Supplementary Figure 1: TargetScan workflow

-	Targe Prediction of mic	ScanHuman croRNA targets Release 7.	2: March 2018	Agan	wal et al.,	2015														
earch fo	r predicted n	nicroRNA targets in mammals	[Go to Targe [Go to Targe [Go to Targe [Go to Targe	etSca etSca	nWorm nFly]															
Select a sp	becies Human	·	[Go to range	etoca																
Enter a hu er an Ense	man gene symbo embl gene (ENSG	l (e.g. "Hmga2") 00000149948) or transcript (ENST000004036	681) ID	s	elect		em cko						nice and	t						
D/OR	the following:		/	-		UII		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Jub		bu	nuo								
		microRNA family miR-137																		
		A family Conserved microRNA families •																		
Select a po	corly conserved bu	it confidently annotated microRNA family Poorty	ly conserved microRNA fa	amilies *																
Select ano	ther miRBase ann at of these families	otation Other miRBase annotations are star miRNAs or RNA fragments misannotal	ted as miRNAs														•			
	croRNA name (e.g																			
bmit Rese																				
adly conserved = co	ved = conserved acros nserved across most n	s most vertebrates, usually to zebrafish nammals, but usually not beyond placental mammals																		
getScan pr	redicts biological ta sites with mismatc	argets of miRNAs by searching for the presence hes in the seed region that are compensated by scores of the sites (Agarwal et al., 2015). As an	y conserved 3' pairin	ng (Frie	dman et al	, 2009) and c	entered	sites i	Shin e	t al., 2	010).	In mammals, pr	edictions a	re ranked	based on	the predicted	efficacy of targ	eting as calci	ulated usi
ned by UC	CSC whole-genome	e alignments. Conserved targeting has also bee	en detected within op	pen rea	ding frame	s (ORI	Fs). A I	sting of	f these	ORF s	sites ca	an be f	found at the bot	tom of Sup	plemental	Table 2 o	f Lewis et al.,	2005.		
(Lewis et a	age of TargetScan al., 2005; Grimson ImPNA containing	Release 7.2 retrieves predicted regulatory targ et al., 2007; Friedman et al., 2009; García et al each site (Nam et al., 2014), and uses undated	al., 2011). Compared	to prev	ious releat	ses Re	elease	USES 8	an impi	se pres roved n	methoo	d to pre	edict targeting e	efficacy (the	e context+	+ model,	es 2.0, 2.1, 3. Agarwal et al.	, 3.1, 4.0 - 4.2 , 2015), uses 3'	UTR profiles	that indic
5-2018 Whiteh	esearch Computing ead Institute for Biomedical	Research					2010 c Targets Questions	can Relea barcewi	ise 7.2 i.mit.edu									v	Thitehead Institute	for Biomedica C
O Typ	pe here to search	🕘 🛱 🧮 😫	TargetScanHuman															rft		E 6/14/2
Targetscan	Human 7.2: predicted	× +																		-
· > C			tscan.cgi?species=Huma	an&gid=	&mir_sc=m	R-1378	lmir_c=8	tmir_nc=	=8tmir_v	nc=&m	iirg=									- \$
→ C Apps	Not secure Not secure Prediction of mi R-137 ipts with conserve	tScanHuman	1.2: March 2018 tes and 326 poorly co	Agar	wal et al.,		amir_c=8	omir_nc=	=8cmir_v	nc=&m	iirg=									÷
Apps Apps Apps Apps Apps Apps Apps Apps	Not secure Not secure Prediction of mi R-137 ipts with conserve that these predicte only poorly conserv by cumulative wei	d sites, containing a total of 1498 conserved sitt d sites, containing a total of 1498 conserved sitt d sites, containing a total of 1498 conserved sitt d targets include some false positives. [Read pield context+ score. [Sort table by agg	1.2: March 2018 tes and 326 poorly or more] redicted targets, irre regate Pct]	Agar	wal et al.,	2015	ation]					a tie)	Downloa	sri table]						☆
