

**Reversal of Aberrant Cancer Methylome and Transcriptome upon Direct  
Reprogramming of Lung Cancer Cells**

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## **Supplementary Information**

### **Supplementary Table Legends**

**Table S1** List of aberrantly methylated promoters (AMP).

**Table S2** List of AMPs identified in cancer cells that were hypomethylated upon reprogramming.

**Table S3** List of commonly upregulated genes in lung cancer.

**Table S4** List of URs identified in cancer cells that were downregulated upon reprogramming.

**Table S5** List of OGs identified in cancer cells that were downregulated upon reprogramming.

**Table S6** List of TSs identified in cancer cells that were upregulated upon reprogramming.

**Table S7** Primer sequences.

## Supplementary Figure Legends

**Figure S1** Bisulfite sequencing analysis was used to quantify the methylation levels in iPC cells and parent cancer cells. (a) iPCH358 and iPCH460 were unmethylated in *HOXA5* gene promoters as shown by bisulfite sequencing. (b) Bisulfite sequencing analysis revealed high significant increases in methylation levels in iPC cells for *KRT19* gene. White circles represent unmethylated CpGs; black circles denote methylated CpGs. Numbers indicate the percentage of methylated CpGs.

**Table S1: Lists of aberrantly methylated promoters (AMP)**

References	Descriptions	Genes
Human Lung Cancer EpiTect Methyl qPCR Arrays	Apoptosis & Anti-apoptosis	ACIN1  APC BRCA1 CADM1 CDKN1C CDKN2A CDKN2A CDKN2B DAPK1 ENG FHIT PGF PTEN PYCARD RECK SFN TNFRSF10C TNFRSF25 TWIST1
	Bone Morphogenesis Signaling Pathway	GREM1
	Cell Adhesion & Migration	APC CADM1 CDH1 CDH13 CTNNB1 DLC1 ENG OPCML
	Cell Adhesion Molecule-Like Genes	ROBO1 THBS1
	Cell Cycle, Growth, Differentiation & Development	AKAP12 ALDH1A3 APC BRCA1

	<p>CADM1  CCNA1  CCND2  CDKN1A  CDKN1C  CDKN1C  CDKN2A  CDKN2B  CEBPA  DLC1  FHIT  GADD45G  GREM1  HOXC9  HOXD1  IGFBP3  MLH1  ONECUT2  PGF  PRDM2  PTEN  RARB  RASSF1  RASSF2  RASSF4  SFN  SPARC  TCF21  TGFBI  TWIST1  WIF1  XPC</p>
Chemokines, Cytokines & Receptor	<p>CXCL12  IL20RA  TNFRSF10C  TNFRSF25</p>
Neuronal Adaptor Protein	<p>APBA1</p>
DNA Damage Repair	<p>APC  BRCA1</p>

	CDKN1A FANCF MLH1 RASSF1 RASSF4 WRN XPC XRCC5
DNA Methyltransferases	MGMT PRDM2
Drug Metabolism	CYP1A1 CYP1B1 GSTP1
Dual Oxidase	DUOX2
Extracellular Matrix Remodeling	LOX SLIT2 SPARC TGFB1 THBS1 WIF1
Oncogene	PAX5
Tumor Suppressors	DIRAS3 MT1G SCGB3A1
Growth Factors	GDNF IGFBP7 PGF WIF1
GTPase Activating Proteins	RASGRF2 DAB2IP
Heparan Sulfate Biosynthetic Enzyme	HS3ST2
Histidine Triad Gene Family	FHIT
Hormone Receptor	ESR1
Hypoxia Response	PTEN
Inflammation	PYCARD
Insulin Signaling Pathway	CDX2 IGFBP3
Lipid Metabolism	LRP1B
Nuclear Receptors	ESR1

	RARB
Oncogene	ENG
One Carbon Unit Metabolism	MTHFR
p53 Signaling Pathway	RPRM XPC
PI3 Kinase Signaling Pathway	PTEN
Proteases & Protease Inhibitors	CTSZ PRSS3 THBS1
Protein Kinases & Protein Kinase Adaptor Proteins	AKAP12 DAB2IP PRKCDBP
Pure Cerebellar Ataxia	SYNE1
Retinoid Acid Signaling	ALDH1A3 RARB
TGF $\beta$ Signaling Pathway	BRCA1
Transcription Factors	CDX2 CEBPA GATA4 GATA5 GATA6 HOXA5 HOXC9 HOXD1 MSX1 ONECUT2 PAX5 PRDM1 RUNX3 TCF21 TGFBI TWIST1
Tumor Suppressor Gene Candidates	APC BRCA1 CDKN1A CDKN1C CDKN2A CDKN2A CDKN2B

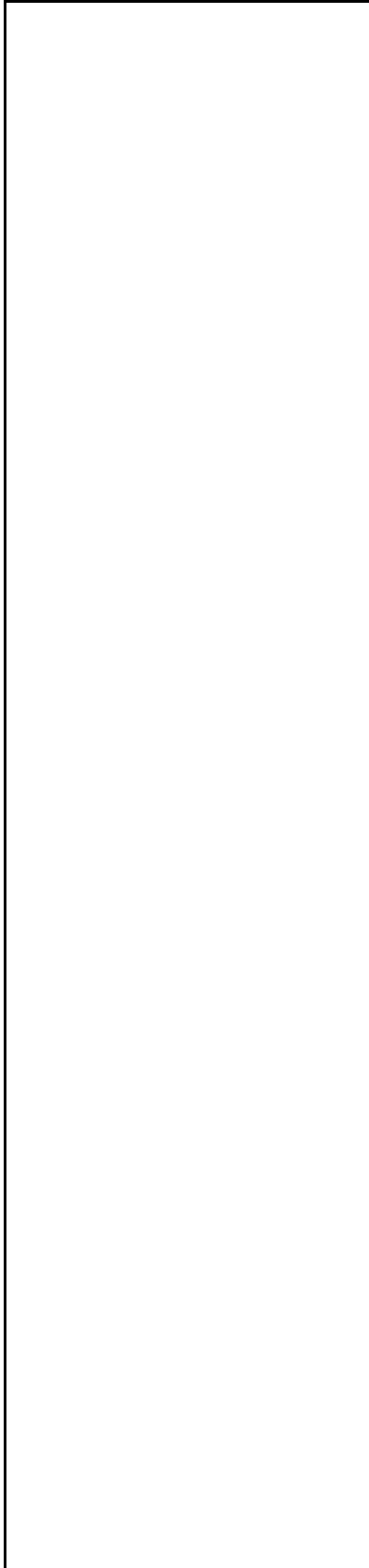
		<p>ENG LRP1B MLH1 PRKCDBP PTEN RASSF1 RASSF2 RECK RUNX3 SFN XPC</p>
	Wnt Signaling	<p>APC SFRP1 SFRP2 SFRP4</p>
	Others	<p>C20orf85 GP1BB RAMP2 ZMYND10 HTR1B</p>
<p>Shames D.S. et al. A genome-wide screen for promoter methylation in lung cancer identifies novel methylation markers for multiple malignancies. Plos Med 2006; 3(12): e486</p>	Well-established methylation markers that have tumor suppressor activity	<p>CDH1 p16 RASSF1 SFRP1 TIMP3</p>
	Novel methylation candidates in NSCLC	<p>BIK CCNA1 DUSP1 LOX TFPI2 TWIST1</p>
<p>Zöchbauer-Müller S et al. Aberrant DNA methylation in lung cancer: biological and clinical implications. Oncologists 2002; 7 (5): 451-457</p>	Methylated genes in lung cancers	<p>APC CDH1 CDH13 DAPK1 FHIT MGMT P16 RARB</p>



