Epigenome and transcriptome changes in *KMT2D*-related Kabuki syndrome Type 1 iPSCs, neuronal progenitors and cortical neurons

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ABSTRACT

Kabuki syndrome type 1 (KS1) is a neurodevelopmental disorder caused by loss-of-function variants in *KMT2D* which encodes a H3K4 methyltransferase. The mechanisms underlying neurodevelopmental problems in KS1 are still largely unknown. Here, we track the epigenome and transcriptome across three stages of neuronal differentiation using patient-derived induced pluripotent stem cells (iPSCs) to gain insights into the disease mechanism of KS1. In KS1 iPSCs we detected significantly lower levels of functional *KMT2D* transcript and KMT2D protein, and lower global H3K4me1 and H3K4me2 levels. We identify loss of thousands of H3K4me1 peaks in iPSCs, neuronal progenitors (NPs) and early cortical neurons (CNs) in KS1. We show that the number of lost peaks increase as differentiation progresses. We also identify hundreds of differentially expressed genes (DEGs) in iPSCs, NPs and CNs in KS1. In contrast with the epigenomic changes, the number of DEGs decrease as differentiation progresses. Our analysis reveals significant enrichment of differentially downregulated genes in areas containing putative enhancer regions with H3K4me1 loss. We also identify a set of distinct transcription factor binding sites in differentially methylated regions and a set of DEGs related to KS1 phenotypes. We find that genes regulated by SUZ12, a subunit of Polycomb Repressive complex 2, are over-represented in KS1 DEGs at early stages of differentiation. In conclusion, we present a disease-relevant human cellular model for KS1 that provides mechanistic insights for the disorder and could be used for high throughput drug screening for KS1.

INTRODUCTION

KMT2D encodes a trithorax-related histone 3 lysine 4 (H3K4) methyltransferase, which is part of the COMPASS complex that primarily binds to enhancer regions and maintains global levels of H3K4me1(1, 2). Mouse *Kmt2d* knockouts are embryonic lethal(3) and it is required for exit of mouse embryonic stem cells (ESCs) from the naive pluripotent state, but is dispensable for maintenance of cell-identity(4, 5). KMT2D is also crucial for the development of several organs including the brain(6, 7).

Rare mono-allelic *KMT2D* variants cause Kabuki syndrome (KS) Type 1 (KS1, OMIM#147920)(8, 9). KS type 2 is caused by rare hetero- or hemizygous variants in a H3K27 demethylase encoding *KDM6A* gene (OMIM#300867)(10, 11). KS1 is characterised by distinct facial dysmorphism, mild to moderate intellectual disability, developmental delay, a range of internal organ malformations (congenital heart defects, skeletal defects, cleft palate and genitourinary malformations) and systemic problems (endocrine disorders, deafness, immune defects)(12).

Current animal and cellular models for KS1 have provided valuable insights into the disease mechanisms(7, 13, 14). *Kmt2d* zebrafish morphants showing reduced hindbrain and midbrain size(6), and learning and memory impairment were reported in a *Kmt2d*$^{+/\beta Geo}$ murine model(7). Suppression of oxygen-responsive gene expression has been seen in induced pluripotent stem cells (iPSCs) derived from patients with nonsense *KMT2D* variants(15). Changes in locus-specific loss of gene expression were reported in KS1 iPSC models with truncating *KMT2D* variants(16). Of note, most studies have used models with null variants, even though ~10% KS1-causing variants are missense(17). Furthermore, most studies have used single cell types, thus our knowledge about the impact of KS1-causing *KMT2D* variants at different stages of differentiation is lacking.

Here, we track the epigenomic and transcriptional panorama across three stages of neuronal differentiation using patient-derived iPSCs to gain insights into disease mechanism of KS1. We show that in iPSCs, KS1 causing variants result in loss of KMT2D function and alter the H3K4me1 and transcriptional landscapes in a correlated manner. We show that epigenomic differences between KS1 and control cells increase with differentiation progression, but the transcriptional changes become less abundant. Our analysis also reveals a set of potential transcriptional regulators and their cis-regulatory elements, differentially expressed genes (DEGs) and master regulators that likely underpin the KS1 phenotypes.

RESULTS

KS1 causing variants result in loss of *KMT2D* function in iPSCs

IPSCs were generated either from fibroblasts in the HipSci program (www.hipsci.org/#/cells) or in house from fibroblasts or peripheral blood mononuclear cells and used three controls and three individuals

with molecularly confirmed KS1. Our cohort included one individual each with frameshift (NM_003482.4: *KMT2D*; c.5527dupA, p.(Pro1849Ter)), missense (c.16019G>A, p.(Arg5340Gln)), and nonsense (c.16180G>T, p.(Glu5394Ter)) variants (**Figure 1A** and **Supplementary Table 1**).

Firstly, to investigate the effect of KS1 variants at the pluripotent stem cell stage, we generated a merged iPSC RNAseq dataset of 53 control lines and 7 KS1 lines (4 replicates with the missense variant, 2 with the nonsense variant and one with the frameshift variant) (**Supplementary Figure S1**). Most disease causing *KMT2D* variants are predicted to result in haploinsufficiency but it has not been proven to the best of our knowledge(8). We, therefore, assessed the level of *KMT2D* mRNA using the merged RNAseq data. We did not observe significant difference in the total *KMT2D* mRNA level between controls and KS1 iPSCs (total *KMT2D* reads) (**Figure 1B** and **Supplementary Figure S2A**). However, quantification of reference and mutant *KMT2D* transcripts revealed that the reference *KMT2D* reads (REF) were significantly lower in all KS1 iPSCs compared to controls (**Figure 1B** and **Supplementary Figure S2B-C**). Interestingly, level of reference *KMT2D* reads (REF) in KS1 iPSCs was higher compared to reads with mutations (ALT) (**Figure 1B**). Furthermore, level of reads with missense variants was significantly higher compared to the reads with truncating variants, due to potential action of nonsense-mediated decay (**Figure 1B**).

Next, we performed Western blotting on nuclear protein extracts from iPSCs, which revealed a significant decrease in KMT2D protein level in nuclei of all KS1 iPSCs, including the one with the missense variant, compared to control iPSCs (**Figure 1C**). As KMT2D is a H3K4 methyltransferase, we quantified the total levels of H3K4me1, H3K4me2, and H3K4me3 histone marks in all three KS1 and control iPSCs by Western blotting. In all three lines, including in the one with the missense variant, we observed a significant decrease in the levels of H3K4me1 and H3K4me2 histone marks but not in H3K4me3 histone mark (**Figure 1D**). Next, we examined the DepMap portal (https://depmap.org/portal/) for the levels of 42 different histone marks in cancer cell lines with *KMT2D* mutations and compared to cell lines without *KMT2D* damaging mutations (**Supplementary Figure S3**). We found H3K4me1 and H2K4me2 levels to be most significantly reduced in cell lines with *KMT2D* mutations compared to cell lines without *KMT2D* mutations.

Next, we evaluated if loss of KMT2D function led to any changes in the molecular pluripotency state of KS1 iPSCs. In the merged RNAseq dataset, we did not find significant differences in the expression of key genes related to pluripotency in KS1 iPSCs compared to control iPSCs (**Figure 1E**). We validated these results by RTq-PCR and immunofluorescence staining for SOX2, NANOG and OCT4 (**Supplementary Figure S4**).

Overall, these data show that KS1-causing heterozygous *KMT2D* variants, including missense variants, are associated with loss of function that is reflected in significant decrease in levels of H3K4me1/me2. The loss of function resulting from KS1-causing heterozygous *KMT2D* variants does not result in major changes in pluripotency-associated gene expression.

H3K4me1 landscape is dysregulated in KS1 iPSCs

KMT2D is a major H3K4 mono-methyltransferase essential for enhancer activation during cell differentiation(1, 3). Since we observed a significant global decrease in H3K4me1 in our cell lines (**Figure 1D**), we decided to investigate the H3K4me1 landscape in KS1 in more detail. As limited studies have been conducted on KS1 animal or cellular models with missense variants, we performed H3K4me1 ChIPseq in one KS1 (c.16019G>A, p.(Arg5340Gln)) and one control iPSC line, both in triplicate. We detected 9,309 out of 205,973 peak sites to be significantly differentially methylated (FDR<0.05; $-1>\log_2 FC>1$). Of these, 8,146 sites (87.5% of all differentially methylated peak sites) showed loss, and 1,163 sites showed gain in the H3K4me1 peak signal (**Figure 2A-C**). H3K4me1 peak site losses were enriched in cell-type independent EpiMap annotated enhancer regions (fisher's test; p-value < $2.2e^{-16}$) (**Figure 2C** and **Supplementary Figure S5A** and **S6**).

To identify transcription factor binding sites predicted to be affected by changes in H3K4me1 levels, we performed motif analysis on significantly differentially methylated peak sites. This showed these sites to be significantly enriched for motifs predicted to be binding sites for Zinc Finger (ZNF) transcription factors family members, as well as the transcription factor WT1 (**Figure 2D**). Cell-type-independent enhancers with H3K4me1 loss were enriched for the WT1 transcription factor motif, while cell-type-independent promoters with H3K4me1 loss were enriched for the EGR1 motif (**Supplementary Figure S5B-C**). KS1 sites that gained H3K4me1 peaks showed significant enrichment for KLF1 transcription factor binding site (**Figure 2D**).

Overall, these data show significant dysregulation of the H3K4me1 landscape in KS1 iPSCs, especially in the enhancer regions.

