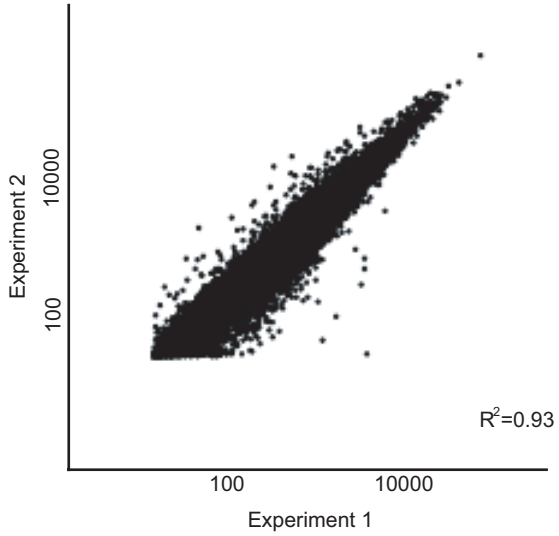
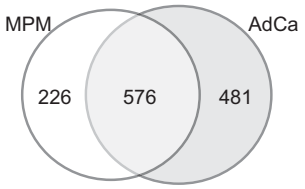
Goto et al. Supplementary Figure 1



Goto et al. Supplementary Figure 2

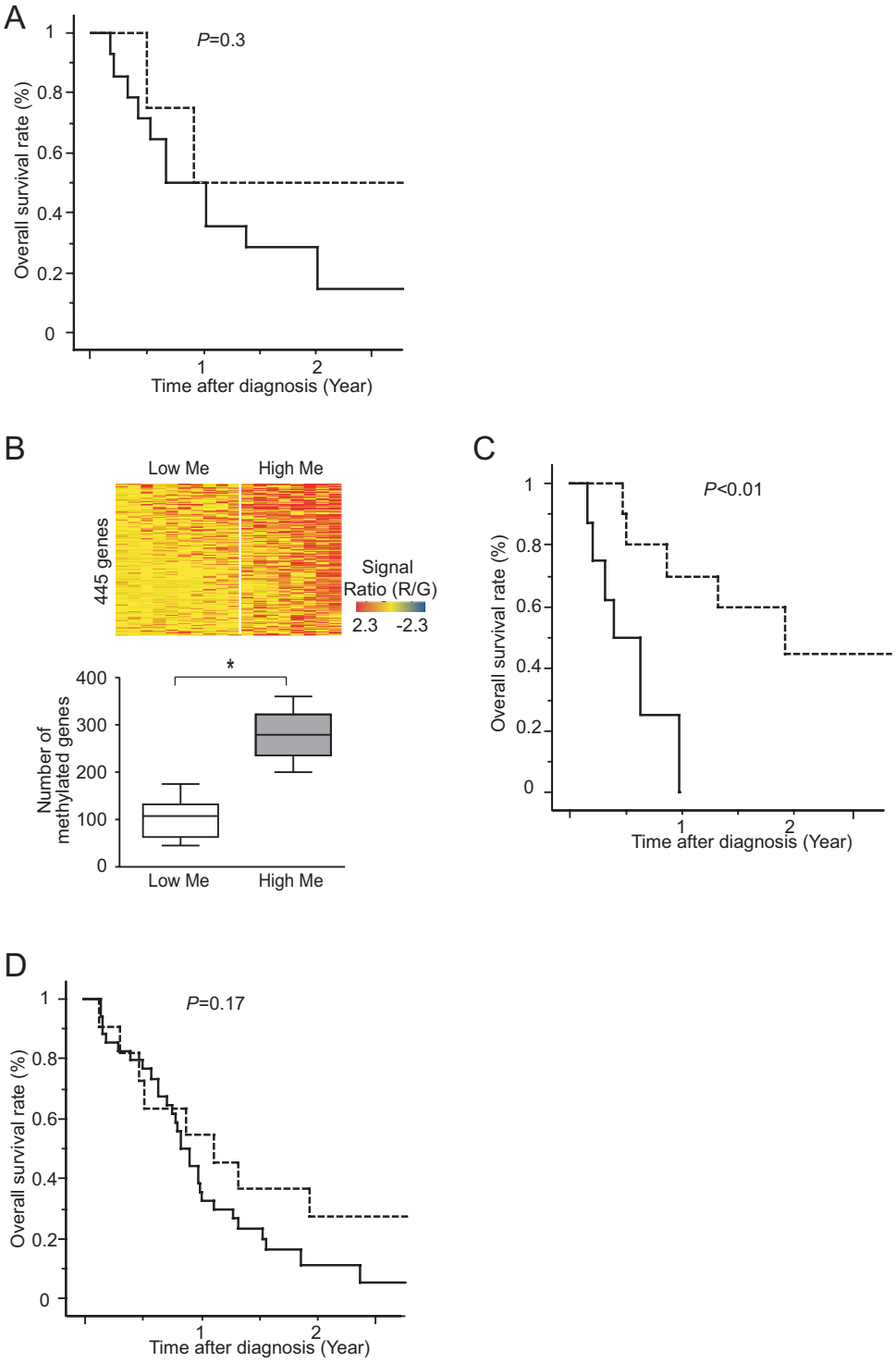
A



B

C

Goto et al. Supplementary Figure 3



Supplementary figure legend

Figure S1. Reproducibility of methylation analysis. Replicate experiments were done with six MPMs. Averaged signal intensity (log scale) obtained from six MPMs is plotted on the *X axis* (first experiment) and the *Y axis* (the second experiment). The coefficient of determination (R^2) in linear regression model is indicated.

Figure S2. Venn diagrams analysis on DNA methylation in MPMs and AdCas. Genes methylated in more than 20% cases of each group were analyzed. *A*, Number of hypermethylated genes in MPM and AdCa. *B*, Number of DNA methylation targets in smokers and non-smokers. *C*, Number of DNA methylation targets with and without asbestos exposure (AE) in MPM.

Figure S3. Kaplan-Meier analysis of MPM patient survival. *A*, MPMs with less methylation (*black circle* in Fig. 1C) tended to have longer survival rates (*broken line*) than MPMs with more methylation (*solid line*, P=0.3). *B*, *Upper column*, heat-map overview of hierarchical cluster analysis of DNA methylation data of 18 MPMs using 445 genes (*Y-axis*). Two cases were excluded from the original array samples because of missing data of patient survival. Color corresponds to methylation level as indicated in the log2-transformed scale bar beside the matrix. *Red* and *blue* reflect high and low