Supplementary Information

Supplementary Table 1: Study Participants

	Age	Sex	Race	Relationship	N Lines
F1	**46**	**Female**	**Asian**	**Daughter**	**3**
M1	**73**	**Male**	**Asian**	**Father**	**2**
F2	**35**	**Female**	**Caucasian**	**Unrelated**	**1**

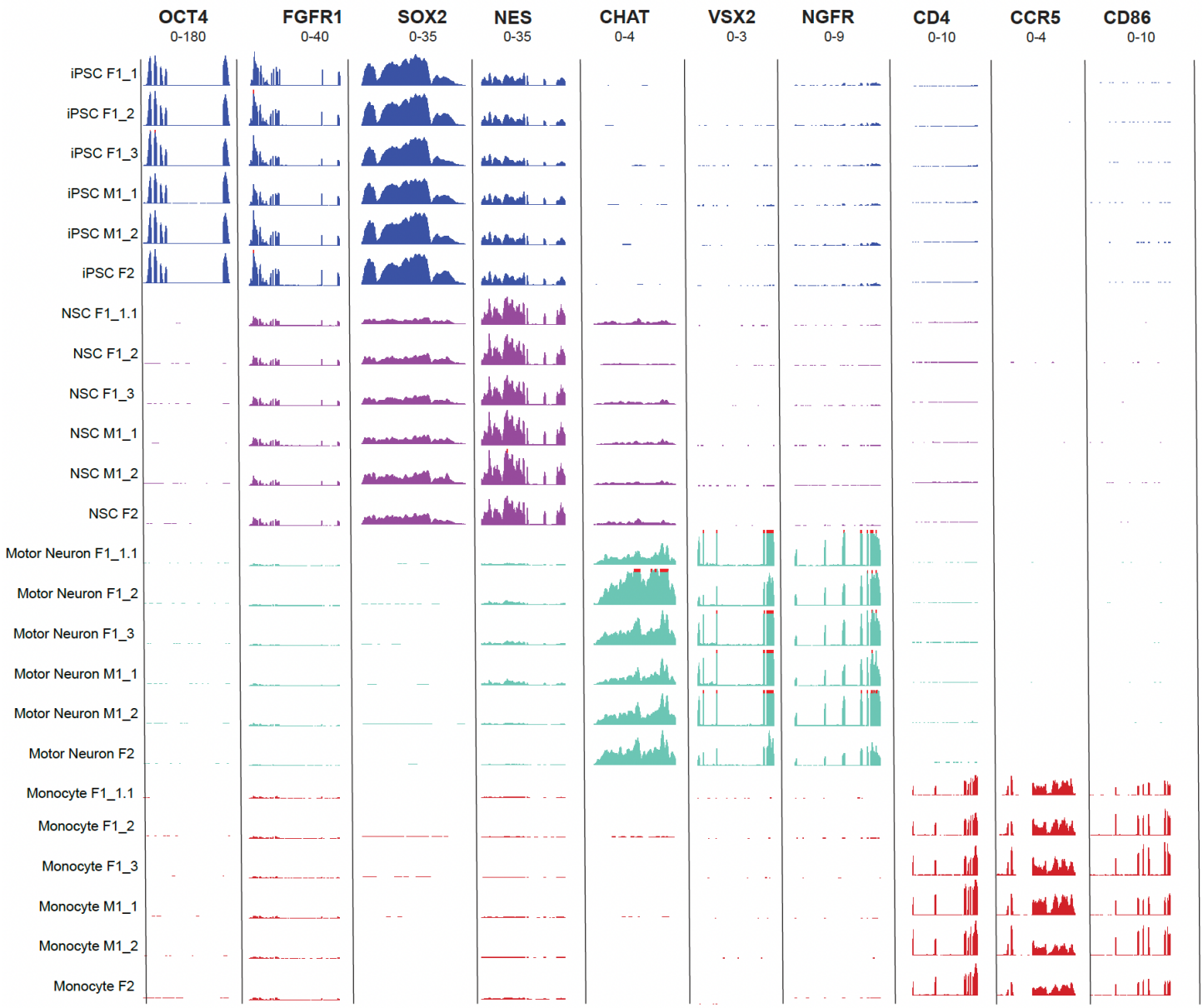
Table describing the age, sex, race, familial relationship, and number of clones derived from each of the donors from whom iPSCs were derived.

Supplementary Table 2: iPSC lines

Clone	Donor	Pool/Clone
F1_1	F1	Pool
F1_2	F1	Pool
F1_3	F1	Clone
M1_1	M1	Pool
M1_2	M1	Clone
F2_1	F2	Clone

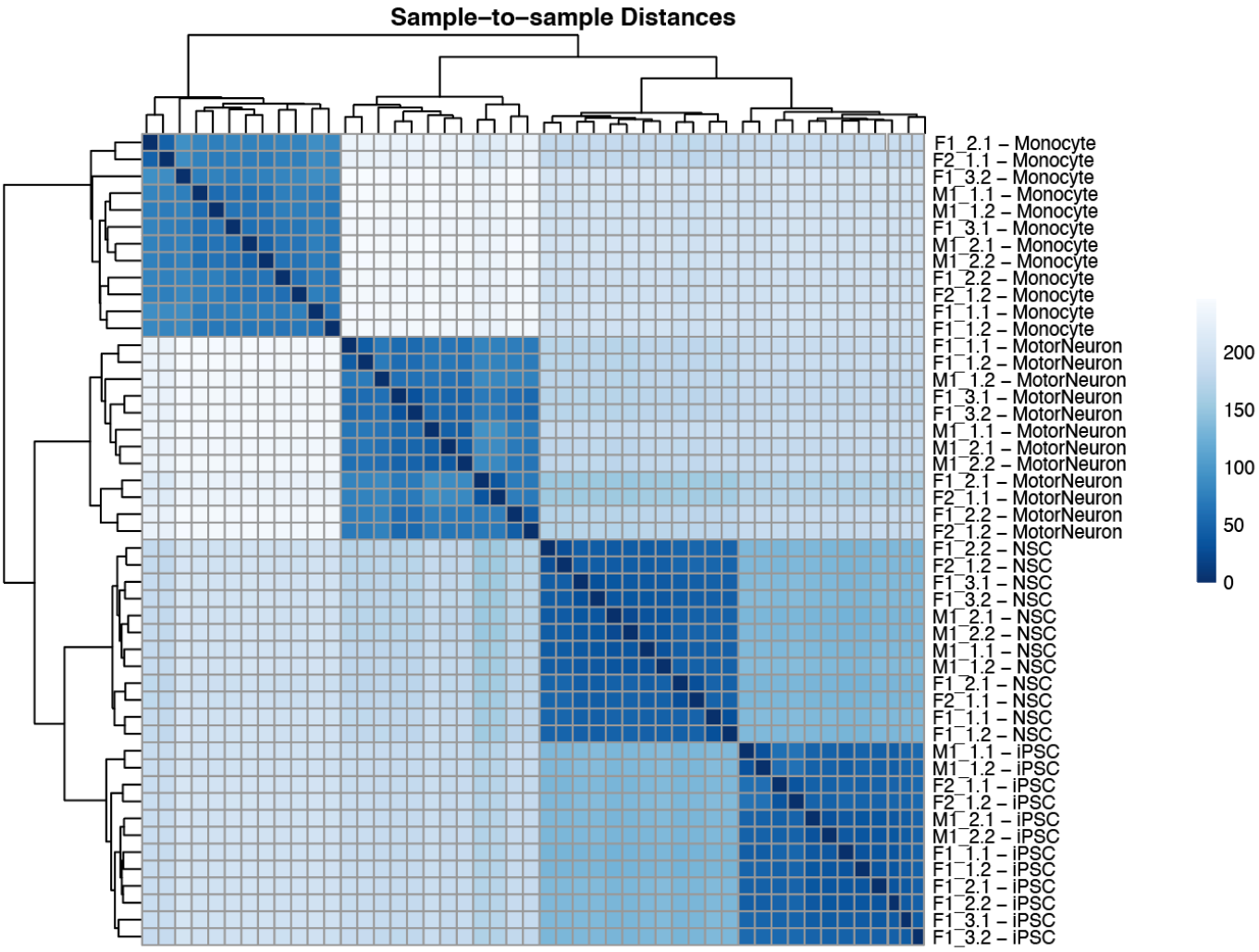
Table describing the donor of origin, of each line, and whether it was derived as a pool or a clonal line.

Supplementary Figure 1: Marker Gene Expression



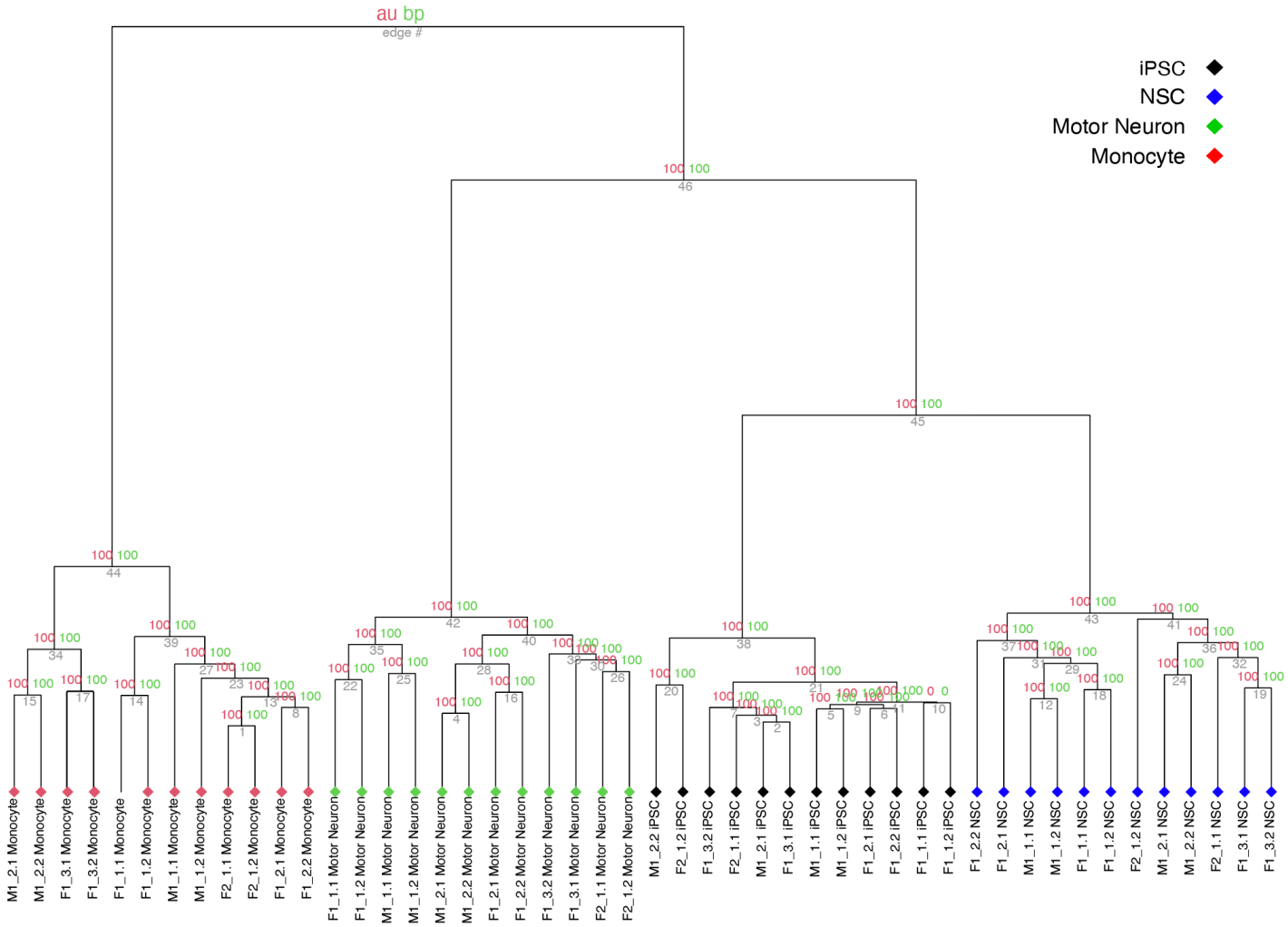
Gene expression profiles from each line for marker genes of iPSCs, NSCs, Motor Neurons, and Monocytes. Gene expression profiles were generated using the WashU Epigenome browser, which represent RNA-seq read counts across the gene. Y-axis limits for each of the genes vary by column and are listed under the gene name.

