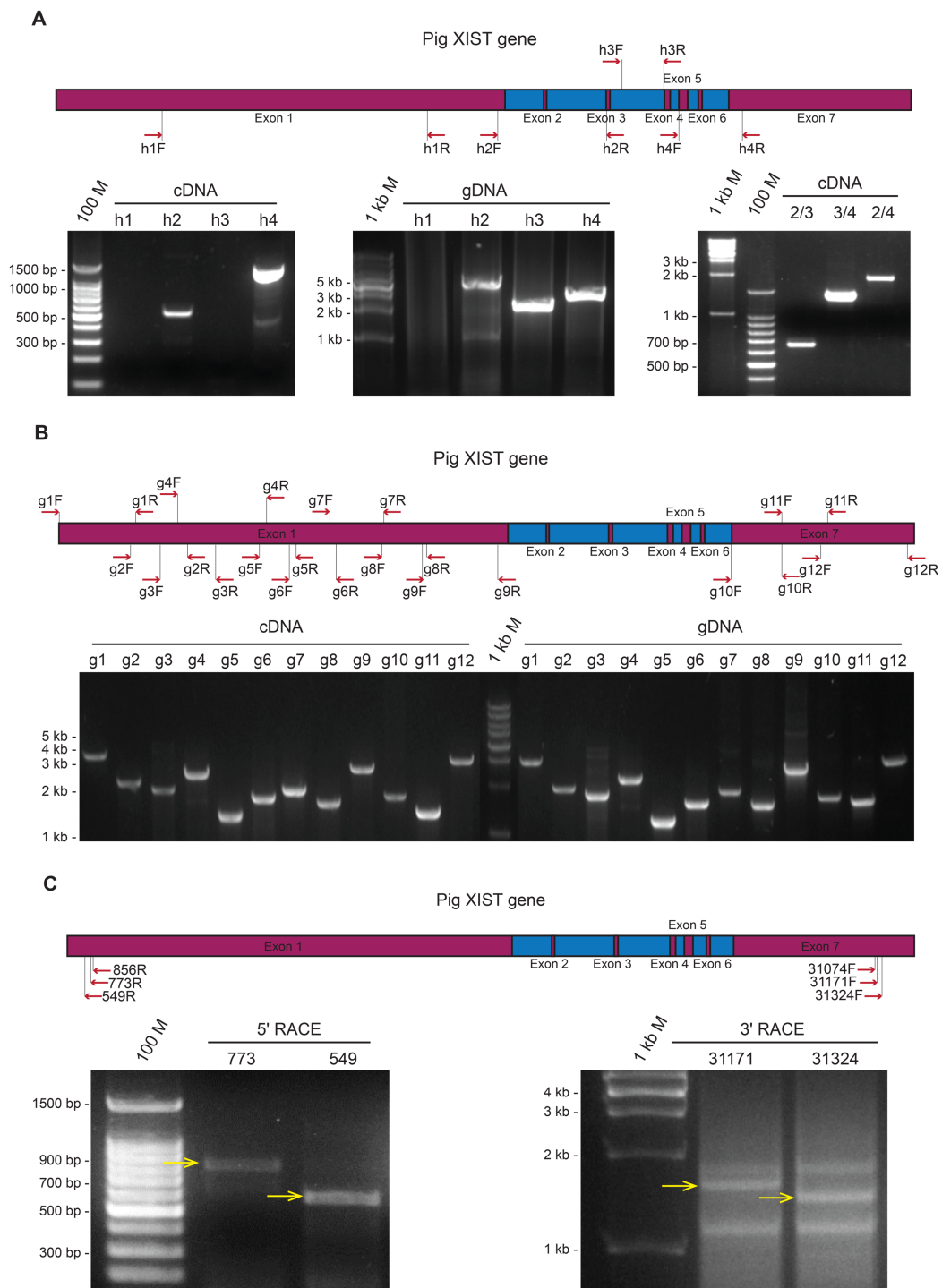**Figure S1**

Figure S1 Identification of the full-length RNA sequence of porcine *XIST*.