The transcriptome is altered in KS1 iPSCs and is correlated with the H3K4me1 landscape

Altered H3K4me1 landscape is predicted to result in changes in the transcriptome. We, therefore, performed RNAseq on control and KS1 (c.16019G>A) iPSCs (**Supplementary Figure S7A**) and detected 909 significant DEGs (FDR<0.05, -1>Log2FC>1). Of these, 554 DEGs were downregulated while 355 were upregulated (**Figure 3A**). Gene Ontology (GO) overrepresentation analysis on the 909 DEGs detected biological categories related to organ morphogenesis and development, cell adhesion and actin and extracellular structure to be significantly overrepresented in DEGs (FDR<0.05) (**Figure 3B**). Notably, DEGs related to stem cell differentiation (*TBX2, TWIST1*), mesenchyme development (*GBX2, MEF2C*), negative regulation of locomotion (*ANGPT2, GREM1*), morphogenesis of an epithelium (*AJAP1, GDF7*) and regulation of neuron projection development (*POU3F2, NTRK2*) were upregulated while actin filament-based movement (*TNNC2*, *ACTA1*) and sensory perception of light stimulus (*TULP1*, *AIPL1*, *CRYBB1*) were downregulated (**Figure 3A**). GO categories for ear development (*TSHZ1*, *BMP5*), neuron projection (*GDF7*, *CNTN6*), sensory organ morphogenesis

161 (*DIO3*, *NTRK2*), embryonic organ development (*PAX5*, *KDR*) and heart morphogenesis (*SNAI2*, *PITX2*)
162 included both up and downregulated DEGs (**Figure 3A**).
163
164 Next, we performed transcription regulator enrichment analysis on DEGs. This revealed SUZ12, a
165 component of the Polycomb Repressive Complex 2 (PRC2), as the top regulatory factor among the
166 upregulated DEGs (adjusted p-value < 0.05) (**Table 1**).
167
168 Downregulation of several genes within a 110 Kb region on chromosome 19 was previously reported in
169 KS1 iPSCs suggesting locus-specific targeting of KMT2D (16). We, therefore, asked if any clusters of
170 DEGs were present in our dataset as well. We found significant enrichment of downregulated DEGs
171 located on chromosome 1, 16, 17 and 19 (hypergeometric test, FDR< 0.0001) (**Figure 3C** and
172 **Supplementary Figure S7C**). We also detected a region on chromosome 19, which overlaps with the
173 previously reported downregulated cluster at 19q13.33 (16).
174
175 Next, we asked if there was correlation between the altered H3K4me1 signals and gene expression in
176 our cell model. For this, we analysed expression of genes within ±100kb of differentially lost H3K4me1
177 regions. We found several regions of the genome with clusters of reduced H3K4me1 peaks and
178 downregulated genes with significant enrichment of downregulated DEGs on chromosome 1, 16, 17
179 (hypergeometric test, FDR < 0.0001) (**Figure 3C** and **Supplementary Figure S7C**). (**Figure 3C**). We
180 also found H3K4me1 and gene expression levels to be significantly correlated based on the ±100kb
181 distance between gene TSS and H3K4me1 peak (p-value < 0.05; hypergeometric test) (**Figure 3D** and
182 **Table 2**). Most of these genes correspond to areas near cell-type independent enhancer regions with
183 loss of H3K4me1 (**Supplementary Figure S7D**).
184
185 Overall, these data show that at the stem cell stage there are significant changes in expression of genes
186 related to the KS1 phenotype, which are over-represented by regions of DNA associated with SUZ12
187 recruitment.
188

189 The neuronal progenitor and neural epigenomes are altered in KS1

190 Having shown the epigenomic changes at the stem cells stage, we asked if similar changes could also
191 be present in differentiating cells. Learning difficulties are seen in 95% individuals and epilepsy is
192 present in 25% individuals affected by KS1(9, 18). We, therefore, differentiated the KS1 (c.16019G>A)
193 and control iPSCs into neuroepithelium after 10 days of SMAD signalling inhibition (19) giving rise to
194 neural rosettes (**Supplementary Figure S8A**) and later into early cortical neurons (Day 30) (**Figure 4A**
195 and **Supplementary Figure S9A**). After the formation of the rosettes, cells were enriched for
196 progenitors by FACs for a $CD44^{-}CD184^{+}CD24^{+}$ population at Day 18 and for neuronal cells by sorting
197 for a $CD44^{-}CD184^{-}CD24^{+}$ population at Day 30 (**Figure 4A**). Both control and KS1 cells expressed key
198 markers of neuronal progenitors such as *PAX6*, *FOXG1, SOX2, NES* and *OTX2*, and of neuronal cells
199 such as *TBR1, MAP2* and *GRIA2* (**Figure 4B**).
200

201 We performed H3K4me1 ChIPseq on sorted neural progenitors and neuronal cells. In neural
202 progenitors, we detected 22,975 differentially methylated sites (FDR<0.05; -1>Log2FC>1). Of these,
203 15,452 (67.2%) sites showed loss and 7,523 showed gain in H3K4me1 in KS1 cells (**Figure 4C-4E** and
204 **Supplementary Figure S8**). In neurons, we detected 25,858 differentially methylated sites (FDR<0.05;
205 -1>Log2FC>1). Of these, 21,586 sites showed loss in H3K4me1 and 4,272 showed gain in H3K4me1
206 (**Figure 4D-4F** and **Supplementary Figure S9**). Of the H3K4me1 peak site losses, 5,796 (37.5%) in
207 neural progenitor and 8,321 (38.5%) in neurons correspond to cell-type independent enhancer regions
208 (**Figure 4E-F** and **Supplementary Figure S6B-C**).
209
210 Motif analysis on neuronal progenitors revealed that the sites where H3K4me1 was lost in KS1 cells
211 were predicted to target for ZNF family of transcription factors as well as OTX, RARG and RFX5 while
212 sites where H3K4me1 was gained were predicted to be targets for IKZF1, KLF4, FOXO6, TFAP2C and
213 EWSR1-FLI1 (**Figure 4G**). ZNF460, PATZ1, PITX1 and ZKSCAN1 were found to be associated with
214 cell-type independent enhancers with H3K4me1 loss while ELF1, TFAP2C and KLF1 with cell-type
215 independent enhancers with H3K4me1 gain (**Supplementary Figure S8D**). In neuronal cells, loss of
216 H3K4me1 sites were predicted to be bound by ZNF transcription factor family members, BHLHA15,
217 KLF4, NFIC and ESRRA (**Figure 4H**). ZNF transcription factor family members, NEUROD1, ARGFX,
218 NFIB and NFIC motifs were found to be associated with cell-type independent enhancers with
219 H3K4me1 loss (ZNF was also found in cell-type independent promoters with H3K4me1 loss)
220 (**Supplementary Figure S9D-E**).
221
222 Next, we compared the significantly differentially methylated peaks across the three stages of neuronal
223 differentiation. We identified 88 H3K4me1 regions (74 losses and 14 gains) that were affected across
224 all stages in the KS1 lines (**Figure 4I**). Three hundred H3K4me1 loss peaks were maintained between
225 iPSC and neural progenitor stage and more than 700 between neural progenitor and neuronal cells
226 stage (hypergeometric test; p-value<0.0001) (**Figure 4I**).
227
228 Overall, in our KS1 model we witness increasing dysregulation of the H3K4me1 landscape with
229 advancing differentiation from iPSCs to neurons.
230

231 The transcriptome is altered in KS1 neuronal progenitors and neurons

232 Finally, we investigated the transcriptome of KS1 neuronal progenitors and neurons by RNAseq
233 (**Supplementary Figure S7B**). In neuronal progenitors, we detected 447 DEGs (FDR<0.05, -
234 1<LogFC>1). Of these, 264 DEGs were downregulated while 183 DEGs were upregulated in KS1
235 neuronal progenitors (**Figure 5A**). GO analysis on the 447 DEGs revealed biological categories related
236 to organ development, cell fate commitment and extracellular structure (FDR<0.05) (**Figure 5C**).
237 Notably, DEGs related to neuron projection guidance (*FEZ1*, *VANGL2*) and cilium organization (*CDK10*,
238 *DNALI1*) were downregulated whereas morphogenesis of epithelium (*AJAP1, IRX2*) and embryonic
239 organ development (*TBX1, EN2*) were upregulated. GO categories for urogenital system development
240 (*PAX8*, *AMH*), negative regulation of nervous system development (*INPP5F*, *SOX8*), and synapse

organisation (*SLC7A11*, *NTNG2*) were contributed by both up- and downregulated DEGs. In neuronal cells, we detected a lower number of DEGs with only 116 DEGs (FDR<0.05, -1>Log2FC>1) and 147 DEGs (FDR<0.1, -1>Log2FC>1) (**Figure 5B**). Of these, 31 (44; FDR<0.1) DEGs were downregulated while 85 (103; FDR<0.1) DEGs were upregulated (**Figure 5B**). GO analysis on the 147 DEGs (FDR<0.1) showed biological categories related to related to nerve development (*TBX1*, *NGFR, EMX1*) contributed by both up and down DEGs while GO categories related to pattern specification process (*HOXB2*, *HOXB3*, *BARX1*), autonomous nervous system development (*SOX10*, *TBX1*) were upregulated (**Figure 5D**).

Transcription factor enrichment analysis revealed SUZ12 as top regulatory factor for upregulated DEGs in neural progenitors (adjusted p-value < 0.05) (**Table 1**). SUZ12 was also the top most hit for neurons, although not statistically significant. Additionally, we found significant enrichment of downregulated DEGs located on chromosome 1, 16, 17 in neural progenitors and in 1 and 5 in neuronal cells (hypergeometric test, p-value < 0.0001) (**Supplementary Figure S10-11**).

Next, to analyse which changes in the transcriptome were in common at all three stages of neuronal differentiation, we compared DEGs between the three differentiation stages. Interestingly, we observed 50 significant DEGs (13 down- and 37 upregulated) in common across all three differentiation stages (**Figure 5E**). Intersection analysis showed most genes were significantly dysregulated between the iPSC and neural progenitor stage (exact test; p<0.0001).

To identify possible direct associations between H3K4me1 loss and downregulated genes across multiple stages of differentiation in our model, we extracted genes, which are downregulated and have transcription start sites within ±100kb of H3K4me1 loss. We identified 30 such genes in common between iPSC and neural progenitor stages, of which 4 (*CNTN4*, *NOVA2*, *GAS8* and *TRIM46*) are involved into axogenesis, neuronal projection guidance and microtubule formation (**Figure 5F**).

Overall, in our KS1 model we witness a decrease in the number of DEGs with advancing neuronal differentiation.