→ C Apps	Not secure Not secure Prediction of mi R-137 ipts with conserve that these predicte only poorly conserv by cumulative wei	www.targetscan.org/cgi-bin/targetscan/vert_72/target ScanHuman croRNA targets d sites, containing a total of 1498 conserved site d targets include some false positives. [Read to d targets seare not show. [Vew top p	tes and 326 poorly cc more] predicted targets, irre regate Pc1] prevalent, based on : Name Page	Agar	wal et al., ed sites. e of site co tags (or th Link to sites in	2015 onserva	ation]	longes	at 3' UT	R, in c v conset	ase of rved sit	tes 6m 1er- sit	[Downloa er Representative mRNA	ad table] Cumulative weighted context=	2 Total context+	Aggregat	Previous IngetScan			÷
Apps Apps	Not secure	d sites, containing a total of 1498 conserved site of largets include some false positives [Read r yield context+2 coces] Gottalible by aggr anscript per gene, selected for being the most p Gere name	1.2: March 2018 tes and 326 poorly co more] regate Pcr] prevalent, based on 7 gr up up up up	Agar onserve spectiv 3P-seq ags porting R+5	wal et al., ed sites. e of site co tags (or th Link to sites in UTRs	2015 DINSERVA Corr total 8r	ation] with the nserved 7mer 7met	longes r- 7mer- A1	st 3' UT Poorh r total 8	R, in c gronset mer 7m	ase of rved sit	tes Grin Al	er Representativ es miRNA	e Cumulativ weighted context++ score	context+ score		publication(s)			÷
Apps Apps	Not secure Add secure A	d sites, containing a total of 1498 conserved still distes, containing a total of 1498 conserved still not targets include some false positives. [Read a ved sites are not shown. Vew top p ginted context++ score (Sort table by agg) core selected for being the most p Ceres same PDZ and LM domain 3	1.2: March 2018 tes and 326 poorly co more] regate Pcr] prevalent, based on Num seg seg seg seg seg seg seg seg	Agar onserve spectiv 3P-seq ags porting R+5 58 2	wal ef al., ed sites. e of site co tags (or th Link to sites in UTRs Sites in UTR	2015 Dinserva e one v Cor total 8n 1	ation] with the nserved 7mer 7mer 1 0	longes sites r. 7mer. A1 0	st 3' UT Poort total 8 3	R, in c consee	ase of rved sit	tes her- 1 0	er Representativ miRNA	e Cumulativ weighted context++ score	context+ score	< 0.1	publication(s) 2007, 2009, 2011			÷
Apps Apps Apps Apps Apps Apps Apps Apps	Not secure Not secure Prediction of min	A service of the serv	1.2: March 2018 tes and 326 poorly co more] regate Pcr] prevalent, based on Num seg seg seg seg seg seg seg seg	Agar onserve spectiv 3P-seq ags porting R+5 58 58 218 2	wal et al., ed sites. e of site co tags (or th Link to Sites in UTRs Sites in UTR	2015 Dinserva e one v Cor total 8r 1 2	ation] with the nserved 7mer 7met	Ionges sites r. 7merc A1 0 0	st 3' UT Poorty total 8 3 0	R, in c conset mer 7m 1 0	ase of rved sitting rved sittin	tes Ner- Sit 1 0 0 0	er Representativ miRNA) hsa-miR-137) hsa-miR-137	Cumulativ weighted context++ score -0.88 -0.84	-0.95		publication(s) 2007, 2009, 2011 2007, 2009, 2011			÷
Apps Apps Apps Apps Apps Apps Apps Apps	Not secure Not secure Prediction of mi R-137 Ips with conserve that these prediction Not secure that these prediction Ref R-137 Ips with conserve Ref Ref	A sites, containing a total of 1498 conserved site d sites, containing a total of 1498 conserved site d targets include some faite positives. (Field and d targets include some faite positives.) (Field and d targets targets and d targets and	12: March 2018 tes and 326 poorly co more] regate Pcr] prevalent, based on i regate 2 regate	Agar onserve ispectiv 3P-seq porting R+5 58 58 218 218 23390 5	wal et al., d sites. e of site co sites in UTRs Sites in UTR Sites in UTR	2015 0005erva 6 00e V Corr total 8n 1 2 2	ation] with the nserved 1 0 2 0 2 0	longessites sites 0 0 0	t 3' UT Poort total 8 3 0	R, in c v conset imer 7m 1 0	ase of sit ner- 7m ns 7m 1 1 0 (0 (tes her sit 1 0 0 0 0 0	es Representativ miRNA) hsa-miR-137) hsa-miR-137) hsa-miR-137	e Cumulativ weighted context+- score -0.88 -0.84 -0.83	-0.95 -0.84 -0.83	< 0.1 > 0.99 0.92	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011			
