44	4	GGCGATGATGAGTCCTTCAGCAGCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGCGATGATGAGTCCTTCAGCAGCT
MTOR	45	4	GAGGGCCAACTCGATGCTTCTGATG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGAGGGCCAACTCGATGCTTCTGATG
MTOR	46	4	GTGTGACTTCAGCGATGTCTTGTGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTGTGACTTCAGCGATGTCTTGTGA
MTOR	47	4	GGCAGCTCTCTCACCCAGCAGAACA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAG

MTOR	52	4	AGTTTGTACTGGATAACCTCCTCCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGTTTGTACTGGATAACCTCCTCCA
MTOR	53	4	ATGTCTTCATGAGGGCTGACCACAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATGTCTTCATGAGGGCTGACCACAA
MTOR	54	4	CAGGCTTGCATACTTGAGCCAGGTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCAGGCTTGCATACTTGAGCCAGGTT
MTOR	55	4	TTGCGGGCACTCTTCCACATGTTTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTAGAGTGAGTAGTAGTGGAGTTTTTCGCGGCACTCTTCCACATGTTTT
MTOR	56	4	TCATTGATGCCCTGTAGATTCAGCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCATTGATGCCCTGTAGATTCAGCT
MTOR	57	4	TTTCTTCTTCTCATCGCGGGCTTGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTAGAGTGAGTAGTAGTGGAGTTTTTTCTTCTTCATCGCGGGCTTGG
MTOR	58	4	GGCAGTGGTGGCGTTGGTGATGTTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGCAGTGGTGGCGTTGGTGATGTTG
MTOR	59	4	CCAAGGGTCTGGGCGTATCAATTCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCAAGGGTCTGGGCGTATCAATTCT
MTOR	60	4	GTGAGAAGCTGGTGAATGAGACGTC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTGAGAAGCTGGTGAATGAGACGTC
MTOR	61	4	TCAGAATCTTGTTGGCTGCATTGTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCAGAATCTTGTTGGCTGCATTGTG
MTOR	62	4	AGGGTGTTGCTGTGCTCACACATGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGGGTGTTGCTGTGCTCACACATGT
MTOR	63	4	TCTTCCAGGCCTTCATGCCACATCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCTTCCAGGCCTTCATGCCACATCT
MTOR	64	4	AACATGCCTTTCACGTTCCTTTCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAACATGCCTTTCACGTTCCTTTCCC
MTOR	65	4	CATTAAATCTCGACCATAGGCCTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCATTAAATCTCGACCATAGGCCTGA
MTOR	66	4	TGTACTTCCTGCACCACTCTTGGGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGTACTTCCTGCACCACTCTTGGGC
MTOR	67	4	GAGGCAGCTGCTTTGAGATTCGTCG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGAGGCAGCTGCTTTGAGATTCGTCG
MTOR	68	4	ACATATTGCAGCTCTAAGGATGTGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTACATATTGCAGCTCTAAGGATGTGA
MTOR	69	4	CATATGTTCCTGGCACAGCCAATTC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCATATGTTCCTGGCACAGCCAATTC
MTOR	70	4	TGAATGCGAATGATTGGCTGGTTGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGAATGCGAATGATTGGCTGGTTGG
MTOR	71	4	TTTAGAAGGAAAACAAACTCATGTCCG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTTAGAAGGAAAACAAACTCATGTCCG
MTOR	72	4	CTCATCCTGGCGCAGATCTTCATGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTCATCCTGGCGCAGATCTTCATGG
MTOR	73	4	GATGTTGGGTCATTGGCCAGAAGGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGATGTTGGGTCATTGGCCAGAAGGG
MTOR	74	4	GCCCGAGTTGGTCGATAAAGGGATG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCCCGAGTTGGTCGATAAAGGGATG
MTOR	75	4	CAACATGATGCGATGCTCGATGTTG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCAACATGATGCGATGCTCGATGTTG
MTOR	76	4	TTTTCAGCCACAGCAGCTTGGCCAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTTCAGCCACAGCAGCTTGGCCAG
MTOR	77	4	ACCTCCATCACTGTGTGGCATGTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACCTCCATCACTGTGTGGCATGTGA
MTOR	78	4	GGTCATAGACAAAGGCTTCCAGCAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGTCATAGACAAAGGCTTCCAGCAC
MTOR	79	4	AGTGTCATCATGAGAGAAGTCCCGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGTGTCATCATGAGAGAAGTCCCGA
MTOR	80	4	TTTTCATGGGATGTCGCTTGTTTGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTTTCATGGGATGTCGCTTGTTTGA
MKI67	1	5	TTTGTTGCTGTGAATATTGTACAGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTGTTGCTGTGAATATTGTACAGGG
MKI67	2	5	AGGAGGCAAGTTTTCATCAAATAGTTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGGAGGCAAGTTTTCATCAAATAGTTC
MKI67	3	5	AGGACCTACGGCGTTGATCACTGGCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGGACCTACGGCGTTGATCACTGGCA
MKI67	4	5	CTTTCTCCCTCCTCTCTTAGGAACCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTTCTCCCTCCTCTCTTAGGAACCT
MKI67	5	5	AGGGTCGAGCAGGCACATGTACTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGGGTCGAGCAGGCACATGTACTTTT
MKI67	6	5	AGGGCTTGCAGAGCATTTATCAGATG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGTGCTCAGAGCATTTATCAGATG
MKI67	7	5	GACCTGTTTGCAGTGGATACTGTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGACCTGTTTGCAGTGGATACTGTTTT
MKI67	8	5	CTGTATATTCCTGAACTCTGTAGACCTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTCTGTATATTCCTGAACTCTGTAGACCTT
MKI67	9	5	AGTAGTGTTGCCTTCTGACCTCTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGTAGTGTTGCCTTCTGACCTCTTTT
MKI67	10	5	TATCAGGCAAGCTCTTGAGGTCTGTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATCAGGCAAGCTCTTGAGGTCTGTC
MKI67	11	5	TTTTGCCTTTCTCACTCTTTGGTGCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTTGCCTTTCTCACTCTTTGGTGCC
MKI67	12	5	TTGTAATGACTGGCAGGGCATTTTAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTTGTAATGACTGGCAGGGCATTTTAG
MKI67	13	5	CCTGACGTCCGTGTGAACTTGCCGAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCCTGACGTCCGTGTGAACTTGCCGAC
MKI67	14	5	ATCTCCTGCTGGCTCTCTGTGCGTGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTATCTCCTGCTGGCTCTCTGTGCGTGT
MKI67	15	5	TTCATTCAGTTACACGGGCTGCTGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATTCCAGTTACACGGGCTGCTGG
MKI67	16	5	CCTCTTCCTTAGGCGTTCTTGGCCAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTCTTCCTTAGGCGTTCTTGGCCAC
MKI67	17	5	AGTCTGTAGCTGTCTTTTGCTGCCAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGTCTGTAGCTGTCTTTTGCTGCCAG
MKI67	18	5	AGCCACTAATTCCTCGGTGTGACCAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGCCACTAATTCCTCGGTGTGACCAG
MKI67	19	5	ATGGCATTAGATTCCTGCACGCTAAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTATGGCATTAGATTCCTGCACGCTAAG
MKI67	20	5	CCACTGCTTCTTCAGTATGACCAGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCACTGCTTCTTCAGTATGACCAGGG
MKI67	21	5	TCTTGGGCTGCCTTCTTGTGCTTGTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCTTGGGCTGCCTTCTTGTGCTTGTT
MKI67	22	5	CTTCTGTACGTCCCTTTTCTCCAAAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTCTGTACGTCCCTTTTCTCCAAAG
MKI67	23	5	TCAGTGCATACTGGTGTCTGGAAGAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCAGTGCATACTGGTGTCTGGAAGAG
MKI67	24	5	TGGTAGTTTTCTCGTGAGTCGTGGGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGGTAGTTTTCTCGTGAGTCGTGGGC
MKI67	25	5	TTTCCTGAGTGCGAAGAATTCTTCTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTTCCTGAGTGCGAAGAATTCTTCTT
MKI67	26	5	TCTCACCACTTACTGCTGGTTTGGGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCTCACCACTTACTGCTGGTTTGGGT
MKI67	27	5	TTTGCAGGCTACTTTGGCAGTTTTAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTTGCAGGCTACTTTGGCAGTTTTAT
MKI67	28	5	CCGTCGCTTGGAGCTTGCTGGGTTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCGTCGCTTGGAGCTTGCTGGGTTTT
MKI67	29	5	GCTTTCATGCTCTTACCATCTCCTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCTTTCATGCTCTTACCATCTCCTGT
MKI67	30	5	AGACTTTCCCTTAGGAGTTCTCAGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGACTTTCCCTTAGGAGTTCTCAGCT
MKI67	31	5	AGCTCTGTAGGATACTTTGGTAGTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGCTCTGTAGGATACTTTGGTAGTTTT
MKI67	32	5	TGGCGTTTGTTTCCTAAATGCTAAAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTTGGGATGTATTGAAGGAGGATTTTTTGCCTCTGTTGTTTCCTAAATGCTAAAA
MKI67	33	5	CTGAAGCCAGTCAGTTCTTCTAGAGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTGAAGCCAGTCAGTTCTTCTAGAGC
MKI67	34	5	TATCAGTGCATGGTGTCTGGAAAAGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATCAGTGCATGGTGTCTGGAAAAGC
MKI67	35	5	TGGGCCGTTGCTTTGTGTTTGTTGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGGGCCGTTGCTTTGTGTTTTGTTGGG
MKI67	36	5	CTCTACGTCTGCTTTCTTGAGGCTTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCTACGTCTGCTTTCTTGAGGCTTC
MKI67	37	5	TGAGTCGTTGCTTGGAGCTTGTTGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGAGTCGTTGCTTGGAGCTTGTTGGG
MKI67	38	5	AAACGCTTTGATGCTCTTTCCATCTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAAACGCTTTGATGCTCTTTCCATCTC
MKI67	39	5	TTGGGCCTCTTCCTTAGGTGTTCTTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTGGGCCTCTTCCTTAGGTGTTCTTG
MKI67	40	5	CCTCAGTGTGGTCTGGTGTCTGGAAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTCAGTGTGGTCTGGTGTCTGGAAG
MKI67	41	5	TGTGTGGTCTGTGTGAGCTGCTTCAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGTGTGGTCTGTGTGAGCTGCTTCAG
MKI67	42	5	TATCCTCATCTCCTGGTACTTTTGTCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATCCTCATCTCCTGGTACTTTGTCT
MKI67	43	5	GAGTTCTTGGCTGCCTCTTGCTACCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGAGTTCTTGGCTGCCTCTTGCTACCA
MKI67	44	5	TTTCAAGCCAGCCAAGTCTTCTAGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTTCAAGCCAGCCAAGTCTTCTAGGG
MKI67	45	5	TGGTAGTTTTCTCATGAGTCGTGGGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGGTAGTTTTCTCATGAGTCGTGGGC
MKI67	46	5	TGGACTGTGGCTTGAAGATTGTTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGGACTGTGGCTTGAAGATTGTTGGG
MKI67	47	5	CTTAGGAGTTTGTGGCCATCTTTTGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTTAGGAGTTTGTGGCCATCTTTTGC
MKI67	48	5	GGAGTCTGTGGCTGTCTCTTGCTGCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGAGTCTGTGGCTGTCTCTTGCTGCC
MKI67	49	5	TGTCTGGAAGAGTTCTTTGAAGCCAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGTCTGGAAGAGTTCTTTGAAGCCAA
MKI67	50	5	TTCTTTCATGTCCACTTTCACCAGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTTGGGATGTATTGAAGGAGGATTTTTTCTTTCATGTCCACTTTCACCAGGG
MKI67	51	5	CTCTGTGTGTGTTTGCGTAGTCTCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTCTGTGTGTGTTTGCGTAGTCTCCC
MKI67	52	5	GCTTTGATGCTCTTACTATCTCCTGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCTTTGATGCTCTTACTATCTCCTGT
MKI67	53	5	TGAAGTCAACCAGGTCTTCTAGAGCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGAAGTCAACCAGGTCTTCTAGAGCA
MKI67	54	5	TGGCAGTGTCTGTTAGTTCTGGTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGACGTCTGTTAGTTCTGGTGGG
MKI67	55	5	GTGTGTGCTTTGCCCTGATGTTTGCG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGTGTGTGCTTTGCCCTGATGTTTGCG
MKI67	56	5	TCATCACCGCTTGCTGGTTCTTTGTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCATCACCGCTTGCTGGTTCTTTGTG
MKI67	57	5	TTCCTCTTCTACTGGGTTTGGTTTCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTCCTCTTCTACTGGGTTTGGTTTCT
MKI67	58	5	TTAGGTGCTCTTGGCCTTCTCCTGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTTGGGATGTATTGAAGGAGGATTTTTTAGGTGCTCTTGGCCTTCTCCTGCT
MKI67	59	5	CGCAGGGTATTTTAGTGGCTTTGCCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCGCAGGGTATTTTAGTGGCTTTGCCA
MKI67	60	5	ACGTGTCCTGAGATGCCTCTTTGTGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTACGTGTCCTGAGATGCCTCTTTGTGC
MKI67	61	5	CCTGATGTTTGTGTGAACTTGACTGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCCTGATGTTTGTGTGAACTTGACTGC
MKI67	62	5	CTGGTTCTTTGTCTGCATCCGTGGTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTGGTTCTTTGTCTGCATCCGTGGTT
MKI67	63	5	TGGAGCCGGTGTCTGTTTTGCAGATT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGGAGCCGGTGTCTGTTTTGCAGATT
MKI67	64	5	CGTCTCCTGCTGCCAGTTACACTTGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCGTCTCCTGCTGCCAGTTACACTTGC
MKI67	65	5	CGGTGTCTTCTAGTTCTGGTGATGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCGGTGTCTTCTAGTTCTGGTGATGAT
MKI67	66	5	TGTCCTGGGCCGTCTCTTTGAGCTTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGTCCTGGGCCGTCTCTTTGAGCTTG
MKI67	67	5	GCTTTCGTGCCTTTGCCCTCACCTAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCTTTCGTGCCTTTGCCCTCACCTAC
MKI67	68	5	TCTCCTGCTGCCAATTACATCTTCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCTCCTGCTGCCAATTACATCTTCTG
MKI67	69	5	TTGTGATTTTACAGGGTCTCTGGTGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTGTGATTTTACAGGGTCTCTGGTGC
MKI67	70	5	TGACGCTTCCATCTTTGCCACCTCCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGACGCTTCCATCTTTGCCACCTCCC
MKI67	71	5	ACGGGTTCGGATGATTTGCCTCTTGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTACGGGTTCGGATGATTTGCCTCTTGC
MKI67	72	5	CTTTGTTGGTTTTCATGTCGTTGCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTTGTTGGTTTTCATGTCGTTGCTG
MKI67	73	5	TCTTTCTGCTAATACAAAGACCTCAGTTA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCTTTCTGCTAATACAAAGACCTCAGTTA
MKI67	74	5	CTGGATTCTGAATGTCCATCTCTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTGGATTCTGAATGTCCATCTCTGGG
MKI67	75	5	AAGCACCTTTTGTTCTCAGTGACTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAAGCACCTTTTGTTCTCAGTGACTTT
MKI67	76	5	GGGAGCTCTCATTCTGTCTAGCAGAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGGAGCTCTCATTCTGTCTAGCAGAC
MKI67	77	5	TTCTGCATGAGAACCTTCGCACTCTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTCTGCATGAGAACCTTCGCACTCTT
MKI67	78	5	CTTTCTTGATCTCAGGCACATGGAGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTTCTTGATCTCAGGCACATGGAGT
MKI67	79	5	TGGATTTTCTGCACACCTCTTGACAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGGATTTTCTGCACACCTCTTGACAC
MKI67	80	5	TTGACACACACATTGTCCTCAGCCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAA

