

Supplementary Table S1. All High Probability Off-Target Effects in Promoter Regions from Designed gRNA Templates

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
O-AY623602	42	AGAAATCCCTGGATCTTTGGG						chr12:57446538-57446560	0.871	3	0.585
O-AY623602	42	AGAAATCCCTGGATCTTTGGG	TRUE		SCCPDH			chr1:246920083-246920105	0.813	4	0.703
O-AB485669	42	AGAGATCCCTGGATCTTTGGA						chr12:57446538-57446560	0.836	3	0.585
O-AB485669	42	AGAGATCCCTGGATCTTTGGA	TRUE		SCCPDH			chr1:246920083-246920105	0.780	4	0.703
O-AB485669	42	AGAGATCCCTGGATCTTTGGA	TRUE		ZPLDI			chr3:102047288-102047310	0.722	2	0.788
O-KU168297	42	AGAGATCCCTGGATCTTTGGG						chr12:57446538-57446560	0.783	4	0.585
C-KC156213	42	AGACATCCCTGATTTGTGGG						chr12:108226404-108226426	0.844	4	0.642
O-KU168282	40	GCAGAAATCCCTGGATCTCTG	TRUE		ITGA9			chr3:37542153-37542175	0.754	4	0.605
A1-AB287379	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
A1-AB287379	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
A1-AB287379	78	CTACTTCCCTGATTTGGCAGA						chr6:27068888-2706910	0.875	2	0.563
B-HM469982	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:20768095-20768117	0.799	4	0.862
B-HM469982	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
B-HM469982	78	CTACTTCCCTGATTTGGCAGA	TRUE		AUTS2			chr6:27068888-2706910	0.875	2	0.563
G-KU168277	78	ATTCTTCCAGATTTGGCAGA	TRUE		MYLK4			chr7:69465760-69465782	0.714	4	0.573
A1-AB253429	77	GCTACTTCCCTGATTTGGCAG	TRUE		AUTS2			chr5:20768095-20768117	0.799	4	0.862
A1-AB253429	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
A1-AB253429	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
B-EF363127	78	CTACTTCCCTGATTTGGCAAA						chrX:31060581-31060603	0.711	3	0.522
C-AB485645	78	CTACTTCCCTGATTTGGCAAA						chrX:31060581-31060603	0.711	3	0.522
D-JX236679	78	CTACTTCCCTGATTTGGCAAA	TRUE		MYLK4			chrX:31060581-31060603	0.711	3	0.522
G-AF196748	78	ATACTTCCAGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.772	3	0.563
A1-AB485632	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
A1-AB485632	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
A1-AB485632	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
B-AB604947	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
B-AB604947	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
B-AB604947	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
D-KU168272	78	TTACTTCCCTGATTTGGCAAA						chrX:31060581-31060603	0.711	3	0.522
G-KU168302	78	ATTCTTCCAGATTTGGCAGA	TRUE		AUTS2			chr7:69465760-69465782	0.714	4	0.573
A1-AF196742	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
A1-AF196742	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
A1-AF196742	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
B-GQ386793	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
B-GQ386793	77	GCTACTTCCCTGATTTGGCAG	TRUE		MYLK4			chr5:34093603-34093625	0.799	4	0.862
B-GQ386793	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
D-JX236668	78	CTACTTCCCTGATTTGGCAAA						chrX:31060581-31060603	0.711	3	0.522
G-AB287004	78	ATTCTTCCAGATTTGGCAGA	TRUE		AUTS2			chr7:69465760-69465782	0.714	4	0.573
B-AB731663	77	GCTACTTCCCTGATTTGGCAG						chr5:20768095-20768117	0.799	4	0.862
B-AB731663	77	GCTACTTCCCTGATTTGGCAG	TRUE		AUTS2			chr5:34093603-34093625	0.799	4	0.862
B-AB731663	78	CTACTTCCCTGATTTGGCAGA	TRUE		MYLK4			chr6:27068888-2706910	0.875	2	0.563
G-AF196747	78	ATTCTTCCAGATTTGGCAGA	TRUE		AUTS2			chr7:69465760-69465782	0.714	4	0.573
A1-AB287379	95	AGAAATACACACAGGCCA	TRUE		LINC00861			chr8:126962194-126962216	0.875	2	0.514