levels of methylation, respectively. MPM could be divided into two groups, groups with high frequency of methylation (High Me, n=8) and low frequency of methylation (Low Me, n=10). *Lower column*, Box and whisker plot analysis of the number of methylated genes out of 445 genes in the High Me group (279.1±19.3 genes) and Low Me group (104.0±12.6 genes). *, P<0.01. The mean is marked by a line inside the box whose ends denote the upper and lower quartiles. Error bars represent 5

and 95 percentile values. *C*, Patients with high methylation lived significantly shorter (*solid line*) than those with low methylation (*broken line*, $P<0.01$). *D*, A total of 45 MPMs were classified into two groups according to the methylation status of *TMEM30B*, *KAZALD1*, and *MAPK13*. Patients with no methylation (*broken line*) tended to live longer than those with methylation in at least one gene (*solid line*) ($P=0.17$).

Supplementary Table 1. Methylation level examined by pyrosequencing analysis in tumor and normal tissues

	MPM		Normal mesothelium		AdCa		Normal lung	
	Mean	(95% CI)	Mean	(95% CI)	Mean	(95% CI)	Mean	(95% CI)
PGR	9.2	(13.9-4.7)	7.1	(10.2-4.0)	16.9	(27.1-6.6)	6.0	(6.8-5.3)
RASSF1A	11.4	(21.6-1.2)	4.9	(8.7-1.1)	20.8	(34-7.5)	8.7	(11.6-5.8)
p16	5.6	(7.8-3.3)	3.9	(8.2-0)	23.7	(34.0-13.5)	4.9	(5.9-4.0)
SFRP1	5.3	(6.4-4.1)	6.1	(10.1-2.2)	14.5	(20.8-8.1)	9.4	(10.5-8.3)
TNFRSF10C	23.3	(31.6-15.0)	2.6	(13.9-0)	4.9	(7.1-2.6)	5.2	(6.1-4.4)

Supplementary Table 2. Summary of bisulfite PCR and pyrosequencing primers, RT-PCR primers and MSP primers

