

Figure S1. Functional analysis of differentially expressed lncRNAs. (A and B) GO enrichment analysis of the (A) upregulated and (B) downregulated lncRNAs in the categories biological process, cellular component and molecular function. (C and D) Top 10 most significantly enriched signaling pathways of the (C) upregulated and (D) downregulated lncRNAs. lncRNA, long non-coding RNA; GO, gene ontology; hsa, *Homo sapiens*.

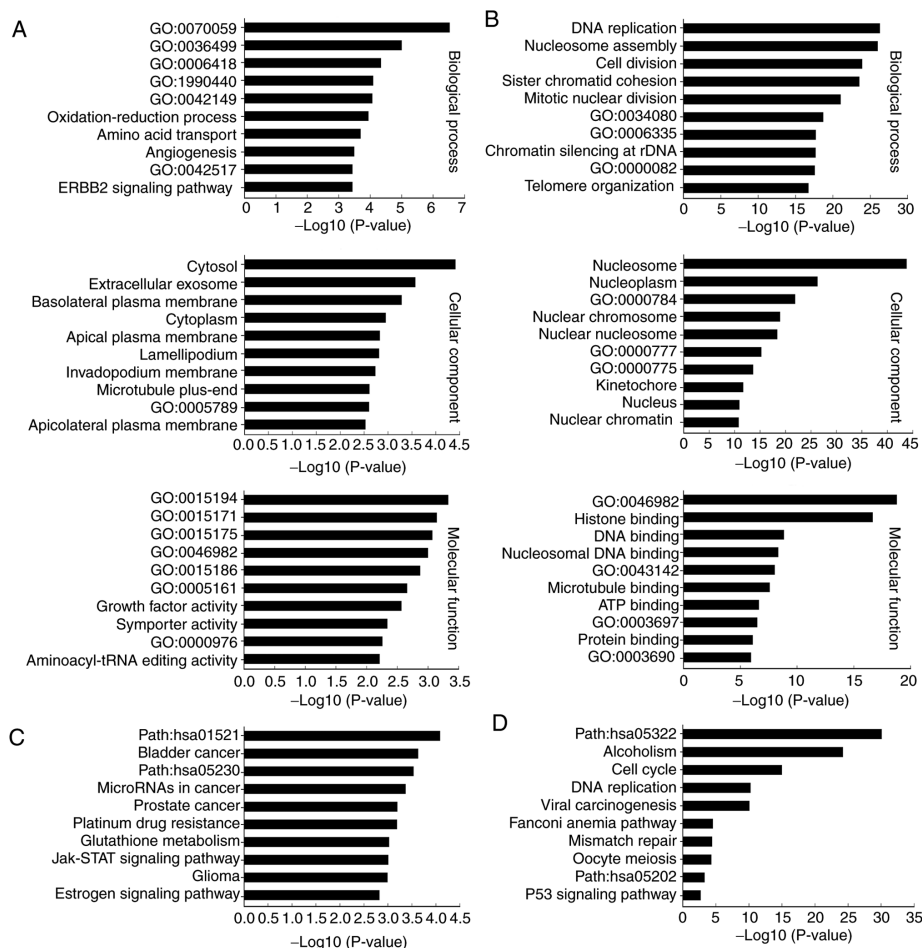


Figure S2. Link and overlap between differentially expressed lncRNAs and mRNAs in the EGFR tyrosine kinase inhibitor resistance pathway. Circles represent lncRNAs; squares represent mRNAs; red represents upregulated expression; blue represents downregulated expression. lncRNA, long non-coding RNA; EGFR, epidermal growth factor receptor; lnc., the symbol of LNCipedia ID; ENST, the symbol of Ensembl ID; NONHSAT, the symbol of NONCODE ID; NR, the symbol of RefSeq ID; T, the symbol of mitranscriptome ID.

