

Supplementary table 1

sgRNA name	Sequence	Gene	Exon	Protein domain targeted	Predicted On-target efficiency
GUIDES_sg001	GTTGACTGGGAGAGAACACG	<i>ABCA1</i>	46	ABC_tran	0.707186352
GUIDES_sg002	GTGTTCTAAAAGAGAAACAC	<i>ABCA1</i>	50	-	0.684107302
GUIDES_sg003	GTGCAGTGTCTCTCCTACAC	<i>ADAMTS6</i>	28	-	0.720054847
GUIDES_sg004	ACCAGTCATGTCCACCACAG	<i>ADAMTS6</i>	26	-	0.71972146
GUIDES_sg005	CAAGGGTAAAAAGCCCCCG	<i>AFAP1</i>	16	-	0.759587174
GUIDES_sg006	GGAAAGAAAAGACCTTCGAG	<i>AFAP1</i>	17	-	0.753862205
GUIDES_sg007	CAACTATAACGTGAGCCAG	<i>ALDH9A1</i>	10	Aldedh	0.764185557
GUIDES_sg008	TATGAACAATGCTGTAAAGG	<i>ALDH9A1</i>	6	Aldedh	0.704113168
GUIDES_sg009	GTGCTGTGAGCTGGGAAGTG	<i>ANAPC1</i>	39	-	0.69840945
GUIDES_sg010	ATGGCTCTTCCTGTAGGACG	<i>ANAPC1</i>	27	-	0.641611628
GUIDES_sg011	CCCCAGCCAATATTCACCGG	<i>ANGPT1</i>	9	Fibrinogen_C	0.666179972
GUIDES_sg012	AATATGGATGTCAATGGGGG	<i>ANGPT1</i>	8	Fibrinogen_C	0.630390739
GUIDES_sg013	TAACGTGTAGATGCCATTCG	<i>ANGPT2</i>	5	Fibrinogen_C	0.692502215
GUIDES_sg014	TGTGACATGGAAGCTGGAGG	<i>ANGPT2</i>	6	Fibrinogen_C	0.647042655
GUIDES_sg015	ACTCGCTCTCAGGTTCCAGG	<i>ANGPTL2</i>	5	Fibrinogen_C	0.761119961
GUIDES_sg016	CACCAGCATGTCACGCACAG	<i>ANGPTL2</i>	2	RasGEF	0.753686491
GUIDES_sg017	CTTTGTGGGAGAATCCACCA	<i>ANKH</i>	14	ANKH	0.705623542
GUIDES_sg018	TGAGGGCGCATCTCACCGGG	<i>ANKH</i>	13	ANKH	0.671178514
GUIDES_sg019	CTTCGACATGCCCGCAACG	<i>ANTXR1</i>	10	Anth_lg	0.66965417
GUIDES_sg020	CAGAACTGGAGATAAAAGAG	<i>ANTXR1</i>	12	Anth_lg	0.661995855
GUIDES_sg021	CTGCTGGACCAGAAATTCGG	<i>ARHGEF12</i>	39	-	0.715629912
GUIDES_sg022	TCTCTGGGGTCATAATCATG	<i>ARHGEF12</i>	38	-	0.682338139
GUIDES_sg023	TACCAAATATGCCCAACAG	<i>ATXN2</i>	21	-	0.746394842
GUIDES_sg024	ATTACAGGACTATAGACATG	<i>ATXN2</i>	22	-	0.705381212
GUIDES_sg025	ATGGGCCAGGACTTCCAGG	<i>BCAS3</i>	35	-	0.763805308
GUIDES_sg026	TGAACTGGATGAGATAACTG	<i>BCAS3</i>	36	-	0.749363581
GUIDES_sg027	AGTTTTTAGGCTGAAACTGG	<i>CAPZA1</i>	6	F-actin_cap_A	0.671121892
GUIDES_sg028	GGAATAATGGTCTTTCACAT	<i>CAPZA1</i>	5	F-actin_cap_A	0.61837895
GUIDES_sg029	TAAACACCTCAACGATGACG	<i>CAV1</i>	3	Caveolin	0.697766064
GUIDES_sg030	TGGGGGCAAATACGTAGACT	<i>CAV1</i>	1	Caveolin	0.638532867
GUIDES_sg031	GATGTGCAGACAGCTGAGGG	<i>CAV2</i>	23	Caveolin	0.699222046