Bisulfite PCR and pyrosequencing primers

Genes	Primer sequences	Sequencing primers	Condition (°C)
C20orf100	Forward GTTTAGGGTAGGTTGGAGTTAAG Reverse-Universal GGGACACCGCTGATCGTTTATCTCCTACCTCATCCCCACTA	TTTTAGGGTTTTTTTTTAAT	53 (3) 52 (4) 50 (5) 48 (40)
BMP6	Forward-Universal GGGACACCGCTGATCGTTTATTTTTAAGAGGTTTTTTTGGTGAT Reverse CCTTCCTAACCCTCAATCCTTATCT	CAATCCTTATCTCTCATAAT	53 (3) 52 (4) 50 (5) 48 (40)
TNFRSF10C	Forward ATTTAGGTTTTTTTGGAGGTGTTAGG Reverse-Universal GGGACACCGCTGATCGTTTACCTTACATCTCTAATCAAACTCCCAAA	TGTGGGAATTTTTTTA	62 (3) 60 (4) 58 (5) 55 (40)
HELZ	Forward GGGGTAGGAGAAAGGGAGAAAAT Reverse-Universal GGGACACCGCTGATCGTTTACCCCAACTAACCCCTTCC	ATGAGGGTGAATTTTTAAT	55 (50)
hsa-mir-9-1	Forward AGAGGGAAATGGGGTATTAGAAA Reverse-Universal GGGACACCGCTGATCGTTTACCTCAAACACCAAAATACAAACAC	TTTTTTGGGTTTGGA	60 (50)
C9orf106	Forward GGGTGTTTGTATTTAAGGTGTTTATAG Reverse-Universal: GGGACACCGCTGATCGTTTAATCTCCRCCAACCAAAC	GGGGTTGTTTTGGGTA	58 (3) 56 (4) 54 (5) 50 (40)
HOXA11	Forward TTTTTTGTTAAGGATGGGGATAGA Reverse-Universal GGGACACCGCTGATCGTTTAAACCACCCTCATCAAAATCCATTAT	AGTGGAGAATTATGTTAAGT	55 (50)
TP53I11	Forward AGATGGTGTGGTTTGTTTATTTA Reverse-Universal GGGACACCGCTGATCGTTTACRAAAACCRCCTACAAAAA	TTGTTAGGAAAGTTATTTTG	53 (3) 52 (4) 50 (5) 48 (40)
LHX1	Forward GGAAGGAGGTTAGAAAGGAAATTTA Reverse-Universal GGGACACCGCTGATCGTTTATACCTCCCTCTAACCCCACAAT	AAGGAAAAGGAGAGAAAGT	53 (3) 52 (4) 50 (5) 48 (40)
ANK1	Forward TGAGGTGAGTTAGTTAGTTTTAGTTG Reverse-Universal GGGACACCGCTGATCGTTTAAATAACCCCCTCCTAACATCTC	TTTTTTAAGTTTTTAAGGTT	60 (50)
PENK	Forward AGGAAAAGAGTYGGGTGTTTTAGGTAGT Reverse-Universal GGGACACCGCTGATCGTTTACCCRACCRACAACTTTTAAAT	GGGTGTTTTAGGTAGTTT	53 (3) 52 (4) 50 (5) 48 (40)
EDG4	Forward TTGAGGAGTGATTGGAGGTTTAG Reverse-Universal GGGACACCGCTGATCGTTTAACCTCTCCAAACTAAAAAAAAAATAA	GGTTTAGGTGAGGTTTGTA	60 (50)