A1-AB287379	97	AAATTACACACAGGCCAGG						chr9:34356238-34356260	0.807	4	0.538

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Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
A1-AB287379	105	ACCAGGCCACGGAAATCAGAT	TRUE		VANGL2			chr1:160370369-160370391	0.758	4	0.624
C-AF196733	97	AATTACACACCGGGACCCAGG						chr9:34356238-34356260	0.800	4	0.538
D-AB485651	94	GCAAAACACTACAGGGCCAGG	TRUE		EPS8			chr12:15794978-15795000	0.746	4	0.629
D-AB485651	105	ACAGGGCCAGGGATTAGATA						chr8:57160913-57160935	0.708	4	0.756
D-AB485651	112	CCAGGGATTAGATATCCACT						chr4:55887307-55887329	0.788	4	0.788
G-KUI168277	95	AAATTACACACACAGGGCCCA		TRUE	LINC00861			chr8:126962194-126962216	0.875	2	0.514
G-KUI168277	97	GAATTACACACAGGGCCCAAG						chr9:34356238-34356260	0.807	4	0.538
O-XY623602	104	CACAGGACACAGGAACCCAGG		TRUE	LINC00861			chr8:103757690-103757712	0.783	3	0.559
A1-AB253429	95	AGAAATTACACACAGGGCCCA		TRUE	LINC00861			chr8:126962194-126962216	0.875	2	0.514
A1-AB253429	97	AATTACACACAGGGCCCAAG						chrX:87503599-87503621	0.929	1	0.582
A1-AB253429	97	AATTACACACAGGGCCCAAG						chr10:19237281-19237303	0.824	2	0.535
A1-AB253429	97	AATTACACACAGGGCCCAAG						chr2:107868897-107868919	0.807	3	0.547
A1-AB253429	97	AATTACACACAGGGCCCAAG						chr12:49536199-49536221	0.706	4	0.667
G-AF196748	95	AGAAATTACACATCAGGACCA	TRUE		SETDB1			chr1:150904508-150904530	0.824	2	0.514
A1-AB485632	95	AGAAATTACACACAGGGCCCA	TRUE		LINC00861			chr8:126962194-126962216	0.875	2	0.514
A1-AB485632	97	AATTACACACAGGGCCCAAG						chr9:34356238-34356260	0.807	4	0.538
G-KUI168302	110	GGCCAGGGACTAGACTCCCA		TRUE	SGCD			chr5:174135570-174135592	0.923	2	0.649
A1-AF196742	112	CCAGGGCCAGATTCCCGCT		TRUE				chr5:155517179-155517201	0.750	3	0.763
A1-AF196742	97	AATTACACACAGGACCCAGG						chr9:34356238-34356260	0.857	4	0.538
A1-AF196742	103	ACACAGGACCCAGGGCCCAAG	TRUE		NTSR1			chr20:61393217-61393239	0.867	3	0.617
A1-AF196742	103	ACACAGGACCCAGGGCCCAAG						chr6:94887281-94887303	0.706	4	0.574
A1-AF196742	110	GACAGGGCCAGATTCCCGCT	TRUE		SNORD109B			chr15:25424827-25424849	0.725	4	0.765
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT	TRUE		FAM90A1			chr12:8374111-83741133	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr4:9178179-9178201	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT		TRUE	LOC100506990			chr8:12029963-12029985	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT	TRUE		FAM90A25P			chr8:12272282-12272304	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7117721-7117743	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7125343-7125365	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7132965-7132987	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7140587-7140609	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7148209-7148231	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT	TRUE		FAM66B			chr8:7406270-7406292	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT		TRUE				chr8:7413915-7413937	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT	TRUE		FAM90A7P			chr8:7421565-7421587	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT	TRUE		FAM90A7P			chr8:7429210-7429232	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT		TRUE		DEFB103B_1		chr8:7436859-7436881	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7576260-7576282	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7583908-7583930	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7591556-7591578	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7599203-7599225	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7606851-7606873	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7614499-7614521	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7622147-7622169	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7629795-7629817	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7877203-7877225	0.721	3	0.914