The altered KS1 transcriptome is consistent

Most of our neuronal differentiation work was based on a single missense mutant and we observed the biggest differences in the Day 0 and Day 18 transcriptomes (**Figure 5E**). We, therefore, decided to validate our results via RNAseq at Day 18 in neural progenitors from our original control and mutant lines, and in two additional controls and patient-derived iPSCs with distinct mutations (c.5527dupA, c.16180G>T). We found several up- and downregulated DEGs to follow the same gene expression trend (adjusted p-value<0.05; -1<Log2FC>1) (**Figure 5G**). Furthermore, 331/447 DEGs from our original Day 18 DEGs dataset (**Figure 5A**) have the same gene expression trend in KS1 samples as in the validation Day 18 DEGs dataset (Spearman correlation; rho = 0.61; p-value < 0.0001) (**Figure 5G**). Additionally, transcription factor enrichment analysis performed on the Day 18 validation dataset

281 confirmed SUZ12 as a key transcriptional regulator for upregulated DEGs reinforcing its main role in
282 gene regulation in KS1 (**Table 1**).
283
284 Overall, these results validate our findings in additional cell lines harbouring distinct *KMT2D* mutations.
285

286 ## DISCUSSION

287 Although the underlying disease mechanism of KS1 has been examined previously(7, 15, 16), several
288 questions about the pathological mechanism of the neurological issues in the disorder remain
289 unanswered. Here, we studied patient-derived iPSC models to interrogate the basis of neurological
290 phenotypes of KS1.
291
292 Firstly, haploinsufficiency has been the proposed mechanism for nonsense or frameshift variants in
293 KS1, but it has not been previously proven. We observed ALT:REF read ratios to be significantly lower
294 in iPSCs with nonsense or frameshift variants in comparison with the iPSCs with missense variants
295 (**Figure 1B**). This observation suggests partial nonsense mediated mRNA decay of the mutant
296 transcripts with premature termination codon. Interestingly, the absolute level of REF allele counts was
297 higher in iPSCs with nonsense or frameshift variants than the ones with missense variants, which is
298 likely explained by mRNA decay triggered transcriptional adaptation(20). The lower levels of reference
299 transcripts in mutant cells with nonsense or frameshift variants in comparison with the controls is also
300 reflected in the protein levels (**Figure 1C**). The KMT2D protein levels were also significantly lower in
301 iPSCs with the missense variant, even though the overall transcript levels in these lines were not
302 significantly different from controls. This indicates possibly reduced stability of the protein with the amino
303 acid substitution. The p.(Arg5340GIn) variant is located in the FYR-N motif which may alter the total
304 charge of the domain and/or the protein stability(21). It is possible that other KS1 causing missense
305 variants could cause loss of function through other mechanisms such as altered protein-protein or
306 protein-chromatin interactions or loss of enzyme activity or mislocalization. In contrast with a previous
307 report of decrease in H3K4me3 levels in a KS1 mouse model(7), but in line with the known role of
308 KMT2D as a H3K4 mono-methyltransferase(1, 3), we found a significant decrease in overall cellular
309 H3K4me1 levels at the iPSC stage (**Figure 1D**). This is also in line with the finding of analysis of 33
310 KS1 and 36 healthy controls' enhancer signatures related to H3K4me1 and H3K4me2 in peripheral
311 blood mononuclear cells of patients with KS1(14).
312
313 Our experiments also show dysregulation of H3K4me1 and transcriptome landscapes in KS1 iPSCs,
314 neuronal progenitors and neurons (**Figures 2-5**). The vast majority of differentially methylated
315 H3K4me1 peaks were losses, which is in line with the known role of KMT2D as a H3K4
316 methyltransferase(1, 2). Importantly, we find significant correlation between the H3K4me1 and
317 transcriptome dysregulation. This suggests that several of the downregulated DEGs are likely to be
318 direct consequences of loss of H3K4me1 rather than secondary to network disruption. We suspect that
319 these correlations in KS1 may be an underestimate as we only considered regions 100Kb up and
320 downstream of DEGs as well as H3K4me1 peaks with ±1 fold change for our analysis, which ignores

321 potential long-range enhancer activity and potential *trans*-acting effects of H3K4me1 deposition.
322 Furthermore, we observed 'large blocks of dysregulation' rather than it being evenly spread throughout
323 the genome suggesting that certain regions of the genome are more susceptible to loss of KMT2D.
324 Interestingly, with progress in differentiation, we observed an increase in loss of H3K4me1 peaks but
325 decrease in downregulated DEGs. This could reflect higher dependency of H3K4me1 regulation on
326 KMT2D at the pluripotent stage. Network level adaption could be an alternative explanation.
327
328 The analysis of transcription factor binding sites in our ChIPseq dataset revealed several transcription
329 factors that may be important in KS1 pathology **(Figures 2 and 4)**. KLF(22) and ZNF (23) family
330 transcription factors play crucial roles in cellular processes such as cell growth, differentiation,
331 apoptosis, and response to environmental stimuli. Wilms Tumour 1 (WT1) expression is required in
332 early kidney development and pathogenic mutations in *WT1* gene are associated with genitourinary
333 phenotypes(24) Estrogen-related receptors (ESRR) regulate genes involved in energy homeostasis,
334 including fat and glucose metabolism and mitochondrial biogenesis(25). Regulatory factor X-5 (RFX5)
335 is involved in regulation of major histocompatibility class II and *RFX5* mutations result in
336 immunodeficiency(26). IKAROS family zinc finger 1 (IKZF1) is involved in lymphocyte development and
337 pathogenic variants in IKZF1 are associated with immunodeficiency(27). OTX2 is critical for early
338 embryonic development, particularly in the development of the brain and sensory organs(28). The
339 effects of retinoic acid on gene expression is mediated by RARG, influencing various biological
340 processes, including development, differentiation, and homeostasis(29). FOXO6 is involved in
341 regulation of Hippo signalling during craniofacial development, with $FoxO6^{-/-}$ have facial overgrowth(27).
342 ETS variant (ETV) transcription factors are required for hippocampal dendrite development(30), while
343 TFAP2C is vital for early development, specifically in morphogenesis(31). Additionally, ETS protein can
344 regulate immune responses and the development of immune-related cells(32).
345
346 In our RNAseq datasets, we detected several DEGs important in lineage commitment and neuronal
347 differentiation (**Figures 3 and 5**). In particular, *PAX8,* important in tissue and organ formation
348 particularly in kidney, thyroid gland and brain(33), is upregulated in KS1 neural progenitor cells. *PAX5,*
349 involved in early neural tube development and regionalization(34), is also upregulated in KS1 iPSC and
350 neural progenitor cells. Its dysregulation in KS1 cells might affect the correct formation of the neural
351 tube, contributing to the KS1 intellectual disability phenotype. We also found SUZ12 to be a master
352 regulator of many of the upregulated DEGs in our datasets (**Table 1**). SUZ12 is a component of PRC2
353 required for the H3K27 tri-methylation mark(35). Further studies will be required to clarify the complex
354 relationships between the chromatin and transcriptional landscape in KS1.
355
356 In conclusion, these results establish heterozygous truncating or missense *KMT2D* variants cause KS1
357 through a loss of function mechanism and result in significant dysregulation of H3K4me1 and the
358 transcriptome landscape across different stages of neuronal differentiation. The H3K4me1 and
359 transcriptome landscapes of KS1 are correlated and their dysregulation seem to occur in discreet blocks

360 across the genome. With advancing differentiation from iPSCs to neurons, the dysregulation of
361 H3K4me1 landscape increase but the number of DEGs decrease.
362

363 MATERIAL AND METHODS

364 Generation, validation and culture of induced pluripotent stem cells

365 Skin biopsies and blood samples were obtained from individuals using standard procedures. Fibroblast
366 cells were cultured in DMEM, 10% foetal bovine serum, 1% L-glutamine at 37°C in a humidified 5%
367 CO_2 incubator. Fibroblast cells or peripheral blood mononuclear cells (for Ctrl 2) were reprogrammed
368 into iPSC by using Sendai viral vectors (CytoTuneTM −iPS 2.0 Sendai Reprogramming Kit-
369 ThermoFisher). Control iPSC (wigw2 - Ctrl 1) and KS1 iPSCs (ierp4 - iPSC 3, aask4 - iPSC 1, oadp4 -
370 iPSC 2) were generated by HipSci (https://www.hipsci.org/#/cohorts/kabuki-syndrome) while control
371 iPSCs (JF191b(36) - Ctrl 2, SW171a(37) - Ctrl 3) were generated in house under local ethics (REC
372 11/H1003/3; IRAS ID 64321 or REC 18/EE0250 IRAS246779). All were grown on Vitronectin N-terminal
373 fragmented (Life Technologies) coated dishes, using Essential 8 medium (StemCELL Technologies).
374 Cells were routinely passaged when 80% confluent using 0.1% EDTA-PBS without Ca^{2+} and Mg. All
375 cell lines were cultured at 37°C in a humidified 5% CO_2 incubator.
376

377 Neuronal differentiation

378 HiPSCs were differentiated to cortical neuron using a protocol adapted from Shi et al 2012(19). At the
379 start of the protocol, on Day 0, cells were plated on Matrigel (Corning) and cultured using E8 medium
380 (StemCell Technologies) supplemented with FGF2 (10ng/ml). On Day 1, neuronal differentiation was
381 undertaken using neuronal induction medium supplemented with SMAD signalling inhibitors, Noggin
382 (500ng/ml, Tocris) or Dorsomorphin (Abcam) and SB43154 (10uM, Tocris). On Day 10, cells were
383 passaged and plated on a poly-l-ornithine (Sigma) and murine laminin L2020 (20µg/ml, Sigma)
384 substrate for neuronal maintenance and maturation. On Day 12, small-elongated cells generate rosette
385 structures resembling early neural tubes which were propagated in culture using FGF2 (20ng/ml) for
386 about 3 days. On Day 18, cells were passaged using Dispase (StemCell Technologies), plated on a
387 poly-l-ornithine and laminin substrate for neuronal maturation and cultured up to Day 30.
388

389 Fluorescence-activated cell sorting (FACS)

390 Single cell suspensions from neural progenitor (Day 18) and neuronal (Day 30) culture were stained
391 and sorted with an Aria Fusion flow cytometer (BD Biosciences). Cells were blocked in PBS-5%FBS for
392 30 minutes and incubated with cell surface antibodies, CD44-PE (561858), CD24-FITC (560992) and
393 CD184-APC (560936) for 30 minutes at 4°C. After staining, cells were washed in PBS-5%FBS and
394 filtered through a 0.22 µm filter before sorting and acquisition. All antibodies used for staining were
395 purchased from BD Bioscience. Cells used for RNAseq and ChIPseq were sorted for $CD44^-$ $CD24^+$ and
396 $CD184^+$ for the progenitor stage at Day 18 and for $CD44^-$ $CD24^+$ and $CD184^-$ (BD Bioscience) for
397 neurons at Day 30.
398

