

Identification of candidate miRNAs in early-onset and late-onset prostate cancer by network analysis

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Supplementary Table 2. Over-representation analysis of co-expressed genes with hub miRNA using LO-PCa data.

hub miRNA	Gene Set	Size	Expect	Ratio	Overlap	FDR
hsa_miR_31_5p	LIU_PROSTATE_CANCER_DN	473	1.98	3.54	7	0.003
hsa_miR_205_5p	LIU_PROSTATE_CANCER_DN	473	4.81	2.91	14	1.16E-04
hsa_miR_224_3p	LIU_PROSTATE_CANCER_DN	473	7.07	2.69	19	1.93E-05
hsa_miR_3545_3p	LIU_PROSTATE_CANCER_DN	473	9.33	2.25	21	4.73E-04

Only statistically significant associations are shown. Size means the number of genes in the pathway, Expect means the expected number of genes in the pathway co-expressed by chance with the miRNA, Ratio means the additional number of times that there are more genes co-expressed with the miRNA compared with the expected number, Overlap means the number of co-expressed genes that are part of the pathway. FDR is the false discovery rate of the overlap.

