

Genes best correlating with the selected gene

Mikhail Dozmorov

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Correlation analysis

Top 10 genes positively correlated with MIA

	symbol	description
9149	MIA	melanoma inhibitory activity [Source:HGNC Symbol;Acc:7076]
16978	TTYH1	tweety family member 1 [Source:HGNC Symbol;Acc:13476]
15122	SOX10	SRY (sex determining region Y)-box 10 [Source:HGNC Symbol;Acc:11190]
13658	SCRG1	stimulator of chondrogenesis 1 [Source:HGNC Symbol;Acc:17036]
13458	S100A1	S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:10486]
5059	FAHD2A	fumarylacetoacetate hydrolase domain containing 2A [Source:HGNC Symbol;Acc:24252]
17671	WWP2	WW domain containing E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:16804]
8284	LCTL	lactase-like [Source:HGNC Symbol;Acc:15583]
9108	MFI2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 [Source:HGNC S
13469	S100B	S100 calcium binding protein B [Source:HGNC Symbol;Acc:10500]

Top 10 genes negatively correlated with MIA

	symbol	description	Length	
5661	FOXA1	forkhead box A1 [Source:HGNC Symbol;Acc:5021]	10056	-0.000000
2407	CCDC125	coiled-coil domain containing 125 [Source:HGNC Symbol;Acc:28924]	52634	-0.000000
8389	LIMA1	LIM domain and actin binding 1 [Source:HGNC Symbol;Acc:24636]	107758	-0.000000
11380	PGGT1B	protein geranylgeranyltransferase type I, beta subunit [Source:HGNC Symbol;Acc:8895]	52042	-0.000000
631	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2 [Source:HGNC Symbol;Acc:13208]	13351	-0.000000
385	AGGF1	angiogenic factor with G patch and FHA domains 1 [Source:HGNC Symbol;Acc:24684]	35983	-0.000000
5419	FBXO38	F-box protein 38 [Source:HGNC Symbol;Acc:28844]	58901	-0.000000
15230	SPG11	spastic paraplegia 11 (autosomal recessive) [Source:HGNC Symbol;Acc:11226]	100982	-0.000000
5935	GATA3	GATA binding protein 3 [Source:HGNC Symbol;Acc:4172]	21594	-0.000000
5396	FBXL5	F-box and leucine-rich repeat protein 5 [Source:HGNC Symbol;Acc:13602]	77140	-0.000000
3939	DCAF5	DDB1 and CUL4 associated factor 5 [Source:HGNC Symbol;Acc:20224]	102269	-0.000000

Genes positively (n = 1394) and negatively (n = 332) correlating with the selected gene MIA at $p < 0.05$ cutoff and pearson correlation coefficient cutoff: >0.2 . Legend:

- **symbol, description** - gene symbols/description
- **cor,** 'pval - Pearson correlation coefficient, and p-value of correlation significance

Full correlation results are saved in results/Results_MIA_BRCA.xlsx file.

Functional enrichment analysis

KEGG canonical pathway enrichment analysis

- Genes positively and negatively correlated with the MIA are tested for pathway enrichment separately.
- Each table has enrichment results for both positively/negatively correlated genes. The “direction” column indicate which pathways are enriched in “UP”- or “DN”-regulated genes for positively/negatively correlated genes, respectively.
- Use the “Search” box for each table, to filter the results for “UP” or “DN” only. Search is global within the table, case insensitive.
- FDR cutoff of the significant enrichments - 0.3.

Legend: “database” - source of functional annotations, “category” - name of functional annotation, “pval” - unadjusted enrichment p-value, “qval” - FDR-adjusted p-value, “genes” - comma-separated differentially expressed genes enriched in a corresponding functional category, “direction” - UP/DN, an indicator whether genes are up- or downregulated.

[1] "KEGG pathway run on 1726 genes without distinguishing them by directionality."
[1] "Running KEGG_2019_Human analysis"

	database	category	pval	qval	genes
51	KEGG_2019_Human	Ribosome	6.291e-04	1.570e-01	RPL5,R
29	KEGG_2019_Human	Spliceosome	1.094e-03	1.570e-01	SF3A3,I
48	KEGG_2019_Human	Wnt signaling pathway	2.224e-03	1.703e-01	CHD8,L
11	KEGG_2019_Human	Ribosome biogenesis in eukaryotes	2.373e-03	1.703e-01	UTP15,I
13	KEGG_2019_Human	RNA polymerase	3.934e-03	2.258e-01	POLR2,
2	KEGG_2019_Human	Glycosaminoglycan biosynthesis	4.923e-03	2.355e-01	B4GALT
5	KEGG_2019_Human	Basal cell carcinoma	6.979e-03	2.862e-01	WNT6,7
26	KEGG_2019_Human	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	8.092e-03	2.865e-01	TCF7L2
30	KEGG_2019_Human	Mitophagy	8.984e-03	2.865e-01	MAPK9
39	KEGG_2019_Human	Primary bile acid biosynthesis	1.220e-02	3.204e-01	CYP27A