GUIDES_sg032	CGGCGTACTCGAGGCCGCTG	<i>CAV2</i>	22	Caveolin	0.674769146
GUIDES_sg033	TCAGGAAGCCAAAGTCCCAG	<i>CDH11</i>	19	Cadherin	0.765145054
GUIDES_sg034	GGATTGTGAATGATTCAGG	<i>CDH11</i>	20	Cadherin	0.686839641
GUIDES_sg035	GGGTTATCTCGTGTGCCAAG	<i>COL24A1</i>	60	COLFI	0.662833491
GUIDES_sg036	GAAATTGCAGAAAACCTCAA	<i>COL24A1</i>	61	COLFI	0.614109727
GUIDES_sg037	AAGCGGCCAGACTTCTGCG	<i>CTTNBP2</i>	25	-	0.737788504
GUIDES_sg038	GCCAGGTTGTCTTTTCACAG	<i>CTTNBP2</i>	24	-	0.682279464
GUIDES_sg039	AACATTCCCAGCATGTACGG	<i>DGKG</i>	22	DAGK_acc	0.746132205
GUIDES_sg040	GTACTTTGAATTTGGCACCT	<i>DGKG</i>	21	DAGK_acc	0.610555363
GUIDES_sg041	GACCACAAATGAATGCCGGG	<i>EFEMP1</i>	9	EGF_CA	0.7383367

GUIDES_sg042	TCACCACTTGGTATCCCTGG	<i>EFEMP1</i>	8	EGF_CA	0.711733541
GUIDES_sg043	ACGCTCTCTTTATCAGACTG	<i>EMCN</i>	19	Endomucin	0.716120299
GUIDES_sg044	GTTTTAGAAGGTGATGCATC	<i>EMCN</i>	15	Endomucin	0.500046723
GUIDES_sg045	AGGACTCCCAGGGACACCTG	<i>EMID1</i>	11	Collagen	0.633805274
GUIDES_sg046	GCTGCCCAGCAGACCTTGG	<i>EMID1</i>	13	Collagen	0.50154336
GUIDES_sg047	GCAGTGGACCAATCCAGCTA	<i>ETS1</i>	13	Ets	0.590477455
GUIDES_sg048	CACTAAAGAACAGCAACGAC	<i>ETS1</i>	8	SAM_PNT	0.507782957
GUIDES_sg049	ATGTTTCAGTTGTAGGCACAA	<i>FBXO32</i>	7	-	0.680491123
GUIDES_sg050	AACTTGTCGGATGTACCCA	<i>FBXO32</i>	8	-	0.665922839
GUIDES_sg051	ACAGTTCAGAGAGTGACGTG	<i>FER</i>	26	Pkinase	0.744231001
GUIDES_sg052	ATGTCTCGTCAAGAGGATGG	<i>FER</i>	25	Pkinase	0.666176654
GUIDES_sg053	GCCTGCAGATTAGCCTCAA	<i>FERMT2</i>	17	PH	0.635135622
GUIDES_sg054	CTGAGGTTTCATCTGATGAGC	<i>FERMT2</i>	15	PH	0.496718402
GUIDES_sg055	GGAGTTCATCCTCAACAATG	<i>FMNL2</i>	23	FH2	0.656016612
GUIDES_sg056	TTCACAAACCGGACAAAGAC	<i>FMNL2</i>	24	FH2	0.52306371
GUIDES_sg057	TGTGTACACACTACAGCTGG	<i>FNDC3B</i>	31	fn3	0.726749897
GUIDES_sg058	GCTCTCCCAGTTCAGTACA	<i>FNDC3B</i>	30	fn3	0.69274705
GUIDES_sg059	GCTGAGCAACAAGACAGAGG	<i>GAS7</i>	19	-	0.715444147
GUIDES_sg060	GCTTGCGAAGGTCGGCAATG	<i>GAS7</i>	18	-	0.692490099
GUIDES_sg061	GCCCACACTCTCCAAGCACA	<i>GNB1L</i>	3	-	0.656080017
GUIDES_sg062	GCAGGCTCCAGATGTGTACC	<i>GNB1L</i>	2	WD40	0.572759585
GUIDES_sg063	TGAACAGAGAGACTTCTGAG	<i>KALRN</i>	59	PH	0.713929927
GUIDES_sg064	CTTCCTGAGATACAGTGAGA	<i>KALRN</i>	56	RhoGEF	0.590046749
GUIDES_sg065	TGATTACTGGAAGTACGGGG	<i>KREMEN1</i>	5	WSC	0.732200895