Supplementary Figure 2: Distance Heatmap of RNA-seq for each celltype



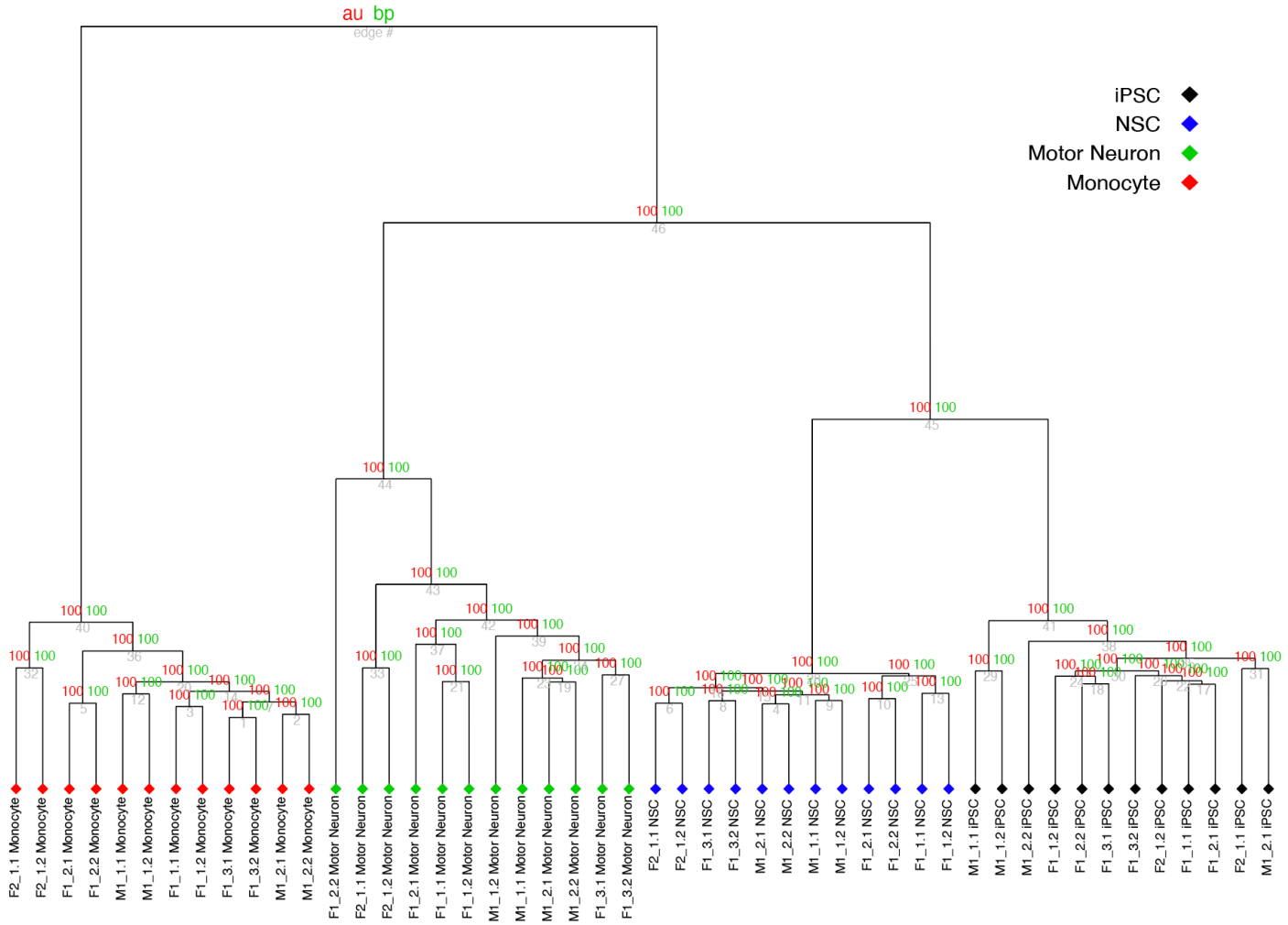
Heatmap of R-log transformed Euclidean distance of gene expression between every sample from every cell type.

Supplementary Figure 3: Bootstrapped Hierarchical Clustering of CpG Methylation by Cell Type



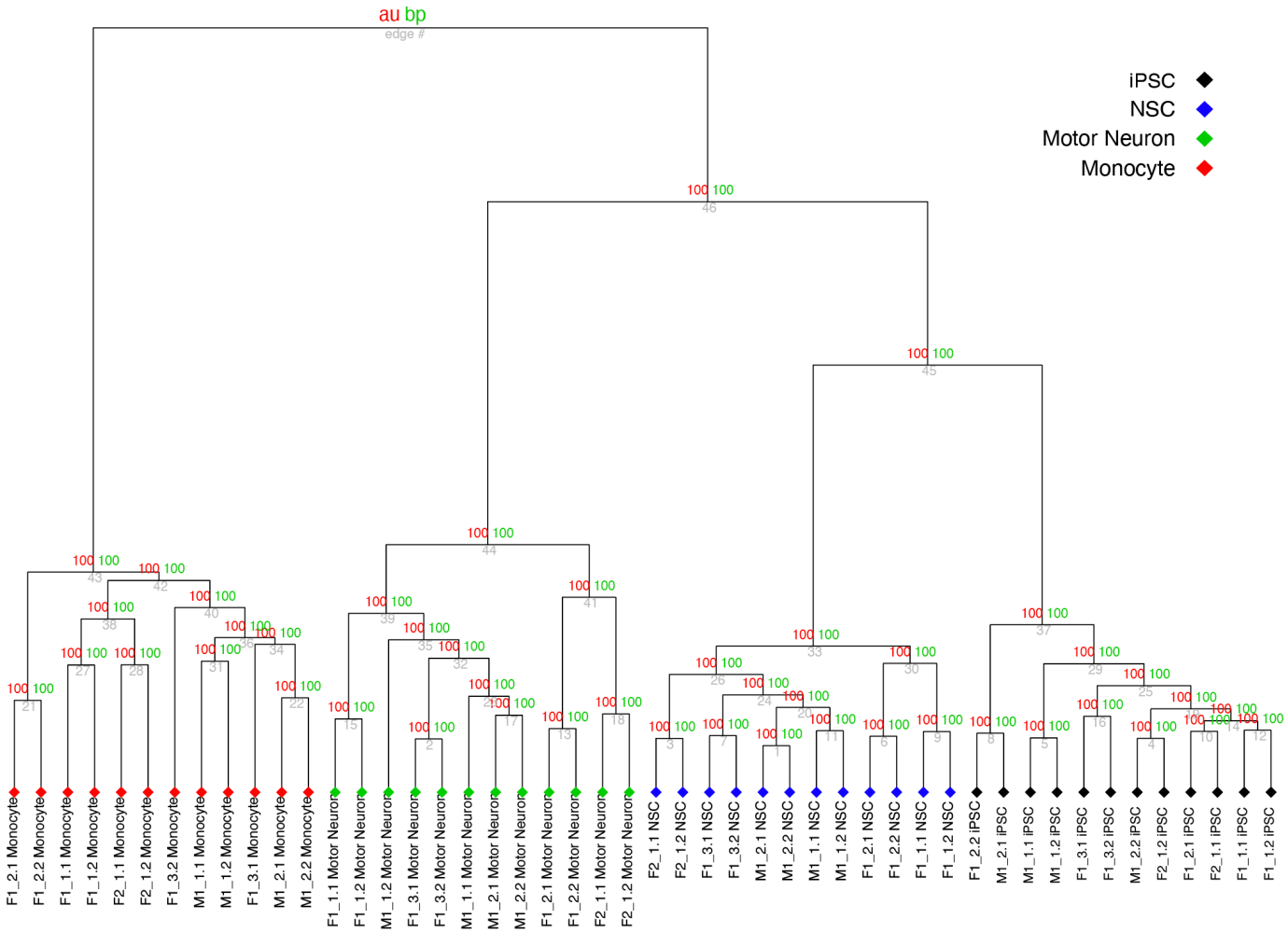
Input for methylation clustering was CpG methylation percentage of CpGs with variance >0.05 across samples.10,000 bootstraps were performed. The correlation distance metric was employed, with complete clustering. BP (red number) is the percentage of bootstraps the node is present in. AU (green number) is the adjusted unbiased P-value. Final nodes in red are Monocyte samples, final nodes in green are Motor Neuron samples, final nodes in black are iPSC samples, and final nodes in blue are NSC samples.

Supplementary Figure 4: Bootstrapped Hierarchical Clustering of Normalized Reads in ATAC Peaks by Cell Type



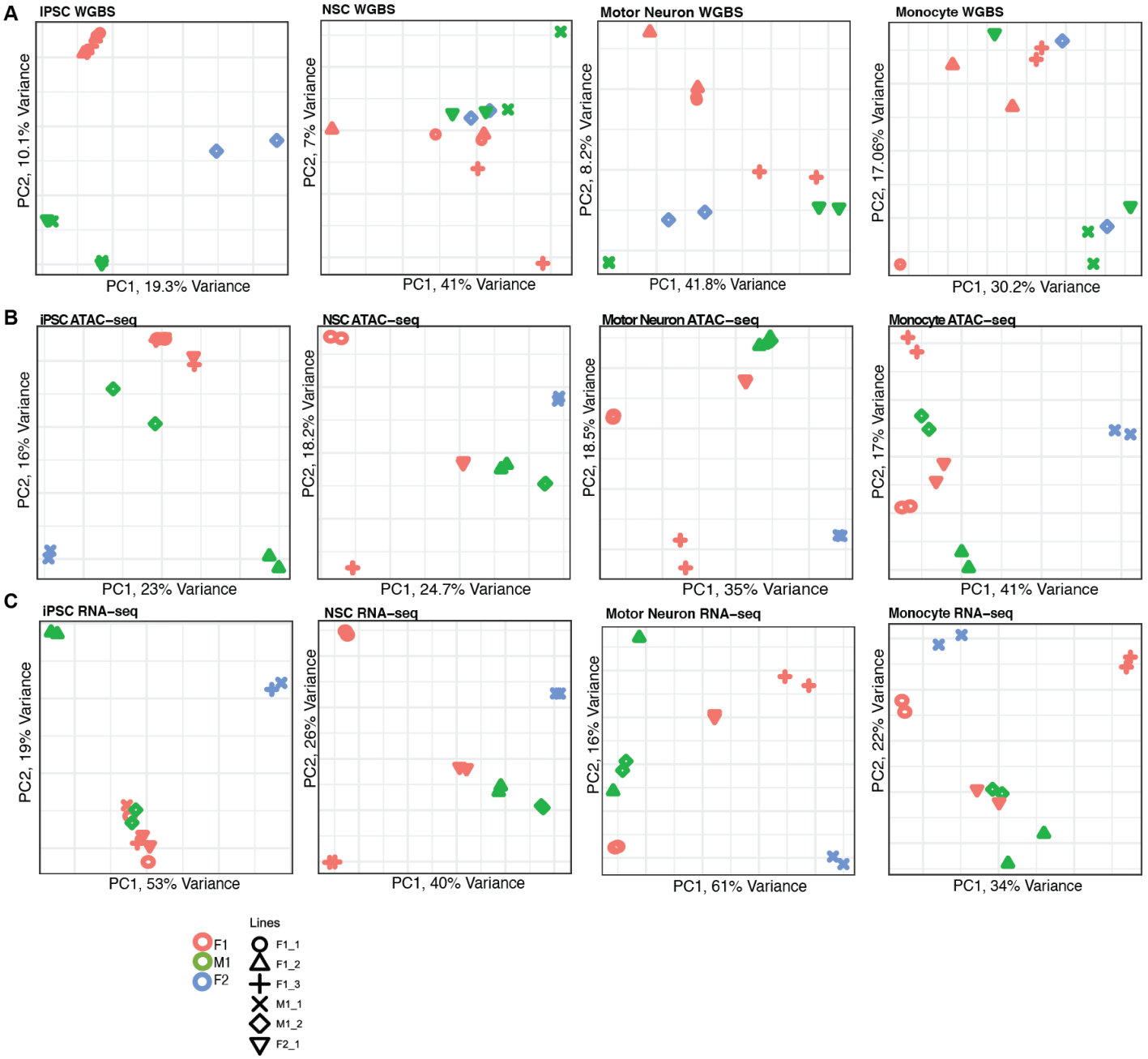
Input for chromatin accessibility clustering was DiffBind-normalized ATAC-seq reads under peaks with variance > 0.3 across samples. 10,000 bootstraps were performed. The correlation distance metric was employed, with complete clustering. BP (red number) is the percentage of bootstraps the node is present in. AU (green number) is the adjusted unbiased P-value. Final nodes in red are Monocyte samples, final nodes in green are Motor Neuron samples, final nodes in black are iPSC samples, and final nodes in blue are NSC samples.