Apps Appp Apps Appp Apps Appp Appp Appp Appp	Not secure Not secure Tediction of mi	A sites, containing a total of 1498 conserved site croRNA torgets Release 7. d sites, containing a total of 1498 conserved site d targets include some false positives. [Read r d targets include some false some false to the some false PDZ and LM domain 3 riteoracleoprotein. PTB-binding 2 nuclear transport factor 2. His export factor 2 mitogen-activated protein kinase 10	1.2: March 2018 tes and 326 poorly co more] prevalent based on i support of the second support of the second s	Agar onserve ispectiv 3P-seq ass optimg R+5 58 58 218 5 5 5 5 5 5 5 5	wal et al., d sites. e of site co sites in UTRs Sites in UTR Sites in UTR	2015 DINSERVA 6 ONE V Corr total 8r 1 2 2 4	ation] with the mer 7mm 1 0 2 0 2 0 2 2	longes sites r- 7merc A1 0 0 0 0	t 3' UT Poorty total 8 3 0 0	R, in c ronset imer 7m 1 0 0	ase of rved sit ner- 7m A 1 1 2 0 0 0 0 0	tes Frincher Situation 1000000000000000000000000000000000000	er Representativ miRNA) hsa-miR-137) hsa-miR-137	e Cumulativ weighted context+- score -0.88 -0.84 -0.83	-0.95	< 0.1 > 0.99 0.92	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2011 2007, 2009,			ф.,
Apps C Apps A	Not secure Not secure rediction of mi	A sites, containing a total of 1498 conserved site of the second	12: March 2018 tes and 326 poorly co more] prevalent, based on i prevalent, based on i transport	Agar onserve ispectiv 3P-seq asporting 18+5 58 218 5 5 5 5 5 5 5 5 5	wal et al., d siles. e of sile cc sites in UTRS Sites in UTR Sites in UTR Sites in UTR Sites in UTR	2015 DINSERVA e ONE V total 8r 1 2 2 4 4 4 1	ation] with the mer 7ms 1 0 2 0 2 0 2 2 0 3 1 0	longess sites - 7mer- 741 0 0 0 0 0 0 1 1 0	t 3' UT Poort) total 8 3 0 0 0 0 0	R, in c / conset imer 7 n 1 0 3 0 0 0 0	ase of nor- 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0	tes 6m her- 1 0 0 0 0 1 0 1 0 1 0 0	Representative miRNA bisa-miR-137	Cumulativ weighted context++ score -0.88 -0.83 -0.83 -0.83 -0.79 -0.78	-0.95 -0.84 -0.83 -0.83 -0.79 -0.78	< 0.1 > 0.99 0.92 > 0.99 > 0.99 > 0.99 ORF	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2007, 2009, 2011			- *
Apps Apps	Not secure Not secure Not secure Not secure Not Not Secure Not Secure Not Secure Secure Not Secure Secur	d sites, containing a total of 1498 conserved site d sites, containing a total of 1498 conserved site d targets include some false postforwards d targets include some false postforwards d targets include some false postforwards d targets include some false postforwards (Sort table by aggr anscript per gene, selected for being the most p (Gene name) PDZ and LM domain 3 riboruckeproteik, PTB-kinding 2 rucker transport factor 2 2 mington-activated protein kinase 10 settogen-related receptor gamma	1.2: March 2018 Ites and 326 poorly co more] regate Pcr] revalent, based on a support revalent, based o	Agar onserve spectiv 3P-seq as spotting R+5 58 \$ 58 \$ 218 \$ 5	wal ef al., d sites. e of site cc tags (or th sites in UTR Sites in UTR Sites in UTR