GUIDES_sg066	TTACTGGTGCCAGTTAGAGG	<i>KREMEN1</i>	4	WSC	0.660612633
GUIDES_sg067	CAGGGACTCGATGATCATGG	<i>LMO7</i>	34	LIM	0.767439497
GUIDES_sg068	GATCCTGACTTCAGCTCCTG	<i>LMO7</i>	35	LIM	0.666458078
GUIDES_sg069	CTTCGACGAGACCTCGAAGG	<i>LMX1B</i>	4	Homeobox	0.713403988
GUIDES_sg070	GTGCAAGGGTGACTACGAGA	<i>LMX1B</i>	3	LIM	0.675803927
GUIDES_sg071	ACGTCTCGGATGGTGCTGAG	<i>ME3</i>	18	Malic_M	0.711900963
GUIDES_sg072	AGAGAAAGAAGGTGTACCGA	<i>ME3</i>	14	Malic_M	0.683948993
GUIDES_sg073	TAGTACTTCCCATGTGCCAG	<i>MECOM</i>	24	-	0.69054325
GUIDES_sg074	ACTGTGGCAAGATTTTCCA	<i>MECOM</i>	20	zf-C2H2	0.638498746
GUIDES_sg075	GGACTTCTGCTCAAAGAGGG	<i>MYOF</i>	56	-	0.689398449
GUIDES_sg076	TGCATGGGTTGGTGAACCAG	<i>MYOF</i>	58	-	0.68114604
GUIDES_sg077	AAAGGTA CTCTGAAACATGG	<i>PARD3B</i>	24	-	0.748915706
GUIDES_sg078	TGGTCTCTTTCTGGAGACAG	<i>PARD3B</i>	25	-	0.687131379
GUIDES_sg079	TCTGGGAGATGAGCAAGCAG	<i>PDE7B</i>	11	PDEase_I	0.63710316
GUIDES_sg080	TCTTTCTGTTGATTACAAAG	<i>PDE7B</i>	12	PDEase_I	0.626787508
GUIDES_sg081	CGTGAGACTCCAGTCACAGG	<i>PKHD1</i>	20	-	0.721146822
GUIDES_sg082	ATGGGATAGCCCCAAGCAGG	<i>PKHD1</i>	16	-	0.648027027
GUIDES_sg083	TACTCAGGGGATCACCAGCG	<i>PLEKHA7</i>	28	-	0.733493753
GUIDES_sg084	CCCCGA ACTCTACAGCCAG	<i>PLEKHA7</i>	25	-	0.727012157
GUIDES_sg085	GCTGCCCACTGCATACACGA	<i>PRSS23</i>	3	Trypsin	0.707785666

GUIDES_sg086	AACATCAGTGAAGTTATCCA	<i>PRSS23</i>	3	Trypsin	0.589826381
GUIDES_sg087	CAGTGGTGTCTGGGAACACCG	<i>PTPRJ</i>	26	Y_phosphatase	0.752294442
GUIDES_sg088	GTTTCGGTAAAGGTCCTTG TG	<i>PTPRJ</i>	24	Y_phosphatase	0.742428198
GUIDES_sg089	TGGCAAAAAGGTTTCCATCG	<i>RALGPS1</i>	25	PH	0.63983389
GUIDES_sg090	CGAAAGAAGATAATTACAAG	<i>RALGPS1</i>	11	RasGEF	0.632295378
GUIDES_sg091	AGAGGTACCAGATGGGACTG	<i>RUNX2</i>	5	Runt	0.707376125
GUIDES_sg092	CATGGCGGAAGCATTCTGGA	<i>RUNX2</i>	11	Runx1	0.681198759
GUIDES_sg093	TGGAATTCCTACCACAGCG	<i>SPTBN1</i>	36	PH	0.712246448
GUIDES_sg094	TCAGTCTTAACCATTCCCAT	<i>SPTBN1</i>	31	Spectrin	0.683179693
GUIDES_sg095	GGGCTGGCTATGATAAACTG	<i>TES</i>	6	LIM	0.774116567
GUIDES_sg096	CCATGAGTTGTCTCCAGAG	<i>TES</i>	5	PET	0.735126362
GUIDES_sg097	GAAGCTCCGAGAGTCTCTG	<i>TIMP3</i>	3	TIMP	0.703685264
GUIDES_sg098	CTATGATGGCAAGATGTACA	<i>TIMP3</i>	4	TIMP	0.591387438
