

Supplementary Materials:

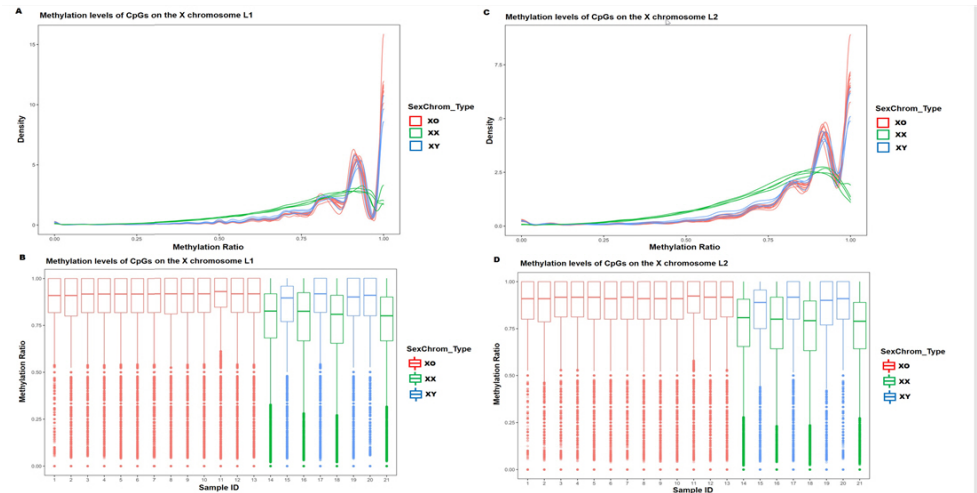


Figure S1. The methylation levels of 13 TS individuals and 8 healthy controls in the L1 and L2 regions on the chrX. The methylation density (A) and methylation ratio (B) of each sample in the L1 regions. The methylation density (C) and methylation ratio (D) of each sample in the L2 regions. (Red: TS, Green: female controls, and Blue: male controls).

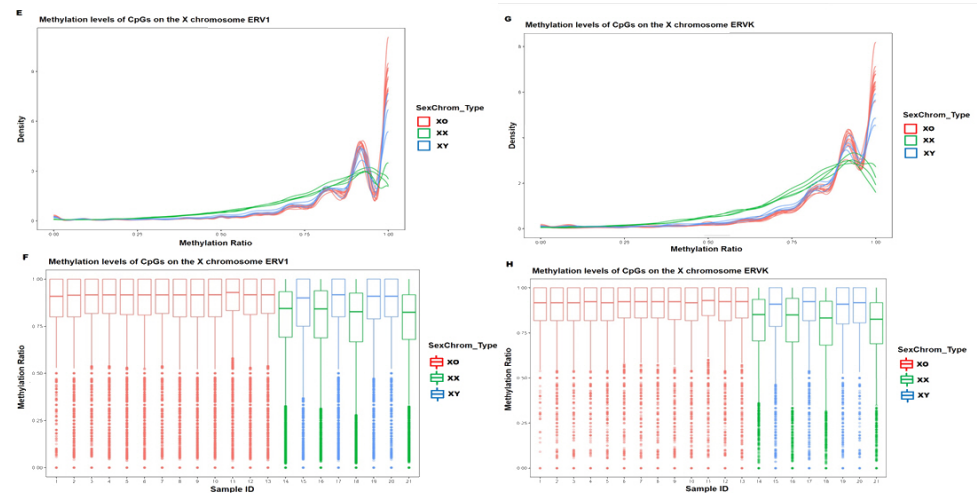


Figure S2. The methylation levels of 13 TS individuals and 8 healthy controls in the ERV1 and ERVK regions on the chrX. The methylation density (E) and methylation ratio (F) of each sample in the ERV1 regions. The methylation density (G) and methylation ratio (H) of each sample in the ERVK regions. (Red: TS, Green: female controls, and Blue: male controls).

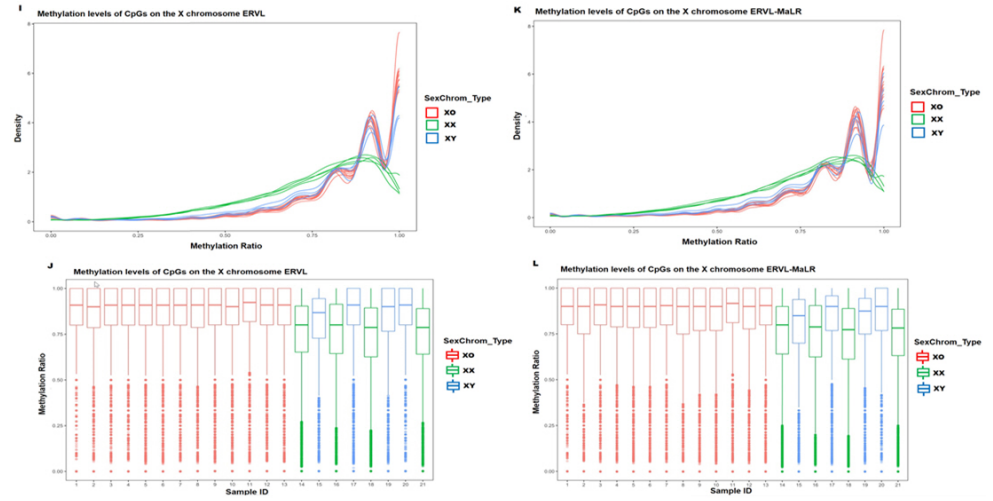


Figure S3. The methylation levels of 13 TS individuals and 8 healthy controls in the ERVL and ERVL-MaLR regions on the chrX. The methylation density (I) and methylation ratio (J) of each sample in ERVL regions. The methylation density (K) and methylation ratio (L) of each sample in the ERVL-MaLR regions. (Red: TS, Green: female controls, and Blue: male controls).

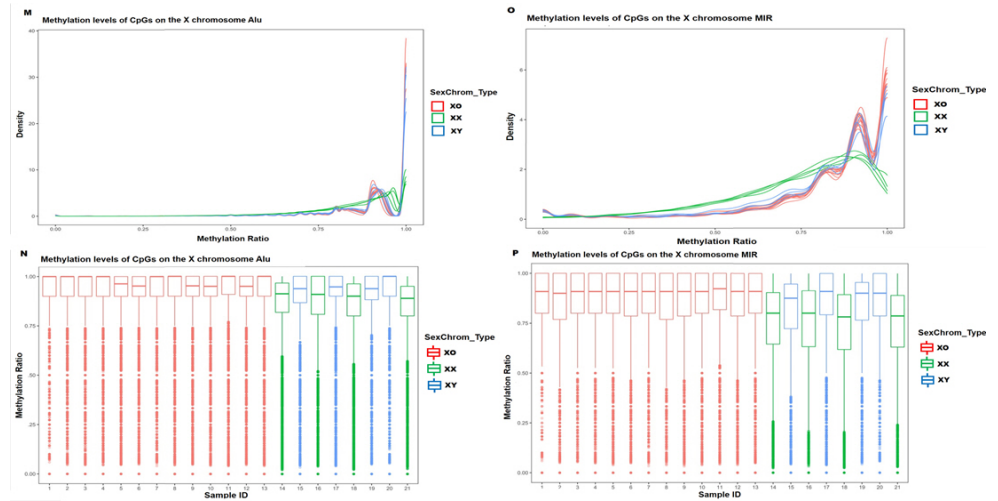


Figure S4. The methylation levels of 13 TS individuals and 8 healthy controls in the Alu and MIR regions on the chrX. The methylation density (M) and methylation ratio (N) of each sample in Alu regions. The methylation density (O) and methylation ratio (P) of each sample in the MIR regions. (Red: TS, Green: female controls, and Blue: male controls).