BRCA1	4	6	CCACATGCAAGTTTGAAACAGAACTAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCACATGCAAGTTTGAAACAGAACTAC
BRCA1	5	6	AGTAATAAACTGCTGTTCTCATGCTGTA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGTAATAAACTGCTGTTCTCATGCTGTA
BRCA1	6	6	CAGCCTTTTCTACATTCATTCTGTCTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCAGCCTTTTCTACATTCATTCTGTCTTT
BRCA1	7	6	GCCCATCTGTTATGTTGGCTCCTTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCCCATCTGTTATGTTGGCTCCTTG
BRCA1	8	6	CCGCCTATCATTACATGTTTCCTTACT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCGCCTATCATTACATGTTTCCTTACT
BRCA1	9	6	CTGCTATTTAGTGTTATCCAAGGAACATC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGCTATTTAGTGTTATCCAAGGAACATC
BRCA1	10	6	TCTGGAAAACCACTCATTAACTTTCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCTGGAAAACCACTCATTAACTTTCTG
BRCA1	11	6	ACTTTGGCATTTGATTCAGACTCCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACTTTGGCATTTGATTCAGACTCCC
BRCA1	12	6	TCTACCTCATTTAGAACGTCCAATACATC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCTACCTCATTTAGAACGTCCAATACATC
BRCA1	13	6	TTTTCAGTTACATGGCTTAAGTTGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTTGTGATGGAAGTTAGAGGGTTTTTTTTCAGTTACATGGCTTAAGTTGGG
BRCA1	14	6	TGGCTCAGTAACAAATGCTCCTATAAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTTGGGATGTATTGAAGGAGGATTTTTGGCTCAGTAACAAATGCTCCTATAAT
BRCA1	15	6	TCCTCAGGATGAAGGCCTGATGTAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCCTCAGGATGAAGGCCTGATGTAG
BRCA1	16	6	GAACTGCCAAATCTGCTTTCTTTGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAACTGCCAAATCTGCTTTCTTTGAT
BRCA1	17	6	ATCACTTGACCATTCTGCTCCGTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTATCACTTGACCATTCTGCTCCGTTT
BRCA1	18	6	TCGAGTGATTCTATTGGGTTAGGATTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCGAGTGATTCTATTGGGTTAGGATTTT
BRCA1	19	6	GTTCAAGCGCATGAATATGCCTGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTCAAGCGCATGAATATGCCTGGT
BRCA1	20	6	AGGTGGGCTTAGATTTCTACTGACT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGGTGGGCTTAGATTTCTACTGACT
BRCA1	21	6	CTGACTGGCATTTGGTTGTACTTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGACTGGCATTTGGTTGTACTTTT
BRCA1	22	6	CTTCCATGAGTTGTAGGTTTCTGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTTCCATGAGTTGTAGGTTTCTGCT
BRCA1	23	6	TTTACTTGTCTGTTCATTTGGCTTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTTGTGATGGAAGTTAGAGGGTTTTTTACTTGTCTGTTCATTTGGCTTGT
BRCA1	24	6	AGCTCTGGGAAAGTATCGCTGTCAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGCTCTGGGAAAGTATCGCTGTCAT
BRCA1	25	6	TGGAAGGCTAGGATTGACAAATTCTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGGAAGGCTAGGATTGACAAATTCTTT
BRCA1	26	6	GGTCTTCAGCATTATTAGACACTTTAACTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGTCTTCAGCATTATTAGACACTTTAACTG
BRCA1	27	6	GCTACTCTCTACAGATCTTTCAGTTTGC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCTACTCTCTACAGATCTTTCAGTTTGC
BRCA1	28	6	CCATAATCAGTACCAGGTACCAATGAAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCATAATCAGTACCAGGTACCAATGAAA
BRCA1	29	6	AACAACCATGAATTAGTCCCTTGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAACAACCATGAATTAGTCCCTTGGG
BRCA1	30	6	TGGATACTTAAAGCCTTCTGTGTCATT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGGATACTTAAAGCCTTCTGTGTCATT
BRCA1	31	6	GCGCTTTGAAACCTTGAATGTATTCTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCGCTTTGAAACCTTGAATGTATTCTG
BRCA1	32	6	CCTGGATTTGAAAACGGAGCAAATG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTGGATTTGAAAACGGAGCAAATG
BRCA1	33	6	TTGTTTCTTTAAGGACCCAGAGTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTTTCTTTAAGGACCCAGAGTGG
BRCA1	34	6	AGCCTGCAGTGATATTAACTGTCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGCCTGCAGTGATATTAACTGTCTG
BRCA1	35	6	GCCTCCTTTGATACTACATTTGGCATTAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCCTCCTTTGATACTACATTTGGCATTAT
BRCA1	36	6	CCTCTGAACTGAGATGATAGACAAAACC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTCTGAACTGAGATGATAGACAAAACC
BRCA1	37	6	GGTGGTATACGATATGGGTTTTGTAAAAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGTGGTATACGATATGGGTTTTGTAAAAG
BRCA1	38	6	CCATTTCTCTTTCAGGTGACATTGAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCATTTCTCTTTCAGGTGACATTGAA
BRCA1	39	6	CACTTCATTAGTACTGGAACCTACTTCAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCACTTCATTAGTACTGGAACCTACTTCAT
BRCA1	40	6	CTGTTTCTACCTAGTTCTGCTTGAATG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTGTTTCTACCTAGTTCTGCTTGAATG
BRCA1	41	6	ACTTTGTTTATAGACCTCAGGTTGCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACTTTGTTTATAGACCTCAGGTTGCA
BRCA1	42	6	ATTTCAGGATGCTTACAATTACTTCCAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTATTTCAGGATGCTTACAATTACTTCCAG
BRCA1	43	6	GAACAAACCTGAGATGCATGACTAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGAACAAACCTGAGATGCATGACTAC
BRCA1	44	6	CATCATCTAACAGGTCATCAGGTGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCATCATCTAACAGGTCATCAGGTGT
BRCA1	45	6	TCCTTTCTGGACGCTTTTGCTAAAA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCCTTTCTGGACGCTTTTGCTAAAA
BRCA1	46	6	GTGAAAGGGCTAGGACTCCTGCTAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTGAAAGGGCTAGGACTCCTGCTAA
BRCA1	47	6	TTCTGAGGACTCTAATTTCTTGGCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCTTTCTGAGGACTCTAATTTCTTGGCC
BRCA1	48	6	GAAGCTCTTCATCCTCACTAGATAAGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAAGCTCTTCATCCTCACTAGATAAGT
BRCA1	49	6	TCTTAGACAGACACTCGGTAGCAAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCTTAGACAGACACTCGGTAGCAAC
BRCA1	50	6	GTTACTGCAGTCATTTAAGCTATTCTTCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTTACTGCAGTCATTTAAGCTATTCTTCA
BRCA1	51	6	AGAACATTTTGTTTCCTCACTAAGGTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGAACATTTTGTTTCCTCACTAAGGTG
BRCA1	52	6	TCACTGCACTGTGAAGAAAACAAGC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCACTGCACTGTGAAGAAAACAAGC
BRCA1	53	6	GTTTGGAAGAACCAATCAAGAAAGGAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTTGGAAGAACCAATCAAGAAAGGAT
BRCA1	54	6	TCCCTGGCTTTCAGACTGATGCCTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCCCTGGCTTTCAGACTGATGCCTC
BRCA1	55	6	CATTTCCTGCTGGAGCTTTATCAGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCATTTCCTGCTGGAGCTTTATCAGG
BRCA1	56	6	TGCTGTTCTAACACAGCTTCTAGTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGCTGTTCTAACACAGCTTCTAGTT
BRCA1	57	6	CTCAAGGGCAGAAGAGTCACTTATG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCAAGGGCAGAAGAGTCACTTATG
BRCA1	58	6	AGGGTATTCACTACTTTTCTGTGAAGTTA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGGGTATTCACTACTTTTCTGTGAAGTTA
BRCA1	59	6	AACTATCTGCAGACACCTCAAACTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAACTATCTGCAGACACCTCAAACTT
BRCA1	60	6	ACCTTTCCACTCCTGGTTCTTTATTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTACCTTTCCACTCCTGGTTCTTTATTTT
BRCA1	61	6	CTCTTGAGATGGGTAGTTTCTATTCTGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCTTGAGATGGGTAGTTTCTATTCTGA
BRCA1	62	6	TCCTCCACATCAACAACCTTAATGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTCCACATCAACAACCTTAATGA
BRCA1	63	6	CCTTGGCAAGTAAGATGTTTCCGTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCTTGGCAAGTAAGATGTTTCCGTC
BRCA1	64	6	GCTGATTCCAGATTCCAGGTAAGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCTGATTCCAGATTCCAGGTAAGGG
BRCA1	65	6	GTTGCCAACACGAGCTGACTCTGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTGCCAACACGAGCTGACTCTGGG
BRCA1	66	6	ACTTTCAATGCAGAGGTTGAAGATG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTACTTTCAATGCAGAGGTTGAAGATG
BRCA1	67	6	ATCAGTAGTATGAGCAGCAGCTGGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTATCAGTAGTATGAGCAGCAGCTGGA
BRCA1	68	6	CACTTTCTTCCATTGCATTATACCCAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCACTTTCTTCCATTGCATTATACCCAG
BRCA1	69	6	CACCCACTCTCGGGTCACCACAGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCACCCACTCTCGGGTCACCACAGGT
BRCA1	70	6	GGCTGCAGTCAGTAGTGGCTGTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGCTGCAGTCAGTAGTGGCTGTGGG
BRCA1	71	6	CAGATTTCCAAGGGAGACTTCAAGC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAGATTTCCAAGGGAGACTTCAAGC
BRCA1	72	6	TCAATTGGTGGCGTTTAAATGGTTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCAATTGGTGGCGTTTAAATGGTTTT
BRCA1	73	6	TGAGGCCAAGCCACTCTGTGCTTCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGAGGCCAAGCCACTCTGTGCTTCC
BRCA1	74	6	AGAAGTAAACTTAGGGAAACCAGCTATT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGAAGTAAACTTAGGGAAACCAGCTATT
BRCA1	75	6	CCCAAGGACTATTCTGACTTTAAGTCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCAAGGACTATTCTGACTTTAAGTCA
BRCA1	76	6	CCAATGTTCCACTCCAACATTTGAGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCAATGTTCCACTCCAACATTTGAGA
BRCA1	77	6	GGAATGGATTATATACCAGAGCTACAACA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGAATGGATTATATACCAGAGCTACAACA
BRCA1	78	6	ATCACCTCAAAGAAAGCAACAGCTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTATCACCTCAAAGAAAGCAACAGCTT
BRCA1	79	6	ACAGTCCTGGATAATGGGTTTATGAAAA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACAGTCCTGGATAATGGGTTTATGAAAA
BRCA1	80	6	GTCTTCACTGCCCTTGCACACTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTCTTCACTGCCCTTGCACACTGGG
NCOA2	1	7	TCACATTCTCTGACACAAACACAAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCACATTCTCTGACACAAACACAAC
NCOA2	2	7	TCAGCTCTTCTTGGTTATACCTTAGATAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTCAGCTCTTCTTGGTTATACCTTAGATAC
NCOA2	3	7	CGACAATTGAAGGTATGGCTGTTCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCGACAATTGAAGGTATGGCTGTTCC
NCOA2	4	7	GCGAAGCACTGCATAGTTTCATATT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCGAAGCACTGCATAGTTTCATATT
NCOA2	5	7	CAAGAGTGCCATCAGACAAGGAAAA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAAGAGTGCCATCAGACAAGGAAAA
NCOA2	6	7	GATGAGTTTGCTCTTCGTTTGTGCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGATGAGTTTGCTCTTCGTTTGTGCA
NCOA2	7	7	ATTGCTACTGAGGGTCATGTCCTGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTATTGCTACTGAGGGTCATGTCCTGA
NCOA2	8	7	TCCTTTGGGCCATTTATGGGAAAAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCCTTTCTGGGCCATTTATGGGAAAAT
NCOA2	9	7	TCATGCCAGGGCTGCTTTGTGAGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCATGCCAGGGCTGCTTTGTGAGGG
NCOA2	10	7	TGAAAGCATGGAGGTGGGCTGTCCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGAAAGCATGGAGGTGGGCTGTCCT
NCOA2	11	7	GGAGCTGTTGGTATAACTATGGCTAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGAGCTGTTGGTATAACTATGGCTAT
NCOA2	12	7	GCCAACGATGACCCTAATGAGACCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCCAACGATGACCCTAATGAGACCC
NCOA2	13	7	CAAGCTTCCCATCTTGCTGAGTGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCATCTTGCTGAGTGGG
NCOA2	14	7	CCAGTTGTACCTTCAGAGGGCTCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCCAGTTGTACCTTCAGAGGGCTCCC
NCOA2	15	7	CCGTCAGCTCTCTCACTGCTCACGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCGTCAGCTCTCTCACTGCTCACGG
NCOA2	16	7	GCCCTTTGCTGTCATGCAGTCTGCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCCCTTTGCTGTCATGCAGTCTGCT
NCOA2	17	7	ACCCAGAACCAGGCAAGCTACCTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACCCAGAACCAGGCAAGCTACCTGT
NCOA2	18	7	CTTCTCCTTGAGCGAGGTTCCATGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCTCCTTGAGCGAGGTTCCATGT
NCOA2	19	7	TGTTAACTTGGCCAAGTCCACAGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTTAACTTGGCCAAGTCCACAGGG
NCOA2	20	7	TGGCTCAGGTCTTTGCCTGTGGCTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCCTTGGCCATTTGCCTGTGGCTT
NCOA2	21	7	GCGAAGTAGTGCATTCTCTTTCTTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCGAAGTAGTGCATTCTCTTTCTTCT
NCOA2	22	7	TACTGTCCAGTCTCTCAAGTTTGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTACTGTCCAGTCTCTCAAGTTTGGG
NCOA2	23	7	GCTCATCTCCTCCTTCTCAGTTTTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCTCATCTCCTCCTTCTCAGTTTTC
NCOA2	24	7	CTATTCTGCAAATCATCCAAAATCTCCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCTATTCTGCAAATCATCCAAAATCTCCT
NCOA2	25	7	TTGCTTGTCAACTGATCCAGCAGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGCTTGTCAACTGATCCAGCAGGG
NCOA2	26	7	GTGAGTTGCATGAGGTCATTGATGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGTGAGTTGCATGAGGTCATTGATGA
NCOA2	27	7	TCTGGTTTGGCAATAACCTGCCCAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGGTTTGGCAATAACCTGCCCAG
NCOA2	28	7	GCTTTGCAATGTGATGTCAAGTGGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCTTTGCAATGTGATGTCAAGTGGT
NCOA2	29	7	TCCCTTGATTACCCATCATTCCTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCCCTTGATTACCCATCATTCCTGG
NCOA2	30	7	TGACTCTCACAGCCGAACTCTGCGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGACTCTCACAGCCGAACTCTGCGG
NCOA2	31	7	TTCCGAATCATACCTCCTTGGACTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTCCGAATCATACCTCCTTGGACTG
NCOA2	32	7	CTGAAGCGTCTGTCTTTGGCCAGGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAAT

NCOA2	36	7	TGGTGTGAAAGTTTGGATCTTGCAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGGTGTGAAAGTTTGGATCTTGCAT
NCOA2	37	7	AAGATGCTGGTTCAGGATTTCCCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAAGATGCTGGTTCAGGATTTCCCTC
NCOA2	38	7	TGCTGTTGCTGATGCATTTGTCTCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGCTGTTGCTGATGCATTTGTCTCT
NCOA2	39	7	CATGCTTGGTGTCATATTCAACCCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCATGCTTGGTGTCATATTCAACCCT
NCOA2	40	7	ATAGTTGCTGGCATACCACTAGGAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTATAGTTGCTGGCATACCACTAGGAG
NCOA2	41	7	GGACTCTGTGTATGTGCCATTCGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGACTCTGTGTATGTGCCATTCGGG
NCOA2	42	7	CTGGGTTGGCCTGAGACTGTTGCAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCTGGGTTGGCCTGAGACTGTTGCAT
NCOA2	43	7	CTGCTCATGCCACCTGTGTTGGTCG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGCTCATGCCACCTGTGTTGGTCG
NCOA2	44	7	TGCTGATCTGTCCTGTCATCTGGTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGCTGATCTGTCCTGTCATCTGGTT
NCOA2	45	7	ACTGGAAGTGTTTTGAGCAAGTGAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACTGGAAGTGTTTTGAGCAAGTGAG
NCOA2	46	7	GGGTTGAAACAAATAGACACAGCTCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGGGTTGAAACAAATAGACACAGCTCT
NCOA2	47	7	CTGTCTGGATGCGAGCTTCAGACTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGTCTGGATGCGAGCTTCAGACTG
NCOA2	48	7	AAGGTGAATGCAGTGAACAGACTGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTAAGGTGAATGCAGTGAACAGACTGA
NCOA2	49	7	TGACATGGGTATGAAATTTGCCTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGACATGGGTATGAAATTTGCCTGT
NCOA2	50	7	ACAAGAGCATGGTTCTCCTTAAATACATA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTACAAGAGCATGGTTCTCCTTAAATACATA
NCOA2	51	7	CCCAAATTCAGGCTTTAGCTTAAAACAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCCAAATTCAGGCTTTAGCTTAAAACAT
NCOA2	52	7	GCTGTCCACGGTGTCTGTCCTGCTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCTGTCCACGGTGTCTGTCCTGCTT
NCOA2	53	7	AGAGATACGACTGTGACTTTTGTTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGAGATACGACTGTGACTTTGTTGG
NCOA2	54	7	TCTTTCCAACATGGTCTTTAGAGCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTCTTTCCAACATGGTCTTTAGAGCT
NCOA2	55	7	AATATTTGCTAATGTTAACAGCCCTCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAATATTTGCTAATGTTAACAGCCCTCTC
NCOA2	56	7	AGGTGAACCAGTTTGGTTTTAACAAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTAGGTGAACCAGTTTGGTTTTAACAAA
NCOA2	57	7	CTGACAGGGAAGAAGAGATGCTGAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGACAGGGAAGAAGAGATGCTGAT
NCOA2	58	7	GGCTTACCTGGTTTCTGTAGCTTATATT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGGCTTACCTGGTTTCTGTAGCTTATATT
NCOA2	59	7	GCTCGATTGGTATCAAGCCTTAACTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCTCGATTGGTATCAAGCCTTAACTTT
NCOA2	60	7	GCTATCAATTTAAACACACTGGCGTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGCTATCAATTTAAACACACTGGCGTTTT
NCOA2	61	7	TTCGGCTTAGTCAGCACTGCTAAAA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTCGGCTTAGTCAGCACTGCTAAAA
NCOA2	62	7	CCTGCTTAGTAACATGTAGTCTTTCTAAGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCCTGCTTAGTAACATGTAGTCTTTCTAAGG
NCOA2	63	7	CTTTGGGCTATATCTCTTCCTATATTTCCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTTTGGGCTATATCTCTTCCTATATTTCCA
NCOA2	64	7	GCAACATTTTCAGACTGTCTACTTACCAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCAACATTTTCAGACTGTCTACTTACCAT
NCOA2	65	7	ACTGGTGGCCACTGAGAAGTGTTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACTGGTGGCCACTGAGAAGTGTTGT
NCOA2	66	7	GGAGAAAAGTAGAGCCTTTTGAGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGAGAAAAGTAGAGCCTTTTGAGGG
NCOA2	67	7	TTGTATGCCACATGAGCCTCAGCCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTATGCCACATGAGCCTCAGCCC
NCOA2	68	7	GTGCTGTGTGAAGTTAAAAGTCATTCTA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGTGCTGTGTGAAGTTAAAAGTCATTCTA
NCOA2	69	7	AGATAGTTTTGGACGGTGTTGTAGTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGATAGTTTTGGACGGTGTTGTAGTG
NCOA2	70	7	AAATACAGCGGGCAGATGGATAAAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTAAATACAGCGGGCAGATGGATAAAA
NCOA2	71	7	CCTTCAAAACAGCAATGATCACGAA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCTTCAAAACAGCAATGATCACGAA
NCOA2	72	7	ACCTGATTGAAACCGTAAGAGAATTTATC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTACCTGATTGAAACCGTAAGAGAATTTATC
NCOA2	73	7	CAGGCCATAAGAGATACACATAGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAGGCCATAAGAGATACACATAGGG
NCOA2	74	7	TGCAAGTGGATCTGTGCCACCCATT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGCAAGTGGATCTGTGCCACCCATT
NCOA2	75	7	TTGTGCAGAGGATGCTTTGCTCTTA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTGCAGAGGATGCTTTGCTCTTA
NCOA2	76	7	GTCTATAAAGAAACACCAGGGAGAAAATTC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTGTCTATAAAGAAACACCAGGGAGAAAATTC
NCOA2	77	7	GGACAGCTATGTAGGAATATACAAGACT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGACAGCTATGTAGGAATATACAAGACT
NCOA2	78	7	AGCTTTCTCCTGAAGAACCATAGTTAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTAGCTTTCTCCTGAAGAACCATAGTTAA
NCOA2	79	7	AATACAAACATCAATGCAGGTGAACA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAATACAAACATCAATGCAGGTGAACA
NCOA2	80	7	CTACCTTTGCATAAACTGCTCACAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTCTACCTTTGCATAAACTGCTCACAC
BRCA2	1	8	GTGGAGTTTTAAATAGGTTTGGTTCGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTGGAGTTTTAAATAGGTTTGGTTCGT
BRCA2	2	8	AGCCAGCTGATTATAAGATGGTTTCC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGCCAGCTGATTATAAGATGGTTTCC
BRCA2	3	8	TGGTTCCACTTCAGATACAAATGAGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGGTTCCACTTCAGATACAAATGAGTA
BRCA2	4	8	GGCTTCTGATTTGCTACATTTGAATCTAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGCTTCTGATTTGCTACATTTGAATCTAA
BRCA2	5	8	TTCACAGGCCAAAGACGGTACAACTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTCACAGGCCAAAGACGGTACAACTT
BRCA2	6	8	ATTTAGACCTGAAAGGGTTAGTTGAGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATTTAGACCTGAAAGGGTTAGTTGAGA
BRCA2	7	8	GTGGCAAAGAATTCTCTGAAGTAAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGTGGCAAAGAATTCTCTGAAGTAAGAA
BRCA2	8	8	GCTTCTCTGATTTTGGTAGGCTAGAAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTTCTCTGATTTTGGTAGGCTAGAAA
BRCA2	9	8	ATATTGCCTGCTTTACTGCAAGAATG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATATGCCTGCTTTACTGCAAGAATG
BRCA2	10	8	AGTTTGGATCAGTCATATGACCTGAAAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGTTTGGATCAGTCATATGACCTGAAAA
BRCA2	11	8	CCAGCTTCCATTATCAATTAAATTTGGAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTCCAGCTTCCATTATCAATTAAATTTGGAC
BRCA2	12	8	GGGCTGAACAGTTAATTAGTTCTGATTTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGGCTGAACAGTTAATTAGTTCTGATTTT
BRCA2	13	8	TTGAATGTTGTACTGGGTGACATGCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTGAATGTTGTACTGGGTGACATGCT
BRCA2	14	8	GCTGGCATTTTCATGATCATATAAAAGAC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTGGCATTTTCATGATCATATAAAAGAC
BRCA2	15	8	TTGCCTCTAGAAATCATGACTAGGTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTGCCTCTAGAAATCATGACTAGGTTT
BRCA2	16	8	CTTTGAGCTTGTCTGACATTTTGTATGAT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTTGAGCTTGTCTGACATTTTGTATGAT
BRCA2	17	8	CTTGAAGGTGATGCTACTCTCATGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTTGAAGGTGATGCTACTCTCATGTA
BRCA2	18	8	CCTTTCATTAGCTACTTGGAAGACAAAAT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCTTTCATTAGCTACTTGGAAGACAAAAT
BRCA2	19	8	TTGAAAATGGGTTCGTTTACACAAGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGAAAATGGGTTCGTTTACACAAGT
BRCA2	20	8	TGTGTCTCCATATAAAACCATGGTAGAG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTGTGTCTCCATATAAAACCATGGTAGAG
BRCA2	21	8	CCTGCTTGGAAAATAACATCTGAGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCTGCTTGGAAAATAACATCTGAGGG
BRCA2	22	8	CCTTTTGGCTAGGTGTTAAATTATGGTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCTTTTGGCTAGGTGTTAAATTATGGTT
BRCA2	23	8	CTTCTGCAATATGTAGCTTGGTTTTCTAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTTCTGCAATATGTAGCTTGGTTTTCTAA
BRCA2	24	8	ATCTGGTTTTCAGGCACTTCAAATGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATCTGGTTTTCAGGCACTTCAAATGT
BRCA2	25	8	GCATTCATTATGACATGAAGATCAGCATC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATTCATTATGACATGAAGATCAGCATC
BRCA2	26	8	TGCTGCTGTCTACCTGACCAATCGAT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTGCTGTCTACCTGACCAATCGAT
BRCA2	27	8	CACTGCCATCAAATTCTAAGTTATGAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCACTGCCATCAAATTCTAAGTTATGAGAA
BRCA2	28	8	CAGTAAATAGCAAGTCCGTTTCATCTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCAGTAAATAGCAAGTCCGTTTCATCTT
BRCA2	29	8	ATCTGAGTGTTTCCCTCCTTCATAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATCTGAGTGTTTCCCTCCTTCATAAA
BRCA2	30	8	TTCTTGAGCTTTCGCAACTTCCAAAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTTCTTGAGCTTTCGCAACTTCCAAAA
BRCA2	31	8	GCAATTCTTCTGGTTTCTGATCAAAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCAATTCTTCTGGTTTCTGATCAAAGAA
BRCA2	32	8	TCTGTTTCCTCATAACTTAGAATGTCCA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTCTGTTTCCTCATAACTTAGAATGTCCA
BRCA2	33	8	CTTTTCATCACGTTCGGGTTGTCCCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCATCACGTTCGGGTTGTCCCT
BRCA2	34	8	GCTGTATGAAAACCCAATAGAGTAGGTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTGTATGAAAACCCAATAGAGTAGGTT
BRCA2	35	8	AGGGTCTTTGCCCATTGATGGCTAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAGGGTCTTTGCCCATTGATGGCTAAA
BRCA2	36	8	CCACAGTCTCAATAGAAACAAGGTTTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTCCACAGTCTCAATAGAAACAAGGTTTT
BRCA2	37	8	GGCTGAATTTTCAATGACTGAATAAGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGCTGAATTTTCAATGACTGAATAAGGG
BRCA2	38	8	GTTCCTCAACGCAAATATCTTCATTTACA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTTCCTCAACGCAAATATCTTCATTTACA
BRCA2	39	8	ACGATTTTACCACTGGCTATCCTAAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACGATTTTACCACTGGCTATCCTAAAT
BRCA2	40	8	CCTCTGAATCCAATGCCTCGTAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCCTCTGAATCCAATGCCTCGTAA
BRCA2	41	8	CTTTCTCCAATCCAGACATATTTTGGTTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTTTCTCCAATCCAGACATATTTTGGTTA
BRCA2	42	8	GTTTCCAAACTAACATCACAAGGTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTGTTTCCAAACTAACATCACAAGGTGA
BRCA2	43	8	GACTTGCTTGGTACTATCTTCTATTTCAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGACTTGCTTGGTACTATCTTCTATTTCAG
BRCA2	44	8	GCTGGTCTGAATGTTCGTTACTTTTAAA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGCTGGTCTGAATGTTCGTTACTTTTAAA
BRCA2	45	8	AACTTGCTTTCCACTTGCTGTACTAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAACTTGCTTTCCACTTGCTGTACTAA
BRCA2	46	8	GTGAAGACTATGCTCAGTTCTGATTAAATC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTGAAGACTATGCTCAGTTCTGATTAAATC
BRCA2	47	8	GGTTTCTCTTATCAACACGAGGAAGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGTTTCTCTTATCAACACGAGGAAGTA
BRCA2	48	8	TTCCATTTCTGAGTTTACACAGTGCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTTAGAGTGAGTAGTAGTGGAGTTTTTTCCATTTCTGAGTTTACACAGTGCT
BRCA2	49	8	CACTTTGGTTCCTAATACCAACTGTTG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCACTTTGGTTCCTAATACCAACTGTTG
BRCA2	50	8	GTTCATCATCTTCCATAAAAGCTTTAGCA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTTCATCATCTTCCATAAAAGCTTTAGCA
BRCA2	51	8	CATTTCCTCATTTTCGGGACATGTAAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCATTTCCTCATTTTCGGGACATGTAAAA
BRCA2	52	8	CGGTAAAATTTGGATTCTGTATCTCTTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCGGTAAAATTTGGATTCTGTATCTCTTGA
BRCA2	53	8	CCTGAAACTGCTAAATTGCTTGAAGAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCTGAAACTGCTAAATTGCTTGAAGAT
BRCA2	54	8	TGCCTGTAGTAATCAAGTGTCTCATTTT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTTGCCTGTAGTAATCAAGTGTCTCATTTT
BRCA2	55	8	CACTGTTCAACTCTGTGAAAATGTGATT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCACTGTTCAACTCTGTGAAAATGTGATT
BRCA2	56	8	ATCATCAGAGCCATGTCCATCAATGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATCATCAGAGCCATGTCCATCAATGT
BRCA2	57	8	ACAGACTGCCTGGCTGTGGAAAGACG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACAGACTGCCTGGCTGTGGAAAGACG
BRCA2	58	8	ATCCACCATCAGCCAACTGTATTCCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATCCACCATCAGCCAACTGTATTCCT
BRCA2	59	8	GCTGTGTCATCCCTTTCCATTATCTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTGTGTCATCCCTTTCCATTATCTTT
BRCA2	60	8	AGAAGTTTCAGATATATTTGCGCTCAATG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAGAAGTTTCAGATATATTTGCGCTCAATG
BRCA2	61	8	ATCTAACTGGGCCTTAACAGCATACC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATCTAACTGGGCCTTAACAGCATACC
BRCA2	62	8	GCCATTCTTTAAGACAGCTAAGAGGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGG

BRCA2	68	8	AAACCTTGTTCCTTTTGTTCAGCAGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTAAACCTTGTTCCTTTTGTTCAGCAGA
BRCA2	69	8	GGTCTATCCAAAACTTTATTGCCAGTAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGTCTATCCAAAACTTTATTGCCAGTAAA
BRCA2	70	8	ATTTGGATTCTGGTCGCCACTGGAGG	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTATTTGGATTCTGGTCGCCACTGGAGG
BRCA2	71	8	CTCTTTTGGACTAGCAGAAAACACAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTCTTTTGGACTAGCAGAAAACACAG
BRCA2	72	8	GTTTTCTGCTTCATTGCAAAGTATGTC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGTTTTCTGCTTCATTGCAAAGTATGTC
BRCA2	73	8	AGACAGGTGTGGAAACAGACTTCCTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAGACAGGTGTGGAAACAGACTTCCTT
BRCA2	74	8	CAGTTCTTTTGGTCATCAATCTCTTTCT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCAGTTCTTTTGGTCATCAATCTCTTTCT
BRCA2	75	8	GCAGCCGGAGAAACAAATGTACAAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCAGCCGGAGAAACAAATGTACAAAT
BRCA2	76	8	CTTTATGGGTGTTTCGTATTTGGTGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTCTTTATGGGTGTTTCGTATTTGGTGC
BRCA2	77	8	TTCTTCGTCAGCTATTGAATTACTTTCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCTTCGTCAGCTATTGAATTACTTTCC
BRCA2	78	8	ACAAAAGAGCTTGGGTATTTATCAATGC	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTACAAAAGAGCTTGGGTATTTATCAATGC
BRCA2	79	8	GAGATGTAGTACAACGTCGTTTCAGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGAGATGTAGTACAACGTCGTTTCAGT
BRCA2	80	8	GGCCTGGGAACTCTCCTGTTCTTTGA	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGT	AGAGTGAGTAGTAGTGGAGTTTTAGAGTGAGTAGTAGTGGAGTTTTGGCCTGGGAACTCTCCTGTTCTTTGA
CENPF	1	9	CTTTTCAGGTTTGTACCCTCGGTTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTTTTCAGGTTTGTACCCTCGGTTTT
CENPF	2	9	CCTGGAAATTCACTTGTGACTCCTTG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCTGGAAATTCACTTGTGACTCCTTG
CENPF	3	9	GCATCTCTTTTCCCTATTTGCAAAGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATCTCTTTTCCCTATTTGCAAAGT
CENPF	4	9	CTGCTAGAATTGTCAAAGAAACTGCTA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGCTAGAATTGTCAAAGAAACTGCTA
CENPF	5	9	GAAACTTATTCACTTGGCCTTTCATTTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCAACTTGGCCTTTCATTTC
CENPF	6	9	TCATCCCTACATTTGTTCAAAACTTTCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCATCCCTACATTTGTTCAAAACTTTCTC
CENPF	7	9	TGTTTGGAAAGAACGCTGTTGACGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGTTTGGAAAGAACGCTGTTGACGGG
CENPF	8	9	GCCTTCATCTGGATGCACTCCTGGTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCCTTCATCTGGATGCACTCCTGGTC
CENPF	9	9	GATCTGACTCGCCTGGAACGCCTGTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGATCTGACTCGCCTGGAACGCCTGTT
CENPF	10	9	TGTTCTTGAGTTCTGCCTCCAGGTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGTTCTTGAGTTCTGCCTCCAGGTGG
CENPF	11	9	CCAGATCAGCCACAGCAAGCTTCAGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCAGATCAGCCACAGCAAGCTTCAGT
CENPF	12	9	ACTCTTTCTCTGTCTTGCTTAACTTATCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACTCTTTCTCTGTCTTGCTTAACTTATCA
CENPF	13	9	CGTTCTTACTCTCTCGTTGTATTCATGAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCGTTCTTACTCTCTCGTTGTATTCATGAC
CENPF	14	9	CTGGGTCTCTACCTCCACTGACTTAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGGGTCTCTACCTCCACTGACTTAC
CENPF	15	9	CATATTCGGCATGCAAGTCTTGGTAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCATATTCGGCATGCAAGTCTTGGTAA
CENPF	16	9	GCTGATCAAAAGCCAAAAGACTTCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCTGATCAAAAGCCAAAAGACTTCTC
CENPF	17	9	TCAACTCTATTTTGTAGGATGGCAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCAACTCTATTTTGTAGGATGGCAGAA
CENPF	18	9	TTTGCAGGTCTGAGTTCATCTGTTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTTGTGATGGAAGTTAGAGGGTTTTTTTGCAGGTCTGAGTTCATCTGTTTT
CENPF	19	9	CTGTTCTGCTTTCATGAGATTTTCTTCTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTGTTCTGCTTTCATGAGATTTTCTTCTA
CENPF	20	9	AGTCTTCAAGTAGATGGTTGCTCTTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGTCTTCAAGTAGATGGTTGCTCTTTT
CENPF	21	9	GCATTAATTTCCTTAAGAGTCCCATTCTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATTAATTTCCTTAAGAGTCCCATTCTC
CENPF	22	9	CTCTCACTTTTCTGGATTAAGTTCATCTTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCTCACTTTTCTGGATTAAGTTCATCTTC
CENPF	23	9	ACTAGTGCATTCATTTAGCAAGCATTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACTAGTGCATTCATTTAGCAAGCATTC
CENPF	24	9	CTTCCTTTAGCTGTTCCAACTCATTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTTCCTTTAGCTGTTCCAACTCATTTT
CENPF	25	9	CATCAGCTGTTCATTCTCTTGTAATAAGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCATCAGCTGTTCATTCTCTTGTAATAAGT
CENPF	26	9	AGAGTTCCTAATTGGTTCTGATTCTAGAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTAGAGTTCCTAATTGGTTCTGATTCTAGAT
CENPF	27	9	CCAACTGCGCATTATAACTATCTAGAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCAACTGCGCATTATAACTATCTAGAGAA
CENPF	28	9	TCATGAGGCCCTGAAATATACTTTTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCATGAGGCCCTGAAATATACTTTTCT
CENPF	29	9	CATTGTTGTTTGCAGAGAGCACTGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCATTGTTGTTTGCAGAGAGCACTGAA
CENPF	30	9	GAGTTCATACTTTTCAGCCTGCAGTA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGAGTTCATACTTTTCAGCCTGCAGTA
CENPF	31	9	CTCCTGGTATGTCTTCCACTAACTCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTCCTGGTATGTCTTCCACTAACTCA
CENPF	32	9	CTCGTCCAATGGAGCCAAAGACACAG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCGTCCAATGGAGCCAAAGACACAG
CENPF	33	9	CCAAATTTTCGGCCTTTAATGAGTCAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCAAATTTTCGGCCTTTAATGAGTCAA
CENPF	34	9	CTTGAAAGTTTCTCAGATTCGTTGACA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTTGAAAGTTTCTCAGATTCGTTGACA
CENPF	35	9	TGCTAAGACTAGAGCTGTCAGGCACA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCTAAGACTAGAGCTGTCAGGCACA
CENPF	36	9	GGGTTTCTTTCCTGGTCAGATTCTCC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGGTTTCTTTCCTGGTCAGATTCTCC
CENPF	37	9	CAAGCTCTTGCCTTTCAGAACTTAATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCAAGCTCTTGCCTTTCAGAACTTAATA
CENPF	38	9	TTCTGACAAATACTGCTTCCTAAGGC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCTGACAAATACTGCTTCCTAAGGC
CENPF	39	9	CAGTTGTTCCGTCTGTTTCTTTTCTG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCAGTTGTTCCGTCTGTTTCTTTTCTG
CENPF	40	9	ACCGAGAACTTAAGTCCAGACCTTGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACCGAGAACTTAAGTCCAGACCTTGT
CENPF	41	9	TGGTGTTCTTTCTGTAGTTTCTGAAGTAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGGTGTTCTTTCTGTAGTTTCTGAAGTAT
CENPF	42	9	CTGGAGGCTCATAATTGGTATCTGGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTGGAGGCTCATAATTGGTATCTGGG
CENPF	43	9	GCATTAGGACCAGAAAATGACAATTCAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGCATTAGGACCAGAAAATGACAATTCAG
CENPF	44	9	TCTCATTTGATGTCTCTTTTACCCGC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCTCATTTGATGTCTCTTTTACCCGC
CENPF	45	9	TGAGGCCTTCAGAAGTTTCTACTCTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGAGGCCTTCAGAAGTTTCTACTCTC
CENPF	46	9	ACGTGATGATTTATCTGCATGCATTTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTACGTGATGATTTATCTGCATGCATTTC
CENPF	47	9	CTTGTGACCACTGAGAGTTCTTCTTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTCTTGTGACCACTGAGAGTTCTTCTTC
CENPF	48	9	CTAATTCTCCACGAAGCTGGTTTCTC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTAATTCTCCACGAAGCTGGTTTCTC
CENPF	49	9	GTTTTGTCTTTTAACAGCTCACTCACAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTTTTGTCTTTTAACAGCTCACTCACAT
CENPF	50	9	GATTCCTTGACAAGCAATTCTTTCTCTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGATTCCTTGACAAGCAATTCTTTCTCTTT
CENPF	51	9	TTTCTCGATGCCTCTTCTCAGCTGAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTTCTCGATGCCTCTTCTCAGCTGAT
CENPF	52	9	TTTTCATCGGCCTCAATGCGAACTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTTTTCATCGGCCTCAATGCGAACTCT
CENPF	53	9	ATTCCCTTTCAAGGTTCTCAACTTTATC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTATCCCTTTCAAGGTTCTCAACTTTATC
CENPF	54	9	TAGCTCCTGGTTTTCTTCTGACATCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTAGCTCCTGGTTTTCTTCTGACATCT
CENPF	55	9	CTGGCCATCTCTTCTATTTGTGTTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTGGCCATCTCTTCTATTTGTGTTTT
CENPF	56	9	CTTGCTCCTTTTCTTCTAACAGACTTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTTGCTCCTTTTCTTCTAACAGACTTTT
CENPF	57	9	TGTTCTGTGGCCTTCATAATTTCTTG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGTTCTGTGGCCTTCATAATTTCTTG
CENPF	58	9	GCTCTTCCTCTATTGGTGGGTCTAGA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCTTCCTCTATTGGTGGGTCTAGA
CENPF	59	9	CCTTCAGTTGTTGTAAGACACAGAGC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCTTCAGTTGTTGTAAGACACAGAGC
CENPF	60	9	CCTTAAGTAAATCTGCATGATGCTCAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCCTTAAGTAAATCTGCATGATGCTCAC
CENPF	61	9	GCATGCTCTTGGTTTGTCCTGGCTAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATGCTCTTGGTTTGTCCTGGCTAT
CENPF	62	9	CTAATTCAGATATTCGCTCTTGCTCTTTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTAATTCAGATATTCGCTCTTGCTCTTTT
CENPF	63	9	CTCTCTCATTGAGCTCTTTTAATTGTGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTCTCTCATTGAGCTCTTTTAATTGTGT
CENPF	64	9	CTACTAAGATTCTGCTCTTTGGCCTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTACTAAGATTCTGCTCTTTGGCCTT
CENPF	65	9	GCTGCTCTTGGTCTTGAATTTGATTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCTGCTCTTGGTCTTGAATTTGATTTT
CENPF	66	9	TTTGGATTGTAGCACTTGGATCTTCT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTTGTGATGGAAGTTAGAGGGTTTTTTTGGATTGTAGCACTTGGATCTTCT
CENPF	67	9	CATTCTCTAGATTCTTGTAAGAACTCTGC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCATTCTCTAGATTCTTGTAAGAACTCTGC
CENPF	68	9	CAGTTTCCTTTTGCAGTCATTTTTGTTTAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCAGTTTCCTTTTGCAGTCATTTTTGTTTAC
CENPF	69	9	TTTCTAGTGTGAGCTCCTTCAATTGA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTTCTAGTGTGAGCTCCTTCAATTGA
CENPF	70	9	GCAATCTAGGCTCTTCTTCAATTCAC	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGCAATCTAGGCTCTTCTTCAATTCAC
CENPF	71	9	GTTTGTTTGTGTCCAAAAGCAAAGCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTTTGTTTGTGTCCAAAAGCAAAGCC
CENPF	72	9	CTCGGTATGTCTGGATTTCTACTTCAT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTCTCGGTATGTCTGGATTTCTACTTCAT
CENPF	73	9	GCTTGAAGTTGAGAGAGTTCTTTCTG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTTGAAGTTGAGAGAGTTCTTTCTG
CENPF	74	9	TGTTAATTCATCGACCTTGGTATCCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTGTTAATTCATCGACCTTGGTATCCA
CENPF	75	9	TGTGTCTCTAACATCTCTTTAGCTTTCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGTGTCTCTAACATCTCTTTAGCTTTCT
CENPF	76	9	TAGCAAAGGAGACCCTCGGGAATCTT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTAGCAAAGGAGACCCTCGGGAATCTT
CENPF	77	9	TTTGCCTCTTGCCTGAAGCTTTATTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTTGCCTCTTGCCTGAAGCTTTATTT
CENPF	78	9	TCTACCATTCTCCCATATTCCACTGG	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTTCTACCATTCTCCCATATTCCACTGG
CENPF	79	9	GCTGGTCCGAGTTGCCATGGTTGTTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTGGTCCGAGTTGCCATGGTTGTTC
CENPF	80	9	GGATAGCGCTAACTTCTGTGCAGCCA	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGT	TGTGATGGAAGTTAGAGGGTTTTTGTGATGGAAGTTAGAGGGTTTTGGATAGCGCTAACTTCTGTGCAGCCA
CKAP5	1	10	CACTGCATTGGAATCAGTGACAAATTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCACTGCATTGGAATCAGTGACAAATTTT
CKAP5	2	10	AGTGCAGCTTCTAATCCTTTCAATTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGTGCAGCTTCTAATCCTTTCAATTG
CKAP5	3	10	GCTTTAGGTTGATTGAACACCTTACTTAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTTTAGGTTGATTGAACACCTTACTTAC
CKAP5	4	10	AGATCTCTATGCCCAGCTCCTTGGCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGATCTCTATGCCCAGCTCCTTGGCT
CKAP5	5	10	CAAGCCTTTCAGGAGCTCTTCTTGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCAAGCCTTTCAGGAGCTCTTCTTGAA
CKAP5	6	10	GGCCACTATGATCTTGGGATTCTTATT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGCACCTATGATCTTGGGATTCTTATT
CKAP5	7	10	GCTTCATCTCGAACAGCCTTCTCTCG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTTCATCTCGAACAGCCTTCTCTCG
CKAP5	8	10	CCATCTGTAAATCTCCACAGCAATTAGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCATCTGTAAATCTCCACAGCAATTAGT
CKAP5	9	10	TTGGGAACGAAGAAATCGAGTAGGTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGGGAGGGATTGAAGGATATTTTGGGAACGAAGAAATCGAGTAGGTC
CKAP5	10	10	TATTTGTGGCACCTCATCACCATCAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATTTGTGGCACCTCATCACCATCAT
CKAP5	11	10	GTCATAAAAGTCTTTGGGAAGTTTGGAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGTCATAAAAGTCTTTGGGAAGTTTGGAAA
CKAP5	12	10	GGGCCTCTTTTCTCTCTTGCCATTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGGCCTCTTTTCTCTCTTGCCATTTT
CKAP5	13	10	TGCCAAAGCCACCAACATGACATTGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCCAAAGCCACCAACATGACATTGG
CKAP5	14	10	CCAACAGCCAGGCCAGTAAGACATTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCAACAGCCAGGCCAGTAAGACATTT
CKAP5	15	10	TTGTACCACTTGAGGTTTCTTTCTCTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTGTACCACTTGAGGTTTCTTTCTCTT
CKAP5	16	10	AAGATTGCATCAATTGCCTCCTGCAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAAGATTGCATCAATTGCCTCCTGCAG
CKA

