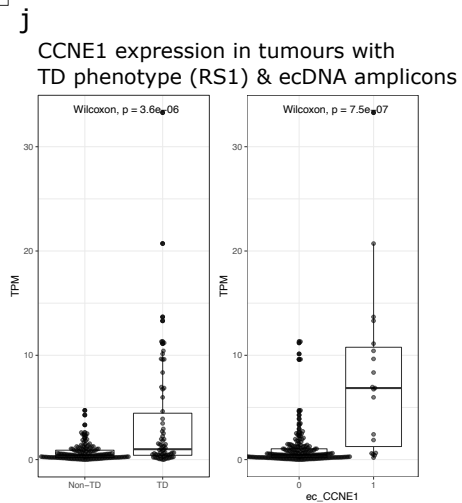
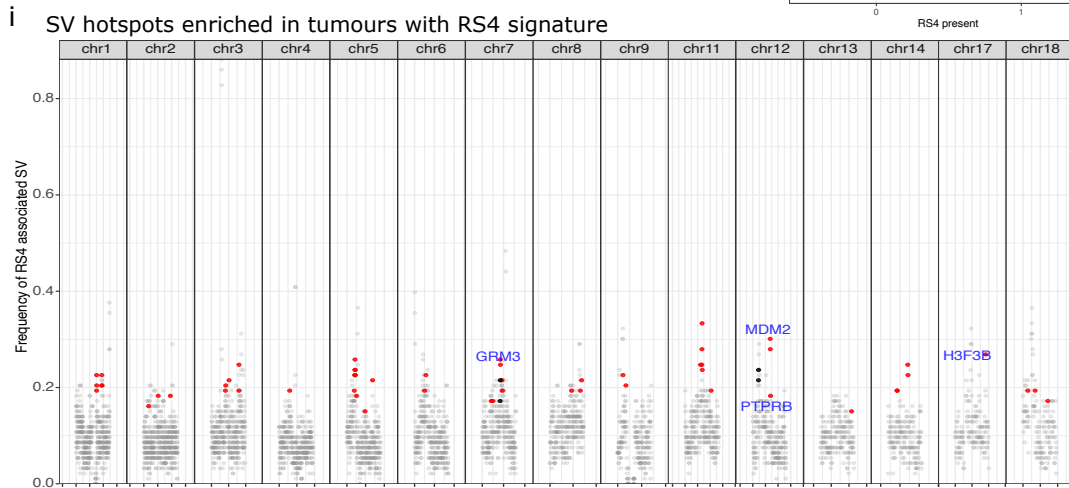
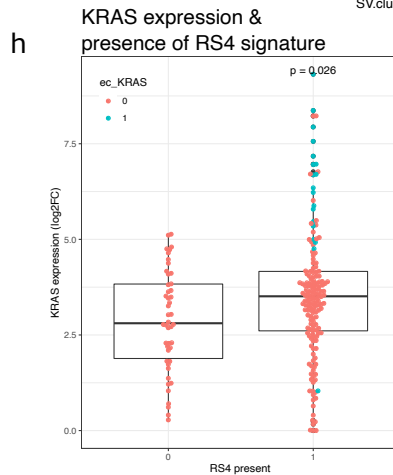
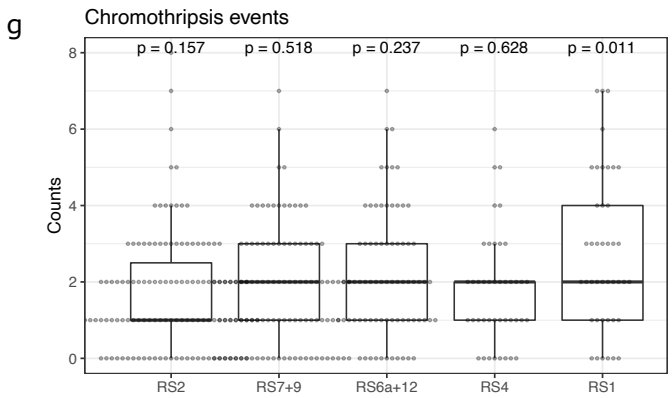
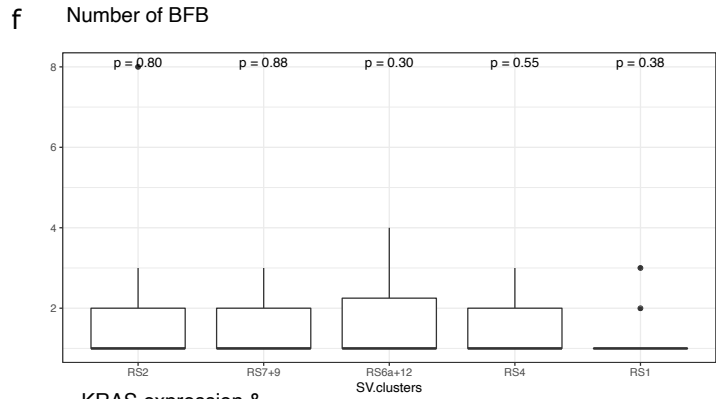
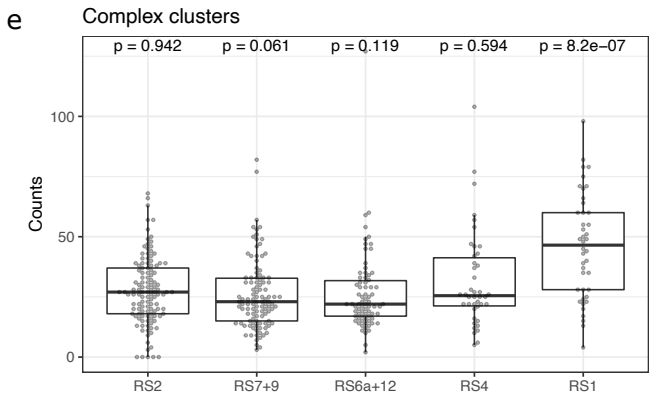