(A) PCR products of homologous regions amplified in porcine cDNA and genome. Red arrowheads indicate the primer positions. (B) PCR products of overlapped overlapping primers amplified in porcine cDNA and genome. Red arrowheads indicate the primer positions. (C) Identification of the transcriptional start site and transcriptional stop site of porcine *XIST* using 5′-RACE and 3′-RACE respectively. To avoid interruptions of undesirable nonspecific bands, we designed two reverse primers at different positions. Therefore, the sizes of correct bands is dependent on the different primer positions. Yellow arrowheads indicate the correct bands. Red arrowheads indicate the primer positions.

Figure S2

A

S4

Chr X

XIST

Maternal_Allele
Paternal_Allele

Relative expression level

B

S5

Chr X

XIST

Maternal_Allele
Paternal_Allele

Relative expression level

C

S6

Chr X

XIST

Maternal_Allele
Paternal_Allele

Relative expression level

D

pEFs

Chr X

XIST

Maternal_Allele
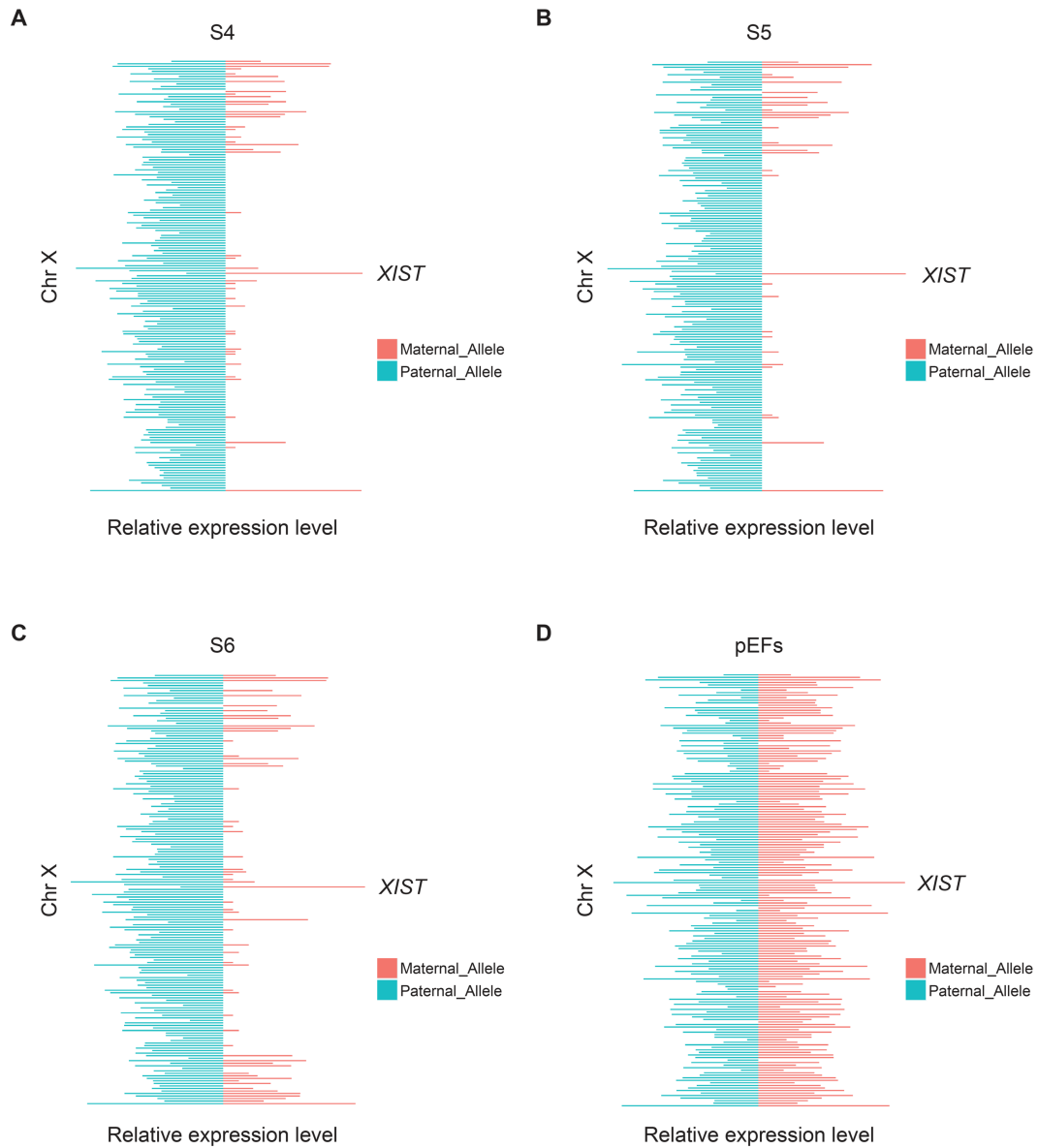Paternal_Allele

Relative expression level

Figure S2 The allelic expression of X-linked genes in three clonal cell lines and porcine embryonic fibroblasts (S4, S5, and S6). All three clonal cell lines showed non-random maternal X inactivation. Most of X-linked genes detected are subject to X inactivation