CKAP5	20	10	AGTACCCAATGCTTCAAATGCGGCAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGTACCCAATGCTTCAAATGCGGCAT
CKAP5	21	10	GTTTGTCCACATCAGCTAGGAATGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTTTGTCCACATCAGCTAGGAATGGG
CKAP5	22	10	CAGGCAGAGGTTTGAATTCCTTCTTA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCAGGCAGAGGTTTGAATTCCTTCTTA
CKAP5	23	10	AGAGGTCCTGGTTTGGGTGCAGAAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAGAGGTCCTGGTTTGGGTGCAGAAAT
CKAP5	24	10	GGTTCCAGTATTCCCTGCGCCTCCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGGTTCCAGTATTCCCTGCGCCTCCTG
CKAP5	25	10	ACAAGCCAGCCTTTCTTTCCAGTTAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACAAGCCAGCCTTTCTTTCCAGTTAC
CKAP5	26	10	CCTGGCATGGCATTTCAGTTCGGTCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTGGCATGGCATTTCAGTTCGGTCC
CKAP5	27	10	ACAACCTGAGCTGACGTTTTGGAAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACAACCTGAGCTGACGTTTTGGAAAA
CKAP5	28	10	CTCCAATCTTGTCCACAAGGCCATCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCTCCAATCTTGTCCACAAGGCCATCT
CKAP5	29	10	TTTGGGATTCTTTTGTGAGAAAGCCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTTGTGGAGGGATTGAAGGATATTTTTTGGGATTCTTTTGTGAGAAAGCCA
CKAP5	30	10	TACAGATACATCACGCCAAGCAGGGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTACAGATACATCACGCCAAGCAGGGT
CKAP5	31	10	TCATCTGGTTCATCTCCATCTTCTCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCATCTGGTTCATCTCCATCTTCTCC
CKAP5	32	10	GCAAAAGATCAACGACATCATTGCTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCAAAAGATCAACGACATCATTGCTC
CKAP5	33	10	GGAAGTTCACCTATATTCGGTTGGATAAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGGAAGTTCACCTATATTCGGTTGGATAAAT
CKAP5	34	10	AATCATTGAGTCGACCCTTCAAGGCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAATCATTGAGTCGACCCTTCAAGGCA
CKAP5	35	10	CCAAGCATTCACAGTCGCTAGGGCAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCAAGCATTCACAGTCGCTAGGGCAG
CKAP5	36	10	AGCCATTCCTTCATGCCAGTCTGTTC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGCCATTCCTTCATGCCAGTCTGTTC
CKAP5	37	10	GGTAGTTTCTCAGCCAGCCAGCCCAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGGTAGTTTCTCAGCCAGCCAGCCCAG
CKAP5	38	10	GAACACAAAGGATAAGGTCTGTAGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAACACAAAGGATAAGGTCTGTAGGG
CKAP5	39	10	TCTTGGGCCTTCTTTCGCACATCTCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCTTGGGCCTTCTTTCGCACATCTCC
CKAP5	40	10	CCTAAATGCATCATGAAGAATGGCAAG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCCTAAATGCATCATGAAGAATGGCAAG
CKAP5	41	10	GCATGTTAACTTTGGCTTTCTCTAGC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATGTTAACTTTGGCTTTCTCTAGC
CKAP5	42	10	TGCTTTAGTGGGTGGAGCAGGCTTGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTGCTTTAGTGGGTGGAGCAGGCTTGG
CKAP5	43	10	TGCTCTTTTCCATTTGGAACAACAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCTCTTTTCCATTTGGAACAACAAT
CKAP5	44	10	GTTGCTCAATGTATTCATCCCGTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTTGCTCAATGTATTCATCCCGTGGG
CKAP5	45	10	TGAGTGAAACATCTCATCTTGTAACCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGAGTGAAACATCTCATCTTGTAACCA
CKAP5	46	10	GCAAGGGCTTTGTTATGATGCTGAAA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCAAGGGCTTTGTTATGATGCTGAAA
CKAP5	47	10	TCAGGACGCTTGTATTGGTGTCAAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGGGATGTATTGAAGGAGGATTTTCAGGACGCTTGTATTGGTGTCAAAA
CKAP5	48	10	CACTTAGCAAGGTGAAGAGCAATTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTCACTTAGCAAGGTGAAGAGCAATTTT
CKAP5	49	10	CGAACATCTTTACGAATGACATCCTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCGAACATCTTTACGAATGACATCCTTT
CKAP5	50	10	GATAAAGGGAAACATCTTGCTAGCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGATAAAGGGAAACATCTTGCTAGCTG
CKAP5	51	10	TGCGTACAGCATTGTCACGGTCTCCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCGTACAGCATTGTCACGGTCTCCT
CKAP5	52	10	TCCAATCAGTTTGAACACCTGATCCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCCAATCAGTTTGAACACCTGATCCC
CKAP5	53	10	CTCTTTGCTGACCGCTTAATCCTCTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTCTTTGCTGACCGCTTAATCCTCTC
CKAP5	54	10	TATGTTCTGTGCACGCTGAGGTTTCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTATGTTCTGTGCACGCTGAGGTTTCT
CKAP5	55	10	CCTCAGGATGCCCACTCATGCTTCGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCTCAGGATGCCCACTCATGCTTCGG
CKAP5	56	10	CTGGAATTCTCGGCGGACCATCTGGG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTCTGGAATTCTCGGCGGACCATCTGGG
CKAP5	57	10	GTTCAGGAATAAGGACTGGCTCAAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTTCAGGAATAAGGACTGGCTCAAAA
CKAP5	58	10	GAAGTGTGGAGAAACAGCCCGGATCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAAGTGTGGAGAAACAGCCCGGATCT
CKAP5	59	10	CTGGCTACTTGGGAGATAATGAAATTG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTCTGGCTACTTGGGAGATAATGAAATTG
CKAP5	60	10	GAGCTTGGATACTTGTGTTGATGTCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGAGCTTGGATACTTGTGTTGATGTCA
CKAP5	61	10	TGGCCGGACATGGCTTCAGCTTTGTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGGCCGGACATGGCTTCAGCTTTGTC
CKAP5	62	10	GCATAAAAGTGGCTATCAGAAACTGATCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGCATAAAAGTGGCTATCAGAAACTGATCA
CKAP5	63	10	GATCTCGTCCTTCTCCAATTTCTCAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGATCGTCCTTCTCCAATTTCTCAT
CKAP5	64	10	GTTGCCAATGATACAGCTATACAACTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTTGCCAATGATACAGCTATACAACTT
CKAP5	65	10	TCAAGATCTTCAATCCGAGAATCCAG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCAAGATCTTCAATCCGAGAATCCAG
CKAP5	66	10	TCACAGAGCGGATGACCTGTTGTCCT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCACAGAGCGGATGACCTGTTGTCCT
CKAP5	67	10	CTAGCAGGCTGTCTTGGAGCAAAACA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTAGCAGGCTGTCTTGGAGCAAAACA
CKAP5	68	10	CTCTGAGAATTTGGGAGAACTGGCTG	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTCTCTGAGAATTTGGGAGAACTGGCTG
CKAP5	69	10	TTGCATTGCTTCAGTTTCTCTTTGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTGCATTGCTTCAGTTTCTCTTTGGG
CKAP5	70	10	GTCTTTAGGGTCCTTATGGGAAATTCA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTGTCTTTAGGGTCCTTATGGGAAATTCA
CKAP5	71	10	ATCATCGTTAGGTGGTCCAGGATCTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATCATCGTTAGGTGGTCCAGGATCTT
CKAP5	72	10	ATGGGCCTCCAGCTCAGACTCGTTTT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTATGGGCCTCCAGCTCAGACTCGTTTT
CKAP5	73	10	TTTCCTTATCAGACTTGCTCCCAGTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTTCCTTATCAGACTTGCTCCCAGTC
CKAP5	74	10	AAATCATTCACTTTGGCCTTTGATGA	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAAATCATTCACTTTGGCCTTTGATGA
CKAP5	75	10	GCTCTGGAAGAACTGTGAGGAATTTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCTCTGGAAGAACTGTGAGGAATTTT
CKAP5	76	10	TCAATCACCCGAAGGCCTCTTTCGAC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTTCAATCACCCGAAGGCCTCTTTCGAC
CKAP5	77	10	GCACACATGTGACTTCCATCTGAGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCACACATGTGACTTCCATCTGAGGG
CKAP5	78	10	AGCCTTTCCAAGTAGACAGATGGCCC	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTGGGATGTATTGAAGGAGGATTTTAGCCTTTCCAAGTAGACAGATGGCCC
CKAP5	79	10	GCATGTCTGTGGAAGAGGCGACAGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCATGTCTGTGGAAGAGGCGACAGTA
CKAP5	80	10	CTCCCGGAGCTGAGAGAGTTTGCTGT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGAT	GGGATGTATTGAAGGAGGATTTTCTCCCGGAGCTGAGAGAGTTTGCTGT
NCOA	1	11	GCGATCCTTTCCTCTTATGTGAGTCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCGATCCTTTCCTCTTATGTGAGTCT
NCOA	2	11	TTTATTTTCTTGCTCCCTGCGCCTC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTTATTTTCTTGCTCCCTGCGCCTC
NCOA	3	11	ACTCAAGCTGTCAATGTCACTAATGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTACTCAAGCTGTCAATGTCACTAATGT
NCOA	4	11	CGACTGTTTTCTTCAAAATCTTGCATTTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCGACTGTTTTCTTCAAAATCTTGCATTTG
NCOA	5	11	TGTACATCGTCATCAGTTGTTGATTTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGTACATCGTCATCAGTTGTTGATTTC
NCOA	6	11	CCTTGACTACTTGATGAGATGTCTGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCCTTGACTACTTGATGAGATGTCTGAT
NCOA	7	11	ATTCTCCCTTCACAGTTCACAACAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATTCTCCCTTCACAGTTCACAACAA
NCOA	8	11	AGCTGGTTACATTCTCTGACACAAAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGCTGGTTACATTCTCTGACACAAAT
NCOA	9	11	TTCTTCACAAATTCTGCATGATCCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTCTTCACAAATTCTGCATGATCCC
NCOA	10	11	TAGCATCCTGCAGTTAAAGGTATGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTAGCATCCTGCAGTTAAAGGTATGG
NCOA	11	11	TACTTCATAACGCTGGCAAGCTTCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTACTTCATAACGCTGGCAAGCTTCT
NCOA	12	11	TTGGCTGTGACACAGTGAAACACTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTGGCTGTGACACAGTGAAACACTG
NCOA	13	11	GTAGTATCTTGCTTGGTCATAAAGGATTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGTAGTATCTTGCTTGGTCATAAAGGATTC
NCOA	14	11	TCTCAGGGAACTAGTATCAATAGAGATGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTCTCAGGGAACTAGTATCAATAGAGATGAT
NCOA	15	11	GGTTCTCTGCCCTGAGGTTGGAAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGTTCTCTGCCCTGAGGTTGGAAAA
NCOA	16	11	TTCTTGGAACAGCTGTCTGGCATAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTTCTTGGAACAGCTGTCTGGCATAA
NCOA	17	11	ATGTCTGGACTTTGAGGGTAGCAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTATGTCTGGACTTTGAGGGTAGCAAA
NCOA	18	11	CGATGATATGAATTCCCATGATGAAAGGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCGATGATATGAATTCCCATGATGAAAGGT
NCOA	19	11	GGGAATTGACATTCCAGAATTAGTGTCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTGGAATTGACATTCCAGAATTAGTGTCA
NCOA	20	11	GATACTAGGATTGACCGAGGGATTTAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGATACTAGGATTGACCGAGGGATTTAC
NCOA	21	11	ATGTTGCTGTTGGATGGTGGCAATG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTATGTTGCTGTTGGATGGTGGCAATG
NCOA	22	11	CTGCTGGCGGTTTATTCTGGTGGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCTGCTGGCGGTTTATTCTGGTGGAT
NCOA	23	11	AAACTTCCTTGGCTGTTGCTAGAAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAAACTTCCTTGGCTGTTGCTAGAAT
NCOA	24	11	TACAATCTGACTTCCGGGTGAGCAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTACAATCTGACTTCCGGGTGAGCAT
NCOA	25	11	AAAGAGGGATTACTGCTCTGTGAAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAAAGAGGGATTACTGCTCTGTGAAC
NCOA	26	11	TGTACCTTCCATAGGAGAATTATTGAGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTACCTTCCATAGGAGAATTATTGAGG
NCOA	27	11	GGAATTGTTTGGCATCCTGGGCCTT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGAATTGTTTGGCATCCTGGGCCTT
NCOA	28	11	GGAGAGCTTAATGTCGAAATATTAGGAGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGAGAGCTTAATGTCGAAATATTAGGAGG
NCOA	29	11	CTGGGATGTTTGAATAAGATCGGTTATT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTGGGATGTTTGAATAAGATCGGTTATT
NCOA	30	11	GGTCCTTCATTCATACCCTGTAAAGATG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGTCCTTCATTCATACCCTGTAAAGATG
NCOA	31	11	GTGAGCTCATCTGCCTGAGGACTGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGAGCTCATCTGCCTGAGGACTGG
NCOA	32	11	TGCTGGTTGTATATTTAATCTGCTAGGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGCTGGTTGTATATTTAATCTGCTAGGT
NCOA	33	11	GAGCTGTTGTCAGATTGAATCATTTCATT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGAGCTGTTGTCAGATTGAATCATTTCATT
NCOA	34	11	CCCTGAATCCAGAGGTTTGCCATCA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCCCTGAATCCAGAGGTTTGCCATCA
NCOA	35	11	TGTGACTGGTTTGAGAGTATTTACTGTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGTGACTGGTTTGAGAGTATTTACTGTC
NCOA	36	11	GCAGTTGTTGTCAAAAGCTGCACTA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCAGTTGTTGTCAAAAGCTGCACTA
NCOA	37	11	AAGACAGGACATCTTTGCAGCTTGT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTAAGACAGGACATCTTTGCAGCTTGT
NCOA	38	11	AGAGGGACAAGAACCTCCTGAAGAG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTAGAGGGACAAGAACCTCCTGAAGAG
NCOA	39	11	CCCTCCTGTAAGAGCCGGTGTAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTCCCTCCTGTAAGAGCCGGTGTAGAA
NCOA	40	11	CAGACAAAGTGGTGATATCTGAGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTCAGACAAAGTGGTGATATCTGAGGG
NCOA	41	11	GTTTCCTTGTACCTGTCCAGTCACT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTGTGGAGGGATTGAAGGATATTTGTTCCTTGTACCTGTCCAGTCACT
NCOA	42	11	GGAGCTGATGGTCTTTTGATTCTTTT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGGAGCTGATGGTCTTTTGATTCTTTT
NCOA	43	11	CCACTTTCACCTTTACATCATCCAGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCACTTTCACCTTTACATCATCCAGG
NCOA	44	11	TGTATTACATGGATCCATCTGTTCTTTCT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTGTATTACATGGATCCATCTGTTCTTTCT
NCOA	45	11	ACTGGCTCTGGGCCTCCAGTTTTAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACTGGCTCTGGGCCTCCAGTTTTAT
NCOA	46	11	TGATCAAACTGGTCAAGGTCAGCTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGATCAAACTGGTCAAGGTCAGCTG
NCOA	47	11	ACCGCACCATCCATCCTGTCTGTCT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACCGCACCATCCATCCTGTCTGTCT
NCOA	48	11	GGATCTCCGATTTGATGGTTACACTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTTGATGGTTACACTG
NCOA	49	11	GATCGCCTGTTCCTGGTTGTCCAAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGATCGCCTGTTCCTGGTTGTCCAAA
NCOA	50	11	GCTGTCACTGTATTATTTGTCCATGGAA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTATAGGAAATGGTGGTAGTGTTTTGCTGTCACTGTATTATTTGTCCATGGAA
NCOA	51	11	CCAGCTGTTCAAGAAGAGCCTTCTC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTCCAGCTGTTCAAGAAGAGCCTT

