

Supplementary Figure 1: TargetScan workflow

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TargetScanHuman 7.2
Release 7.2: March 2018
Agarwal et al., 2015

Search for predicted microRNA targets in mammals

1. Select a species: Human

2. Enter a human gene symbol (e.g. "Hmga2") or an Ensembl gene (ENSG00000149948) or transcript (ENST00000403681) ID

3. Do one of the following:

- Select a broadly conserved* microRNA family: miR-137
- Select a conserved* microRNA family: Conserved microRNA families
- Select a poorly conserved but confidently annotated microRNA family: Poorly conserved microRNA families
- Select another miRBase annotation (Other miRBase annotations)
- Enter a microRNA name (e.g. "miR-9-5p")

Select the microRNA of choice and click on submit button

B

Human | miR-137

1314 transcripts with conserved sites, containing a total of 1498 conserved sites and 326 poorly conserved sites.

Please note that these predicted targets include some false positives. [Read more]

Genes with only poorly conserved sites are not shown. [View top predicted targets, irrespective of site conservation]

Table sorted by cumulative weighted context++ score [Sort table by aggregate PCT]

The table shows at most one transcript per gene, selected for being the most prevalent, based on 3P-seq tags (or the one with the longest 3' UTR, in case of a tie). [Download table]

Target gene	Representative transcript	Gene name	Number of 3P-seq tags supporting UTR + 5'	Link to sites in UTRs	Conserved sites			Poorly conserved sites			Representative miRNA	Cumulative weighted context++ score	Total context++ score	Aggregate PCT	Previous TargetScan publication(s)			
					total	8mer	7mer	total	8mer	7mer								
POLM3	ENST00000284770.5	PDZ and LIM domain 3	58	Sites in UTR	1	1	0	0	3	1	1	0	hsa-miR-137	-0.88	-0.95	< 0.1	2007, 2009, 2011	
RAVER2	ENST00000371672.4	ribonucleoprotein, PTD-binding 2	218	Sites in UTR	2	2	0	0	0	0	0	0	hsa-miR-137	-0.84	-0.84	> 0.99	2007, 2009, 2011	
NXT2	ENST00000372106.1	nuclear transport factor 2-like export factor 2	390	Sites in UTR	2	2	0	0	0	0	0	0	hsa-miR-137	-0.83	-0.83	0.92	2007, 2009, 2011	
MAPK10	ENST00000395169.3	mitogen-activated protein kinase 10	5	Sites in UTR	4	2	2	0	0	0	0	1	hsa-miR-137	-0.83	-0.83	> 0.99	2011	
ESRRG	ENST00000361525.3	estrogen-related receptor gamma	5	Sites in UTR	4	0	3	1	0	0	0	0	1	hsa-miR-137	-0.79	-0.79	> 0.99	2007, 2009, 2011
RPS13	ENST00000252634.1	ribosomal protein S13	41	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.78	-0.78	ORF	2007, 2009, 2011	
MTF	ENST00000328528.6	microphthalmia-associated transcription factor	593	Sites in UTR	4	2	1	1	1	1	0	0	hsa-miR-137	-0.77	-0.85	> 0.99	2011	
OSGEP	ENST00000355666.1	D-sialylglycoprotein endoepitope	335	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.72	-0.72	0.87	2009, 2011	
TMSB15B	ENST00000354223.1	thymosin beta 15B	211	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.72	-0.72	< 0.1	2011	
APL2	ENST00000258530.3	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	434	Sites in UTR	1	1	0	0	1	1	0	0	hsa-miR-137	-0.71	-0.73	< 0.1	2009, 2011	
TCF4	ENST00000354452.3	transcription factor 4	394	Sites in UTR	2	1	0	1	0	0	0	0	hsa-miR-137	-0.71	-0.84	0.99	2009, 2011	
NEUROD4	ENST00000242994.3	neuronal differentiation 4	5	Sites in UTR	2	2	0	0	0	0	0	1	hsa-miR-137	-0.71	-0.71	0.94	2009, 2011	
KLF12	ENST00000377669.2	Kruppel-like factor 12	251	Sites in UTR	4	3	1	0	1	0	1	0	3	hsa-miR-137	-0.69	-0.74	> 0.99	2007, 2009, 2011
SOCG	ENST00000218667.3	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	5	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.68	-0.68	0.81	2011	
ASPH	ENST00000356457.5	aspartate beta-hydroxylase	3013	Sites in UTR	2	1	0	1	1	0	0	1	hsa-miR-137	-0.68	-0.83	0.91	2007, 2009, 2011	
SERP1	ENST00000239944.2	stress-associated endoplasmic reticulum protein 1	3242	Sites in UTR	1	1	0	0	1	1	0	0	hsa-miR-137	-0.68	-1.05	0.92	2007, 2009, 2011	
TMEM218	ENST0000032156.1	transmembrane protein 218	553	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.67	-0.68	< 0.1	2007, 2009, 2011	
EPHA7	ENST00000365303.4	EPH receptor A7	213	Sites in UTR	3	2	1	0	0	0	0	0	hsa-miR-137	-0.66	-0.73	0.99	2007, 2009, 2011	
EPHA2	ENST00000355666.1	EPH receptor A2	5	Sites in UTR	4	3	1	0	0	0	0	0	hsa-miR-137	-0.65	-0.65	0.93	2007, 2009, 2011	