C-KCI156124	112	CCAGGGTTCAGATTCCCGCT						chr8:7884851-7884873	0.721	3	0.914
D-JX236668	112	CCAGGGATTAGATATCCACT						chr4:55887307-55887329	0.788	4	0.788
D-JX236668	95	AAAATTACACACAGGGCCCA	TRUE		LINC00861			chr8:126962194-126962216	0.700	3	0.514

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Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
D-JX236668	97	AATTACACACAGGGCCAGG						chr9:34356238-34356260	0.807	4	0.538
G-AB287004	110	GGCCAGGGACTAGACTCCCA		TRUE	<i>LINC00861</i>			chr5:174135570-174135592	0.923	2	0.649
A1-AB253422	95	AGAATTATACACAGGGCCA						chr8:126962194-126962216	1.000	1	0.514
A1-AB253422	95	AGAATTATACACAGGGCCA						chr10:86657342-86657364	0.753	4	0.503
A1-AB253422	97	AATTATACACAGGGCCAGG						chr9:34356238-34356260	0.869	3	0.538
A1-AB253422	97	AATTATACACAGGGCCAGG						chrX:875035599-87503621	0.714	1	0.582
A1-AB253422	99	TTATACACAGGGCCAGGGA		TRUE	<i>SSU72</i>			chr1:1494938-1494960	0.723	4	0.582
G-AF196747	103	ACACCAGGACAGGACTAG		TRUE	<i>TMEM209</i>			chr7:129827361-129827383	0.779	2	0.684
G-AF196747	110	GACCAGGACTAGACTCCCA						chr5:174135570-174135592	0.738	3	0.649
A1-AB287379	154	CTAGTACCAGTTGATCCAGG						chr9:83857865-83857887	0.738	3	0.715
B-HM469982	157	GTACCAGTGGAGCCAGAGAA						chr3:30237368-30237390	0.707	3	0.552
B-HM469982	160	CCAGTGGAGCCAGAGAAAGT						chr3:149941221-149941243	0.788	4	0.573
D-AB485651	157	GTACCAGTTGAGCCACAGGT		TRUE	<i>C4orf22</i>			chr4:81481621-81481643	0.754	3	0.785
O-AY623602	158	TACCAGTGTGAGAACTGAG		TRUE				chr1:119242210-119242232	0.800	4	0.510
B-EF363127	154	CTAGTACCAGTTGAGACAGA		TRUE	<i>ATG2A</i>			chr11:64684245-64684267	0.760	3	0.634
B-EF363127	159	ACCAGTGGAGCAGAGAAAGG		TRUE	<i>RALYL</i>			chr8:85158379-85158401	0.791	4	0.628
B-EF363127	160	CCAGTGGAGCAGAGAAAGT						chr2:207485890-207485912	0.701	4	0.643
G-AF196748	157	GTACCAGTGGATCCAGCAGA						chr3:149941221-149941243	0.909	3	0.573
G-KUI68302	157	GTACCAGTGGATCCAGCAGA						chr3:14715437-14715459	0.813	1	0.604
O-KUI68298	154	CTAGTACCAGTTGAGAAAGA						chr3:14715437-14715459	0.813	1	0.604
O-KUI68298	154	CTAGTACCAGTTGAGAAAGA						chr15:37680272-37680294	0.852	3	0.602
O-KUI68298	158	TACCAGTGTGAGAAAGAGG		TRUE	<i>RAPIA</i>			chr1:112094876-112094898	0.737	3	0.539
O-KUI68298	159	ACCAGTGTGAGAAAGAGG						chr22:34570763-34570785	0.738	4	0.634
O-KUI68298	159	ACCAGTGTGAGAAAGAGG		TRUE	<i>DSP</i>			chr6:7563874-7563896	0.824	4	0.559
B-GQ386793	157	GTACCAGTGGAGCCAGAGAA						chr8:37876383-37876405	0.735	4	0.551
B-GQ386793	160	CCAGTGGAGCCAGAGAAAGT						chr3:30237368-30237390	0.707	3	0.552
G-AB287004	156	AGTACCAATAGATCCAGCAG		TRUE	<i>DLGAP2</i>			chr3:149941221-149941243	0.788	4	0.573
F1-AB485657	158	TACCAGTTGAGCCAGAGGAG	TRUE		<i>WDR78</i>			chr8:1616110-1616132	0.781	3	0.559
G-AF196747	156	AGTACCAATGAAACCAGAAAG						chr1:67299340-67299362	0.714	2	0.628
O-KUI68282	155	TAGTGCCAGTTGCAAGGAG						chr2:240647785-240647807	0.829	2	0.537
O-KUI68282	159	GCCAGTGTCAAAGGAGGAGG		TRUE	<i>TOM1L2</i>			chr6:142124604-142124626	0.813	4	0.506
B-HM469982	165	GGAGCCAGAGAGGTAGAAAG						chr17:17791260-17791282	0.743	3	0.545
