

Deep sequencing and *in silico* analyses identify MYB-regulated gene networks and signaling pathways in pancreatic cancer

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Supplementary Information

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Supplementary Table 1: List of genes modulated upon MYB-silencing in MiaPaCa cell line with fold change $\geq \pm 1.5$ and p-value ≤ 0.05

Exp Fold Change	Exp p-value	Entrez Gene Name
-1.719	3.74E-02	AASDHPPT
-1.708	3.72E-02	AATF
1.93	1.70E-02	ABCA7
4.266	4.40E-03	ABCC3
-1.852	2.96E-02	ABCC4
5.283	1.00E-04	ABCG1
2.278	4.23E-02	ABHD16B
1.95	4.54E-02	ABHD8
-1.752	3.84E-02	ABLIM1
2.078	1.55E-02	ABTB1
-2.323	9.95E-03	ABTB2
2.209	8.50E-03	ACADS
1.949	2.15E-02	ACADVL
-2.95	1.13E-02	ACOX2
4.323	1.65E-03	ADAMTS4
2.412	1.67E-02	ADCY5
-1.647	5.00E-02	ADI1
-5.061	2.70E-02	ADM
-2.734	1.71E-02	ADORA2A
-1.866	2.66E-02	AEN
-1.709	3.96E-02	AGGF1
1.951	1.27E-02	AGRN
-2.092	4.55E-03	AK4
2.08	1.35E-02	AKAP12
-3.285	5.00E-05	ALDH1A1
1.752	2.78E-02	ALDH1A3
2.071	7.10E-03	ALDH3B1
-2.746	5.00E-05	ALDH9A1
-2.798	5.75E-03	ALDOC
-2.192	1.87E-02	ALG10
-2.034	1.38E-02	ALG10B
-5.145	9.00E-04	ALOXE3
-1.692	4.30E-02	ALYREF
-1.768	4.23E-02	AMMECR1
-1.804	2.60E-02	AMOTL2
-6.314	3.35E-02	ANKRD1
-1.987	2.34E-02	ANKRD26
-1.697	3.94E-02	ANKRD28

-1.843	4.13E-02	ANKRD32
-3.424	4.28E-02	ANKRD5
2.606	1.18E-02	ANKRD9
-2.08	7.30E-03	ANLN
-2.046	9.60E-03	ANXA1
-2.857	2.43E-02	ANXA10
-1.662	4.53E-02	AP3M1
1.814	4.40E-02	APLP1
-1.749	2.95E-02	ARHGAP12
-1.745	4.33E-02	ARHGAP18
5.177	2.15E-03	ARHGAP31
-1.848	1.96E-02	ARHGAP32
-1.763	3.67E-02	ARID1A
1.748	4.86E-02	ARRDC2
-2.03	6.95E-03	ARRDC3
1.847	3.84E-02	ARSA
1.874	1.75E-02	ASNS
-1.891	1.60E-02	ATAD2
-2.226	1.09E-02	ATAD5
-2.592	2.55E-03	ATF3
1.855	3.86E-02	ATHL1
1.709	3.96E-02	ATP13A2
1.964	1.00E-02	ATP8B2
-2.869	9.60E-03	AUNIP
-1.722	3.87E-02	BAG3
2.622	4.00E-03	BAI2
-1.971	2.31E-02	BARD1
-1.915	2.38E-02	BARX2
2.26	1.09E-02	BBC3
-1.706	3.82E-02	BCAR1
2.143	2.41E-02	BCAT1
2.206	1.06E-02	BCL7A
-2.326	1.25E-03	BCLAF1
-4.773	3.01E-02	BCO2
2.197	4.22E-02	BEAN1
-5.805	5.00E-05	BIRC3
3.238	8.90E-03	BIRC7
-2.388	8.50E-03	BLM
1.856	1.96E-02	BLVRB
2.513	2.94E-02	BMF
-1.777	2.43E-02	BMS1

-1.922	1.26E-02	BNIP3L
-1.783	3.17E-02	BRCA1
-2.206	7.25E-03	BRCA2
-1.866	1.87E-02	BRCC3
-1.742	4.38E-02	BRE
-1.85	2.47E-02	BTF3
-2.094	1.40E-02	BTG2
-2.693	2.03E-02	BTN2A3P
-2.079	2.92E-02	C11orf82
1.81	2.92E-02	C12orf57
-3.652	2.88E-02	C15orf48
2.037	2.25E-02	C17orf103
2.002	4.22E-02	C19orf26
-3.774	5.00E-05	C1orf110
-2.239	1.24E-02	C1orf226
2.196	1.76E-02	C5orf4
2.447	3.15E-03	C6orf1
-2.093	3.65E-02	C8orf46
2.853	1.62E-02	CACNA2D2
2.121	1.27E-02	CACNB3
-2.21	4.40E-03	CASP2
-4.057	5.00E-05	CAV1
-1.806	1.98E-02	CBFB
-1.678	4.43E-02	CCAR1
-1.747	4.40E-02	CCDC137
-2.515	1.70E-03	CCDC58
-2.105	4.40E-03	CCDC68
-1.923	1.53E-02	CCNF
-2.485	6.25E-03	CCRN4L
-1.779	2.91E-02	CD109
1.707	4.08E-02	CD9
-2.374	2.05E-02	CDA
-1.92	3.17E-02	CDC25A
-2.15	5.30E-03	CDC6
-1.837	3.24E-02	CDC7
-2.022	9.30E-03	CDCA5
-1.721	3.30E-02	CDCA7
-1.956	1.11E-02	CDK1
-1.855	2.57E-02	CDK2
-3.886	5.00E-05	CDK6
-3.599	1.75E-03	CDKN1A

1.801	3.30E-02	CEBPB
-1.707	3.21E-02	CENPE
-1.718	3.43E-02	CEP55
1.841	3.87E-02	CFD
-1.715	4.86E-02	CHAF1B
-1.867	2.53E-02	CHAMP1
1.862	1.53E-02	CHD3
-1.746	3.66E-02	CHEK1
-2.71	4.00E-04	CHORDC1
2.133	3.60E-03	CHPF
-1.748	3.91E-02	CHRAC1
2.806	7.90E-03	CHRD
2.347	3.30E-02	CHRM4
2.891	2.33E-02	CHST11
-1.834	2.97E-02	CHST3
-2.991	1.50E-04	CITED2
-1.698	3.84E-02	CKAP2
-1.788	3.48E-02	CKAP2L
-1.808	2.40E-02	CKS1B
1.664	4.88E-02	CLIP2
1.965	1.55E-02	CLIP4
-1.763	3.12E-02	CLNS1A
-1.956	1.41E-02	CLOCK
-3.289	5.00E-05	CLSPN
-1.771	3.37E-02	CMSS1
1.853	2.04E-02	COL18A1
1.725	3.99E-02	COL4A2
2.427	9.00E-04	COL6A2
-1.703	3.93E-02	COPS3
-2.054	4.21E-02	CPSF1
3.837	1.14E-02	CREB3L3
2.416	1.70E-03	CREBRF
2.152	2.22E-02	CRELD1
2.258	4.25E-03	CRELD2
1.731	3.55E-02	CRLF1
-1.664	4.64E-02	CTNNAL1
-1.829	3.43E-02	CTSC
1.867	1.86E-02	CTSL1
1.742	2.96E-02	CUL7
-1.844	3.12E-02	CWF19L1
-4.886	1.38E-02	CXCL2

