

Table S2

Gene to gene fragments						
Generic crRNAs						
#	Pool	Target gene(s)	Cut site	Direction	crRNA sequence	On-target score
1	1	3DS2; 2DL9; 2DL6; 2DL8; 3DL4; 2DS4; 2DL7; DP	intron 4	Forward	ATAACAGAGGACAGACACAG	81,2
2	1	3DS2; 2DL9; 2DL6; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP; 3DL1	intron 4	Forward	CAGACCAGGTGTCATAACAG	76,9
3	1	3DL3; 2DL9; 2DL6; 2DL5; 2DL8; 3DL5; 3DL4; 2DL7; DP; DL4; 3DL1	intron 4	Forward	GACAAGGAAGAACCTCCCTG	76,0
4	1	3DL3; 2DL9; 2DL6; 2DS4; 2DL7	intron 4	Forward	GTGTGAGGGGAGCTGTGACA	64,4
5	1	3DS2; 2DL9; 2DL6; 2DL8; 3DL5; 3DL4; 2DL7; DP	intron 4	Forward	ACATCAAGTCACCAATCCA	64,2
6	1	3DS2; 2DL6; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP; 3DL1	intron 3	Reverse	CCTATGTGGATGGAGCCTGG	71,7
7	1	3DS2; 2DL6; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP	intron 3	Reverse	GAATTGGAATCCTTGGCAGG	64,0
8	1	3DS2; 3DL5; 3DL4; DP; 2DL4; 3DL1	intron 3	Reverse	ACACCCCCACCAGAAAGCTCT	58,1
12	1	3DL3; 3DL1	exon 4	Reverse	GCATCTGTAGGTCCCTGCAA	70,1
14	1	2DL9; 2DL6; 2DL5; 2DL8	exon 3	Reverse	CTGTGACCACGATCACCGAG	76,5
15	1	3DS2; 3DL5; 3DL4; 2DL7; 2DL4	exon 3	Reverse	CTGTGACCACGATCACCGAG	80,5
16	1	2DL9; 2DL6; 2DL5; 2DL8	intron 3	Reverse	CCTGTGACCACGATCACCGAG	74,6
17	1	3DS2; 3DL5; 3DL4; 2DL7; 2DL4	intron 3	Reverse	CCTGTGACCATGATACCAG	75,9
18	1	2DL9; 2DL6; 2DL5; 2DL8	intron 3	Reverse	ACCTGTGACCACGATCACCA	67,3
19	1	2DL5; 2DL4	intron 3	Forward	ATTGTAGCCCAGGAAGAACAA	70,3
20	1	2DL5; 2DL4	intron 3	Forward	AGTTAAAAAACCACAAAGAA	66,9
Specific crRNAs						
9	1	3DL3	exon 4	Reverse	CGTCTCTCCGATTCACCA	67,1
10	1	3DL3	exon 4	Reverse	TGACCTGGAAACCCGATCG	71,4
11	1	3DL1	exon 4	Reverse	CATCATGGATCTGCTCAACG	73,4
13	1	3DL3	intron 4	Forward	CAGGGAAGATAAAAGATGTG	69,0
21	1	LILR	intron 5	Forward	GAGGAATCATGCTTAGACTG	61,8
22	1	LILR	intron 5	Forward	AGACTGAGGGTAGAACAGATGG	71,3
23	1	LILR	intron 5	Forward	CAGTGCTACACTGAGACGAA	64,7
24	1	FCAR	intron 2	Reverse	TGGGGCTCACACCCATTAGG	62,5
25	1	FCAR	intron 2	Reverse	AGAAGACATGGATGGACGTG	63,0
26	1	FCAR	intron 2	Reverse	GGGAATACTAGCTAACACAGGG	75,5
