Genes best correlating with the selected gene

Mikhail Dozmorov

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Correlation analysis

Genes positively (n = 3567) and negatively (n = 2101) 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/BRCA_results_MIA_RNASeq2___UP.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.

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[1] "Running KEGG_2016 analysis"
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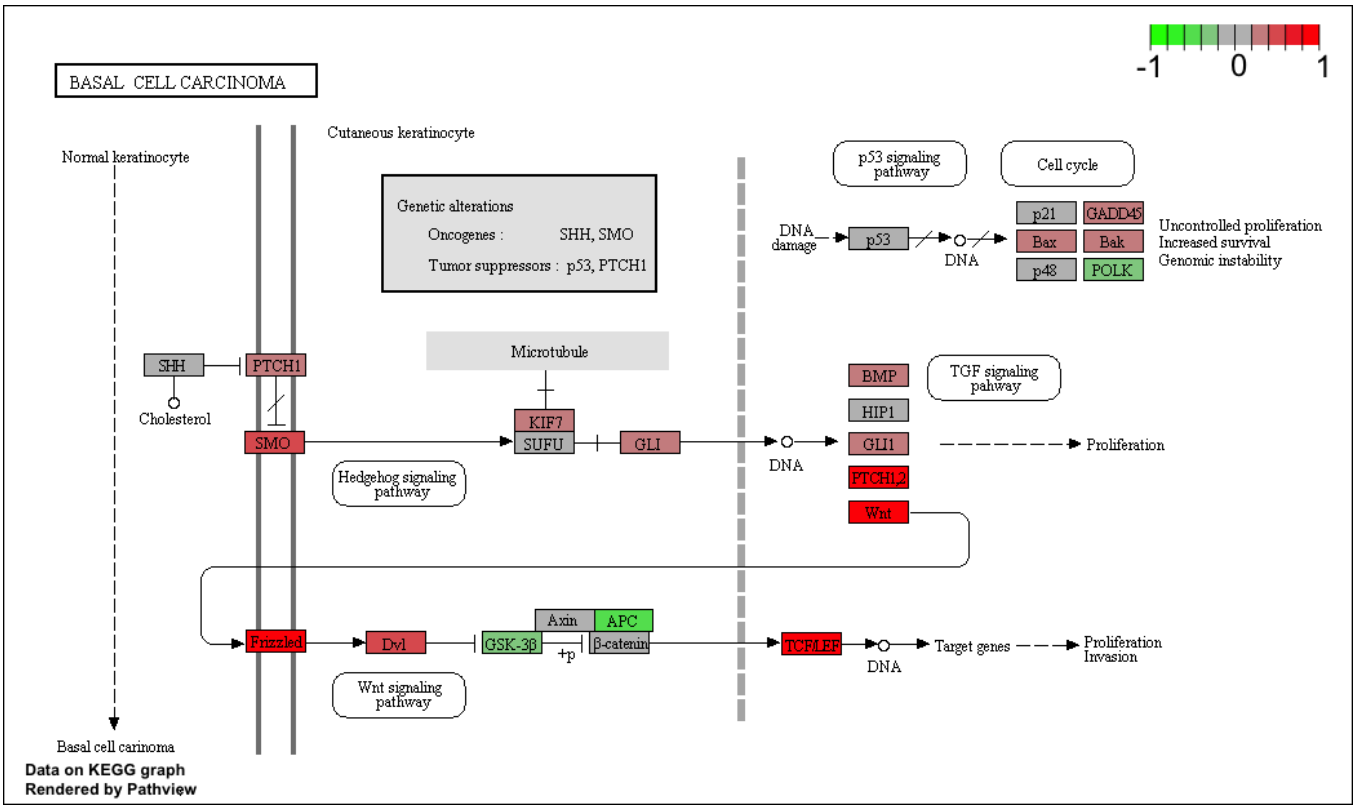
database	category	pval	qval
KEGG_2016	Ribosome_Homo sapiens_hsa03010	3.665e-18	1.059e-15
KEGG_2016	Cytokine-cytokine receptor interaction_Homo sapiens_hsa04060	1.211e-08	1.750e-06
KEGG_2016	TNF signaling pathway_Homo sapiens_hsa04668	1.028e-06	9.906e-05
KEGG_2016	NF-kappa B signaling pathway_Homo sapiens_hsa04064	9.370e-05	4.513e-03
KEGG_2016	Primary immunodeficiency_Homo sapiens_hsa05340	7.503e-05	4.337e-03
KEGG_2016	Glycosphingolipid biosynthesis - lacto and neolacto series_Homo sapiens_hsa00601	3.575e-05	2.583e-03
KEGG_2016	Focal adhesion_Homo sapiens_hsa04510	3.218e-04	1.162e-02
KEGG_2016	HTLV-I infection_Homo sapiens_hsa05166	3.929e-04	1.262e-02
KEGG_2016	Basal cell carcinoma_Homo sapiens_hsa05217	2.903e-04	1.162e-02
KEGG_2016	PI3K-Akt signaling pathway_Homo sapiens_hsa04151	1.415e-03	3.146e-02


BASAL CELL CARCINOMA
-1
0
1
Normal keratinocyte
Cutaneous keratinocyte
Genetic alterations
Oncogenes : SHH, SMO
Tumor suppressors : p53, PTCH1
p53 signaling pathway
Cell cycle
DNA damage
p53
DNA
p21
GADD45
Bax
Bak
p48
POLK
Uncontrolled proliferation
Increased survival
Genomic instability
Microtubule
SHH
PTCH1
Cholesterol
SMO
KIF7
SUFU
GLI
Hedgehog signaling pathway
DNA
BMP
HIP1
GLI1
PTCH1,2
Wnt
TGF signaling pahway
Proliferation
Axin
APC
Frizzled
Dvl
GSK-3β
+p
β-catenin
TCF/LEF
DNA
Target genes
Proliferation
Invasion
Wnt signaling pathway
Basal cell carinoma
Data on KEGG graph
Rendered by Pathview