Supplementary Figure 5: Bootstrapped Hierarchical Clustering of Normalized Gene Expression by Cell Type



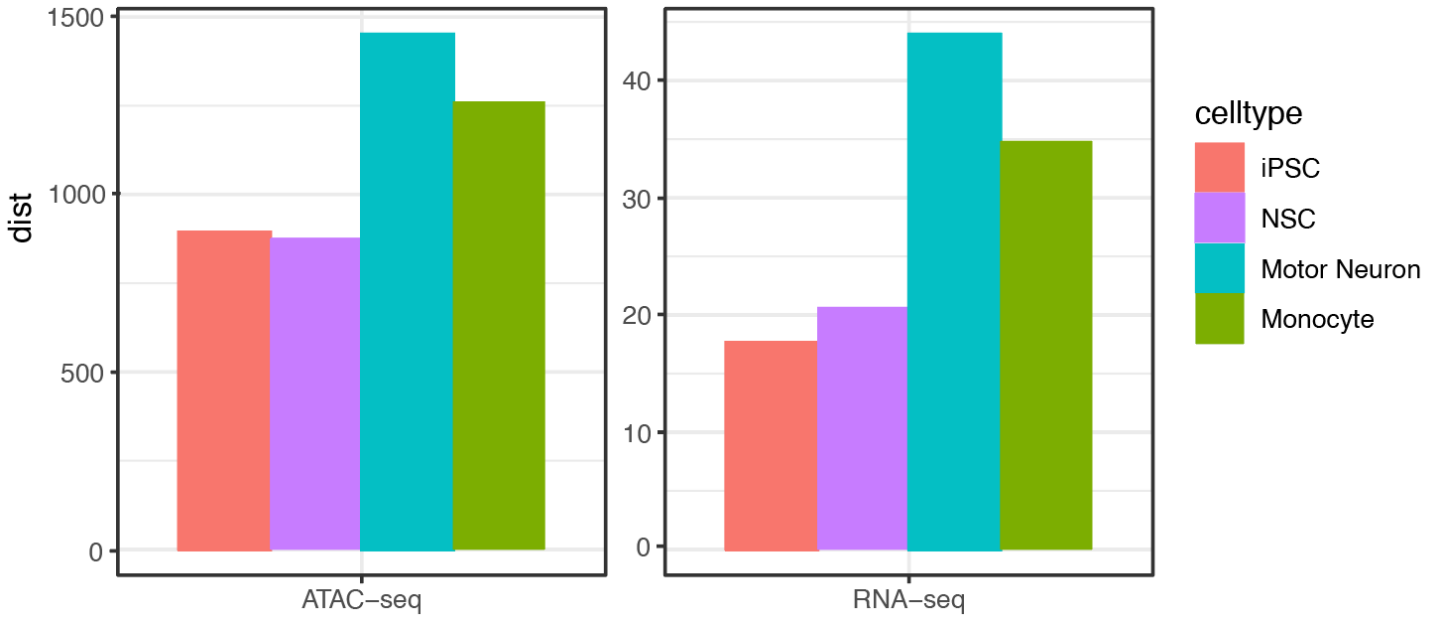
Input for the gene expression clustering was DESeq2-normalized gene expression values with variance > 0.3 across samples. 10,000 bootstraps were performed. The correlation distance metric was employed, with complete clustering. BP (red number) is the percentage of bootstraps the node is present in. AU (green number) is the adjusted unbiased P-value for a one-sided test. Final nodes in red are Monocyte samples, final nodes in green are Motor Neuron samples, final nodes in black are iPSC samples, and final nodes in blue are NSC samples.

Supplementary Figure 6: PCA of WGBS, ATAC-seq, RNA-seq colored by Donor



A. PCAs of CpG methylation for each of the differentiated cell lines. The points are colored by donor, and shaped by technical replicate. Observations are the methylation levels (percentages) of CpGs with variance>0.05 among samples. N=26166086. **B.** PCAs of reads within ATAC peaks for each of the differentiated cell lines. PCAs of reads within ATAC peaks for each of the differentiated cell lines. Each observation is the number of reads under a peak, normalized by library size in DiffBind. N=344,343 **C.** PCAs of exonic gene expression for each of the differentiated cell lines. Each observation is the number of exonic reads within a gene, normalized by sequencing depth and RNA composition in DeSEQ2. N= 37683.

Supplementary Figure 7: Cell Type Cluster Euclidean Distances in ATAC and RNA-seq



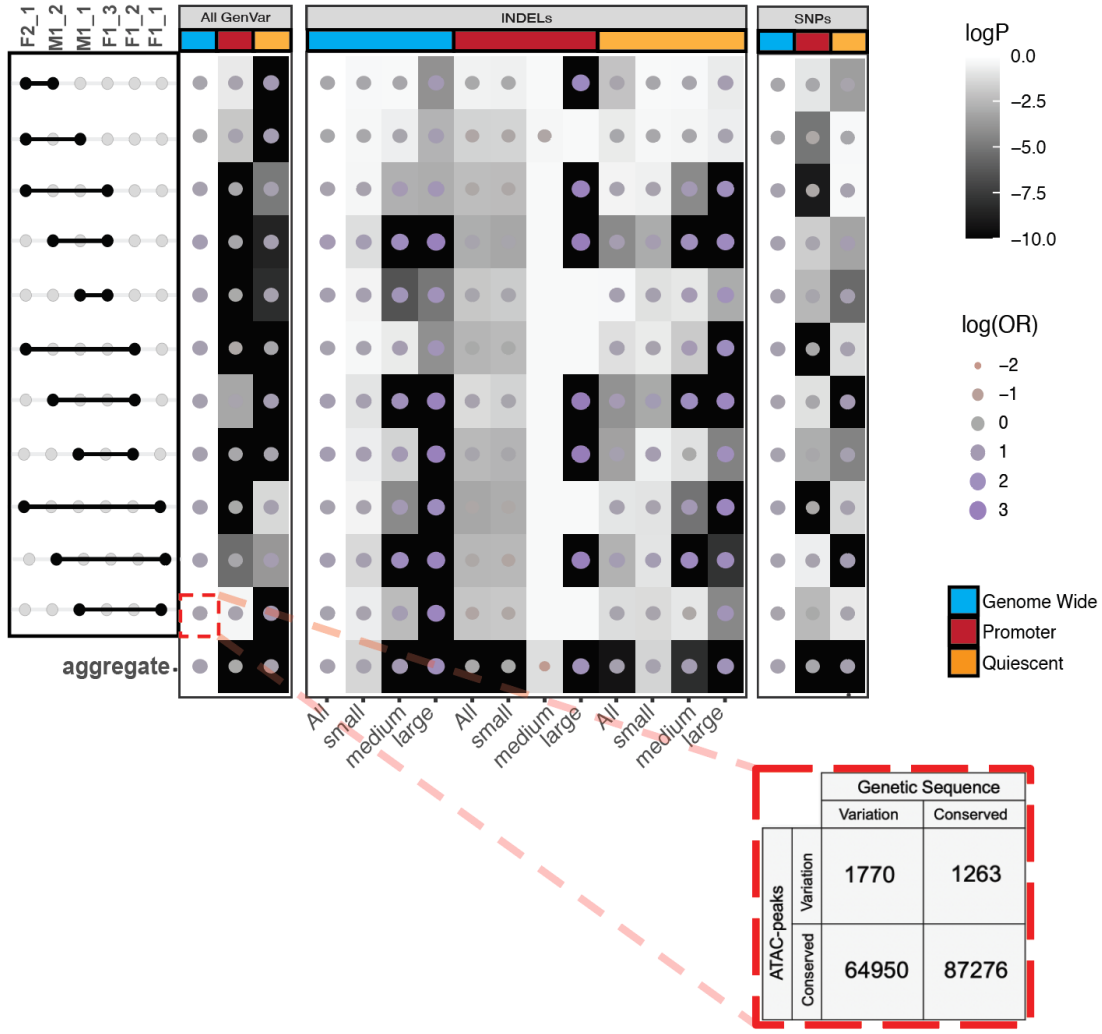
Bar plot of intra-cluster Euclidean distances, as calculated between the two farthest samples of each cell type. ATAC-seq Euclidean distances were calculated using reads under called peaks. RNA-seq distances were calculated using exonic read counts for each line sample.

Supplementary Table 3: GO of DEGs between M1 iPSC Samples

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
0.067755982	3	5	23.61504425	GO:0072047 proximal/distal pattern formation involved in nephron development	IRX1 IRX2 IRX3
0.067755982	3	5	23.61504425	identity	IRX1 IRX2 IRX3
0.067755982	3	4	23.61504425	identity	IRX1 IRX2 IRX3
0.088439384	3	9	17.71128319	GO:0061004 pattern specification involved in kidney development	IRX1 IRX2 IRX3
0.088439384	3	9	17.71128319	specification	IRX1 IRX2 IRX3
0.088439384	5	41	8.433944374	development	HES1 IRX1 IRX2 PDGFB EGR1
0.088761695	5	47	7.379701327	GO:0042551 neuron maturation	LGI4 C3 TBX6 SPTBN4 AGRN
0.129617499	6	121	5.247787611	GO:0006766 vitamin metabolic proc.	CYP27A1 CYP26A1 CYP2R1 CYP26C1 SLC2A3 SLC2A1
0.088761695	7	93	5.00925181	GO:0001656 metanephros development	PDGFB HES1 GREB1L IRX1 IRX2 IRX3 EGR1
0.106780033	7	216	4.72300885	GO:0009566 fertilization	TRPC6 SPESP1 OVGP1 ACRBP PCSK4 SPTBN4 SYCP2
0.106780033	8	186	4.106964217	GO:0050954 sensory perception of mechanical stimulus	PDZD7 MYO15A KCNA1 BARHL1 SPTBN4 EPS8L2 SPNS2 STRC
0.088439384	10	210	3.871318729	GO:0008016 reg. of heart contraction	ADM RNF207 TMEM38A SPTBN4 NOS3 IRX3 HRC TNNI3 FOXN4 SLC8A2
0.088761695	10	215	3.63308373	GO:0009612 response to mechanical stimulus	TCAP KCNA1 IGFBP2 SLC2A1 BTG2 FOS PDZD7 STRC BNIP3 TLR5
0.088439384	11	247	3.510344415	GO:0060047 heart contraction	TNNI3 ADM RNF207 TCAP TMEM38A SPTBN4 NOS3 IRX3 HRC FOXN4 SLC8A2
0.088439384	11	258	3.417966931	GO:0003015 heart proc.	TNNI3 ADM RNF207 TCAP TMEM38A SPTBN4 NOS3 IRX3 HRC FOXN4 SLC8A2
0.106780033	13	377	2.842551622	GO:0003002 regionalization	HES1 BHLHE41 BHLHE40 C3 FOXN4 TBX6 BTG2 MSX1 IRX1 IRX2 TCAP IRX3 CYP26C1
0.106780033	15	491	2.604600469	GO:0007389 pattern specification proc.	HES1 BHLHE41 BHLHE40 TBX6 RNF207 C3 RAX FOXN4 BTG2 MSX1 IRX1 IRX2 TCAP IRX3 CYP26C1
0.088439384	20	681	2.373371281	GO:0061061 muscle structure development	TCAP FER1L5 PDGFB LGALS1 HES1 IGFBP5 EGR1 BHLHE41 GDF15 EGLN1 ADM BTG2 NPHS1 MSX1 FOS IRX3 TNNI3 ID2 OBSL1 MYL6
0.067755982	35	1644	1.949355068	GO:0000003 reproduction	BIK DNAH1 TRPC6 TCTE1 SYCP2L SYCP2 SPESP1 OVGP1 TEKT2 PTGDS ACRBP ENO2 HES1 PCSK4 IGFBP2 IGFBP5 SLC2A1 EGR1 C3 GAMT EGLN1 GREB1L ADM SPTBN4 SYCE2 MSX1 NOS3 FOS JUNB CSMD1 TLR5 UTF1 MMP23B PDGFB CGB7
0.088439384	34	1635	1.898135944	GO:0022414 reproductive proc.	BIK DNAH1 TRPC6 TCTE1 SYCP2L SYCP2 SPESP1 OVGP1 TEKT2 PTGDS ACRBP ENO2 HES1 PCSK4 IGFBP2 IGFBP5 SLC2A1 EGR1 C3 GAMT EGLN1 GREB1L ADM SPTBN4 SYCE2 MSX1 NOS3 FOS JUNB CSMD1 TLR5 UTF1 PDGFB CGB7