MMP25	Forward-Universal GGGACACCGCTGATCGTTTAGAGGGGATTTGGGAAGAGAA Reverse CCAACCAAAAAATAACCCCTACC	ACCCAAAAACCCTCC	58 (3) 56 (4) 54 (5) 50 (40)
SFRP1	Forward TGTTTTTTAAGGGGTGTTGA Reverse (5'-Biotin) CTCCRAAAACTACAAAACTAAAAT	GTTTGGTTTTAGTAAAT	61 (3) 59 (4) 57 (5) 55 (40)
NF2	Forward-Universal GGGACACCGCTGATCGTTTATTGGTGGAGTTATTTTAAAGGAGG Reverse ACAACCCRAAACCTACTCCC	ACCAAAATAAACAAAACTTT	60 (50)
MGMT	Forward TTGGTAAATTAAGGTATAGAGTTTT Reverse (5'-Biotin) AAACAATCTACGCATCCT	GGAAGTTGGGAAGG	60 (3) 59 (4) 57 (5) 55 (40)
PGR	Forward TGATTGAGTTGAAGGTAAAG Reverse (5'-Biotin) GGGACACCGCTGATCGTTTA	GGATTTTTATTGTTGTGT	58 (3) 56 (4) 54 (5) 52 (40)
p16	Forward GGTTGTTTTYGGTTGGTGTTTT Reverse (5'-Biotin) ACCCTATCCCTCAAATCCTCTAAAA	TTTTTGTTTGGAAAGAT	58 (3) 56 (4) 54 (5) 52 (40)
RASSF1A	Forward GGGGGAGTTTGAGTTTATTGA Reverse (5'-Biotin) CTACCCCTTAACTACCCCTTCC	GATTTTATTTGGGG	55 (50)
TMEM30B	Forward TTGGGAGGGTGTGGGTATT Reverse -Universal GGGACACCGCTGATCGTTTACCAAACCCRAAAACTACTC	TAAAAATTTATTTGAGTTGG	55 (50)
KAZALD1	Forward GTAGTGGGGAGGAAGAAGGAG Reverse -Universal GGGACACCGCTGATCGTTTACCRCAACCCAAAACTAATTCCC	GGTAGTTGGGTGGGTAAG	60 (50)
MAPK13	Forward(5'-Biotin) GGAGGGAATTGGGAAGTATTGTTT Reverse CACRCCCRAACCTATCCA	AACCTATCCAACCCT	55 (50)

For those with a Universal tailed primer, the following additional primer is added: Universal (5'-Biotin)

GGGACACCGCTGATCGTTTA

Number in parentheses indicate cycles at that temperature.

MSP primers

Genes		Primer sequences	Condition (°C)
TMEM30B	M	Forward TTGGGAGGGTGTGGGTATTGTTC Reverse ACGCGCGAACTAACCGAAT	55(35)
	U	Forward GGAATTGGGAGGGTGTGGGTATTGTTT Reverse ACCTCCCTCTCCACACCAC	65(35)
KAZALD1	M	Forward GCGGGTCGTAGTATTTGTCG Reverse AACAAAACCAACCACCTTCG	55(35)
	U	Forward TTATTTGTGGGTTGTAGTATTTGTT Reverse AAACCAACCACCTTCATCTCC	60(35)
MAPK13	M	Forward CGTGTTTTCGACGTACGTCGGTAGC Reverse ACCGCTAAATAACCCCGAAA	60(35)
	U	Forward GGTTTTGTTGGGTAGTTTT Reverse TCCCACCTACCAACTCACC	62(3) 60(4) 58(5) 55(28)

Numbers in parentheses indicate cycles at that temperature.

Quantitative MSP primers

Genes	Primer sequences
TMEM30B	Forward CGAGTAGTTTTCGGGTTTGC Reverse ACCGACGCGCGAACTAAC
KAZALD1	Forward GGTAAGTTTGCGGTCGTTTTC Reverse AACAAAACCAACCACCTTCG
MAPK13	Forward TCGTTTTGGGTTGGTTTTTC Reverse CCTTAAAATCCGCGATCAAA
LINE1	Forward TTTTAAAGTTGTTAGATAGGGATATTTAAGTTTGTA Reverse AAAAACCTACCTACCTCTATAAACTCCACC

RT-PCR primers

Genes	Primer sequences
ANK1	Forward AGAGGAGCAATTCACGGATGA Reverse ACAAGTCTATCTGTCGAACCACCTT
PENK	Forward GACGTGCAGCTACCGCCTAG Reverse GAAGGCAGTTTACCTTCACATTCC
GAPDH	Forward TCCCATCACCATCTTCCAG Reverse ATGAGTCCTTCCACGATACC
PGR	Hs00172183_m1
GAPDH	Hs00266705_g1