399 ## Immunofluorescence staining

400 Cells grown in 12-well plates were fixed with 4% paraformaldehyde for 15 minutes at room temperature.
401 Samples were permeabilised with 0.5% Triton X-100 in PBS for 10 minutes at room temperature. Then
402 blocking solution (1% BSA in PBS) was applied for 10 minutes at room temperature. Blocking solution
403 was removed and an antibody recognising one of NANOG, OCT4, or SOX2 (4903S, 2890S, 3579S,
404 Life Technologies) was applied overnight at 4°C. After washing three times with PBS, cells were
405 incubated with secondary antibodies of Alexa FluorTM 488 goat anti-rabbit (A11008, Invitrogen) for 45
406 minutes at room temperature in the dark. After washing three times with PBS, samples were stained
407 with DAPI (4083S, Cell signalling technology) for 5 minutes. Finally, samples were washed with PBS.
408 Pictures were taken using an epifluorescence microscope (Olympus U-LH100HG) and cellSens
409 software. Images are representative of three independent experiments.
410

411 ## Western blot

412 Nuclear protein samples were isolated from iPSCs using NE-NER™ Nuclear and Cytoplasmic
413 Extraction Reagents (ThermoFisher Scientific, Cat#: XJ355181). Then protein samples were quantified
414 using BCA™ protein assay kit- reducing agent compatible (ThermoFisher Scientific, Cat#: 23250).
415 Electrophoresis was carried out using 10% Bis-Tris Gels and NuPAGE MES SDS Running Buffers
416 (Invitrogen) or 3~8% Tris-Acetate Gels (Invitrogen) and Tris-Acetate SDS Running Buffer (Life
417 Technologies) for KMT2D. Twenty to forty µg of nuclear protein extracts were loaded into the
418 polyacrylamide gel and electrophoresed for 45-60 minutes at 120V. Gels were blotted onto
419 nitrocellulose membranes using Mini iBlot Gel Transfer Stacks Nitrocellulose (Invitrogen) for H3K4me1,
420 me2 and me3, or wet transferred at 200mA over night at 4°C using transfer buffer (pH 8.3) contained
421 glycine, tris base, sodium dodecyl sulfate, methanol and water. After blocking non-specific binding, the
422 membranes were incubated with specific anti-H3K4me1 (ab8895, Abcam), anti-H3K4me2 (C15410035,
423 Diagenode), anti-H3K4me3 (ab8580, Abcam), anti-KMT2D (ab213721, Abcam), and anti-HSP90
424 (4874S, Cell Signalling) overnight at 4°C. Then, the membrane was incubated with a secondary
425 fluorescent labelled goat anti-rabbit antibody (IRDye 800CW LiCor) and the signal was developed using
426 an Odyssey M imaging machine. Images were analysed using ImageJ by measuring the integrated
427 density of the bands. Three experimental replicates were performed.
428

429 ## Gene expression analysis

430 Cells were collected by centrifugation and total RNAs were extracted using RNeasy Mini kit (Qiagen)
431 according to the manufacturer's protocol. RNA concentration was measured using a NanoDrop 2000
432 spectrophotometer (Thermo Scientific). One µg of RNA was reverse transcribed with random hexamers
433 primer (Promega) to generate cDNA using the M-MLV Reverse Transcriptase kit (Promega), according
434 to manufacturer's protocol. Quantitative real-time PCR (qRT-PCR) reactions were performed in
435 triplicate on a Bio-Rad CFX394 Real Time system (Bio-Rad) using Power SYBR Green PCR Master
436 mix (Applied Biosystems). For each sample, 2 µl cDNA (2 ng/µl) was incubated in a final volume of 10
437 µl with 5 µl of Power SYBR Green PCR Master mix (Applied Biosystems) and 0.5 µl of both the forward
438 and reverse target-specific primer (10 µM, Sigma). The expression of each target gene was evaluated

439 using a relative quantification approach ($2^{-\Delta CT}$ method) with GAPDH as the internal reference for human
440 genes.
441

442 RNA sequencing and analysis

443 RNAs were extracted using RNeasy Mini kit (Qiagen) according to the manufacturer's protocol. Library
444 preparation was performed by the Genomic technologies core facility at the University of Manchester.
445 Samples were sequenced using NextSeq500 (Dataset 1 – DS1, Dataset 3 – DS3) or Illumina HiSeq
446 2000 sequencer (Dataset 2 from HipSci consortium – DS2). Unmapped paired reads were output in
447 BCL format and converted to FASTQ format using bcl2fastq v2.17.1.14. Prior to the alignment, RNAseq
448 reads were trimmed to remove any adapter or poor-quality reads using Trimmomatic v0.36 with options:
449 "ILLUMINACLIP:Truseq3-PE-2_Nextera-PE.fa:2:30:10 SLIDINGWINDOW:4:20 MINLEN:35"(38). The
450 filtered reads were mapped to the human reference genome (hg19/GRCh37) with comprehensive
451 Gencode v19 genome annotation using STAR v2.5.3a with default options(39). Duplicate reads were
452 marked using Samtools 1.9(40) and sorted by name. Reads were attributed to genes using
453 FeatureCounts tool in Subread v2.0.0(41) in paired-end mode. Prior to the differential gene expression
454 analysis, genes which have less than 10 reads in >3 samples were filtered out, as well as genes on sex
455 chromosomes. Differential gene expression analysis was performed using DESeq2 v1.40.2 using Wald
456 test with Benjamini Hochberg p value adjustment (p adjusted<0.05). EdgeR was used to calculate
457 counts per million. GO over-representation analysis was performed using WebGestalt tool (2019
458 version). EnrichR(42, 43) was used for transcription regulator enrichment analysis. PEGS(44) tool was
459 used to calculate enrichment of differentially expressed genes adjacent to differential ChIP-Seq
460 H3K4me1 peaks. Statistical analysis of overlap of differentially expressed genes across timepoints was
461 performed using SuperExactTest package within R v4.3.1. To assess clustering of DEGs in a statistical
462 manner, we performed hypergeometric test for over-enrichment of DEGs in 10Mb genomic bins across
463 autosomes (excluding patches, haplotypes and undefined contigs).
464 For validation heatmap generation and gene-based Z-score transformation of RNASeq count data
465 pheatmap package within R v4.3.1 was used. Separate DGE analysis was performed for validation
466 dataset 3 (-1<Log2 FC>1, adjusted p-value <0.05). Then DEGs from Dataset 1 were intersected with
467 DEGs from validation Dataset 2 or 3 and plot them in a heatmap representation.
468

469 Chromatin Immunoprecipitation Sequencing and Analysis

470 ChIPseq has been performed using the True MicroChIP kit from Diagenode following the
471 manufacturer's protocol. Briefly, cells were collected and DNA-protein was cross-linked using 36.5%
472 formaldehyde. Then cells were lysed and chromatin was sheared by sonication (Bioruptor NextGen).
473 Sheared chromatin was incubated with H3K4me1 Antibody (5326, Cell signalling) overnight at 4°C.
474 Library preparation was performed by the Genomic technologies core facility at the University of
475 Manchester.
476 Unmapped paired-end sequences from an Illumina HiSeq4000 sequencer were output in BCL format
477 and converted to FASTQ format using bcl2fastq v2.20.0.422, during which adapter sequences were
478 removed. Unmapped paired-reads of 76 bp were interrogated using a quality control pipeline consisting

479 of FastQC v0.11.3 (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and FastQ Screen
480 v0.9.2(45). Prior to the alignment, reads were trimmed to remove any adapter or poor-quality sequence
481 using Trimmomatic v0.36(38), and truncated at a sliding 4bp window, starting 5', with a mean quality
482 <Q20, then removed if the final length was less than 35bp. The filtered paired-reads were mapped to
483 the human reference sequence analysis set (hg19/GRCh37) from the UCSC browser, using Bowtie2
484 v2.3.0(46). Mapped reads were then filtered using Samtools v0.1.19 to retain only high-confidence
485 concordant pairs (-f 2 -q30), followed by the removal of reads mapping to the mitochondrial genome
486 and to unassembled parts of the reference genome. Peak calling was performed using MACS2
487 v2.1.2(47) using the parameters ' --format BAMPE --gsize hs --keep-dup 1 --bdg --SPMR --qvalue 0.05'.
488 Candidate regions were further filtered by fold enrichment score. Differential binding analysis was run
489 on peaks which were found in at least 2 samples using DiffBind v2.10.0 on R v4.3.1
490 (http://bioconductor.org/packages/release/bioc/vignettes/DiffBind/inst/doc/DiffBind.pdf(48) and R Core
491 Team 2023). The input was the binding region coordinates and associated q-values from MACS2, and
492 mapped reads for each sample. Differential binding analysis was performed based on the comparison
493 of KS1 versus control samples with Benjamini-Hochberg adjusted p-value threshold of 0.05.
494 Bedtools(49) intersect tools was used to intersect enhancer regions from EpiMap repository(50) based
495 on iPSC DF19.11, BSS01370 Neural Progenitor or BSS01366 Neural cells with H3K4me1 regions from
496 ChIP-Seq analysis with minimum intersect ratio of 0.5 in relation to enhancer region. Deeptools
497 v3.4.3(51) was used to compare the distribution and intensity of H3K4me1 peaks across samples in
498 different genomic regions. BamCompare was used to subtract ChIP input reads from each sample,
499 whilst being simultaneously normalised to bins per million (BPM) with bin size of 20. ComputeMatrix
500 created a matrix of reads for the normalised reads of each sample relative to the sites of interest used
501 for visualisation, which was then passed to plotHeatmap for visualisation of read distribution within
502 regions of interest. HOMER software was used for annotation of peaks(52).
503 Analysis of ChIP-seq data between different cell time points was performed using ChIPpeakAnno
504 v3.36.0 package within R v4.3.1.
505 For motif analysis, unique peak summits from samples within differential H3K4me1 regions were
506 extracted using Bedtools(49) intersect. Flanking regions of ±250bp were added to the peak summits
507 (Bedtools(49) slop) and fasta sequences within those regions were extracted using Bedtools(49)
508 getfasta. MEME-TomTom within MEME-ChIP was used to search JASPAR CORE(53) vertebrates,
509 UniProbe Mouse(54) and Jolma 2013 Human and Mouse databases(55) for enriched motifs within
510 differential H3K4me1 regions.
511

512 **Statistical analysis**

513 Two-tailed T-test was performed to analyse the differences in mean expression values of KMT2D and
514 intensity of H3K4me1/2/3. Hypergeometric test was performed to assess over-representation of DEGs
515 per chromosome and per chromosomal bins. Two-tailed Fisher's test was performed to analyse the
516 association of H3K4me1 loss within the enhancer regions. Spearman correlation test was performed to
517 compare correlation of Log2 Fold Changes of DEGs from Dataset 1 Neural Progenitors and Log 2 Fold
518 Changes calculated from Dataset 3 Neural Progenitors.

