Supplementary Table S2. Off-target filtering in essential gene candidates reveals 91 HC_OTEs and their re-scoring removes 16 corresponding genes. Seed heptamers are highlighted in red within the oligonucleotide sequence

Gene	Refseq ID	Supplier ID	Oligonucleotide sequence	Seed Freq$_{\mathrm{HITS}}$	Seed Freq$_{\mathrm{LIB}}$	p-value	miRNA matches	%3'UTR	Gene removed
ARHGEF1	NM_004706	TRCN0000033565	CCGGCATGGCAGAATGCCTGTTCTTCTCGAGAAGAACAGGCATTCTGCCATGTTTTTG	4	17	0.026	hsa-miR-4773	19	✓
CD300LF	NM_139018	TRCN0000060563	CCGGCCGTGCAGTGTGTTTACAGATCTCGAGATCTGTAAACACACTGCACGGTTTTTG	7	23	0.001	hsa-miR-3686	15	✓
CDC34	NM_004359	TRCN0000007301	CCGGGAGTGTGATCTCCCTCCTGAACTCGAGTTCAGGAGGGAGATCACACTCTTTTT	3	8	0.014	hsa-miR-4779	25	✓
CDC34	NM_004359	TRCN0000007300	CCGGTCGGGAGTACACAGACATCATCTCGAGATGATGTCTGTGTACTCCCGATTTTT	4	18	0.031	hsa-miR-654-3p	12	
DHX38	NM_014003	TRCN0000001171	CCGGGCAGTGGAAGAACAATAATTACTCGAGTAATTATTGTTCTTCCACTGCTTTTT	3	5	0.003	hsa-miR-944	26	✓
HS3ST3B1	NM_006041	TRCN0000035817	CCGGCAAGCACTTCTACTTCAACAACTCGAGTTGTTGAAGTAGAAGTGCTTGTTTTTG	7	37	0.012	hsa-miR-653	12	✓
IFITM1	NM_003641	TRCN0000057500	CCGGCTTCTTGAACTGGTGCTGTCTCTCGAGAGACAGCACCAGTTCAAGAAGTTTTTG	3	12	0.045	hsa-miR-3065-3p	15	✓
KISS1	NM_002256	TRCN0000059065	CCGGCCTGCCGAACTACAACTGGAACTCGAGTTCCAGTTGTAGTTCGGCAGGTTTTTG	5	29	0.045	hsa-miR-145	13	✓
KISS1	NM_002256	TRCN0000059064	CCGGGCAGCTAGAATCCCTGGGCCTCTCGAGAGGCCCAGGGATTCTAGCTGCTTTTTG	2	4	0.026	hsa-miR-1915	26	
LILRA2	NM_006866	TRCN0000056847	CCGGCGACAGATTTGTTCTGTATAACTCGAGTTATACAGAACAAATCTGTCGTTTTTG	4	20	0.044	hsa-let-7f-2-3p	13	✓
MS4A1	NM_021950	TRCN0000061522	CCGGCAGCATACAATCTCTGTTCTTCTCGAGAAGAACAGAGATTGTATGCTGTTTTTG	4	17	0.026	hsa-miR-4773	19	✓
OLR1	NM_002543	TRCN0000060521	CCGGGCAAACCTAACTCACCAGAAACTCGAGTTTCTGGTGAGTTAGGTTTGCTTTTTG	4	15	0.016	hsa-miR-4299	11	✓
PRSS12	NM_003619	TRCN0000050978	CCGGCGGCTTTGATTCTGTCCTCAACTCGAGTTGAGGACAGAATCAAAGCCGTTTTTG	4	19	0.037	hsa-miR-1224-5p	10	✓

RAB13	NM_002870	TRCN0000048122	CCGGCGAGAATATTCAGAACTGGATCTCGAGATCCAGTTCTGAATATTCTCGTTTTTG	5	29	0.045	hsa-miR-145	13	✓
RAMP3	NM_005856	TRCN0000060982	CCGGGAAGGCTTTCGCAGACATGATCTCGAGATCATGTCTGCGAAAGCCTTCTTTTTG	4	18	0.031	hsa-miR-654-3p	12	✓
TGS1	NM_024831	TRCN0000060828	CCGGGCTCGCAATAATGCAGAAGTTCTCGAGAACTTCTGCATTATTGCGAGCTTTTTG	7	36	0.010	hsa-mir-544a	17	✓