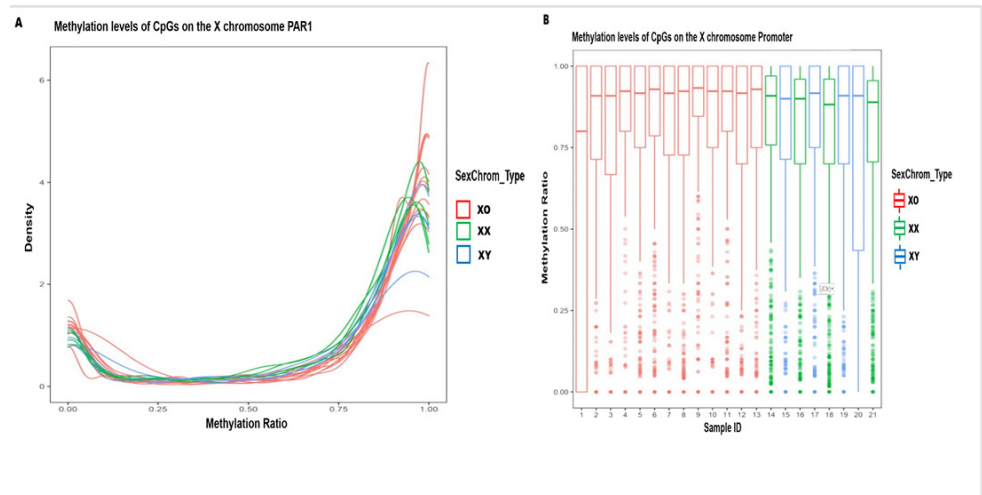


Figure S5. The methylation levels of 13 TS individuals and 8 healthy controls in the PAR1 regions on the chrX. The methylation density (A) and methylation ratio (B) of each sample in the PAR1

regions. (Red: TS, Green: female controls, and Blue: male controls).

Table S1. The phenotypes and genetic information of patients with 45X0 Turner syndrome.

[illegible]

Cardiac malformation														4/13
Bicuspid aortic valve (HP:0001647)	-	-	-	+	-	-	-	-	+	-	-	-	+	3/13
Aortic root dilation (HP:0002616)	-	+	-	+	-	-	-	-	+	-	-	-	-	3/13
Renal malformation														4/13
Medullary nephrocalcinosis (HP:0012408)	-	-	-	-	-	-	-	-	-	+	-	-	-	1/13
Horseshoe kidney (HP:0000085)	-	-	-	-	-	-	-	-	-	-	-	+	+	2/13
Hydronephrosis (HP:0000126)	-	-	-	-	-	-	-	-	-	-	-	+	-	1/13
Nephrolithiasis (HP:0000787)	-	+	-	-	-	-	-	-	-	-	-	-	-	1/13
Specific learning disability (HP:0001328)	+	+	-	-	-	-	-	-	-	-	-	-	-	2/13
Hypothyroidism (HP:0000821)	-	+	+	-	-	-	-	-	-	-	-	-	-	2/13

* Origin of chrX: M, maternal origin and P, paternal origin.

Table S2. Differentially methylated genes identified among the three groups of Turner syndrome 45X0 and controls 46XY and 46XX.

Gene	Set	Number
CNTNAP3	XO/XXhyper	8
BCOR	XO/XXhyper	
AC004870.3	XO/XXhyper	
AK2	XO/XXhyper	
MYT1L	XO/XXhyper	
OPCML	XO/XXhyper	
GRK1	XO/XXhyper	
RP11-453F18__B.1	XO/XXhyper	
MVB12B	XO/XXhypo	117
CXorf40A	XO/XXhypo	
RPL10	XO/XXhypo	
RP4-537K23.4	XO/XXhypo	
NDUFA1	XO/XXhypo	
VMA21	XO/XXhypo	
KLF8	XO/XXhypo	
RPL36A	XO/XXhypo	
RPL36A-HNRNP2	XO/XXhypo	
HUWE1	XO/XXhypo	
TBC1D25	XO/XXhypo	
AF196779.12	XO/XXhypo	
WDR45	XO/XXhypo	
ZNF630	XO/XXhypo	
PIM2	XO/XXhypo	
F8	XO/XXhypo	
RP11-85L21.4	XO/XXhypo	
SYP	XO/XXhypo	
TIMM17B	XO/XXhypo	
IKBKG	XO/XXhypo	
NUDT10	XO/XXhypo	
TMEM255A	XO/XXhypo	
ELK1	XO/XXhypo	
FAM127B	XO/XXhypo	
CCDC22	XO/XXhypo	
TMEM185A	XO/XXhypo	
BTBD11	XO/XXhypo	
WDR13	XO/XXhypo	
ESX1	XO/XXhypo	

PHF8	XO/XXhypo
ZNF674-AS1	XO/XXhypo
PNCK	XO/XXhypo
MAGED2	XO/XXhypo
KIAA2022	XO/XXhypo
WNK3	XO/XXhypo
G6PD	XO/XXhypo
CHST7	XO/XXhypo
ARHGEF9	XO/XXhypo
TAF9B	XO/XXhypo
TM4SF2	XO/XXhypo
TSPAN7	XO/XXhypo
EIF2AK4	XO/XXhypo
BCORL1	XO/XXhypo
PCDH19	XO/XXhypo
RP3-326L13.2	XO/XXhypo
SCML1	XO/XXhypo
CACNA1F	XO/XXhypo
WAS	XO/XXhypo
GPR50-AS1	XO/XXhypo
RP4-769N13.6	XO/XXhypo
RP4-769N13.7	XO/XXhypo
RAB33A	XO/XXhypo
SYN1	XO/XXhypo
ATP6AP1	XO/XXhypo
TRMT2B	XO/XXhypo
TRMT2B-AS1	XO/XXhypo
HS6ST2	XO/XXhypo
TIMM8A	XO/XXhypo
MORC4	XO/XXhypo
MAGIX	XO/XXhypo
IRAK1	XO/XXhypo
DLG3	XO/XXhypo
OTUD5	XO/XXhypo
AR	XO/XXhypo
AC115618.1	XO/XXhypo
HAUS7	XO/XXhypo
NHS	XO/XXhypo
MAGT1	XO/XXhypo
NUDT11	XO/XXhypo
NDUFB11	XO/XXhypo
PTCHD1	XO/XXhypo
CROCC	XO/XXhypo
U1	XO/XXhypo
BHLHB9	XO/XXhypo
HDAC6	XO/XXhypo
EBP	XO/XXhypo
LINC00086	XO/XXhypo
LONRF3	XO/XXhypo
ZBTB33	XO/XXhypo
BEX4	XO/XXhypo
ELF4	XO/XXhypo
NKAPP1	XO/XXhypo
TAZ	XO/XXhypo
RP11-66N11.8	XO/XXhypo
ZNF41	XO/XXhypo
HMGB3	XO/XXhypo
EMD	XO/XXhypo
SLC25A5-AS1	XO/XXhypo
STARD8	XO/XXhypo
MID1IP1	XO/XXhypo
MOSPD1	XO/XXhypo
FLNA	XO/XXhypo
LANCL3	XO/XXhypo
CXorf40B	XO/XXhypo
MAGEE1	XO/XXhypo