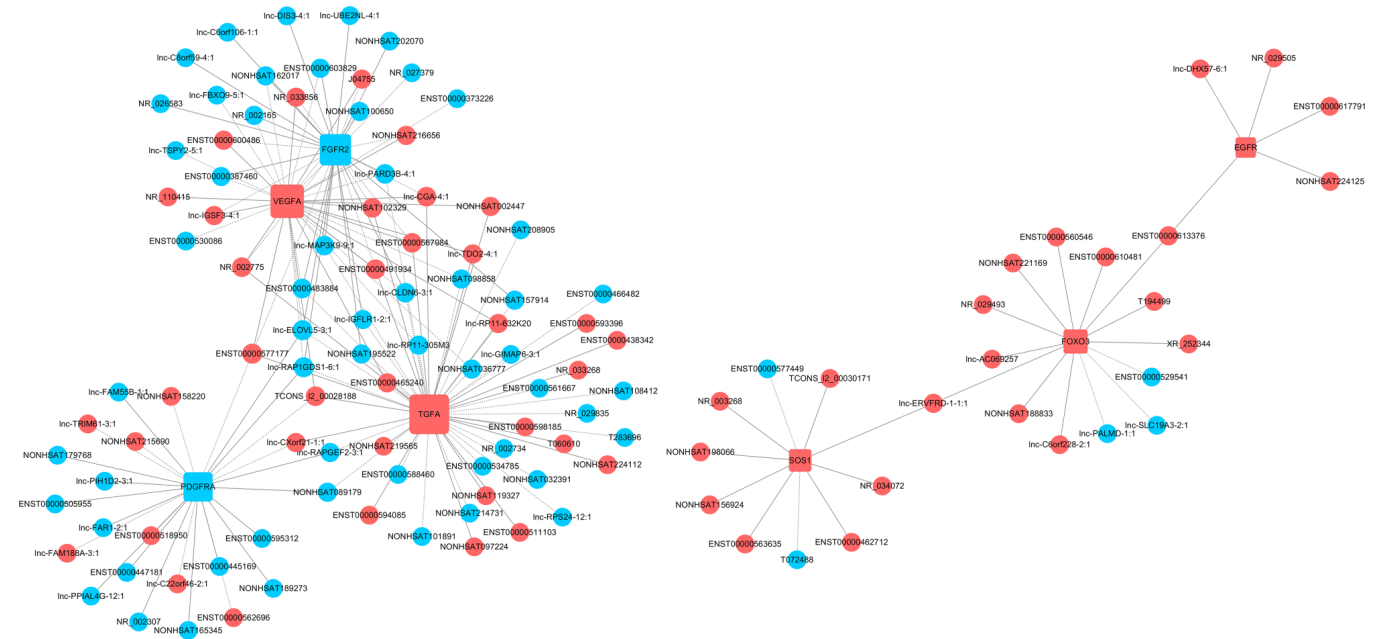


Figure S3. The interactions between differentially expressed lncRNAs and mRNAs in the FOXO signaling pathway. Circles represent lncRNAs; squares represent mRNAs; red represents upregulated expression; blue represents downregulated expression. lncRNA, long non-coding RNA; FOXO, forkhead box O; lnc., the symbol of LNCipedia ID; ENST, the symbol of Ensembl ID; NONHSAT, the symbol of NONCODE ID; NR, the symbol of RefSeq ID; T, the symbol of mitranscriptome ID.