ACKNOWLEGMENTS

We thank KS1 individuals and their families for providing the samples. We acknowledge the support of Great Ormond Street Hospital Charity (V4621), Newlife Charity (Grant reference 16-17/10), Manchester University Hospitals NHS Foundation Trust Kabuki Research Fund no. 629396, the NIHR Manchester Biomedical Research Centre (NIHR203308), and the MRC Epigenomics of Rare Diseases Node (MR/Y008170/1). We also thank Julieta O'Flaherty and Steven Woods for the control iPSCs (JF191b(36), SW171a(37)) and the Genomic Technologies Core Facility at the University of Manchester for RNA and ChIP library preparation and sequencing. This study makes use of control and KS1 iPSCs and RNAseq data generated by the HipSci consortium (www.hipsci.org), funded by The Wellcome Trust and the MRC.

FIGURE LEGENDS

Figure 1. Analysis of KMT2D expression in KS1 iPSCs.

A) Schematic representation of *KMT2D* exons and protein domains and regions with the different *KMT2D* variants highlighted in light pink, dark pink and red for missense, nonsense and frameshift mutations, respectively. (Dataset 1: DS1; Dataset 2: DS2). **B)** Log counts per million (CPM+1) mapped reads for *KMT2D* transcript detected in the integrated RNAseq analysis. REF shows reads with reference – no mutation (light blue; ***p<0.0001, *p<0.05) and ALT shows reads with mutation (pink/red). **C)** Western blot for KMT2D and scatter plot showing KMT2D quantification relative to loading control, HSP90 (n=3; * p<0.05). **D)** Representative image for Western blots for H3K4me1, H3K4me2 and H3K4me3 and scatter plots showing their quantification relative to loading control, HSP90 (n=3; *p<0.05). **E)** Log counts per million (CPM+1) mapped reads for pluripotency related transcripts detected in the integrated RNAseq analysis.

Figure 2. Loss of H3K4me1 in KS1 iPSCs.

A) Heatmap of H3K4me1 peaks (subset of consensus regions 20,000 out of 205,973; black), H3K4me1 loss regions (n=8146; blue), and H3K4me1 gain regions (n=1163; red). **B)** Volcano plot showing loss (blue) and gain (red) in H3K4me1. **C)** Bar graph showing number of H3K4me1 peaks in relation to enhancer and promoter regions for total, loss and gain in mono-methylation. **D)** Top TF motifs predicted in differential H3K4me1 peaks (loss and gain of H3K4me1 in binding regions) between KS1 and control.

Figure 3. Correlation between changes in transcripts and H3K4me1 in KS1 iPSCs.

A) Volcano plot showing down and up regulated genes on autosomal chromosomes in KS1 compared to controls (adjp<0.05, -1>log2FC>1). Genes highlighted are related to the GO categories in blue and red. Top 3 genes with highest or lowest log2FC are highlighted by black text. **B)** WebGestalt was performed on DEGs (adjp < 0.05; -1>log2FC>1) between KS1 iPSC and control iPSC. Gene ontology categories for biological processes are shown in the bar graphs (FDR<0.05). Red bars correspond to

558 up DEGs, blue to down DEGs and red and blue to both. **C)** Karyoplot showing up (red) and down (blue)
559 DEGs on each chromosome. Lime-green regions represent 100Kb up and downstream regions within
560 H3K4me1 loss. Different grey colours represent the different G band staining and red represents
561 centromere. Blue lines above chromosomes represent regions of enrichment of downregulated DEGs
562 and red lines for upregulated DEGs (FDR < 0.05; hypergeometric test) **D)** Scatter plot showing change
563 in expression and change in H3K4me1 within ±100kb of DEGs.
564

565 **Figure 4. Loss of H3K4me1 in KS1 neural progenitors and neurons.**

566 **A)** Schematic representation of the neuronal differentiation protocol **B)** RNAseq analysis showing
567 transcript level for key neural progenitor markers in control and KS1 samples at stem cell, progenitor
568 and neuronal stages. **C-D)** Line graph of H3K4me1 peaks (black), H3K4me1 loss regions (blue), and
569 H3K4me1 gain regions (red) for neuronal progenitors and neurons. **E-F)** Bar graph showing number of
570 H3K4me1 peaks in relation to enhancer and promoter regions for total, loss and gain in mono-
571 methylation. **G-H)** Top TF motifs predicted in differential H3K4me1 peaks (loss and gain of H3K4me1
572 in binding regions) between KS1 and control. **I)** Intersection analysis showing H3K4me1 peaks in
573 common between iPSC, Progenitor and Neurons (hypergeometric test; ****p<0.0001) between KS1
574 (c.16019G>A) and control.
575

576 **Figure 5. Changes in the transcriptome in KS1 neural progenitors and neurons**
577 **and comparison of transcriptomic and epigenomic changes during neuronal**
578 **differentiation.**

579 **A-B)** Volcano plot showing down and up regulated genes on autosomal chromosomes in KS1 compared
580 to controls (adjp<0.05, -1>log2FC>1 in red/blue; adjp<0.1, -1>log2FC>1 in light-red/light-blue). Top 3
581 genes with highest or lowest log2FC are highlighted in black. **C-D)** WebGestalt was performed on DEGs
582 (adjp<0.1, -1>log2FC>1) between KS1 and control in neuronal progenitor and neuronal cells. Gene
583 ontology categories for biological processes are shown in the bar graphs (FDR<0.1) Red bars
584 correspond to upregulated (up) DEGs, blue to downregulated (down) DEGs and red and blue to both.
585 **E)** Intersection analysis showing DEGs in common between iPSC, progenitor and neurons between
586 KS1 (c.16019G>A) and control (exact test; ****p<0.0001). **F)** Intersection analysis showing Down DEGs
587 and H3K4me1 loss peaks in common between iPSC, progenitor and neurons between KS1
588 (c.16019G>A) and control. **G)** Comparison of Log2 Fold Changes of DEGs from the original dataset
589 (DS1) and validation dataset (DS3) at progenitor stage (Day18). Genes within Gene Ontology
590 categories are highlighted in blue and red. Top 3 genes with highest or lowest log2FC are highlighted
591 in black.
592

TABLES

Table 1. Consensus Transcription factor (TF) analysis.

CHEA and ENCODE consensus transcription factor (TF) analysis for upregulated (UP), downregulated (DOWN) and both up and downregulated (UP and DOWN) DEGs (adjp<0.05) at the three different differentiation stages and in the validation dataset.

Table 2. Hypergeometric analysis of gene-peak associations across different genomic distances.

A) Association of DEGs and differential H3K4me1 peaks in iPSCs. **B)** Association of DEGs and differential H3K4me1 peaks in Neural Progenitors. **C)** Association of DEGs and differential H3K4me1 peaks in Neurons. Associations with p-value < 0.05 of downregulated DEGs and loss of H3K4me1 are in blue, and associations with p-value < 0.05 of upregulated DEGs and gain of H3K4me1 are in red.