ChIP-PCR primers

Genes	Primer sequences
ERa	Forward CCGGGCCTCCAACTTTAAGT Reverse GAAGCTGCTCTTTGGGATCG
p16	Forward AGACAGCCGTTTTACACGCAG Reverse CACCGAGAAATCGAAATCACC
p21	Forward GGTGTCTAGGTGCTCCAGGT Reverse GCACTCTCCAGGAGGACACA
TRIM36	Forward CTCGATGGCCTTCATTTCAC Reverse GCGGGTGTATCGAATTTGTC
ANK1	Forward GGGAGGAGGTGCTCTTGTAA Reverse GACTCACCGCAGCCTCTG
PENK	Forward GTCGCCTCCACGTCTACCTA Reverse CCAAGTGCAAAGTGTCAGGA
ITGb8	Forward ACACCATTAGTTGCAGCTTTGC Reverse GCTGCCGACTTGTCTTTGC Probe CCCGTCTGCGGAGC
PRB	Forward GCCTGAAGTTTCGGCCATAC Reverse CAGGGCCGAGGGAAGAGT Probe TATCTCCCTGGACGGGC
TP73	Forward GGCGTCGGGCACAGAGT Reverse ACCCGACCGCGATCTTC Probe ACCGGCGTCCCCAG

MYT1	Forward TGGACAAACATAGGCACCTTCTG Reverse AGTCCGGTGGAGTCCTGTGT Probe TGGCCGAGGCTCA
NALP9	Forward TCTTTCTTTTCCCTCTGGAGACA Reverse CCGAAAAAAAAGATTCTGCCATA Probe CTCAGTTCACAATCCT
MOBKL2A	Forward CCGCGGGACCGAGTCT Reverse GACCGGACCTACTTTCCTTAAAGG Probe AGACCCCTGCACGCC
NF2	Forward GGACGGAGCGGGAAAGTC Reverse ACGCATAGATGCTGCGATTG Probe TGCCTACCTTGGCCTT
SDC1	Forward CGGGTGCAGCTGTTTAAACTAA Reverse CGTTCTTCCTGCACTCCACAA Probe CCCCAAGTCTCCAGCAC
SIX5	Forward GGAGGGAAAACAAAGGGAGAA Reverse GCTCTCCACTCGGGTCTCTGT Probe CACAGACAGACGGGAGG
MGMT	Forward AAAGGTACGGGCCATTTGG Reverse GGCGCCTTCCCAGCTT Probe TAAGGCACAGAGCCTC

Supplementary Table 3. ChIP-chip and ChIP-PCR in pyrosequencing in MPM cell lines

ChIP-PCR	ChIP-chip		Sensitivity (%)	Specificity (%)
	Positive (K27me3/input>1.5)	Negative (K27me3/input ≤1.5)		
Positive	9	2	82	82
Negative	2	9		

ChIP-PCR was conducted using 11 genes (*MGMT*, *NF2*, *MOBKL2A*, *ITGb8*, *SDC1*, *SIX5*, *PGR*, *TP73*, *ER*, *TRIM36*, and *p16*) and compared with the ChIP-chip analysis.

Relative ratio of K27me3/ H3 in ChIP-PCR over 0.07 considered as enrichment of K27me3.

Supplementary Table 4. MCAM ratio and methylation level in pyrosequencing in MPM cell lines, 20 MPMs, and 20 AdCas

Pyrosequencing	MCAM		Sensitivity (%)	Specificity (%)
	Positive (Cy5/Cy3>2.0)	Negative (Cy5/Cy5≤2.0)		
Positive	23	9	82	90
Negative	5	80		

Methylation status of 18 genes (*HELZ*, *NF2*, *BMP6*, *SFRP1*, *C9orf106*, *MMP25*, *TP53I11*, *hsa-mir-9-1*, *ANK1*, *TNFRSF10C*, *HOXA11*, *EDG4*, *PENK*, *LHX1*, *C20orf100*, *MGMT*, *PGR* and *p16*) was analyzed in two MPM cell lines as well as 20 cases of MPM and AdCa by pyrosequencing. Methylation-positive indicates methylation levels of the genes were greater than 15%. We compared the MCAM (signal ratio of Cy5/Cy3>2.0 or Cy5/Cy5≤2.0) and methylation status (positive or negative) in pyrosequencing and found a high concordance between the two.