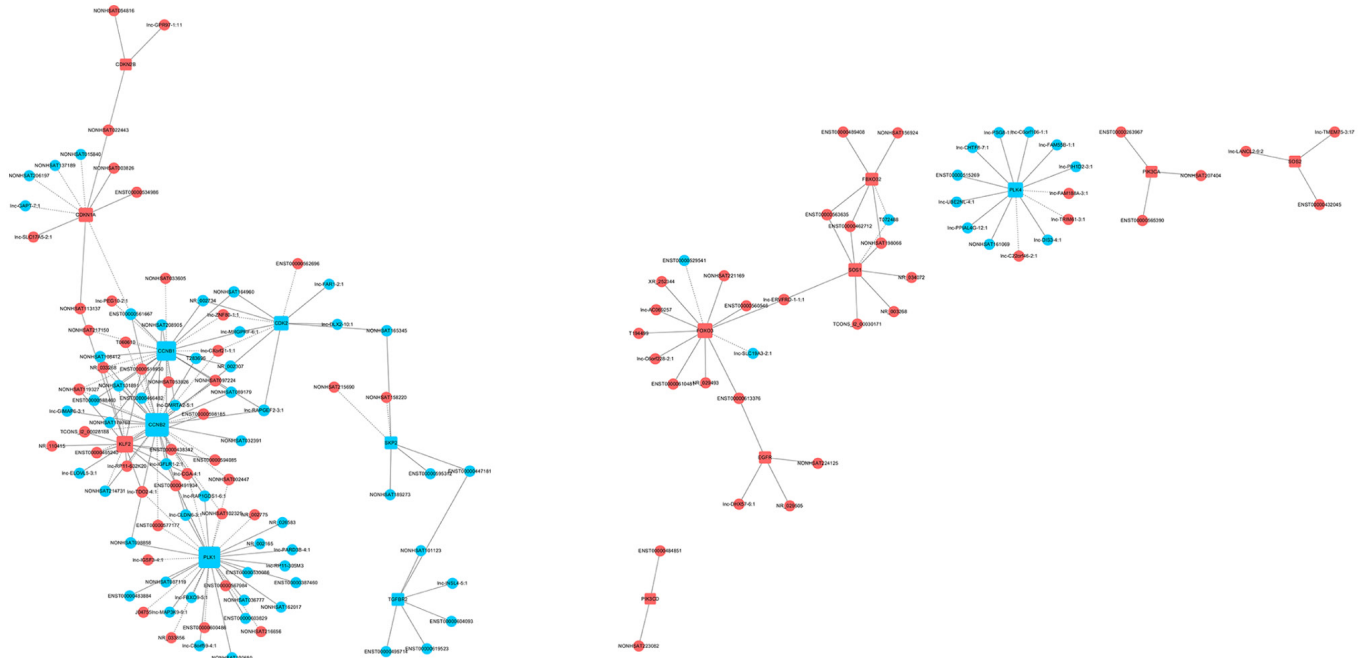


Figure S4. Link and overlap between differentially expressed lncRNAs and mRNAs in the p53 signaling pathway. Circles represent lncRNAs; squares represent mRNAs; red represents upregulated expression; blue represents downregulated expression. lncRNA, long non-coding RNA; p53, tumor protein P53 (TP53); lnc., the symbol of LNCipedia ID ID; ENST, the symbol of Ensembl ID; NONHSAT, the symbol of NONCODE ID; NR, the symbol of RefSeq ID; T, the symbol of mitranscriptome ID.