-2.048	1.27E-02	CXCL5
1.699	4.21E-02	CYBA
2.097	3.72E-02	CYS1
-1.78	2.50E-02	DARS
1.786	3.62E-02	DBP
-2.257	6.90E-03	DCLRE1B
-2.124	6.55E-03	DDR2
-1.81	4.20E-02	DDX11
-1.805	2.67E-02	DDX39A
-1.697	4.61E-02	DDX41
-2.051	3.91E-02	DEM1
-1.76	2.81E-02	DEPDC1
-25.269	4.28E-02	DES
-1.911	1.73E-02	DHX9
-5.186	1.00E-03	DKK1
2.285	3.87E-02	DLL1
-2.078	1.58E-02	DNA2
-1.753	3.26E-02	DNAJA1
-1.85	2.94E-02	DNAJC9
1.773	3.06E-02	DNASE2
-1.851	2.22E-02	DNMBP
-1.874	4.21E-02	DPCD
-1.953	9.35E-03	DROSHA
-2.095	3.05E-02	DTL
1.822	2.08E-02	DVL1
-2.464	9.20E-03	E2F8
1.756	3.89E-02	ECI1
-1.824	4.83E-02	EED
1.73	3.86E-02	EGFL7
-2.214	2.55E-03	EGFR
1.822	2.26E-02	EGR1
2.61	1.29E-02	EGR3
-2.169	2.80E-03	EHF
-1.674	4.40E-02	EI24
-1.67	4.98E-02	EIF3M
-1.724	3.52E-02	EIF4EBP2
1.761	3.08E-02	ELFN1
-1.033	2.73E-02	ENO1-AS1
2.412	1.58E-02	EPAS1
-2.817	3.60E-02	EPB41L4B
-1.755	4.61E-02	EPC1

-2.32	8.45E-03	ERCC6L
1.941	3.18E-02	ERO1LB
-3.395	3.50E-04	ESCO2
-1.821	4.50E-02	ESRG
-1.869	2.63E-02	ETS1
-2.384	3.50E-03	EXO1
-1.826	2.28E-02	EXOSC2
-2.042	7.45E-03	EZH2
-2.028	1.70E-02	FAIM
-3.778	2.00E-04	FAM111B
2.803	5.50E-04	FAM129A
-1.958	9.80E-03	FAM136A
-2.373	3.55E-03	FAM13B
4.404	3.15E-02	FAM149A
-1.854	3.01E-02	FAM162A
3.807	4.76E-02	FAM171B
-2.531	9.00E-03	FAM173B
2.126	3.84E-02	FAM176B
-2.531	1.23E-02	FAM198B
-10.342	4.93E-02	FAM212A
-1.994	4.96E-02	FAM54A
-2.474	8.55E-03	FAM5C
-2.725	2.95E-03	FAM9C
-1.95	3.53E-02	FANCM
-1.707	4.00E-02	FARP2
1.764	3.52E-02	FBXL16
-2.068	1.00E-02	FBXO5
2.177	7.45E-03	FBXW4
2.029	2.58E-02	FCGRT
-1.886	2.62E-02	FEM1C
-2.158	7.65E-03	FEN1
-2.792	4.60E-02	FGF5
-1.986	1.55E-02	FGFR1OP
2.438	6.15E-03	FHL1
2.421	3.45E-02	FIBCD1
-2.145	1.08E-02	FIGNL1
2.535	1.56E-02	FNDC4
-2.498	3.50E-04	FOSL1
2.481	2.40E-02	FRS3
-1.942	8.30E-03	FRYL
1.793	2.78E-02	FURIN

-2.698	1.50E-04	FUS
2.717	2.15E-02	FYN
-1.844	2.31E-02	FZD4
-1.822	2.81E-02	G3BP1
2.419	5.55E-03	GABARAPL1
-2.659	6.50E-04	GADD45A
3.437	2.25E-02	GALNTL1
2.284	4.03E-02	GATA2
3.464	1.50E-04	GATSL3
2.456	1.74E-02	GBX2
3.729	3.50E-04	GDF15
2.419	4.70E-02	GDPD1
-2.306	3.50E-03	GEN1
-1.937	1.57E-02	GINS1
-1.996	1.92E-02	GINS2
-2.014	1.37E-02	GINS3
-1.775	2.43E-02	GINS4
-1.896	1.28E-02	GJC1
5.113	6.55E-03	GLDN
2.259	1.67E-02	GNAO1
-2.687	3.74E-02	GNG2
2.117	4.40E-03	GPC1
1.865	4.83E-02	GPR137B
1.716	3.86E-02	GRAMD1A
2.188	4.21E-02	GRAMD1B
3.479	5.00E-05	GRB7
-1.77	3.82E-02	GRPEL1
-1.726	3.94E-02	GSPT1
-2.155	4.15E-03	GTF2A1
-1.9	1.65E-02	GTF3C6
2.222	2.88E-02	HAGHL
2.058	7.35E-03	HCN2
1.899	2.27E-02	HDAC5
-2.689	3.00E-04	HDAC9
11.707	2.50E-04	HEATR6
1.842	4.37E-02	HECA
2.435	2.31E-02	HECW1
-2.527	2.25E-03	HELLS
1.873	1.64E-02	HELZ2
-1.82	4.91E-02	HENMT1
1.919	1.08E-02	HERPUD1

2.128	2.15E-02	HES4
5.375	2.09E-02	HES7
-4.461	5.00E-05	HIF1A
-4.13	3.33E-02	HIF1A-AS2
-1.853	1.54E-02	HIGD1A
-7.523	4.47E-02	HIST1H1B
-4.451	3.96E-02	HIST1H1E
-8.682	3.60E-02	HIST2H2BF
-1.735	3.28E-02	HK2
-2.111	1.28E-02	HKDC1
2.175	4.49E-02	HLA-A
5.045	4.30E-03	HLA-B
2.345	4.79E-02	HLA-C
-1.914	2.23E-02	HMGB1
-1.708	4.33E-02	HMGB3
-1.777	2.40E-02	HMMR
3.481	5.00E-05	HMOX1
-1.68	4.42E-02	HNRNPD
-1.756	3.06E-02	HNRNPH3
-2.092	4.80E-03	HNRNPM
-1.823	4.33E-02	HNRNPU
2.111	5.20E-03	HOXB8
2.774	1.50E-04	HOXB9
-1.87	2.77E-02	HSP90AB2P
2.241	1.02E-02	HSPA5
-1.75	3.83E-02	HSPH1
1.719	3.45E-02	HYOU1
2.371	1.05E-03	ICAM5
3.323	2.40E-02	ID4
2.582	4.16E-02	IDUA
1.694	4.85E-02	IER5L
2.239	1.52E-02	IFI27L2
-2.167	6.25E-03	IFIT1
-2.306	7.15E-03	IFIT3
-2.261	8.05E-03	IFLTD1
-1.837	4.45E-02	IFT172
2.025	8.10E-03	IGFBP6
1.931	4.47E-02	IGSF8
-3.163	6.40E-03	IKZF2
2.083	1.54E-02	ILF3-AS1
-1.935	1.41E-02	INPP4B