NCOA	52	11	GTTTCATCTTTGCCACTAAGGAAGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTTTCATCTTTGCCACTAAGGAAGG
NCOA	53	11	ATCTCTCTGATAATACATCTAATCCACCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTATCTCTCTGATAATACATCTAATCCACCC
NCOA	54	11	AAAGGTGGCGTTGCTTGTTGTGGTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTAAAGGTGGCGTTGCTTGTTGTGGTG
NCOA	55	11	TGCCTTGGAAAGGGCTAGGGAGATT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGCCTTGGAAAGGGCTAGGGAGATT
NCOA	56	11	GTGTTACTTGAACAGGCATCGTCCC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTGTTACTTGAACAGGCATCGTCCC
NCOA	57	11	GCCGGAGGTCTGTTTAGAGTTTGCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGCCGGAGGTCTGTTTAGAGTTTGCC
NCOA	58	11	TAGTTGAAGTCGAAGCTGGTTAGGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTAGTTGAAGTCGAAGCTGGTTAGGT
NCOA	59	11	AAGATAGCTTGCCGATTTTGGTGTA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAAGATAGCTTGCCGATTTTGGTGTA
NCOA	60	11	TGTTGCATGCCTGATCTCATATTGAT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTTGCATGCCTGATCTCATATTGAT
NCOA	61	11	CTGTTGACTGTACAGTTCCCGCTGA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCTGTTGACTGTACAGTTCCCGCTGA
NCOA	62	11	GCTGCTGTATTAGCTGCCTCTGTCG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGCTGCTGTATTAGCTGCCTCTGTCG
NCOA	63	11	AGATGAGGGAGGGAGGTTGTTCCCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAGATGAGGGAGGGAGGTTGTTCCCA
NCOA	64	11	TGTGGAGCACCCTGAGGAAGACGGG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTGGAGCACCCTGAGGAAGACGGG
NCOA	65	11	AAACGGGCTGGTAGAAGCAGGTGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTAAACGGGCTGGTAGAAGCAGGTGGG
NCOA	66	11	ATGCTTCAGGATTTGCTGCTAGTTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTATGCTTCAGGATTTGCTGCTAGTTG
NCOA	67	11	ACTGTCCTCCTATGTTTCCTGTCAT	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTACTGTCCTCCTATGTTTCCTGTCAT
NCOA	68	11	TGCATCTGAGGATTGATTCCAGTGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTGCATCTGAGGATTGATTCCAGTGC
NCOA	69	11	GGAGCAAAGTTGGCCTCACCTTGGG	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGGAGCAAAGTTGGCCTCACCTTGGG
NCOA	70	11	CACCATGGAGCTCCCAGGGCTTAGA	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTCACCATGGAGCTCCCAGGGCTTAGA
NCOA	71	11	GAGGCAGGTGGAGTTTGCTGGAGAA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTGAGGCAGGTGGAGTTTGCTGGAGAA
NCOA	72	11	GGCCTTCATGTCTGGTGACTGATAC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGGCCTTCATGTCTGGTGACTGATAC
NCOA	73	11	TGGTTCTGGACAGCTTGACTGAACA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTGGTTCTGGACAGCTTGACTGAACA
NCOA	74	11	GTATACTCCTGGCTGTGCAGGCGTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGTATACTCCTGGCTGTGCAGGCGTG
NCOA	75	11	TCATGTTCTGAACATTCGTATTTCCAC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTCATGTTCTGAACATTCGTATTTCCAC
NCOA	76	11	CTCATCTGCATCTGGGCCATCATTG	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTCTCATCTGCATCTGGGCCATCATTG
NCOA	77	11	TTGCAGTAGAGGCCTGTGTGTCTCA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTTTGCAGTAGAGGCCTGTGTGTCTCA
NCOA	78	11	TTTGAGAAGGTCAGTGGATGAGAGC	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTTTGAGAAGGTCAGTGGATGAGAGC
NCOA	79	11	CCAGGCTGGTTCAGGTAAGGGTCCC	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATA	TGTGGAGGGATTGAAGGATATTTTGTGGAGGGATTGAAGGATATTTCCAGGCTGGTTCAGGTAAGGGTCCC
NCOA	80	11	TGACGTGGGCTTTTGAGTTCCCAGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGT	ATAGGAAATGGTGGTAGTGTTTTTATAGGAAATGGTGGTAGTGTTTTTGACGTGGGCTTTTGAGTTCCCAGT

Phasor Transform Expressions

The first-order phasor transform of the lifetime intensity photon histogram $I(t)$:

$$S = \frac{\int_0^T I(t)\sin(\omega t)dt}{\int_0^T I(t)dt} \tag{1}$$

$$G = \frac{\int_0^T I(t)\cos(\omega t)\,dt}{\int_0^T I(t)\,dt} \tag{2}$$

Where T is the period between excitation pulses (or modulation period), and $\omega = \frac{2\pi}{T}$ the pulsation frequency such that the period of trigonometric functions matches the excitation period T.