		RASSF1 TIMP-3
Rauch T et al. Homeobox gene methylation in lung cancer studied by genome-wide analysis with a microarray-based methylated CpG island recovery assay. PNAS (2007) 104 (13): 5527-5532	Preferential targets for DNA methylation in cancer cell lines and in early-stage lung cancer	HOXA1 HOXA2 HOXA3 HOXA4 HOXA5 HOXA6 HOXA7 HOXA9 HOXA10 HOXA11 HOXA13 HOXB1 HOXB2 HOXB3 HOXB4 HOXB5 HOXB6 HOXB7 HOXB8 HOXB9 HOXC4 HOXC5 HOXC6 HOXC8 HOXC9 HOXC10 HOXC11 HOXC12 HOXC13 HOXD1 HOSD3 HOXD4 HOXD8 HOXD9 HOXD10 HOXD11

		HOXD12 HOXD13 EN1 EN2 LHX1 PAX2 PAX3 PAX5 PAX6 PAX7 PAX9 SIX2 SIX3
<p>Tsou JA et al (2002). DNA methylation analysis: a powerful new tool for lung cancer diagnosis. <i>Oncogene</i> (2002) 12: 21 (35): 5450-5461</p>		AR APC BCL2 CALCA CDH1 CDH13 CDKN2A DAPK1 EDN1 EGFR ESR1 ESR2 FHIT GDF10 GSTP1 HIC1 HOXB HTR1B MGMT MTHFR MYOD1 PGR PTGS2 PTHLH RARB

		RASSF1 PRDM2 S100A2 PRKCDBP TIMP3 CADM1
Helman et al. (2011) DNA hypermethylation in lung cancer is targeted at differentiation-associated genes. <i>Oncogene</i> (2011) 1-8	Tumor vs normal sample	MSC SOX2 BARHL2 HOXD9 SALL3 PRDM13 LOC442425 PROX1 OTX1 C20orf103 ST8SIA3 IRX2 SOX21 VAX1 LRRTM1 FOXD3 TFAP2A RUNX1 WT1 FAM19A2 EN1 SIM2 INSM1 ZNF497 HOXD13 ECAT1 BOLL NXPH1 ZIC4 DMRT3 KATNAL2 LOC389549



FLJ46347  
ONECUT2  
CBLN4  
LBXCOR1  
PAX6  
SIX6  
GSC  
EPS8L1  
HOXD10  
PCDHGA12  
EN2  
HMX2  
NRN1  
PCGF4  
PAX9  
ALX3  
SLC32A1  
OSR2  
TRIM59  
HOXC13  
MAFB  
LHX9  
SIM1  
ZIC1  
LHX2  
ZNF577  
SPATA17  
MEIS1  
GP5  
TBX15  
FOXF2  
ZIC3  
HOXC11  
GRIK2  
DLX5  
HTRA4  
HOXD12  
FOXD2

	ZNF146
	DLX6
	NKX2-3
	HOXB13
	VAX2
	HOXC4
	NR2E1
	DPP6
	OTX2
	PRDM14
	IRX1
	HOXA1
	OSR1
	GRK7
	TWIST1
	SIX3
	TFAP2C
	HOXD3
	TITF1
	SSTR1
	PRDM1
	PCDHGA11
	ZNF329
	MSX1
	HOXD8
	HOXA9
	ZNF274
	CDX2
	FOYG1B
	SFMBT2
	KIAA1024
	DMRT2





Legend:

B - Beta (measure of methylation proportion)

Brank - Beta Rank (refer below)

M - M-value ( $\log_2(\text{methylated probe}/\text{unmethylated probe})$ )

FDR - P-value adjusted by False Discover Rate

H358 $\cap$ H460

<b>Beta Rank</b>	<b>Beta</b>
1	[0.0, 0.2)
2	[0.2, 0.4)
3	[0.4, 0.6]
4	(0.6, 0.8]
5	(0.8, 1.0]



**Table S3: List of commonly upregulated genes in lung cancer**

References	Descriptions	Gene
<p>Beer DG et al. Gene-expression profile predict survival of patients with lung adenocarcinoma. Nat Med 2002; 8(8): 816-24</p>	<p>Tumor samples vs normal</p>	<p>ADM  AGFG1  ALDH3B2  ALDOA  BZW1  CDC6  CDS1  CRK  CSTB  DBP  DEFB1  EIF1  ERBB2  FADD  FEZ2  FUCA1  FURIN  FUT3  FXVD3  GAPDH  GARS  GCNT1  GRB7  H2AFZ  HCFC1R1  HMBS  HPCAL1  HSPA8  HSU53209  INHA  ITGA2  KIAA0020  KIAA0317  KRT18  KRT19  KRT7</p>