1.744	3.38E-02	INSIG1
-2.216	4.46E-02	IQCC
-1.681	4.76E-02	IQCE
1.754	3.41E-02	IRF2BPL
-3.275	2.85E-02	ISPD
1.732	4.44E-02	ITGA5
1.811	3.01E-02	ITGB4
1.736	4.66E-02	JMY
2.154	3.95E-03	JUND
-1.748	2.86E-02	KAT6B
2.255	4.21E-02	KCNAB2
7.627	6.55E-03	KCNJ4
6.492	2.25E-02	KCNK3
4.687	3.19E-02	KCP
-1.851	2.09E-02	KCTD9
1.779	3.87E-02	KDM6B
2.456	2.25E-02	KIAA1211
2.121	2.46E-02	KIAA1244
-1.706	4.63E-02	KIAA1279
-1.91	4.56E-02	KIAA1524
-1.9	1.29E-02	KIF11
-2.077	7.60E-03	KIF18A
1.962	9.15E-03	KIF1A
-2.008	8.35E-03	KIF20B
-1.836	1.79E-02	KIF23
-1.893	1.54E-02	KIF4A
1.963	2.67E-02	KIFC2
-2.062	4.15E-02	KLF4
2.478	1.65E-03	KLF9
2.053	3.91E-02	KLHL17
2.331	8.00E-04	KLHL24
-1.782	2.45E-02	KNTC1
2.32	1.14E-02	KREMEN2
-2.056	4.54E-02	KRT13
-11.957	5.65E-03	KRT16
-1.85	3.05E-02	KRT80
-4.133	5.00E-05	LDHA
1.745	3.69E-02	LENG8
1.906	1.54E-02	LGALS3BP
1.978	4.25E-02	LHX1
-1.679	4.86E-02	LIN7C

-2.234	9.50E-03	LIN9
-1.707	4.08E-02	LIPA
-1.907	3.35E-02	LLPH
1.688	4.91E-02	LMF2
-2.065	6.50E-03	LMNB1
1.993	3.30E-02	LMO7
3.662	4.10E-02	LOC344887
-2.238	5.00E-03	LOC389831
-2.184	1.76E-02	LOC441666
-4.432	2.89E-02	LOC646736
1.983	9.25E-03	LPCAT3
-2.462	4.05E-03	LPXN
2.409	2.10E-03	LRP10
1.919	1.46E-02	LRRC33
4.86	2.00E-04	LTBP1
2.377	3.70E-03	LTBP4
-1.828	1.96E-02	LUC7L3
-1.936	1.58E-02	LYAR
2.032	1.58E-02	MACROD1
-1.911	2.65E-02	MAGOHB
-1.749	2.99E-02	MALAT1
-1.708	4.02E-02	MALL
-2.005	4.78E-02	MAML2
2.163	3.55E-03	MAN2B1
1.731	4.97E-02	MANF
-2.678	2.46E-02	MAP2
-2.061	5.60E-03	MARCKSL1
-1.941	1.42E-02	MASTL
-4.147	1.81E-02	MB
-2.883	9.00E-04	MCM10
-1.896	1.73E-02	MCM2
-2.124	2.60E-03	MCM3
-2.23	2.05E-03	MCM4
-1.929	1.27E-02	MCM5
-1.836	1.90E-02	MCMBP
-2.306	5.85E-03	MCTP1
-1.751	3.02E-02	MCU
-2.296	1.60E-03	MDM2
2.027	1.66E-02	MEIS3
-1.722	3.65E-02	MELK
2.064	2.23E-02	MESDC1

3.263	1.60E-03	METRN
2.59	7.55E-03	MFSD3
1.718	4.68E-02	MIB2
2.27	6.30E-03	MICAL1
-2.914	2.86E-02	MIR137HG
-5.189	2.36E-02	MIR210HG
-1.764	3.90E-02	MKI67IP
2.35	2.40E-03	MKNK2
3.644	2.50E-03	MMP14
2.154	9.60E-03	MNT
-1.959	9.25E-03	MORF4L1
-1.856	2.36E-02	MPHOSPH9
2.145	3.45E-03	MRC2
-2.125	1.35E-02	MRPL1
2.012	4.30E-02	MSI1
-1.876	2.00E-02	MSL2
5.974	4.21E-02	MSLN
-2.017	3.66E-02	MT1A
-3.109	7.65E-03	MT1M
-2.626	2.09E-02	MTERF
1.73	4.49E-02	MVD
-1771.85	5.00E-05	MYB
-2.071	8.15E-03	MYBL1
-2.151	1.24E-02	MYH16
-15.566	3.50E-04	MYH7
-1.791	4.33E-02	MYOF
-2.751	7.00E-04	MYPN
4.046	1.15E-02	N4BP2L1
-1.867	2.91E-02	NAA15
2.087	1.67E-02	NAGLU
-1.655	4.93E-02	NAP1L4
-1.796	3.77E-02	NARF
1.814	4.71E-02	NAT14
-2.029	2.80E-02	NCAPG
-1.737	3.02E-02	NCAPG2
-1.852	3.57E-02	NCAPH
-1.746	4.88E-02	NCBP1
-1.9	2.82E-02	NCOA5
-1.914	1.41E-02	NDC80
2.039	8.50E-03	NEAT1
-1.675	4.14E-02	NET1

-4.251	3.19E-02	NEURL3
-2.068	4.75E-02	NFIB
2.842	4.47E-02	NIPAL4
-1.906	4.92E-02	NMI
2.688	1.12E-02	NOG
-1.862	1.62E-02	NOL11
-1.857	2.14E-02	NOL9
-2.25	1.45E-03	NOP58
-2.318	2.50E-02	NOS1AP
2.362	3.52E-02	NOXA1
-1.75	4.08E-02	NPAT
2.088	9.90E-03	NPDC1
-2.438	1.91E-02	NPIP
-2.275	1.65E-03	NR2F2
-3.14	7.00E-04	NRIP1
-3.631	6.45E-03	NRP1
-1.916	1.55E-02	NSRP1
-1.943	1.23E-02	NT5C2
-2.124	4.50E-03	NT5DC2
2.277	2.66E-02	NUDT18
-1.678	4.36E-02	NUP153
-1.711	3.58E-02	NUP155
-1.949	9.40E-03	NUP50
4.56	1.00E-04	NUPR1
-1.724	3.61E-02	NXF1
2.423	4.57E-02	NXPH4
-7.717	2.79E-02	OAS2
-2.688	1.27E-02	OASL
2.196	4.98E-02	OCEL1
-2.55	4.50E-04	ODC1
1.917	3.33E-02	OGDHL
3.35	7.00E-04	OLFM2
1.973	2.33E-02	ORAI3
-2.066	1.49E-02	ORC1
-1.812	3.50E-02	ORC6
-1.799	3.69E-02	OSBPL3
-2.535	9.60E-03	OSR1
-2.659	4.00E-02	P2RY2
-1.91	1.18E-02	P4HA1
-1.804	2.20E-02	PA2G4
-1.757	3.29E-02	PAICS

