

Figure S1

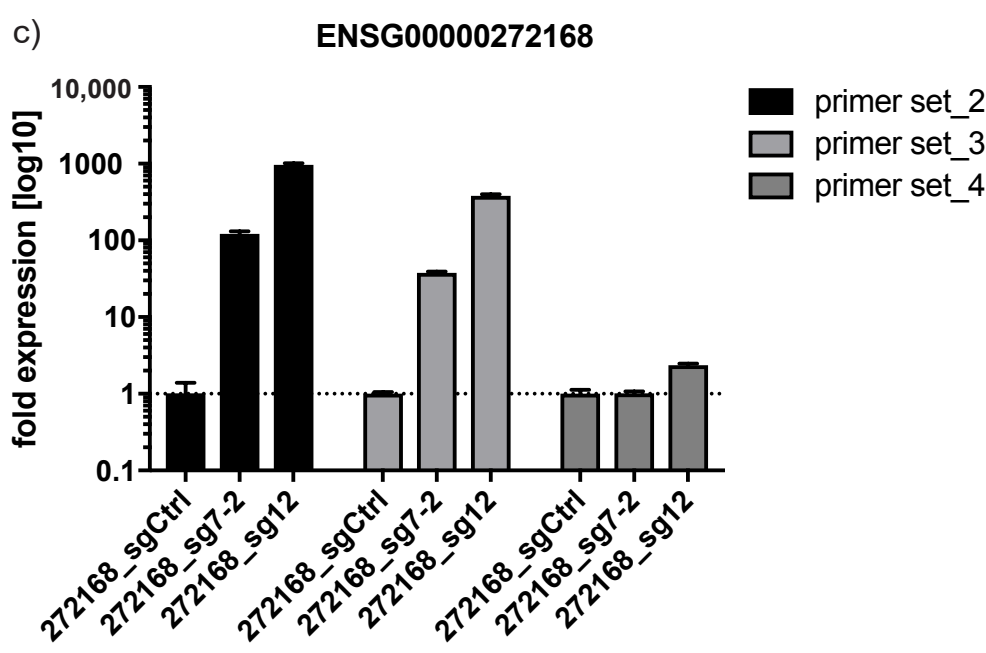
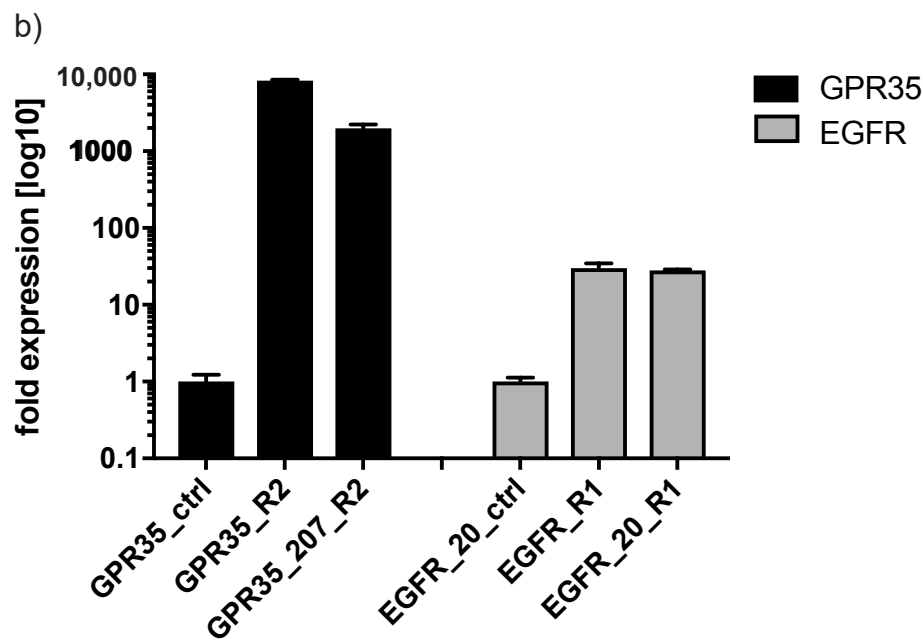
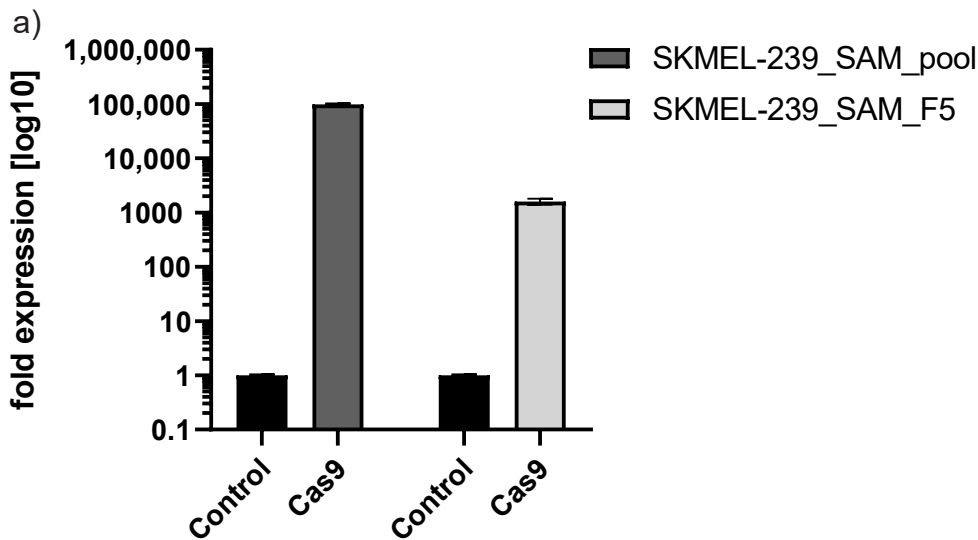


