

Supplementary Figure 1: TargetScan workflow

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TargetScanHuman 7.2
 Prediction of microRNA targets
 Release 7.2: March 2018 Agawal et al., 2015

Search for predicted microRNA targets in mammals
 [Go to TargetScanMouse]
 [Go to TargetScanWorm]
 [Go to TargetScanFly]
 [Go to TargetScanFish]

1. Select a species: Human

AND

2. Enter a human gene symbol (e.g. "Hmga2") or an Ensembl gene (ENSG0000049948) or transcript (ENST00000403681) ID

AND/OR

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")

[Submit] [Reset]

* broadly conserved = conserved across most vertebrates, usually to zebrafish
 conserved = conserved across most mammals, but usually not beyond placental mammals

TargetScan predicts biological targets of miRNAs by searching for the presence of conserved 8mer, 7mer, and 6mer sites that match the seed region of each mRNA (Lewis et al., 2005). As an option, predictions with only poorly conserved sites are also provided. Also identified are sites with mismatches in the seed region that are compensated by conserved 3' pairing (Friedman et al., 2009) and centered sites (Shin et al., 2010). In mammals, predictions are ranked based on the predicted efficacy of targeting as calculated using cumulative weighted context++ scores of the sites (Agawal et al., 2015). As an option, predictions are also ranked by their probability of conserved targeting (P_{CT}; Friedman et al., 2009). TargetScanHuman considers matches to human 3' UTRs and their orthologs, as defined by UCSC whole-genome alignments. Conserved targeting has also been detected within open reading frames (ORFs). A listing of these ORF sites can be found at the bottom of Supplemental Table 2 of Lewis et al., 2005.

This search page of TargetScan Release 7.2 retrieves predicted regulatory targets of mammalian microRNAs. Many targets are the same as those presented in previous versions of the TargetScan site (Releases 2.0, 2.1, 3.0, 3.1, 4.0, 4.2, 5.0, 5.2, 6.0, 6.2, 7.0 and 7.1 (Lewis et al., 2005; Grimson et al., 2007; Friedman et al., 2009; Garcia et al., 2011). Compared to previous releases, Release 7 uses an improved method to predict targeting efficacy the context++ model (Agawal et al., 2015), uses 3' UTR profiles that indicate the fraction of mRNA containing each site (Nawa et al., 2014), and uses updated miRNA families curated from Chiaroni et al., 2014 and Friedman et al., 2015.

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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 P_{CT}]

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			8mer sites	Representative miRNA	Cumulative weighted context++ score	Total context++ score	Aggregate P _{CT}	Previous TargetScan publication(s)	
					total	8mer	7mer	6mer	total	7mer							6mer
POLM3	ENST00000284770.5	POZ 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	ENST00000371072.4	ribonucleoprotein, PTB-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	ENST00000361529.3	estrogen-related receptor gamma	5	Sites in UTR	4	0	3	1	0	0	0	1	hsa-miR-137	-0.79	-0.79	> 0.99	2007, 2009, 2011
RPS13	ENST0000025634.1	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
MTF	ENST00000328528.6	microphthalmia-associated transcription factor	593	Sites in UTR	4	2	1	1	1	0	0	0	hsa-miR-137	-0.77	-0.85	> 0.99	2011
OSGEP	ENST00000555866.1	D-sialylglycoprotein endoepididymase	335	Sites in UTR	1	1	0	0	0	0	0	0	hsa-miR-137	-0.72	-0.72	0.87	2009, 2011
TMS615B	ENST00000540220.1	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
APPL2	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	ENST00000242984.3	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	3	hsa-miR-137	-0.69	-0.74	> 0.99	2007, 2009, 2011
SOCG	ENST00000218667.3	sarcoglycan, gamma (350kDa 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	313	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	ENST00000532156.1	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	ENST00000369303.4	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	ENST00000369303.4	EPH receptor A2	5	Sites in UTR	4	3	1	0	0	0	0	0	hsa-miR-137	-0.66	-0.66	0.93	2007, 2009, 2011

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