Schematic alignment of retrocopies encoded by the reference genomes.
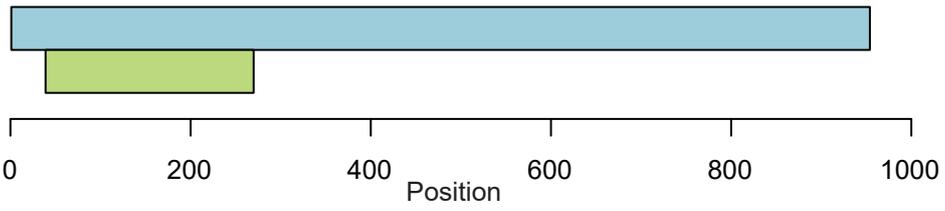The size and relative location of parental and child copies are drawn to scale. The parental genes and retrocopies were marked in blue and green, respectively. We translated retrocopies by aligning parental proteins against retrocopies with exonerate (Slater and Birney 2005). Frame-shifting indels and premature termination codons were marked as "F" and "*", respectively. Some retrocopies (e.g., *ENSMUSG00000084064*) do not have such mutations. Finally, the remaining longest continuous coding regions were highlighted in light red. For each gene pair except *retro-Kmt2d*, one panel is presented. In the case of *retro-Kmt2d*, since the retroposed region is tiny relative to the parental locus, one additional enlarged version is also shown. In the case of "*Super*" which involves four parental genes, we do not show a figure given its complex structure. Notably, two parental gene derived sequences already accumulated one premature termination codon, while the other two sequences do not harbor any loss-of-function mutations.

ENSANGG00000011308
ENSDARG00000002400_r
ENSDARG00000032849_r
ENSDARG00000011511_r
ENSDARG00000076317_r
ENSDARG00000091935
ENSGALG00000006009_r

ENSGALG00000000312_r
ENSGALG00000011896_r
ENSGALG00000001041_r
ENSMUSG00000024866_r
retro−Kmt2d
ENSMUSG00000084064
ENSMUSG00000083892