		<p> KYNU  MSH3  NFYC  NME2  P2RX5  PDAP1  PDE7A  PEX7  POLD3  PPIF  REG1A  RPS26  RPS3  RPS6KB1  RTCD1  S100P  SCGB2A2  SERPINE1  SLC20A1  SLC2A1  STARD3  STC1  STX1A  TMF1  TP63  TPBG  TTLL12  TUBA4A  UGP2  VDAC2  VEGFA  WNT1  WNT10B </p>
<p> Kettunen E et al. Differentially expressed genes in nonsmall cell lung cancer: expression profiling of cancer-related genes in squamous cell lung cancer. <i>Cancer Genet Cytogenet</i> 2004; 149(2): 98-106 </p>	<p>Tumor samples</p>	<p> COL2A1  DSC3  IGFBP5  ITGA6  ITGB4  JAG1 </p>

		<p>KRT10  KRT14  KRT2  MIF  NGFR  RARG</p>
<p>Risch A &amp; Plass C. Lung Cancer epigenetics and genetics. Int J Cancer 2008; 123(1): 1-7</p>	<p>Review citing from studies on tumor samples</p>	<p>BCL2  CCND1  EGFR  MYC</p>
<p>Valk K et al. Gene-expression profiles of non-small cell lung cancer: Survival Prediction and New Biomarkers. Oncology 2010; 79(3-4): 283-292</p>	<p>Tumor Samples vs. normal</p>	<p>ANLN  ASPM  AURKA  AURKB  BIK  BUB1B  CCNA2  CCNB1  CCNB2  CCT5  CDC20  CDC45  CDCA8  CDK1  CDKN3  CEP55  CKS1B  COL3A1  COL7A1  FAP  FEN1  FOXM1  GMNN  HMMR  IGFBP3  KIAA0101  KIF11  KIF14  LOXL2</p>

		MCM2 MDK MIF MMP1 MMP11 MMP9 MYBL2 NCAPH NDC80 PAK1 PTTG2 SPP1 TIMP1 TK1 TMPRSS4 TTK TYMS UHRF1
Hou et al. Gene Expression-Based Classification of Non-Small Cell Lung Carcinomas and Survival Prediction. PloS one 2010; 5(4): e10312	Tumor vs Normal	ABP1 ADAM12 ADAM28 ADAMDEC1 AIM2 AK4 AKR1B10 ANKRD22 ANLN ARNTL2 ASPM ATAD2 AURKA AURKB BCL11A BIRC5 BLM BRIP1 BUB1 BUB1B C11orf80

	C16orf75
	C2CD4A
	C4orf7
	C7orf68
	C9orf140
	CASC5
	CCDC34
	CCNA2
	CCNB1
	CCNB2
	CCNE1
	CCNE2
	CDC20
	CDC45
	CDC6
	CDCA2
	CDCA3
	CDCA5
	CDCA7
	CDCA8
	CDK1
	CDKN2A
	CDKN3
	CDT1
	CENPA
	CENPE
	CENPF
	CENPK
	CENPN
	CEP55
	CHEK1
	CLDN10
	COCH
	COL10A1
	COL11A1
	COL1A1
	COL3A1
	COL5A2
	CPS1

		CRABP2
		CTHRC1
		CTTN
		CXCL13
		CXCL9
		CXorf61
		CYP24A1
		DEPDC1
		DEPDC1B
		DERL3
		DLGAP5
		DNAH14
		DNAJC12
		DSCC1
		DSP
		DTL
		DUSP4
		E2F8
		ECT2
		EGLN3
		EPR1
		ERO1L
		EXO1
		EZH2
		FAM72A
		FAM72B
		FAM72C
		FAM72D
		FAM83A
		FAM83D
		FANCI
		FAP
		FBXO32
		FCRL5
		FERMT1
		FGB
		FGL1
		FLJ40330
		FNDC1

		FOXM1
		GABBR1
		GALNT14
		GCNT3
		GIN1
		GIN2
		GJB2
		GNG4
		GOLM1
		GPT2
		GPX2
		GREM1
		GTSE1
		HELLS
		HIST1H2BC
		HIST1H2BD
		HIST1H2BG
		HIST1H2BH
		HIST3H2A
		HJURP
		HMGB3
		HMGB3L1
		HMMR
		HN1
		HOXC10
		HOXC6
		HS6ST2
		IGF2BP3
		IGFBP3
		IGHA1
		IGHA2
		IGHD
		IGHG1
		IGHG2
		IGHG3
		IGHG4
		IGHM
		IGHV1-69
		IGHV2-70

		IGHV3-23
		IGHV3-48
		IGHV4-31
		IGHV4-59
		IGK@
		IGKC
		IGKV1-5
		IGKV3-20
		IGKV3D-15
		IGKV4-1
		IGL@
		IGLJ3
		IGLV1-36
		IGLV1-40
		IGLV1-44
		IGLV3-19
		IQGAP3
		KIAA0101
		KIF11
		KIF14
		KIF15
		KIF18B
		KIF20A
		KIF23
		KIF2C
		KIF4A
		KISS1R
		KNTC1
		KRT17
		KRT6A
		KRT6B
		KRT6C
		LGR4
		LGSN
		LOC100290006
		LOC100291917
		LOC652694
		LOC84740
		LOC96610



		LRRC15
		LY6K
		MAD2L1
		MAGEA3
		MAGEA6
		MCM10
		MCM2
		MCM4
		MDK
		MELK
		MGC29506
		MKI67
		MLF1IP
		MMP1
		MMP12
		MMP9
		MND1
		MS4A1
		MYBL2
		NCAPG
		NDC80
		NEK2
		NFE2L3
		NMU
		NUF2
		NUSAP1
		OIP5
		ORC6L
		PAEP
		PAFAH1B3
		PAICS
		PBK
		PCP4
		PI15
		PITX2
		PLEK2
		POSTN
		POU2AF1
		PPAT

		PRC1
		PRR11
		PSAT1
		PTTG1
		PYCR1
		RAD51
		RAD51AP1
		RALGPS2
		RASSF6
		RFC4
		RNASEH2A
		RRM2
		SCG5
		SERPINB5
		SGOL2
		SHCBP1
		SIX1
		SLAMF7
		SLC12A8
		SLC16A14
		SLC2A1
		SLC2A5
		SLC44A5
		SLC6A10P
		SLC6A8
		SOX4
		SPAG4
		SPAG5
		SPC25
		SPINK1
		SPP1
		SRD5A1
		STIL
		SULF1
		SYT13
		TFAP2A
		TFF1
		THBS2
		THY1