Figure S1. Functional assessment of CRISPRa system in SKMEL-239_SAM_pool and F5 by qPCR expression analysis of Cas9 (a), EGFR and GPR35 (b) and a randomly expressed lncRNA ENSG00000272168 (c).

Figure S2

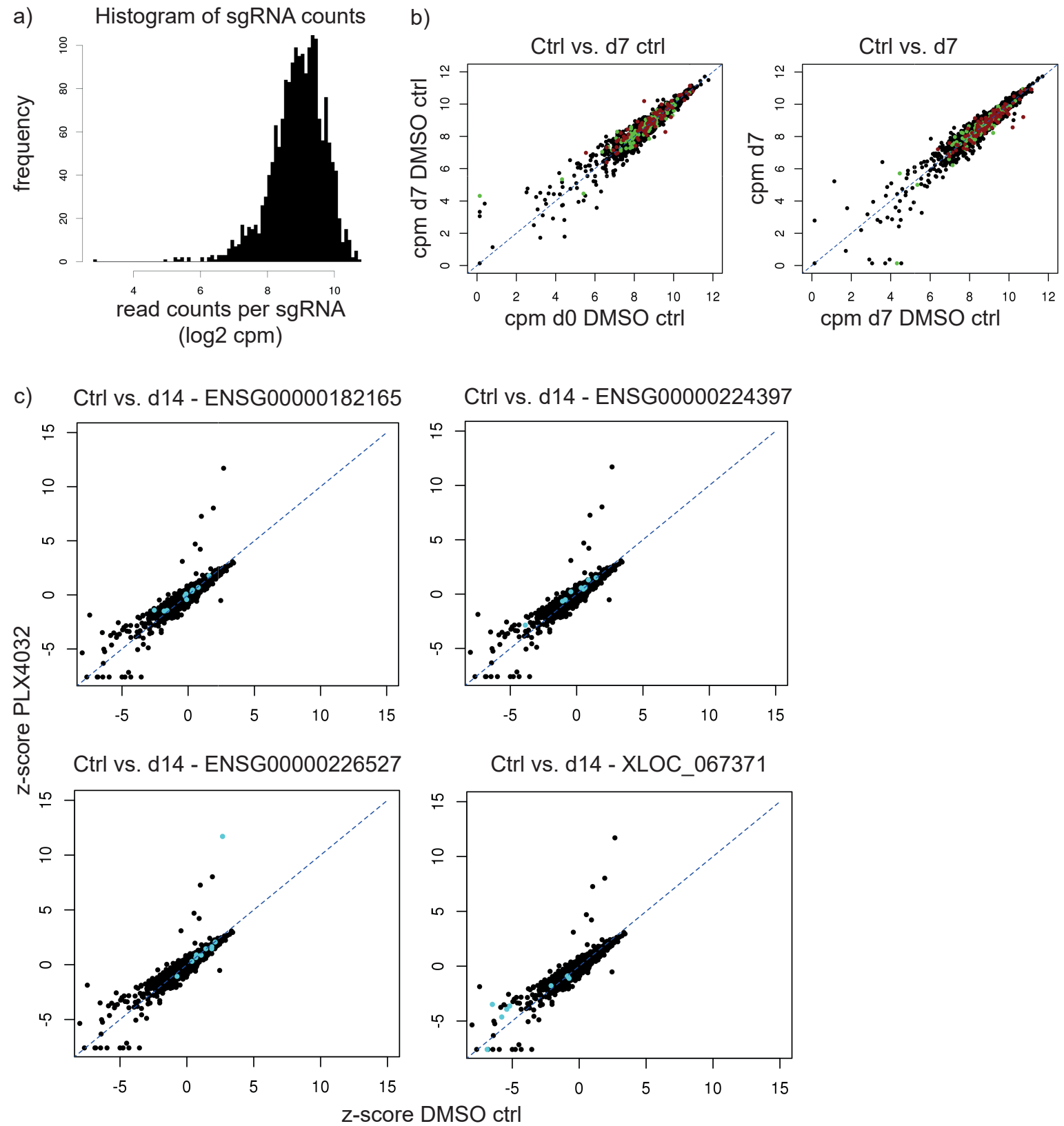


Figure S2. (a) CRISPRa sgRNA plasmid library validation. Histogram shows a log2 read counts in cpm against frequency. (b) control sample validation at day 7 of (left) cpm of day 0 of DMSO control versus cpm at day 7 DMSO control, (right) cpm of day 0 of DMSO control versus cpm at day 7. (c) sgRNA representation of all ten sgRNAs per all four validated lncRNA candidates ENSG00000185168 (aka LINC00482), ENSG00000224397 (aka PELATON), XLOC067371, ENSG00000226527 referring BRAFi resistance in melanoma shown as z-score normalization of DMSO negative control against PLX4032 treated cells at day 14.

Figure S3

qPCR validation lncRNA candidates (day 7)