GUIDES_sg099	AGTCCTTGATGTAAGAAAG	<i>TMCO1</i>	9	DUF841	0.652850785
GUIDES_sg100	GAAACAATAACAGAGTCAGC	<i>TMCO1</i>	5	DUF841	0.622258097
GUIDES_sg101	AGAGACTTTGAAGTGAACGA	<i>TNS1</i>	42	PTB	0.715095311
GUIDES_sg102	CAGAAGGTGACAGTGTGAG	<i>TNS1</i>	43	PTB	0.675343539
GUIDES_sg103	GCCGACTGGTGACCTCATGG	<i>TRIOBP</i>	3	-	0.713915639
GUIDES_sg104	GGGAGCAGGAGGCAGGAACG	<i>TRIOBP</i>	4	-	0.656603289
GUIDES_sg105	TAAACCACTGGAGTTCACGG	<i>TXNRD2</i>	20	Pyr_redox_dim	0.785275668
GUIDES_sg106	TCATCATTGCTACTGGAGGG	<i>TXNRD2</i>	8	Pyr_redox_2	0.706088692
GUIDES_sg107	GGTGAAGCTCCTGATTGCAG	<i>ZNF280D</i>	27	-	0.700021186
GUIDES_sg108	GAAGAAAGTAAAGAAGTTG	<i>ZNF280D</i>	15	-	0.599965492
GUIDES_sg109	ATGGAGTTCCGCGACCACGT	<i>ABO</i>	7	CDS	0.6563
GUIDES_sg110	CCGGTCCCCAGCGTCACGCG	<i>ABO</i>	7	CDS	0.6687
GUIDES_sg111	CCACCTGGTACATCGCCTCA	<i>TEX41</i>	2	TRANSCRIPT	0.6631
GUIDES_sg112	AACTCAAGACATTGGAACCA	<i>TEX41</i>	5	TRANSCRIPT	0.6251
GUIDES_sg113	AATGTGGTAGCCCAAGACAG	<i>CYP1B1</i>	5	p450	0.775320729
GUIDES_sg114	GTGGCCACTGATCGGAAACG	<i>CYP1B1</i>	3	p450	0.726256031
GUIDES_sg115	GCAAGCCATGAGCCTGTACG	<i>FOXC1</i>	1	-	0.747984594
GUIDES_sg116	TCGTCGTCCCTGAGTCACGG	<i>FOXC1</i>	1	-	0.730741126
GUIDES_sg117	GATTGTGGTGAACCTCCGTG	<i>GMDS</i>	8	Epimerase	0.727535334
GUIDES_sg118	GTTGCAGAATGATGAGCCGG	<i>GMDS</i>	10	Epimerase	0.65599947
GUIDES_sg119	CCTCCCGCACGCGCACACAG	<i>LTBP2</i>	35	EGF	0.755863507
GUIDES_sg120	CAGGCAGACATAACCAGGCA	<i>LTBP2</i>	31	EGF_CA	0.708717
GUIDES_sg121	GGTCATACTCAAAAACCTGG	<i>MYOC</i>	3	OLF	0.763937898
GUIDES_sg122	ATGCCAGTATACCTTCAGTG	<i>MYOC</i>	1	-	0.722928246
GUIDES_sg123	TCTTGCGAAGGAAGTCCAGA	<i>TEK</i>	17	Pkinase	0.627785812
GUIDES_sg124	ATCTAATGAGACAATGCTGG	<i>TEK</i>	22	Pkinase	0.626682424
NonTargeting Human_0001	ACGGAGGCTAAGCGTCGCAA	-	-	-	-
NonTargeting Human_0002	CGCTTCCGCGGCCCGTTCAA	-	-	-	-
NonTargeting Human_0003	ATCGTTTCCGCTTAACGGCG	-	-	-	-

NonTargeting Human_0004	GTAGGCGCGCCGCTCTCTAC	-	-	-	-
NonTargeting Human_0005	CCATATCGGGGCGAGACATG	-	-	-	-
NonTargeting Human_0006	TACTAACGCCGCTCCTACAG	-	-	-	-
NonTargeting Human_0007	TGAGGATCATGTCGAGCGCC	-	-	-	-
NonTargeting Human_0008	GGGCCCCGCATAGGATATCGC	-	-	-	-
NonTargeting Human_0009	TAGACAACCGCGGAGAATGC	-	-	-	-
NonTargeting Human_0010	ACGGGCGGCTATCGCTGACT				