

Supplement files

Supplement 1. Hub genes constituting the core of the major protein-protein interaction network

Upregulated					Downregulated				
Gene	log ₂ FC	Degree	Betweenness	Eigen Vector	Gene	log ₂ FC	Degree	Betweenness	Eigen Vector
<i>CDKN2A</i>	1.1	28	1183	0.224	<i>CDK1</i>	-2	32	1110	0.275
<i>CDKN1A</i>	4.4	25	566	0.224	<i>TOP2A</i>	-2.6	29	1967	0.219
<i>IKBKB</i>	1.5	20	772	0.126	<i>PLK1</i>	-3.1	25	840	0.233
<i>HIST2H2BE</i>	1.4	18	720	0.109	<i>BRCA1</i>	-1.1	24	450	0.219
<i>PRKACA</i>	0.8	16	733	0.119	<i>CDC20</i>	-3.6	22	487	0.214
<i>NFKBIA</i>	1.5	15	872	0.073	<i>CDK7</i>	-3.6	22	606	0.172
<i>GADD45A</i>	4	13	215	0.119	<i>HDAC2</i>	-2.6	22	966	0.138
<i>PSMB8</i>	1.1	10	508	0.103	<i>EZH2</i>	-3.9	20	355	0.186
					<i>FOXO3</i>	-2	20	725	0.147
					<i>MNAT1</i>	-2.1	15	212	0.122
					<i>TBP</i>	-2.8	14	333	0.073
					<i>CAB39</i>	-2.3	9	290	0.061
					<i>IGF1R</i>	-2	9	594	0.061

Supplement 2. Top-40 differentially expressed genes with the most significant change in expression

Upregulated		Downregulated	
Gene	log ₂ FC	Gene	log ₂ FC
<i>PMAIP1</i>	5.1	<i>TLE1</i>	-6.9
<i>CDKN1A</i>	4.4	<i>JMJD6</i>	-6.7
<i>GADD45A</i>	4.0	<i>CCNA2</i>	-5.2
<i>GATA2</i>	4.0	<i>KEAP1</i>	-5.2
<i>GADD45B</i>	3.5	<i>MTF2</i>	-5.1
<i>ALDOC</i>	2.9	<i>KAT6A</i>	-5.0
<i>FOXO4</i>	2.3	<i>AURKA</i>	-5.0
<i>CTSL</i>	2.3	<i>NRIP1</i>	-4.8
<i>HSPB1</i>	2.2	<i>ATP1B1</i>	-4.6
<i>NENF</i>	2.1	<i>CDC25A</i>	-4.3
<i>TCTA</i>	2.0	<i>USP6NL</i>	-4.3
<i>STK25</i>	1.9	<i>EZH2</i>	-3.9
<i>HES1</i>	1.8	<i>RFC2</i>	-3.7
<i>PECR</i>	1.8	<i>FOXJ3</i>	-3.7
<i>PRAF2</i>	1.7	<i>CDC25B</i>	-3.6
<i>NFKBIA</i>	1.5	<i>CDC20</i>	-3.6
<i>IKBKB</i>	1.5	<i>MBNL1</i>	-3.6
<i>RRAGA</i>	1.5	<i>CDK7</i>	-3.6
<i>HIST2H2BE</i>	1.4	<i>MAP3K4</i>	-3.6
<i>TICAM1</i>	1.4	<i>NUP85</i>	-3.5

Supplement 3. The top-10 enriched KEGG pathways of upregulated differentially expressed genes

Pathway ID	Pathway description	Genes	<i>p</i>
hsa05166	HTLV-I infection	<i>ZFP36, ICAM1, CDKN1A, CDKN2A, RELB, TGFB3,</i>	<0.001

		<i>FZD1, NFKBIA, PRKACA, IKBKB, PIK3R3, TERT</i>	
hsa04115	p53 signaling pathway	<i>BID, CDKN1A, CDKN2A, PMAIP1, SFN, GADD45B, GADD45A</i>	<0.001
hsa05169	Epstein-Barr virus infection	<i>ICAM1, CDKN1A, RELB, NFKBIA, HSPB1, PRKACA, HSPA1A, IKBKB, PIK3R3</i>	0.001
hsa05220	Chronic myeloid leukemia	<i>CDKN1A, CDKN2A, TGFB3, NFKBIA, IKBKB, PIK3R3</i>	0.004
hsa04068	FoxO signaling pathway	<i>CDKN1A, TGFB3, GADD45B, IKBKB, PIK3R3, FOXO4, GADD45A</i>	0.007
hsa04210	Apoptosis	<i>BID, DFFA, NFKBIA, IKBKB, PIK3R3</i>	0.019
hsa04110	Cell cycle	<i>CDKN1A, CDKN2A, TGFB3, SFN, GADD45B, GADD45A</i>	0.026
hsa04010	MAPK signaling pathway	<i>RELB, TGFB3, HSPB1, PRKACA, HSPA1A, GADD45B, IKBKB, GADD45A</i>	0.029
hsa05161	Hepatitis B	<i>CDKN1A, TICAM1, TGFB3, NFKBIA, IKBKB, PIK3R3</i>	0.037
hsa05203	Viral carcinogenesis	<i>CDKN1A, CDKN2A, HIST2H2BE, NFKBIA, PRKACA, PMAIP1, PIK3R3</i>	0.038

KEGG= Kyoto Encyclopedia of Genes and Genomes; HTLV-I= Human T-cell lymphotropic virus type 1; FoxO= forkhead box transcription factors of the class O; MAPK= mitogen-activated protein kinase

Supplement 4. Significantly enriched KEGG pathways of downregulated differentially expressed genes

Pathway ID	Pathway description	Genes	<i>p</i>
hsa04110:	Cell cycle	<i>CDK1, HDAC2, CCNB2, PLK1, CDK6, CDC20, CDK7, CCNA2, CDC25A, CDC25B</i>	<0.001
hsa04914:	Progesterone-mediated oocyte maturation	<i>CDK1, IGF1R, CCNB2, PLK1, CCNA2, CDC25A, CDC25B</i>	0.001
hsa05203:	Viral	<i>USP7, CDK1, HDAC2, TBP, CDK6,</i>	0.015

	carcinogenesis	<i>CDC20, CCNA2, TBPL1</i>	
hsa04152:	AMPK signaling pathway	<i>IGF1R, PRKAG2, PPARG, CAB39, FOXO3, CCNA2</i>	0.037
hsa05169:	Epstein-Barr virus infection	<i>USP7, CDK1, HDAC2, TBP, CCNA2, HSPA8, TBPL1</i>	0.037
hsa04068:	FoxO signaling pathway	<i>USP7, IGF1R, CCNB2, PLK1, PRKAG2, FOXO3</i>	0.037

KEGG= Kyoto Encyclopedia of Genes and Genomes; AMPK= AMP-activated protein kinase; FoxO= forkhead box transcription factors of the class O