		TK1 TMPRSS4 TNNT1 TOP2A TPX2 TRIM59 TRIP13 TTK TUBB2B TYMS UBD UBE2C UBE2S UBE2T UCHL1 UCK2 UGT1A1 UGT1A10 UGT1A3 UGT1A4 UGT1A5 UGT1A6 UGT1A7 UGT1A8 UGT1A9 UGT8 UHRF1 WDR72 ZWILCH ZWINT
Zhang WC, et al. Glycine Decarboxylase Activity Drives Non-Small Cell Lung Cancer Tumor-initiating cells and tumorigenesis. Cell (2012).	Tumor samples enriched with CD166	ABCC3 AGR2 AKR1B10 ANLN BAIAP2L1 C1orf106 C6orf168 CD24 CDC20

		CDCA7
		CDH1
		CDH3
		CEACAM1
		CLDN10
		CLDN3
		COL10A1
		COL1A1
		COL1A2
		COL3A1
		CP
		CRABP2
		CXCL13
		CXCL14
		DNAJC12
		DNAJC12
		DNAJC12
		EPCAM
		ERO1L
		FAM199X
		FERMT1
		GCNT3
		GGCT
		GREM1
		HIST1H2BD
		HMGA1
		HMGB3
		HS6ST2
		IGF2BP3
		IGFBP2
		IGFBP3
		KCNK1
		KDEL2
		KDEL3
		KIAA0101
		KIAA0101
		LAPTM4B
		LCN2
		LSR

		MDK MMP1 MMP12 MMP7 NME1 NME1 NME1 NQO1 PAICS PAICS PHLDA2 PLA2G4A PPAP2C PRDX4 PSAT1 PTGFRN RRM2 S100A2 S100P SLC7A11 SMPDL3B SORD SPINK1 SPP1 SRD5A1 ST14 SULF1 THBS2 TMEM106B TMPRSS4 TOP2A TRIM2 WFDC2 ZWINT
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**Table S5: List of OGs identified in cancer cells that were downregulated upon reprogramming.**

List of OGs identified in H358 that were downregulated upon reprogramming												
geneSymbol	geneName	entrezID	accNum	IMR90_M	H358_M	iPCH358_M	piPCH358_log	log(H358_M-IMR90_M)	log(iPCH358_M-H358_M)	FDR(H358_M-IMR90_M)	FDR(iPCH358_M-H358_M)	FDR(piPCH358_M-IPCH358_M)
EFNA1	Homo sapiens ephrin-A1 (EFNA1), transcript variant 1, mRNA.	1942	NM_004428.2	4.247927513	9.418225588	6.76431591	6.375399729	5.170298074	-2.653893997	0.000232311	0.004491135	1
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA.	2919	NM_001511.1	5.695097871	9.572064793	4.247927513	4.247927513	3.876696922	-5.324137279	0	0.039708178	1
CXCL2	Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA.	2920	NM_002089.3	4.247927513	7.322556059	4.247927513	4.247927513	3.074628546	-3.074628546	0	0.009583053	1
ID1	Homo sapiens inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), transcript variant 2, mRNA.	3397	NM_181353.1	8.237489413	11.47685306	6.050191838	7.076549726	3.239363644	-5.42666122	1.026357889	0.000857332	0.783285728
JUP	Homo sapiens junction plakoglobin (JUP), transcript variant 2, mRNA.	3728	NM_021991.1	8.874473618	11.05583735	8.453374153	8.539220587	2.181363732	-2.602463197	0.085846434	0.00714489	1
S100P	Homo sapiens S100 calcium binding protein P (S100P), mRNA.	6286	NM_005980.2	4.247927513	11.20758241	4.247927513	4.247927513	6.959654898	-6.959654898	0	0.001103273	1
SPP1	Homo sapiens secreted phosphoprotein 1 (SPP1), transcript variant 2, mRNA.	6696	NM_000582.2	4.247927513	7.861902468	4.247927513	4.390022365	3.613974954	-3.613974954	0.142094852	5.05E-05	7.78E-05
RUNX2	Homo sapiens runt-related transcription factor 2 (RUNX2), transcript variant 2, mRNA.	860	NM_001015051.2	4.683202761	7.007194709	4.247927513	4.247927513	2.323991948	-2.759267195	0	0.019028605	1
MAP3K8	Homo sapiens mitogen-activated protein kinase kinase kinase 8 (MAP3K8), mRNA.	1326	NM_005204.2	4.247927513	6.602793522	4.247927513	4.247927513	2.354866008	-2.354866008	0	0.011213193	1
EPHA1	Homo sapiens EPH receptor A1 (EPHA1), mRNA.	2041	NM_005232.3	4.247927513	8.757376071	4.247927513	4.247927513	4.509448558	-4.509448558	0	0.000675135	1
ERBB3	Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3), transcript variant s, mRNA.	2065	NM_001009515.1	4.247927513	9.430702958	6.9268915	7.424687304	5.182775445	-2.504013808	0.497998153	0.000389518	1
EREG	Homo sapiens epiregulin (EREG), mRNA.	2069	NM_001432.2	4.247927513	6.917788748	4.247927513	4.247927513	2.669861234	-2.669861234	0	0.010247191	1
LCN2	Homo sapiens lipocalin 2 (LCN2), mRNA.	3934	NM_005564.3	4.247927513	13.33485101	4.208386711	4.247927513	9.086923493	-9.126464296	0.039540803	0.00263334	0.003694607
TACSTD2	Homo sapiens tumor-associated calcium signal transducer 2 (TACSTD2), mRNA.	4070	NM_002353.1	4.247927513	12.6099518	4.247927513	4.247927513	8.36202429	-8.36202429	0	5.47E-06	7.68E-06
EPCAM	Homo sapiens epithelial cell adhesion molecule (EPCAM), mRNA.	4072	NM_002423.2	4.247927513	13.06746186	7.315248288	7.508466913	8.819534345	-5.752213571	0.193218626	9.93E-06	0.001180033
MMP7	Homo sapiens matrix metalloproteinase 7 (matrylsin, uterin) (MMP7), mRNA.	4316	NM_002423.2	4.247927513	8.627443131	4.247927513	4.247927513	4.379515617	-4.379515617	0	0.010466226	0.013421766
MST1R	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R), mRNA.	4486	NM_002447.2	4.247927513	7.957914935	4.247927513	4.247927513	3.709987421	-3.709987421	0	0.001706729	0.00243089
SREBF1	Homo sapiens sterol regulatory element binding transcription factor 1 (SREBF1), transcript variant 1, mRNA.	6720	NM_001005291.1	7.618162029	9.737849243	5.719248909	5.311239609	2.119687215	-4.018600334	-0.40800984	0.034905336	0.002138814
VAV1	Homo sapiens vav 1 guanine nucleotide exchange factor (VAV1), mRNA.	7409	NM_005428.2	4.247927513	6.361477763	4.294463376	4.797047463	2.11355025	-2.067014387	0.502584087	0.015403121	0.021208353
ARHGEF5	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 5 (ARHGEF5), mRNA.	7984	NM_005435.3	4.247927513	6.256147764	4.247927513	4.247927513	2.00822025	-2.00822025	0	0.000147284	0.000239621
PEG10	Homo sapiens paternally expressed 10 (PEG10), transcript variant 1, mRNA.	23089	NM_015068.3	4.247927513	7.753477147	4.247927513	4.247927513	2.879620386	-3.505549634	0	0.011853366	7.44E-05
CBLC	Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence c (CBLC), mRNA.	23624	NM_012116.2	4.247927513	6.264549688	4.247927513	4.247927513	2.016622174	-2.016622174	0	0.022934193	0.028138718
RAB38	Homo sapiens RAB38, member RAS oncogene family (RAB38), mRNA.	23682	NM_022387.1	6.292413066	8.968600584	5.281151141	5.979301154	2.676187518	-3.687449443	0.698150013	9.24E-05	0.003663093
RAB25	Homo sapiens RAB25, member RAS oncogene family (RAB25), mRNA.	57111	NM_020387.2	4.247927513	11.65646491	4.247927513	4.247927513	7.408537397	-7.408537397	0	1.30E-05	2.06E-05
RAB17	Homo sapiens RAB17, member RAS oncogene family (RAB17), mRNA.	64284	NM_022449.1	4.247927513	9.661579232	4.247927513	4.247927513	5.413651718	-5.413651718	0	7.03E-05	0.000106336

