

Table S1. Genes used in significance analysis.

Collecta ID	gene symbol	constructs	SL-ratio	P-value
CLL-H-000022	A1BG	3	0.090	0.251
CLL-H-027496	A2BP1	5	0.042	0.219
CLL-H-000028	A2M	5	0.087	0.238
CLL-H-000033	A4GALT	4	0.028	0.359
CLL-H-027501	AAAS	4	0.015	0.328
CLL-H-000044	AACS	4	-0.164	0.219
CLL-H-000050	AADAC	3	-0.113	0.362
CLL-H-000054	AADAT	4	0.287	0.032
CLL-H-027506	AAK1	5	0.086	0.140
CLL-H-000059	AANAT	5	-0.054	0.460
CLL-H-000065	AARS	3	-0.069	0.435
CLL-H-000071	AARS2	4	0.220	0.087
CLL-H-000075	AASDH	3	0.021	0.379
CLL-H-000080	AASDHPPT	5	0.043	0.322
CLL-H-000087	AASS	4	-0.136	0.294
CLL-H-027511	AATF	4	0.198	0.049
CLL-H-027516	AATK	4	0.374	0.004
CLL-H-000097	ABCA1	5	-0.077	0.402
CLL-H-000103	ABCA10	3	0.054	0.333
CLL-H-000108	ABCA12	3	-0.318	0.073
CLL-H-000114	ABCA13	5	0.081	0.214
CLL-H-000120	ABCA2	5	0.092	0.242
CLL-H-000132	ABCA4	4	0.247	0.070
CLL-H-000136	ABCA5	5	0.137	0.140
CLL-H-000142	ABCA6	4	0.101	0.237
CLL-H-000148	ABCA7	4	0.038	0.334
CLL-H-000153	ABCA8	3	-0.088	0.393
CLL-H-000158	ABCA9	3	-0.164	0.250
CLL-H-000164	ABCB1	3	-0.181	0.242
CLL-H-000170	ABCB10	3	-0.092	0.384
CLL-H-000176	ABCB11	3	0.159	0.153
CLL-H-000180	ABCB4	4	0.120	0.180
CLL-H-000190	ABCB6	4	0.047	0.303
CLL-H-000201	ABCB8	6	-0.082	0.387
CLL-H-000207	ABCB9	5	0.131	0.162
CLL-H-000212	ABCC1	5	-0.216	0.135
CLL-H-027521	ABCC10	5	0.025	0.275
CLL-H-027526	ABCC11	5	0.075	0.153
CLL-H-027532	ABCC12	4	-0.176	0.164
CLL-H-000218	ABCC2	3	-0.011	0.446
CLL-H-000224	ABCC3	5	-0.129	0.270
CLL-H-000230	ABCC4	5	0.070	0.256
CLL-H-000235	ABCC5	3	-0.160	0.269
CLL-H-000241	ABCC6	3	-0.331	0.094
CLL-H-027536	ABCC9	5	0.085	0.127
CLL-H-000250	ABCD1	4	-0.150	0.249

Table S2. Genes included in GO-annotation cluster enrichment analysis.

gene symbol	SL-ratio (log2)	p-value	p-value (-log10)
ACO2	-0.413	0.023	1.63
ACSL1	-0.397	0.031	1.51
AMPH	-0.464	0.042	1.37
ANGPTL4	-0.381	0.027	1.56
ANGPTL6	-0.54	0.008	2.09
ATP4B	-0.358	0.045	1.34
ATP6AP1	-0.369	0.045	1.35
C10ORF110	-0.362	0.04	1.4
CCNA2	-0.707	0.041	1.38
CCNT1	-0.432	0.006	2.19
CD40	-0.42	0.04	1.4
CD52	-0.376	0.045	1.34
CDX2	-0.398	0.042	1.38
CELSR2	-0.392	0.037	1.44
CNTN5	-0.489	0.002	2.64
COL1A2	-0.402	0.032	1.49
CPSF4	-0.381	0.024	1.61
CPT2	-0.445	0.012	1.9
CRNKL1	-0.399	0.018	1.76
CSNK1G3	-0.479	0.02	1.71
CXCL9	-0.372	0.045	1.35
CYP4B1	-0.354	0.017	1.77
DHTKD1	-0.353	0.039	1.41
DPYSL5	-0.444	0.035	1.46
DYRK3	-0.398	0.018	1.74
ECT2	-0.424	0.012	1.91
ETV3	-0.486	0.019	1.73
FREM2	-0.358	0.013	1.88
GOT1	-0.407	0.022	1.66
GPR155	-0.432	0.02	1.71
GZMA	-0.52	0.012	1.92
HUS1	-0.455	0.041	1.39
IFT57	-0.467	0.033	1.48
IL4R	-0.578	0.002	2.71
IMP4	-0.379	0.009	2.05
INGX	-0.379	0.022	1.65
IRF4	-0.407	0.047	1.32
ISG15	-0.453	0.009	2.04
ITGB6	-0.387	0.042	1.38
KCNE1	-0.585	0.011	1.97
NUP98	-0.455	0.013	1.89
OPRL1	-0.382	0.033	1.48
OR6C74	-0.38	0.009	2.04
PACAP	-0.384	0.016	1.79
PDE4A	-0.473	0.017	1.78
PDE7A	-0.354	0.038	1.42