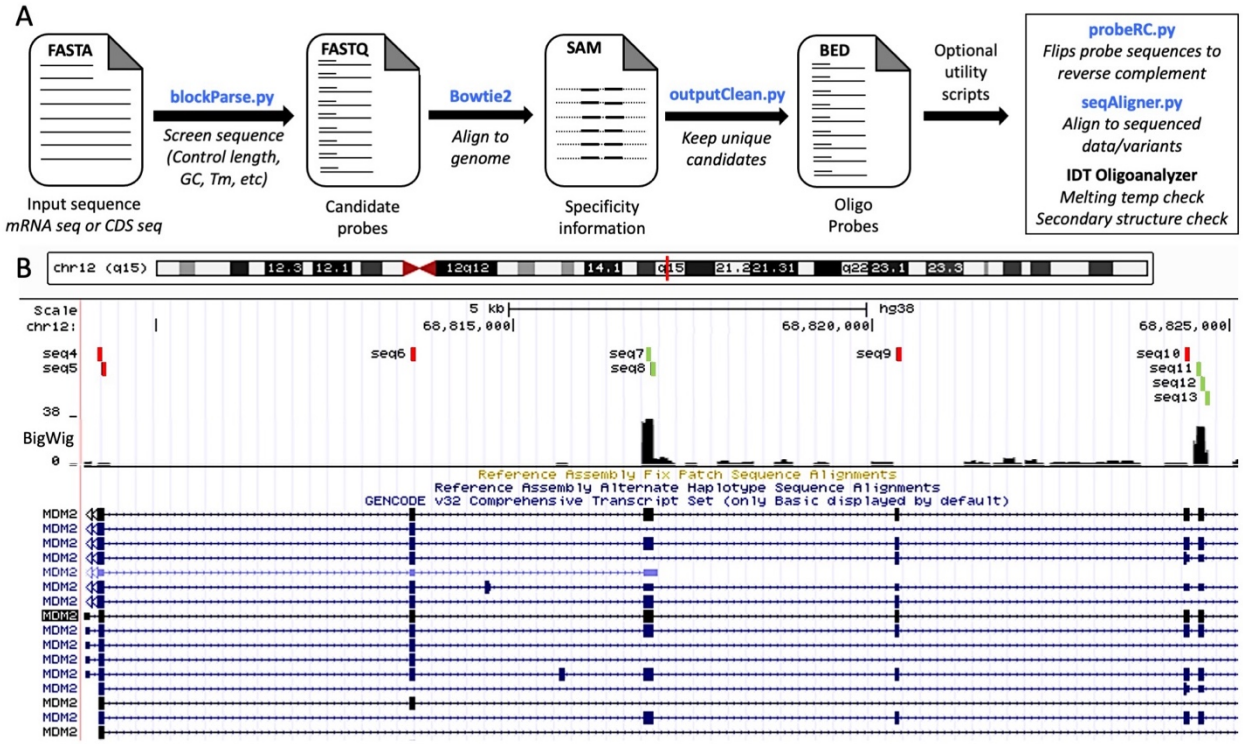
The first-order phasor transform of the spectral intensity photon histogram $I(\lambda)$:

$$S = \frac{\int_{\lambda_0}^{\lambda_f} I(\lambda)\sin(\omega\lambda - \omega\lambda_0)\;d\lambda}{\int_{\lambda_0}^{\lambda_f} I(\lambda)\,d\lambda} \tag{3}$$

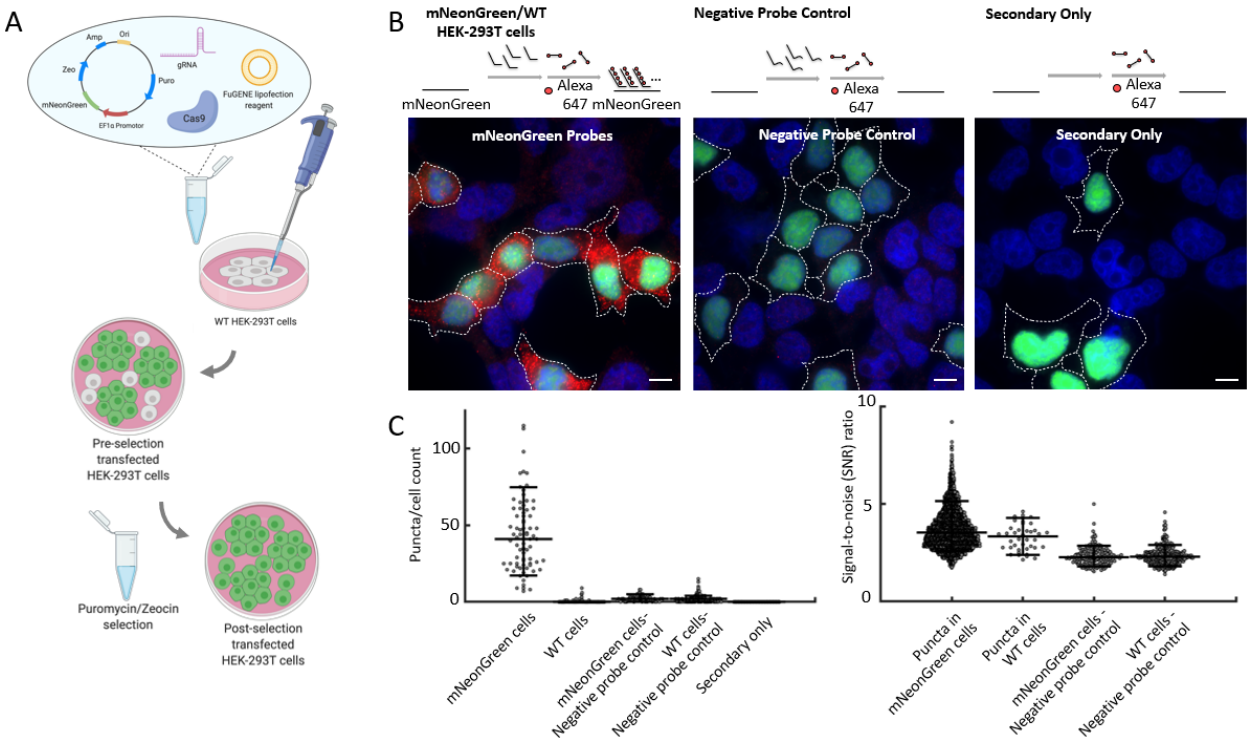
$$G = \frac{\int_{\lambda_0}^{\lambda_f} I(\lambda)\cos(\omega\lambda - \omega\lambda_0)\;d\lambda}{\int_{\lambda_0}^{\lambda_f} I(\lambda)\,d\lambda} \tag{4}$$

Where λ_0 and λ_f are the limits of the spectral band of the detector, and $\omega = \frac{2\pi}{\lambda_f - \lambda_0}$ the pulsation frequency such that the period of trigonometric functions matches the spectral bandwidth.

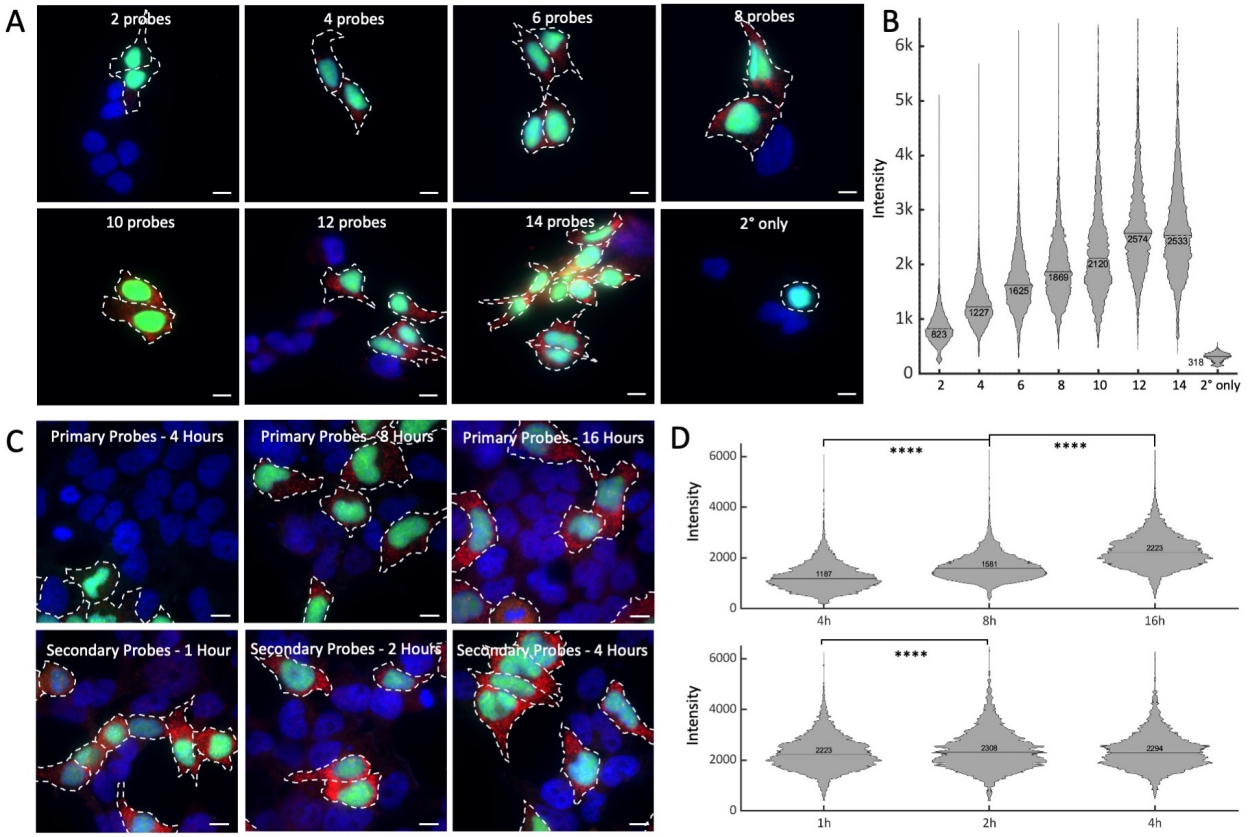
Figures



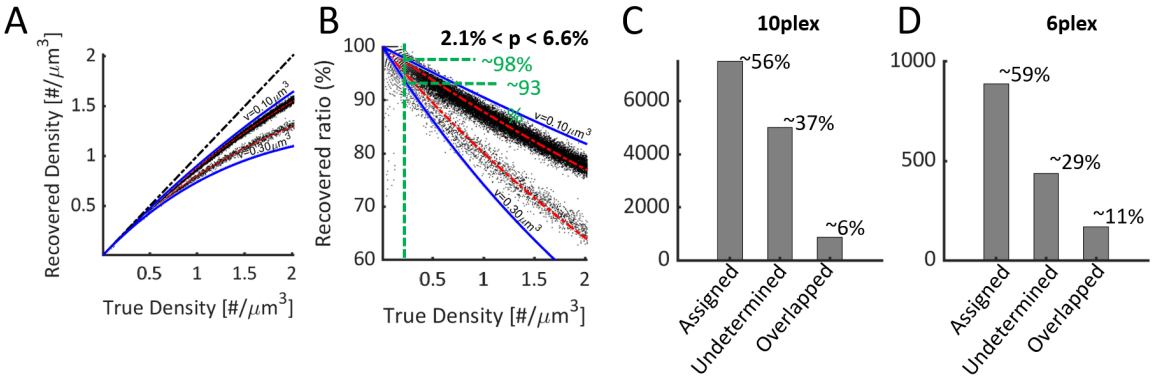
Supplementary Figure 1. Schematic overview of probe design process. A) A modified version of Oligominer was used to design primary probes. **B)** In the seqAligner.py script, the probes (labeled "seq#") go through BLAT and are aligned to the RNA sequencing data, as seen on the UCSC Genome Browser. The BigWig browser track shows a histogram of the read counts and probes are aligned and compared to the read counts of the region they overlap with. Probes that overlapped with more than 5% of the highest read count were used (green) and those that aligned with regions considered as "low read count" (5% or less) were removed from the final probe list (red).



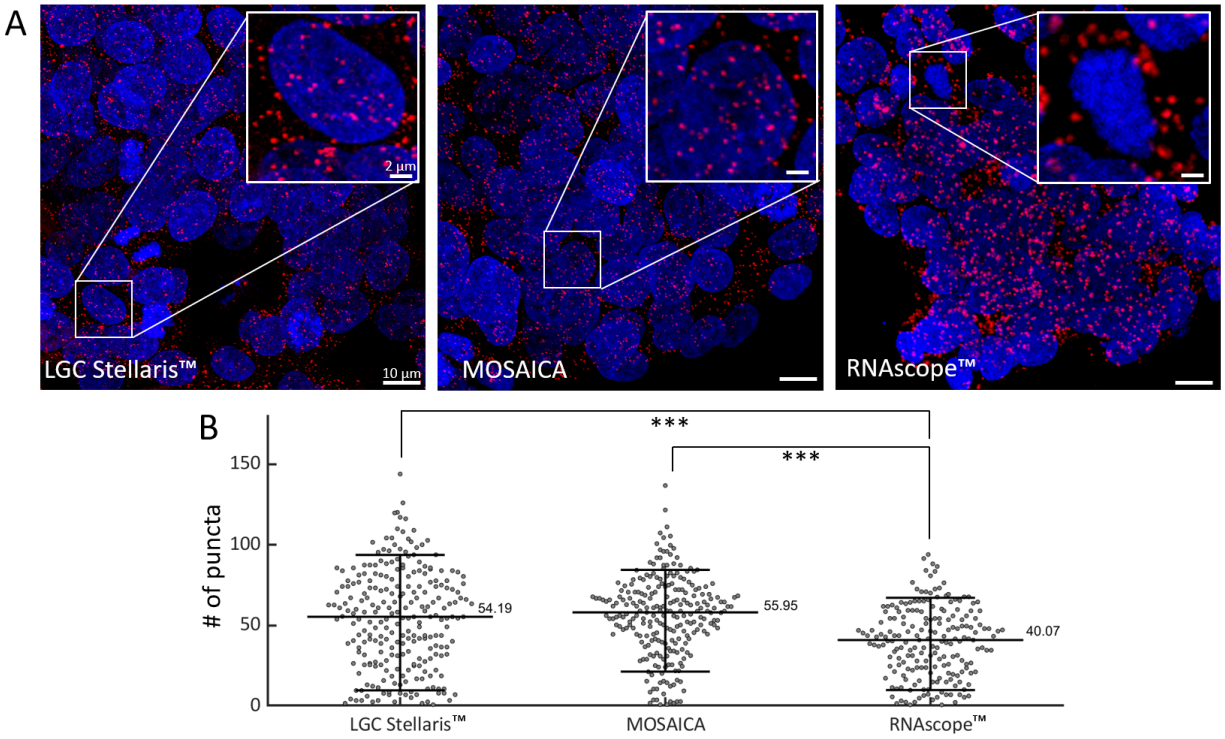
Supplementary Figure 2. Validation of probe hybridization in mNeonGreen cells. A) *Schematic of engineering of mNeonGreen HEK293T-X cells. Engineered mNeonGreen plasmids were transfected into HEK293T-X cells with FuGENE HD Transfection Reagent. Three days after transfection, the cells were then selected with Puromycin and Zeocin.* ***B)*** *Schematic and representative images of each condition. The primary probes were designed to be complementary to mNeonGreen transcripts. A dopachrome tautomerase (DCT) primary probe negative control, which uses primary probes targeting sequences not present in the mNeonGreen HEK-293T-X cells but can still bind to secondary fluorescent oligonucleotides, was used to indicate any nonspecific binding which can occur with primary probe labeling. A negative control where only secondary probes were added but no primary probes were added was used as a reference for nonspecific binding from secondary probes alone. For each condition, the concentration of each primary probe (14 in total) was 1 nM and the secondary probe was 5 nM. Scale bar = 10 µm.* ***C)*** *Plots to quantify the detected puncta per cell and signal-to-noise (SNR) ratio under different conditions. Left, scatter plot showing puncta number per cell (n=755 cells). Right, signal-to-noise ratio (SNR). SNR=each signal intensity/the mean of background noise (n=3,860 puncta).*