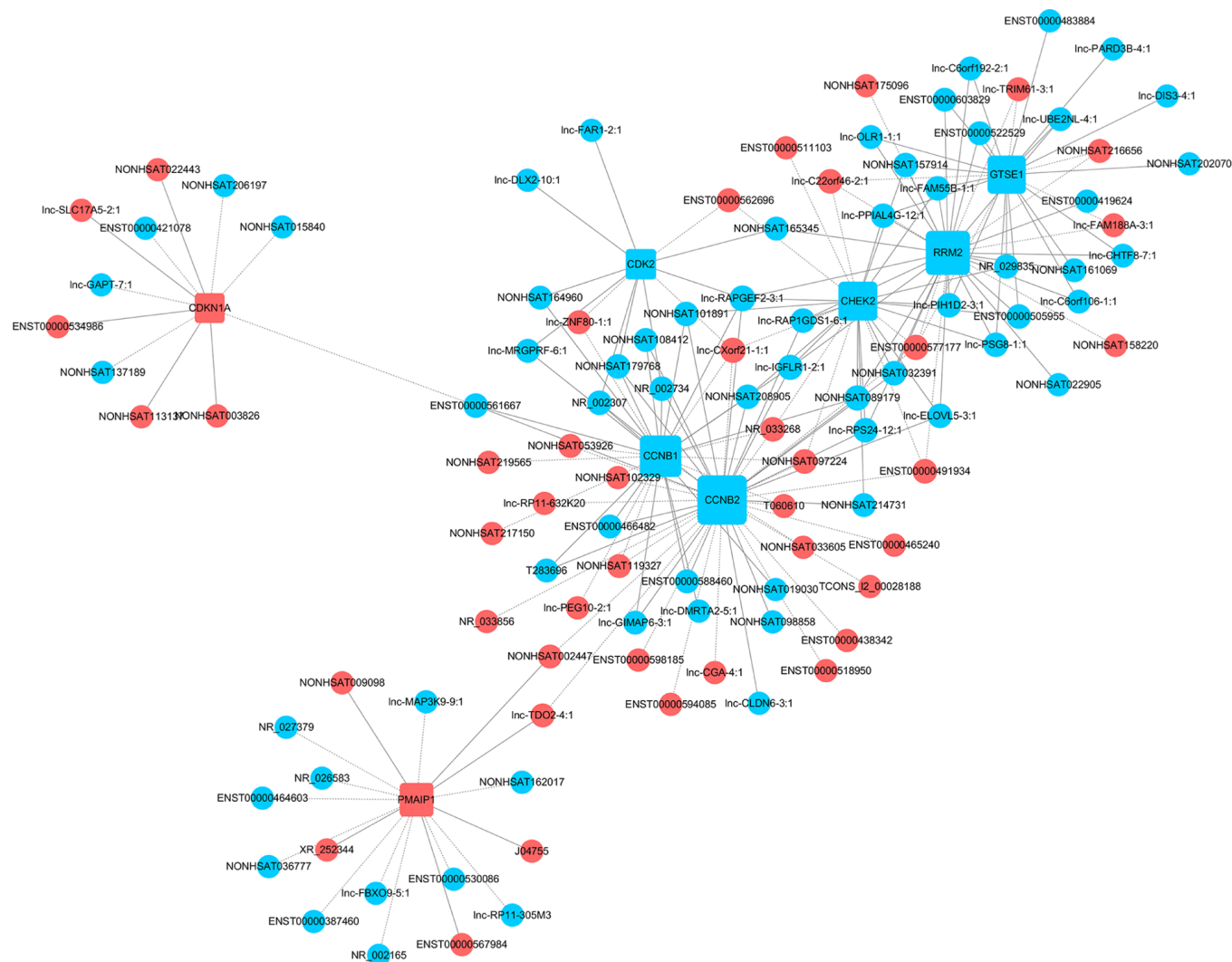


Figure S6. lncRNA-mRNA co-expression network. Green represents lncRNAs; red represents mRNAs. The size of the squares represents the P-value with a larger size indicating a smaller P-value. lncRNA, long non-coding RNA; ENST, the symbol of Ensembl ID; NONHSAT, the symbol of NONCODE ID; NR, the symbol of RefSeq ID.

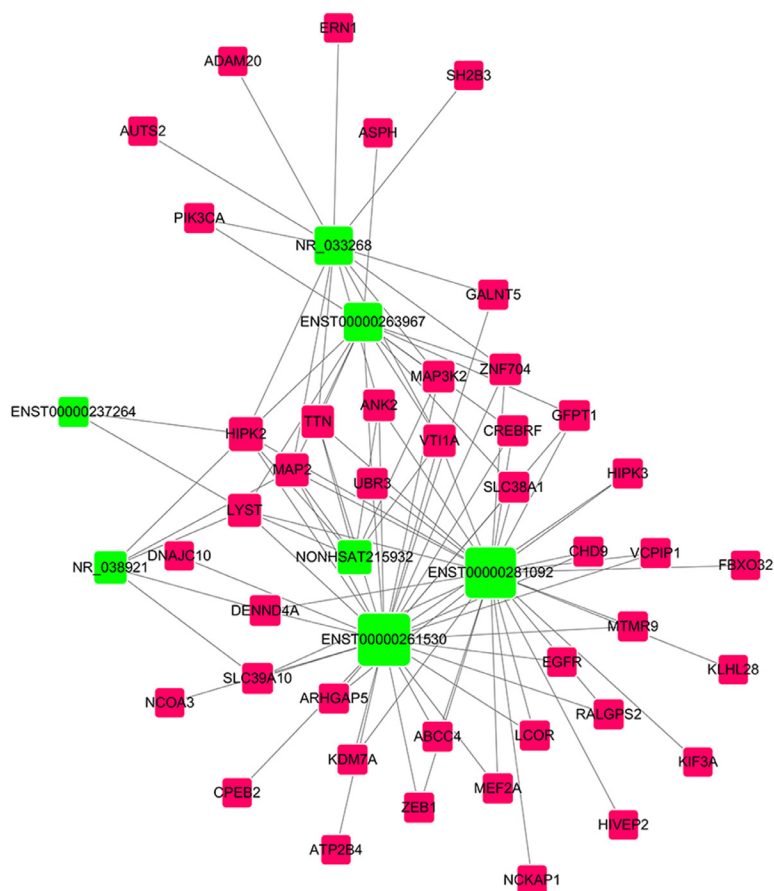


Figure S7. circRNA-mRNA co-expression network. Yellow represents circRNAs; red represents mRNAs. The size of the squares represents the P-value with a larger size indicating a smaller P-value. circRNA, circular RNA; hsa, *Homo sapiens*.