A

Placenta 2

Chr X

Maternal_Allele
Paternal_Allele

Hybrid placentas of
Duroc sow and Rongchang boar

Placenta 3

Chr X

Maternal_Allele
Paternal_Allele

Hybrid placentas of
Duroc sow and Rongchang boar

B

Placenta 2

Chr X

Maternal_Allele
Paternal_Allele

Hybrid placentas of
Rongchang sow and Duroc boar

Placenta 3

Chr X

Maternal_Allele
Paternal_Allele

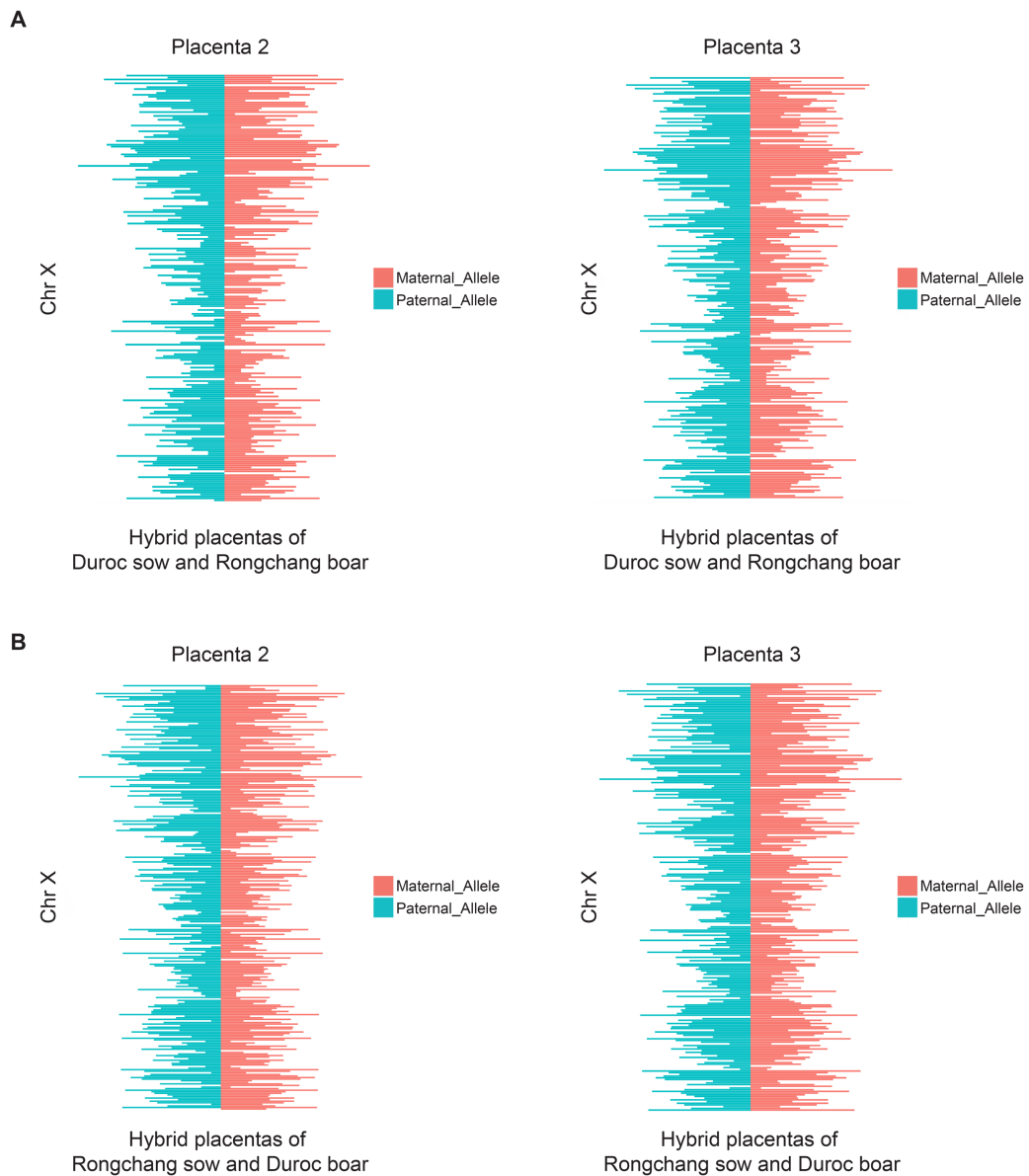Hybrid placentas of
Rongchang sow and Duroc boar