TAF7L	XO/XXhypo	
RAI2	XO/XXhypo	
SAMD11	XO/XXhypo	
SLC25A5	XO/XXhypo	
ZMYM3	XO/XXhypo	
BEX1	XO/XXhypo	
SRPX	XO/XXhypo	
IDS	XO/XXhypo	
ARHGAP6	XO/XXhypo	
UBL4A	XO/XXhypo	
RBMX2	XO/XXhypo	
PRRG1	XO/XXhypo	
PGK1	XO/XXhypo	
C1GALT1C1	XO/XXhypo	
AFF2	XO/XXhypo	
FMR1	XO/XXhypo	
LINC00629	XO/XXhypo	
SRPK3	XO/XXhypo	
IL13RA1	XO/XXhypo	
DOCK11	XO/XXhypo	
HOOK2	XO/XXhypo	
DNASE1L1	XO/XXhypo	
HOXB3	XO/XYhyper	3
HOXB-AS3	XO/XYhyper	
DTX2	XO/XYhyper	
TAF1	XO/XYhypo	
MVB12B	XO/XYhypo	
TNS1	XO/XYhypo	
AC093609.1	XO/XYhypo	16
MPL	XO/XYhypo	
EIF2AK4	XO/XYhypo	
FOXI2	XO/XYhypo	
BTBD11	XO/XYhypo	
HOXA3	XO/XYhypo	
HOXA-AS2	XO/XYhypo	
HOXA4	XO/XYhypo	
RP1-170O19.22	XO/XYhypo	
SPRN	XO/XYhypo	
CYP2E1	XO/XYhypo	
NAPRT1	XO/XYhypo	
CTU1	XO/XYhypo	
BCOR	XY/XXhyper	8
TAF1	XY/XXhyper	
RP11-453F18__B.1	XY/XXhyper	
LMTK3	XY/XXhyper	
AK2	XY/XXhyper	
SPRN	XY/XXhyper	
CYP2E1	XY/XXhyper	
AC093609.1	XY/XXhyper	
DNASE1L1	XY/XXhypo	121
FAM156B	XY/XXhypo	
DOCK11	XY/XXhypo	
AMMECR1	XY/XXhypo	
SSR4	XY/XXhypo	
FZD1	XY/XXhypo	
BEX1	XY/XXhypo	
ARX	XY/XXhypo	
EFNB1	XY/XXhypo	
C1GALT1C1	XY/XXhypo	
FAM157C	XY/XXhypo	
GPC3	XY/XXhypo	
TSPAN6	XY/XXhypo	
UBL4A	XY/XXhypo	
FMR1	XY/XXhypo	
HS6ST2	XY/XXhypo	
FAM156A	XY/XXhypo	

IDS	XY/XXhypo
AFF2	XY/XXhypo
RBMX2	XY/XXhypo
NHS	XY/XXhypo
SLITRK4	XY/XXhypo
SLC25A5	XY/XXhypo
PRRG1	XY/XXhypo
TM4SF2	XY/XXhypo
PABPC1L2A	XY/XXhypo
KIAA2022	XY/XXhypo
SRPX	XY/XXhypo
STARD8	XY/XXhypo
RAI2	XY/XXhypo
PGK1	XY/XXhypo
LANCL3	XY/XXhypo
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ARHGAP6	XY/XXhypo
CXorf40B	XY/XXhypo
MOSPD1	XY/XXhypo
WNK3	XY/XXhypo
MID1IP1	XY/XXhypo
NUDT11	XY/XXhypo
HMGB3	XY/XXhypo
TAF7L	XY/XXhypo
PCDH19	XY/XXhypo
SLC25A5-AS1	XY/XXhypo
ZBTB33	XY/XXhypo
ZNF41	XY/XXhypo
RP4-537K23.4	XY/XXhypo
EMD	XY/XXhypo
SOWAHD	XY/XXhypo
LONRF3	XY/XXhypo
BCORL1	XY/XXhypo
ZMYM3	XY/XXhypo
TAZ	XY/XXhypo
EBP	XY/XXhypo
NKAPP1	XY/XXhypo
ELF4	XY/XXhypo
HDAC6	XY/XXhypo
LINC00086	XY/XXhypo
GPR50-AS1	XY/XXhypo
NDUFB11	XY/XXhypo
PTCHD1	XY/XXhypo
PHF8	XY/XXhypo
BHLHB9	XY/XXhypo
WDR45	XY/XXhypo
RPL36A-HNRNPH2	XY/XXhypo
AC115618.1	XY/XXhypo
HAUS7	XY/XXhypo
OTUD5	XY/XXhypo
MAGT1	XY/XXhypo
DLG3	XY/XXhypo
MAGIX	XY/XXhypo
IRAK1	XY/XXhypo
MORC4	XY/XXhypo
AR	XY/XXhypo
ZNF630	XY/XXhypo
TIMM8A	XY/XXhypo
RP3-326L13.2	XY/XXhypo
SYN1	XY/XXhypo
TRMT2B	XY/XXhypo
TRMT2B-AS1	XY/XXhypo
ZNF75D	XY/XXhypo
ATP6AP1	XY/XXhypo

RP4-769N13.6	XY/XXhypo
RP4-769N13.7	XY/XXhypo
WAS	XY/XXhypo
NUDT10	XY/XXhypo
CACNA1F	XY/XXhypo
RAB33A	XY/XXhypo
SCML1	XY/XXhypo
TSPAN7	XY/XXhypo
CHST7	XY/XXhypo
HUWE1	XY/XXhypo
G6PD	XY/XXhypo
ZNF674-AS1	XY/XXhypo
MAGED2	XY/XXhypo
SYP	XY/XXhypo
WDR13	XY/XXhypo
TAF9B	XY/XXhypo
PNMA6A	XY/XXhypo
ARHGEF9	XY/XXhypo
CCDC22	XY/XXhypo
FAM127B	XY/XXhypo
TMEM185A	XY/XXhypo
ESX1	XY/XXhypo
TMEM255A	XY/XXhypo
PNCK	XY/XXhypo
ELK1	XY/XXhypo
TIMM17B	XY/XXhypo
F8	XY/XXhypo
RP11-85L21.4	XY/XXhypo
PIM2	XY/XXhypo
AF196779.12	XY/XXhypo
TBC1D25	XY/XXhypo
RPL36A	XY/XXhypo
RPL10	XY/XXhypo
CXorf40A	XY/XXhypo
VMA21	XY/XXhypo
KLF8	XY/XXhypo
NDUFA1	XY/XXhypo
SRPK3	XY/XXhypo

Table S3. Enriched GO and pathway lists.