UBOX5	NM_014948	TRCN0000004439	CCGGCGGCGGTATCCCTTGTATCAACTCGAGTTGATACAAGGGATACCGCCGTTTTT	3	4	0.001	hsa-miR-381, hsa-miR-300	12	✓
XAB2	NM_020196	TRCN0000074412	CCGGGCAGTATGACATGTTCAACATCTCGAGATGTTGAACATGTCATACTGCTTTTTG	7	37	0.012	hsa-miR-653	12	✓
ABCB8	NM_007188	TRCN0000059876	CCGGTCACGAGTTCATCACCAGTTTCTCGAGAAACTGGTGATGAACTCGTGATTTTTG	4	15	0.016	hsa-miR-4299	11	
ACYP1	NM_001107	TRCN0000050444	CCGGCGACAAAGCAAACTTCAACAACTCGAGTTGTTGAAGTTTGCTTTGTCGTTTTTG	7	37	0.012	hsa-miR-653	12	
ANKH	NM_054027	TRCN0000059324	CCGGCCTGGGCTACTACAAGAACATCTCGAGATGTTCTTGTAGTAGCCCAGGTTTTTG	5	26	0.030	hsa-miR-578	14	
ANTXR1	NM_018153	TRCN0000063220	CCGGCAAGGCATCATCCACTCAATTCTCGAGAATTGAGTGGATGATGCCTTGTTTTTG	2	5	0.041	hsa-miR-4758-5p	10	
ARL9	NM_206919	TRCN0000065293	CCGGGCAGCCTATCACATTACAGATCTCGAGATCTGTAATGTGATAGGCTGCTTTTTG	7	23	0.001	hsa-miR-3686	15	
C19ORF61	NM_019108	TRCN0000061848	CCGGCCTAGTCTTCTTGCAGAACAACTCGAGTTGTTCTGCAAGAAGACTAGGTTTTTG	7	36	0.010	hsa-mir-544a	17	
CCDC76	NM_019083	TRCN0000062719	CCGGGCATTGTTATTGCACTCTGTTCTCGAGAACAGAGTGCAATAACAATGCTTTTTG	3	10	0.027	hsa-miR-4797-5p	16	
CD2BP2	NM_006110	TRCN0000057487	CCGGGTGTACCAGGAAACAAGGGAACTCGAGTTCCCTTGTTTCCTGGTACACTTTTTG	3	9	0.020	hsa-miR-623	10	
CD300C	NM_006678	TRCN0000062982	CCGGGCACCTCAGGTCCTCCCACGACTCGAGTCGTGGGAGGACCTGAGGTGCTTTTTG	3	5	0.003	hsa-miR-30b-3p, hsa-miR-3689a-3p, hsa-miR-3689b-3p, hsa-miR-3689c	35	
CDCA4	NM_145701	TRCN0000072627	CCGGGCTTGAAGACAGTGTCCTCATCTCGAGATGAGGACACTGTCTTCAAGCTTTTTG	4	19	0.037	hsa-miR-1224-5p	10	

CDK10	NM_003674	TRCN0000000689	CCGGCTACAACAACCTGAAGCACAACTCGAGTTGTGCTTCAGGTTGTTGTAGTTTTT	5	27	0.035	hsa-miR-218-5p	14	
CTHRC1	NM_138455	TRCN0000062247	CCGGGTGAAGGAATTGGTGCTGGATCTCGAGATCCAGCACCAATTCCTTCACTTTTTG	3	12	0.045	hsa-miR-3065-3p	15	
CYBB	NM_000397	TRCN0000064589	CCGGCTTGGCTGAAACCCTGAGTAACTCGAGTTACTCAGGGTTTCAGCCAAGTTTTTG	2	5	0.041	hsa-miR-1266, hsa-miR-4518	17	
CYP11A1	NM_000781	TRCN0000064276	CCGGGCTGAGCAAAGACAAGAACATCTCGAGATGTTCTTGTCTTTGCTCAGCTTTTTG	5	26	0.030	hsa-miR-578	14	
CYP2E1	NM_000773	TRCN0000064174	CCGGGCTCCAGCTTTACAATAATTTCTCGAGAAATTATTGTAAAGCTGGAGCTTTTTG	3	5	0.003	hsa-miR-944	26	
CYP2F1	NM_000774	TRCN0000064190	CCGGCGATGTCATCACCCTCCTTAACTCGAGTTAAGGAGGGTGATGACATCGTTTTTG	3	8	0.014	hsa-miR-4779	25	
CYP2R1	NM_024514	TRCN0000064501	CCGGGCCTCAGTCTTCTTGTATAATCTCGAGATTATACAAGAAGACTGAGGCTTTTTG	3	4	0.001	hsa-miR-381, hsa-miR-300	12	