ENSMUSG00000083549
retro−Rplp0
retro−Eef1g
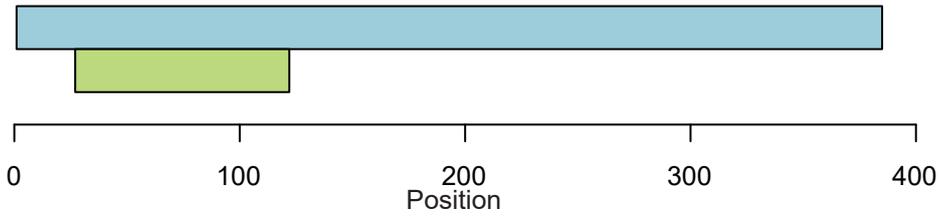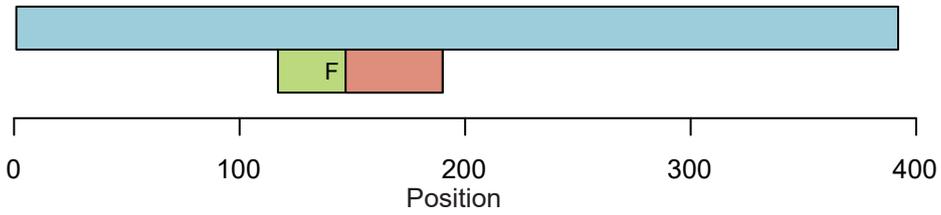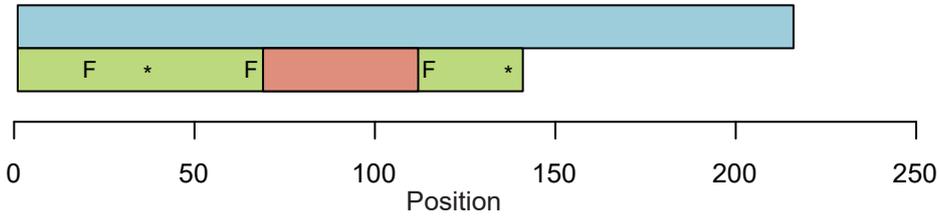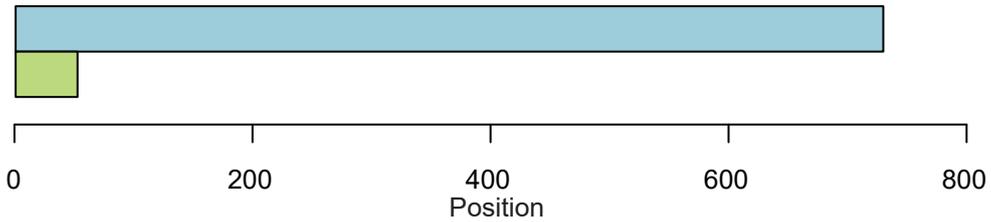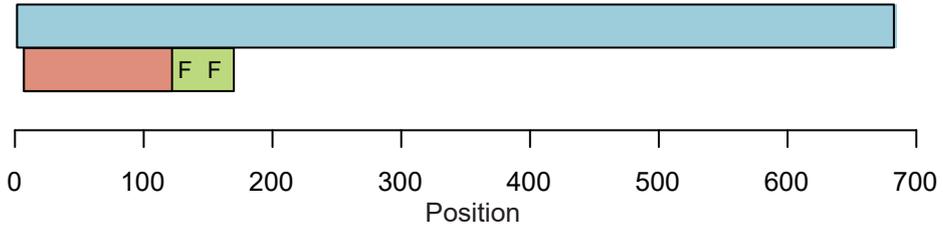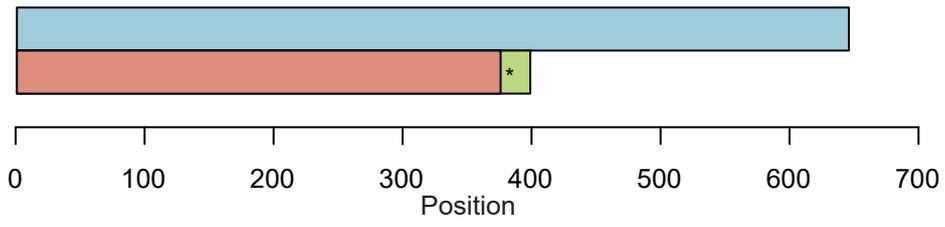*ENSG00000218772*
ENSG00000254722
ENSG00000230535

Color code
☐ Parental gene
☐ Child gene
☐ Longest continuous sequence
F   Frame shift
*   Stop codon

