

Table S2:

Gene Symbol	Full Gene Name	Entrez Gene ID	RefSeq	siRNA ID	Antisense siRNA Sequence	SH4-HASPB-GFP	SH4-Yes-mCherry
Lipid Metabolism							
ACADVL	acyl-Coenzyme A dehydrogenase, very long chain	37	NM_000018	s208	AAACUGUUAUUGACAUAUCCcc	3.4	6.1
MVD	mevalonate (diphospho) decarboxylase	4597	NM_002461	s224074	UUUUUAAACUGGUCCUGGUGca		2.8
SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	27293	NM_014474	s26101	UGCUAUGACGCGGAUGAUGCht	5.0	
SREBF2	sterol regulatory element binding transcription factor 2	6721	NM_004599	s28	UUUGACCUUUUGCAUCAUCCaa	2.1	
Transport Factors							
COPA (α-COP)	coatamer protein complex, subunit alpha	1314	NM_004371	s3369	AAAGCGAGUUUUCUCAUCht	7.6	5.5
COPB1 (β-COP)	coatamer protein complex, subunit beta 1	1315	NM_016451	s3371	UGGAUUAGCAUGACAGACht	7.0	4.2
				s3372	UCUUUGACUUUACAUCUCht	6.1	2.6
KIF20B	kinesin family member 20B	9585	NM_016195	s18420	UCGAUAUUCUUUAACUUGht	2.6	
				s18421	UGCUGAACUAUACGUUUGgg	2.6	
RAN	RAN, member RAS oncogene family	5901	NM_006325	s11768	UUCUUUGUAUAACUCUCGat		6.5
				s11769	UUUCCUGUCCUUAUAUCCac		4.8
Protein Phosphorylation							
PRKCA (PKCα)	protein kinase C, alpha	5578	NM_002737	s11093	UGCAGGAUUUAGUGGAGCGgg	4.3	3.3
PRKCB	protein kinase C, beta	5579	NM_212535	s11096	AAAUCCGCAUGAUUCAUCcgg	3.3	2.6
PTPRD	protein tyrosine phosphatase, receptor type, D	5789	NM_001040712	s11540	UACAUUCGCGUAUCUAUUCht	2.4	
Other Protein Modifications							
ACY3	aspartoacylase (aminocyclase) 3	91703	NM_080658	s40752	UUCGCGAUUAAGCAGGUGCCcc	2.8	3.2
GALNTL4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl/galactosaminyltransferase-like 4	374378	NM_198516	s51536	AAAGUUGUCAUAUUUGAUGht	2.7	
LIPT2	lipoyl(octanoyl) transferase 2 (putative)	387787	XM_370636	s226411	AAUUGAGAAUAUGACAUAUCjat	5.0	5.3
NAA35	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	60560	NM_024635	s34135	UUUACGUACUUUUGCCGUCCat	3.9	3.4
Membrane Receptors							
BAI3	brain-specific angiogenesis inhibitor 3	577	NM_001704	s1878	UGGAUUGCUAAGCUCAUUCat	3.2	
CDH26	cadherin 26	60437	NM_021810	s34067	AGCAGGAGUAGAGUGUAUGht	3.1	2.8
IL7R	interleukin 7 receptor	3575	XM_001127146	s7325	UGUUUAGUAAGUAAGGAUCCaa	2.5	3.5
ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	3685	NM_002210	s7569	UAGGGUACACUUCAGACCag	4.9	7.1
ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	3688	NM_002211	s7575	AGCCGUGUAACAUUCCUCCag	4.4	3.2
				s7576	UAAUCGCAAAACCAACUCGtg	5.0	3.2
				s7574	UGCUGUUCUUUUGCUACGGht	3.6	
LILRB5	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5	10990	NM_006840	s21637	AAAAAGAAAGUGUCUAUCUGa	2.4	
OR10V1	olfactory receptor, family 10, subfamily V, member 1	390201	NM_001005324	s52738	UCAGGGUCAGGUGAGAAUGga	2.9	2.5
TGFBRI	transforming growth factor, beta receptor I	7046	NM_004612	s14073	AGUCUUUACAACGUAGUACCct		5.0
Gene Regulation and Expression							
EIF4A3	eukaryotic translation initiation factor 4A3	9775	NM_014740	s18876	UUCACGAACCUGAAUAUCCaa	3.3	3.9
				s18877	UGAUCUGCUUGAUUGCUCht	4.5	4.0
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	3178	NM_002136	s6710	UUUAUCUGGUACCAUUAUUCaa		2.4