Category	Category ID	GO	Description	PARENT_GO	LogP	Enrichment	Z-score	#TotalGen eInLibrary	#GeneIn nGO	#GeneIn HitList	#GeneIn GOAnd HitList	%InGO	STDV %InGO	GeneID	Hits	Log(q-value)	Gene List
GO Biological Processes	19	GO:000423	mitophagy	19_GO:0008152 metabolic process	-5.2	33	11	30,242	28	132	4	3	1.5	292 6901 10013 10075	SLC25A5 TAFAZZIN HDAC6 HUWE1	-0.82	MyList
GO Biological Processes	19	GO:0090042	tubulin deacetylation	19_GO:0008152 metabolic process	-4.6	53	12	30,242	13	132	3	2.3	1.3	2316 10013 5627 1	FLNA HDAC6 BEX4	-0.78	MyList
GO Biological Processes	19	GO:000422	autophagy of mitochondrion	19_GO:0008152 metabolic process	-4.5	14	7.8	30,242	81	132	5	3.8	1.7	292 6901 10013 10075 11152	SLC25A5 TAFAZZIN HDAC6 HUWE1 WD R45	-0.78	MyList
GO Biological Processes	19	GO:0061726	mitochondrion disassembly	19_GO:0009987 cellular process	-4.5	14	7.8	30,242	81	132	5	3.8	1.7	292 6901 10013 10075 11152	SLC25A5 TAFAZZIN HDAC6 HUWE1 WD R45	-0.78	MyList
GO Biological Processes	19	GO:0051090	regulation of DNA- binding transcription factor activity	19_GO:0050789 regulation of biological process	-3.9	4.7	5.2	30,242	440	132	9	6.8	2.2	367 2316 3654 6 872 8321 8517 2 8952 55859 4402 75	AR FLNA IRAK1 TA F1 FZD1 IKBK CCD C22 BEX1 EIF2AK4	-0.25	MyList
GO Biological Processes	19	GO:1903008	organelle disassembly	19_GO:0009987 cellular process	-3.8	10	6.4	30,242	114	132	5	3.8	1.7	292 6901 10013 10075 11152	SLC25A5 TAFAZZIN HDAC6 HUWE1 WD R45	-0.25	MyList
GO Biological Processes	19	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	19_GO:0048518 positive regulation of biological process	-3.8	7.4	5.8	30,242	186	132	6	4.5	1.8	2316 3654 7105 8517 11040 2895 2	FLNA IRAK1 TSPAN 6 IKBK PIM2 CCDC 22	-0.25	MyList
GO Biological Processes	19	GO:0061912	selective autophagy	19_GO:0008152 metabolic process	-3.6	13	6.8	30,242	69	132	4	3	1.5	292 6901 10013 10075	SLC25A5 TAFAZZIN HDAC6 HUWE1	-0.16	MyList
GO Biological Processes	19	GO:0016236	macroautophagy	19_GO:0008152 metabolic process	-3.5	5.4	5.1	30,242	295	132	7	5.3	2	292 4943 6901 8 517 10013 10075 11152	SLC25A5 TBC1D25 T FAZZIN IKBK HD AC6 HUWE1 WDR45	-0.08	MyList
GO Biological Processes	19	GO:0007005	mitochondrion organization	19_GO:0009987 cellular process	-3.4	4.1	4.6	30,242	509	132	9	6.8	2.2	292 1678 4694 6 901 10013 10075 10245 11152 54 539	SLC25A5 TIMM8A N DUF41 TAFAZZIN H DAC6 HUWE1 TIMM 17B WDR45 NDUFB11	-0.056	MyList
WikiPath ways	27	WP2858	Ectoderm differentiation		-3.4	8	5.5	30,242	144	132	5	3.8	1.7	10013 23133 232 29 54880 170302	HDAC6 PHF8 ARHG EF9 BCOR ARX	-0.056	MyList

GO Biological Processes	19	GO:0046777	protein autophosphorylation	19_GO:0008152 metabolic process	-3.3	6.1	5.1	30,242	227	132	6	4.5	1.8	3654 6011 6872 11040 65267 440275	IRAK1 GRK1 TAF1 PI M2 WNK3 EIF2AK4	-0.056	MyList
GO Biological Processes	19	GO:0061919	process utilizing autophagic mechanism	19_GO:0009987 cellular process	-3.3	3.9	4.5	30,242	528	132	9	6.8	2.2	292 4943 6901 8406 8517 10013 10075 11040 11152	SLC25A5 TBC1D25 T AFAZZIN SRPX IKBK G HDAC6 HUWE1 PI M2 WDR45	-0.056	MyList
GO Biological Processes	19	GO:0006914	autophagy	19_GO:0008152 metabolic process	-3.3	3.9	4.5	30,242	528	132	9	6.8	2.2	292 4943 6901 8406 8517 10013 10075 11040 11152	SLC25A5 TBC1D25 T AFAZZIN SRPX IKBK G HDAC6 HUWE1 PI M2 WDR45	-0.056	MyList
Reactome Gene Sets	6	R-HSA-9609507	Protein localization		-3.1	7	5.1	30,242	163	132	5	3.8	1.7	1678 2010 6901 8266 10245	TIMM8A EMD TAFA ZZIN UBL4A TIMM17 B	0	MyList
GO Biological Processes	19	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	19_GO:0023052 signaling	-3.1	5.5	4.7	30,242	249	132	6	4.5	1.8	2316 3654 7105 8517 11040 28952	FLNA IRAK1 TSPAN 6 IKBK G PIM2 CCDC 22	0	MyList
Reactome Gene Sets	6	R-HSA-9012999	RHO GTPase cycle		-3.1	4.1	4.4	30,242	449	132	8	6.1	2.1	395 537 2010 4810 7454 9754 23229 139818	ARHGAP6 ATP6AP1 EMD NHS WAS STA RD8 ARHGEF9 DOC K11	0	MyList
KEGG Pathway	24	ko03022	Basal transcription factors		-3	15	6.3	30,242	45	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
GO Biological Processes	19	GO:0051091	positive regulation of DNA-binding transcription factor activity	19_GO:0050789 regulation of biological process	-3	5.3	4.6	30,242	260	132	6	4.5	1.8	367 3654 6872 8321 8517 55859	AR IRAK1 TAF1 FZD 1 IKBK G BEX1	0	MyList
Reactome Gene Sets	6	R-HSA-194315	Signaling by Rho GTPases		-3	3.2	4	30,242	707	132	10	7.6	2.3	367 395 537 2010 2316 4810 7454 9754 23229 139818	AR ARHGAP6 ATP6 AP1 EMD FLNA NH S WAS STARD8 ARH GEF9 DOCK11	0	MyList
Reactome Gene Sets	6	R-HSA-76042	RNA Polymerase II Transcription Initiation And Promoter Clearance		-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
Reactome Gene Sets	6	R-HSA-73779	RNA Polymerase II Transcription Pre-Initiation And Promoter Opening		-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
Reactome Gene Sets	6	R-HSA-73776	RNA Polymerase II Promoter Escape		-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
Reactome Gene Sets	6	R-HSA-75953	RNA Polymerase II Transcription Initiation		-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList

Reactome Gene Sets	6	R-HSA-167162	RNA Polymerase II HIV Promoter Escape	-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList	
Reactome Gene Sets	6	R-HSA-167161	HIV Transcription Initiation	-2.9	15	6.2	30,242	47	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList	
KEGG Pathway	24	hsa03022	Basal transcription factors	-2.9	14	6.1	30,242	48	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList	
Reactome Gene Sets	6	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	-2.9	3.2	3.9	30,242	723	132	10	7.6	2.3	367 395 537 2010 2316 4810 7454 9754 23229 139818	AR ARHGAP6 ATP6AP1 EMD FLNA INH1 WAS STARD8 ARHGEF9 DOCK11	0	MyList	
GO Biological Processes	19	GO:0043433	negative regulation of DNA-binding transcription factor activity	-2.9	6.2	4.7	30,242	185	132	5	3.8	1.7	19_GO:0050789 regulation of biological process	2316 3654 6872 28952 440275	FLNA IRAK1 TAF1 CDC22 EIF2AK4	0	MyList
Reactome Gene Sets	6	R-HSA-1793185	Chondroitin sulfate/dermatan sulfate metabolism	--2.9	14	6	30,242	50	132	3	2.3	1.3	2719 3423 56548	GPC3 IDS CHST7	0	MyList	
GO Biological Processes	19	GO:0071478	cellular response to radiation	-2.9	6.1	4.7	30,242	187	132	5	3.8	1.7	19_GO:0050896 response to stimulus	2002 2332 6011 6872 440275	ELK1 FMR1 GRK1 TAF1 EIF2AK4	0	MyList
GO Biological Processes	19	GO:0009896	positive regulation of catabolic process	-2.8	3.7	4	30,242	493	132	8	6.1	2.1	19_GO:0048518 positive regulation of biological process	292 2332 2719 6872 8517 10075 11040 28952	SLC25A5 FMR1 GPC3 TAF1 IKBK HUWE1 PIM2 CCDC22	0	MyList
GO Biological Processes	19	GO:0007249	I-kappaB kinase/NF-kappaB signaling	-2.8	4.9	4.3	30,242	281	132	6	4.5	1.8	19_GO:0023052 signaling	2316 3654 7105 8517 11040 28952	FLNA IRAK1 TSPAN6 IKBK PIM2 CCDC22	0	MyList
GO Biological Processes	19	GO:2000300	regulation of synaptic vesicle exocytosis	-2.8	13	5.7	30,242	54	132	3	2.3	1.3	19_GO:0051179 localization	2332 6853 6855	FMR1 SYN1 SYP	0	MyList
Reactome Gene Sets	6	R-HSA-1638091	Heparan sulfate/heparin (HS-GAG) metabolism	-2.7	12	5.7	30,242	55	132	3	2.3	1.3	2719 3423 90161	GPC3 IDS HS6ST2	0	MyList	
GO Biological Processes	19	GO:0006360	transcription by RNA polymerase I	-2.7	12	5.7	30,242	55	132	3	2.3	1.3	19_GO:0008152 metabolic process	2316 6872 23133	FLNA TAF1 PHF8	0	MyList
Reactome Gene Sets	6	R-HSA-71387	Metabolism of carbohydrates	-2.7	4.7	4.2	30,242	295	132	6	4.5	1.8	2539 2719 3423 5230 56548 90161	G6PD GPC3 IDS PGK1 CHST7 HS6ST2	0	MyList	

GO Biological Processes	19	GO:0010257	NADH dehydrogenase complex assembly	19_GO:0009987 cellular process	-2.7	12	5.5	30,242	57	132	3	2.3	1.3	4694 6901 54539	NDUFA1 TFAFAZZIN NDUFB11	0	MyList
GO Biological Processes	19	GO:0032981	mitochondrial respiratory chain complex I assembly	19_GO:0009987 cellular process	-2.7	12	5.5	30,242	57	132	3	2.3	1.3	4694 6901 54539	NDUFA1 TFAFAZZIN NDUFB11	0	MyList
GO Biological Processes	19	GO:0071482	cellular response to light stimulus	19_GO:0050896 response to stimulus	-2.7	7.4	4.7	30,242	124	132	4	3	1.5	2332 6011 6872 440275	FMR1 GRK1 TAF1 EI F2AK4	0	MyList
Reactome Gene Sets	6	R-HSA-1630316	Glycosaminoglycan metabolism		-2.7	7.4	4.7	30,242	124	132	4	3	1.5	2719 3423 56548 190161	GPC3 IDS CHST7 HS 6ST2	0	MyList
GO Biological Processes	19	GO:0050808	synapse organization	19_GO:0009987 cellular process	-2.6	3.8	3.8	30,242	426	132	7	5.3	2	1741 2316 6853 8321 10013 8082 3 139065	DLG3 FLNA SYN1 F ZD1 HDAC6 BHLHB9 SLITRK4	0	MyList
Reactome Gene Sets	6	R-HSA-1268020	Mitochondrial protein import		-2.6	11	5.2	30,242	64	132	3	2.3	1.3	1678 6901 10245	TIMM8A TFAFAZZIN TIMM17B	0	MyList
Canonical Pathways	11	M34	PID TCR PATHWAY		-2.6	11	5.2	30,242	64	132	3	2.3	1.3	2316 7454 8517	FLNA WAS IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-450294	MAP kinase activation		-2.6	11	5.2	30,242	64	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
GO Biological Processes	19	GO:0009416	response to light stimulus	19_GO:0050896 response to stimulus	-2.5	4.3	3.9	30,242	321	132	6	4.5	1.8	778 2002 2332 6 011 6872 440275	CACNA1F ELK1 FMR 1 GRK1 TAF1 EIF2AK 4	0	MyList
Reactome Gene Sets	6	R-HSA-162599	Late Phase of HIV Life Cycle		-2.5	6.6	4.4	30,242	139	132	4	3	1.5	6872 51616 5445 7 89853	TAF1 TAF9B TAF7L MVB12B	0	MyList
Canonical Pathways	11	M153	PID P75 NTR PATHWAY		-2.5	10	5	30,242	68	132	3	2.3	1.3	3654 8517 55859	IRAK1 IKBKG BEX1	0	MyList
GO Biological Processes	19	GO:0051129	negative regulation of cellular component organization	19_GO:0048519 negative regulation of biological process	-2.5	3	3.5	30,242	691	132	9	6.8	2.2	292 367 395 231 6 7454 10013 10 075 23133 58526	SLC25A5 AR ARHGA P6 FLNA WAS HDA C6 HUWE1 PHF8 MI D1IP1	0	MyList
GO Biological Processes	19	GO:0016241	regulation of macroautophagy	19_GO:0050789 regulation of biological process	-2.5	6.5	4.3	30,242	141	132	4	3	1.5	292 4943 8517 1 0013	SLC25A5 TBC1D25 IK BKG HDAC6	0	MyList
GO Biological Processes	19	GO:0071214	cellular response to abiotic stimulus	19_GO:0050896 response to stimulus	-2.5	4.1	3.8	30,242	333	132	6	4.5	1.8	2002 2332 6011 6872 65267 4402 75	ELK1 FMR1 GRK1 T AF1 WNK3 EIF2AK4	0	MyList
GO Biological Processes	19	GO:0104004	cellular response to environmental stimulus	19_GO:0050896 response to stimulus	-2.5	4.1	3.8	30,242	333	132	6	4.5	1.8	2002 2332 6011 6872 65267 4402 75	ELK1 FMR1 GRK1 T AF1 WNK3 EIF2AK4	0	MyList