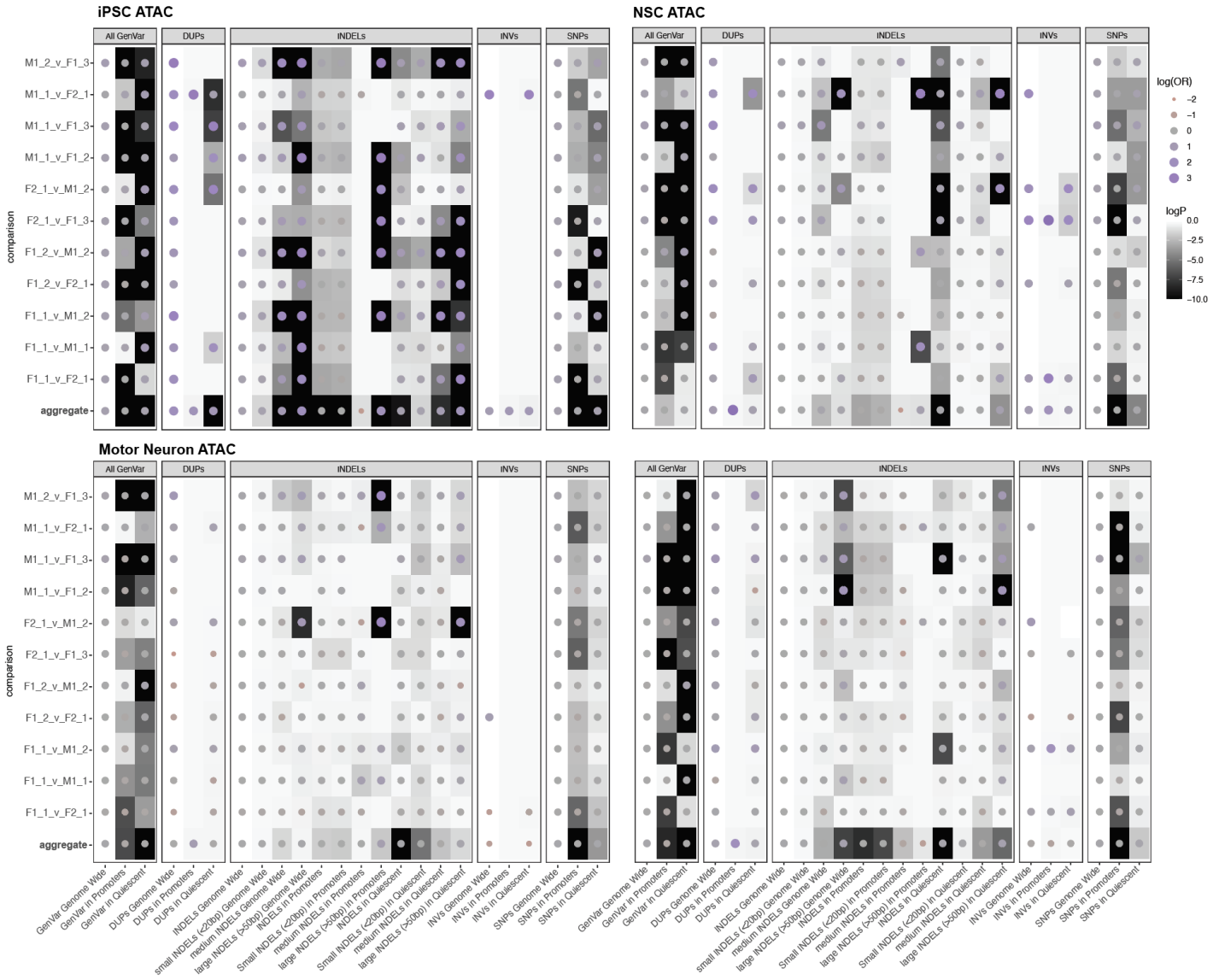
Table of ShinyGo top 20 biological process gene ontology (GO) terms enriched in differentially expressed genes between the two iPSC lines from donor M1. Background gene set was every gene expressed in any iPSC line with > 1 RPKM.

Supplementary Figure 8: Odds Ratio Plot Example



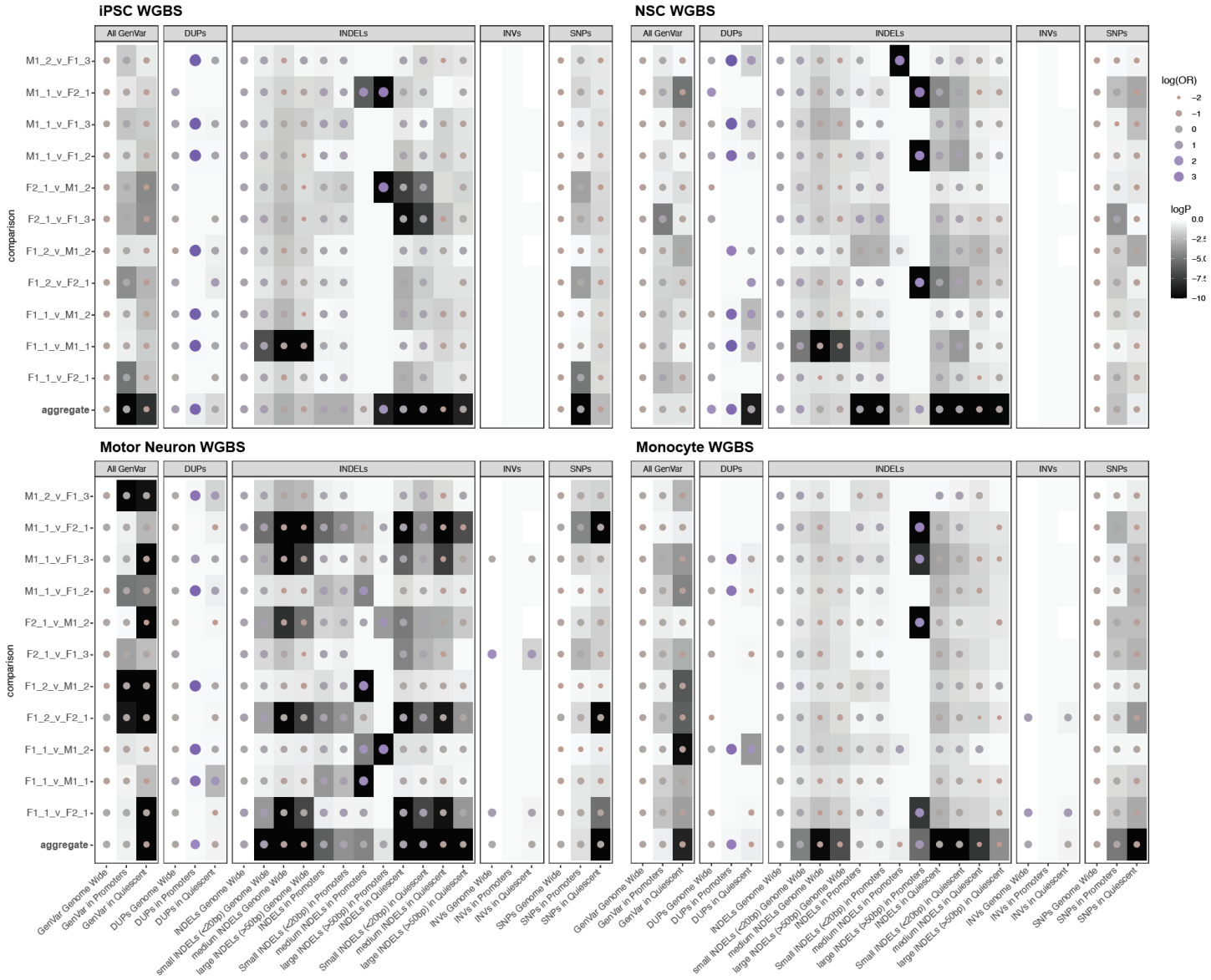
Odds of differential accessibility given genetic variation in iPSCs, NSCs, Motor Neurons, and Monocytes in each clonal comparison. Odds ratios are equal to the odds that a called peak is differentially accessible between clones given that the peak overlaps a genetic variation, divided by the odds of a peak being differentially accessible given that it does not overlap a genetic variation. Odds ratios are calculated in genome wide context (all peaks), as well as specifically peaks that overlap ChromHMM Quiescent/Heterochromatin regions, and peaks that overlap promoters. There are also odds ratios calculated for different types of genetic variation in those genomic contexts, including SNPs, INDELs, DUPs, and INVs. Color and size of circles represents the odds ratios. -log10 P-values are represented by shaded background, and are the result of a test for whether the contextual odds ratios are significantly different than the odds ratio observed in genome-wide context. Corresponding Ns for each comparison can be found in Figure 1 F.

Supplementary Figure 9: ATAC Odds Ratio Plots



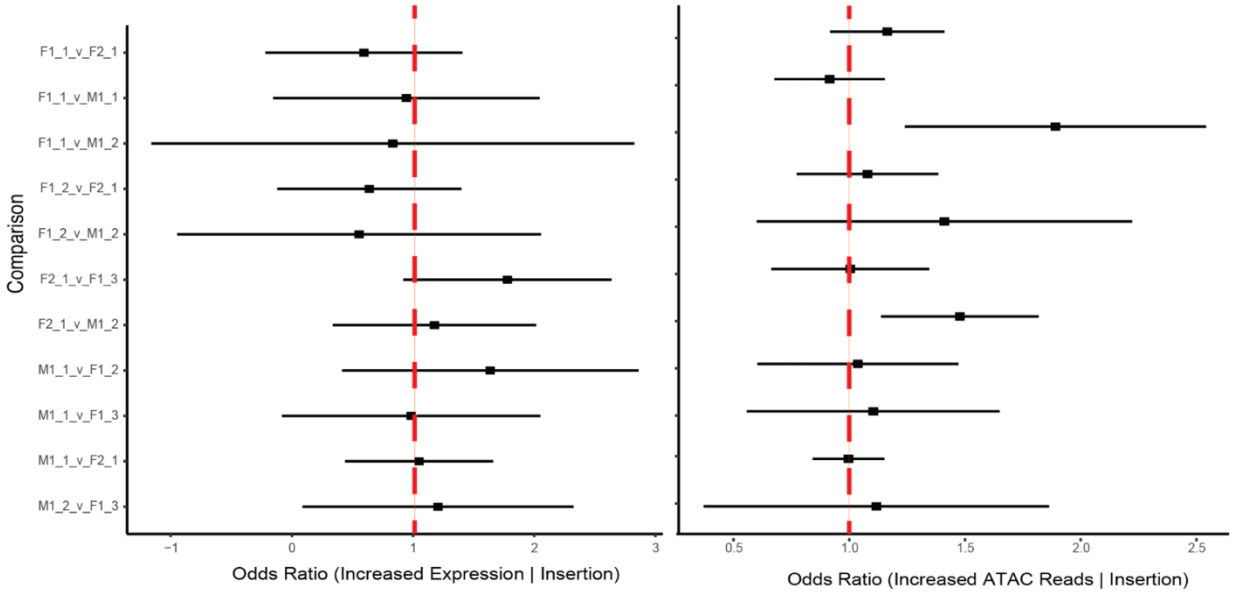
Odds of differential accessibility given genetic variation in iPSCs, NSCs, Motor Neurons, and Monocytes in each clonal comparison. Odds ratios are equal to the odds that a called peak is differentially accessible between clones given that the peak overlaps a genetic variation, divided by the odds of a peak being differentially accessible given that it does not overlap a genetic variation. Odds ratios are calculated in genome wide context (all peaks), as well as specifically peaks that overlap ChromHMM Quiescent/Heterochromatin regions, and peaks that overlap promoters. There are also odds ratios calculated for different types of genetic variation in those genomic contexts, including SNPs, INDELs, DUPs, and INVs. Color and size of circles represents the odds ratios. -log10 P-values are represented by shaded background, and are the result of a test for whether the contextual odds ratios are significantly different than the odds ratio observed in genome-wide context. Corresponding Ns for each comparison can be found in Figure 1F

Supplementary Figure 10: WGBS Odds Ratio Plots



Odds ratios of DMR given genetic variation in iPSCs, NSCs, Motor Neurons, and Monocytes in each clonal comparison. Odds ratios are equal to the odds of a differentially methylated region (DMR), as opposed to a non-differentially methylated CpG island, between clones given that the region overlaps a genetic variation, divided by the odds of a DMR given that it does not overlap a genetic variation. Odds ratios are calculated in genome wide context (all DMRs and non-DMR CpG islands), as well as specifically regions that overlap ChromHMM Quiescent/Heterochromatin regions, and regions that overlap promoters. There are also odds ratios calculated for different types of genetic variation in those genomic contexts, including SNPs, INDELs. Color and size of circles represents the odds ratios. -log10 P-values are represented by shaded background, and are the result of a test for whether the contextual odds ratios are significantly different than the odds ratio observed in genome-wide context. Corresponding Ns for each comparison can be found in Figure 1 E.