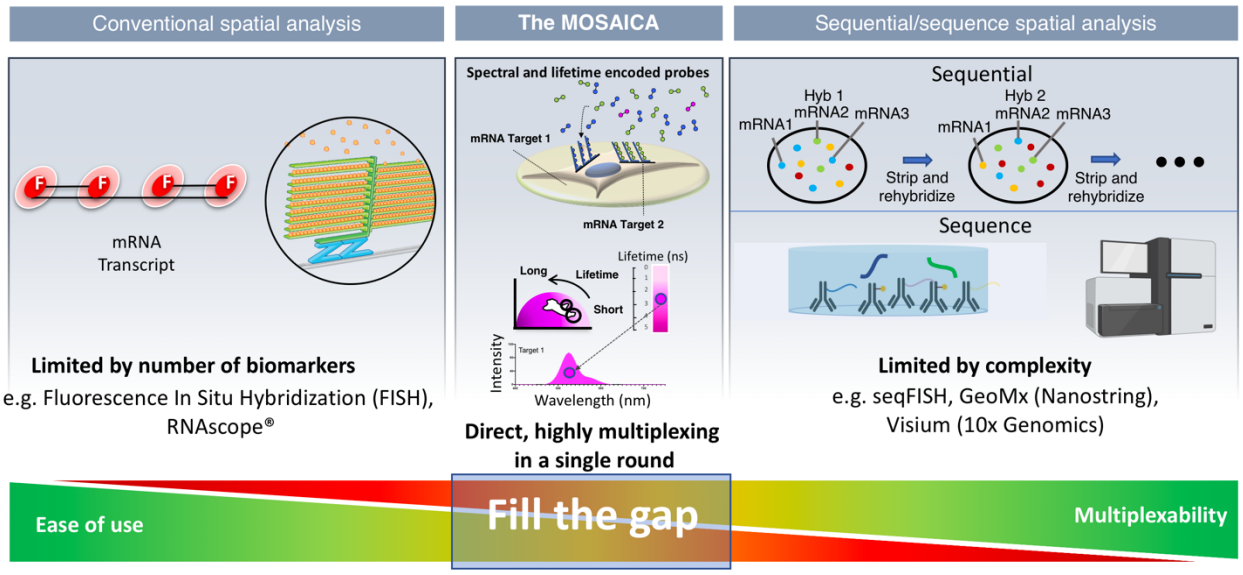
Supplementary Figure 3. Optimization parameters of in situ hybridization conditions. A) *Representative images of mNeonGreen cells with different numbers of primary probes. Conditions included 2, 4, 6, 8, 10, 12, and 14 mNeonGreen primary probes to the HEK293T-X mNeonGreen and WT model. The concentration of each primary probe is constant (5 nM). Scale bars are 10 µm.* ***B)*** *Intensity distribution of detected puncta shows the effects of the number of primary probes on signal intensity (total n ≈ 64k puncta).* ***C)*** *Representative images of mNeonGreen cells with different incubation time of probes. The primary probes hybridization incubation times consisted of 4, 8, and 16 hours. For secondary fluorophore probes, incubation times tested were 1, 2, and 4 hours. Scale bars are 10 µm.* ***D)*** *Intensity distribution of detected puncta as a function of incubation time. Top, primary probe incubation time (total n ≈ 26k puncta). Bottom, secondary probe incubation time (total n ≈ 20k puncta). Pairwise t-test resulted in p-values* $<10^4$ *for conditions marked with ****.*



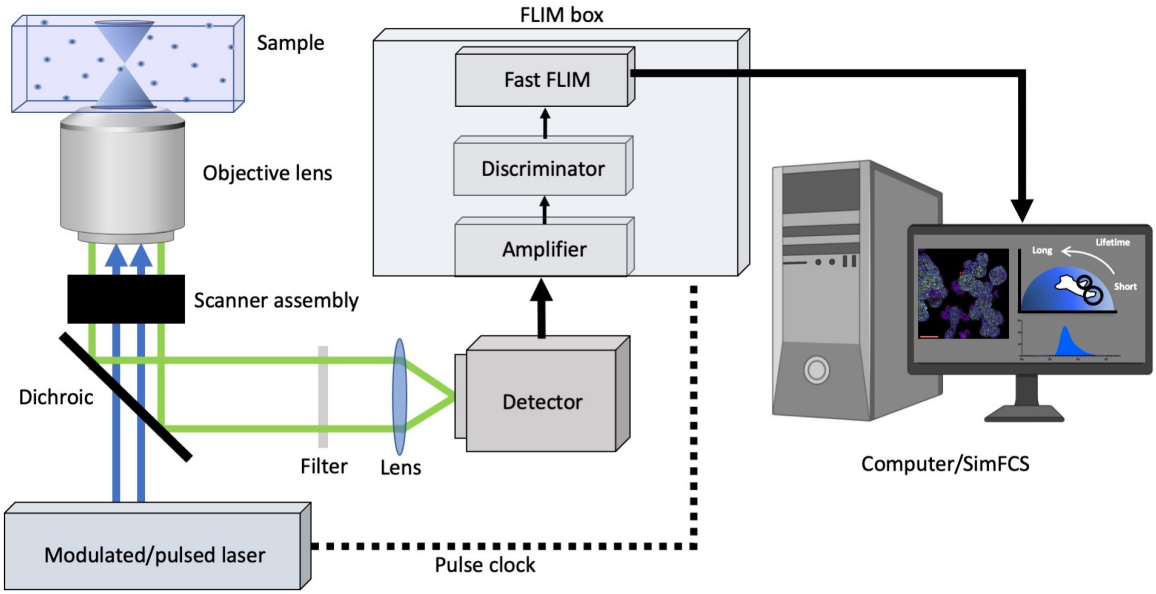
Supplementary Figure 4. Overlapping and inconsistent signal simulations. *Simulations are run at different densities to generate 3D image stacks and puncta are detected using our image processing pipeline.* ***A)*** *Recovered density by our system as a function of the true density for the limit considered puncta volumes (blue) and simulation trends (top trend for 1plex bottom trend for 10-plex).* ***B)*** *Percentage of recovered puncta for the 1plex (top trend, depicting ratio of underestimated due to overlap) and 10-plex (bottom trend, depicting ratio of inconsistent signal due to overlap), again between the limit considered puncta volumes (blue).* ***C,D)*** *Number of puncta assigned to a particular gene, undetermined puncta and overlapped puncta for the 10-plex experiment (Figure 4 in the paper) and 6-plex experiment (Figure 5 in the paper).*



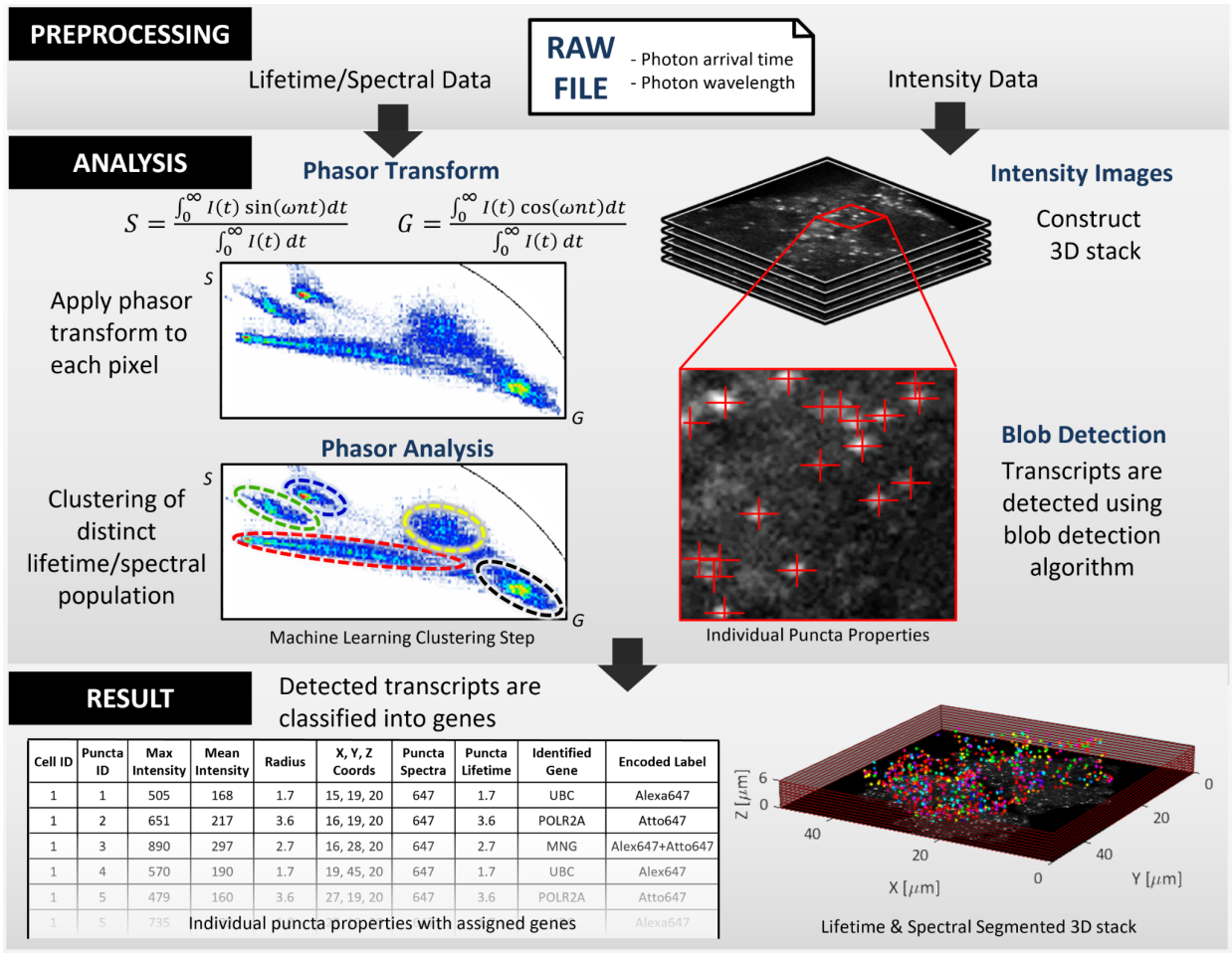
Supplementary Figure 5. *Benchmarking MOSAICA against RNAscope™ and LGC Stellaris™.* ***A)*** *POLR2A gene expression on colorectal cancer SW480 cells following RNAscope™, LGC Stellaris™ and MOSAICA protocols. Scale bars are 10μm.* ***B)*** *Puncta counts per cell volume between three platforms. MOSAICA exhibited comparable puncta per cell count compared to benchmark LGC Stellaris™, whereas RNAscope™ was undercount. Pairwise t-test against null hypothesis that values belong to distributions of equal means were p = 0.4 (LGC Stellaris™ vs MOSAICA), p = $3.4x10^{-4}$ (LGC Stellaris™ vs RNAscope™ and p = $7.8x10^{-4}$ (MOSAICA vs RNAscope™). A sliding volume of $3000μm^3$ was used throughout the image stacks and the number of puncta counts per volume was obtained. This number was then divided into the average number of cells per volume depending on the 3D segmentation of DAPI nuclei.*



Supplementary Figure 6. *Multiplexed spatial transcriptomics with MOSAICA, which is rapid, cost-effective, and easy-to-use, can fill a critical gap between conventional FISH and sequential- and sequencing-based techniques.*



Supplementary Figure 7. Generalized spectral-FLIM Microscopy setup*. A pulsed/modulated light source is used to illuminate the sample and the fluorescence of the sample is collected by a spectral detector (current resolution around 10 nm). The repetition rate can either be supplied by or delivered to the laser which is used by the electronics in the digital frequency domain to obtain a single photon arrival time using the heterodyne principle (current resolution around 50 ps)*



Cell ID	Puncta ID	Max Intensity	Mean Intensity	Radius	X, Y, Z Coords	Puncta Spectra	Puncta Lifetime	Identified Gene	Encoded Label
1	1	505	168	1.7	15, 19, 20	647	1.7	UBC	Alexa647
1	2	651	217	3.6	16, 19, 20	647	3.6	POLR2A	Atto647
1	3	890	297	2.7	16, 28, 20	647	2.7	MNG	Alex647+Atto647
1	4	570	190	1.7	19, 45, 20	647	1.7	UBC	Alex647
1	5	479	160	3.6	27, 19, 20	647	3.6	POLR2A	Atto647
1	5	735							Alexa647

Individual puncta properties with assigned genes

Supplementary Figure 8. Automated pipeline of the processing and analysis. *Raw data consists of a list of detected photons with their times of arrivals. Using the acquisition parameters, dwell time, number of pixels, number of repetitions per image etc. the image stacks are reconstructed. Knowing the laser frequency, a photon histogram for each voxel is built and the phasor transform is applied. The two custom made algorithms work in parallel, one identifying clusters in the phasor space, the other identifying puncta in the intensity space. The two then recombine to result in each transcript being identified, assigned to a particular gene and its morphological properties measured.*