B-HM469982	165	GGAGCCAGAGAGGTAGAAAG						chr6:156402597-156402619	1.000	2	0.505
B-HM469982	167	AGCCAGAGAAAGTAAAGAG		TRUE	<i>RALYL</i>			chr8:41173055-41173077	0.929	1	0.521
C-AF196733	166	GACCCAAAGTAAAGTAAAGA		TRUE	<i>DMMBP-ASI</i>			chr8:85232552-85232574	0.836	2	0.540
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG		TRUE				chr10:101698828-101698850	0.813	2	0.680
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG		TRUE	<i>KCNK2</i>			chr1:215286770-215286792	0.923	3	0.545
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG		TRUE	<i>RHD</i>			chr1:25604058-25604080	0.900	2	0.658
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG		TRUE	<i>RHCE</i>			chr1:25742248-25742270	0.807	4	0.843
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG						chr19:15668376-15668398	0.807	4	0.921
O-AY623602	166	TCAGAAGCTGAGCCAGAAAG						chr19:48885749-48885771	0.746	4	0.636
O-AY623602	167	CAGAAAGTGGCCAGAAAGA		TRUE	<i>ACACA</i>			chr3:112871308-112871330	0.941	3	0.607
A1-AB253429	165	GATGAAGTAAAGTAAAGAGG						chr17:35717329-35717351	0.800	1	0.619
A1-AB253429	166	GGATGAAGTAAAGTAAAGAGG						chr12:63344314-63344336	0.714	1	0.546
A1-AB253429	167	ATGAAGTAAAGTAAAGAGG						chr3:27132976-27132998	0.929	3	0.510
B-EF363127	165	GGAGACAGAGAAAGGTAGAAAG						chr2:108033011-108033033	0.738	3	0.514
B-EF363127	165	GGAGACAGAGAAAGGTAGAAAG						chr15:35001637-35001659	0.831	2	0.654

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Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
B-EF363127	165	GGAGACAGAGAAGGTAGAAG						chr13:114205281-114205303	0.813	4	0.543
B-EF363127	167	AGACAGAGAAAGGTAGAAG	TRUE		<i>DNMBP-ASI</i>		chr10:101698828-101698850	0.938	1	0.680	
B-EF363127	167	AGACAGAGAAAGGTAGAAG	TRUE		<i>FBXLI7</i>		chr5:107410347-107410369	0.789	2	0.503	
B-EF363127	167	AGACAGAGAAAGGTAGAAG	TRUE		<i>CEMIP</i>		chr15:81224835-81224857	0.789	1	0.676	
B-EF363127	167	AGACAGAGAAAGGTAGAAG	TRUE		<i>MNVAT3</i>		chr3:139354366-139354388	0.789	3	0.527	
C-AB485645	167	ACCAAGGAAAGTAGAAGAG	TRUE		<i>LRRC61</i>		chr7:150021447-150021469	0.867	3	0.598	
O-AB485669	166	ACAGAAGATGAGGCAAAAAG	TRUE		<i>QKI</i>		chr6:163969438-163969460	0.818	4	0.586	
O-AB485669	166	ACAGAAGATGAGGCAAAAAG	TRUE				chr11:55821275-55821297	0.733	2	0.880	
O-AB485669	166	ACAGAAGATGAGGCAAAAAG	TRUE				chr16:13521570-13521592	0.720	3	0.690	
C-JN188292	167	ACCCAGGAAAGTAGAAGAG	TRUE		<i>LRRC61</i>		chr7:150021447-150021469	0.867	3	0.598	
G-KUI68302	166	GATCCAGCAGAGGTAGAAGG	TRUE		<i>EXOC6B</i>		chr2:73022009-73022031	0.765	3	0.826	
O-KUI68298	166	TCAGAAGAAGAGGCAGAAAAG	TRUE				chr12:67538797-67538819	0.824	3	0.606	
O-KUI68298	166	TCAGAAGAAGAGGCAGAAAAG	TRUE				chr8:133475166-133475188	0.803	4	0.592	
O-KUI68298	166	TCAGAAGAAGAGGCAGAAAAG	TRUE		<i>KCNQ3</i>		chr6:32125374-32125396	0.795	4	0.575	
B-GQ386793	165	GGAGCCAGAGAAGGTAGAAG	TRUE				chr8:41173055-41173077	0.929	1	0.521	
B-GQ386793	165	GGAGCCAGAGAAGGTAGAAG	TRUE		<i>RALYL</i>		chr8:85232552-85232574	0.836	2	0.540	
B-GQ386793	167	AGCCAGAGAAGGTAGAAGAG	TRUE		<i>DNMBP-ASI</i>		chr10:101698828-101698850	0.813	2	0.680	
G-AB287004	166	GATCCAGCAGAGGTAGAAGG	TRUE		<i>EXOC6B</i>		chr2:73022009-73022031	0.765	3	0.826	
O-KUI68297	166	ACAAAAGAGAGGCAGAAAAG	TRUE				chr1:221242892-221242914	0.933	3	0.534	
O-KUI68297	166	ACAAAAGAGAGGCAGAAAAG	TRUE		<i>TNSI</i>		chr2:218750973-218750995	0.848	3	0.813	
A1-AB253422	167	ATCCAGAGAAAGTAGAAGAG	TRUE				chr12:59865524-59865546	0.878	4	0.680	
G-AF196747	165	GAACCAGAAAGGTAGAAGG	TRUE		<i>CCDC94</i>		chr1:108090386-108090408	0.786	3	0.606	