DERL1	NM_024295	TRCN0000062913	CCGGCCTGCTATTTACCCTGGGTTACTCGAGTAACCCAGGGTAAATAGCAGGTTTTTG	2	4	0.026	hsa-miR-1915	26	
DNAJC16	XM_497656	TRCN0000064151	CCGGCCACATGAATGTGGTCCTCATCTCGAGATGAGGACCACATTCATGTGGTTTTTG	4	19	0.037	hsa-miR-1224-5p	10	
DOCK5	NM_024940	TRCN0000113804	CCGGGCGACTAATAGCATTACAGATCTCGAGATCTGTAATGCTATTAGTCGCTTTTTG	7	23	0.001	hsa-miR-3686	15	
DSCAM	NM_001389	TRCN0000063989	CCGGCCTCATACATTTGCCTCCATACTCGAGTATGGAGGCAAATGTATGAGGTTTTTG	2	5	0.041	hsa-miR-650, hsa-miR-3612	21	
DYNLT1	NM_006519	TRCN0000062181	CCGGCTGTGTAATTATGCAGAAGAACTCGAGTTCTTCTGCATAATTACACAGTTTTTG	7	36	0.010	hsa-mir-544a	17	
EIF4A3	NM_014740	TRCN0000061857	CCGGGCAGTACTATTCCACTCAGATCTCGAGATCTGAGTGGAATAGTACTGCTTTTTG	2	5	0.041	hsa-miR-4758-5p	10	
EIF4B	NM_001417	TRCN0000062602	CCGGCTACCCTATGATGTTACAGAACTCGAGTTCTGTAACATCATAGGGTAGTTTTTG	7	23	0.001	hsa-miR-3686	15	
ENC1	NM_003633	TRCN0000063900	CCGGCGAGTCTGCAATTAACTGGATCTCGAGATCCAGTTAATTGCAGACTCGTTTTTG	5	29	0.045	hsa-miR-145	13	

FCRLA	NM_032738	TRCN0000060517	CCGGGACTTGACTGATGCAAGGGAACTCGAGTTCCCTTGCATCAGTCAAGTCTTTTTG	3	9	0.020	hsa-miR-623	10	
FGF22	NM_020637	TRCN0000058600	CCGGCTCAGGCTTCTACGTGGCCATCTCGAGATGGCCACGTAGAAGCCTGAGTTTTTG	2	5	0.041	hsa-miR-588, hsa-miR-4701-5p	13	
FKBP3	NM_002013	TRCN0000063541	CCGGGATTCGTTTCTTGCAGAACATCTCGAGATGTTCTGCAAGAAACGAATCTTTTTG	7	36	0.010	hsa-mir-544a	17	
GDF2	NM_016204	TRCN0000058366	CCGGGCACATCTTGCTCTTCAACATCTCGAGATGTTGAAGAGCAAGATGTGCTTTTTG	7	37	0.012	hsa-miR-653	12	
GFOD2	NM_030819	TRCN0000064370	CCGGAGTGACACTCAACTTCAACATCTCGAGATGTTGAAGTTGAGTGTCACTTTTTTG	7	37	0.012	hsa-miR-653	12	
HYLS1	NM_145014	TRCN0000072619	CCGGCCCAATCCAAACCTCAGCATACTCGAGTATGCTGAGGTTTGGATTGGGTTTTTG	4	15	0.016	hsa-miR-4728-3p	13	
IFT57	NM_018010	TRCN0000063012	CCGGGCAGAAGATGATGCAGAATTACTCGAGTAATTCTGCATCATCTTCTGCTTTTTG	7	36	0.010	hsa-mir-544a	17	
IGSF10	NM_178822	TRCN0000144401	CCGGCAGGCGTATATCACTGTATAACTCGAGTTATACAGTGATATACGCCTGTTTTTTG	4	20	0.044	hsa-let-7f-2-3p	13	
IL12RB2	NM_001559	TRCN0000058159	CCGGCCTGGGTAACTCTAAGCACAACTCGAGTTGTGCTTAGAGTTACCCAGGTTTTTG	5	27	0.035	hsa-miR-218-5p	14	
IL18BP	NM_005699	TRCN0000058633	CCGGCTGCCTCAGTTAGAAGCACAACTCGAGTTGTGCTTCTAACTGAGGCAGTTTTTG	5	27	0.035	hsa-miR-218-5p	14	
IL1R2	NM_004633	TRCN0000058530	CCGGTGTCCATAATACCCTGAGTTTCTCGAGAAACTCAGGGTATTATGGACATTTTTG	2	5	0.041	hsa-miR-1266, hsa-miR-4518	17	
