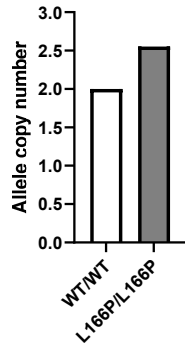
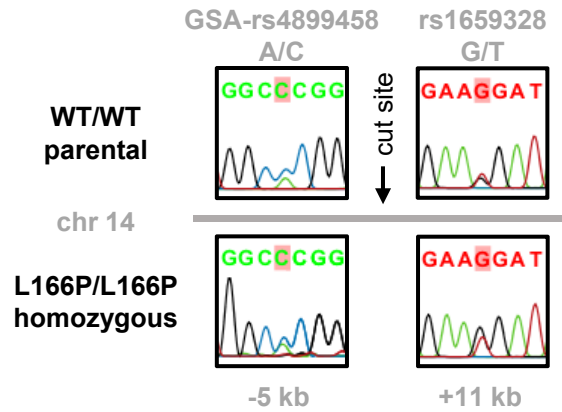


A

ID	Sequence	Mismatch Position	Mismatch Count	MIT	Score	CFD Score	Location	Location Description	Indels detected
gRNA	TAGAGATGATATAATAAGCCAGG	Target							
OT1	GGGAGATAATAAAATAAGCCAGG	**.....*	4		0.70	0.61	2:153724855:153724877:1	intergenic:AC009969.1-UBQLN4P2	None
OT2	AAAAAATGATAAAATAAGCCAGG	*.*.....*	4		0.69	0.52	21:46695806:46695828:1	intron:POFUT2	None
OT3	AAGAAAGGATATAATAAGCCAGG	*.*.....*	3		1.74	0.51	21:31259021:31259043:-1	intergenic:GRIK1-AS1-GRIK1	None
OT4	GTGAAATGATAAAATAAGCCTGG	**.*.....*	4		0.70	0.48	5:178143770:178143792:1	intron:ZNF354A	None
OT5	TAGAGATAAAAAATAAGCCAGG	*.*.*	4		0.17	0.40	2:175393048:175393070:1	intergenic:AC010894.4-AC018890.6	None
OT6	TTAAGATGATAGAATAAGCCCGG	.*.....*	3		1.37	0.27	9:12844099:12844121:1	intergenic:LURAP1L_Y_RNA	None
OT7	GAGACATTAGATAATAAGCCAGG	*.*.*.*	4		1.32	0.23	1:175940964:175940986:-1	intergenic:SCARNA3-RFWD2	None
OT8	TATAAATGATAGAATAAGCCAGG	..*.*.*	3		1.30	0.22	8:24510893:24510915:1	intron:RP11-624C23.1	None
OT9	TGTTGATGAAATAATAAGCCAGG	..***.....*	4		1.24	0.22	13:90205830:90205852:-1	intergenic:RP11-75N6.3-LINC00353	None

B**C****D**