Sites in UTR	2015	ation] met 7mm 1 0 2 0 2 2 0 3 1 0 2 1	Iongess sites r. 7mer. A1 0 0 0 0 0 1 1 0 1	t 3' UT Poorb total 8 3 0 0 0 0 0	R, in c vorset mer 7 n 1 0 0 0 0 0 0	rase of rved sit ner 7m A 1 1 0 (0 (0 (0 (0 (0 (0 (0 (0 (0 (tes 6m her. 1 0 0 0 0 1 0 1 0 1 0 0 0 0 0 0	ee Representative miRNA) hsa-miR-137) hsa-miR-137) hsa-miR-137 1 hsa-miR-137 1 hsa-miR-137	Cumulativ weighted context+- score -0.88 -0.83 -0.83 -0.79	-0.95 -0.84 -0.83 -0.83 -0.79	< 0.1 > 0.99 0.92 > 0.99 > 0.99	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011			- *
Apps Apps	Not secure Not secure Not secure Not secure Not secure Not secure Not Not Secure Not Secure Not Secure Not Secure Secure Secure Not Secure	A sites, containing a total of 1498 conserved site croRNA torgets Release 7. d sites, containing a total of 1498 conserved site d targets include some false postfixews. [Read of d targets include some false postfixews [Read of d targets include some false postfixems] Geties name PDZ and LM domain 3 riteoraceleportein, PTB-binding 2 nuclear transport factor 2-bite sport factor 2 mitogen-atticated protein kinase 10 estrogen-related receptor gamma riteoraphyprobales 13 riteoraphyprobales 15 D site [B]	tes and 326 poorly co more] prevalent based on 3 prevalent, based on 3 prevalent based on 3 support of the second support of the sec	Agar onserve spectiv 3P-seq ass porting 5	wal et al., d sites. e of site cc tags (or th UTRs Sites in UTR Sites in UTR Sites in UTR Sites in UTR Sites in UTR	2015 DINSERVA E ONE V Corr total 8r 1 2 2 4 4 1 1 1 1	ation] with the net 7mm 7mm 7mm 7mm 7mm 7mm 7mm 7mm	Iongess Isites - 7mer- 7mer- 7mer- 7mer- 7mer- 10 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	st 3' UT Poorb 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	R, in c rouser imer 7 n 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of rved sit nor- 7m 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes 6m sit 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Representative miRNA ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137	Currulativ veighted context+ score -0.88 -0.84 -0.83 -0.83 -0.83 -0.79 -0.78 -0.77 -0.72 -0.72	-0.95 -0.84 -0.83 -0.83 -0.79 -0.76 -0.85 -0.72 -0.72	< 0.1 > 0.99 0.92 > 0.99 > 0.99 > 0.99 ORF 0.87 < 0.1	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2009, 2011 2011			÷ ()
Apps Apps	Not secure Not secure Not secure Not secure Not secure Not secure Not Not Secure Not Secure Not Secure Not Secure Secure Not Secure	A sites, containing a total of 1498 conserved site coRNA targets d sites, containing a total of 1498 conserved site d targets include some false postfixers. [Read of d targets include some false postfixers.] [Soft false postfixers.] [Cette tanget false of the sopt factor 2 mitogen-activated protein kinase 10 estrogen-related receptor gamma intercomptones associated transcription factor O-alatelycoprotein endoperdises thought protein Sta adaptor protein, phosphotycosine isteraction. PH domain containing 2	tes and 326 poorly co more] prevalent based on a prevalent, based on a support of the second	Agar onserve spectiv 3P-seq ass porting 5	wal et al., d siles. e of sile cc sites in UTR Sites in UTR	2015 DINSELVA 6 ONE V Corr total 8r 1 2 4 4 1 1 1 1 1 1	ation] with the nserved met 7ms 1 0 2 0 2 0 3 1 0 2 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	Iongess sites (- 7mer- 741 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0 0	t 3' UT Poorb total 8 3 0 0 0 0 0 0 0 1 1 0 0 1	R, in conserver reconserver 11 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of rved sit nor- 7m 1 0	tes Fin ner-sit sit 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ee Representative miRNA ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137	Currulativ veighted context+ score -0.88 -0.83 -0.83 -0.83 -0.83 -0.83 -0.77 -0.78 -0.77 -0.72 -0.72 -0.71	-0.95 -0.84 -0.83 -0.83 -0.79 -0.78 -0.72 -0.72 -0.72 -0.73	< 0.1 > 0.99 0.92 > 0.99 > 0.99 0.000 0.000 0.000 < 0.1 < 0.1	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2011 2011 2009, 2011			÷ (