IL1RAP	NM_002182	TRCN0000058540	CCGGCCCAGTGCATAAACTGTATATCTCGAGATATACAGTTTATGCACTGGGTTTTTG	4	20	0.044	hsa-let-7f-2-3p	13	
IL4	NM_000589	TRCN0000058183	CCGGGTTGACCGTAACAGACATCTTCTCGAGAAGATGTCTGTTACGGTCAACTTTTTG	4	18	0.031	hsa-miR-654-3p	12	
INHA	NM_002191	TRCN0000063903	CCGGGCAGCACTGTGCTTGTATCTACTCGAGTAGATACAAGCACAGTGCTGCTTTTTG	3	4	0.001	hsa-miR-381, hsa-miR-300	12	
KDELR1	NM_006801	TRCN0000063251	CCGGGCTCTATCTCTTCAACTGGATCTCGAGATCCAGTTGAAGAGATAGAGCTTTTTG	5	29	0.045	hsa-miR-145	13	

KLHL2	NM_007246	TRCN0000064967	CCGGGCAGAAATTCAGGTTACAGAACTCGAGTTCTGTAACCTGAATTTCTGCTTTTTG	7	23	0.001	hsa-miR-3686	15	
LCP1	NM_002298	TRCN0000056493	CCGGGCGGACATTTAGGAACTGGATCTCGAGATCCAGTTCCTAAATGTCCGCTTTTTG	5	29	0.045	hsa-miR-145	13	
LENG8	NM_052925	TRCN0000061690	CCGGTGGAGGTCTCAAGTTCAACATCTCGAGATGTTGAACTTGAGACCTCCATTTTTG	7	37	0.012	hsa-miR-653	12	
LILRA4	NM_012276	TRCN0000060560	CCGGCTACATCAGATACACTCTGTACTCGAGTACAGAGTGTATCTGATGTAGTTTTTG	3	10	0.027	hsa-miR-4797-5p	16	
LILRP2	NM_024317	TRCN0000060449	CCGGCTATGACAAATTCACTCTGTACTCGAGTACAGAGTGAATTTGTCATAGTTTTTG	3	10	0.027	hsa-miR-4797-5p	16	
LSAMP	NM_002338	TRCN0000063937	CCGGCTGTGAACTATCCTCCCACTACTCGAGTAGTGGGAGGATAGTTCACAGTTTTTG	3	5	0.003	hsa-miR-30b-3p, hsa-miR-3689a-3p, hsa-miR-3689b-3p, hsa-miR-3689c	35	
LYRM1	NM_020424	TRCN0000064101	CCGGGCCAATTCATCTGCCTCCAATCTCGAGATTGGAGGCAGATGAATTGGCTTTTTG	2	5	0.041	hsa-miR-650, hsa-miR-3612	21	
MS4A3	NM_006138	TRCN0000061661	CCGGCCATAAATGGATCACCAGATTCTCGAGAATCTGGTGATCCATTTATGGTTTTTG	4	15	0.016	hsa-miR-4299	11	
MYO18A	NM_078471	TRCN0000034202	CCGGCGAATTGATGAAGAAGCACAACTCGAGTTGTGCTTCTTCATCAATTCGTTTTTG	5	27	0.035	hsa-miR-218-5p	14	
NDUFB2	NM_004546	TRCN0000064766	CCGGGAATTAGGTATCCCTCCTGATCTCGAGATCAGGAGGGATACCTAATTCTTTTTG	3	8	0.014	hsa-miR-4779	25	
NEURL	NM_004210	TRCN0000034224	CCGGCTCGGCTGTTATGCTGTTCTTCTCGAGAAGAACAGCATAACAGCCGAGTTTTTG	4	17	0.026	hsa-miR-4773	19	
NGF	NM_002506	TRCN0000058404	CCGGACTGGACTAAACTTCAGCATTCTCGAGAATGCTGAAGTTTAGTCCAGTTTTTTG	4	15	0.016	hsa-miR-4728-3p	13	
OR10X1	NM_001004477	TRCN0000061217	CCGGCACAGGTTGTAGCTTACAGATCTCGAGATCTGTAAGCTACAACCTGTGTTTTTG	7	23	0.001	hsa-miR-3686	15	
OR13A1	NM_001004297	TRCN0000062955	CCGGCCTCACAGGTAATGTCCTCATCTCGAGATGAGGACATTACCTGTGAGGTTTTTG	4	19	0.037	hsa-miR-1224-5p	10	