Supplementary Table 5. Gene list of 445 genes in MPMs

Gene Name	Number of methylated MPM cases (n=20) (%)	
ABHD9	7	(35)
ABR	6	(30)
ACP5	8	(40)
ADARB1	7	(35)
ADARB2	9	(45)
ADCY4	7	(35)
ADRA1A	9	(45)
ADRB3	7	(35)
AGXT2L2	7	(35)
AHDC1	6	(30)
AKT1	6	(30)
ALOX12	6	(30)
ALPK3	6	(30)
AMIGO3	6	(30)
ANK1	5	(25)
ANKRD43	6	(30)
ANKZF1	7	(35)
ARHGEF18	8	(40)
ARHGEF4	6	(30)
ARSI	6	(30)
ASCL2	10	(50)
ASCL4	6	(30)
ASTN2	5	(25)
ATP5A1	8	(40)
ATP5G2	8	(40)
AVPI1	5	(25)
B4GALNT2	10	(50)
BAALC	6	(30)
BACH2	8	(40)
BAI1	8	(40)
BANK1	6	(30)
BARHL1	6	(30)
BARX1	6	(30)
BBS10	11	(55)
BC014250:-514	8	(40)
BC038980:147	6	(30)
BCKDK	13	(65)
BCL7A	5	(25)
BIN2	6	(30)
BMP8A	4	(20)
C10orf53	6	(30)

C10orf54	5	(25)
C10orf88	6	(30)
C13orf21	8	(40)
C14orf39	8	(40)
C16orf30	12	(60)
C16orf68	4	(20)
C1orf106	9	(45)
C1orf107	6	(30)
C1orf61	9	(45)
C1orf87	7	(35)
C1QL4	8	(40)
C20orf58	6	(30)
C2orf40	8	(40)
C9orf106	6	(30)
CA10	6	(30)
CACNA1A	5	(25)
CACNA1B	12	(60)
CACNB2	6	(30)
CACNB3	5	(25)
CACNG3	5	(25)
CACNG6	5	(25)
CALCOCO2	10	(50)
CARHSP1	9	(45)
CATSPER2	6	(30)
CCDC107	6	(30)
CCDC63	9	(45)
CCDC8	7	(35)
CD83	7	(35)
CEBPB	8	(40)
CELSR2	10	(50)
CHAD	10	(50)
CHN2	10	(50)
CHST8	7	(35)
CLDN10	10	(50)
CLDN5	9	(45)
CLIC6	7	(35)
CLN6	5	(25)
CLPTM1L	8	(40)
CLUL1	5	(25)
CNTFR	7	(35)
COL1A1	10	(50)
COL24A1	6	(30)
COL2A1	5	(25)

COL9A1	8	(40)
CPXM2	8	(40)
CRYBA2	6	(30)
CSRP2	5	(25)
CTDSP2	5	(25)
CTSZ	5	(25)
CXCL14	5	(25)
CYB561	9	(45)
CYP26C1	12	(60)
DACH2	5	(25)
DDOST	5	(25)
DFNA5	7	(35)
DFNB59	5	(25)
DGKQ	6	(30)
DLG4	9	(45)
DLX1	6	(30)
DLX4	7	(35)
DMRT1	8	(40)
DMRT2	9	(45)
DNAJB2	7	(35)
DPF1	6	(30)
DPF2	7	(35)
DRD4	7	(35)
DUOXA1	7	(35)
DUSP2	6	(30)
DUSP22	6	(30)
DUSP3	8	(40)
DVL3	6	(30)
DYNC1I1	5	(25)
EDG6	9	(45)
EEF1A2	6	(30)
ELA2	10	(50)
ELL3	7	(35)
ELOVL3	6	(30)
EPO	9	(45)
ESX1	6	(30)
EVC2	6	(30)
FAIM2	6	(30)
FAM100A	11	(55)
FAM119A	5	(25)
FAM84A	9	(45)
FANK1	14	(70)
FARP1	12	(60)

FARP2	10	(50)
FBXO39	5	(25)
FBXW4	8	(40)
FERD3L	12	(60)
FGF11	7	(35)
FHL2	8	(40)
FLJ10916	9	(45)
FLJ13236	5	(25)
FLJ21511	6	(30)
FLJ22662	6	(30)
FLJ32447	12	(60)
FLJ39237	6	(30)
FLJ40125	8	(40)
FLJ43980	10	(50)
FLJ44968	8	(40)
FLJ46347	5	(25)
FLJ46831	8	(40)
FLJ90650	12	(60)
FOXD3	8	(40)
FOXJ1	13	(65)
FRMD3	4	(20)
FUCA1	7	(35)
FZD10	10	(50)
GAD2	6	(30)
GATA2	8	(40)
GATA4	5	(25)
GBL	9	(45)
GDF6	7	(35)
GGN	10	(50)
GIPC3	7	(35)
GLB1	9	(45)
GLS2	4	(20)
GNA14	7	(35)
GNAS	7	(35)
GNMT	7	(35)
GNS	7	(35)
GPR25	8	(40)
GPRC5B	6	(30)
GPRIN2	5	(25)
GRAMD2	5	(25)
GRHL1	5	(25)
GRIA2	11	(55)
GRIN2C	6	(30)