Supplementary Figure 11: Directional Impact of INDELs on ATAC and RNA-seq



(Left) Odds ratios: the odds of increased expression given that the gene overlaps an insertion divided by the odds of increased expression in a comparison given that the gene overlaps a deletion. Lines represent 95% Confidence intervals of odds ratios. (Right) Odds ratios: the odds of increased ATAC reads given that the peak overlaps an insertion divided by the odds of increased ATAC reads in a comparison given that the peak overlaps a deletion. Lines represent 95% Confidence intervals of odds ratios. Corresponding Ns for each comparison can be found in Figures 1G and 1F.

Supplementary Table 4: Overlap of Differentially Expressed Genes with Differentially Accessible Peaks and DMRs

comparison	n_diff_exp	n_diff_exp_atac	n_diff_exp_meth	n_diff_exp_atac_meth
F1_1_v_M1_1	344	3	0	0
F1_1_v_F2_1	345	27	4	3
F1_1_v_M1_2	70	2	8	0
M1_1_v_F1_2	294	3	0	0
M1_1_v_F2_1	984	45	6	5
M1_1_v_F1_3	423	5	3	1
F1_2_v_F2_1	297	32	5	5
F1_2_v_M1_2	45	0	4	0
F2_1_v_M1_2	277	33	5	5
F2_1_v_F1_3	322	20	4	3
M1_2_v_F1_3	114	3	3	0

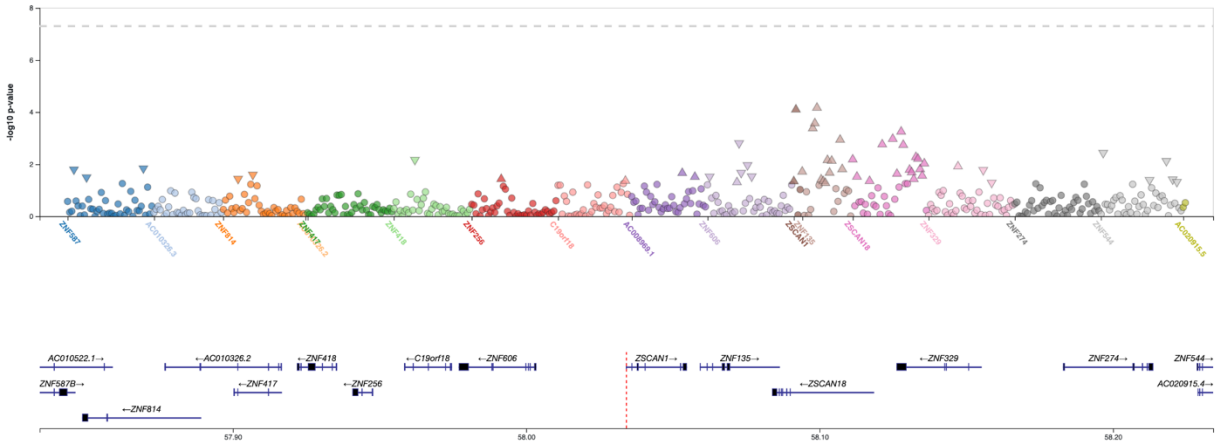
For each iPSC clonal comparison, this table describes the number of differentially expressed genes (n_diff_exp), the number of differentially expressed genes that overlap a differentially accessible peak (n_diff_exp_atac), the number of differentially expressed genes that overlap a DMR (n_diff_exp_meth), and the number of differentially expressed genes that overlap a differentially accessible peak AND a DMR (n_diff_exp_atac_meth).

Supplementary Table 5: Wilcoxon Ranksum P-values for expression differences with or without epigenetic variation

	Gene Overlap			eQTL Overlap
Comparison	**DAP (N)**	**DMR (N)**	**DAP and DMR (N)**	**DAP (N)**
F1_1_v_M1_1	0.191 (49)	6.4e-4 (21)	0.002 (12)	0.129 (8)
F1_1_v_M1_2	0.105(29)	0.49 (39)	0.078 (16)	0.564 (4)
F1_1_v_F2_1	4.6e-5 (130)	0.79 (7)	0.017 (3)	0.922 (15)
F1_2_v_M1_1	0.886 (21)	0.331 (31)	0.256 (9)	0.038 (6)
F1_2_v_M1_2	0.324 (20)	4.1e-4 (27)	4.5e-7 (12)	0.262 (3)
F1_2_v_F2_1	6e-4 (134)	0.455 (5)	5.8e-4 (6)	0.983 (12)
F1_3_v_M1_1	0.082 (23)	0.893 (18)	0.365 (5)	0.365 (3)
F1_3_v_M1_2	0.112 (32)	0.258 (22)	0.342 (4)	0.123 (2)
F1_3_v_F2_1	0.002 (108)	0.723 (17)	0.003 (14)	0.313 (16)
M1_1_v_F2_1	0.002 (184)	0.691 (15)	0.003 (9)	0.989 (25)
M1_2_v_F2_1	0.002 (121)	0.001 (31)	0.09 (12)	0.747 (19)

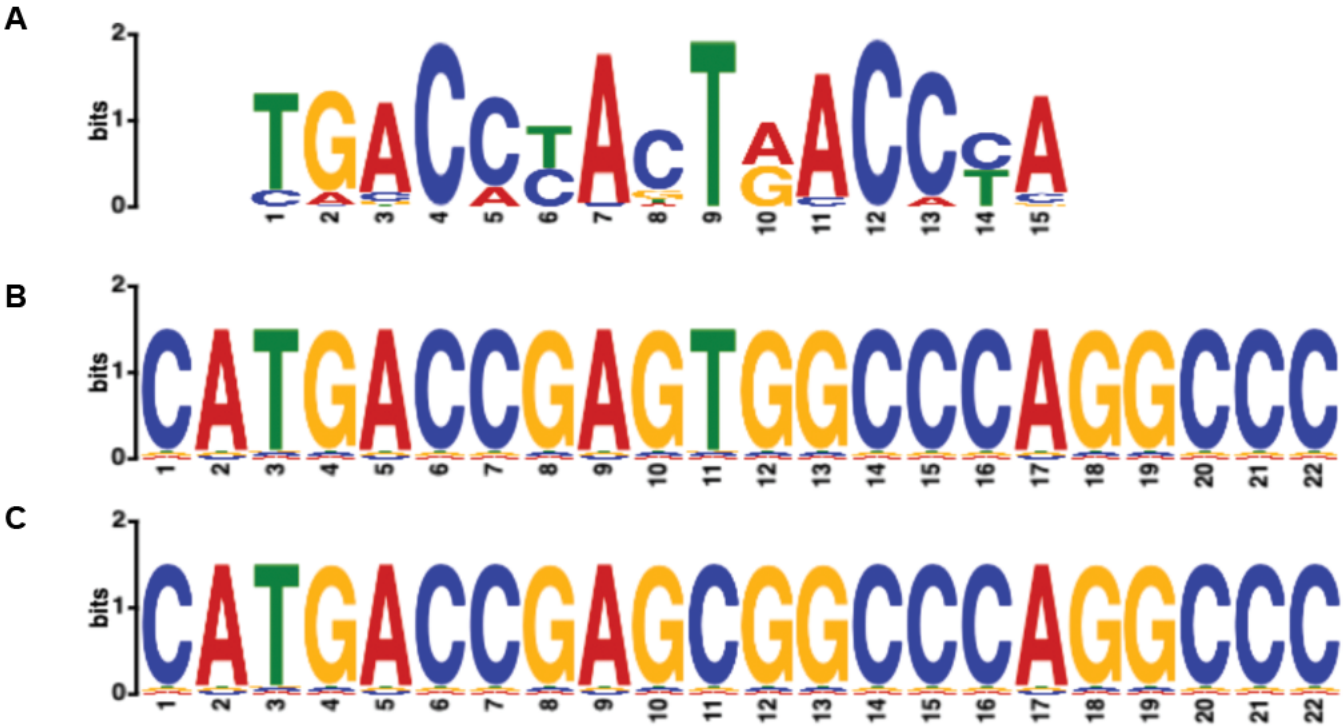
P-values from Wilcoxon Ranksum tests comparing log2 Fold Change gene expression difference between the two samples listed as comparison, under the conditions that the gene overlapped a differentially accessible peak(DAP), a differentially methylated region (DMR), or both, compared to genes that did not overlap any of these. Additionally p-values for tests of each sample comparison for the difference in log2 Fold change gene expression of genes with eQTLs that overlapped a DAP compared to those with eQTLs that did not overlap a DAP.

Supplementary Figure 12: FivEX plot of rs495839 eQTL activity



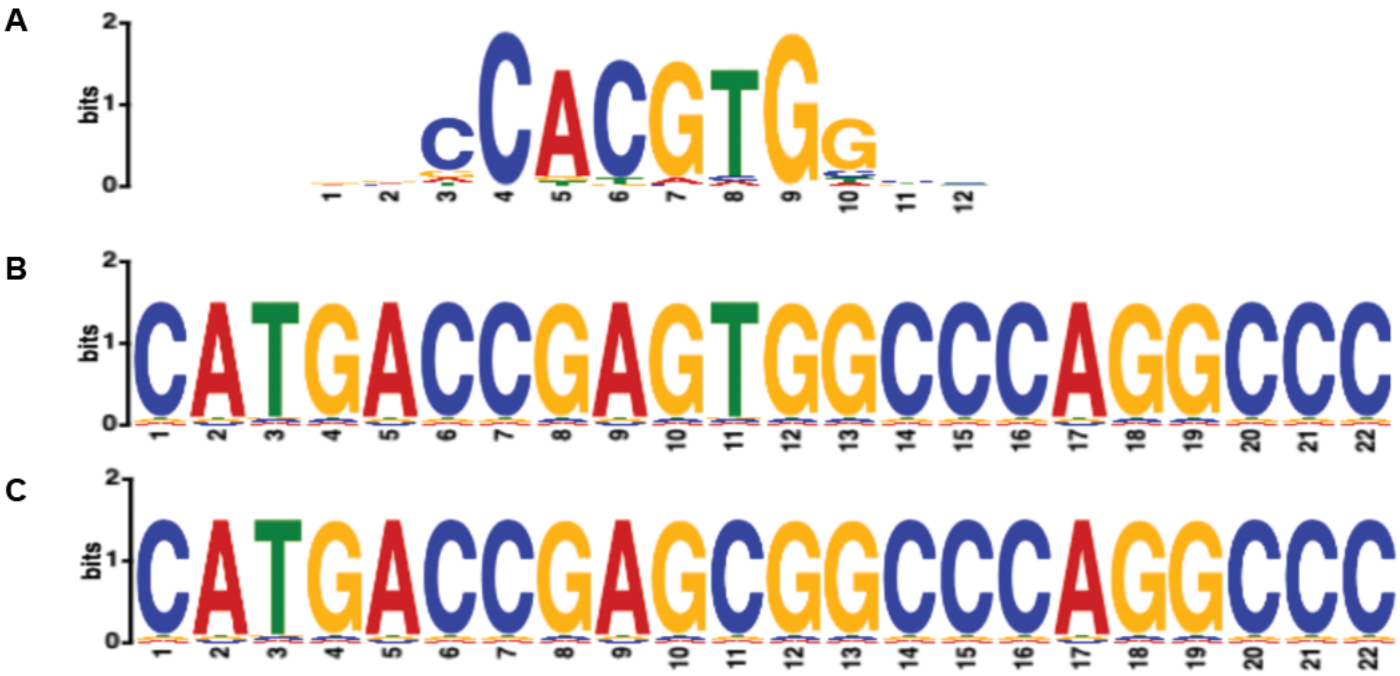
Plot from FivEX showing eQTL results for interactions between SNP rs495839 and gene expression. Each gene is plotted in a different color, with genes along the x axis and -log(P-value) for eQTL on the y-axis. Relative gene locations are plotted in the lower section, with rs495839's location marked by the dotted red line.