2.442	1.10E-03	PANX2
-1.768	3.45E-02	PARVA
2.118	4.85E-03	PBXIP1
-1.717	3.52E-02	PCF11
1.997	4.21E-02	PCK2
-1.835	1.90E-02	PCNA
-1.716	3.87E-02	PCNT
2.168	2.36E-02	PCSK1N
-1.703	4.30E-02	PDCD5
2.164	2.99E-02	PDGFB
-1.86	1.69E-02	PDGFC
1.708	4.40E-02	PDIA5
-2.562	1.35E-03	PDK1
8.891	4.00E-04	PDK4
-3.268	4.50E-04	PER2
-3.196	3.50E-04	PFKFB4
-2.265	2.50E-03	PGAP1
-1.872	2.65E-02	PGK1
1.857	1.74E-02	PGPEP1
-1.679	4.68E-02	PHAX
2.538	7.50E-04	PHGDH
-1.998	2.15E-02	PIGA
1.921	2.54E-02	PIGQ
-1.887	2.22E-02	PIK3R3
2.786	2.50E-04	PIM1
1.769	2.88E-02	PIM3
2.264	1.85E-03	PITPNM1
1.798	4.66E-02	PITX1
3.982	3.15E-03	PKD1L2
-3.502	3.90E-03	PLAC8
5.363	1.77E-02	PLAG1
-1.671	4.59E-02	PLAU
-4.358	2.80E-03	PLCXD3
1.946	1.30E-02	PLD3
-1.805	2.61E-02	PLEKHA2
1.727	3.33E-02	PLIN2
-1.734	3.34E-02	PLK1
1.691	4.94E-02	PLXNA3
-2.25	6.75E-03	PMEPA1
-1.79	2.50E-02	PNN
1.671	4.23E-02	PNPLA6

-1.861	1.48E-02	POLA1
-2.09	9.10E-03	POLD3
-2.609	9.30E-03	POLE2
-3.068	1.00E-04	POLQ
-1.884	3.43E-02	POLR3G
2.401	1.30E-02	PPIC
-1.871	2.05E-02	PPIF
-2.162	1.01E-02	PPM1D
-1.69	4.71E-02	PPME1
-2.287	2.65E-03	PPP1R15A
-2.177	4.20E-03	PPP1R2
1.656	4.67E-02	PPP1R26
-2.004	5.65E-03	PPP4R1
-1.711	3.72E-02	PPP6R3
1.732	4.55E-02	PRAF2
-2.264	2.32E-02	PRICKLE1
-1.904	4.78E-02	PRIM1
-2.184	9.35E-03	PRIM2
-6.571	2.12E-02	PRIMA1
-1.816	2.50E-02	PRMT3
1.745	4.83E-02	PRND
2.698	1.06E-02	PROCR
-1.699	4.59E-02	PRPF3
-1.737	3.19E-02	PRPF38B
-1.793	2.32E-02	PRPF4
-1.699	4.24E-02	PRPF4B
-1.815	1.97E-02	PRPS2
-2.696	1.00E-04	PRRG4
2.265	4.86E-02	PRSS16
-1.87	1.69E-02	PSMD12
-2.036	6.90E-03	PSPC1
2.007	4.24E-02	PTCH1
-2.061	7.00E-03	PTP4A1
2.001	1.40E-02	PTPRU
1.721	3.44E-02	PVRL2
-2.055	3.76E-02	PVT1
2.097	1.10E-02	QPCTL
-1.741	2.88E-02	QSER1
-1.693	4.71E-02	RAB22A
-1.776	3.19E-02	RAB31
1.853	4.89E-02	RAB32

2.604	6.50E-04	RABAC1
-2.457	1.11E-02	RAD51
-2.007	2.89E-02	RAD51C
-1.897	1.75E-02	RAPGEF6
-1.778	3.18E-02	RASAL2
2.093	8.05E-03	RBCK1
-2.287	3.10E-03	RBL1
-1.763	3.00E-02	RBM26
-1.839	2.26E-02	RBMX
-3.582	4.10E-03	RCBTB2
-4.638	5.00E-05	RELA
16.466	5.00E-05	REXO1
-2.553	3.00E-04	RFC3
-1.98	9.35E-03	RFWD3
-2.34	6.00E-03	RGS5
1.783	3.70E-02	RHPN1
-1.902	1.40E-02	RIF1
-3.395	2.60E-03	RIMKLA
-1.823	2.78E-02	RIN2
-1.807	3.17E-02	RIPK1
-1.991	2.62E-02	RIPK4
-1.705	4.54E-02	RNF138
-1.893	1.36E-02	RNF182
3.254	5.50E-04	RNF215
-2.926	3.86E-02	ROCK1P1
-1.861	4.53E-02	RPP14
1.969	1.04E-02	RPS21
2.453	4.83E-02	RPS6KA2
1.722	4.16E-02	RRAGD
2.241	5.70E-03	RRAS
2.198	1.29E-02	RTN4R
1.909	2.44E-02	S100A6
-1.797	2.20E-02	SAFB
-2.095	8.95E-03	SAFB2
-2.288	2.30E-03	SAT1
-1.948	1.98E-02	SBDSP1
2.884	2.04E-02	SCN1B
-2.424	7.45E-03	SDPR
3.423	2.00E-04	SEC24D
-2.217	2.10E-03	SEMA3A
-3.961	5.00E-05	SEMA3C

