

chromosome	strand	from	to	mismatch	gap	spacer
<b>chr5</b>	<b>+</b>	<b>7477585</b>	<b>7477635</b>	<b>0</b>	<b>0</b>	<b>15</b>
chr5	+	28112014	28112249	10	2	198
chr7	-	17711418	17711581	10	1	127
<b>chr9</b>	<b>-</b>	<b>15931407</b>	<b>15931476</b>	<b>10</b>	<b>2</b>	<b>32</b>
chr12	+	5685843	5685985	7	2	105
chr12	-	19269294	19269518	10	2	187
chr13	-	23653665	23654214	7	2	512
chr16	+	21165226	21165700	10	2	437
scaffold693	+	42746	43178	9	2	395
scaffold791	-	31456	31899	10	2	406
ultracontig149	-	166188	166675	6	2	450
ultracontig62	+	293467	293699	9	1	196
ultracontig72	-	2589715	2589917	10	1	166
ultracontig88	-	226571	227065	7	2	457

**Figure S1** Potential off-target site of DJ1-TALENs identified with the e-PCR program. This list shows candidate off-target sites identified as follow three conditions; (1) up to five non-identical bases (mismatches) in each recognition sequence, (2) up to one base pair gap in each recognition sequence, (3) <500 bp spacer length between the two putative recognition regions. Red letters indicate the target site of DJ1-TALENs. Blue letters indicate a potential off-target region analyzed in this study.