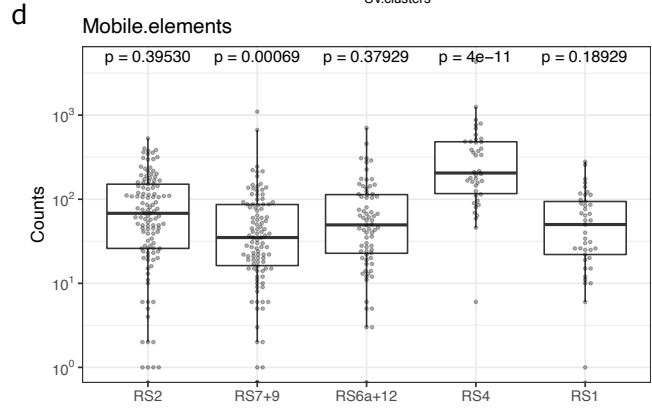
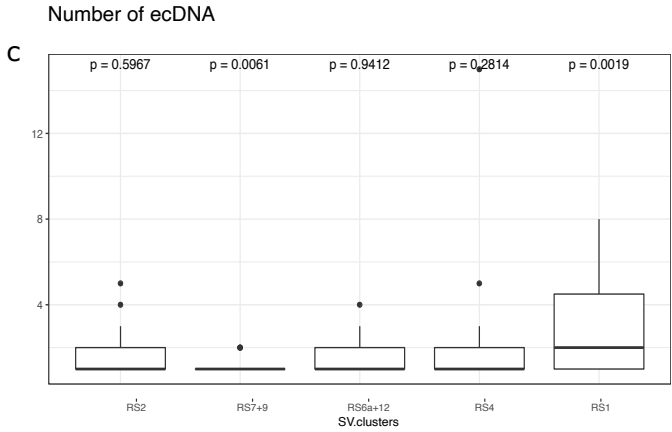
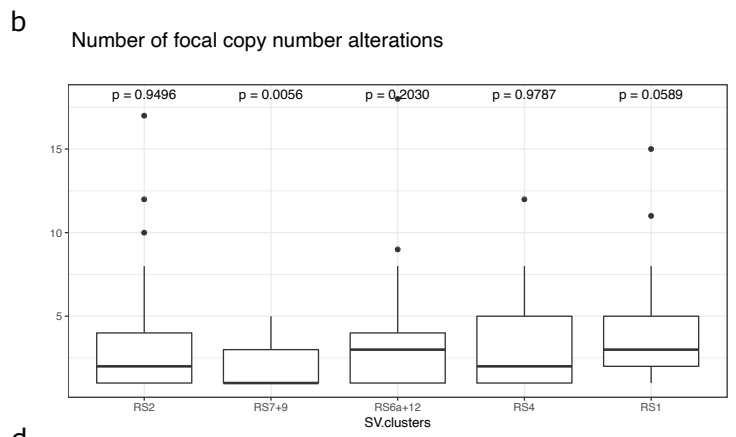
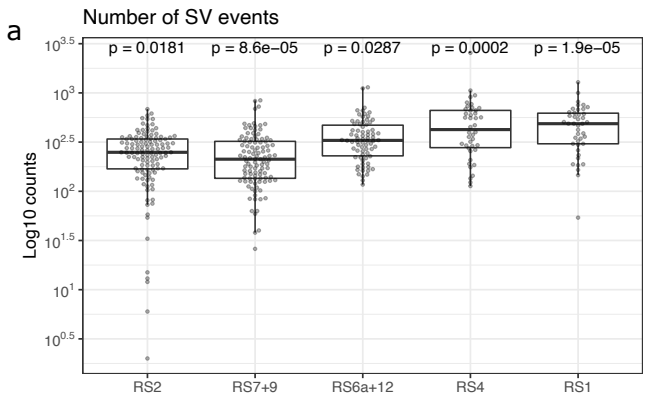
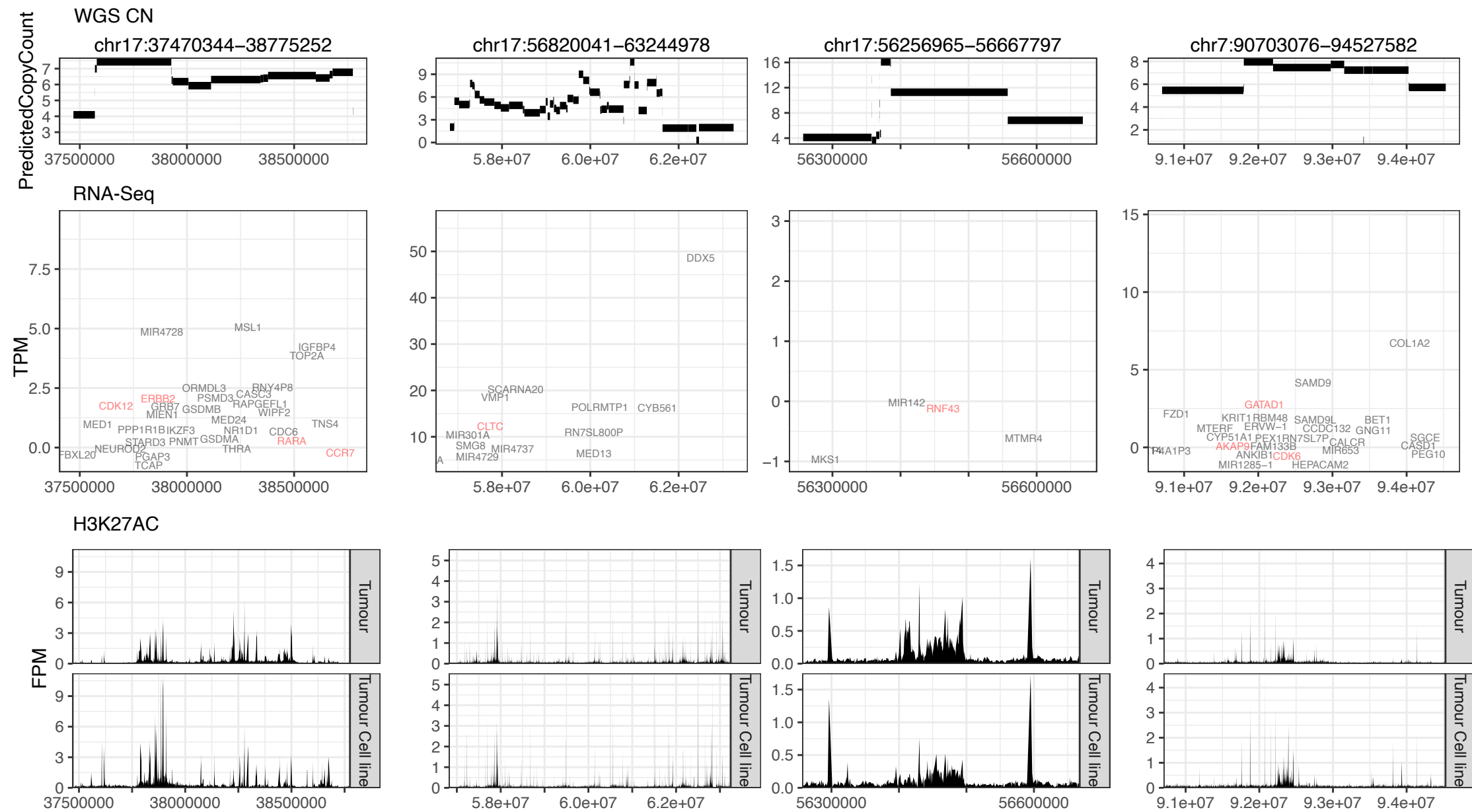


Supplementary Figures		Page