PIWIL1	-0.456	0.022	1.66
PLG	-0.41	0.008	2.07
PMF1	-0.456	0.013	1.87
PRKCI	-0.562	0.007	2.15
PRKRIR	-0.413	0.028	1.56
PUM1	-0.552	0.005	2.31
RAD17	-0.704	0.002	2.74
RBM15	-0.358	0.033	1.48
RFC3	-0.37	0.021	1.68
SELE	-0.714	0.003	2.5
SFRP1	-0.369	0.039	1.41
SLC17A3	-0.394	0.008	2.12
SLC34A1	-0.387	0.021	1.67
SOD1	-0.529	0.023	1.64
SPRED1	-0.37	0.018	1.75
TOP3A	-0.391	0.047	1.33
TUBGCP2	-0.704	0.012	1.93
TXNRD1	-0.467	0.021	1.68
TYMS	-0.744	0.009	2.04
UPF1	-0.404	0.031	1.51
VKORC1	-0.549	0.008	2.07
XPA	-0.356	0.04	1.39
ZNF321	-0.361	0.021	1.67
ZNF687	-0.358	0.006	2.24

Table S3. shRNA expression constructs used in validation.

name	sense	loop	antisense
CHK1_1	GCTGCAAATAGTAGTTCTTGAA	GTTAATATTCATAGC	TTCAGGAACTACTATTTGCAG
CHK1_2	GGTGGTTTATCTGTATGGTATT	GTTAATATTCATAGC	AATACCATGCAGATAAACCAC
CHK1_3	GGAAGATTAAAGGGAAGTTGAT	GTTAATATTCATAGC	ATCAGCTTCCCTTTAATCTTC
HUS1_1	GGAGAACTTCTTCAACGAATTT	GTTAATATTCATAGC	AAATTCGTTGAAGAAGTTCTC
HUS1_2	GCCACTTCACACGAATTAGTAA	GTTAATATTCATAGC	TTACTGATTTCGTGTGAAGTGG
HUS1_3	GCAGCTGCAGTATTTGGAGTTT	GTTAATATTCATAGC	AGACTCCAAATGCTGCAGCTG
IL4R_1	GCCCCGGTAGATTTTCAGAATTTA	GTTAATATTCATAGC	TAGATTCTGAAATCTGCCGGG
IL4R_2	GGCGATGAACAAAGTAGATAGA	GTTAATATTCATAGC	TCTATCTGCTTTGTTTCATCGC
IL4R_3	GCGATGAACAAAGTAGATAGAA	GTTAATATTCATAGC	TTCTATCTGCTTTGTTTCATCG
RAD17_1	GGCGACAAAGTATAACAAGTTA	GTTAATATTCATAGC	TAACTTGTTATACTTTGTTCGC
RAD17_2	GGCCACATTATTAGGTGTGAAT	GTTAATATTCATAGC	ATTCACACCTAATGATGTGGC
RAD17_3	GCGCTCTTTACTTAGGGAATAT	GTTAATATTCATAGC	ATATTCCCTGAGTAAAGAGCG
RFC3_1	GGCTGGAAATGGTGACTIONGAGTA	GTTAATATTCATAGC	TACTCGGTCACTATTTCCAGC
RFC3_2	GGTGCTGCAATTCTACATTTAA	GTTAATATTCATAGC	TTAGATGTAGAATTGCAGCAC
RFC3_3	GCTGCCATAGGTAATATGATTG	GTTAATATTCATAGC	CAATCATGTTACCTGTGGCAG
SOD1_1	GCCGATGTGTTTATTGAAGATT	GTTAATATTCATAGC	AATCTTCAATAGACACATCGG
SOD1_2	GCTGCATGGATTCCATGTTTAT	GTTAATATTCATAGC	ATGAACATGGAATCCATGCAG
SOD1_3	GGTGGAATGAAGAAAGTACAA	GTTAATATTCATAGC	TTGTACTTTCTTCATTTCCAC
TXNRD1_1	GGCTGGATTTCTTGTGGTATT	GTTAATATTCATAGC	AATACCAGCAAGAAATCCAGC
TXNRD1_2	GCACAGGATTAAGGCAATAAAT	GTTAATATTCATAGC	ATTTGTTGCCTTAATCCTGTG
TXNRD1_3	GCTGTATTTACTCCTTTGGAAT	GTTAATATTCATAGC	ATTCCAAAGGAGTAAATACAG
TYMS_1	GGCAAAGAGTGATTGACATCAT	GTTAATATTCATAGC	ATGGTGTCAATCACTCTTTGC
TYMS_2	GCTTTGGGAGATGCATATATTT	GTTAATATTCATAGC	AAATATGTGCATCTCCAAAG
TYMS_3	GCCACTGGTAAATGTAATTGTG	GTTAATATTCATAGC	CACAGTTACATTTGCCAGTGG
WEE1_1	GCTAGAAAGAGTGCAGAATAAT	GTTAATATTCATAGC	ATTGTTCTGCACTCTTTCTAG
WEE1_2	GAGATGAAACAAGACCTGTTAA	GTTAATATTCATAGC	TTAGCAGGTCTTGTTCATCT
WEE1_3	GGCCTTTCTAGGTTAACCATT	GTTAATATTCATAGC	AGTGGTTAACCTGGAAAGGC
XPA_1	GGCACAATGTCATGTTTGTGAT	GTTAATATTCATAGC	ATCACAGACATGACATTGTGC
XPA_2	GGCTGATGATAAACACAAGTTT	GTTAATATTCATAGC	AAGCTTGTGTTTATCATCAGC
XPA_3	GCATGAGTATGGACTAGAAGAA	GTTAATATTCATAGC	TTCTTCTGGTCCATACTCATG
shCTRL	GCCGTTTCGTCGTACGTCGAGCG	GTTAATATTCATAGC	CGCTCGACGTACGACGAACGG