D-AB485651	178	GTAGAGGAGGACACTGAAGG	TRUE		<i>UST</i>		chr19:4253243-4253265	0.900	4	0.515	
D-JX236679	178	GTAGAGGAGGACACTGAAGG	TRUE		<i>UST</i>		chr6:149245619-149245641	0.788	3	0.715	
D-JX236668	178	GTAGAGGAGGACACTGAAGG	TRUE		<i>UST</i>		chr6:149245619-149245641	0.788	2	0.715	
A1-AB287379	221	CTATATGCCAACATGGAATG					chrX:94294537-94294559	0.856	4	0.551	
B-HM469982	224	TGAGCTGCATGGATGGAG					chr11:126028693-126028715	0.774	4	0.567	
D-AB485651	221	CTATATGCCAGCATGGAATG					chr2:148008598-148008620	0.706	4	0.530	
D-AB485651	225	ATGCCAGCATGGAATGGAGG					chr5:160341758-160341780	0.700	4	0.705	
A1-AB253429	221	CTATATGCCAACATGGAATG					chrX:94294537-94294559	0.856	4	0.551	
O-AB485669	225	TTGTAACCATGGCTTTGAAG					chr5:139139708-139139730	0.700	2	0.625	
A1-AB485632	221	CTATATGCCAACATGGAATG					chr8:140387431-140387453	0.735	3	0.679	
C-JN188292	219	CCCTATGAGCCAGCATGGAG	TRUE		<i>SLC35F3</i>		chrX:94294537-94294559	0.856	4	0.551	
G-KUI68302	225	CTGCCAGCATGGAATGGAGG					chr1:234208498-234208520	0.729	4	0.529	
O-KUI68298	220	CCAGTTGTGATCATGGCCA	TRUE		<i>ANKS1A</i>		chr5:160341758-160341780	0.700	4	0.705	
A1-AF196742	221	CTATATGCCAACATGGAATG	TRUE				chr6:35041095-35041117	0.909	2	0.641	
B-GQ386793	224	TGAGCTGCATGGATGGAG	TRUE		<i>COL9A2</i>		chrX:94294537-94294559	0.856	4	0.551	
F1-AF196763	214	CTACACCCCATGAGCCAGCA	TRUE				chr1:40779291-40779313	0.750	3	0.726	
A1-AB253422	221	CTATATGCCAGCATGGAATG	TRUE				chr2:148008598-148008620	0.706	4	0.530	
D-M22639	221	ATGCCAGCATGGAATGGAGG	TRUE		<i>MRPS9</i>		chr5:160341758-160341780	0.827	4	0.705	
D-M22639	225	CTGCCAGCATGGAATGGAGG	TRUE				chr2:105694014-105694036	0.700	4	0.535	
G-AF196747	225	CTGCCAGCATGGAATGGAGG	TRUE				chr5:160341758-160341780	0.700	4	0.705	
O-KUI68282	224	CTTGTAAATCATGGCCCTGAG					chr20:39476871-39476893	0.807	3	0.678	
G-KUI68277	255	AGAAGTCTGGTATGGAGAT					chr2:84300393-84300415	0.753	3	0.525	
C-AB485645	253	AGAGAAGTATTAAGTTGAA					chr1:212812049-212812071	0.878	3	0.539	
O-AB485669	259	ATACTGAAATGCCAGTTTGA					chr9:84782026-84782048	0.807	4	0.632	

(continued)

Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
A1-AB485632	253	AGAGAAACAGTAAATGTGGAA		TRUE	SORCS3			chr10:106500528-106500550	0.762	4	0.706
O-KUI168298	255	GGAAATGCTAAAGTGGCAGT		TRUE	SORCS3		chr2:78287187-78287209	0.765	4	4	0.615
A1-AF196742	253	AGAGAAACAITTAATGTGGAA		TRUE	SORCS3		chr10:106500528-106500550	0.700	4	4	0.706
G-AB287004	259	GTGCTGGTATGGAAGTTTGA					chr9:87916887-87916909	0.713	3	3	0.511
O-KUI168297	259	ATACTGAAATGGCAGTTTGA					chr9:84782026-84782048	0.807	4	4	0.632
F1-AB485657	253	GGAGAAGTACTGATGTGGAA		TRUE	SORCS3		chr9:137933132-137933154	0.941	3	3	0.695
F1-AB485657	253	GGAGAAGTACTGATGTGGAA		TRUE	SORCS3		chr10:106500528-106500550	0.755	4	4	0.706
G-AF196747	255	AGAAAGTCTGGTATGGAGAT					chr2:84300393-84300415	0.753	3	3	0.525
O-KUI168282	259	ATACTGAAATGGCAGTTTGA					chr9:84782026-84782048	0.807	3	3	0.632
B-HM469982	312	GCTGCATCCGGAGTACTACA		TRUE	DIP2C		chr5:162139400-162139422	0.755	4	4	0.513
A1-AB253429	315	ACATCCGGAGTTTTACAAAG					chr10:645683-645705	0.829	4	4	0.618
B-EF363127	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.755	4	4	0.513
C-AB485645	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.839	3	3	0.513
D-JX236679	315	GCTATCCGGAGTACTCAAAG		TRUE	ADAMTS3		chr4:73390611-73390633	0.727	2	2	0.535
G-AF196748	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.755	4	4	0.513
O-AB485669	315	CCACCCAGAGTCTCCCCA					chr12:105633288-105633310	0.947	3	3	0.598