Supplementary Figure 13: NR1D2 Motif alignment with rs495839



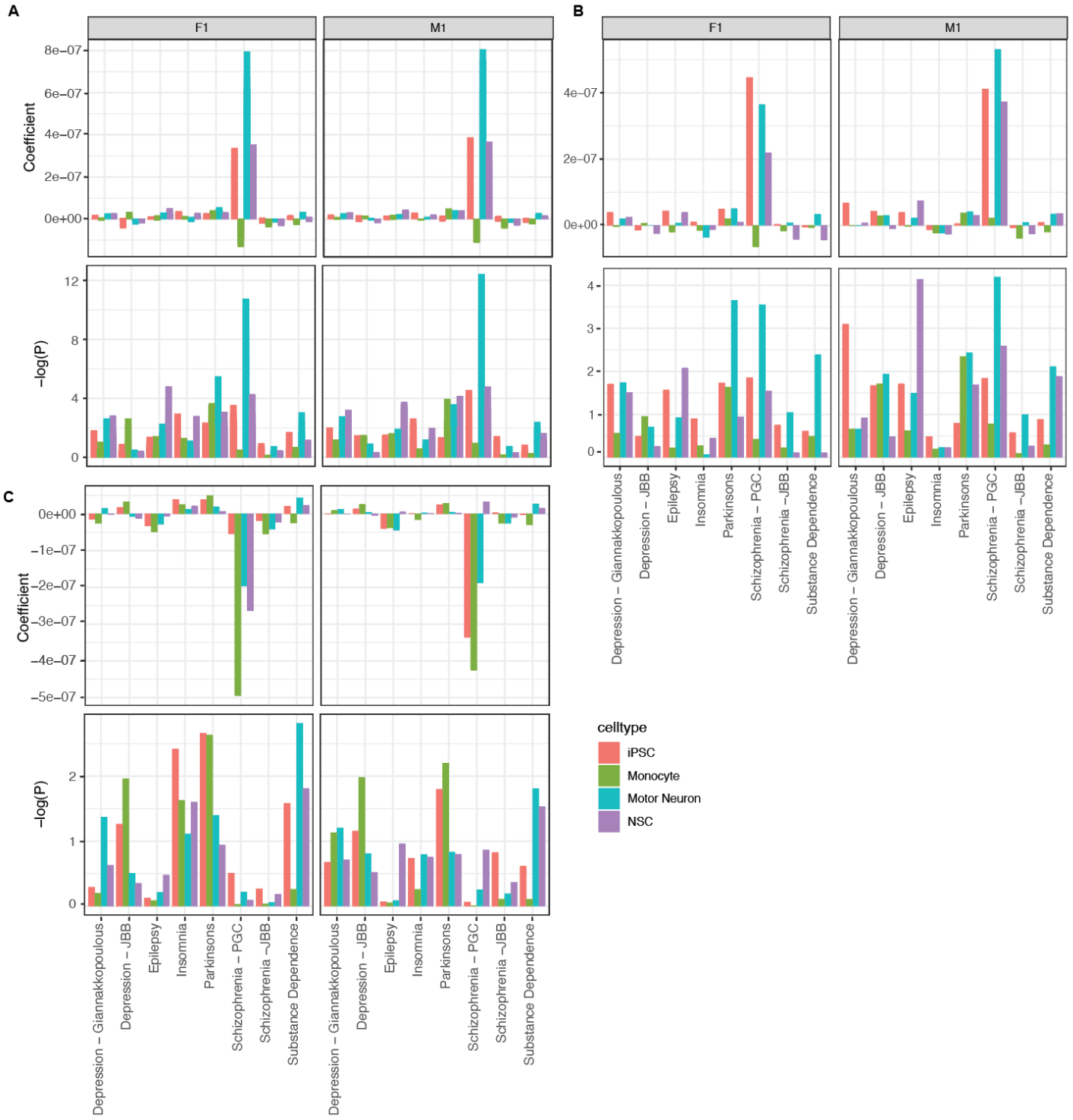
A. Position weight matrix (PWM) logo of NR1D2 binding motif. **B.** Sequence +/- 10bp surrounding rs495839 with reference sequence (T at position 11). **C.** Sequence +/- 10bp surrounding rs495839 with alternative sequence (C at position 11).

Supplementary Figure 14: MYCN Motif alignment with rs495839



A. Position weight matrix (PWM) logo of MYCN binding motif. **B.** Sequence +/- 10bp surrounding rs495839 with reference sequence (T at position 11). **C.** Sequence +/- 10bp surrounding rs495839 with alternative sequence (C at position 11).

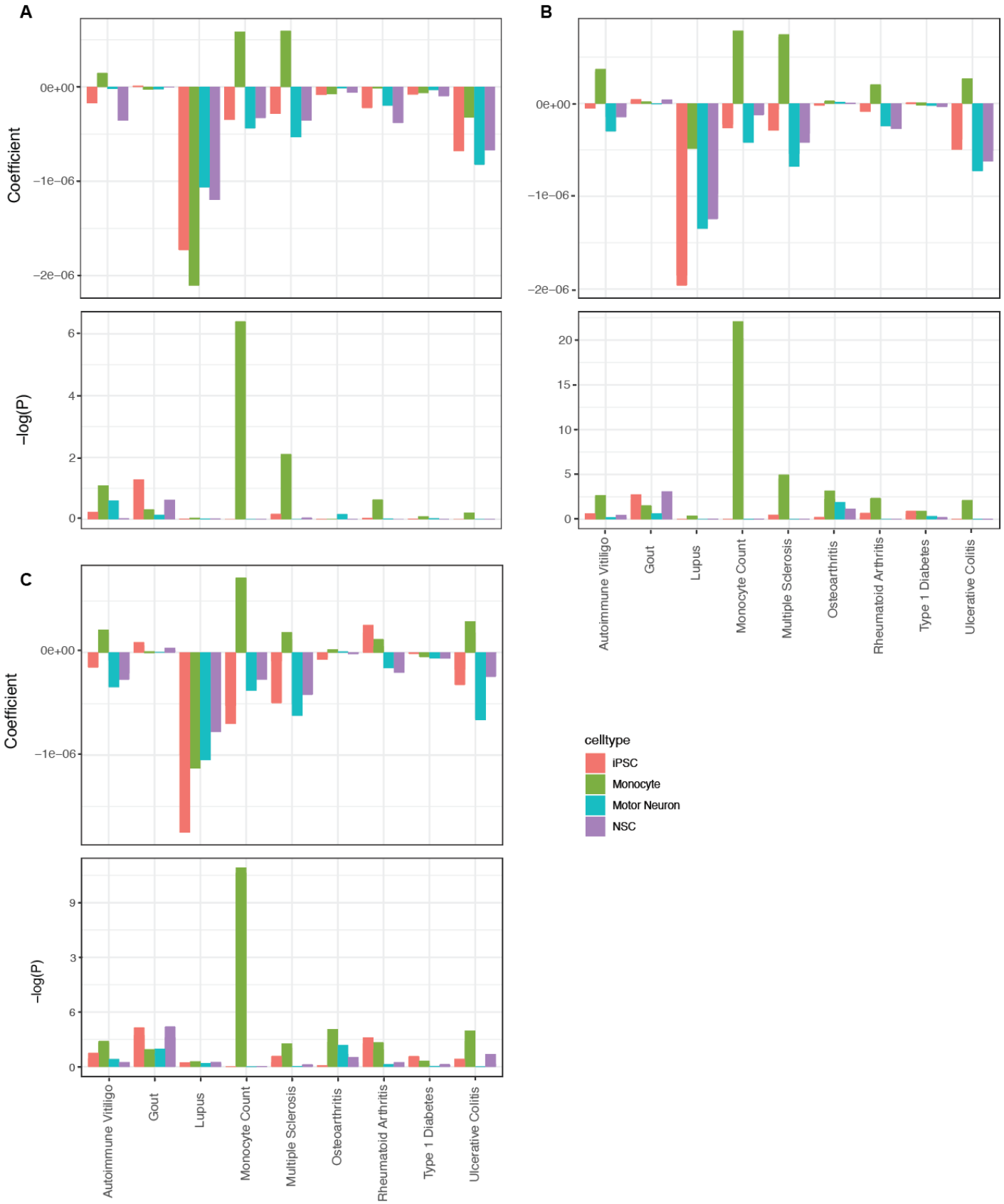
Supplementary Figure 15: Neuronal trait LDSC in Clones from donors with Eastern Asian Background



A. (Upper) Bar chart depicting linkage disequilibrium score regression (LDSC) coefficients of ATAC peaks in any F1 or M1 clone, respectively, compared to randomized genomic regions of equivalent size. A positive coefficient indicates an enrichment of GWAS loci in ATAC peaks. (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **B.** (Upper) Bar chart depicting LDSC coefficients for regression comparing ATAC peaks that were differentially accessible between any line for F1 and M1 to ATAC peaks that were not differentially accessible. (Lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **C.** (Upper) Bar chart depicting LDSC coefficients of ATAC peaks in M1 and F1 clones that

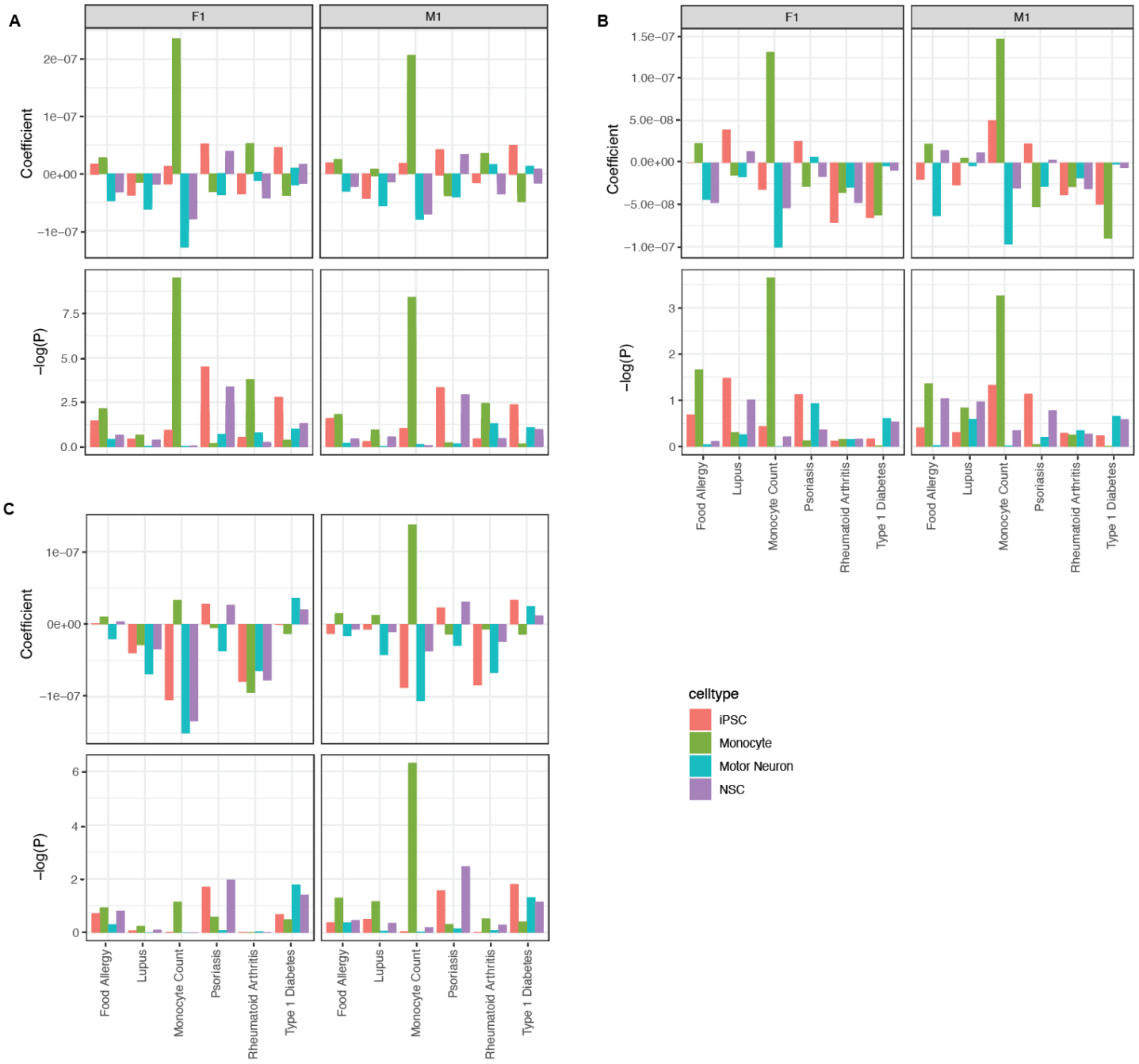
did not overlap a genetic variation compared to ATAC peaks that did overlap a genetic variation. A positive coefficient indicates an enrichment of GWAS loci in peaks without genetic variation (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. Ns for each study can be found in Supplementary Table 6.

