

Supplementary information, Table S3: Potential off-target sites of RAG1 TALENs predicted by e-PCR in the rabbit genome

Rabbit-rag1-TALEN						
seq	strand	from	to	mism	gaps	act_len/exp_len
gi 283557968 ref NW_003159226.1	+	22779832	22780256	5	2	425/0-1000
gi 283557968 ref NW_003159226.1	-	19885750	19886797	6	2	1048/0-1000
gi 283557967 ref NW_003159227.1	-	16096807	16097323	6	2	517/0-1000
gi 283557965 ref NW_003159229.1	+	52618352	52618640	6	2	289/0-1000
gi 283557964 ref NW_003159230.1	+	18196441	18196488	0	0	48/0-1000
gi 283557962 ref NW_003159232.1	+	40761755	40762488	6	1	734/0-1000
gi 283557962 ref NW_003159232.1	-	30856184	30857212	6	2	1029/0-1000
gi 283557959 ref NW_003159235.1	+	9966050	9966680	5	1	631/0-1000
gi 283557955 ref NW_003159239.1	-	4107957	4108758	5	0	802/0-1000
gi 283557943 ref NW_003159251.1	+	15121948	15122170	6	1	223/0-1000
gi 283557943 ref NW_003159251.1	+	15097686	15097909	6	1	224/0-1000
gi 283557943 ref NW_003159251.1	-	15069608	15069830	6	1	223/0-1000
gi 283557943 ref NW_003159251.1	-	15057223	15058003	6	1	781/0-1000
gi 283557942 ref NW_003159252.1	-	70363	70586	6	1	224/0-1000
gi 283557940 ref NW_003159254.1	-	7963067	7964015	6	1	949/0-1000
gi 283557938 ref NW_003159256.1	-	139938	140231	6	2	294/0-1000
gi 283557932 ref NW_003159262.1	-	3010379	3011202	5	1	824/0-1000
gi 283557931 ref NW_003159263.1	+	13600188	13600268	6	2	81/0-1000
gi 283557908 ref NW_003159286.1	-	7872793	7872829	6	1	37/0-1000
gi 283557899 ref NW_003159295.1	+	1627097	1627556	6	0	460/0-1000
gi 283557898 ref NW_003159296.1	-	118323021	1833319	6	2	1018/0-1000
gi 283557897 ref NW_003159297.1	-	1042631	1043351	6	2	721/0-1000
gi 283557895 ref NW_003159299.1	-	45978182	45979003	6	0	822/0-1000
gi 283557894 ref NW_003159300.1	-	4302717	4303142	6	1	426/0-1000
gi 283557892 ref NW_003159302.1	+	6728287	6728409	6	1	123/0-1000
gi 283557879 ref NW_003159315.1	-	4476525	4476635	5	2	111/0-1000

For RAG1 TALENs, 26 potential off-target sites were identified. Among these, two sites highlighted in yellow that had a spacer of <100 bp between two binding sequences were amplified and sequenced. No mutations were found at these sites. The hits in red are the RAG1 target site used in this study. The list of primers can be found in Supplementary Table 4.