-4.5	7.50E-04	SEMA3D
2.505	1.80E-02	SERINC2
2.144	6.10E-03	SERPINA3
-2.385	2.30E-03	SESN2
1.974	8.25E-03	SEZ6L2
-1.721	4.74E-02	SF3B4
-3.491	2.21E-02	SFN
-2.316	1.95E-03	SFPQ
-2.103	4.90E-02	SFXN2
-2.117	5.05E-03	SGOL2
1.959	1.84E-02	SGSH
-2.52	4.25E-03	SH3RF2
2.081	8.70E-03	SHC1
2.522	2.98E-02	SHC2
-1.691	4.71E-02	SHCBP1
-2.493	3.15E-03	SHH
-1.669	4.83E-02	SKA2
-2.575	2.15E-02	SKA3
-1.903	1.26E-02	SKP1
2.01	1.40E-02	SLC16A2
1.99	2.39E-02	SLC16A5
5.584	7.05E-03	SLC17A7
1.96	2.83E-02	SLC20A1
2.695	9.95E-03	SLC22A17
2.257	8.65E-03	SLC22A18
-2.058	5.30E-03	SLC2A1
-2.445	8.50E-04	SLC30A1
-2.134	4.27E-02	SLC38A4
-2.63	3.00E-04	SLC39A10
1.875	1.67E-02	SLC45A1
1.879	3.19E-02	SLC6A6
2.917	1.25E-03	SLC9A3
2.581	2.26E-02	SLC9A5
-1.942	1.06E-02	SLTM
-2.03	9.20E-03	SMAP1
-1.706	3.74E-02	SMC2
-1.903	1.93E-02	SMC4
-1.7	4.00E-02	SMC5
-2.001	6.75E-03	SMCHD1
2.11	9.95E-03	SMPD1
2.92	1.00E-03	SNCG

2.951	2.65E-02	SNORA48
1.573	1.16E-02	SNORD21
3.485	4.28E-02	SNORD36A
-2.245	2.95E-02	SNORD97
2.449	2.86E-02	SNPH
-1.731	4.13E-02	SNRPF
-1.762	3.03E-02	SOGA1
1.926	4.43E-02	SOX8
-3.428	4.61E-02	SPATA17
-1.914	3.25E-02	SPC25
2.786	1.12E-02	SPON1
-1.729	3.91E-02	SPTSSA
-1.842	2.20E-02	SRF
-2.006	7.80E-03	SRRT
-1.742	3.16E-02	SRSF1
-2.006	1.20E-02	SRSF3
-1.99	6.45E-03	SRSF6
-1.742	2.88E-02	SRSF7
-1.698	3.62E-02	STAG1
-1.907	3.40E-02	STC1
-1.938	1.24E-02	STIL
1.768	4.96E-02	STK39
2.386	2.61E-02	STX1B
2.243	1.77E-02	SULT1A1
-1.735	4.74E-02	SUPT16H
-1.822	3.52E-02	SUV39H1
-1.951	1.69E-02	SYNCRIP
2.61	1.29E-02	SYNGR3
-3.673	1.45E-03	SYT1
-2.005	9.40E-03	TAF9B
-1.693	4.11E-02	TARDBP
2.088	2.03E-02	TBC1D10A
1.878	2.51E-02	TBC1D17
-7.789	4.45E-02	TCAP
-1.972	8.15E-03	TCF7
4.87	3.65E-02	TEX22
-2.462	1.47E-02	TEX30
-1.688	4.23E-02	TFAM
-1.979	1.28E-02	TFRC
-1.97	3.58E-02	TGS1
2.091	3.65E-02	THSD4

-1.924	1.30E-02	THUMPD1
-2.435	1.43E-02	TIPIN
-3.275	5.00E-05	TM4SF18
1.969	3.14E-02	TMBIM4
2.534	6.35E-03	TMC6
1.907	2.32E-02	TMEM129
1.835	2.93E-02	TMEM132A
-3.796	2.27E-02	TMEM145
1.935	2.19E-02	TMEM158
4.862	4.13E-02	TMEM221
2.732	9.00E-04	TMEM59L
-2.102	6.05E-03	TMOD3
-3.27	5.00E-05	TMX3
-5.135	3.05E-03	TNFAIP3
-3.362	5.00E-05	TNFRSF10D
-6.887	3.92E-02	TNNC1
-1.938	9.60E-03	TNPO1
-1.7	4.13E-02	TNRC6A
-1.674	4.63E-02	TOMM34
1.819	4.32E-02	TP53I13
2.259	1.87E-02	TPBG
-3.147	2.36E-02	TPI1P2
-1.847	4.90E-02	TPM1
-2.033	7.60E-03	TRA2A
-2.676	1.00E-04	TRA2B
1.896	4.96E-02	TRIM16
-2.009	1.21E-02	TRIM55
-1.665	4.98E-02	TRIP13
-1.863	3.52E-02	TRMT10C
-1.968	1.95E-02	TRMT6
2.068	4.03E-02	TRPV2
2.072	4.69E-02	TUBB3
-1.768	3.29E-02	TWISTNB
-1.747	3.19E-02	U2AF1
-1.832	1.62E-02	UAP1
1.783	3.35E-02	UAP1L1
-1.765	2.84E-02	UBE2C
-2.225	1.50E-02	UBE2D4
-1.679	4.96E-02	UBE2V2
-2.165	2.70E-03	UHRF1
2.137	4.59E-02	ULBP2

-1.793	2.50E-02	UPF2
-2.357	2.00E-03	UPF3B
2.74	2.70E-02	UPK3B
-1.864	1.53E-02	USP1
-2.027	1.06E-02	USP22
-1.867	2.71E-02	USP37
-1.864	3.14E-02	VGLL4
-1.782	4.51E-02	VRK1
-1.656	4.53E-02	WAPAL
-1.796	2.91E-02	WDHD1
-1.724	3.51E-02	WDR43
-2.433	2.35E-03	WDR76
2.309	4.70E-03	WIP1
-2.872	8.50E-04	XRCC2
1.868	4.71E-02	YPEL2
1.881	3.89E-02	YPEL3
2.579	3.89E-02	ZBTB42
2.148	7.10E-03	ZBTB7B
-1.727	4.42E-02	ZC3H7A
-1.702	4.95E-02	ZC3HAV1L
2.52	4.61E-02	ZHX2
-1.837	1.74E-02	ZMIZ2
-2.027	1.15E-02	ZNF107
-2.937	9.75E-03	ZNF235
-2.189	7.25E-03	ZNF267
-2.008	1.42E-02	ZNF326
-1.867	3.16E-02	ZNF367
-1.896	1.46E-02	ZNF395
2.126	2.48E-02	ZNF446
2.405	1.09E-02	ZNF467
-1.964	1.95E-02	ZNF480
3.443	5.55E-03	ZNF516
-2.013	4.13E-02	ZNF551
2.176	1.42E-02	ZNF581
2.797	1.98E-02	ZNF641
-2.75	3.05E-03	ZNF724P
-2.235	3.84E-02	ZSCAN12
1.785	4.93E-02	ZSWIM4
-2.205	4.10E-03	ZWINT

Supplementary Table 2: Network ID assigned on the basis of network score, genes involved in the network, score of the network, focus molecules representing the number of genes in our dataset that are present and top diseases and functions associated with the genes.

