

Table S4

Group Type	Group Name	P-Value	Q-Value
<b>GO Molecular Function</b>	<b>methyltransferase activity</b>	<b>1.90E-08</b>	<b>3.86515E-05</b>
<b>GO Cellular Component</b>	<b>nucleus</b>	<b>3.90E-07</b>	<b>0.000170133</b>
<b>InterPro</b>	<b>Nuclear protein SET</b>	<b>2.20E-07</b>	<b>0.001040343</b>
<b>KEGG Pathway</b>	<b>Nicotinate and nicotinamide metabolism</b>	<b>2.30E-05</b>	<b>0.003830887</b>
<b>KEGG Pathway</b>	<b>Methionine metabolism</b>	<b>6.50E-05</b>	<b>0.005532044</b>
Conserved UTR Motif	CLUSTER_7__MIR-29C MIR-29B MIR-29A MIR196	6.70E-04	0.047902318
<b>GO Molecular Function</b>	<b>DNA binding</b>	<b>1.60E-04</b>	<b>0.169526443</b>
<b>GO Molecular Function</b>	<b>zinc ion binding</b>	<b>1.60E-04</b>	<b>0.169526443</b>
<b>InterPro</b>	<b>SET-related region</b>	<b>7.80E-05</b>	<b>0.184952092</b>
<b>Oncomine Gene Expression Signatures</b>	<b>Localized Prostate Carcinoma PCa ETS - Top 20% over-expressed in ERG+ (xiaojun)</b>	<b>6.50E-05</b>	<b>0.363401091</b>
KEGG Pathway	Purine metabolism	0.01	0.422128373
KEGG Pathway	Selenoamino acid metabolism	0.01	5.41E-01
GO Molecular Function	histone-lysine N-methyltransferase activity	0.001	0.544517978
GO Biological Process	chromatin modification	4.20E-04	0.765878138
Oncomine Gene Expression Signatures	CellLine Vinblastine-newanalysis - Top 20% under-expressed in Indeterminate, Resi	9.00E-04	8.40E-01
Transfac TF Matrix - 1000bp	XFD-3	0.01	0.89845999
Transfac TF Matrix - 1000bp	NF-muE1	0.003	0.927962342
GO Molecular Function	magnesium ion binding	0.002	0.933790176
Transfac TF Matrix - 1000bp	YY1	0.005	0.962902402
GO Molecular Function	transferase activity	0.003	1.01E+00
picTar predicted miRNA target genes	HSA-MIR-29B	0.006	1.045814262
picTar predicted miRNA target genes	HSA-MIR-29C	0.006	1.045814262
Oncomine Gene Expression Signatures	Prostate SPINK1 - Top 10% over-expressed in SPINK1 (LaTulippe)	0.002	1.059810563
Oncomine Gene Expression Signatures	Glioma Grade - Top 5% over-expressed in 4 (Rickman)	0.001	1.08E+00
Oncomine Gene Expression Signatures	Gastric Carcinoma H. Pyroli status - Top 10% under-expressed in positive (Leung)	0.002	1.09E+00
Oncomine Gene Expression Signatures	Parathyroid Type - Top 5% under-expressed in Nonfamilial Multiple Gland Neoplasia	0.002	1.09E+00
Oncomine Gene Expression Signatures	Ovarian Carcinoma Histologic Subtype - Top 10% under-expressed in Mucinous (Sch	0.003	1.10E+00
Oncomine Gene Expression Signatures	Localized Prostate Carcinoma PCa ETS - Top 10% over-expressed in ERG+ (xiaojun)	7.90E-04	1.107844412
Oncomine Gene Expression Signatures	Prostate SPINK1 - Top 5% under-expressed in SPINK1 (Vanaja)	0.002	1.136350429
Transfac TF Matrix - 1000bp	KROX	0.01	1.15E+00
Oncomine Gene Expression Signatures	CellLine Daunorubicin - Top 20% under-expressed in Resistant (Shankavaram)	6.30E-04	1.18E+00
Oncomine Gene Expression Signatures	Parathyroid Type - Top 10% under-expressed in Nonfamilial Multiple Gland Neoplas	0.003	1.180091663
Oncomine Gene Expression Signatures	Ovary Type - Top 5% under-expressed in Ovarian Metastasis to Omentum (Adib)	0.003	1.24E+00