S1	SV signatures extracted from 383 OAC tumours and comparison to Signal reference rearrangement signatures	2
S2	SV signature group correlations	3
S3	Enhancer regions amplified in ecDNA amplicons	4
S4	Distribution of SV hotspots containing driver genes	5
S5	RUNX1 isoform expression analysis and PCR validations	6
S6	Overview of analyses and software	7

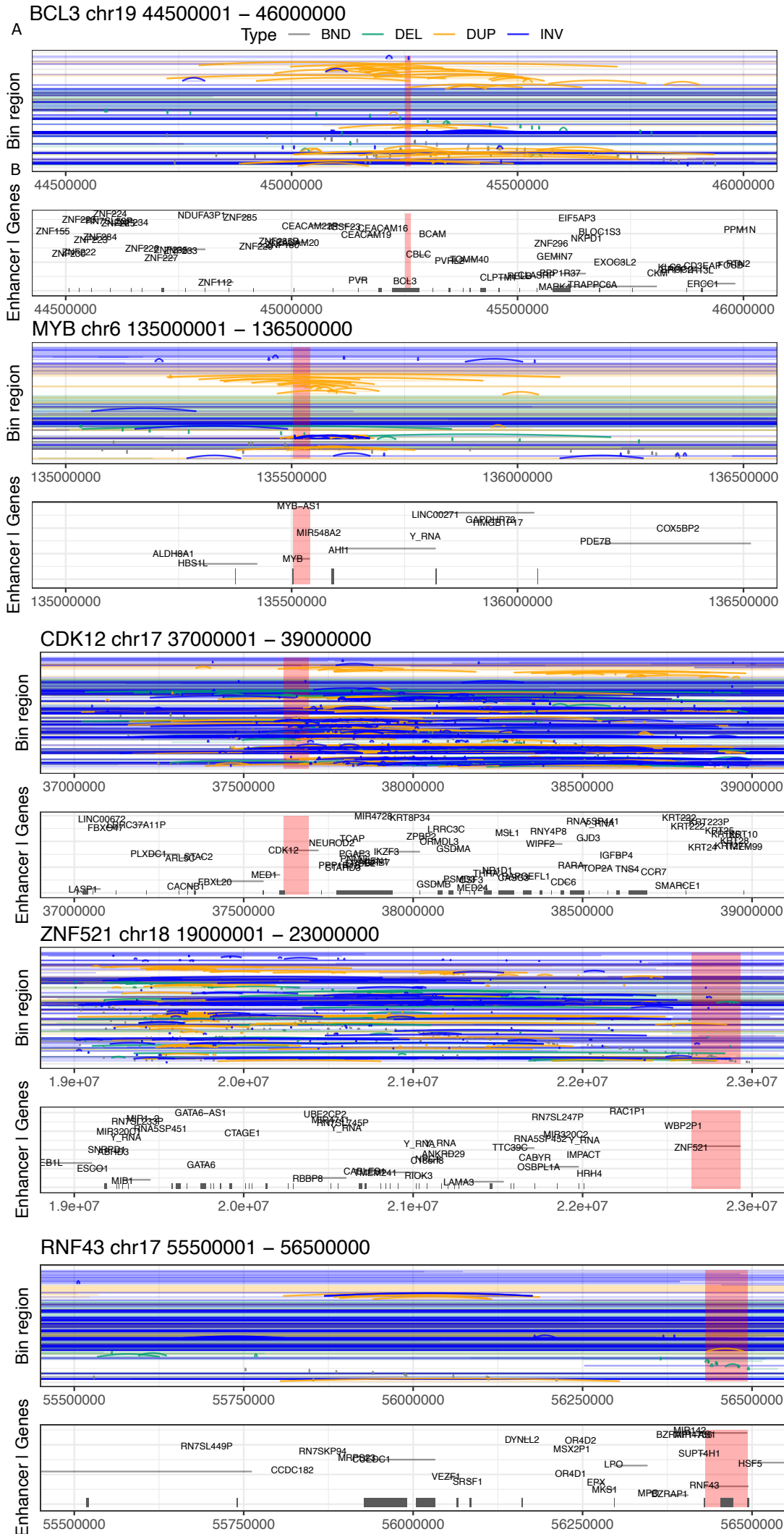


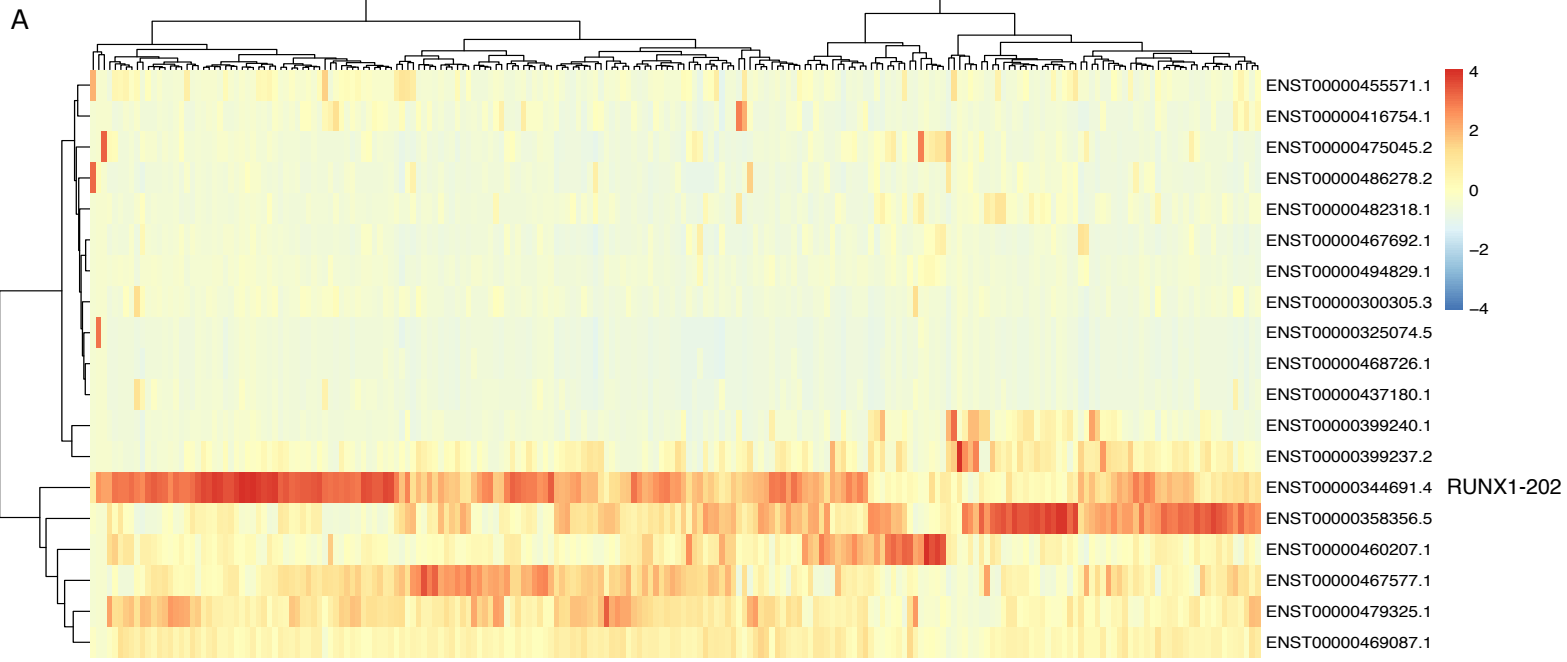


Supplementary\_Fig\_S3. Enhancer regions amplified in ecDNA amplicons. Four example of