List of OGs identified in H460 that were downregulated upon reprogramming										
geneSymbol	geneName	entrezID	accNum	IMR90_M	H460_M	iPCH460_M	log(H460_M-IMR90_M)	log(iPCH460_M-H460_M)	FDR(H460_M-IMR90_M)	FDR(iPCH460_M-H460_M)
EFNA1	Homo sapiens ephrin-A1 (EFNA1), transcript variant 1, mRNA.	1942	NM_004428.2	4.247927513	10.20934074	5.95407019	5.961413228	-4.255270552	0.006105777	0.025092469
CXCL1	Homo sapiens chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha) (CXCL1), mRNA.	2919	NM_001511.1	5.695097871	11.5472057	4.247927513	5.852107828	-7.299278185	0.015147775	0.000967435
CXCL2	Homo sapiens chemokine (C-X-C motif) ligand 2 (CXCL2), mRNA.	2920	NM_002089.3	4.247927513	8.297494621	4.247927513	4.049567107	-4.049567107	0.000372551	0.000624987
ID1	Homo sapiens inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), transcript variant 2, mRNA.	3397	NM_181353.1	8.237489413	10.24989778	5.796304373	2.012408366	-4.453593406	0.009418681	0.044912459
JUP	Homo sapiens junction plakoglobin (JUP), transcript variant 2, mRNA.	3728	NM_021991.1	8.874473618	11.23884483	8.05354804	2.36437121	-3.185296788	0.016545167	0.025085519
S100P	Homo sapiens S100 calcium binding protein P (S100P), mRNA.	6286	NM_005980.2	4.247927513	10.97868416	4.247927513	6.730756644	-6.730756644	0.000675716	0.001177531
SPP1	Homo sapiens secreted phosphoprotein 1 (SPP1), transcript variant 2, mRNA.	6696	NM_000582.2	4.247927513	12.34166532	4.247927513	8.093737807	-8.093737807	9.17E-05	0.00014868
DEFB1	Homo sapiens defensin, beta 1 (DEFB1), mRNA.	1672	NM_005218.3	4.247927513	13.13271334	4.247927513	8.88478583	-8.88478583	3.29E-05	5.32E-05
SERPINB2	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 2 (SERPINB2), mRNA.	5055	NM_002575.1	7.565686581	9.971485427	4.247927513	2.405798846	-5.723557914	0.00855195	2.46E-05
PVT1	Homo sapiens Pvt1 oncogene (non-protein coding) (PVT1), non-coding RNA.	5820	NR_003367.1	5.32386525	11.43545246	4.934155068	6.111587209	-6.501297392	0.000112599	0.001429108
SRC	Homo sapiens v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC), transcript variant 2, mRNA.	6714	NM_198291.1	7.933923882	10.38395416	8.078445065	2.450030279	-2.305509097	0.000108271	0.006480961
RAB20	Homo sapiens RAB20, member RAS oncogene family (RAB20), mRNA.	55647	NM_017817.1	4.247927513	7.919364601	4.247927513	3.671437088	-3.671437088	0.005469648	0.008592697
AKR1B10	Homo sapiens akko-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA.	57016	NM_002099.3	4.247927513	13.24966468	4.247927513	9.001737169	-9.001737169	3.10E-05	5.07E-05
RAB3C	Homo sapiens RAB3C, member RAS oncogene family (RAB3C), mRNA.	115827	NM_138453.2	4.247927513	9.643016759	4.247927513	5.395089245	-5.395089245	0.001098751	0.00190137

**Legend:**

M - M-value (log2(Sample intensity))