Gene fragments						
#	Pool	Target gene(s)	Cut site	Direction	crRNA sequence	On-target score
27	2	3DL3; 3DS2; 2DL9; 2DL5; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP; 3DL1	intron 1	Forward	GTTGTGTTGGTAGCTCTGGA	60,4
28	2	3DL3; 3DS2; 2DL9; 2DL5; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP; 3DL1	intron 1	Forward	TGTGTGGTAGCTCTGGAA	67,1
29	2	2DL6; 2DL8; 2DS4; DP; 3DL1	5'UTR	Forward	GGTCAACATGTTAACCTGCAT	66,7
30	2	3DL3; 3DS2; 2DL5; 3DL5; 3DL4; 2DL7	intron 1	Forward	TGAGTCTGGAAAGGAATCG	64,2
31	2	3DS2; 2DL9; 2DL6; 2DL5; 2DL8; 3DL5; 3DL4; 2DS4; 2DL7; DP; 3DL1	5'UTR	Forward	TGCGCTGCTGAGCTGAGCTG	52,1
37	2	3DL3; 3DL4; 2DL4	3'UTR	Reverse	GTCCAGGGGTGAGAACCCAG	71,5
38	2	3DL3; 3DS2; 2DS4	3'UTR	Reverse	TATTTGATATGTGTCCTCG	72,0
39	2	3DL3; 2DL9; 2DL6; 2DL8; 3DL4; 2DS4	3'UTR	Reverse	GGGGAGGTGGAACAGCATGA	69,5
40	2	3DL3; 2DL9; 2DL6; 2DL8; 3DL4	3'UTR	Reverse	CTGAAAGCTAGTCTGAGGGG	67,3
41	2	3DS2; 2DL9; 2DL6; 2DL8	3'UTR	Reverse	GTCCCATTAACGAAACCATG	74,8
42	2	3DL3; 2DL6; 2DL5; 2DS4	3'UTR	Reverse	ACTCTACAAATGTTCATCG	71,8
43	2	2DL5; 2DL8; 3DL5; 2DL7	3'UTR	Reverse	GGACATGGAATGATAACAG	82,6
44	2	3DL5; 2DL7	3UTR	Reverse	GGGTAGGTGGAACAGTACGT	76,9
48	2	3DL3; 2DL8; 3DL4; 2DS4; 2DL4	3'UTR	Reverse	AACCCAGTGGAGAACAGATG	64,9
52	2	3DS2; 2DL8; 2DS4; 3DL1	3'UTR	Reverse	AGGCTGAAGATAGTCTGAG	65,5
53	2	3DL3; 3DS2; 2DS4; 3DL1	3'UTR	Reverse	TGGAGTCCCAGAGACAAATG	71,9
54	2	3DL3; 2DL9; 2DL6; 2DL8; 3DL5; 3DL4; 2DL7; 3DL1	3'UTR	Reverse	TCCAGAAGCTCAGAGTCCAG	66,9
Specific crRNAs						
32	2	DP	3'UTR	Forward	GACATGAGTATGTTGCAGAG	79,6
33	2	DP	3'UTR	Forward	TTTGAGTAGATACCCAGCAG	71,4
34	2	DP	3'UTR	Forward	CGCTGCAACCTCCACCAACCC	65,2
35	2	2DL4	intron 1	Forward	CATTTCTGAAGCAAGTGAG	69,1
36	2	2DL4	intron 1	Forward	TCTGAAGCAAGTGAGTGGAG	81,0
45	2	2DL4	5'UTR	Reverse	GTGGTAGTTCACTCAAGGG	70,6
46	2	2DL4	5'UTR	Reverse	TCACCTCACATCATGCACAA	74,3
47	2	2DL4	5UTR	Reverse	TTGAATTCTGCACTCACATG	61,2
49	2	DP	3'UTR	Reverse	TTACTGTCCAAGATCAACGC	66,0
50	2	DP	3'UTR	Reverse	CAACCCAAAATTAGGCCAG	65,2
51	2	DP	3'UTR	Reverse	AGACACATCCATCAATCCAC	63,3