Apps Apps	Not secure N	A sites, containing a total of 1498 conserved site coRNA targets d sites, containing a total of 1498 conserved site d targets include some false postfixers. [Read of d targets include some false postfixers.] [Soft false postfixers.] [Cette tanget false of the sopt factor 2 mitogen-activated protein kinase 10 estrogen-related receptor gamma intercomptones associated transcription factor O-alatelycoprotein endoperdises thought protein Sta adaptor protein, phosphotycosine isteraction. PH domain containing 2	12: March 2018 tes and 326 poorly comore] predicted targets, irre-regate Pc1 prevalent, based on a sed and leucine zipper and leucine zipper	Agar spectiv 3P-seq ags nber of -seq ags -seq ags -seq ags -seq	wal ef al., d sites. e of site cc UTRS Sites in UTR Sites in UTR	2015	ation] with the nserved 1 0 2 0 2 0 3 1 0 2 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	Ionges sites r. 7mer. A1 0 0 0 0 1 0 1 0 0 0 0 1 0 0 0 1	st 3' UT Poorf total 8 3 0 0 0 0 0 0 1 0 0 1 0 0 1 0 0	R, in c / conset mer 7 n 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of nor. 7m ns. 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes Fin ner-sit Sin 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ee Representative miRNA ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137 ba-miR-137	Currulativ veighted context+ score -0.88 -0.84 -0.83 -0.83 -0.83 -0.79 -0.78 -0.77 -0.72 -0.72	-0.95 -0.84 -0.83 -0.83 -0.79 -0.76 -0.85 -0.72 -0.72	< 0.1 > 0.99 0.92 > 0.99 > 0.99 > 0.99 ORF 0.87 < 0.1	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2011 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2009, 2011 2009, 2011			÷ (
	Not secure N	A sites, containing a total of 1498 conserved site croRNA torgets Release 7. d sites, containing a total of 1498 conserved site d targets include some false positives. [Read r d targets include some false positive some false [Soft false positive]. [Soft false by aggr anscript per gene, selected for being the most p Cethe name PDZ and LM domain 3 ritoracleoprotein, PTB-binding 2 nuclear transport factor 2-like export factor 2 mitogen-activated protein kinase 10 estrogen-related receptor gamma ritoracphalanias isociated transception factor O-ailadycoprotein endoppediase thronophalanias 13 adapter protein, phosphotyresine interaction, PH domain containing 2 transception tactor 4 Kuppel-like factor 12	tes and 326 poorly co more] prevalent, based on 3 prevalent, based on 3 und leucine zipper and leucine zipper 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Agar onserve spectiv 3P-seq ags nber of -seq ags optiming 12-seq ags 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	d sites. d sites. e of site cc tags (or th sites in UTR Sites in UTR	2015	ation] met 7m 1 0 2 0 2 2 0 3 1 0 2 1 1 0 1 0 1 0 1 0 1 0 2 1 1 0 2 1 1 0 2 1 1 0 2 1 1 0 2 0 2 0 3 1 1 0 2 0 3 1 1 0 2 0 2 0 3 1 1 0 2 0 2 0 3 1 1 0 2 0 2 0 3 1 1 0 2 0 3 1 1 0 2 0 2 0 3 1 1 0 2 0 2 0 3 1 1 0 2 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	Ionges ites r. 7mer. 741 0 0 0 0 1 1 0 0 0 1 1 0 0 1 0 0 1 0 0 1 0	st 3' UT Poort total 8 3 0 0 0 0 0 1 0 0 1 0 0 1 0 0 0 1 0	R, in c / conset mer 7 n 1 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of nor. 7m ns. 