FDR - P-value adjusted by False Discover Rate



H358∩H460

**Table S6: List of TSs identified in cancer cells that were upregulated upon reprogramming.**

List of TSs identified in H358 that were upregulated upon reprogramming													
geneSymbol	geneName	entrezID	accNum	IMR90_M	H358_M	iPCH358_M	piPCH358_M	log(H358_M-IMR90_M)	log(iPCH358_M-H358_M)	log(piPCH358_M-iPCH358_M)	FDR(H358_M-IMR90_M)	FDR(iPCH358_M-H358_M)	FDR(piPCH358_M-iPCH358_M)
ALPL	Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), transcript variant 1, mRNA.	249	NM_000478.3	7.795100115	4.467531584	8.174977981	8.009136379	-3.327568531	3.707446396	-0.165841601	0.01523736	0.004046034	1
CCND2	Homo sapiens cyclin D2 (CCND2), mRNA.	894	NM_001759.2	10.27632147	4.247927513	9.437738181	8.523925386	-6.028393958	5.189810667	-0.913812794	7.03E-05	0.001107741	1
PLAGL1	Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 3, mRNA.	5325	NM_001080951.1	7.105535033	4.247927513	7.126926419	7.151122405	-2.857607519	2.878998906	0.024195986	0.000442278	0.00034159	1
CADM1	Homo sapiens cell adhesion molecule 1 (CADM1), transcript variant 1, mRNA.	23705	NM_014333.3	10.36637441	4.247927513	9.38546736	9.000871995	-6.118446892	5.137539846	-0.38495365	5.70E-05	0.001505054	1
CA12	Homo sapiens carbonic anhydrase XII (CA12), transcript variant 1, mRNA.	771	NM_001218.3	8.524815847	4.247927513	7.109658232	7.38406416	-4.276888333	2.861730719	0.274405928	5.28E-05	0.000341716	1
FBLN1	Homo sapiens fibulin 1 (FBLN1), transcript variant A, mRNA.	2192	NM_006487.2	11.81414526	6.685880878	9.015930357	9.306764265	-5.128264381	2.330049479	0.290833908	0.000142915	0.003334851	1
GAS1	Homo sapiens growth arrest-specific 1 (GAS1), mRNA.	2619	NM_002048.1	8.125312486	4.577930152	10.12927275	9.903133067	-3.547382334	5.551342595	-0.22613968	0.002311989	0.000740814	1
GJA1	Homo sapiens gap junction protein, alpha 1, 43kDa (GJA1), mRNA.	2697	NM_000165.3	10.50714393	4.247927513	7.858575106	8.039972897	-6.259216419	3.610647592	0.181397791	2.84E-05	0.002117823	1
HOXA5	Homo sapiens homeobox A5 (HOXA5), mRNA.	3202	NM_019102.2	9.93139086	7.740408287	12.75976082	12.48903598	-2.190982573	5.01935253	-0.270724842	0.01412541	0.002327925	1
IGFBP5	Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA.	3488	NM_000599.2	15.15831636	4.345068564	6.693926527	7.822641058	-10.8132478	2.348857963	1.128714531	9.24E-06	0.03229626	1
KIT	Homo sapiens v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog (KIT), transcript variant 2, mRNA.	3815	NM_001093772.1	8.133750484	4.361215664	6.669333508	6.521571679	-3.77253482	2.308117844	-0.147761829	0.003151229	0.004131816	1
MAP1B	Homo sapiens microtubule-associated protein 1B (MAP1B), transcript variant 2, mRNA.	4131	NM_032010.1	9.636943555	5.957565475	7.990596854	7.566182125	-3.679378079	2.033031378	-0.424414729	0.010150785	0.030845379	1
HTRA1	Homo sapiens HtrA serine peptidase 1 (HTRA1), mRNA.	5654	NM_002775.3	11.57090207	4.247927513	6.344927155	6.89566172	-7.322974554	2.06999642	0.550734565	5.70E-05	0.012146371	1
SMO	Homo sapiens smoothened homolog (Drosophila) (SMO), mRNA.	6608	NM_005631.3	6.875414771	4.247927513	7.316235762	7.165529396	-2.627487257	3.068308249	-0.150706366	0.000364337	0.000634267	1
UCHL1	Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA.	7345	NM_004181.3	12.91768063	7.221504453	11.77149922	11.68571058	-5.696176182	4.54994772	-0.085788646	0.000164925	0.000633869	1
BTG2	Homo sapiens BTG family, member 2 (BTG2), mRNA.	7832	NM_006763.2	7.054502802	4.247927513	6.646722892	6.147949445	-2.806575289	2.398795378	-0.498773447	0.000852036	0.004289454	1
KAT2B	Homo sapiens K(lysine) acetyltransferase 2B (KAT2B), mRNA.	8850	NM_003884.4	7.259617257	5.015597497	8.171427927	8.523938382	-2.244019761	3.155830431	0.352510455	0.025774379	0.010455759	1
RASSF2	Homo sapiens Ras association (RafGDS/AF-6) domain family member 2 (RASSF2), transcript variant 2, mRNA.	9770	NM_170774.1	7.343944471	4.247927513	6.561671587	6.336537841	-3.096016957	2.313744074	-0.225133746	0.001888477	0.010684353	1
EPB41L3	Homo sapiens erythrocyte membrane protein band 4.1-like 3 (EPB41L3), mRNA.	23136	NM_012307.2	7.332014683	4.247927513	7.860048505	8.353701191	-3.08400717	3.612120992	0.493652686	0.000554104	9.53E-05	0.533196594
TSPYL2	Homo sapiens TSPY-like 2 (TSPYL2), mRNA.	64061	NM_022117.1	7.956868629	5.642638403	8.054215569	7.030405853	-2.314230226	2.411577166	-1.023809716	0.000915075	0.00407643	0.720939221
CCDC136	Homo sapiens coiled-coil domain containing 136 (CCDC136), mRNA.	64753	NM_022742.3	8.456707331	4.914481111	9.161872282	9.540556825	-3.54222622	4.247391171	0.378684542	0.000127179	0.000704154	1

