

**Table S3** List of top 15 potential off-targets of Sry TALEN pair 2

Left Sry TALEN 2 Coord.	Right Sry TALEN 2 Coord.	SP	Left Match	Right Match	% L.M.	% R.M.	Left Score	Right Score	Comb. Score
chrY:1919526- 1919542:-	chrY:1919493- 1919511:+	14	GAATGCATT TATGGTGT	GCTGGGCCAA CTTGTGCCT	100	100	0	0	0
chr2:136965673- 136965689:-	chr2:136965639- 136965657:+	15	GAATaCATTT AaaaTcT	aCTataCCAAct TGTGCaT	70.59	73.68	-5814	-8301	-14115
chr15:70236492- 70236508:+	chr15:70236520- 70236538:-	11	aAATaCATTT AccGTGT	aCTGGaCaAcC TacTGCCT	76.47	68.42	-5507	-12517	-18024
chr16:76949103- 76949119:+	chr16:76949135- 76949153:-	15	GAATGgATTT ATaGTGT	aCaaaaCCAaAT TGTcCCT	88.24	63.16	-8828	-9892	-18720
chr15:87265524- 87265540:-	chr15:87265489- 87265507:+	16	aAAcaCATTT AaaacaT	GCTGGGCCAc CTacTaCCT	52.94	78.95	-11165	-8439	-19604
chr9:69488856- 69488872:-	chr9:69488822- 69488840:+	15	GAATGtATTT ATcaTaT	GCTtaaCCcACT ccTaCCT	76.47	63.16	-8585	-12662	-21247
chr17:33805058- 33805074:+	chr17:33805086- 33805104:-	11	GAATaCATTc ATtTaT	GCTGaGCCaTc TTaTcCCT	70.59	78.95	-11042	-10788	-21830
chr1:139652173- 139652189:+	chr1:139652208- 139652226:-	18	GAATGCATT TATtaTtg	aCaacaCCAAct TtTaCCT	76.47	63.16	-13127	-9730	-22857
chr7:28158072- 28158088:+	chr7:28158103- 28158121:-	14	aAATGCATaT AaGaTaa	aCTaccCCAcCT aaTcCCT	64.71	57.89	-10551	-12419	-22970
chr13:109697953- 109697969:+	chr13:109697989- 109698007:-	19	aAATaCATTTt aGaTGT	GCTaaGCaAAC TaaaGCCT	70.59	68.42	-12622	-11112	-23734
chr1:174769836- 174769852:+	chr1:174769879- 174769897:-	26	aAAatCATTaA TaaTGT	aCTGGcCCAA CTaaTaaCc	64.71	63.16	-10950	-12795	-23745
chr13:81411028- 81411044:+	chr13:81411060- 81411078:-	15	GcAgatAcccAT atTca	ctTccataAgtgTtg ctgc	35.29	15.79	-11956	-12175	-24131
chr9:14021886- 14021902:+	chr9:14021920- 14021938:-	17	aAATGCACtT ATaGgGc	aCTtGGCaAAC TTtTaCCT	70.59	73.68	-12636	-11603	-24239
chrX:61887910- 61887926:+	chrX:61887952- 61887970:-	25	GAAGtCATTa ATaGTaT	aCTaaaCCcACg TGTcCCT	70.59	63.16	-13035	-11752	-24787
chrX:143582738- 143582754:-	chrX:143582699- 143582717:+	20	aAATGCATaT AaaaTag	cCTaaaCCAaAT TaccCCT	58.82	57.89	-13250	-11575	-24825
chr11:35804487- 35804503:+	chr11:35804516- 35804534:-	12	aAATGCACtG ATaaTga	cCTacaCCAAC TTtTeCCc	64.71	63.16	-12943	-12482	-25425

Left and Right Sry TALEN 2 coordinates indicate positions of paired left and right hits in mm9 genome assembly (chrom:start-end:strand); SP, length of the spacer between left and right hits; Left match, the genomic sequence of left hit (Uppercase indicates a match with the consensus. Lowercase indicates mismatch); Left match, the genomic sequence of right hit (Uppercase indicates a match with the consensus. Lowercase indicates mismatch); % L. M., percentage of consensus-matched bases of left hit; % R. M., percentage of consensus-matched bases of right hit; Left Score, the score of left hit (relative to a consensus match); Right Score, the score of right hit (relative to a consensus match); Comb. Score, the combined score of left and right hits.