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes fm 1 0 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	er Representatives mRRA) hse-mR-137	Cumulativ weighted context+- score -0.88 -0.84 -0.83 -0.83 -0.83 -0.83 -0.79 -0.78 -0.77 -0.72 -0.72 -0.71 -0.71	Context+ score -0.95 -0.84 -0.83 -0.83 -0.83 -0.79 -0.78 -0.72 -0.72 -0.72 -0.73 -0.84	< 0.1 > 0.99 0.92 > 0.99 > 0.99 0.000 0.000 0.000 < 0.1 < 0.1 0.99	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2011 2011 2011 2011 2011 2009, 2011 2009, 2011			- -
	Not secure Secure Not s	A service of the	A March 2018 A March 2018 A March 2018 A more and 326 poorly co more) redicided targets, irre regate Pc;1 prevalent, based on i a more a m	Agar onserve spectiv 3P-seq ags porting 5 \$ 218 \$ 5 \$ 218 \$ 5 \$ 218 \$ 5 \$ 218 \$ 5 \$ 218 \$ 5 \$ 211 \$ 5 \$ 5 \$ 211 \$ 5	wal et al., d sites. e of site cc d sites in utra- sites in UTR sites in UTR	2015 DONSERVA E CONE V Cone	ation] with the nserved 1 0 2 0 2 0 2 0 2 1 1 0 2 1 1 0 2 1 1 0 2 1 1 0 2 1 1 0 3 1 1 0 1 0 1 0 2 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	Iongess ittes r 7mer A1 0 0 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 0	1 0 0 0 0 0 1 0 1 0 0 1 0 1 0 1	R, in c mer 7 n 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of rved sit nor- 7m A 1 1 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes Fm ner-sit sit 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 0 0	or ss Representation miRNA semiR-137 hse-miR-137 hse-miR-137	Cumulativ weighted context+- score -0.88 -0.83 -0.83 -0.83 -0.83 -0.83 -0.79 -0.77 -0.77 -0.72 -0.72 -0.71 -0.71 -0.71 -0.69 -0.68	Context+ score -0.95 -0.84 -0.83 -0.83 -0.83 -0.79 -0.78 -0.85 -0.72 -0.72 -0.72 -0.73 -0.84 -0.71 -0.74 -0.66	< 0.1 > 0.99 0.92 > 0.99 > 0.99 ORF > 0.99 0.87 < 0.1 < 0.1 0.99 0.94 > 0.99 0.81	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2010, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011			
	Not secure N	A sites, containing a total of 1498 conserved 3 d sites, containing a total of 1498 conserved 3 met and the second second second 3 d sites are not shown. View top p philed context++ score Containing a mercip per gene, selected for being the most pr d second second 3 d sites are not shown. View top p philed context++ score Containing a d second second 3 d sec	A March 2018 A more) Insert and 326 poorly component Insert and sead on a	Agar onserve spectiv 3P-seq ags porting 18+5 5 8 8 5 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5	wal ef al., add sites. e of site co tags (or the sites is of the site of sites in UTR Sites in UTR	2015 DISERVA 8 ONE V Coo 1 2 3 4 1 1 4 1 1 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 4 1 1 1 2 2 4 4 4 1 1 1 2 2 4 4 4 4 1 1 1 1 2 2 4 4 4 4 1 1 1 1 2 2 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1	ation] with the nserved rm 1 0 2 0 2 0 2 0 3 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0	Ionges ites r. 7mer. A1 0 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 0 0 0 1 1 0 0 0 1	3 UT 1 total 8 3 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	R, in c y conset mer 7 n 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	asso off nrved sill nst 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes Em ner-sit sit 1 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 3 0 0 1 0	or ss Representation miRNA a hsa-miR-137 b hsa-miR-137	Currulativ weighted context	Context+ score -0.95 -0.84 -0.83 -0.83 -0.79 -0.78 -0.72 -0.73 -0.73 -0.73 -0.71 -0.74 -0.68 -0.85	< 0.1 > 0.99 0.92 > 0.99 > 0.99 ORF > 0.99 0.87 < 0.1 < 0.1 0.99 0.94 > 0.99 0.94 > 0.99 0.81 0.91	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011			×
