

Gene Symbol	Gene Name	siRNA ID	Antisense siRNA	RNAi-Screen:		RNAi-Screen:	
				filipin p-value (FDR)	Z-score	DiI-LDL p-value (FDR)	Z-score
AGR2 (poorly characterized)	anterior gradient homolog 2 (Xenopus laevis)	HSS116219	AUAUGUCUGAGUCCAGAUGAGUUGG	3.9E-01	0.3	7.8E-03	-0.6
		HSS116220	UUUCUUUAAAGCUUGACUGUGUGGG	2.0E-01	-1.6	1.4E-04	-1.0
		s20693	UACUGUCAGAGAUGGGUCaa	9.1E-01	0.1	3.1E-01	-0.2
		s20694	UUUCUUUAAAGCUUGACUGtg	3.9E-03	-3.6	1.7E-05	-1.0
ARMCX3 (poorly characterized)	armadillo repeat containing, X-linked 3	HSS122362	UAUACUCUUGCUCUCAUUGCUGUCA	1.5E-02	2.5	3.2E-01	-0.2
		HSS122363	AGACAUCUCAACCAAGCAAAGAACC	3.6E-02	-2.8	6.1E-04	-0.7
		s28338	UUCAUGUAUACUUUAAAGCCtg	4.7E-03	4.2	3.2E-01	-0.2
		s28339	AUACUCAUUAGUAAACAGUCat	9.8E-03	6.1	1.0E+0	0.0
DNAJB9 (poorly characterized)	DnaJ (Hsp40) homolog, subfamily B, member 9	HSS106408	UUGUCAGGGUGGUACUUCUAGGCCA	1.7E-04	6.0	2.4E-02	-0.8
		HSS106410	UGAACAGUCAGUGUAUGUAGUAACC	1.2E-03	3.7	6.6E-05	-1.1
		s8616	UCUUCGUUGAGUGACAGUCct	8.0E-01	-0.4	5.9E-01	-0.1
		s8618	UAGCAUCUGAGAGUGUUUCat	8.6E-01	-0.4	4.8E-01	0.2
DNAJC12 (poorly characterized)	DnaJ (Hsp40) homolog, subfamily C, member 12	HSS148264	UAGCGGGCUCGACUCUCUUCUUGG	9.1E-01	-0.1	6.1E-03	-0.8
		HSS183512	AACCGAAGAUAGUUAUCACAUCACC	5.4E-01	-0.6	2.7E-03	-0.9
		s32166	UCACUGAGUCAUUCAAAGCtt	6.5E-03	4.4	7.5E-01	0.0
		s32168	UUUGUUAACCGAAGAUAGtt	1.5E-02	-2.8	5.5E-01	0.0
DUSP4 (poorly characterized)	dual specificity phosphatas e 4	s4373	AAAGCUGAAGACGAACUGCga	2.2E-02	2.0	2.3E-01	0.4
		s4374	AUAGUGUCCUCAAAGUGGtt	2.8E-01	-0.8	7.1E-14	-1.8
		VHS40973	UACUCUAUGGCUUCAUGAACCCAGG	3.7E-01	-0.8	6.5E-06	-1.2
		VHS40975	AGACAUUCAACAGAGCCGUGAUGCC	3.0E-01	1.1	3.7E-04	-1.1
EIF2AK3 (poorly characterized)	eukaryotic translation initiation factor 2- alpha kinase 3	HSS114059	UUUACUGUGAAGAAACUCCACUGCC	2.7E-04	5.7	1.8E-01	-0.3
		HSS190343	UUCAGAAGAAGAUUUGCUACUGGUG	7.9E-01	0.0	1.2E-06	-1.2
		s18102	UCUUGUCCAUUUCGUCACta	1.6E-01	1.0	3.2E-06	0.9
		s18103	UUUGCGGAUUAUUCUUGUUGta	1.9E-01	1.1	2.4E-01	0.4
FADS1	fatty acid desaturase 1	HSS106078	UGAUGUGGAAGGCCACAAAGGGAUC	3.2E-01	1.2	1.7E-01	-0.3