Oncomine Gene Expression Signatures	Brain Type - Top 5% under-expressed in Astrocytoma (Shai)	0.003	1.24E+00
Oncomine Gene Expression Signatures	Bladder Grade - Top 20% over-expressed in High Grade (Dyrskjot)	0.004	1.32E+00
Oncomine Gene Expression Signatures	Germ Cell Type - Top 10% under-expressed in Seminoma (Sperger)	0.004	1.32E+00
Oncomine Gene Expression Signatures	Esophageal Squamous Cell Carcinoma Family history of cancer - Top 10% over-expre	5.00E-04	1.412679118
Oncomine Gene Expression Signatures	Prostate ETS Status - Top 20% over-expressed in ERG+ (xiaojun)	0.006	1.63E+00
Conserved Promoter Motif	CLUSTER_7__V\$AP1_C	0.009	1.641197672
Oncomine Gene Expression Signatures	Melanoma Type - Top 20% over-expressed in Lymph Node Metastasis, Metastatic Gr	0.01	1.66E+00
Oncomine Gene Expression Signatures	Cancer Type - v1 - Top 10% over-expressed in Endometrial Endometrioid Carcinoma	0.009	1.664373194
Oncomine Gene Expression Signatures	Cancer Type - v1 - Top 10% over-expressed in Metastatic Ovarian Carcinoma (Bittner	0.009	1.70E+00
Oncomine Gene Expression Signatures	Normal Type - Top 5% over-expressed in Uterus (Shyamsundar)	0.008	1.736146304
Oncomine Gene Expression Signatures	Breast Type - Top 10% under-expressed in Breast Carcinoma (Finak)	0.009	1.75E+00
Oncomine Gene Expression Signatures	Diffuse Large B-cell Lymphoma Subtype - Top 5% over-expressed in Activated B-Cell	0.008	1.76E+00
Oncomine Gene Expression Signatures	Sarcoma Type - Top 10% under-expressed in chondroblastoma (Henderson)	0.009	1.76E+00
Oncomine Gene Expression Signatures	B-cell Chronic Lymphocytic Leukemia Disease Status - Top 10% under-expressed in P	0.007	1.781038862
Oncomine Gene Expression Signatures	Breast Type - Top 5% under-expressed in Breast Carcinoma (Finak)	0.008	1.79E+00
Oncomine Gene Expression Signatures	Acute Myeloid Leukemia Karyotype - Top 10% over-expressed in -7 (Oshima)	0.009	1.80E+00
Oncomine Gene Expression Signatures	Normal Type - Top 10% over-expressed in Testis (Su)	0.009	1.80E+00
Oncomine Gene Expression Signatures	CellLine taxotere-newanalysis - Top 20% under-expressed in Resistant (Staunton)	0.007	1.82E+00
Oncomine Gene Expression Signatures	Bladder Patient status A/D - Top 10% under-expressed in DOD (Modlich)	0.007	1.829243916
Oncomine Gene Expression Signatures	CellLine Daunorubicin - Top 5% under-expressed in Resistant (Shankavaram)	0.007	1.91E+00
Literature-defined Concepts	Genes expressed only in human embryonic stem cells as compared to hematopoieti	0.005	3.395497156
<b>InterPro</b>	<b>Pre-SET</b>	<b>0.007</b>	<b>1.11E+01</b>
Oncomine Clusters	Co-expressed across 16 Breast samples (Weigelt_Breast)	0.008	14.52639303
Oncomine Clusters	Co-expressed across 24 Breast samples (Chang_Breast)	0.007	16.73446596
Connectivity Map	MCF Cells Treatment - Top 5% under-expressed in 506, MCF7 treated with valproic a	0.009	27.62173097
Connectivity Map	CellLine Batch - description - Top 5% under-expressed in 109, SKMEL5 treated with n	0.009	27.62173097