amplified regions involved in ecDNA formation (top), expression of genes from the same sample (middle) with driver genes highlighted (red) and H3K27Ac peaks identified in tumours and tumour cell lines from Chen et al (2019).

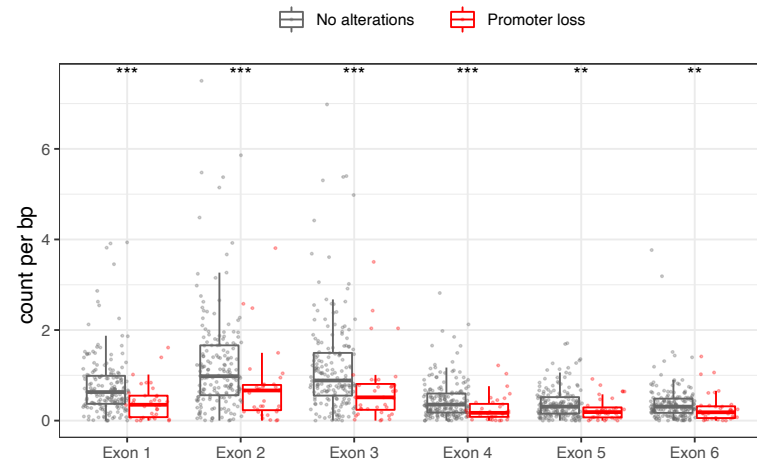


Supplementary\_Fig\_S4 Distribution of SV in hotspot containing BCL3. SVs in A) driver hotspot bin shown as arcs (within bin) and lines (spanning bin). Positions of enhancers and genes showed with driver gene region highlighted (red).