GO Biological Processes	19	GO:0045732	positive regulation of protein catabolic process	19_GO:0048518 positive regulation of biological process	-2.4	4.9	4	30,242	232	132	5	3.8	1.7	2332 2719 6872 10075 28952	FMR1 GPC3 TAF1 HWE1 CCDC22	0	MyList
GO Biological Processes	19	GO:0022411	cellular component disassembly	19_GO:0009987 cellular process	-2.4	3.6	3.6	30,242	448	132	7	5.3	2	292 4943 6901 10013 10075 11152 58526	SLC25A5 TBC1D25 TFAFAZZIN HDAC6 HWE1 WDR45 MID1IP1	0	MyList
Reactome Gene Sets	6	R-HSA-162906	HIV Infection		-2.4	4.9	4	30,242	234	132	5	3.8	1.7	292 6872 51616 54457 89853	SLC25A5 TAF1 TAF9B TAF7L MVB12B	0	MyList
Reactome Gene Sets	6	R-HSA-448424	Interleukin-17 signaling		-2.4	9.5	4.8	30,242	72	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-167172	Transcription of the HIV genome		-2.4	9.4	4.8	30,242	73	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
GO Biological Processes	19	GO:0010639	negative regulation of organelle organization	19_GO:0048519 negative regulation of biological process	-2.4	4	3.7	30,242	348	132	6	4.5	1.8	292 395 7454 10013 10075 58526	SLC25A5 ARHGAP6 WAS HDAC6 HWE1 MID1IP1	0	MyList
Reactome Gene Sets	6	R-HSA-162587	HIV Life Cycle		-2.3	6	4.1	30,242	152	132	4	3	1.5	6872 51616 54457 89853	TAF1 TAF9B TAF7L MVB12B	0	MyList
GO Biological Processes	19	GO:0031346	positive regulation of cell projection organization	19_GO:0048518 positive regulation of biological process	-2.3	3.9	3.6	30,242	353	132	6	4.5	1.8	2316 2332 8321 9696 80823 139818	FLNA FMR1 FZD1 CROCC BHLHB9 DOCK11	0	MyList
WikiPath ways	27	WP4666	Hepatitis B infection		-2.3	6	4.1	30,242	154	132	4	3	1.5	537 2002 3654 8517	ATP6AP1 ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-9013148	CDC42 GTPase cycle		-2.3	5.9	4.1	30,242	155	132	4	3	1.5	7454 9754 23229 139818	WAS STARD8 ARHGAP9 DOCK11	0	MyList
KEGG Pathway	24	hsa05230	Central carbon metabolism in cancer		-2.3	8.8	4.6	30,242	78	132	3	2.3	1.3	2539 8266 29911	G6PD UBL4A HOOK2	0	MyList
GO Biological Processes	19	GO:0051494	negative regulation of cytoskeleton organization	19_GO:0048519 negative regulation of biological process	-2.2	5.6	3.9	30,242	163	132	4	3	1.5	395 7454 10013 58526	ARHGAP6 WAS HDAC6 MID1IP1	0	MyList
GO Biological Processes	19	GO:0007420	brain development	19_GO:0032502 developmental process	-2.2	2.7	3.2	30,242	753	132	9	6.8	2.2	2316 2334 2539 6872 8321 23133 57526 139411 170302	FLNA AFF2 G6PD TAF1 FZD1 PHF8 PCDH19 PTCHD1 ARX	0	MyList

Reactome Gene Sets	6	R-HSA-674695	RNA Polymerase II Pre-transcription Events	-2.2	8.2	4.4	30,242	84	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
Reactome Gene Sets	6	R-HSA-168142	Toll Like Receptor 10 (TLR10) Cascade	-2.2	8.1	4.3	30,242	85	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-975871	MyD88 cascade initiated on plasma membrane	-2.2	8.1	4.3	30,242	85	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-168176	Toll Like Receptor 5 (TLR5) Cascade	-2.2	8.1	4.3	30,242	85	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
GO Biological Processes	19	GO:1902904	negative regulation of supramolecular fiber organization	-2.2	5.5	3.9	30,242	167	132	4	3	1.5	395 7454 10013 58526	ARHGAP6 WAS HDAC6 MID1 IP1	0	MyList
GO Biological Processes	19	GO:0046928	regulation of neurotransmitter secretion	-2.2	8	4.3	30,242	86	132	3	2.3	1.3	2332 6853 6855	FMR1 SYN1 SYP	0	MyList
GO Biological Processes	19	GO:0030901	midbrain development	-2.1	7.6	4.2	30,242	90	132	3	2.3	1.3	2539 6872 8321	G6PD TAF1 FZD1	0	MyList
Reactome Gene Sets	6	R-HSA-975138	TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	-2.1	7.6	4.1	30,242	91	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
GO Biological Processes	19	GO:0034644	cellular response to UV	-2.1	7.6	4.1	30,242	91	132	3	2.3	1.3	2332 6872 440275	FMR1 TAF1 EIF2AK4	0	MyList
GO Biological Processes	19	GO:0042176	regulation of protein catabolic process	-2.1	3.5	3.3	30,242	391	132	6	4.5	1.8	2316 2332 2719 6872 10075 28952	FLNA FMR1 GPC3 TAF1 HUWE1 CCDC22	0	MyList
KEGG Pathway	24	hsa05161	Hepatitis B	-2.1	5.2	3.7	30,242	177	132	4	3	1.5	537 2002 3654 8517	ATP6AP1 ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-975155	MyD88 dependent cascade initiated on endosome	-2.1	7.5	4.1	30,242	92	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-6804756	Regulation of TP53 Activity through Phosphorylation	-2.1	7.5	4.1	30,242	92	132	3	2.3	1.3	6872 51616 54457	TAF1 TAF9B TAF7L	0	MyList
GO Biological Processes	19	GO:0051668	localization within membrane	-2.1	2.8	3.1	30,242	651	132	8	6.1	2.1	367 1678 1741 2316 2719 8266 28952 65267	AR TIMM8A DLG3 FBLN4 GPC3 UBL4A CDC22 WNK3	0	MyList

Reactome Gene Sets	6	R-HSA-168181	Toll Like Receptor 7/8 (TLR7/8) Cascade		-2.1	7.4	4.1	30,242	93	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBK	0	MyList
GO Biological Processes	19	GO:0033108	mitochondrial respiratory chain complex assembly	19_GO:0009987 cellular process	-2.1	7.4	4.1	30,242	93	132	3	2.3	1.3	4694 6901 54539	NDUFA1 TAFAZZIN NDUFB11	0	MyList
GO Biological Processes	19	GO:0044089	positive regulation of cellular component biogenesis	19_GO:0048518 positive regulation of biological process	-2.1	3.1	3.2	30,242	520	132	7	5.3	2	2316 2332 7454 9696 80823 139065 139818	FLNA FMR1 WAS CR OCC BHLHB9 SLITR K4 DOCK11	0	MyList
GO Biological Processes	19	GO:0019693	ribose phosphate metabolic process	19_GO:0008152 metabolic process	-2.1	3.5	3.3	30,242	397	132	6	4.5	1.8	204 2539 5230 6901 55190 170685	AK2 G6PD PGK1 TAFAZZIN NUDT11 NUDT10	0	MyList
Reactome Gene Sets	6	R-HSA-168164	Toll Like Receptor 3 (TLR3) Cascade		-2.1	7.3	4.1	30,242	94	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBK	0	MyList
Reactome Gene Sets	6	R-HSA-9013423	RAC3 GTPase cycle		-2.1	7.3	4.1	30,242	94	132	3	2.3	1.3	395 2010 4810	ARHGAP6 EMD NHS	0	MyList
GO Biological Processes	19	GO:0060322	head development	19_GO:0032502 developmental process	-2.1	2.6	3	30,242	796	132	9	6.8	2.2	2316 2334 2539 6872 8321 23133 57526 139411 170302	FLNA AFF2 G6PD TAF1 FZD1 PHF8 PCDH19 PTCHD1 ARX	0	MyList
GO Biological Processes	19	GO:1903827	regulation of cellular protein localization	19_GO:0051179 localization	-2.1	3	3.1	30,242	527	132	7	5.3	2	367 2010 2316 2719 9696 10075 65267	AR EMD FLNA GPC3 CROCC HUWE1 WINK3	0	MyList
Reactome Gene Sets	6	R-HSA-168138	Toll Like Receptor 9 (TLR9) Cascade		-2.1	7.2	4	30,242	96	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBK	0	MyList
Reactome Gene Sets	6	R-HSA-9013149	RAC1 GTPase cycle		-2	5	3.6	30,242	185	132	4	3	1.5	2010 4810 7454 139818	EMD NHS WAS DOCK11	0	MyList
Reactome Gene Sets	6	R-HSA-166166	MyD88-independent TLR4 cascade		-2	6.9	3.9	30,242	99	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBK	0	MyList
Reactome Gene Sets	6	R-HSA-937061	TRIF(TICAM1)-mediated TLR4 signaling		-2	6.9	3.9	30,242	99	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBK	0	MyList
GO Biological Processes	19	GO:0060996	dendritic spine development	19_GO:0032502 developmental process	-2	6.9	3.9	30,242	99	132	3	2.3	1.3	2332 10013 80823	FMR1 HDAC6 BHLHB9	0	MyList
GO Biological Processes	19	GO:0051588	regulation of neurotransmitter transport	19_GO:0051179 localization	-2	6.9	3.9	30,242	100	132	3	2.3	1.3	2332 6853 6855	FMR1 SYN1 SYP	0	MyList