Figure S3 Biallelic expression of X-linked genes in two other hybrid placentas. Transcriptome-wide distribution of allele-specific expression in E20 hybrid placentas for X-linked genes.

(A) RNA-seq data analysis of two other E20 female hybrid placentas of Duroc sow and Rongchang boar.

(B) RNA-seq data analysis of two other E20 female hybrid placentas of Rongchang sow and Duroc boar.

The expression ratios of maternal and paternal X chromosome for X-linked genes are nearly 1:1.

Figure S4

```
1183  GCAGCATTGCTTAGCATGGCTCTCTGCTTTGTTAGAGTGTTCAAAATGGCGGACCCACTT
1243  TGCCGCAGTGTTCCAGTGGCGGGAAGCCACATTATGGGTGTCTTTGTTCTAGCGTGCAGC
1303  ATGGCGGTGGAAATATTCTGTTACATAGCAAAAGATGGCGGCTCAAGTACTTGCCGCAAT
1363  CGAAAACATGGCGGGCCTTTGTCTTTGCCGTGTGCATTTCCTGACAAATTTTGCCGCAGG
1423  GACAATATGGCTGACCTTGTCATGTGGATAGCATGGCAGTCTGTCACGTGGACGTCATGG
1483  CAGGGGTGTTTGACCGTTACATTCTTGGCGGGCTTTGCACCAGGAGGGCCTGCCGCATTG
1543  TTCAAGATGGCGGGCTTTGCCGCGAAAAAGTGCAGGAGGGATTGGCAGCGTTGGATTGCC
1603  GCCCGACACATCCAATCAGAAAGGGTGGTGGAATTGGTCACAGACAGTTAGTGGAGGATG
1663  GAATTAGTCGGAGTTAGCATAGCACCTCGCTACCGTCTCTATTCAGCCAGTCAGCACCGG
1723  CCACGTTTGTACTACTCCCAGTGGGTG
```

Figure S4 Prediction of DMR in porcine *XIST*. Bases in red indicates a CpG; underlined bases are Zfp57-binding sites.

Figure S5

A

2-cell (0.37%)

4-cell (2.22%)

8-cell (0.00%)

Morula (2.96%)

Female blastocyst (1.48%)

Male blastocyst (2.96%)