Supplementary Figure 16: Immune trait LDSC in Clones from donors with European Background



A. (Upper) Bar chart depicting linkage disequilibrium score regression (LDSC) coefficients of ATAC peaks in any F1 or M1 clone, respectively, compared to randomized genomic regions of equivalent size. A positive coefficient indicates an enrichment of GWAS loci in ATAC peaks. (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **B.** (Upper) Bar chart depicting LDSC coefficients for regression comparing ATAC peaks that were differentially accessible between any line for F1 and M1 to ATAC peaks that were not differentially accessible. (Lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **C.** (Upper) Bar chart depicting LDSC coefficients of ATAC peaks in M1 and F1 clones that did not overlap a genetic variation compared to ATAC peaks that did overlap a genetic variation. A positive coefficient indicates an enrichment of GWAS loci in peaks without genetic variation (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. Ns for each study can be found in Supplementary Table 6.

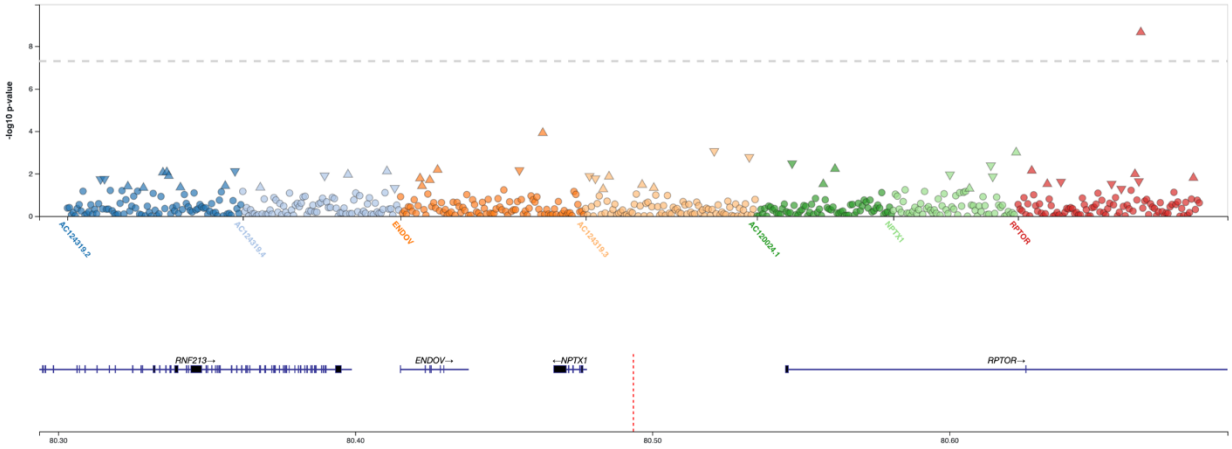
Supplementary Figure 17: Immune trait LDSC in Clones from donors with Eastern Asian Background



A. (Upper) Bar chart depicting linkage disequilibrium score regression (LDSC) coefficients of ATAC peaks in any F1 or M1 clone, respectively, compared to randomized genomic regions of equivalent size. A positive coefficient

indicates an enrichment of GWAS loci in ATAC peaks. (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **B.** (Upper) Bar chart depicting LDSC coefficients for regression comparing ATAC peaks that were differentially accessible between any line for F1 and M1 to ATAC peaks that were not differentially accessible. (Lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. **C.** (Upper) Bar chart depicting LDSC coefficients of ATAC peaks in M1 and F1 clones that did not overlap a genetic variation compared to ATAC peaks that did overlap a genetic variation. A positive coefficient indicates an enrichment of GWAS loci in peaks without genetic variation (lower) Bar chart depicting -log10 p-values of LDSC regression coefficients for each GWAS trait. Ns for each study can be found in Supplementary Table 6.

Supplementary Figure 18: FivEX plot of rs4453556 eQTL activity

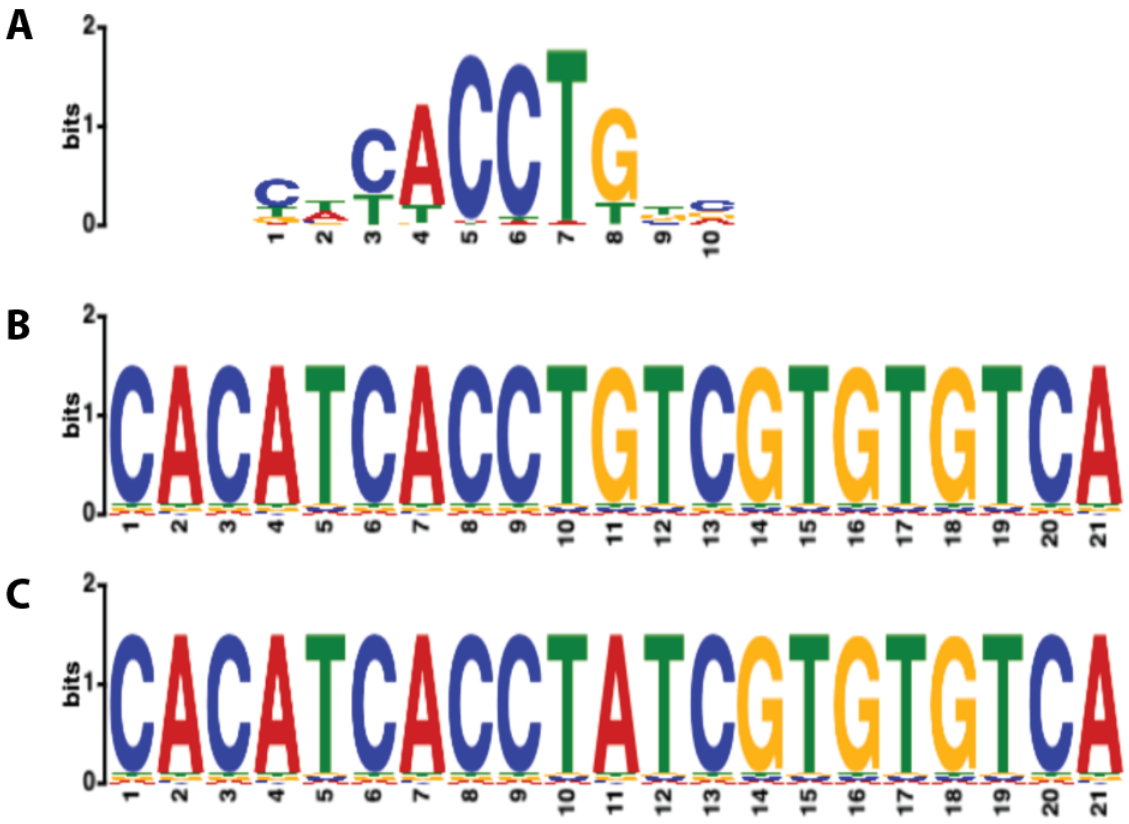


Plot from FivEX showing eQTL results for interactions between SNP rs4453556 and gene expression. Each gene is plotted in a different color, with genes along the x axis and -log(P-value) for eQTL on the y-axis. Relative gene locations are plotted in the lower section, with rs4453556's location marked by the dotted red line.

Supplementary Figure 19: WashU Epigenome Browser Shot of SNP rs4453556

WashU Epigenome Browser Shot of genes NPTX1 and RPTOR in motor neurons. Matplot wrap is a lineplot showing expression (RNA-seq) of each of the samples, color-coded by donor. Read counts from RNA-seq are displayed for each sample, as well as ATAC-seq.

Supplementary Figure 20: ZEB1 Motif alignment with rs4453556



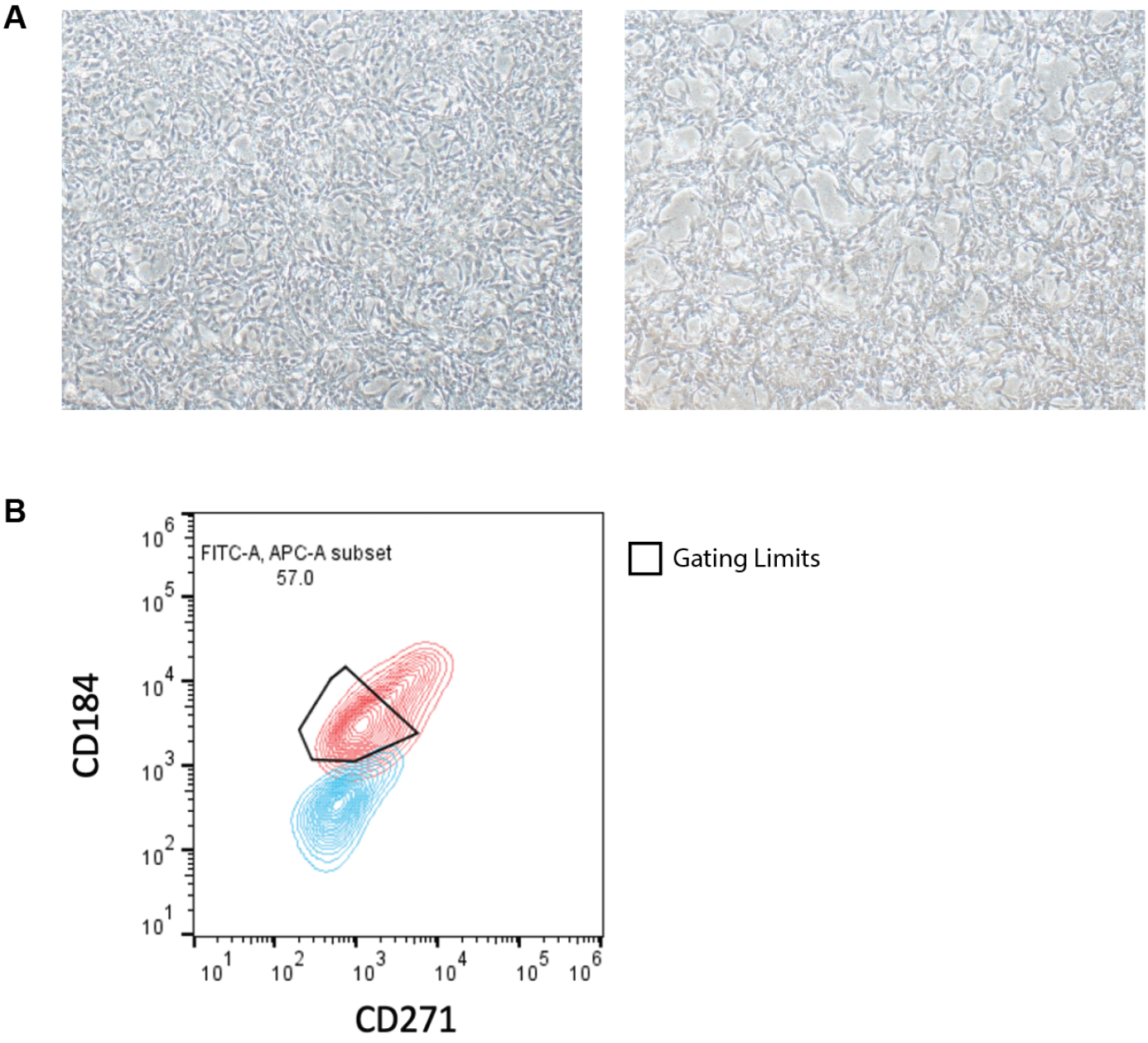
A. Position weight matrix (PWM) logo of ZEB1 binding motif. **B.** Sequence +/- 10bp surrounding rs4453556 with reference sequence (G at position 11). **C.** Sequence +/- 10bp surrounding r rs4453556 with alternative sequence (A at position 11).