GO Biological Processes	19	GO:0006626	protein targeting to mitochondrion	19_GO:0051179 localization	-2	6.9	3.9	30,242	100	132	3	2.3	1.3	1678 10,075 10245	TIMM8A HUWE1 TIMM17B	0	MyList
GO Biological Processes	19	GO:0050890	cognition	19_GO:0032501 multicellular organismal process	-2	3.9	3.3	30,242	296	132	5	3.8	1.7	2334 80823 84061 139411 440275	AFF2 BHLHB9 MAGT1 PTCHD1 EIF2AK4	0	MyList
Reactome Gene Sets	6	R-HSA-9633012	Response of EIF2AK4 (GCN2) to amino acid deficiency		-2	6.8	3.9	30,242	101	132	3	2.3	1.3	6134 6173 44,0275	RPL10 RPL36A EIF2AK4	0	MyList
Reactome Gene Sets	6	R-HSA-168188	Toll Like Receptor TLR6:TLR2 Cascade		-2	6.8	3.9	30,242	101	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
Reactome Gene Sets	6	R-HSA-166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane		-2	6.8	3.9	30,242	101	132	3	2.3	1.3	2002 3654 8517	ELK1 IRAK1 IKBKG	0	MyList
GO Biological Processes	19	GO:0050821	protein stabilization	19_GO:0065007 biological regulation	-2	4.8	3.5	30,242	191	132	4	3	1.5	2316 6872 11040 51616	FLNA TAF1 PIM2 TAF9B	0	MyList

Table S4. Candidate genes of X0_Hypomethylated which were also detected as hypomethylated in TSvs46XX in previous research.

PNAS2020	CLINEPI2015	X0hypo	PNAS2020 CLINEPI2015	PNAS2020 X0hypo	CLINEPI2015 X0hypo	PNAS2020 CLINEPI2015 X0hypo
RP11-1148L6.9	38961	MVB12B	5	NUDT10	CYP2E1	WDR45
PFKFB1	40057	RP4-537K23.4	FTSJ1	TAF9B	HOXA4	CXorf40B
XX-	TLE1	AF196779.12	EFNB1	TIMM17B	EMD	NDUFA1
FW83563B9.5	MGC3207	ZNF630	IGBP1	ZNF674-AS1	CXorf40A	NDUFB11
SNORA70	FAM83A	RP11-85L21.4	APEX2	FAM127B	SYN	ESX1
AL049564.1	GLUD1	IKBKG	CSTF2	RP4-769N13.6	OTUD5	IDS
LINC00894	CST9L	BTBD11	RNF113A	TRMT2B	UBL4A	CHST7
AIFM1	CCL26	TM4SF2	PQBP1	PCDH19	WNK3	PIM2
AF196970.3	NPR2	EIF2AK4	LDOC1	RAI2	ZMYM3	C1GALT1C1
FAM127A	HLA-DQB2	CACNA1F	RBM10	NKAPP1	AFF2	TAF1
SLC25A53	SEC31L2	GPR50-AS1	SLC25A14	RPL36A-HNRNPH2	ARHGEF9	SYN1
ERCC6L	SH3BP2	TRMT2B-AS1	NKAP	F8	MOSPD1	ELK1
FAM104B	LYPD3	AC115618.1	ATG4A	TMEM255A	BCORL1	G6PD
HNRNPH2	ZNF593	HAUS7	PSMD10	NUDT11	RBMX2	LONRF3
OGT	NAV1	CROCC	DKC1	VMA21	NHS	RPL36A
FANCB	HP	U1	DACH2	RP11-66N11.8	PNCK	MAGT1
ZNF674	DHODH	LINC00086	SOX3	HUWE1	PGK1	KLF8
OOEP	AIF1	TAF7L	YIPF6	HS6ST2	TSPAN7	CCDC22
RLIM	STMN1	SAMD11	PRAF2	RP3-326L13.2	TAZ	ARHGAP6
DPPA5	CIA51	DOCK11	GPR101	MORC4		WAS
ZNF81	ZFYVE19	HOOK2	GLA	TBC1D25		MAGEE1
AL022578.1	GPR109B	TNS1	UTP14A	LINC00629		HDAC6
RP11-308D16.2	FYB	MPL	MOSPD2	KIAA2022		TIMM8A
GPKOW	VAMP5	FOXI2	DDX43		TMEM185A	FLNA
RP13-228J13.9	PDZD11	HOXA3	TFE3		AC093609.1	BHLHB9
RP11-348F1.2	TACSTD1	HOXA-AS2	ARMCX5	BEX4		SCML1
RP11-348F1.3	GPR109A	RP1-170O19.22	RPL39	MAGIX		ZBTB33
SPACA5	HTRA4	SPRN	KIF4A	PRRG1		EBP
ZNF182	AMT	NAPRT1	ATRX	PTCHD1		SRPX
THOC2	P2RY2	CTU1	TSPYL2		SLC25A5-AS1	ZNF41
CLCN5	VENTX		MID2		RP4-769N13.7	HMGB3
STK26	FLJ30046		ZCCHC12	SRPK3		IRAK1
TAB3-AS2	F12		NR0B1			IL13RA1
SMIM10	STK31		ZNF449			LANCL3
KRBOX4	ZNF541		OPHN1			AR
ZNF75D	C14orf162		SLC35A2			DLG3
PIH1D3	TRPM2		MAGEH1			DNASE1L1
NUP62CL	DEFA1		IDH3G			PHF8
AL590410.1	EPN3		RBMX			RAB33A
BTB	CCIN		PIGA			SLC25A5
MAMLD1	MAN2A2		COX7B			ELF4
FAM127C	LMO2		ARMCX3			WDR13
SNORD61	CLEC4C		FUNDC2			MAGED2
SMIM10L2B	EPAS1		RAB39B			MID1IP1
AC234775.1	ARS2		NSDHL			RPL10
ARMCX3-AS1	BRD4		CETN2			STARD8
ZCCHC18	C6orf68		NKRF			FMR1
NCL	DYRK4		WDR44			ATP6AP1
HSPB1P2	HPS4		SUV39H1			BEX1
H3F3AP1	TMEM102		ZDHHC15			
RP1-161N10.1	LTBR		LAS1L			
SMAD5-AS1_2	POR		MSN			
RHOXF1P1	ZNF124		FHL1			
CXorf57	RABGEF1		ACSL4			
ZNF280C	AMDHD1		ARAF			
CELSR3-AS1	PPP4R2		MCTS1			
OVCH1-AS1	HMGNI		HDAC8			
AMER1	CIDEB		CXorf56			
DGKK	NFE2		PRDX4			