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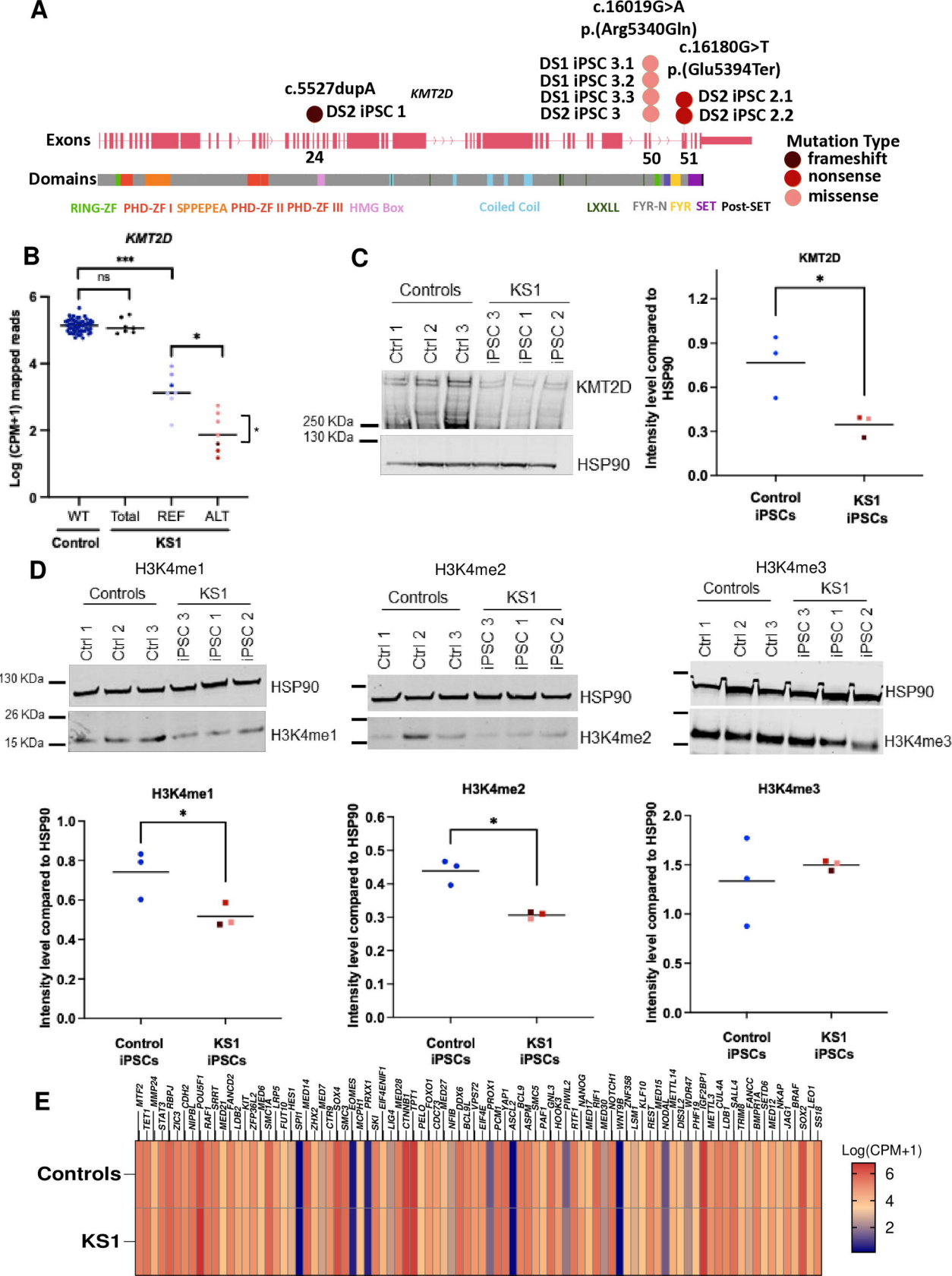
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c.16019G>A
p.(Arg5340Gln)
c.16180G>T
p.(Glu5394Ter)
DS1 iPSC 3.1
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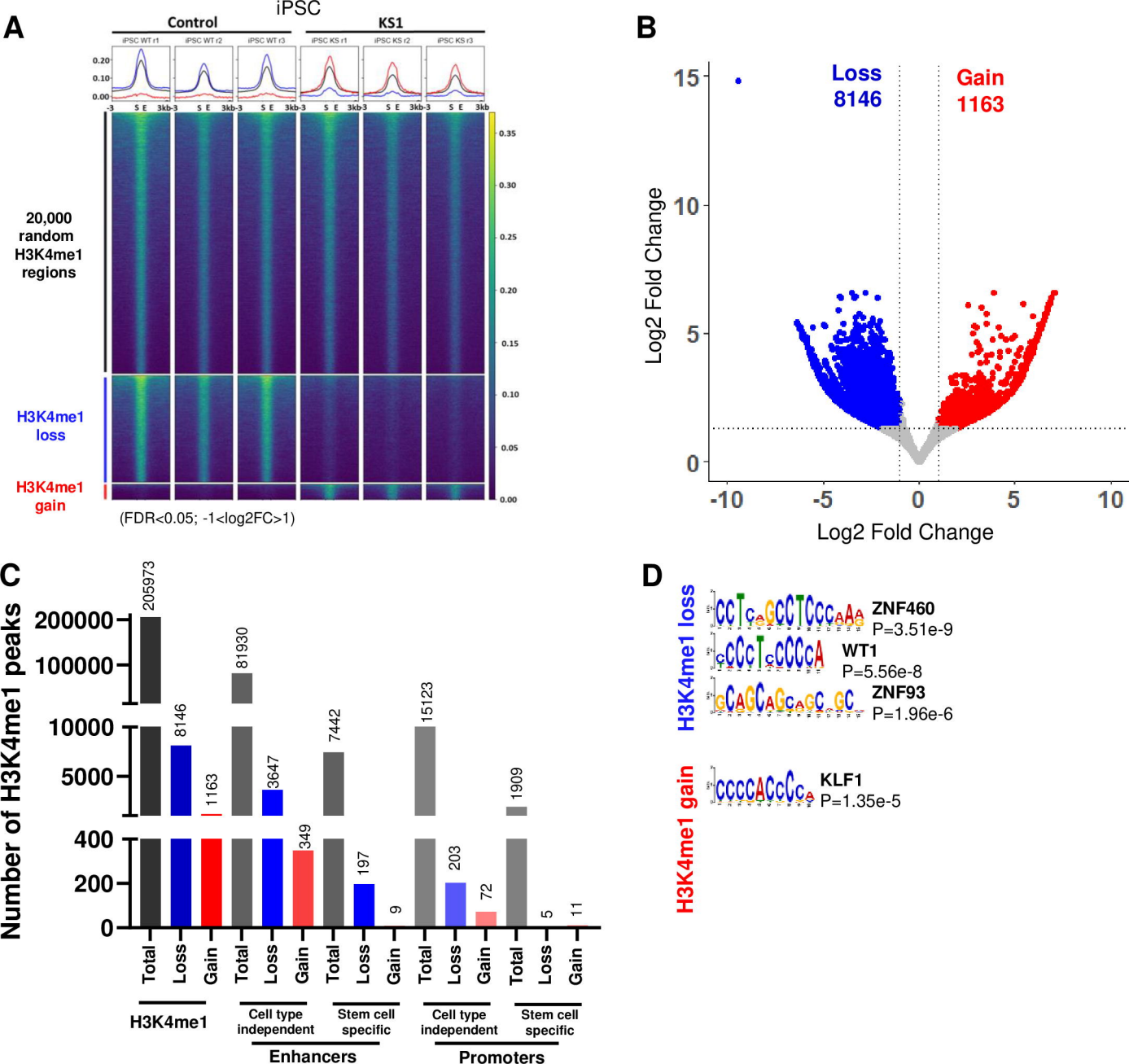
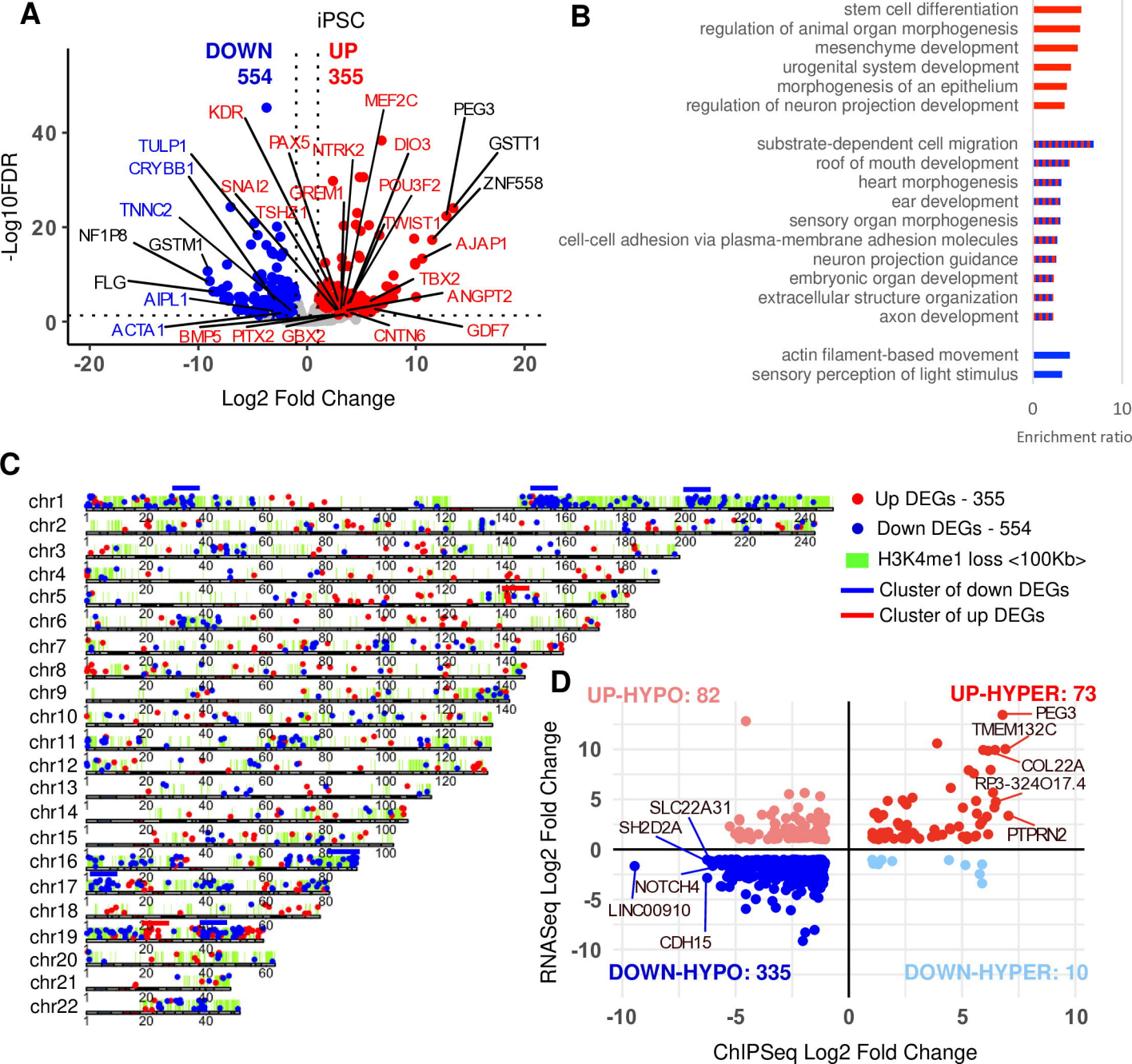
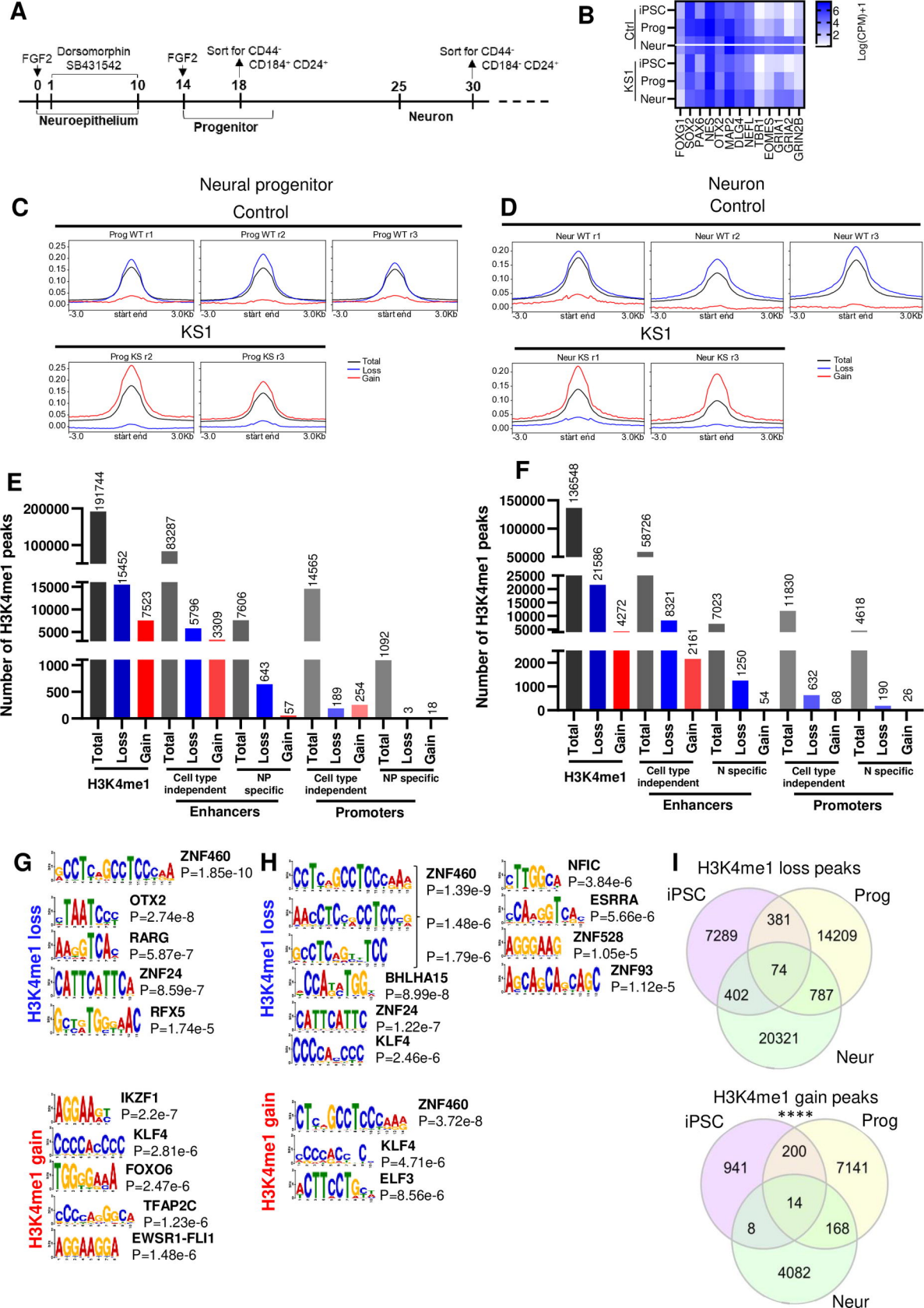
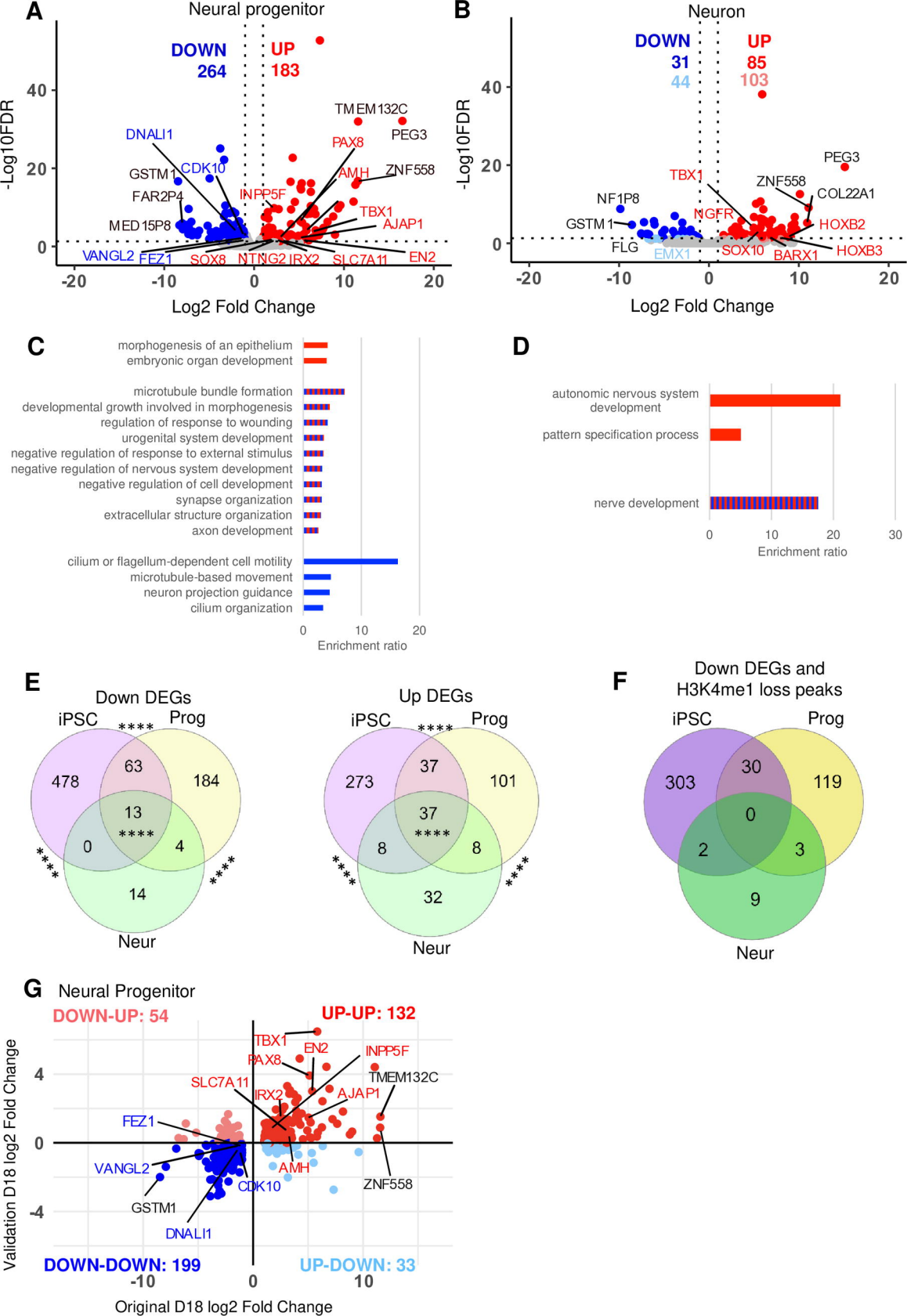
DS1 iPSC 3
DS2 iPSC 2.1
DS2 iPSC 2.2
c.5527dupA
DS2 iPSC 1
KMT2D
Exons
24
50
51
Domains
Mutation Type
frameshift
nonsense
missense
RING-ZF PHD-ZF I SPPEPEA PHD-ZF II PHD-ZF III HMG Box
Coiled Coil
LXXLL FYR-N FYR SET Post-SET
B
KMT2D
Log (CPM+1) mapped reads
WT
Total
REF
ALT
Control
KS1
C
Controls
KS1
Ctrl 1
Ctrl 2
Ctrl 3
iPSC 3
iPSC 1
iPSC 2
KMT2D
HSP90
250 KDa
130 KDa
Intensity level compared to HSP90
Control iPSCs
KS1 iPSCs
D
H3K4me1
H3K4me2
H3K4me3
130 KDa
26 KDa
15 KDa
E
Controls
KS1
Log(CPM+1)