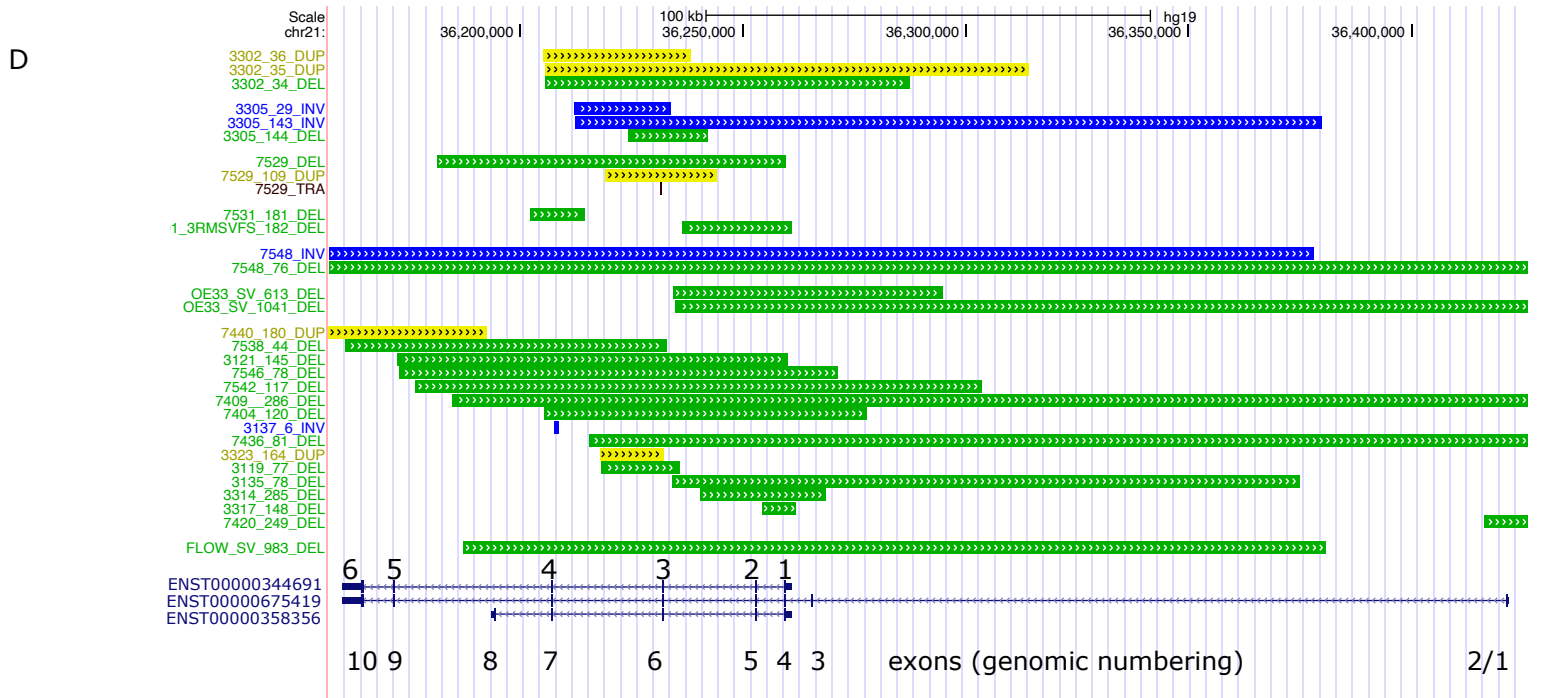
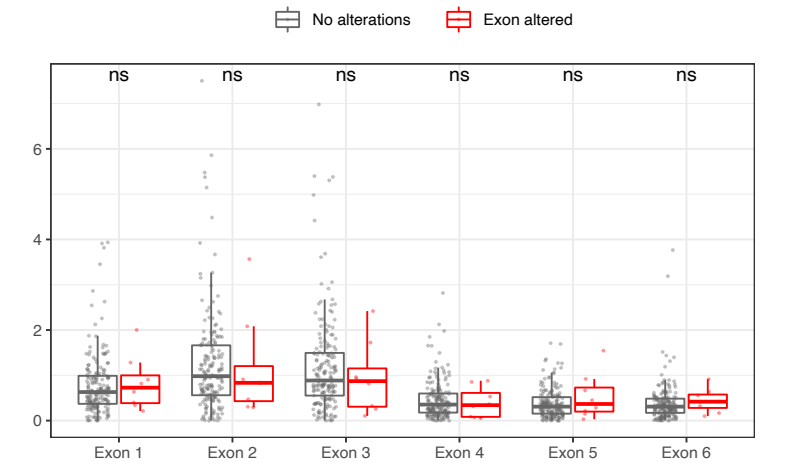




**B** RUNX1-202 exon expression of cases with Promoter 2 loss



**C** RUNX1-202 exon expression of cases without Promoter 2 loss



Supplemental\_Fig\_S6. Overview of analyses and software