B

Female blastocyst in vivo (3.70%)
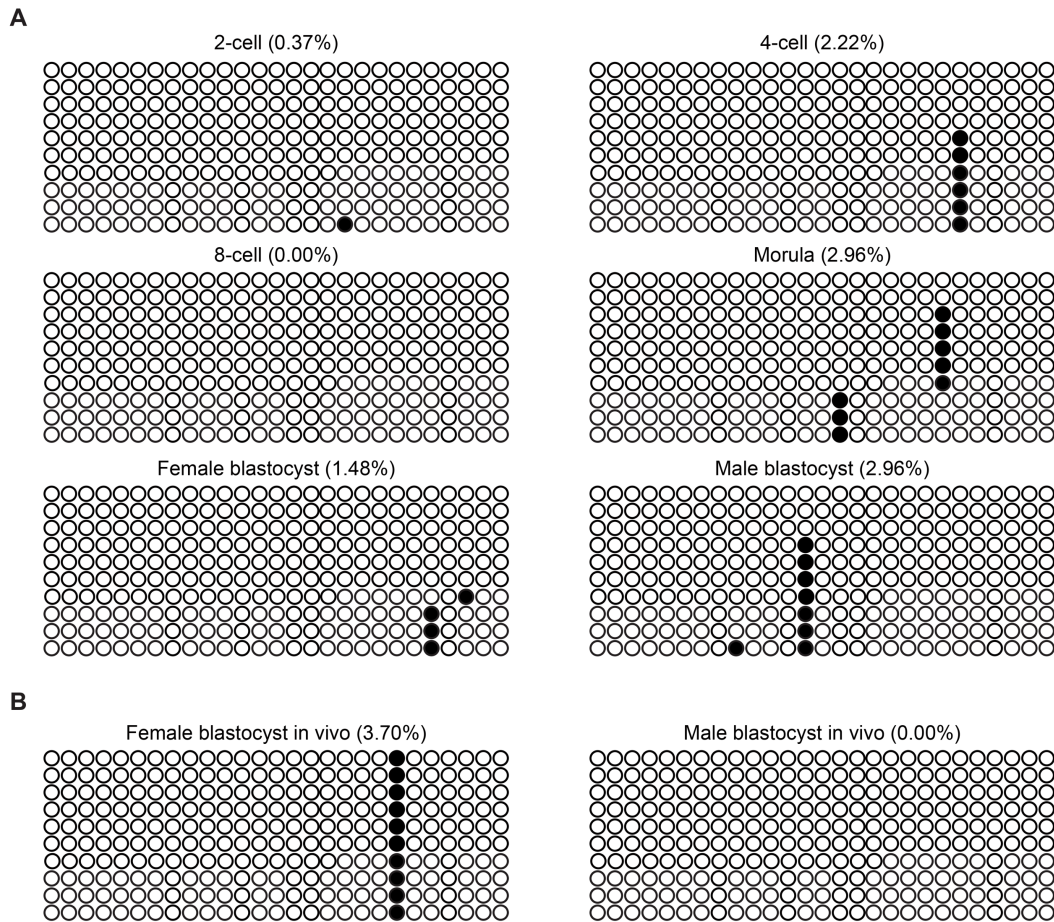
Male blastocyst in vivo (0.00%)

Figure S5 *XIST* DMR methylation in early embryos.

(A) *XIST* DMR methylation in ICSI embryos at different stages. (B) *XIST* DMR methylation in E7 blastocysts *in vivo*. Each circle represents a CpG dinucleotides. The methylation level (%) was based on the methylated CpGs/all examined CpGs; open circles represent unmethylation and filled circles represent methylation.

Table S1. List of primers used in this study.

primer	sequence	
hXIST-1F/1R	ctaggtgtgtcaggaggacc	
	tgtggtacttcaaagggaat	
hXIST-2F/2R	gcctaaagcaccacactgaa	Amplification of homologous regions in porcine cDNA
	tgcggaacttcttagagctg	
hXIST-3F/3R	tcccttttgagaatctggat	
	tcactaacactgtaaggcaa	
hXIST-4F/4R	tgatccttaggtggagatgg	
	gccaaaatactcaaaggtga	
gXIST-1F/1R	ctcctaatattttcttgaca	
	ggcaggagattgagatgatgag	
gXIST-2F/2R	ctgcctctagcattgctgatc	
	cgcattaactatcccaagtacc	
gXIST-3F/3R	ctaggtgtgtcaggaggacc	
	gacagcagtgcaattaagtcc	
gXIST-4F/4R	aatgggctttattgcagctac	
	ggcatgaaaagggagttaagtg	
gXIST-5F/5R	ccatccccaactaactctctt	
	tcccaagtaccctctacagtca	
gXIST-6F/6R	gatgggcttaaatacaactact	Amplification of overlapped regions in porcine genome
	aatcacttaggaggagatggga	
gXIST-7F/7R	caagggactggtaagtatgctt	
	tgggagcctaagttagatcaca	
gXIST-8F/8R	catccctttctgcttctttgtg	
	tgtggtacttcaaagggaat	
gXIST-9F/9R	gccttgtcttgggactgttac	
	gcagctatctcactcctgaaa	
gXIST-10F/10R	tgcggtctgtgtctcgtctt	
	cagggacaggcacagagaag	
gXIST-11F/11R	gccagggactgtgttctgaa	
	ccagggaacatcagataaggat	
gXIST-12F/12R	ctggcatacatttctgctgaat	
	ccaaggctcagagattctatgt	
AUAP	ggccacgcgtcgactagtac	
5RACE-856R	gtaggtccactcacaca	Primers used for 5′ RACE
5RACE-549R	gccaagggggttggagaaagaggg	
5RACE-773R	aacccaacactttccatccatac	