		HSS106079	UAAUCAUCCAGGCCAAGUCCACCCA	1.3E-03	4.3	9.9E-02	-0.5
		s8207	UUUAGUGAGUGGAUGAUGUcg	5.0E-01	-0.5	6.3E-01	0.1
FAM117A (poorly characterized)	family with sequence similarity 117, member A	s37630	UCACCUUCUAGCUCUUGCCag	2.4E-01	1.0	8.1E-02	0.5
		s37631	ACUUGGAAAUCUCUUUCGgt	1.3E-01	1.5	2.3E-01	0.4
FASN	fatty acid synthase	s5031	UUGAUGAUCAGGUCCACGGgeg	6.1E-01	-0.5	5.1E-07	-1.2
		s5032	UUUCUCACAGAUACGCUCcat	1.8E-02	3.5	1.2E-02	-0.6
FGFBP1 (poorly characterized)	fibroblast growth factor binding protein 1	HSS115142	AUUGAGUGCACUCAACCUUGAGAGA	2.9E-02	2.1	2.0E-03	-0.8
		HSS190756	AAUAGACUCUCUCAUCCUUGAGCUU	1.7E-03	3.4	1.6E-02	-0.6
		s19392	AAAAUUCAUGGUCAAUUGag	3.5E-03	5.8	4.0E-09	1.5
		s19394	UUGAGCUUUAGGCAUGAGGtt	1.7E-02	4.3	3.3E-02	0.5
FKBP11 (poorly characterized)	FK506 binding protein 11, 19 kDa	s224198	UGUAUGUGAAGCGUGUCUCca	4.3E-02	1.9	4.9E-01	0.2
		s27896	UCUUAUACAGAGGGUCUCtg	1.5E-01	1.1	6.3E-01	0.0
HMGR	3-hydroxy- 3- methylgluta ryl- Coenzyme A reductase	HSS104864	UUUGCAUGCUCCUUGAACACCUAGC	1.8E-02	2.7	1.7E-01	0.4
		HSS179267	AUAAAUUCUCACAACAAGCUCCCA	4.4E-03	2.9	7.2E-01	0.0
		s143	UCCUUUUAUCACUGCGAACct	2.5E-02	3.7	1.3E-08	1.5
HSPA5 (poorly characterized)	heat shock 70kDa protein 5 (glucose- regulated protein, 78kDa)	HSS105076	UUCAAAUUUGGCCGAGUCAGGGUC	3.8E-03	4.5	3.0E-01	-0.1
		HSS105077	UACCCUUGUCUUCAGCUGUCACUCG	6.3E-02	1.7	6.0E-02	-0.4
		s6980	UCUAGUAUCAUGCGCUCct	1.3E-02	2.8	9.4E-01	0.0
		s6981	UACGCUACAGCUUCAUCUGgg	1.6E-01	-1.1	4.4E-01	0.3

IDH1 (poorly characterized)	isocitrate dehydrogenase 1 (NADP+), soluble	HSS105181	AAAUGAUUCGUGUCAUUUCAUCUCC	6.3E-02	1.4	1.7E-01	-0.4
		HSS105182	AAAUCAGUUGCUCUGUAUUGAUCC	6.8E-01	-0.9	7.0E-05	-1.2
		s7120	UCAAUUCCCAAUGAUUCGtg	3.0E-01	-0.8	1.1E-06	-1.2
		s7121	UUGGUGACUUGGUCGUUGGtg	8.3E-02	1.7	2.6E-01	-0.3
INSIG1	insulin induced gene 1	s7465	AAGAGAGUGACAUUCCUCUgg	6.6E-01	0.2	2.9E-15	2.0
		s7466	UUUGGAUAAAUAUUAUUCt	4.1E-01	0.6	1.5E-02	-0.6
ISG20 (poorly characterized)	interferon stimulated exonuclease gene 20kDa	HSS142681	UAAUCGGUGAUCUCUCCUCAGGCC	2.2E-02	2.6	6.8E-04	-1.0
