

Table S5

CRISPR validation: Results of OFF-Target verification by Sanger sequencing

Gene ID	location	chromosomal location	sequence	PAM	Result-Editing	F primer	R primer	length
Nrsn2	Exon 2	chr2:152,369,584-152,374,334	TGGAGGAAAAGTACATGGTAT GGG	GGG	Yes	TGCCAGATGGTCTCAGAGA	CTCTGCCAGAAGGCATCCAA	591
Zdhhc5	Exon 2	chr2:84,710,597-84,710,619	TGAAGGAAAGCACATGGGAG	GGG	No	GGGCATGTTGGAGCTCTGAT	GCTGCTCTAGTGTGGTGT	493
Abca8a	Exon 39	chr11:110,025,789-110,025,811	TGAAGGAAAATACATGGAAT	TGG	No	GCTGATGAAAATTTAGAGAAAAGCAATGATAAT	AAAAGCCACTGAGCTACTCTCTACAATT	689
Rhbg	Exon 5	chr3:88,245,808-88,245,830	TGGACGACTGGACATGGTAT	GGG	No	CGTTCTGGACGTGGACCTTA	GGCTGCTTAGTAGTGACGGA	517
Fat4	Exon 7	chr3:38,970,701-38,970,723	TGAAGTTAAGTACATGTTAT	TGG	No	AGGCAGTTGAGCTCTTAGGTC	CTTAGAAGAAGCAGACACGCT	541
Wdfy3	Exon 35	chr5:101,889,296-101,889,318	TGGAGGAAAGTACAGGTAT	TGG	No	CAAAGTTGGGTACACCTGAGAAT	TCACAGGCTGGCTTAAAGTGA	539
Ccdc80	Exon 3	chr3:45,095,317-45,095,339	TGCAGGAAAGAACAGGGTAT	GGG	No	GCAGTAGGTCAGCTCGGTATC	ACAGCACCATGCTAAACTTGC	579
Theg1	Exon 6	chr5:77,056,055-77,056,077	TGGAGGAAAGTAGCTGGGAT	TGG	No	CATCGGTGGGAAAAGAGC	TGAACTCGCTCAGAGAACGG	534
Ntm	intron 1	chr9:29,941,757-29,941,779	GGGAGGAAAAGATGTGGTAT	TGG	No	ACAGCAGATTCGGTGATGA	GGGTGGCGGTTAGGATAGTG	526
Zpf644	intron 1	chr5:106,667,595-106,667,617	TGGTGTAAGTACATGGAAG	AGG	No	TATGAGCCATCAGTTCTGCACC	TAGCTGCTATCACAATTCACCTT	437
Spidr	intron 1	chr3:88,245,808-88,245,830	ATGATAAAAGTACATGGTAT	TGG	No	CCAGGATAGCCAAACAATCC	AACTCAAGTGCCCCAGGTG	194
Gm5139-Gm18294	intergenic	chr3:64190048-64190070	TTTTAAAAAGTACATGGTAT	TGG	No	GGAATCGTGAATGGTATTGGTAAGC	ATAGGTAGGGAGATAGTGGGTAGCCTTGTC	680
Gm12010-Gm12011	intergenic	chr11:16210581-16210603	TGTTAAAAAGTACATGGTAT	TGG	No	AGTTCCTGTATCCACTTAGACTTGAGATTGTAC	AGAAAGAAATTTAAGAAGATCACAGAAGACAGAAA	533
Kcnq5-Gm26580	intergenic	chr1:21959279-21959301	TTGGGTAAAGTACATGGTAT	GGG	No	CTCCCTGCTCAGACCTCAA	TTAAGCTCATCTCTGGGTTGAT	560
Olf1353-Olf1352	intergenic	chr10:78977749-78977771	TGATAAAAAAGTACATGGTAT	TGG	No	ACCAAGCAATATGAAAATCTGTATGGCAA	TGTTCTGTTCTGGAAATTTCCCTG	668
Slc10a2-n-R5s94	intergenic	chr8:5212502-5212524	CCATGGAAAAGTACATGGTAT	GGA	No	TACTCAAGTAAAAGGGTAAAAGGA	AGGCCAATGACAGGTGTGA	431
Gm7803-Gm14611	intergenic	chrX:50332539-50332561	AGGTAGAGAGTACATGGTAT	AAG	No	ACATCAAAACCAGCTCCATCCT	TCTGACTTTGAAGAAAATGACCAAA	486