Supplementary Table 6: GWAS Studies

Trait	Ancestry	N Cases	N Controls	DOI
ADHD	EUR	20183	35191	https://doi.org/10.1038/s41588-018-0269-7
Alzheimer's	EUR	71880	383378	https://doi.org/10.1038/s41588-018-0311-9
Autism	EUR	18381	27969	https://doi.org/10.1038/s41588-019-0344-8
Bipolar	EUR	9784	30471	https://doi.org/10.1093/hmg/ddw181
Insomnia	EUR	165820	40220	https://doi.org/10.1038/s41588-018-0333-3
Major Depressive Disorder	EUR	246363	561190	https://doi.org/10.1038/s41593-018-0326-7
OCD	EUR	2688	7037	https://doi.org/10.1038/mp.2017.154
Parkinson's	EUR	37000	1400000	https://doi.org/10.1016%2FS1474-4422(19)30320-5
Monocyte Count	EUR	N=173480		https://doi.org/10.1016/j.cell.2016.10.042
Systemic Lupus Erythematosus	EUR	7219	15991	https://doi.org/10.1038/ng.3434
Type I Diabetes	EUR	18942	501638	https://doi.org/10.1038/s41586-021-03552-w
Ulcerative Collitis	EUR	12882	21770	https://doi.org/10.1038/ng.3760
Multiple Sclerosis	EUR	9772	17376	https://doi.org/10.1038/nature10251
Autoimmune Vitiligo	EUR	4680	39586	https://doi.org/10.1038/ng.3680
Rheumatoid Arthritis	EUR	29880	73758	https://doi.org/10.1038/nature12873
Osteoarthritis	EUR	77052	378169	https://doi.org/10.1038/s41588-018-0327-1
Gout	EUR	4908	334880	https://doi.org/10.1038/s41588-019-0504-x
PTSD	EUR	30000	170000	https://doi.org/10.1038/s41467-019-12576-w
Schizophrenia	EUR	36989	113075	https://doi.org/10.1038/nature13595
Depression	EAS	836	177794	https://doi.org/10.1038/s41588-021-00931-x
Epilepsy	EAS	2466	175788	https://doi.org/10.1038/s41588-021-00931-x
Insomnia	EAS	389	177864	https://doi.org/10.1038/s41588-021-00931-x
Parkinson's	EAS	340	175788	https://doi.org/10.1038/s41588-021-00931-x
Schizophrenia	EAS	99	177794	https://doi.org/10.1038/s41588-021-00931-x
Substance Dependence	EAS	118	178608	https://doi.org/10.1038/s41588-021-00931-x
Schizophrenia	EAS	22778	35362	https://doi.org/10.1038/s41588-019-0512-x
Depression	EAS	15771	178777	https://doi.org/10.1001/jamapsychiatry.2021.2099
Food Allergy	EAS	105721	433663	https://doi.org/10.1038/s41588-021-00931-x
Lupus	EAS	317	175937	https://doi.org/10.1038/s41588-021-00931-x
Monocyte Count	EAS	N=95119		https://doi.org/10.1038/s41588-021-00931-x
Psoriasis Vulgaris	EAS	206	172289	https://doi.org/10.1038/s41588-021-00931-x
Rheumatoid Arthritis	EAS	5348	173268	https://doi.org/10.1038/s41588-021-00931-x
Type I Diabetes	EAS	1219	132032	https://doi.org/10.1038/s41588-021-00931-x

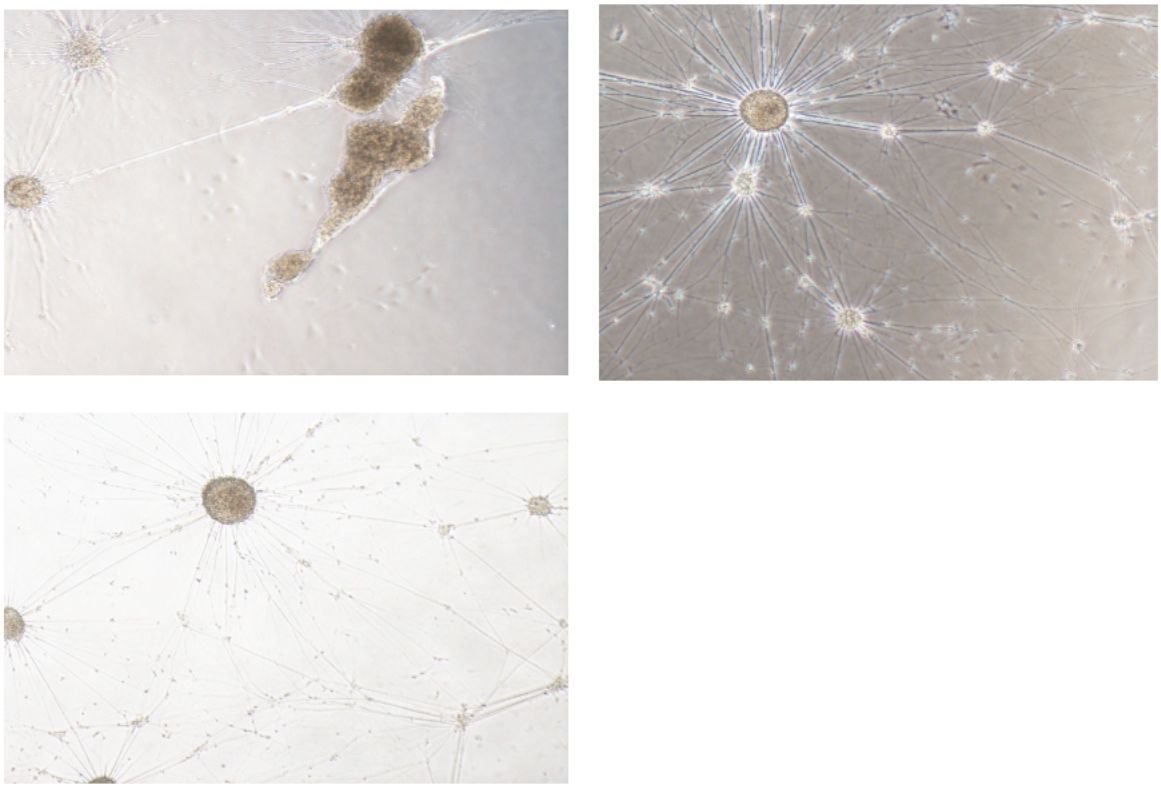
Table of GWAS studies included in LDSC analysis, including trait, ancestry of GWAS study participants (EUR=European, EAS=Eastern Asian), number of cases and controls for each study, and the DOI identification for each study.

Supplementary Figure 21: NSC Images and FACS



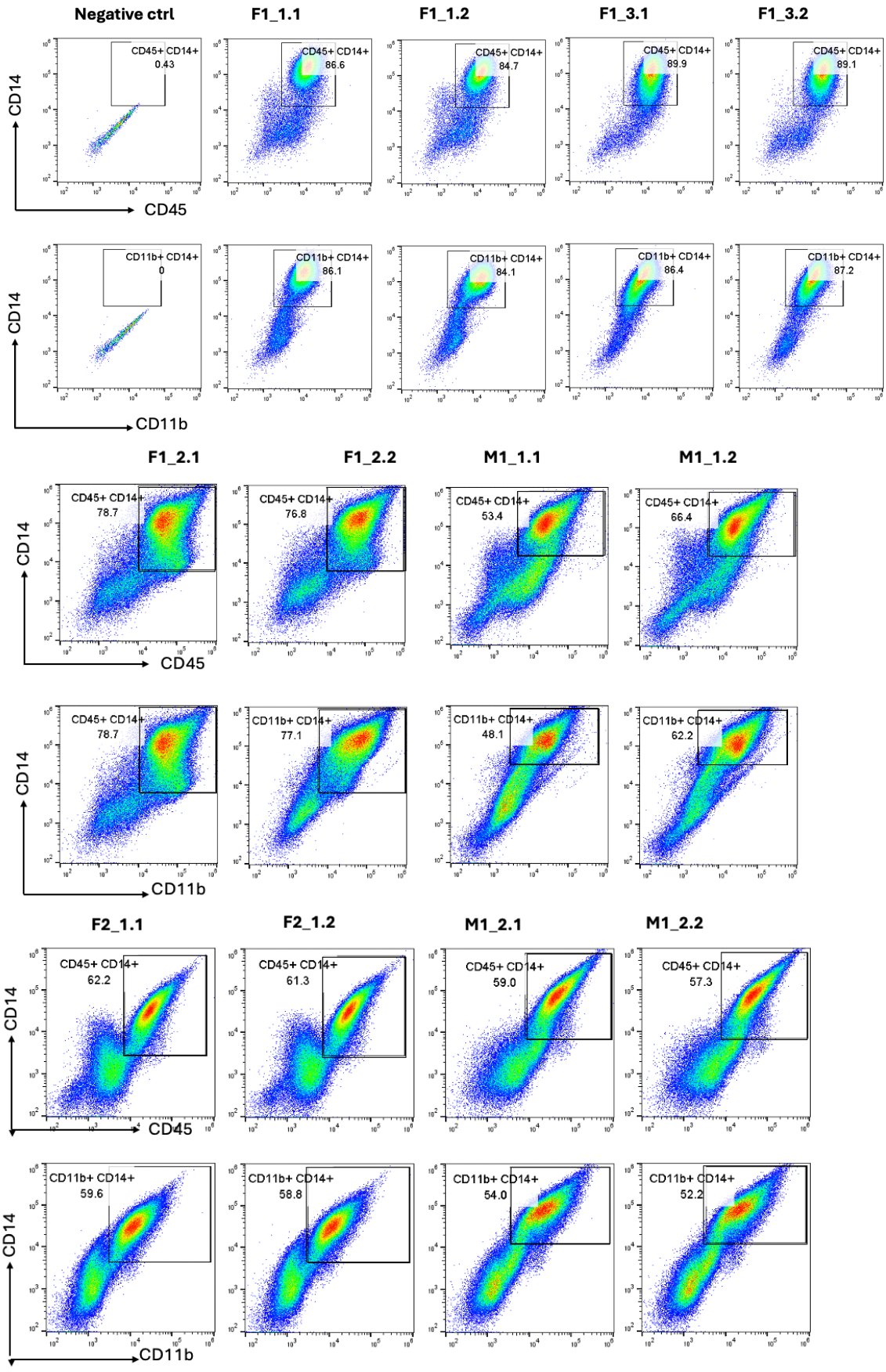
A. Microscopic images of iPS-derived NSC morphology before harvesting. **B.** FACS of NSCs marked for CD184 and CD271. NSCs were sorted to be CD184 positive and CD271 negative, gating criteria depicted by black outline.

Supplementary Figure 22: Motor Neuron Morphology



Microscopic images of iPS-derived motor neuron morphology before harvesting.

Supplementary Figure 23: Monocyte FACS Analysis



Gating from fluorescence activated cell sorting (FACS) of iPS-derived monocytes. Monocytes were sorted to be CD14, CD45, and CD11b positive. Gating criteria is indicated indicated as black outlines.