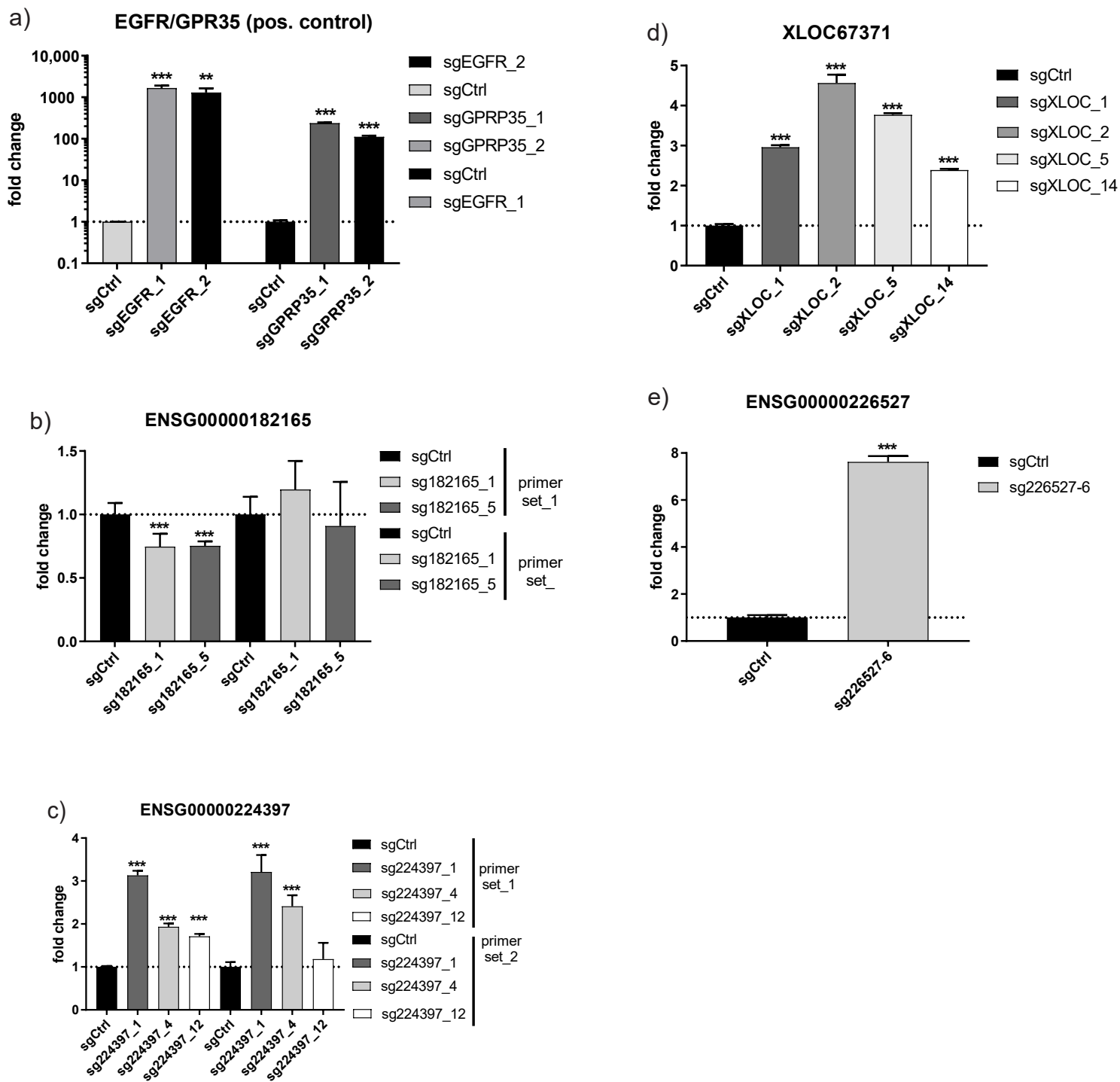