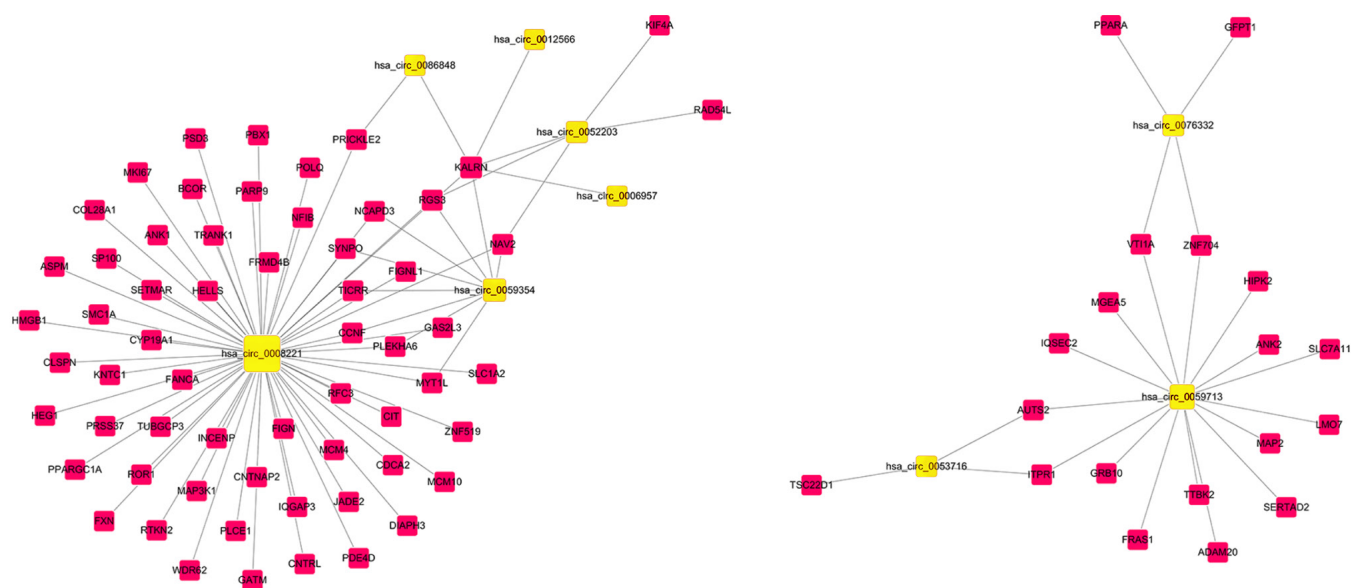


Table SI. Top 10 upregulated and downregulated differentially expressed long non-coding RNAs identified from arrays.