RPS26P35	ribosomal protein S26 pseudogene 35	441377	XM_496991	s54340	UCUUUUAAGAACUCAGCUCht		3.4
RPL21P62	ribosomal protein L21 pseudogene 62	442160	XM_001128707	s54494	UAACUUGUUUUGUUUAACAACaa		2.8
RPS26P8	ribosomal protein S26 pseudogene 8	644191	XM_930072	s55596	UCACAUACAGUUUGGGAAGca		2.7
MBD3L2	methyl-CpG binding domain protein 3-like 2	125997	NM_144614	s42925	UGGAUUUUCUGGUUUCUUCht	3.6	
RPL23AP82	ribosomal protein L23a pseudogene 82	284942	NM_203302	s49770	UCAGGACAAUUCAGGGUGGtg	3.2	2.3
PHF5A	PHD finger protein 5A	84844	NM_032758	s39506	AUAGGAGUCACAAAUACACaa	4.2	3.5
POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	5435	NM_021974	s224297	UGGCAGGUAACGGCGAAUGat	3.7	2.9
				s10809	UGUGGUGAUUCGCUUCUCGht		2.7
PRPF8	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	10594	NM_006445	s20796	UCGUUGUUCACAUAGUAGGca	5.1	8.2
				s20797	AUGCGAUCAAUGUAUUCGCag	3.7	6.8
PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	26121	NM_015629	s25122	UACUUUAUCCCGGAUGAACUhta		2.5
RPL18	ribosomal protein L18	6141	NM_000979	s194744	UAUAACUUGACCAACAGCCtc		3.7
				s194745	UAGGAUCCAGGGUUAGUUUtt		3.0
RPL21	ribosomal protein L21	6144	NM_000982	s12186	UAUCUCGGCUCUUAAGAGUGct		3.0
				s12187	UAACAUUGUAGACUCUUCcag		2.9
RPS25P6	ribosomal protein S25 pseudogene 6	401206	XM_937380	s53508	UAAGUUUAUUGAGCUUGUCCcg	3.8	3.8
SF3A1	splicing factor 3a, subunit 1, 120kDa	10291	NM_001005409	s20117	UCAAUAUCCAGACCUGGUGag		2.8
ZNF326	zinc finger protein 326	284695	NM_182975	s195972	UUCCAUAUAAAGCCCUAGUAug		2.4
Others							
A2M	alpha-2-macroglobulin	2	NM_000014	s819	UCGUUCUUAACCAUACUGhtg	3.2	2.9
ATP6AP2	ATPase, H+ transporting, lysosomal accessory protein 2	10159	NM_005765	s19790	UUUCCGAAAACAACAGACCct		2.3
CACNA1S	calcium channel, voltage-dependent, L type, alpha 1S subunit	779	NM_000069	s2297	UUCCGGUUUAUUUGGGUCCca		4.1
CHERP	calcium homeostasis endoplasmic reticulum protein	10523	NM_006387	s20627	UUUUGUCUCUUCUCCGAGCct	2.8	3.1
DBH	dopamine beta-hydroxylase (dopamine beta-monoxygenase)	1621	NM_000787	s3947	ACUGUAGACCACCUUUCUCCca		2.7
CDC37P1	cell division cycle 37 homolog (S. cerevisiae) pseudogene 1	390688	NM_001080829	s52851	UCUUAUCAUACGCGUACUGhtg		2.9
MAGEB1	melanoma antigen family B, 1	4112	NM_002363	s8455	UUUAUACUUAACGUAGAAGaa	2.3	
SHC1	SHC (Src homology 2 domain containing) transforming protein 1	6464	NM_003029	s12811	AAAUAGAGUAAGUAUGCAUhtg		4.0
SOBP	sine oculis binding protein homolog (Drosophila)	55084	NM_018013	s30136	AAGUAUGUCGCAUUAUUCht	3.4	3.5
TMEM126A	transmembrane protein 126A	84233	NM_032273	s38695	AAUCCAGUAACUUAAGAUGht		2.1
YAP1	Yes-associated protein 1, 65kDa	10413	NM_006106	s20367	UGAUUUAGAAGUAUCUCUga	2.2	
Unknown							
PATE2	prostate and testis expressed 2	399967	NM_212555	s53217	UAAUGAUACAUGCUCUGCCct	3.4	3.6
C12orf36	chromosome 12 open reading frame 36	283422	NM_182558	s49233	UAGUGGAGCAUGAAGUGUCht	3.0	
C16orf71	chromosome 16 open reading frame 71	146562	NM_139170	s44876	UCUGGAUAUCGGGAGGUUUgg	3.2	
FAM108A1	family with sequence similarity 108, member A1	81926	NM_001130111	s230886	UUAAUUUCCGUUUUACGCUjat	2.2	