		HSS142682	AGCCGCUCAUGUCCUUAUCAGUGC	1.8E-02	-2.1	9.0E-03	-0.7
		s7524	UCUGUAAUCGGUGAUCUCUcc	3.1E-02	3.1	8.3E-01	0.0
		s7525	AUUUGAUAGAGCUCCAUCGtt	2.9E-02	2.4	6.3E-01	0.2
LDLR	low density lipoprotein receptor	HSS106010	UUCUCAUUUCCUCUGCCAGCAACGU	4.4E-04	-4.7	1.0E-10	-1.7
		HSS106011	UGUCCUUGCAGUCAUAUUCGGGUC	1.7E-04	-5.5	0.0E+0	-2.0
		s224006	UAUCUUCGCAUCUUCGCUg	4.3E-04	-5.0	0.0E+0	-2.8
LZTFL1 (poorly characterized)	leucine zipper transcription factor-like 1	HSS123079	AAAUUUCCUUGUUUAGGAGUUCUGC	5.7E-02	-1.5	6.1E-03	-0.7
		HSS123080	UUCAAUGGUCUUAACCUUGACUUC	1.1E-02	-2.8	1.8E-05	-1.4
		s29234	UAAGUUACUUAAGUCUUGGgc	1.1E-01	-1.2	2.5E-03	-0.7
		s29235	UAAGAUACCACUUCUCAGCtt	8.6E-01	-0.3	8.2E-01	-0.1
NPC1	Niemann-Pick disease, type C1	HSS107272	AAAUGGUGCAGUUCGUGUUAUACGG	6.4E-08	15.1	2.3E-01	-0.3
		HSS107273	AAUAAUCGUCGAUCCAGGACGAGGG	1.8E-03	5.5	1.6E-01	-0.6
		s237198	AUAUUGCUAUCACAAUUGGtc	1.1E-04	13.9	3.5E-01	-0.1
NUCB2 (poorly characterized)	nucleobindin 2	s9773	UAUAUCUUGAAGGGAUCCaa	6.7E-01	0.3	9.0E-03	0.6
		s9774	UUCUUAACCUUCCUACUUCtt	7.5E-01	0.0	7.5E-01	-0.1
PGM3 (poorly characterized)	phosphoglucosyltransferase 3	HSS107909	UUCAUUGGACUUAUUUCCAUCUCC	1.1E-04	7.2	5.4E-02	-0.5
		HSS107910	UAAGGAAACUGCUAAUUAACGUUGC	1.7E-04	6.0	6.1E-03	-0.7
		s10409	UGAUUGCCUCCUGUAUUCctg	5.7E-02	1.5	9.9E-03	-0.6
		s10410	UCUUGUUGCAGAUUCACAGct	4.0E-01	-0.7	1.2E-02	0.6
RGS1 (poorly characterized)	regulator of G-protein signaling 1	HSS143614	UUUCAUCCAGAUUCCAGAUUGGG	1.7E-03	3.8	3.0E-01	-0.2
		HSS143615	UUUAUAUCUCUUCUGCUUUACAGG	5.4E-01	-1.1	6.5E-06	-1.1
		s11986	UCAUAGAUCUCAGGUAUGCtt	9.2E-01	-0.1	1.5E-02	-0.6
		s11988	UAUUGAUUUUUAGCAGCat	6.2E-01	-0.3	1.4E-01	-0.3
SEC24D (poorly characterized)	SEC24 family, member D (S. cerevisiae)	s19116	UUGUUGUCUAUCCAAGUGCat	1.7E-01	1.1	4.1E-01	0.2
		s19117	UGAUUAACUAGAAUUUCCGg	8.3E-02	1.4	4.8E-01	-0.2
SLC2A14 (poorly characterized)	solute carrier family 2 (facilitated glucose transporter), member 14	HSS152070	AAGCGUUAAACAAAGAGUCCGACGG	2.0E-01	0.7	4.3E-08	-1.5
		HSS152071	AUGAGUCCAGACCAAAGAUUCUGGG	3.8E-03	3.9	1.7E-02	-0.6