A
iPSC
Control
KS1
iPSC WT r1
iPSC WT r2
iPSC WT r3
iPSC KS r1
iPSC KS r2
iPSC KS r3
20,000 random H3K4me1 regions
H3K4me1 loss
H3K4me1 gain
(FDR<0.05; -1<log2FC>1)
B
Loss 8146
Gain 1163
Log2 Fold Change
Log2 Fold Change
C
Number of H3K4me1 peaks
205973
8146
1163
81930
3647
349
7442
197
9
15123
203
72
1909
5
11
Total
Loss
Gain
H3K4me1
Cell type independent
Stem cell specific
Enhancers
Promoters
D
H3K4me1 loss
ZNF460
P=3.51e-9
WT1
P=5.56e-8
ZNF93
P=1.96e-6
H3K4me1 gain
KLF1
P=1.35e-5


A
iPSC
DOWN
554
UP
355
KDR
MEF2C
PEG3
TULP1
PAX5
NTRK2
DIO3
GSTT1
CRYBB1
SNAI2
GREM1
POU3F2
ZNF558
TNNC2
TSHZ1
TWIST1
NF1P8
GSTM1
AJAP1
FLG
TBX2
AIPL1
ANGPT2
ACTA1
BMP5
PITX2
GBX2
CNTN6
GDF7
-Log10FDR
Log2 Fold Change
B
stem cell differentiation
regulation of animal organ morphogenesis
mesenchyme development
urogenital system development
morphogenesis of an epithelium
regulation of neuron projection development
substrate-dependent cell migration
roof of mouth development
heart morphogenesis
ear development
sensory organ morphogenesis
cell-cell adhesion via plasma-membrane adhesion molecules
neuron projection guidance
embryonic organ development
extracellular structure organization
axon development
actin filament-based movement
sensory perception of light stimulus
Enrichment ratio
C
Up DEGs - 355
Down DEGs - 554
H3K4me1 loss <100Kb>
Cluster of down DEGs
Cluster of up DEGs
D
UP-HYPO: 82
UP-HYPER: 73
PEG3
TMEM132C
COL22A
RP3-324O17.4
PTPRN2
SLC22A31
SH2D2A
NOTCH4
LINC00910
CDH15
DOWN-HYPO: 335
DOWN-HYPER: 10
RNASeq Log2 Fold Change
ChIPSeq Log2 Fold Change