ENSANGG00000011308

ENSDARG00000002400_r

ENSDARG00000032849_r
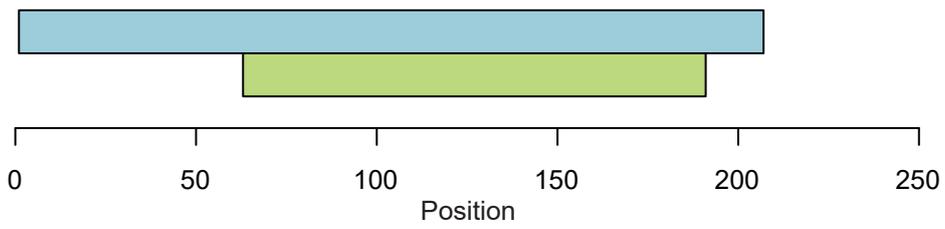
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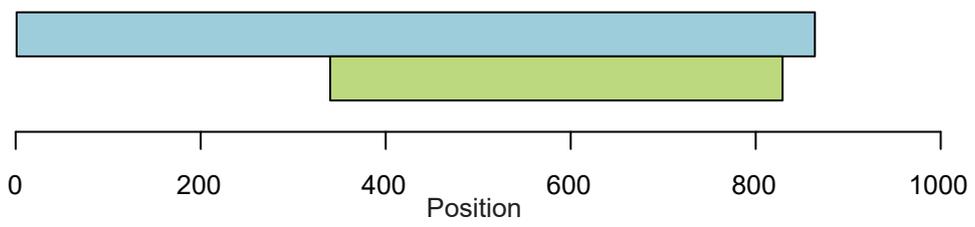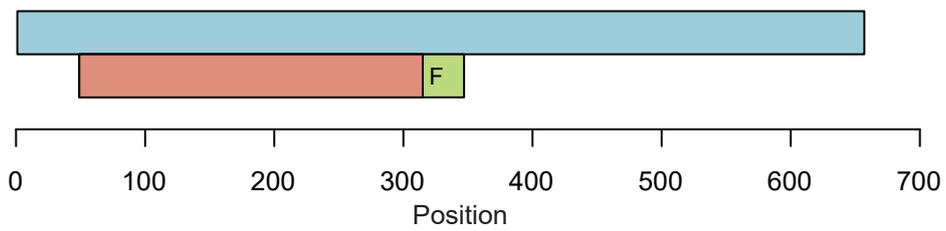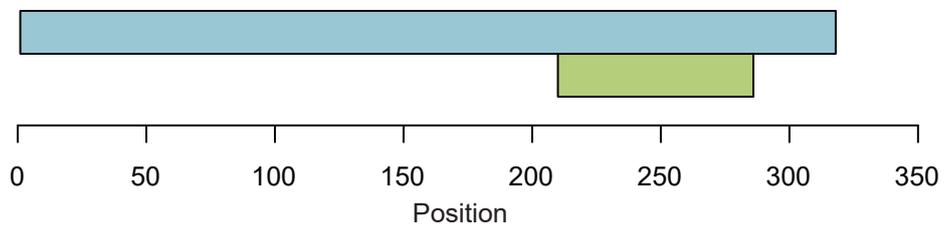
ENSDARG00000076317_r

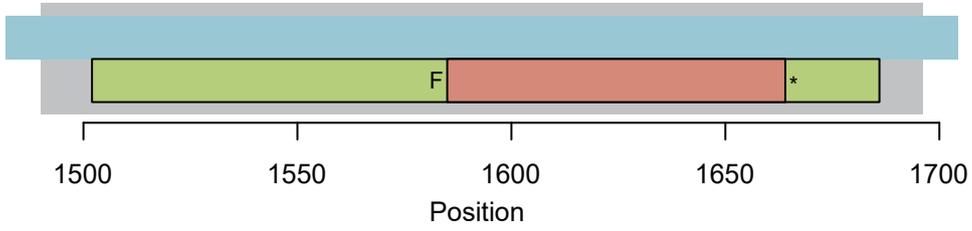*ENSDARG00000091935*

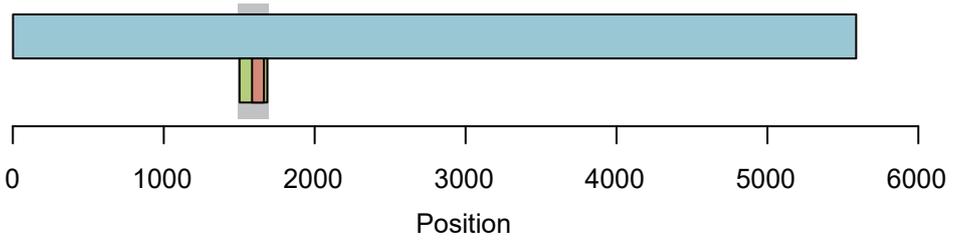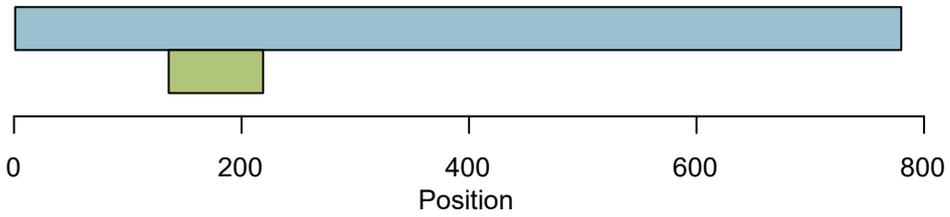ENSGALG00000006009_r