O-AB485669	318	CCCAGAGTCTCCCCAAG		TRUE	NRXN3		chr14:79838771-79838793	0.745	4	4	0.573
A1-AB485632	315	GCTATCCGGAGTACTCAAAG		TRUE	ADAMTS3		chr4:73390611-73390633	0.727	2	2	0.535
D-KUI168272	315	GCATCCGGAGTACTCAAAG		TRUE	ADAMTS3		chr4:73390611-73390633	0.727	2	2	0.535
B-GQ386793	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.755	4	4	0.513
F1-AF196763	315	ACATCCGGAGTACTCAAAG		TRUE	SLC05A1		chr8:70730202-70730224	0.791	4	4	0.592
G-AB287004	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.755	4	4	0.513
O-KUI168297	313	ATCCACCCAGAGCTCTTCCA					chr7:36149956-36149978	0.784	3	3	0.706
B-AB731663	312	GCTGTTCCGGAGTACTACA		TRUE		ZNF83_1	chr19:52690031-52690053	0.739	4	4	0.798
F1-AB485657	315	ACATCCGGAGTACTCAAAG		TRUE	SLC05A1		chr8:70730202-70730224	0.791	4	4	0.592
G-AF196747	312	GCTGCATCCGGAGTACTACA					chr5:162139400-162139422	0.755	4	4	0.513
A1-AB287379	384	GGGAGGTGTGTTTGGGCG					chr9:132232322-132232344	0.714	4	4	0.539
A1-AB287379	395	GTTTGGCGGAGTTGGGGAG					chr10:103333887-103333909	0.750	3	3	0.529
B-HM469982	375	GGACTTCCAGGAGGCGGTG					chr3:193667547-193667569	0.769	3	3	0.715
B-HM469982	385	GCGAGCTGGCCCTGGGCGG					chr1:229896409-229896431	0.714	4	4	0.521
B-HM469982	400	GCGGGACTGGGAGTGGCG		TRUE	DLCI		chr8:12991014-12991036	0.844	3	3	0.560
B-HM469982	400	GCGGGACTGGGAGTGGCG		TRUE	FXSD1		chr19:35632217-35632239	0.731	4	4	0.517
D-AB485651	380	TCCAGGGAGGCGTGACATG					chr5:162920275-162920297	0.923	4	4	0.615
D-AB485651	395	GACATGGCGGGACTGGGAG		TRUE	GRM1		chr5:146658371-146658393	0.857	3	3	0.566
G-KUI168277	375	GGACTTCCGGGAGGCGGTG	TRUE		GLIPR2		chr9:36144888-36144910	0.737	4	4	0.520
G-KUI168277	375	GGACTTCCGGGAGGCGGTG					chr3:193667547-193667569	0.717	4	4	0.715
G-KUI168277	380	TTCCGGGAGGCGTGGACTG					chr12:89346843-89346865	0.738	4	4	0.557
G-KUI168277	390	GCGTGGACTGGAGGCGCTG					chr7:119251043-119251065	0.813	4	4	0.563
O-AY623602	385	TGTGGAGGGATAGGGGCGG					chr9:98458750-98458772	0.754	4	4	0.503
A1-AB253429	384	GGGAGGTGTGTTTGGGCG					chr9:132232322-132232344	0.714	4	4	0.539
A1-AB253429	395	GTTTGGCGGAGTTGGGGAG					chr10:103333887-103333909	0.750	3	3	0.529
B-EF363127	395	GGGAGGTGTGTTTGGGCG		TRUE	CTNND2		chr10:103333887-103333909	0.750	3	3	0.529
B-EF363127	400	GGGAGGTGTGTTTGGGCG		TRUE	DLCI		chr5:11765460-11765482	0.714	2	2	0.634
B-EF363127	400	GGCGGACAGGGAGTGGCG		TRUE	DLCI		chr8:12991014-12991036	0.909	2	2	0.560
C-AB485645	394	GGTCTGGCGGACTGGGAG		TRUE	CAB39L		chr13:49960885-49960907	0.747	4	4	0.517
G-AF196748	375	GGACTTCCAGGAGGCGCGG		TRUE	LRP4		chr11:46921188-46921210	0.764	4	4	0.641
G-AF196748	375	GGACTTCCAGGAGGCGCGG		TRUE	PLA2R1		chr2:160917025-160917047	0.747	4	4	0.801
G-AF196748	394	GGCTGGGAGGCGTGGGGA		TRUE	GRK5		chr10:120971281-120971303	0.733	4	4	0.648
O-AB485669	383	ACGCTGGGAGGACAAAGGGG		TRUE		SLC2A11_3	chr22:23876264-23876286	0.813	4	4	0.614

(continued)

Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
A1-AB485632	384	GGGAGGGTGTGGTTTGGGGC						chr9:132232322-132232344	0.714	4	0.539
A1-AB485632	395	GTTTGGGCGGAGTTGGGGAG					chr10:103333887-103333909	0.750	3	3	0.529
C-JN188292	395	GTCTGGGCGGACTGGGGAG	TRUE		<i>DOK2</i>		chr8:21638068-21638090	0.875	4	4	0.573
C-JN188292	395	GTCTGGGCGGACTGGGGAG					chr8_gl000197_random:36671-36693	0.875	4	4	0.573
D-KUI68272	374	GGACTTTCGGGAGGCGGTG	TRUE		<i>GLIPR2</i>		chr9:36144888-36144910	0.737	4	4	0.520
D-KUI68272	374	GGACTTTCGGGAGGCGGTG					chr3:193667547-193667569	0.717	4	4	0.715
D-KUI68302	394	GGAGCTTCAGGGAGGCGGG					chr1:229896409-229896431	0.714	3	3	0.521
G-KUI68302	394	GGCTGGGAGGGTTGGGGA			<i>GRK5</i>		chr10:120971281-120971303	1.000	3	3	0.648
