

Supplementary Materials: MicroRNA Profile of Lung Tumor Tissues Is Associated with a High Risk Plasma miRNA Signature

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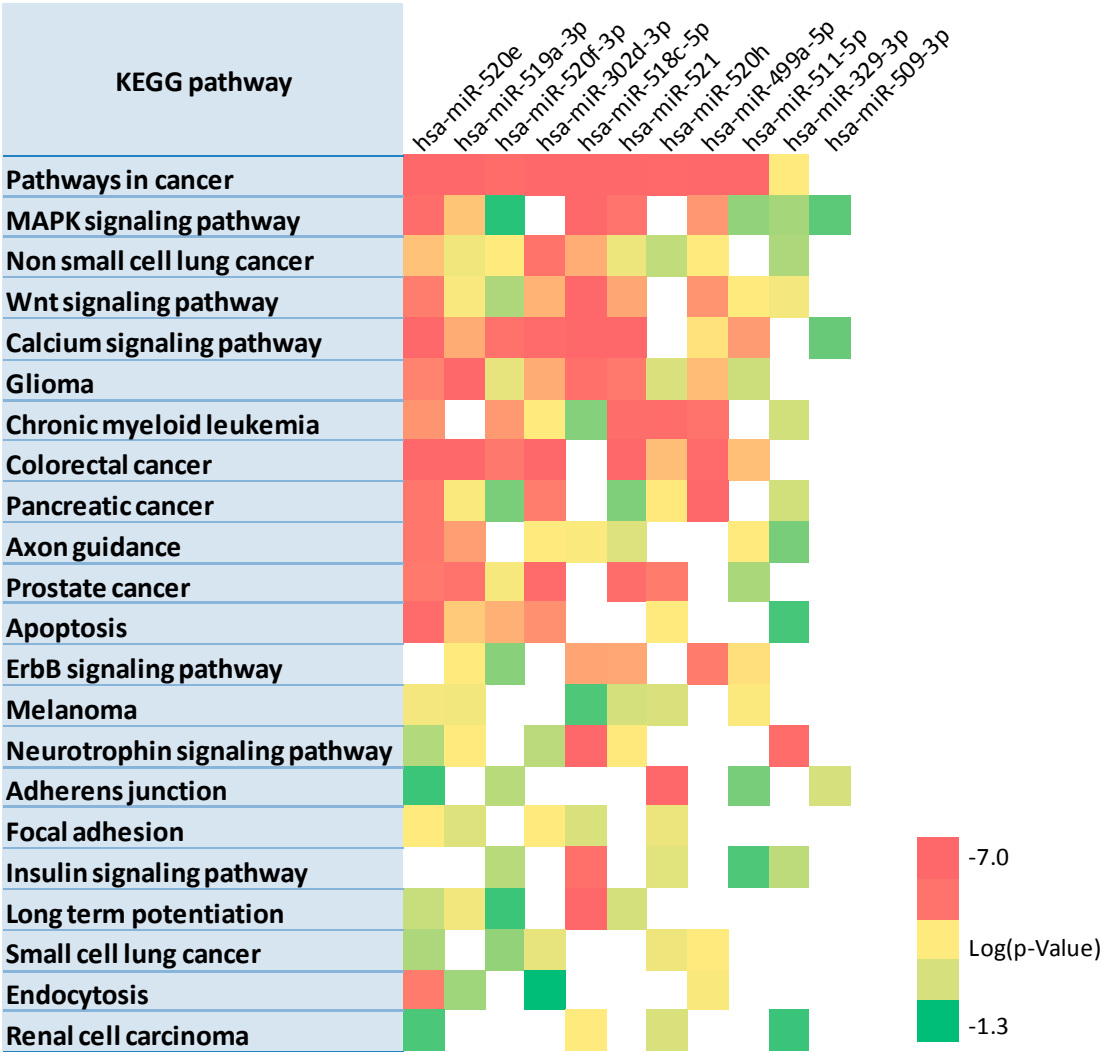


Figure S1. Heat map of KEGG pathway enrichment analysis using miRWalk2.0 and considering 11 mature miRNAs differentially expressed between lung cancer patients with high and intermediate/low risk MSC. Adjusted *p*-value < 0.05 after FDR correction.

Table S1. Class comparison analysis of microRNA expression in tumor tissue of lung cancer patients stratified according to status at five years.

MicroRNA	Parametric <i>p</i> -Value	Permutation <i>p</i> -Value	Geom Mean of Dead Patients	Geom Mean of Alive Patients	Fold-Change
hsa-mir-499a-5p	0.0058	0.0058	1912.49	1152.67	1.67
hsa-mir-212-prec	0.0066	0.0084	1692.4	1241.48	1.37
hsa-mir-429	0.0079	0.0074	1349.96	910.32	1.49

Type of univariate test used: two-sample *t*-test. Permutation *p*-values for significant miRNAs were computed based on 10,000 random permutations. Nominal significance level of each univariate test: 0.01.