Supplementary Figure 2: ToppGene Suite workflow

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ToppGene Suite

A one-stop portal for gene list enrichment analysis and candidate gene prioritization based on functional annotations and protein interactions network

ToppFun: Transcriptome, ontology, phenotype, proteome, and pharmacome annotations based gene list functional enrichment analysis

Select your gene identifier type, paste your sets below or select example set, then submit.

Entry Type:

Example gene sets: (click on "HGNC Symbol" or "Entrez ID" to use the example training and test set of genes)

Training Gene Set:

Paste the genes here

Clear Submit

B

Results

Go To Start Page

Input Parameters [Show Data]

Training Results [Legend: N] [Download: N] [Source: Matrix] Display p-values and Scores as: Scientific (4 significant digits) Table row limit: 50

1: GO: Molecular Function [Display Chart] 3160 input genes in category / 2718 annotations before applied cutoff / 18881 genes in category

ID	Name	Source	pValue	FDR BH	FDR BH*	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0003700 DNA-binding transcription factor activity	6.556E-4	1.71E-4	1.457E-3	1.834E-4	305	1294	
2	GO:0046873 metal ion transmembrane transporter activity	1.223E-7	1.71E-4	1.457E-3	3.423E-4	129	426	
3	GO:0043585 sequence-specific DNA binding	7.866E-6	4.801E-3	4.086E-2	1.977E-2	253	1096	
4	GO:0019101 ubiquitin-like protein transferase activity	7.721E-6	4.801E-3	4.086E-2	2.160E-2	116	441	
5	GO:0011967 regulatory region nucleic acid binding	1.827E-5	4.801E-3	4.086E-2	2.873E-2	205	886	

Show 24 more annotations

2: GO: Biological Process [Display Chart] 3365 input genes in category / 8995 annotations before applied cutoff / 19623 genes in category

ID	Name	Source	pValue	FDR BH	FDR BH*	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0048738 cardiac muscle tissue development	3.709E-4	3.709E-4	3.629E-3	3.709E-4	72	215	
2	GO:0048729 tissue morphogenesis	2.122E-7	9.171E-4	8.976E-3	2.121E-3	183	782	
3	GO:0060537 muscle tissue development	3.683E-7	9.171E-4	8.976E-3	3.691E-3	119	415	
4	GO:0007167 enzyme linked receptor protein signaling pathway	3.896E-7	9.171E-4	8.976E-3	3.861E-3	240	1016	
5	GO:0007087 heart development	4.588E-7	9.171E-4	8.976E-3	4.584E-3	155	585	

Show 45 more annotations

3: GO: Cellular Component [Display Chart] 3410 input genes in category / 1155 annotations before applied cutoff / 15861 genes in category

ID	Name	Source	pValue	FDR BH	FDR BH*	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0005759 Golgi stack	5.686E-4	5.453E-3	4.175E-2	6.752E-3	45	132	
2	GO:0005758 endosome	5.284E-4	5.453E-3	4.175E-2	1.891E-2	191	626	
3	GO:0044031 Golgi apparatus part	2.803E-5	1.023E-2	7.035E-1	3.073E-2	214	928	
4	GO:0005139 Golgi membrane	3.462E-5	1.023E-2	7.035E-1	4.890E-2	170	716	
5	GO:0011984 organelle subcompartment	5.322E-5	1.261E-2	8.816E-1	6.105E-2	90	341	

Show 24 more annotations

4: Human Phenotype [Display Chart] 885 input genes in category / 1518 annotations before applied cutoff / 4707 genes in category

ID	Name	Source	pValue	FDR BH	FDR BH*	Bonferroni	Genes from Input	Genes in Annotation
1	HP:0100687 Brachydactyly (hand)	7.737E-4	1.603E-2	1.696E-1	4.764E-2	91	319	
2	HP:0001056 Brachydactyly	6.278E-4	1.603E-2	1.696E-1	6.016E-2	127	483	
3	HP:0010207 Short digit	6.278E-4	1.603E-2	1.696E-1	6.016E-2	127	483	
4	HP:0100532 Pulmonary sequestration	2.044E-5	2.304E-2	2.219E-1	1.203E-1	19	39	
5	HP:0000750 Delayed speech and language development	2.225E-5	2.304E-2	2.219E-1	1.363E-1	109	407	

Show 18 more annotations