List of TSs identified in H460 that were upregulated upon reprogramming													
geneSymbol	geneName	entrezID	accNum	IMR90_M	H460_M	iPCH460_M	piPCH460_M	log(H460_M-IMR90_M)	log(iPCH460_M-H460_M)	log(piPCH460_M-iPCH460_M)	FDR(H460_M-IMR90_M)	FDR(iPCH460_M-H460_M)	FDR(piPCH460_M-iPCH460_M)
ALPL	Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), transcript variant 1, mRNA.	249	NM_000478.3	7.795100115	4.247927513	7.957177189	7.957177189	-3.547172602	3.709249675	-0.012769538	0.012769538	0.010224651	1
CCND2	Homo sapiens cyclin D2 (CCND2), mRNA.	894	NM_001759.2	10.27632147	4.51690323	10.01807229	10.01807229	-5.759418242	5.501169065	-0.001252837	0.006359006	0.006359006	1
PLAGL1	Homo sapiens pleiomorphic adenoma gene-like 1 (PLAGL1), transcript variant 3, mRNA.	5325	NM_001080951.1	7.105535033	4.419983748	7.208899781	7.208899781	-2.685551285	2.788916033	0.001543689	0.005068682	0.005068682	1
CADM1	Homo sapiens cell adhesion molecule 1 (CADM1), transcript variant 1, mRNA.	23705	NM_014333.3	10.36637441	5.379390016	9.585978902	9.585978902	-4.98706539	4.206669886	0.006236772	0.014985263	0.014985263	1
CDKN2A	Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 3, mRNA.	1029	NM_058197.3	7.888719191	4.247927513	11.16717146	11.16717146	-3.640791678	6.919243942	0.00040259	0.000861878	0.000861878	1
CDKN2B	Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 2, mRNA.	1030	NM_078487.2	6.503157508	4.247927513	6.395097179	6.395097179	-2.255229995	2.147169665	0.000217071	0.015729684	0.015729684	1
FOXO3	Homo sapiens forkhead box O3 (FOXO3), transcript variant 2, mRNA.	2309	NM_201559.2	11.09002897	8.108814853	10.57977939	10.57977939	-2.981214115	2.470964533	0.015147775	0.03525379	0.03525379	1
SLIT2	Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA.	9353	NM_004787.1	6.96545246	4.424805712	9.18802115	9.18802115	-2.540646748	4.763215438	0.015450578	0.023359656	0.023359656	1

Legend:

M - M-value (log2(Sample intensity))

FDR - P-value adjusted by False Discover Rate

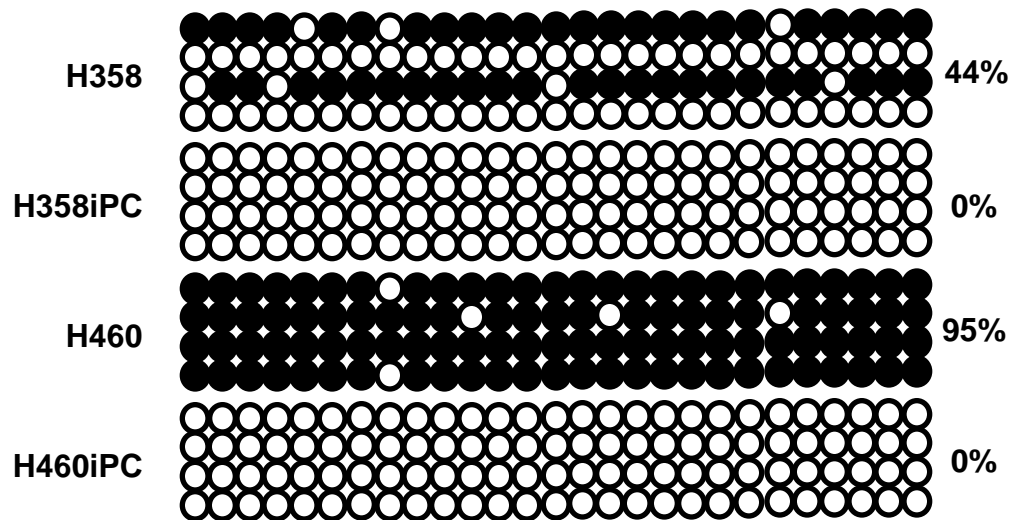
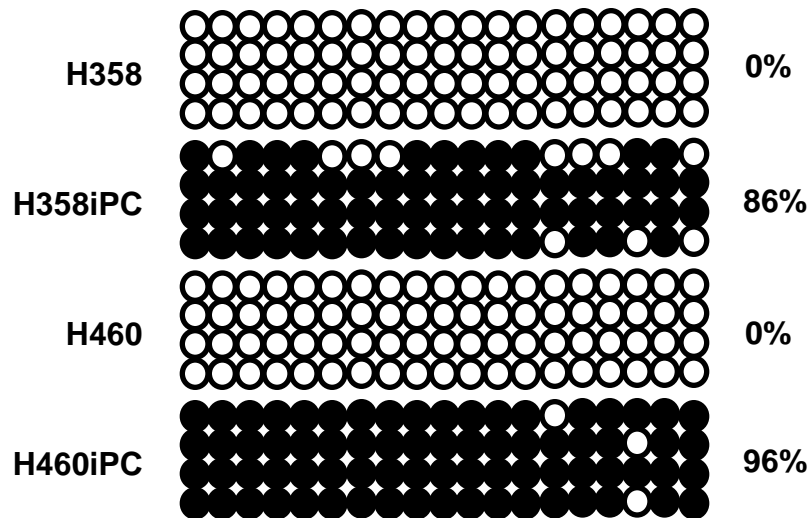
H358∩H460