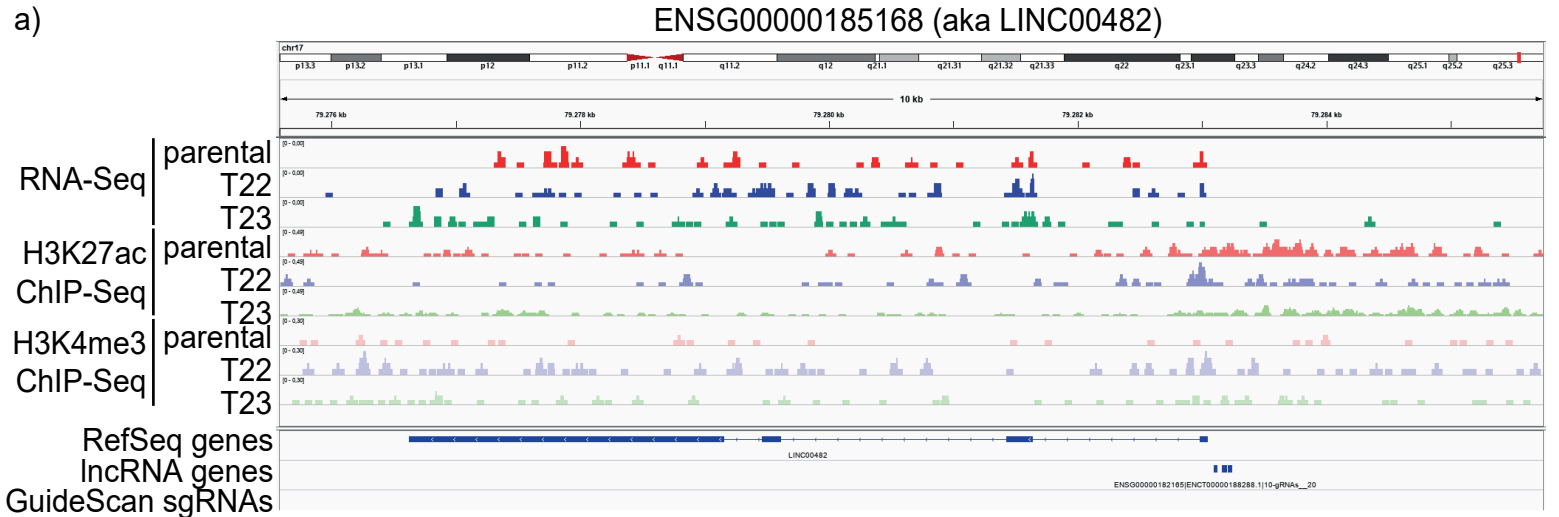