A1-AF196742	373	GGACTTTCAGGGAGGCGGTG					chr8:49363277-49363299	0.737	3	3	0.571
A1-AF196742	376	ACTTTCAGGGAGGAGTGG					chr2:238822868-238822890	0.765	3	3	0.607
A1-AF196742	389	GGAGTGGTTGGCGGAGTGG			<i>IFT122</i>		chr3:129229408-129229430	0.941	3	3	0.505
A1-AF196742	397	TTGGCGGAGTGGGAGTGG			<i>SDK2</i>		chr17:71555711-71555733	0.723	3	3	0.507
B-GQ386793	375	GGACTTTCAGGGAGGCGGTG					chr3:193667547-193667569	0.769	3	3	0.715
B-GQ386793	385	GGAGGCGTGGCTGGGGCGG					chr1:229896409-229896431	0.714	3	3	0.521
B-GQ386793	400	GCGGACTGGGAGTGGCGG			<i>DLCI</i>		chr8:12991014-12991036	0.844	3	3	0.560
B-GQ386793	400	GCGGACTGGGAGTGGCGG			<i>FXYP1</i>		chr19:35632217-35632239	0.731	4	4	0.517
C-KC156124	394	GGTCTGGCGGACTGGGAG			<i>CAB39L</i>		chr13:49960885-49960907	0.747	4	4	0.517
C-KC156124	400	GGCGGACTGGGAGTGGCCA			<i>ATP2B4</i>		chr1:203645478-203645500	0.708	4	4	0.625
D-JX236668	373	GGGACTTTCAGGGAGGAGT	TRUE		<i>CCDC136</i>	HILPDA_1	chr7:128455924-128455946	0.867	2	2	0.505
D-JX236668	379	TTCCAGGAGGAGTAACAGG			<i>CBR4</i>		chr4:169900257-169900279	0.820	3	3	0.617
D-JX236668	395	ACAGGGCGGGACTGGGAG			<i>KIF19</i>		chr17:72336104-72336126	0.817	4	4	0.566
D-JX236668	395	ACAGGGCGGGACTGGGAG					chr3:6172058-6172080	0.817	4	4	0.646
F1-AF196763	394	CCAGAGGGCGGACAAAGGA			<i>EXOC7</i>		chr4:174649420-174649442	0.871	4	4	0.818
F1-AF196763	394	CCAGAGGGCGGACAAAGGA			<i>PEBP4</i>		chr17:74083006-74083028	0.800	4	4	0.869
F1-AF196763	395	CAGAGGGCGGACAAAGGAG				KIAA1967_2	chr8:22604104-22604126	0.913	3	3	0.533
G-AB287004	394	GGCTGGGAGGGCTGGGGGA			<i>GRK5</i>	KIAA1967_1	chr10:120971281-120971303	0.733	4	4	0.648
O-KUI68297	383	AGCTGGGAGGGACAAAGGGG				SLC2A11_3	chr22:23876264-23876286	0.813	4	4	0.614
A1-AB253422	384	GGGAGGGTGTGGTTGGGGC					chr9:132232322-132232344	0.714	4	4	0.539
A1-AB253422	395	GTTTGGGCGGAGTTGGGGAG					chr10:103333887-103333909	0.750	3	3	0.529
B-AB731663	375	GGACTTTCAGGGAGGCGGTG					chr3:193667547-193667569	0.769	3	3	0.715
B-AB731663	385	GGAGGCGTGGCTGGGGCGG					chr1:229896409-229896431	0.714	3	3	0.521
B-AB731663	400	GCGGACTGGGAGTGGCGG			<i>DLCI</i>		chr8:12991014-12991036	0.844	3	3	0.560
B-AB731663	400	GCGGACTGGGAGTGGCGG			<i>FXYP1</i>		chr19:35632217-35632239	0.731	4	4	0.517
D-M22639	374	GGACTTTCGGGAGGCGGTG	TRUE		<i>GLIPR2</i>		chr9:36144888-36144910	0.737	4	4	0.520
D-M22639	374	GGACTTTCGGGAGGCGGTG					chr3:193667547-193667569	0.717	4	4	0.715
D-M22639	379	TTCCGGGAGGCGTGGACTG					chr12:89346843-89346865	0.738	4	4	0.557
F1-AB485657	382	CCAGAGGGCGGACAGAGGG	TRUE		<i>LOXL4</i>		chr10:100022646-100022668	0.875	4	4	0.552
F1-AB485657	382	CCAGAGGGCGGACAGAGGG				FBXO2_1	chr1:11653942-11653964	0.734	4	4	0.816
						FBXO6_3					
						FBXO2_2					
						FBXO4_1					
						FBXO6_2					
						FBXO4_2					
F1-AB485657	382	CCAGAGGGCGGACAGAGGG					chr10:133184476-133184498	0.730	4	4	0.701
F1-AB485657	394	CCAGAGGGCGGACTGGGGGA					chrX:1226723-1226745	0.726	3	3	0.560
F1-AB485657	394	CCAGAGGGCGGACTGGGGGA					chrY:1176723-1176745	0.726	3	3	0.560
G-AF196747	394	GGCTGGGAGGGCTGGGGGA	TRUE		<i>GRK5</i>		chr10:120971281-120971303	0.733	4	4	0.648

(continued)

Supplementary Table S1. (Continued)

Sample	Position	gRNA template	In exon	In intron	Gene	In promoter	Promoters	UCSC coordinates	CFD score	Mismatches	gRNA efficacy
O-KU168282	383	AGTGTGGGAGGGATAAGGGG						chr9:36169095-36169117	1.000	3	0.626
D-AB485651	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
G-KU168277	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