Not I-dT	aactggaagaattcgcggccgcaggaattttttttttttttttt	
3-P1	aactggaagaattcgcggccgcag	
3RACE 31171F	tgcgcttgctccttccttaacaat	Primers used for 3′ RACE
3RACE 31324F	caagccacaactggttttgaaaca	
3RACE 31074F	ggggcaaggcttagttcctcacta	
XIST-SNP-F/R	tggactggagttggatgg	
	gtctctcaagtggagtgg	
XISTouter-SNP-F/R	tatgccagaccatgctgtga	
	gaggaaaagagaggactgaaat	
G6PD-F/R	tgaggtttgccaacaggatc	Amplification of X-linked genes
	tcccatcgctcgttctcca	
HPRT1-F/R	cagcgtcgtgattagtgatg	
	ttgcattgttttgccagtg	
ZBTB33-F/R	ggtaacgatccaccacatac	
	agtatcaacattacagtattggg	
SY-F/R	caggaggatcgctgcaactggac	
	cttaatggctaatcacgggaacaac	Primers used for sex determination
SX-F/R	aagggctgaaggtctgaagt	
	gcctccttctcctcagcaga	
XISTDMR1F/1R	aatggtgattttgattttgt	
	acatccttaaaaaaacctta	Primers used for XIST DMR methylation
XISTDMR2F/2R	gtagtattgtttagtatggt	
	acccactaaaaataatacaaac	

Table S2. Detail information of X-linked genes containing SNP between Rongchang and Duroc alleles.

X-linked gene	Accession Number	SNP position	Duroc	Rongchang
G6PD	XM_003360515	1119	T	G
HPRT1	NM_001032376	397	A	C
ZBTB33	XM_003135334	4910	T	C

Table S3. Escape genes and inactive genes from inactive X in clonal cell lines

Genes escaped from inactive X		Genes subject to inactive X		
0.5≤allelic ratio≤1	0.1<allelic ratio<0.5	allelic ratio ≤0.1		
ARHGAP6	CHM	ABCB7	HTATSF1	RAB9A
GEMIN8	DDX3X	ABCD1	HUWE1	RBM10
KDM6A	FAM3A	AFF2	IL13RA1	RNF113A
MXRA5	FUNDC1	AIFM1	IQSEC2	RP2
TBL1Y	GPR143	AMOT	IRAK1	SEPT6
TXLNG	IDH3G	APOOL	KCND1	SLC25A43
ZRSR2	IKBKG	ARAF	LAMP2	SLC35A2
	LDOC1	ARHGEF6	LONRF3	SLC38A5
	MAP3K15	ARMCX2	MAGED1	SLC9A6
	MTMR1	ARMCX3	MAGED4B	SMC1A
	PDHA1	ARMCX6	MAGIX	SMS
	PRPS2	ATG4A	MAGT1	SNX12
	SH3KBP1	ATP6AP2	MECP2	SRPX
	STS	ATP7A	MED12	SRPX2
	SYAP1	BCOR	MED14	TAF9B
		CASK	MORF4L2	TBC1D25
		CCDC160	MOSPD1	TCEAL2
		CCDC22	MPP1	TCEAL8
		CD99L2	MSL3	TCEAL9
		CH242-123K13.1	MSN	TCEANC
		CHRDL1	NDUFA1	TFE3
		CLCN4	NKAP	TIMM8A
		COX7B	NKRF	TIMP1
		CSTF2	NSDHL	TMEM47
		CTPS2	NXT2	TREX2
		CXorf38	OGT	TRMT2B
		CXorf56	PBDC1	TSPAN6
		DKC1	PDK3	TSPYL2
		DYNLT3	PGK1	TSR2
		EGFL6	PGRMC1	UBA1
		ELK1	PHKA2	UPRT
		FAM155B	PIN4	USP11
		FAM199X	PIR	WDR45
		FOXO4	PJA1	WWC3
		G6PD	PLS3	XPNPEP2
		GPC4	PLXNA3	ZDHHC9
		GPR173	PORCN	ZMYM3

		GPRASP2	PPEF1	ZNF275
		HCCS	PRICKLE3	ZNF674
		HDAC6	PRPS1	ZNF75D
		HSD17B10	PRRG1	