A
FGF2
Dorsomorphin
SB431542
FGF2
Sort for CD44⁻ CD184⁺ CD24⁺
Sort for CD44⁻ CD184⁻ CD24⁺
0 1 10 14 18 25 30
Neuroepithelium
Progenitor
Neuron
B
Ctrl
KS1
iPSC
Prog
Neur
Log(CPM)+1
FOXG1 SOX2 PAX6 NES OTX2 MAP2 DLG4 NEFL TBR1 EOMES GRIA1 GRIA2 GRIN2B
Neural progenitor
Neuron
C
Control
KS1
Prog WT r1
Prog WT r2
Prog WT r3
Prog KS r2
Prog KS r3
start end
Total
Loss
Gain
D
Control
KS1
Neur WT r1
Neur WT r2
Neur WT r3
Neur KS r1
Neur KS r3
E
Number of H3K4me1 peaks
191744 15452 7523 83287 5796 3309 7606 643 57 14565 189 254 1092 3 18
Total Loss Gain Total Loss Gain Total Loss Gain Total Loss Gain Total Loss Gain
H3K4me1
Cell type independent
NP specific
Cell type independent
NP specific
Enhancers
Promoters
F
Number of H3K4me1 peaks
136548 21586 4272 58726 8321 2161 7023 1250 54 11830 632 68 4618 190 26
Total Loss Gain Total Loss Gain Total Loss Gain Total Loss Gain Total Loss Gain
H3K4me1
Cell type independent
N specific
Cell type independent
N specific
Enhancers
Promoters
G
H3K4me1 loss
ZNF460 P=1.85e-10
OTX2 P=2.74e-8
RARG P=5.87e-7
ZNF24 P=8.59e-7
RFX5 P=1.74e-5
H3K4me1 gain
IKZF1 P=2.2e-7
KLF4 P=2.81e-6
FOXO6 P=2.47e-6
TFAP2C P=1.23e-6
EWSR1-FLI1 P=1.48e-6
H
H3K4me1 loss
ZNF460 P=1.39e-9
P=1.48e-6
P=1.79e-6
BHLHA15 P=8.99e-8
ZNF24 P=1.22e-7
KLF4 P=2.46e-6
NFIC P=3.84e-6
ESRRA P=5.66e-6
ZNF528 P=1.05e-5
ZNF93 P=1.12e-5
H3K4me1 gain
ZNF460 P=3.72e-8
KLF4 P=4.71e-6
ELF3 P=8.56e-6
I
H3K4me1 loss peaks
iPSC
Prog
Neur
7289 381 14209 74 402 787 20321
H3K4me1 gain peaks
iPSC
Prog
Neur
****
941 200 7141 14 8 168 4082


A
Neural progenitor
DOWN
264
UP
183
-Log10FDR
Log2 Fold Change
TMEM132C
PEG3
PAX8
DNALI1
GSTM1
CDK10
AMH
ZNF558
FAR2P4
INPP5F
TBX1
MED15P8
AJAP1
VANGL2
FEZ1
SOX8
NTNG2
IRX2
SLC7A11
EN2
B
Neuron
DOWN
31
44
UP
85
103
PEG3
TBX1
ZNF558
COL22A1
NF1P8
NGFR
GSTM1
HOXB2
FLG
EMX1
SOX10
BARX1
HOXB3
C
morphogenesis of an epithelium
embryonic organ development
microtubule bundle formation
developmental growth involved in morphogenesis
regulation of response to wounding
urogenital system development
negative regulation of response to external stimulus
negative regulation of nervous system development
negative regulation of cell development
synapse organization
extracellular structure organization
axon development
cilium or flagellum-dependent cell motility
microtubule-based movement
neuron projection guidance
cilium organization
Enrichment ratio
D
autonomic nervous system development
pattern specification process
nerve development
Enrichment ratio
E
Down DEGs
iPSC
Prog
Neur
478
63
184
13
0
4
14
Up DEGs
iPSC
Prog
Neur
273
37
101
37
8
8
32
F
Down DEGs and H3K4me1 loss peaks
iPSC
Prog
Neur
303
30
119
0
2
3
9
G
Neural Progenitor
DOWN-UP: 54
UP-UP: 132
DOWN-DOWN: 199
UP-DOWN: 33
Validation D18 log2 Fold Change
Original D18 log2 Fold Change
TBX1
EN2
INPP5F
PAX8
TMEM132C
SLC7A11
IRX2
AJAP1
FEZ1
VANGL2
AMH
CDK10
ZNF558
GSTM1
DNALI1

Stage	DEGs	Term	Overlap	P-value	Adj P-value
iPSC	UP	SUZ12 CHEA	93/1684	8.92E-24	8.74E-22
		AR CHEA	34/1095	0.001	0.055
		TP53 CHEA	14/319	0.002	0.058
	DOWN	EZH2 ENCODE	17/338	0.014	0.653
		REST CHEA	49/1280	0.014	0.653
		REST ENCODE	16/383	0.069	0.999
	UP and DOWN	SUZ12 CHEA	144/1684	5.20E-14	5.26E-12
		SMAD4 CHEA	38/584	0.017	0.708
		EZH2 ENCODE	24/338	0.021	0.708
Neural Progenitor	UP	SUZ12 CHEA	31/1684	1.37E-04	0.012
		SALL4 CHEA	7/355	0.045267	0.999996
		RAD21 ENCODE	16/1265	0.118198	0.999996
	DOWN	GATA2 CHEA	14/772	0.144067	0.999995
		ZEB1 ENCODE	3/106	0.164940	0.999995
		STAT3 CHEA	4/177	0.206557	0.999995
	UP and DOWN	SUZ12 CHEA	48/1684	0.048317	0.999995
		STAT3 CHEA	6/177	0.205444	0.999995
		KLF4 CHEA	26/987	0.219578	0.999995
Neuron	UP	SUZ12 CHEA	15/1684	0.004000	0.245000
		EZH2 CHEA	3/237	0.080143	0.999996
		KLF4 CHEA	6/987	0.242292	0.999996
	DOWN	IRF8 CHEA	1/121	0.171601	0.998295
		HDAC2 ENCODE	1/175	0.238640	0.998295
		FOXA2 ENCODE	1/316	0.389870	0.998295
	UP and DOWN	SUZ12 CHEA	16/1684	0.033848	0.999996
		EZH2 CHEA	3/237	0.159055	0.999996
		KLF4 CHEA	7/987	0.348239	0.999996
Neural Progenitor – validation datasets	UP	SUZ12 CHEA	6/1684	0.00194	0.0329
		SUZ12 ENCODE	1/105	0.0856	0.515
		REST CHEA	3/1280	0.0909	0.515
	DOWN	GATA2 CHEA	1/772	0.241	0.371
		NFE2L2 CHEA	1/1022	0.307	0.371
		REST CHEA	1/1280	0.371	0.371
	UP and DOWN	SUZ12 CHEA	6/1684	0.0127	0.228
		REST CHEA	4/1280	0.0638	0.547
		SUZ12 ENCODE	1/105	0.119	0.547

A

iPSC

Peak set	Interval	iPSC_DGE_DOWN	p-value	iPSC_DGE_UP	p-value
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	5000	0	1	25	1E-12
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	25000	4	0.987119325	41	1E-12
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	50000	8	0.990802013	50	1.40546E-11
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	100000	16	0.995582584	63	3.66108E-11
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	150000	26	0.988047687	76	5.39185E-11
iPSC_KSvsWT_FDR0.05_log2FC1_Gain	200000	29	0.999412021	84	1E-12
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	5000	110	2.74261E-11	4	0.999980277
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	25000	214	1.78334E-11	21	1
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	50000	256	1E-12	39	1
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	100000	308	1E-12	62	1
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	150000	338	2.02831E-11	84	1
iPSC_KSvsWT_FDR0.05_log2FC1_Loss	200000	351	2.69212E-09	95	1

B

Neural progenitor

Peak set	Interval	Prog_DGE_DOWN	p-value	Prog_DGE_UP	p-value
Prog_KSvsWT_FDR0.05_log2FC1_Gain	5000	14	0.200926	37	1E-12
Prog_KSvsWT_FDR0.05_log2FC1_Gain	25000	35	0.631637	58	4.52E-10
Prog_KSvsWT_FDR0.05_log2FC1_Gain	50000	52	0.934551	74	1.98E-07
Prog_KSvsWT_FDR0.05_log2FC1_Gain	100000	74	0.999698	88	0.002872
Prog_KSvsWT_FDR0.05_log2FC1_Gain	150000	95	0.999985	99	0.073142
Prog_KSvsWT_FDR0.05_log2FC1_Gain	200000	113	0.999996	107	0.304067
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	5000	19	0.00581	2	0.993048
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	25000	62	0.013411	21	0.993861
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	50000	92	0.139876	36	0.999894
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	100000	126	0.83926	55	1
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	150000	137	0.999887	71	1
Prog_KSvsWT_FDR0.05_log2FC-1_Loss	200000	151	0.999999	81	1

C

Neuron

Peak set	Interval	Neur_DGE_DOWN	p-value	Neur_DGE_UP	p-value
Neur_KSvsWT_FDR0.05_log2FC1_Gain	5000	1	0.431159	8	0.000151
Neur_KSvsWT_FDR0.05_log2FC1_Gain	25000	1	0.894369	17	7.05E-05
Neur_KSvsWT_FDR0.05_log2FC1_Gain	50000	3	0.768472	22	0.000684
Neur_KSvsWT_FDR0.05_log2FC1_Gain	100000	3	0.977701	26	0.037156
Neur_KSvsWT_FDR0.05_log2FC1_Gain	150000	5	0.977017	30	0.178229
Neur_KSvsWT_FDR0.05_log2FC1_Gain	200000	5	0.996821	37	0.117381
Neur_KSvsWT_FDR0.05_log2FC1_Loss	5000	3	0.598051	5	0.928874
Neur_KSvsWT_FDR0.05_log2FC1_Loss	25000	6	0.877893	12	0.998469
Neur_KSvsWT_FDR0.05_log2FC1_Loss	50000	10	0.867032	18	0.99995
Neur_KSvsWT_FDR0.05_log2FC1_Loss	100000	14	0.949907	27	1
Neur_KSvsWT_FDR0.05_log2FC1_Loss	150000	14	0.998383	34	1
Neur_KSvsWT_FDR0.05_log2FC1_Loss	200000	15	0.999797	40	1