Figure S3. qPCR expression validation of all lncRNA candidates and EGFR positive control after 7 days using diverse primer sets for some lncRNAs. ** $p < 0.01$, *** $p < 0.001$.

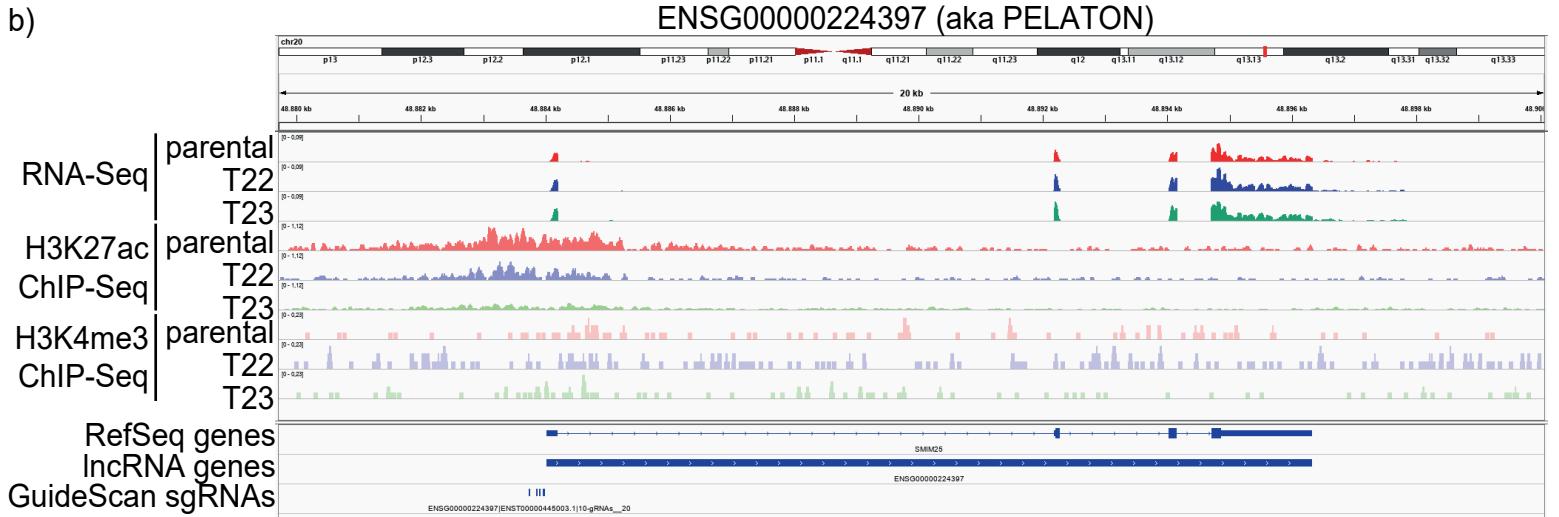
Figure S4. IGV genome browser tracks representing one replicate out of three for RNA-sequencing, H3K27ac and H3K4me3 ChIP-Seq for validated lncRNA candidates ENSG00000185168 (a), ENSG00000224397 (b), XLOC067371 (c), ENSG00000226527 (d) referring BRAFi resistance in melanoma which are expressed in SKMEL-239 parental, T22 and T23. RefSeq and new lncRNA as well as sgRNAs are shown as blue bars at the bottom.

Figure S4

a)



b)



c)



d)