	Not secure N	A sites, containing a total of 1498 conserved 31 Sectors 21 Sectors 21 Sectors 21 Sectors 22 Sectors	A March 2018 A more) redicted targets, irre- regate P _{C1} revalent, based on a redicted targets, irre- regate P _{C1} revalent, based on a redicted targets, irre- revalent, based on a redicted targets, irre- reditargets, irre- redicted targets, irre-	Agar onserver spectiv 3P-seq ags porting 12+5 5 8 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8	wal ef al., add sites. e of site cc tags (of the units) sites in UTR Sites in UTR	2015 DINSELVE E ODE 1 C OT total 8 1 2 4 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 1 1 2 2 4 1 1 1 2 2 4 1 1 1 2 2 4 1 1 1 1 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1	ation] with the net 7m 7m 2 0 2 0 2 0 2 0 2 1 1 0 2 1 1 0 2 1 1 0 2 1 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	Ionges sites c. 7mer. A1 0 0 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 0 1	t 3' UT Poort total 0 3 0 0 0 0 0 1 0 0 1 0 0 1 0 0 1 1 0 0 1 1 0 0 1 1 0 1 1 0 1 1 0 1 1 0 1 1 1 1 0 1	R, in c / conset immer 7 m 1 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of nor- 7m ns 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0	tes Em mer-sit sit 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 1 0 0 0	or Representative mRNA basemR-137 hasemR-137 bhasmR-137 hasemR-137	Currulativ weighted context	Context+ score -0.95 -0.84 -0.83 -0.83 -0.79 -0.78 -0.72 -0.72 -0.72 -0.73 -0.73 -0.71 -0.71 -0.71 -0.71 -0.68 -0.83 -1.05	< 0.1 > 0.99 0.92 > 0.99 ORF > 0.99 ORF > 0.99 0.87 (0.1 0.99 0.94 > 0.99 0.81 0.91 0.91 0.91	publication(s) 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2007, 2009, 2011 2011 2011 2007, 2009, 2011			<u></u>
	Not secure N	A sites, containing a total of 1498 conserved site distagets include some false positives. (Read in wed sites, containing a total of 1498 conserved site and sites are of shown	A March 2018 A March 2018 A sand leucine zipper a s	Agar spectiv 3P-seq spectiv 3P-seq spectiv 3P-seq spectiv 3P-seq spectiv 3P-seq spectiv 3P-seq spectiv spe	wal et al., d siles. e of sile cc tags (or th sites in UTR Sites in UTR	2015	ation] with the net 7m 7m 7m 7m 7m 7m 7m 7m 7m 7m	longes ites 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1 3' UT Poort total 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	R, in c r conset imer 7 m 1 0 0 0 0 0 0 0 0 0 0 0 0 0	ase of nor- 7m nai 7m 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	tes Em ber-sit 6 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	or ss Representation miRNA a hsa-miR-137 b hsa-miR-137	Currulativ weighted context	Context+ score -0.95 -0.84 -0.83 -0.83 -0.79 -0.78 -0.72 -0.73 -0.73 -0.73 -0.71 -0.74 -0.68 -0.85	< 0.1 > 0.99 0.92 > 0.99 > 0.99 ORF > 0.99 0.87 < 0.1 < 0.1 0.99 0.94 > 0.99 0.94 > 0.99 0.81 0.91	publication(s) 2007, 2009, 2011 2011 2017, 2009, 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2009, 2011 2007, 2009, 2011 2011 2011 2007, 2009, 2011 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2011 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2011 2007, 2009, 2011 2007, 2009, 2011 2009, 2011 2007, 2009, 2007, 200			ά