S2: Functional enrichment analysis results of the selected shared miRNAs by DAVID

Annotation Cluster 1			Enrichment Score: 2.2139595316990444						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR001806:Small GTPase superfamily	7	10.14493	0.002502	6093, 3480, 1021, 658, 558, 9641, 7048	5.014397	0.466827	0.466827	3.204603
UP_KEYWORDS	Prenylation	7	10.14493	0.005578	6093, 3480, 1021, 658, 558, 9641, 7048	4.25811	0.931021	0.257035	7.692687
INTERPRO	IPR005225:Small GTP-binding protein domain	7	10.14493	0.008185	6093, 3480, 1021, 658, 558, 9641, 7048	3.922968	0.872921	0.497243	10.13292
UP_SEQ_FEATURE	nucleotide phosphate-binding region:GTP	7	10.14493	0.012197	6093, 3480, 1021, 658, 558, 9641, 7048	3.597901	0.954052	0.459926	14.74503
UP_KEYWORDS	GTP-binding	7	10.14493	0.002202	6093, 3480, 1021, 658, 558, 9641, 7048	3.314397	0.966827	0.366827	13.2046
GOTERM_MF_DIRECT	GO:0005525~GTP binding	7	10.14493	0.005578	6093, 3480, 1021, 658, 558, 9641, 7048	3.25811	0.931021	0.257035	12.69269
INTERPRO	IPR027417:P-loop containing nucleoside triphosphate hydrolase	7	10.14493	0.008185	6093, 3480, 1021, 658, 558, 9641, 7048	2.922968	0.772921	0.297243	8.132921
Annotation Cluster 2			Enrichment Score: 1.1690672404320173						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR017441:Protein kinase, ATP binding site	4	5.797101	0.088106	388, 387, 57799, 3845	3.751847	1	0.865198	73.28044
UP_SEQ_FEATURE	domain:Protein kinase	4	5.797101	0.104556	388, 387, 57799, 3845	3.47843	1	0.336893	74.5316
INTERPRO	IPR000719:Protein kinase, catalytic domain	4	5.797101	0.201399	388, 387, 57799, 3845	2.54846	1	0.813176	94.85441
INTERPRO	IPR011009:Protein kinase-like domain	4	5.797101	0.620938	388, 387, 57799, 3845	1.241986	1	1	99.99967
Annotation Cluster 3			Enrichment Score: 0.8240050727833905						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR

KEGG_PATHWAY	hsa04662: B cell receptor signaling pathway	3	4.347826	0.097872	3725, 3845, 5296	5.563607	1	0.22057	70.77023
GOTERM_BP_DIRECT	GO:0038095~Fc-epsilon receptor signaling pathway	3	4.347826	0.162338	3725, 3845, 5296	4.101612	1	0.829416	94.34144
KEGG_PATHWAY	hsa04915: Estrogen signaling pathway	3	4.347826	0.17569	3725, 3845, 5296	3.877666	1	0.351151	90.04632
KEGG_PATHWAY	hsa05231: Choline metabolism in cancer	3	4.347826	0.181198	3725, 3845, 5296	3.80088	1	0.356596	90.81213
Annotation Cluster 4			Enrichment Score: 0.2177609173953829						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
INTERPRO	IPR015880:Zinc finger, C2H2-like	4	5.797101	0.522885	57621, 7227, 4150, 6935	1.432685	1	1	99.99336
INTERPRO	IPR007087:Zinc finger, C2H2	4	5.797101	0.555328	57621, 7227, 4150, 6935	1.36634	1	1	99.99734
SMART	SM00355: ZnF_C2H2	4	5.797101	0.765176	57621, 7227, 4150, 6935	0.996088	1	1	99.99998
Annotation Cluster 5			Enrichment Score: 0.19675435143030948						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	3	4.347826	0.563826	57621, 4150, 6935	1.574557	1	0.999999	99.9993
UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	3	4.347826	0.621212	57621, 4150, 6935	1.418381	1	1	99.99991
INTERPRO	IPR013087:Zinc finger C2H2-type/integrase DNA-binding domain	3	4.347826	0.733418	57621, 4150, 6935	1.149971	1	1	100
Annotation Cluster 6			Enrichment Score: 0.05445250695329712						
Category	Term	Count	%	PValue	Genes	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_KEYWORDS	Transmembrane helix	16	23.18841	0.870252	658, 596, 599, 4035, 914, 858, 3690, 8754, 351, 3480, 8829, 558, 4582, 7852, 7048, 999	0.847072	1	0.995601	100
UP_KEYWORDS	Transmembrane	16	23.18841	0.873388	658, 596, 599, 4035, 914, 858, 3690, 8754, 351, 3480, 8829, 558,	0.844524	1	0.995546	100

					4582, 7852, 7048, 999				
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	16	23.18841	0.903214	658, 596, 599, 4035, 914, 858, 3690, 8754, 351, 3480, 8829, 558, 4582, 7852, 7048, 999	0.818488	1	0.999951	100