Seq name	Target ID	Regulation	P-value	Log (fold change)	Chromosomal location
A_21_P0010854	NR_027916	Up	9.26x10 ⁻⁵	5.384749	Chr10
CUST_H6L_73811	NR_002775	Up	8.08x10 ⁻⁷	4.403029	Chr11
A_21_P0013475	ENST00000511103	Up	5.90x10 ⁻⁵	4.130445	Chr8
A_21_P0013514	TCONS_I2_00028188	Up	2.93x10 ⁻⁵	4.002797	Chr8
CUST_H6L_10603	lnc-TIPARP-1:1	Up	1.93x10 ⁻⁴	3.816623	Chr3
CUST_H6L_38098	NONHSAT158109	Up	2.79x10 ⁻⁴	3.813126	Chr10
A_33_P3363188	NR_033856	Up	4.31x10 ⁻⁶	3.719438	ChrUn
CUST_H6L_74661	ENST00000491934	Up	5.53x10 ⁻⁶	3.59376	Chr10
A_24_P68908	NR_033752	Up	3.69x10 ⁻⁴	3.464309	Chr3
A_21_P0013028	TCONS_I2_00024286	Up	2.33x10 ⁻³	3.211028	Chr6
CUST_H6L_22666	lnc-PARD3B-4:1	Down	3.57x10 ⁻⁸	-3.758980	Chr2
CUST_H6L_26307	ENST00000465336	Down	3.68x10 ⁻³	-3.541194	Chr4
CUST_H6L_08737	NR_033888	Down	5.40x10 ⁻⁴	-3.467148	Chr19
A_32_P153979	NONHSAT098858	Down	1.06x10 ⁻⁵	-3.393622	Chr4
CUST_H6L_34036	NONHSAT149976	Down	3.35x10 ⁻⁴	-3.286985	Chr1
CUST_H6L_17499	lnc-JPH4-3:1	Down	4.68x10 ⁻⁴	-3.153543	Chr14
CUST_H6L_00288	NR_029835	Down	3.77x10 ⁻⁵	-3.062367	Chr4
CUST_H6L_08739	lnc-PSG8-1:1	Down	1.98x10 ⁻⁴	-3.058501	Chr19
CUST_H6L_20927	lnc-CD177-1:2	Down	3.75x10 ⁻³	-2.928761	Chr19
CUST_H6L_28349	lnc-GJA10-11:1	Down	6.22x10 ⁻⁵	-2.923585	Chr6

Chr, chromosome; ChrUn, the clone contigs that can't be confidently placed on a specific chromosome.

Table SII. Top 10 upregulated and downregulated differentially expressed circRNAs identified from arrays.

Seq name	Gene symbol	Target ID	Regulation	P-value	Log (fold change)	Chromosomal location
CUST_H6C_06499	ABL2	hsa_circ_0015430	Up	8.83x10 ⁻⁴	2.160168	Chr1
CUST_H6C_12308	INTS2	hsa_circ_0045038	Up	0.011022	1.974050	Chr17
CUST_H6C_13232	SNRPA	hsa_circ_0051144	Up	0.046030	1.619331	Chr19
CUST_H6C_03851	CEP350	hsa_circ_0006924	Up	0.030010	1.614593	Chr1
CUST_H6C_00264	SPIRE1	hsa_circ_0000829	Up	0.023407	1.606566	Chr18
CUST_H6C_07639	RRM1	hsa_circ_0020947	Up	0.024381	1.541213	Chr11
CUST_H6C_12111	EFTUD2	hsa_circ_0044105	Up	0.018382	1.507833	Chr17
CUST_H6C_18254	MRPS10	hsa_circ_0076332	Up	9.70x10 ⁻⁴	1.485887	Chr6
CUST_H6C_10995	C16orf62	hsa_circ_0038348	Up	0.041508	1.425772	Chr16
CUST_H6C_13166	COX6B1	hsa_circ_0050629	Up	0.006291	1.398831	Chr19
CUST_H6C_12561	L3MBTL4	hsa_circ_0046757	Down	0.022583	-2.499965	Chr18
CUST_H6C_07327	ABCC2	hsa_circ_0019440	Down	0.007746	-2.152122	Chr10
CUST_H6C_00262	L3MBTL4	hsa_circ_0000824	Down	0.040183	-2.104184	Chr18
CUST_H6C_13373	PPP6R1	hsa_circ_0052203	Down	3.60x10 ⁻⁴	-2.036634	Chr19
CUST_H6C_07480	HTRA1	hsa_circ_0020272	Down	0.004949	-2.014538	Chr10
CUST_H6C_12724	TPGS2	hsa_circ_0047462	Down	0.031517	-1.878515	Chr18
CUST_H6C_20058	INTS8	hsa_circ_0084954	Down	0.032446	-1.854020	Chr8
CUST_H6C_21226	ATP7A	hsa_circ_0091119	Down	0.033960	-1.835343	Chrx
CUST_H6C_19223	PEX1	hsa_circ_0081024	Down	0.002933	-1.807396	Chr7
CUST_H6C_09385	PDS5B	hsa_circ_0029966	Down	0.042588	-1.801153	Chr13

Hsa, *Homo sapiens*; circ/circRNA, circular RNA; Chr, chromosome.