ENSGALG00000000312_r
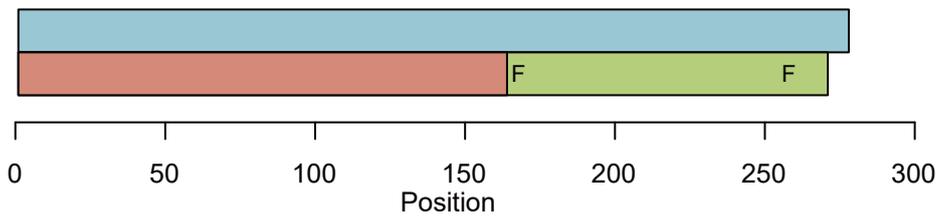
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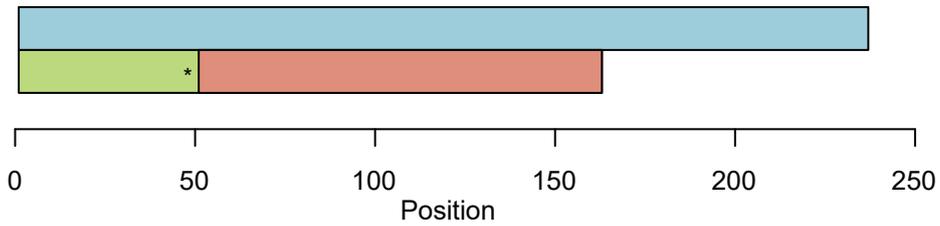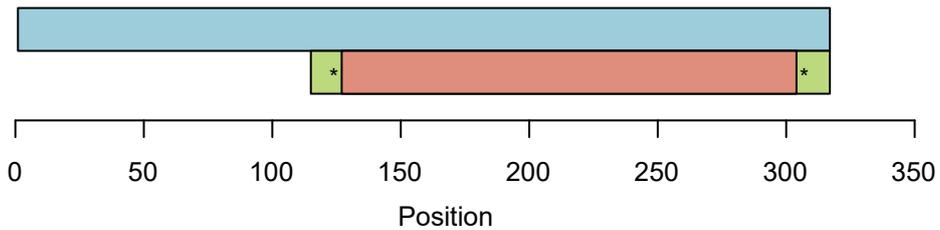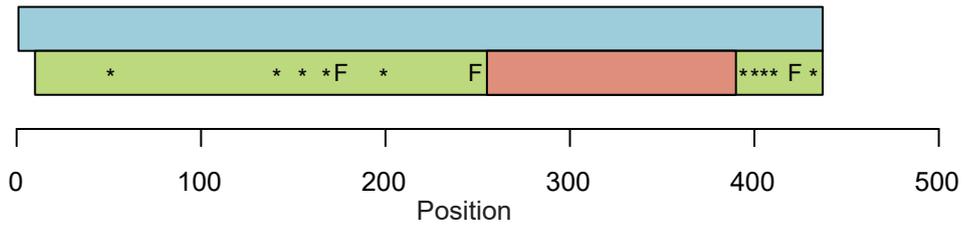
ENSGALG00000001041_r

ENSMUSG00000024866_r

retro−Kmt2d

ENSMUSG00000084064

ENSMUSG00000083892

ENSMUSG00000083549

retro−Rplp0

retro−Eef1g

ENSG00000218772

ENSG00000254722

ENSG00000230535