GRINA	9	(45)
GRP	6	(30)
H2AFY	13	(65)
HAAO	7	(35)
HAND1	8	(40)
HBQ1	7	(35)
HEBP2	5	(25)
HIF3A	6	(30)
HLX1	7	(35)
HNRPF	9	(45)
HOMER2	7	(35)
HOXA11	10	(50)
HOXA6	12	(60)
HOXA9	11	(55)
HOXC10	8	(40)
HOXD4	11	(55)
HOXD8	10	(50)
HR	9	(45)
HRAS	6	(30)
hsa-mir-124a-3:-454	7	(35)
hsa-mir-542:-4759	6	(30)
HSBP1	6	(30)
HSF4	7	(35)
HTATIP2	5	(25)
HTR2C	6	(30)
HYOU1	7	(35)
IER5L	10	(50)
IFNGR2	6	(30)
IGF2BP1	8	(40)
INSM2	6	(30)
INTS3	6	(30)
IRX4	7	(35)
ISL2	6	(30)
ITIH5	9	(45)
KAZALD1	6	(30)
KCNA3	9	(45)
KCNAB1	9	(45)
KCNAB3	9	(45)
KCNG1	6	(30)
KCNIP1	5	(25)
KCNJ14	7	(35)
KCNJ3	9	(45)
KCNK10	8	(40)

KHK	7	(35)
KIAA0247	5	(25)
KIAA1688	7	(35)
KIF17	5	(25)
KIF3C	5	(25)
KLHDC7B	9	(45)
KLHDC8A	5	(25)
KLHL34	11	(55)
L3MBTL	5	(25)
LAD1	6	(30)
LAMP1	6	(30)
LHFPL2	7	(35)
LHX1	13	(65)
LHX2	8	(40)
LHX3	9	(45)
LIMD2	14	(70)
LIME1	8	(40)
LIN28	10	(50)
LMO6	5	(25)
LMX1A	5	(25)
LOC388969	7	(35)
LOXL1	8	(40)
LRFN4	6	(30)
LRRC45	8	(40)
LTBP2	5	(25)
LY6H	10	(50)
LY6K	7	(35)
MADCAM1	6	(30)
MAFB	7	(35)
MAL	6	(30)
MAP2K5	5	(25)
MAP3K8	5	(25)
MAPK13	5	(25)
MAPRE3	7	(35)
ME1	8	(40)
MEGF11	11	(55)
MEOX2	11	(55)
MFSD4	14	(70)
MFSD7	11	(55)
MGC24975	11	(55)
MGC39900	5	(25)
MGC61598	9	(45)
MT1H	12	(60)

MTL5	15	(75)
MXRA7	5	(25)
MYH14	6	(30)
MYOD1	9	(45)
N6AMT2	6	(30)
NAB1	9	(45)
NDRG4	5	(25)
NEFM	6	(30)
NETO1	6	(30)
NEURL	8	(40)
NFATC1	7	(35)
NKX2-3	9	(45)
NKX6-2	5	(25)
NPHS2	6	(30)
NPM2	7	(35)
NPPB	5	(25)
NPR2	11	(55)
NPTX2	10	(50)
NRG1	6	(30)
NRK	5	(25)
NRXN1	10	(50)
NTN1	6	(30)
NTSR1	5	(25)
NUAK1	7	(35)
NUB1	7	(35)
NXPH1	6	(30)
OTX1	6	(30)
P2RY2	12	(60)
PACSIN3	6	(30)
PADI2	5	(25)
PAPSS2	7	(35)
PARD6G	7	(35)
PAX2	8	(40)
PAX3	12	(60)
PAX5	7	(35)
PAX7	11	(55)
PDE8B	6	(30)
PDLIM1	5	(25)
PDPN	6	(30)
PDXK	6	(30)
PENK	13	(65)
PFKFB2	6	(30)
PGR	4	(20)