OR2T27	NM_001001824	TRCN0000061596	CCGGCCTCAGGGACATCCTGTATATCTCGAGATATACAGGATGTCCCTGAGGTTTTTG	4	20	0.044	hsa-let-7f-2-3p	13	

OR51D1	NM_001004751	TRCN0000060717	CCGGCCAGGAGATCGAGTTCAACATCTCGAGATGTTGAACTCGATCTCCTGGTTTTTG	7	37	0.012	hsa-miR-653	12	
OSMR	NM_003999	TRCN0000058683	CCGGGCACTCCATAAGGAATAATTTCTCGAGAAATTATTCCTTATGGAGTGCTTTTTG	3	5	0.003	hsa-miR-944	26	
PAFAH1B1	NM_000430	TRCN0000050964	CCGGCGTATGGGATTACAAGAACAACTCGAGTTGTTCTTGTAATCCCATACGTTTTTG	5	26	0.030	hsa-miR-578	14	
PDE5A	NM_001083	TRCN0000048746	CCGGCCTCGGTTCAATGCAGAAGTTCTCGAGAACTTCTGCATTGAACCGAGGTTTTTG	7	36	0.010	hsa-mir-544a	17	
PNN	NM_002687	TRCN0000072280	CCGGCGCATCGAATTTGCAGAACAACTCGAGTTGTTCTGCAAATTCGATGCGTTTTTG	7	36	0.010	hsa-mir-544a	17	
PNRC1	NM_006813	TRCN0000063279	CCGGGCATTTGAAGAAATCAGCATTCTCGAGAATGCTGATTTCTTCAAATGCTTTTTG	4	15	0.016	hsa-miR-4728-3p	13	
PROM1	NM_006017	TRCN0000062143	CCGGCCCAACATCATCCCTGTTCTTCTCGAGAAGAACAGGGATGATGTTGGGTTTTTG	4	17	0.026	hsa-miR-4773	19	
PSMD3	NM_002809	TRCN0000058122	CCGGCCATGAGGTTTCCTCCCAAATCTCGAGATTTGGGAGGAAACCTCATGGTTTTTG	3	5	0.003	hsa-miR-30b-3p, hsa-miR-3689a-3p, hsa-miR-3689b-3p, hsa-miR-3689c	35	
RARRES1	NM_002888	TRCN0000063373	CCGGCCCTTGGAAATAGTCAGCATACTCGAGTATGCTGACTATTTCCAAGGGTTTTTG	4	15	0.016	hsa-miR-4728-3p	13	
RBP5	NM_031491	TRCN0000059911	CCGGCTGGAACTGACTGCAAGGGATCTCGAGATCCCTTGCAGTCAGTTCCAGTTTTTG	3	9	0.020	hsa-miR-623	10	
SEMA6D	NM_020858	TRCN0000063212	CCGGGCAGTCTATTACAGACATAATCTCGAGATTATGTCTGTAATAGACTGCTTTTTG	4	18	0.031	hsa-miR-654-3p	12	
SORL1	NM_003105	TRCN0000062949	CCGGGCTGCTAGTAACTTTACAGAACTCGAGTTCTGTAAAGTTACTAGCAGCTTTTTG	7	23	0.001	hsa-miR-3686	15	
SOX30	NM_007017	TRCN0000017424	CCGGCCCTATTACGATGAAGCACAACTCGAGTTGTGCTTCATCGTAATAGGGTTTTT	5	27	0.035	hsa-miR-218-5p	14	
TNFRSF25	NM_003790	TRCN0000058512	CCGGCGGTGACTTCCACAAGAAGATCTCGAGATCTTCTTGTGGAAGTCACCGTTTTTG	5	26	0.030	hsa-miR-578	14	
TUBA4A	NM_006000	TRCN0000072401	CCGGTCTGTGAAACTGGTGCTGGAACTCGAGTTCCAGCACCAGTTTCACAGATTTTTG	3	12	0.045	hsa-miR-3065-3p	15	

TXN2	NM_012473	TRCN0000064199	CCGGGTTAGAGAAGATGGTGGCCAACTCGAGTTGGCCACCATCTTCTCTAACTTTTTG	2	5	0.041	hsa-miR-588, hsa-miR-4701-5p	13	
VPS26A	NM_004896	TRCN0000065140	CCGGGATCTTATTGTTCACCAGCTTCTCGAGAAGCTGGTGAACAATAAGATCTTTTTG	4	15	0.016	hsa-miR-4299	11	
VPS26B	NM_052875	TRCN0000065273	CCGGGCGGGACATCAACAAGAAGTTCTCGAGAACTTCTTGTTGATGTCCCGCTTTTTG	5	26	0.030	hsa-miR-578	14	