**Table S7: Primer sequences**

Primers	Sequence 5' - 3'	Applications
hGAPDH F	TCG ACA GTC AGC CGC ATC T	qPCR
hGAPDH R	CTA GCC TCC CGG GTT TCT CT	
hSOX2 F	CAA GAT GCA CAA CTC GGA GA	
hSOX2 R	GCT TAG CCT CGT CGA TGA AC	
hOCT3/4 F	GAA GGA TGT GGT CCG AGT GT	
hOCT3/4 R	GCC TCA AAA TCC TCT CGT TG	
hNANOG F	ACC TTC CAA TGT GGA GCA AC	
hNANOG R	ACT GGA TGT TCT GGG TCT GG	
hFGF4 F	GCT GGC TTA AGG ATG GAC AG	
hFGF4 R	ACG CTC TCC ATC ACG AGA CT	
hPAX6 F	CTT GGG AAA TCC GAG ACA GA	
hPAX6 R	CTA GCC AGG TTG CGA AGA AC	
hCDX2 F	AAA GGC TTG GCT GGT GTA TG	
hCDX2 R	GTC AGG CCT GGA GTC CAA TA	
hBRACHYURY F	CCA CCT TCC AAG TGA AGC TC	
hBRACHYURY R	CGA AGT CCA TGA GCA GCA TA	
hGATA4 F	CCA AGC AGG ACT CTT GGA AC	
hGATA4 R	GGG AAG AGG GAA GAT TAC GC	
hFOXA2 F	GCT ACT CCT CCG TGA GCA AC	
hFOXA2 R	TAC GTG TTC ATG CCG TTC AT	
hMSX1 F	GAG TTC TCC AGC TCG CTC AG	
hMSX1 R	TCT CCA GCT CTG CCT CTT GT	
hKRT19 F	TAG ACC CAG ACC CAC AGA CC	
hKRT19 R	CAG CCC CTG TAG GTC ACA AT	
hCD24 F	GAG ACT CAG GCC AAG AAA CG	
hCD24 R	CCT GTT TTT CCT TGC CAC AT	
hKRT7 F	CAG GAA CTC ATG AGC GTG AA	
hKRT7 R	GTA GGT GGC GAT CTC GAT GT	
hKYNU F	GGG AAA TTC TCT TGG CCT TC	
hKYNU R	CCC CAC TTC ATG ACC ATA GG	
hSERPINB5 F	CGG GGT AGT TGG CAG AAA TA	
hSERPINB5 R	TGG GAA GAA GAG CTT CCA AA	
hDUSP4 F	GGG AGG AGG GAA CAA GCT AC	
hDUSP4 R	ACC TCT AAG CTG GCA CTC CA	
hPPAP2C F	CTG TAT GTG CAG GCA CGA CT	
hPPAP2C R	AAA GGC CAC CAG GAA GAA CT	
hSTX1A F	GAC CGC TTC ATG GAT GAG TT	
hSTX1A R	CGT TCT CTG CGA TCT TGT CA	
hS100P F	TAC CAG GCT TCC TGC AGA GT	
hS100P R	CAA TTT ATC CAC GGC ATC CT	
hAGR2 F	TAT GGC ATG GTG TGC AAA GT	
hAGR2 R	AGT GGC GAA AGA AGG TGC TA	
hHOXA7 F	ACC TAC ACG CGC TAC CAG AC	
hHOXA7 R	AGG TAG CGG TTG AAG TGG AA	
hRPRM F	GCA AAC CTG TCG GAG TCA AT	
hRPRM R	GGC ATG AGG ACT TTC AGA GG	
hHOXA5 F	AGC ACA TGC TCT TTG CCT CT	
hHOXA5 R	CTT CAT TCT CCG GTT TTG GA	
hHOXD13 F	TAT GGG TCT GGG ATT GTG GT	
hHOXD13 R	GCC ACA TTG ATT CAG CCT CT	
hGALNT14 F	CTG AGA TGC ACA CTG CTG G	
hGALNT14 R	CGT TGT GGA AGG TGA TGA TG	
hAPC Methylated F	ATT TTC GTC GGG AGT TCG TC	MSP
hAPC Methylated R	CAA CCA CAT ATC GAT CAC GTA CG	
hAPC Unmethylated F	TTT TGT TGG GAG TTT GTT GA	
hAPC Unmethylated R	CAA CCA CAT ATC AAT CAC ATA CA	
hHOXC9 Methylated F	GCG TTA TAT GCG GAT TTG GTT C	
hHOXC9 Methylated R	ACG TAA TAA CGA CCC CCG AC	
hHOXC9 Unmethylated F	TGT TAT ATG TGG ATT TGG TTT GA	
hHOXC9 Unmethylated R	AAA AAC ATA ATA ACA ACC CCC AAC	

hHOXA7 Methylated F	GCG AGG TTA TTG TAG AGT TCG G	
hHOXA7 Methylated R	AAA ACC CCT TTA CGT CCG AC	
hHOXA7 Unmethylated F	TGG TGA GGT TAT TGT AGA GTT TGG	
hHOXA7 Unmethylated R	TCA AAA CCC CTT TAC ATC CAA C	
hKRT19 Methylated F	TAG GTT TTC GAG GAG GAC GA	
hKRT19 Methylated R	AAA CGA CGA CTC CGT ACG TT	
hKRT19 Unmethylated F	GTA GGT TTT TGA GGA GGA TGA	
hKRT19 Unmethylated R	CCT AAA CAA CAA CTC CAT ACA TT	
hHOXA5 Methylated F	TTT TTT GTT TTT CGG GTC GT	
hHOXA5 Methylated R	CAA ACT TAT CCC CCT AAC GAA	
hHOXA5 Unmethylated F	GGT TTT TTT GTT TTT TGG GTT GT	
hHOXA5 Unmethylated R	CCA AAC TTA TCC CCC TAA CAA A	
hHOXD13 Methylated F	GTT TCG GGG AGT TTC GGT AC	
hHOXD13 Methylated R	ATA CAC CTA ACT ATT CCA CCC GTT	
hHOXD13 Unmethylated F	TTT TGG GGA GTT TTG GTA TGA	
hHOXD13 Unmethylated R	ATA CAC CTA ACT ATT CCA CCC ATT	
hRPRM Methylated F	TGG GAG CGT ATT CGG ATA CG	
hRPRM Methylated R	AAC CCA ACG ACA CTA ATC GCC	
hRPRM Unmethylated F	TGG GAG TGT ATT TGG ATA TGG	
hRPRM Unmethylated R	AAA AAC CCA ACA ACA CTA ATC ACC	
hS100P Methylated F	TTG TTA GGG AGG AGT TAT CGG	
hS100P Methylated R	TTC TAT TCA ACC CAA CCG AA	
hS100P Unmethylated F	TTG TTA GGG AGG AGT TAT TGG	
hS100P Unmethylated R	TTC TAT TCA ACC CAA CCA AA	
KRT19 F	GGT TTT ATT TGT GGA TTT TTT TA	Bisulfite sequencing
KRT19 R	AAA CAA AAA CCT AAA CCC TCC C	
HOXA5 F	TTG TTA TAA TGG GTT GTA ATT TTA ATT	
HOXA5 R	TAA AAC ATA TAC TTA ATT CCC TCC TAC	

**a***HOXA5***b***KRT19***Legends**

- Unmethylated
- Methylated