PGRMC1	7	(35)
PHKA2	5	(25)
PHOX2A	5	(25)
PIP5K2A	7	(35)
PKP1	11	(55)
PLEC1	11	(55)
PLXNC1	5	(25)
POMC	8	(40)
POP7	7	(35)
POU4F2	5	(25)
POU6F1	7	(35)
PPARD	6	(30)
PPP1R14A	8	(40)
PPP3R2	6	(30)
PQLC2	7	(35)
PRAC	8	(40)
PRDM14	10	(50)
PREX1	7	(35)
PRIMA1	8	(40)
PROKR2	6	(30)
PRR5	6	(30)
PRUNE	6	(30)
PTF1A	6	(30)
PTGER1	5	(25)
PTPRG	7	(35)
PTPRN2	8	(40)
PUS7	7	(35)
PXDNL	7	(35)
PYDC1	6	(30)
RAB37	8	(40)
RAET1G	6	(30)
RAET1L	7	(35)
RAMP2	6	(30)
RARRES1	6	(30)
RASGRF2	5	(25)
RAX	6	(30)
RBM35A	7	(35)
RBM35B	7	(35)
RCOR2	9	(45)
REC8	7	(35)
REPS1	5	(25)
REST	5	(25)
RFNG	7	(35)

RILP	10	(50)
RND2	9	(45)
RNF126	6	(30)
RNF130	9	(45)
RNF144	6	(30)
RP13-15M17.2	5	(25)
RPP25	5	(25)
RTKN	9	(45)
SALL1	8	(40)
SAT2	8	(40)
SCARF2	8	(40)
SCGB3A1	9	(45)
SCRIB	6	(30)
SCT	12	(60)
SCUBE1	6	(30)
SDCBP2	12	(60)
SEMA3F	5	(25)
SH2D3C	6	(30)
SH3PX3	6	(30)
SHROOM2	7	(35)
SIVA1	4	(20)
SLC13A5	5	(25)
SLC18A2	6	(30)
SLC22A3	9	(45)
SLC25A30	8	(40)
SLC26A5	9	(45)
SLC2A10	6	(30)
SLC35E1	5	(25)
SLC6A2	10	(50)
SLC9A3	8	(40)
SLCO4A1	5	(25)
SLFN13	14	(70)
SMURF1	10	(50)
SOX11	6	(30)
SOX14	8	(40)
SOX15	6	(30)
SOX3	9	(45)
SPOCK1	5	(25)
ST6GALNAC4	8	(40)
ST8SIA5	6	(30)
SUMO3	5	(25)
SURF6	6	(30)
SUV420H1	11	(55)

SV2C	6	(30)
SYT5	4	(20)
TAC1	9	(45)
TACC2	5	(25)
TBX15	10	(50)
TBX4	13	(65)
TCF2	10	(50)
TCF21	10	(50)
TCL1A	7	(35)
TDGF1	12	(60)
TDRD10	7	(35)
TF	7	(35)
TLX2	8	(40)
TLX3	8	(40)
TM2D3	5	(25)
TMEM132D	6	(30)
TMEM139	7	(35)
TMEM176B	5	(25)
TMEM178	6	(30)
TMEM179	7	(35)
TMEM25	6	(30)
TMEM30B	7	(35)
TMEM61	6	(30)
TMEM8	6	(30)
TMEM88	9	(45)
TMUB1	6	(30)
TNFRSF10C	10	(50)
TNFRSF25	5	(25)
TPM2	8	(40)
TRAPPC1	9	(45)
TRAPPC5	8	(40)
TSP50	5	(25)
TSPAN5	6	(30)
TTC27	6	(30)
TUBA4A	8	(40)
TUBB2B	6	(30)
TUBGCP3	7	(35)
TXNDC5	7	(35)
UBE2I	5	(25)
UFC1	6	(30)
UPB1	8	(40)
URM1	9	(45)
VAX2	6	(30)

VHL	5	(25)
VSX1	10	(50)
WIT1	8	(40)
WNK3	4	(20)
WNT3	12	(60)
WWC3	5	(25)
XKR4	9	(45)
ZBTB4	6	(30)
ZIC1	7	(35)
ZNF154	8	(40)
ZNF259	9	(45)
ZNF385	8	(40)
ZNF526	10	(50)
ZNF628	7	(35)
ZNF667	6	(30)
ZNF768	10	(50)
ZPBP	5	(25)