RAC1P4	NR1I2	ABCB7
ARHGAP36	SFTPD	SLITRK4
LINC01201	HSPA2	KLHL34
GPRASP1	BRCA2	RRAGB
RP11-314A15.2	HAL	XKRX
FAM122B	SLC22A3	XK
FGF13-AS1	FBXL5	MECP2
AC131011.1	ITGB1BP1	PGRMC1
MBNL3	RPS6KC1	IL1RAPL2
HDX	ENTPD1	FAM58A
PBDC1	ARID3A	PHKA1
APOOL	APOB	CNKSR2
TSR2	P2RY13	MBTPS2
RP1-274L7.1	LPO	PCSK1N
RP6-24A23.3	BTBD6	HTATSF1
MYCLP1	SERPINF1	FAM122C
TSPAN6	ZNF266	NONO
RP3-389A20.5	CTBP1	FGD1
LAGE3	BIRC4BP	RAP2C
SAT1	KLF1	POU3F4
RP13-314C10.5	RAB8A	SNX12
FAM156A	CD244	SH3BGR1
ZC4H2	HSPC159	SMS
HMGN5	TIGD5	FAM50A
KANTR	LGP1	UPF3B
RP11-236P24.3	IL27	INGX
PRICKLE3	CACYBP	CHM
NXT2	CTSG	SYTL4
MORF4L2-AS1	RPS6KA1	PIN4
LINC00893	FLJ25084	ATP6AP2
RP1-137H15.2	IFITM3	ARX
PCYT1B-AS1	SCMH1	UXT
LINC01285	GPR21	PHKA2
SMIM10L2A	AQP9	GNL3L
WDR53	LYAR	MTM1
ZXDB	PRTN3	GABRQ
AL158069.1	FLJ40919	MTMR8
FAM155B	GSG1	TMLHE
Y_RNA	LYZ	AMOT
snoU13	H2BFS	NAP1L2
MID1IP1-AS1	SEPT10	ZIC3
CENPI	ELA2	SLITRK2
LINC01381	UNQ830	GPC4
UXT-AS1	CEACAM6	MAGEE2
TLE1P1	NKG7	ATP7A
RNU6-800P	IER2	UBE2A
RP13-43E11.1	SPAG4	PRPS2
AL035088.1	SGK2	EDA
LINC01560	LAIR1	TCEAL1
RPS26P11	SLC44A2	PRPS1
VPS28	PABPN1	MTMR1
MSL3	PARVG	USP51
ZDHHC9	ACYP2	CDX4
MIR718	CLEC5A	TCEAL8
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RP5-1091N2.9	KLHDC7B	GSPT2
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RP13-210D15.8	RBM35B	GLUD2
BTF3P8	KCNE1	RP2
RAP2C-AS1	GATAD2B	RPS6KA3
CDR1-AS	C18orf22	PAK3
BX842568.4	HIST1H2AJ	TCEAL2
RPS6KA6	ATP6V1E2	GPC3
CXorf58	KCNQ1	SLC10A3
APOO	FUT7	STAG2

MAP3K15	CYP27B1	GRIA3
ENOX2	LOC158160	TMSB4X
SASH3	FCGR3B	MAOA
MIR5003	P518	PKD3
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FCF1P4	CSF3R	ARMCX6
PJA1	KNS2	HPRT1
RP11-287D1.4	KIAA0427	DYNLT3
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RP5-1000K24.2	GLRX2	SLC7A3
CFP	C6orf105	SCML2
NCBP2L	LGALS4	USP11
FGF13	CLEC12A	ARMCX1
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DUSP9	CCT6A	IL1RAPL1
RP13-188A5.1	GPR84	ZNF185
CENPVP3	ZNF696	ABCD1
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CMC4	MGC11257	UBQLN2
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UPRT	FLJ35773	PHF6
AL772400.1	LOC92345	ERAS
DERL2	C14orf58	PLP2
POLA1	CIZ1	PDHA1
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POU5F1	SLC22A18	
AC234031.1	PILRA	
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RP11-641J8.1	FLJ35530	
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AC003001.1	FKBP11	
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RNF128	RNF14	
RP11-521C20.5	FXYP1	
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FOXO4	SLC45A1	
AC005041.11	PNPLA2	
CTD-2269E23.4	CSTA	
RP1-164F3.8	MYL9	
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AL691477.1	TATDN1	
TREX2	IL21R	
RNU6-894P	PREX1	
RP11-21G20.3	SH3BP5	
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AMMECR1-IT1	LOC132321	
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CITED1	AGXT	
MIR3202-2	C15orf5	
RP5-972B16.2	MGC41945	
BX842568.2	APOA4	
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GPR45	P2RX1	
GHc-857G6.7	PIP3-E	
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RP11-68I3.4	CLTCL1	
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CHIC1	SEC61G	
MAP2K4P1	GPR25	

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RP11-412D9.4	NDUFS2
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LINGO3	CYP7B1
RP11-149B9.2	GRB7
SPIN3	MS4A6A
COL4A5	DLK1
RP11-62J1.4	IFNGR2
RP11-548B3.3	FOLR3
SOWAHD	FCN1
FZD2	LCN2
RP11-320G24.1	XYLB
AF196972.9	IL19
FMR1-AS1	URP2
JADE3	ZNF710
OR11N1P	RPUSD3
RP1-149M18.4	THSD3
CFAP47	FFAR3
FMR1-AS1_2	KCNQ1DN
RNF5P1	SPATC1
PRDM9	EIF2B3
PNMA5	SYCP1
CH17-340M24.3	ABTB1
BEX5	RNASE3
TMSB15A	PTGFRN
ARHGEF6	FUT3
OSBPL5	NOL3
RP5-998H6.2	SLC26A8
CSNK1G2P1	USP10
MYCBPAP	NAGPA
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	TIGD2
	SERPINB10
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	GABRR1
	EPHA2
	TFAP2E
	ACPP
	LEP
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	CEBPE
	GP5
	PRR3
	AZU1
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	RAB34
	TP53I3
	BCL2
	TREM2
	TACSTD2
	MPO
	CEP1
	CSPG5
	CASP6
	C19orf24

CPM
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VWCE
RAC3
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VTN
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HIVEP3
LYK5
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CEACAM3
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LRPAP1
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UCK1
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CBFA2T3

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LAIR2
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PLXDC1
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HRASLS5
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MRPL28
POU3F1
TRPM6
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HNRPF
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BEX2

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CXorf41
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SMARCA1
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ZNF6
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CLDN2
AVPR2

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FSHPRH1
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COVA1
NOX1
RBBP7
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FRMPD4
MAGED1
PNPLA4
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CXorf21
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TCEAL4
CYSLTR1
NLGN3
PCTK1
CLIC2
GLRA2
PLXNB3
AGTR2
TLR7
BGN
RENBP
PRRG3
SMC1L1
KCND1
CXorf12