O-AY623602	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
A1-AB253429	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
D-JX236679	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
G-AF196748	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
O-AB485669	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
A1-AB485632	417	GTTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
D-KU168272	417	GTTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.857	3	0.691
D-KU168272	417	GTTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.827	4	0.843
D-KU168272	417	GTTAACCCCTCAGATGCTGCA						chr4:172066842-172066864	0.704	3	0.835
G-KU168302	418	CTAACCCCTCAGAAGCTGCAT			ULK4			chr3:41359425-41359447	0.704	3	0.835
O-KU168298	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
A1-AF196742	417	GCTAACCCCTCAGATGCTGCA						chr17:35124135-35124157	0.779	4	0.691
C-KC156124	417	GCCAAAGCCCTCAGATGCTGCA						chr7:54454451-54454473	0.700	3	0.695
D-JX236668	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
F1-AF196763	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
G-AB287004	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
O-KU168297	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
A1-AB253422	417	GCCAAAGCCCTCAGATGCTGCA						chr17:54454451-54454473	0.753	4	0.695
D-M22639	417	CTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
G-AF196747	418	CTAACCCCTCAGAAGCTGCAT						chr17:35124135-35124157	0.724	3	0.576
O-KU168282	417	GCTAACCCCTCAGATGCTGCA						chr7:114526254-114526276	0.779	4	0.691
G-KU168277	477	TAGACCAGATTTGAGCCTGG						chr19:43234740-43234762	0.717	4	0.608
G-KU168277	477	TAGACCAGATTTGAGCCTGG						chr19:43259950-43259972	0.717	4	0.608
G-AF196748	477	TAGACCAGATTTGAGCCTGG						chr19:43234740-43234762	0.717	4	0.608
G-AF196748	477	TAGACCAGATTTGAGCCTGG						chr19:43259950-43259972	0.717	4	0.608
G-KU168302	477	TAGACCAGATTTGAGCCTGG						chr19:43234740-43234762	0.717	4	0.608
G-KU168302	477	TAGACCAGATTTGAGCCTGG						chr19:43259950-43259972	0.717	4	0.608
O-KU168298	479	AATCAGGCTCAGCCCGGGA						chr19:1948101-1948123	0.714	4	0.532
A1-AF196742	479	GACCAGATAGAGCCCGGAG						chr1:194703942-194703964	0.933	4	0.583
C-KC156124	477	TAGACCAGATTTGAGCCTGG						chr19:43234740-43234762	0.717	4	0.608
C-KC156124	477	TAGACCAGATTTGAGCCTGG						chr19:43259950-43259972	0.717	4	0.608
F1-AF196763	477	TAGACCAGATTTGAGCCTGG						chr19:43234740-43234762	0.717	4	0.608
F1-AF196763	477	TAGACCAGATTTGAGCCTGG						chr19:43259950-43259972	0.717	4	0.608
G-KU168277	500	CTCTCTGCTAGCAAGGGAA						chr8:94190055-94190077	0.809	4	0.812
C-KC156124	503	TCTGGCCATCTAGAGAACC						chr10:133521808-133521830	0.836	3	0.684
G-AF196747	500	CTCTCTGCTAGCAGGGGAA						chr7:78117028-78117050	0.867	2	0.840
O-AY623602	546	TGCTTTTGAGTGAGAGCAG						chr2:188927750-188927772	0.751	2	0.681
B-AB731663	544	TGCTCTGAGTGCTTAAAG	TRUE					chr7:130035972-130035994	0.700	4	0.584
A1-AF196742	600	AGAGATACCTCAGACCAATG	TRUE					chr12:109366191-109366213	0.738	4	0.645
B-AB731663	607	CCTCAGACCAATTAAGTCAG				TRUE	CHP2_1	chr16:23754470-23754492	0.750	3	0.566
							CHP2_2				
C-KC156213	600	AGAGATCCCTCAGATCCATT	TRUE					chr10:22174409-22174431	0.750	2	0.598
C-KC156213	600	AGAGATCCCTCAGATCCATT	TRUE					chr15:77144670-77144692	0.750	2	0.598
C-KC156213	600	AGAGATCCCTCAGATCCATT						chr1:75649945-75649967	0.750	2	0.598
C-KC156213	600	AGAGATCCCTCAGATCCATT						chr4:71964816-71964838	0.750	2	0.559
C-KC156213	600	AGAGATCCCTCAGATCCATT	TRUE					chr14:60114158-60114180	0.750	3	0.665