ID	Molecules in Network	Score	Focus Molecules	Top Diseases and Functions
1	ALYREF,BARD1,BCLAF1,CCAR1,CHD3,CUL7,DDX39A,ERCC6L,HNRNPH3,HNRNPU,KCNK3,KIFC2,LOC102724594/U2AF1,MALAT1,NCBP1,NOL9,NOL11,NSRP1,PCF11,Pkc(s),PNN,RBMX,SAFB,SAFB2,SMCHD1,SRR T,SRSF1,SRSF3,SRSF6,SRSF7,STC1,TRA2A,TRA2B,UPF3B,WDR43	54	34	RNA Post-Transcriptional Modification, Molecular Transport, RNA Trafficking
2	AK4,AP3M1,ARFGEF3,CD C7,CKAP2,CMSS1,DCLRE1B,EGFR,EIF3M,GINS1,GINS2,GINS3,GINS4,HES4,HMGB3,KCTD9,Mcm,MCM4,MCM5,MCM10,MCMBP,MT1M,NT5DC2,nucleotidyltransferase,OAS2,ORC6,PLD3,POLA1,POLD3,PRIM1,PRIM2,Primase,PRMT3,TRMT10C,WDHD1	49	32	Cellular Assembly and Organization, Cancer, Hematological Disease
3	ARSA,ATM/ATR,BLV RB,Bvr,CLIP2,CLSPN,CRLF1,EXO5,FAIM,GJC1,KCNJ4,KIAA1524,LIN7C,LUC7L3,MIB2,MRN,NFkB (complex),PDCD5,PIM3,PLAG1,PPIC,PPM1D,PPME1,PSPC1,RAB31,Rfc,RFWD3,RIF1,RIPK4,RPA,SLC22A18,SOGA1,TIPIN,TMX3	41	29	Cell Cycle, DNA Replication, Recombination, and Repair, Neurological Disease
4	AEN,ALOXE3,ANKRD32,ATP13A2,BCR (complex),BRINP3,CACNA2D2,CKAP2L,CXCL5,ESCO2,	41	29	Cancer, Connective Tissue Disorders, Developmental Disorder

	FAM111B,FAM173B,GADD45A,Iga,Immunoglobulin,KIF18A,KIF1BP,LENG8,MAP1LC3,MHC Class II (complex),MTFR2,NFIB,NRROS,NUPR1,POLE2,PRND,PVT1,RIMKLA,SLC6A6,SRCC (family),SUV39H1,SYNCRIP,TFRC,UAP1,ZNF581			
5	ASNS,CDC6,Cdc25B/C,CDK1,CDK2,FUS,GEN1,HIST2H2BF,HNRNPM,IGSF8,Interferon alpha,KCNAB2,KIF23,LLPH,LYAR,MCM3,MYOF,NAT14,NPDC1,p85 (pik3r),PCNA,PLK1,PRPF3,PRPF4,PRPF38B,PRPF4B,PSMD12,RABAC1,Rb,RNA polymerase II,RPS21,SEC24D,SF3B4,SFPQ,snRNP	41	29	RNA Post-Transcriptional Modification, Cellular Assembly and Organization, Cell Cycle
6	ANKRD26,ANKRD28,ATAD2,ATAD5,ATPase,BLM,BRCA1,BRCC3,BTF3,Cbp/p300,DHX9,DNA2,DUB,ERO1LB,EXO1,FEN1,FIGNL1,G3BP1,Gsk3,GTF2A1,Holo RNA polymerase II,I kappa b kinase,KIF20B,LMNTD1,MC M2,NMI,PA2G4,PGK1,RAB22A,RAD51,SUPT16H,TAF9B,TFIIE,USP1,USP22	39	28	DNA Replication, Recombination, and Repair, Cell Cycle, Cancer
7	ABLIM1,Angiotensin II receptor type 1,ANLN,APLP1,Arf,BARX2,CBFB,CDCA7,CDKN1A,CEP55,Cofilin,CTNNAL1,DROSHA,Erm,ETS1,FActin,HIGD1A,ICAM5,IKZF2,LGALS3BP,LPCAT3,MTERF1,Notch,OLFM2,P4HA1,Pias,PITPNM1,Rock,Secretase gamma,Smad,SPON1,SRF,TCF7,TMBIM4,TPM1	33	25	Cell-mediated Immune Response, Cellular Development, Cellular Function and Maintenance

8	AASDHPPT, DNASE2, GRPE L1, HLA-A, HLA-B, HLA-C, IFIT1, IFIT3, Ifn, IFN alpha/beta, IFN Beta, IFN type 1, Ifnar, IL-2R, IL12 (complex), JAK, KDM6B, LD HA, MHC Class I (complex), MHC I-Î±, NAA15, NT5C2, NUDT18, OASL, PAICS, PHGDH, POLR3G, PRRG4, SDPR, SEZ6L2, SHC1, SNORD21, SNRPF, Tlr, UPF2	31	24	Dermatological Diseases and Conditions, Immunological Disease, Inflammatory Disease
9	AMOTL2, BTG2, CDCA5, CDK2-CyclinE, ERBB, ERK, ETS, FRS3, GRB7, HOXB9, IGFBP6, KIF4A, KLF9, LIN9, MAGOHB, MKNK2, MYBL1, Ncor, NCAPG, NCAPG2, NCAPH, NRG (family), PITX1, PLIN2, Rxr, SERCA, SH3RF2, SMC2, SMC4, STAG1, T3-TR-RXR, thyroid hormone receptor, TMOD3, VitaminD3-VDR-RXR, WAPAL	30	24	DNA Replication, Recombination, and Repair, Cell Cycle, Cellular Assembly and Organization
10	C15orf48, CEBPB, CFD, Cg, CHRAC1, DNAJA1, EPAS1, EZH2, FAM198B, GTPase, HIF1A, Histone h3, HOXB8, Hsp70, Hsp90, HSPA5, HSPH1, Ige, IL12 (family), MANF, NIFK, NR2F2, PDIA5, Proinsulin, RAPGEF6, RCBTB2, RFC3, SMAP1, SNCG, STAT5a/b, TFAM, TM4SF18, TMEM132A, VRK1, ZNF267	30	26	Cellular Compromise, Embryonic Development, Organ Development
11	ARHGAP32, ARRDC3, CCRN4L, CHAF1B, CHST3, CHST11, CLNS1A, CLOCK, Cyclin D1/cdk4, DBP, EED, EIF4EBP2, EPC1, Fcgr1, GATA2, Gmcsf, Hat, HISTONE, histone deacetylase, Histone	29	24	Behavior, Carbohydrate Metabolism, Nervous System Development and Function