Table SIII. Top 10 upregulated and downregulated differentially expressed mRNAs identified from arrays.

Seq name	Gene symbol	Target ID	Regulation	P-value	Log (fold change)	Chromosomal location
A_23_P163402	CYP1A1	NM_000499	Up	1.52×10^{-8}	5.820367	Chr15
A_24_P245379	SERPINB2	NM_002575	Up	1.24×10^{-4}	5.725936	Chr18
A_23_P257971	AKR1C1	NM_001353	Up	2.85×10^{-4}	5.393709	Chr10
A_33_P3242623	SLC7A11	NM_014331	Up	2.35×10^{-5}	5.365624	Chr4
A_21_P0013512	-	ENST00000518311	Up	1.62×10^{-6}	3.964775	Chr8
A_23_P104318	DDIT4	NM_019058	Up	5.35×10^{-6}	3.932167	Chr10
A_23_P145694	ASNS	NM_001673	Up	2.19×10^{-6}	3.868033	Chr7
A_23_P209055	CD22	NM_001771	Up	5.50×10^{-4}	3.741541	Chr19
A_24_P408736	GALNT5	NM_014568	Up	1.54×10^{-5}	3.683576	Chr2
A_33_P3376965	CHAC1	NM_024111	Up	9.35×10^{-6}	3.654356	Chr15
A_33_P3300312	DMBT1	NM_007329	Down	2.09×10^{-4}	-4.813966	Chr10
A_23_P375372	FGA	NM_021871	Down	9.88×10^{-8}	-4.286443	Chr4
A_23_P148088	FGG	NM_000509	Down	4.55×10^{-6}	-4.226823	Chr4
A_33_P3241334	PSG9	ENST00000595404	Down	0.003910	-3.908162	Chr19
A_23_P71328	MATN2	NM_030583	Down	2.13×10^{-4}	-3.882849	Chr8
A_23_P383009	IGFBP5	NM_000599	Down	5.33×10^{-6}	-3.687989	Chr2
A_24_P282251	FGA	NM_021871	Down	3.79×10^{-6}	-3.490662	Chr4
A_23_P318904	SERTAD4	NM_019605	Down	3.22×10^{-4}	-3.297592	Chr1
A_33_P3229122	HIST1H2BF	NM_003522	Down	6.41×10^{-6}	-3.292424	Chr6
A_23_P363174	HIST1H2AL	NM_003511	Down	4.17×10^{-5}	-3.242636	Chr6

Chr, chromosome.

Table SIV. Top 10 upregulated and downregulated differentially expressed miRNAs identified from arrays.

miRNA_ID	Regulation	P-value	Log (fold change)
hsa-miR-3929	Up	2.54x10 ⁻¹¹	5.419062
NC_000017.11_32431 ^a	Up	1.20x10 ⁻⁵	4.100887
NC_000019.10_34428	Up	0.021921	3.527191
hsa-miR-4758-3p	Up	0.011080	3.525005
hsa-miR-4435	Up	0.022009	3.520458
NC_000016.10_31515	Up	3.96x10 ⁻⁷	3.512116
hsa-miR-6511b-5p	Up	0.015544	3.425316
NC_000014.9_29046	Up	1.56x10 ⁻⁶	3.302415
NC_000023.11_37419	Up	0.043582	3.288825
hsa-miR-3189-3p	Up	0.040889	3.269043
hsa-miR-548d-3p	Down	0.015999	-4.352009
hsa-miR-675-5p	Down	0.002370	-4.292261
hsa-miR-520c-3p	Down	0.000806	-4.184770
hsa-miR-302b-5p	Down	0.005188	-4.029381
hsa-miR-518b	Down	0.000122	-3.878700
hsa-miR-498	Down	0.009706	-3.871208
hsa-miR-205-5p	Down	1.03x10 ⁻²⁰	-3.555738
NC_000011.10_25384	Down	1.92x10 ⁻⁷	-3.438426
hsa-miR-1268b	Down	0.000232	-3.291232
NC_000010.11_23646	Down	0.006373	-3.192637

^aRepresents another byproduct miRNA. hsa, *Homo sapiens*; miRNA/miR, microRNA.