		s44617	AUCAUAUGCAGAGUCCUUCtt	3.0E-01	0.6	3.1E-02	-0.6
		s44619	AAGAUAAUAAAACGUAGGct	5.4E-01	0.4	6.0E-02	0.4
SPP1 (poorly characterized)	secreted phosphoprotein 1	HSS144072	AUUGCUCUCAUCAUUGGCUUCCGC	8.6E-01	-0.3	5.1E-02	-0.4
		HSS186069	AUCAGAAGCGCGUUCAGGUCCUGG	3.8E-03	-3.4	3.0E-04	-1.1
		s13375	AGAACUCCAGAAUCAGCCtg	1.1E-02	3.5	1.9E-03	0.8
		s13377	UUUCGUUGGACUUAUUCGaa	1.2E-01	1.1	2.5E-01	0.3
SQLE	squalene epoxidase	s198	UUAGUUGAUGCAGGGAUCCat	4.0E-01	-0.6	2.1E-06	-1.1
		s199	UUCUUGAUUUCUCCAGUCtc	1.5E-02	4.4	2.6E-01	0.4
TMEM41B (poorly characterized)	transmembrane protein 41B	HSS162367	AUCGUUCGGCAGUCUCCUUUCGC	8.6E-01	-1.1	1.7E-05	-1.0
		HSS162368	AAAUGGACACAAUAUAAGGAGUGA	3.7E-01	-1.8	1.6E-01	-0.3
		s53992	UUGUAUACAACUGGUCUCCca	6.1E-02	-1.3	0.0E+0	-2.3
		s53993	UGCUGAUCCAGCUUCUACc	7.5E-03	4.4	7.2E-01	0.1
TRIM2	tripartite	HSS118585	UUUCCAGUCUGUACAUGCUUGCGG	8.6E-01	-0.5	4.4E-01	0.2

(poorly characterized)	motif containing 2	HSS118585	UUUCCAGUGCUGUACAUGCUUGCGG	8.6E-01	-0.5	4.4E-01	0.2
		HSS118586	UUAUUUCUUCUUUGGUACCCACUC	1.1E-03	-4.8	2.8E-07	-1.5
		s23555	UGGUGGUUAAGAUCGUCCga	1.1E-02	3.3	2.9E-11	-1.5
		s23556	UACCGUCCAGGCAUAUACtg	9.9E-01	-0.2	3.7E-04	-0.8
TUBA1A (poorly characterized)	tubulin, alpha 1a	HSS144577	UGGAUGGUACGCUUGGUCUUGAUGG	3.8E-02	1.7	1.8E-03	-1.0
		HSS144578	UAGUAUAGGUUGGACGCUCAUAUC	2.6E-01	-2.1	3.9E-02	-0.6
		s15400	ACAAUUUGACCUAUUAACct	4.5E-02	2.1	1.8E-07	1.4
		s15401	UACUGAUCAGACCACAACtt	3.5E-01	0.6	3.9E-02	-0.5
WIPI1 (poorly characterized)	WD repeat domain, phosphoinositide interacting 1	HSS123809	AUAUCCAGGAGGGUCUUAACAGCU	2.9E-02	-3.3	2.9E-01	-0.2
		HSS123810	AUAGAGAGAGCACAUAGACCUGUUG	1.7E-03	-4.1	3.0E-01	-0.3
		s30081	UCAUGGGCAGCAAUAGUGCag	5.1E-02	-1.6	2.8E-02	-0.5
		s30083	UUCUGGAUCGUUGAGAGGGta	6.3E-02	2.4	4.4E-01	-0.3
ZNF165 (poorly characterized)	zinc finger protein 165	HSS111629	UGACAUUAAGUGCUGGUCCAGGAGG	6.2E-01	0.0	4.7E-06	-1.3
		HSS111630	UUCAGCUUUGGCAUGGAUCUACUG	2.4E-02	-2.6	2.6E-05	-1.2
		s15225	UGUUUAGCAAGUUUUGGGCtc	7.5E-03	3.2	1.1E-01	0.4
		s15226	UUUACCAAACCUUCAUCtg	8.9E-01	0.0	2.4E-02	0.6