	h4,KAT6B,Mapk,MORF4L1, MutS alpha,NPAT,PER2,PIGA,PIG Q,SHC2,SLC20A1,sulfotrans ferase,SULT1A1,TGS1,TIP6 0,ZBTB7B			
12	AATF,ADCY5,APC (complex),BNIP3L,Cdc25,C DC25A,Cdk,CHEK1,CKS1B, COPS3,Cyclin B,DTL,E3 RING,FANCM,FBXL16,FB XO5,FBXW4,GNAO1,Lh,LI PA,LMO7,Lpa receptor,Pka,PTP4A1,PTPase, PTPRU,RAB32,RASAL2,RB L1,SKP1,SNPH,Sod,TNRC6 A,tyrosine kinase,UBE2C	29	24	Cell Cycle, DNA Replication, Recombination, and Repair, Connective Tissue Development and Function
13	Akt,ANKRD1,atypical protein kinase C,CDK4/6,CLIP4,Collagen type VI,CREB3L3,DES,INPP4B,J UN/JUNB/JUND,LPXN,MIC AL1,MYPN,N- Cadherin,Neurotrophin,NFkB (family),NRP1,PBXIP1,PLA C8,PLEKHA2,Plexin A,PLXNA3,PVRL2,RIN2,RR AS,Sema3,SEMA3A,SEMA3 C,SEMA3D,SLC22A17,SLC 39A10,TCAP,TRIM55,UBE2 ,Ube3	29	23	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cell Morphology
14	ADAMTS4,Alpha catenin,Ap1,ARHGAP31,AR RDC2,BCAT1,BIRC3,CaMK II,CASP2,DEPDC1,FURIN,I kb,IKK (complex),Ikk (family),LMNB1,MAP2,NFA T (complex),NOP58,PP1- C,Ppp2c,PPP4R1,PRKAC,PR OCR,QPCTL,Rac,RBCK1,RI PK1,RNF138,S100A6,SMC5, TARDBP,TCR,TNFAIP3,UB E2D4,Ubiquitin	27	22	Gastrointestinal Disease, Hepatic System Disease, Inflammatory Disease
15	aldehyde dehydrogenase (NAD),ALDH,ALDH1A1,AL	25	22	Developmental Disorder, Neurological Disease, Organismal

	DH1A3,ALDH3B1,ALDH9A1,BIRC7,c-Src,CCNF,CHRD,Ctbp,DDX11,DKK1,DVL1,Ecm,Frizzled,Gli,HECW1,Hedgehog,HELLS,Integrin alpha 3 beta 1,KIF11,KREMEN2,LRP,LRP10,LTBP4,MSI1,PPP6R3,PRICKLE1,PTCH1,STIL,TCF,TMEM158,Vegf,Wnt			Injury and Abnormalities
16	26s Proteasome,Actin,AGGF1,Alpha Actinin,ANXA10,BAG3,BEAN1,BMS1,caspase,CD3,chemokine,Ck2,cytochrome C,DPCD,GTF3C6,HMGB1,Infingamma,MACROD1,MAN2B1,MAPK12,MDM2,MT1A,NAP1L4,NPIPA8 (includes others),NXF1,OGDHL,ORA13,PNPLA6,PPP1R26,PRPS2,RAG1,RAG2,SP100,TPBG,ZNF326	24	22	Developmental Disorder, Connective Tissue Disorders, DNA Replication, Recombination, and Repair
17	ARID1A,BMF,Cdc2,CDK1/2,Collagen Alpha1,Collagen type V,Cyclin A,Cyclin A/Cdk2,Cyclin E,DARS,DDR2,E2f,E2F8,EXOSC2,Fetal Hemoglobin,GC-GCR dimer,GSPT1,I13r,Jnk,KNTC1,LTBP1,MELK,MRC2,MSLN,NET1,PMEPA1,SESN2,SKA2,SKA3,Smad2/3,Stat3-Stat3,SWI-SNF,TNFRSF10D,USP37,WDR76	23	20	Cell Cycle, Hereditary Disorder, Neurological Disease
18	ABCC4,Alpha tubulin,Beta Tubulin,CACNB3,Caveolin,CENPE,Cytokeratin,DNMBP,Dynamin,Dynein,FAM162A,GABARAPL1,HK2,HLA Class I,KIR,KRT13,KRT16,MALL,	23	20	Hereditary Disorder, Neurological Disease, Cell Death and Survival

	PCNT,PDK1,Pgk,PI3K (complex),RPS6KA,SCN1B,SPTSSA,STX1B,Syntaxin,SYT1,TBC1D17,TBC1D10A,TUBB3,tubulin (complex),tubulin (family),ULBP2,Vdac			
19	ADII,AGRN,BCAR1,BRCA2,BRCA1-BRCA2-FANCD2-FANCN-RAD51,COL18A1,Collagen type I,Collagen type IV,Collagen(s),CRELD2,CTSL,DDX41,elastase,FARP2,Filamin,FYN,GDF15,GPIIB-III A,HCN2,HERPUD1,Integrin,Integrin alpha 4 beta 1,Integrin β ,ITGB4,Laminin,Laminin1,MMP14,Na ⁺ ,K ⁺ -ATPase,NCOA5,ORC1,PARVA,Ptk,RAD51C,Rap1,XRCC2	23	20	Cellular Movement, Cell Cycle, DNA Replication, Recombination, and Repair
20	20s proteasome,Calcineurin A,Calcineurin protein(s),CHORDC1,CITED2,DLL1,DNA-methyltransferase,FGF5,FHL1,FOSL1,Hdac,HDAC5,HDAC9,HEATR6,HSP,LHX1,MARCKSL1,MB,MEF2,MHC CLASS I (family),MNT,MYH7,Myosin,Nfat (family),NRIP1,ODC1,OSR1,PDK4,PPIF,PPP1R2,Ras,Rsk,SAT1,TOMM34,Tropomyosin	22	22	Molecular Transport, Small Molecule Biochemistry, Cardiovascular System Development and Function
21	Alp,AMPK,CAV1,CPSF1,Creb,CXCL2,EGR1,EGR3,EHF,Fgf,Fgfr,GBX2,HMOX1,INSIG1,Insulin,ITGA5,KLF4,MAP2K1/2,MASTL,MCU,Mek,MTORC1,MYB,Nos,NOS1A P,p70 S6k,Pdgf (complex),PDGF BB,PLC gamma,PP1 protein complex	22	19	Cell Death and Survival, Cell-mediated Immune Response, Cellular Development

	group,RPS6KA2,SERPINA3,SHH,Tgf beta,TRPV2			
22	AMER1,AMMECR1,ANKS1A,AUNIP,C19orf26,CDK6,CLTC,DLG4,EGR1,ELAVL1,EPO,FAM13B,FBXW11,FE M1C,GATA3,GSK3B,GSPT1,KDR,KITLG,KLHL17,KLHL24,MESDC1,MNT,N4BP2L1,NRAS,PAX6,PIM1,PRKCD,RBX1,REXO1,RPP14,TWISTNB,YTHDF1,ZNF395,ZSWIM4	22	19	Cell Cycle, Cellular Development, Hematological System Development and Function
23	AKAP12,Collagen type II,CYBA,Cyclin D,ERK1/2,GPC1,Hla-abc,HMMR,Igf,NADPH oxidase,NCK,NDC80,NOG, Pak,PCSK1N,PDGF (family),Pdgf Ab,PDGF-AA,PDGFB,PDGFC,PFKFB4,PHAX,PIK3R3,Pkg,RGS5,RTN4R,SLC9A5,SMAD1/5,Smad1/5/8,Sos,SPC25,VAV,Via-4,ZHX2,ZWINT	20	18	Cell Cycle, Cellular Assembly and Organization, DNA Replication, Recombination, and Repair
24	ABCG1,ABTB1,AChR,ADM,ALDOC,CD9,CTSC,Fc gamma receptor,Fc receptor,FCGRT,FGFR1OP,glutathione peroxidase,GOT,hemoglobin,IgG,IgG1,Igg3,IgG2a,Igh (family),Igm,Ldh (complex),MHC,MHC II,MIR124,OSBPL3,PI3K (family),POLQ,PPP1R15A,RELA,SFN,SHCBP1,SLC2A1,SLC30A1,TMC6,TRIM16	20	18	Tissue Morphology, Embryonic Development, Lymphoid Tissue Structure and Development
25	alcohol group acceptor phosphotransferase,APC/APC2,Arp2/3,BBC3,CAK,calpain,CDA,CDK6,CDK1-Cyclin B,Collagen type III,GADD45,Gcn51,HIST1H1B,HIST1H1E,Histone H1,ID4,Importin	18	17	Cardiovascular System Development and Function, Cell Morphology, Hematological System Development and Function

	alpha,Importin beta,JMY,KIF1A,Nucleoporin, NUP50,NUP153,NUP155,P-TEFb,P38 MAPK,PIM1,PP2A,STK39,Transportin, TNNC1,TNPO1,Transportin,UHRF1,VGLL4			
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Supplementary Table 3: Ten enriched canonical pathways; ratio of the genes present in our dataset to the number of genes that map to that pathway in the IPA library, z-score and p-values. A positive z-score implies activation of the pathway while a negative score implies predicted inhibition; NaN stands for “Not a Number” where the activation state could not be inferred. Genes presented in **red**, also identified by the **↑** symbol, indicate upregulation of the genes in the dataset, genes represented in black are downregulated.

	Canonical pathway	Genes	Ratio	Z score	P value
1.	Chromosomal Replication Pathway	CDC6, CDC7, CDK2, CDK6, MCM2, MCM3, MCM4, MCM5, ORC1, ORC6	10/27 (0.37)	NaN	1.66E-08
2.	DNA Damage Signaling (BRCA1-mediated)	ARID1A, BARD1, BLM1, BRCA1, BRCA2, BRCC3, BRE, CDKN1A, CHEK1, FANCM, GADD45A, PLK1, RAD51, RBL1, RFC3	15/78 (0.192)	-2.53	1.01E-07
3.	G2/M DNA Damage Regulatory Pathway	BRCA1, CDK1, CDKN1A, CHEK1, CKS1B, GADD45A, MDM2, PLK1, PPM1D, SFN, SKP1	11/49 (0.224)	0.302	1.01E-06
4.	ATM Signaling	BLM, BRCA1, CDC25A, CDK1, CDK2, CDKN1A, CHEK1, GADD45A, MDM2, RA51, SMC2	11/59 (0.186)	-1.897	7.02E-06
5.	P53 Signaling	↑BBC3 , BRCA1, CDK2, CDKN1A, CHEK1, GADD45A, HDAC9, HIF1A, ↑JMY , MDM2, PCNA, PIK3R3, SFN, STAG1	14/98 (0.143)	0.632	1.07E-05
6.	G1/S Cell Cycle Regulatory Pathway	CDC25A, CDK2, CDK6, CDKN1A, ↑HDAC5 , HDAC9, MDM2, PA2G4, RBL1, SKP1, SUV39H1	11/64 (0.172)	0.333	1.58E-05
7.	Homologous Recombination Repair Pathway	BRCA1, BRCA2, GEN1, POLA1, RAD51	5/14 (0.357)	NaN	9.08E-05
8.	Pancreatic Adenocarcinoma Signaling	BRCA2, CDK2, CDKN1A, EGFR,	13/106 (0.123)	-0.333	1.11E-04

		↑HMOX, MDM2, PA2G4, PDGFC, PIK3R3, ↑PLD3, RAD51, RELA			
9.	Mismatch Repair Pathway	EXO1, FEN1, PCNA, RC3	4/16 (0.25)	NaN	2.14E- 03
10	Hif1 α Signaling	HIF1A, LDHA, MDM2, ↑MMP14, PDGFC, PIK3K3, ↑RRAS, SLC2A1	8/102 (0.078)	NaN	3.08E- 02

Supplementary Table 4: Table of primers used in our study to validate the RNA-seq data along with the primers used for ChIP assay.

S.No.	Gene	Primer Sequence
1.	GAPDHF GAPDHR	CAC CGT CAA GGC TGA GAA C
		GAC TCC ACG ACG TAC TCA G
2.	ADMF ADMR	ATG AAG CTG GTT TCC GTC G
		GAC ATC CGC AGT TCC CTC TT
3.	SHHF SHHR	CTC GCT GCT GGT ATG CTC G
		ATC GCT CGG AGT TTC TGG AGA
4.	MDM2F MDM2R	GAA TCA TCG GAC TCA GGT ACA TC
		TCT GTC TCA CTA ATT GCT CTC CT
5.	ALDH1A1F ALDH1A1R	CTG CTG GCG ACA ATG GAG T
		CGC AAT GTT TTG ATG CAG CCT
6.	HDAC5F HDAC5R	TCT TGT CGA AGT CAA AGG AGC
		GAG GGG AAC TCT GGT CCA AAG
7.	BBC3F BBC3R	GCC AGA TTT GTG AGA CAA GAG G
		CAG GCA CCT AAT TGG GCT C
8.	MYBF MYBR	TCA GGA AAC TTC TTC TGC TCA CA
		AGG TTC CCA GGT ACT GCT
9.	LDHAF LDHAR	ATG GCA ACT CTA AAG GAT CAG C
		CCA ACC CCA ACA ACT GTA ATC T
10.	HIF1AF HIF1AR	GAA CGT CGA AAA GAA AAG TCT CG
		CCT TAT CAA GAT GCG AAC TCA CA
11.	KLF4F KLF4R	CAG CTT CAC CTA TCC GAT CCG
		GAC TCC CTG CCA TAG AGG AGG
12.	GLUT1F GLUT1R	AAC TCT TCA GCC AGG GTC CAC
		CAC AGT GAA GAT GAT GAA GAC
13.	EGFRF EGFRR	CCC ACT CAT GCT CTA CAA CCC
		TCG CAC TTC TTA CAC TTG CGG
14.	RELAF RELAR	GTG GGG ACT ACG ACC TGA ATG
		GGG GCA CGA TTG TCA AAG ATG
15.	RELMYBPF2 RELMYBPR2	GGC TTT GCT CCA GAC CCG GC
		GGT GGG TCC GCC GAT TAC TCA C
16.	EGFRMYBPF EGFRMYBPR3	GTC CAG AGG GGC AGT GCT G
		GAC CTA GTC TCC GGC GGG