

Arlt et al. Supplemental File S1.

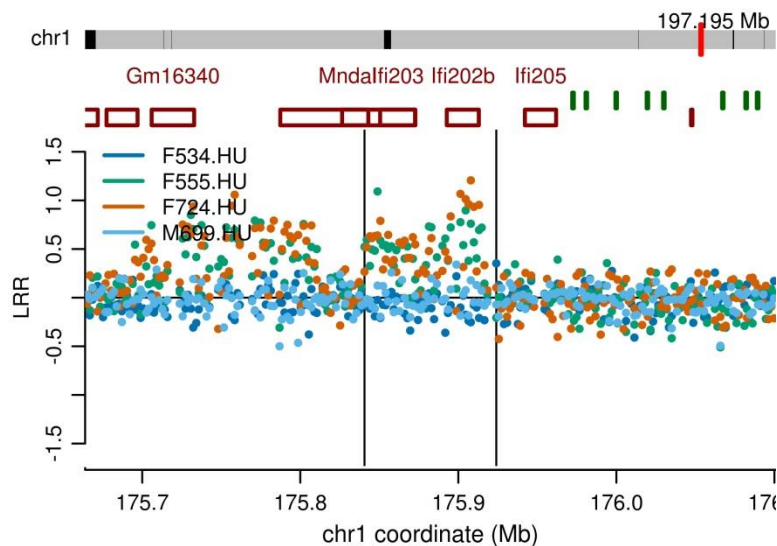
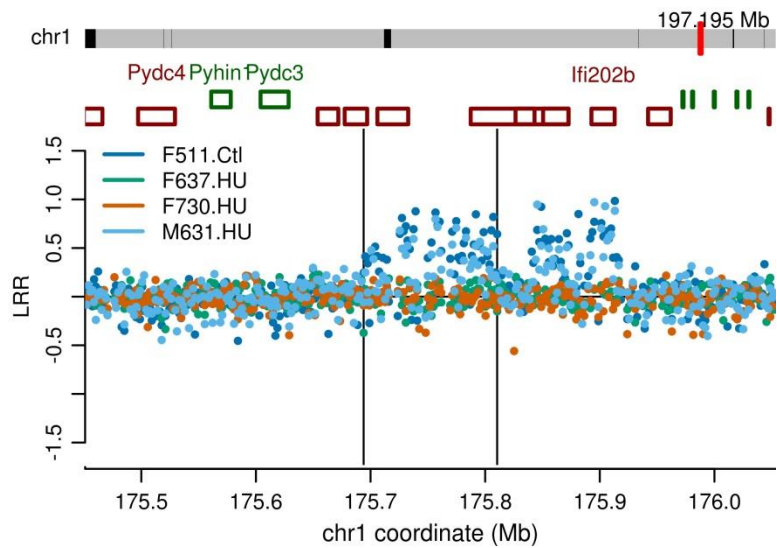
This file contains data image panels for all called germline CNVs from the Arlt et al. study of mice treated with hydroxyurea (HU). Panels are organized by experiment, sorted by chromosome/coordinate within each experiment, to match the accompanying Excel table.

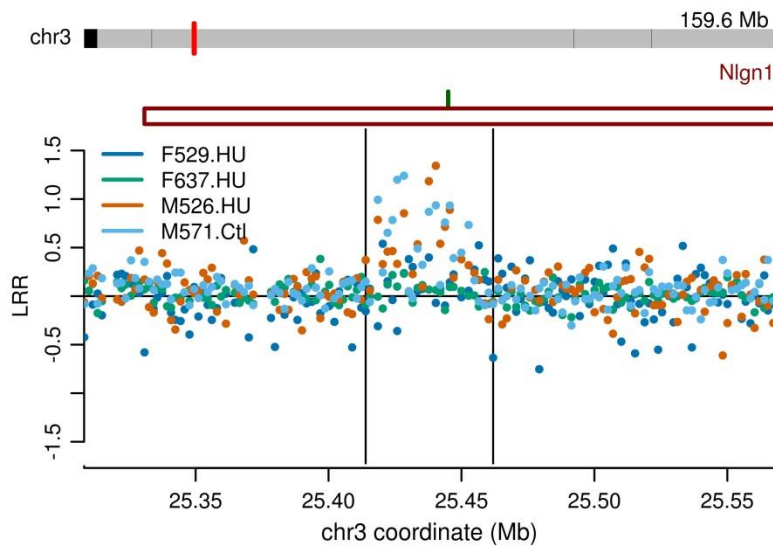
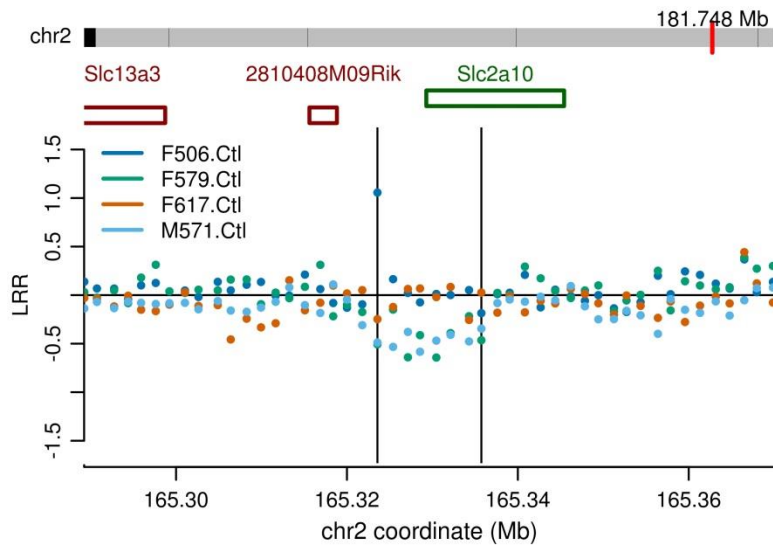
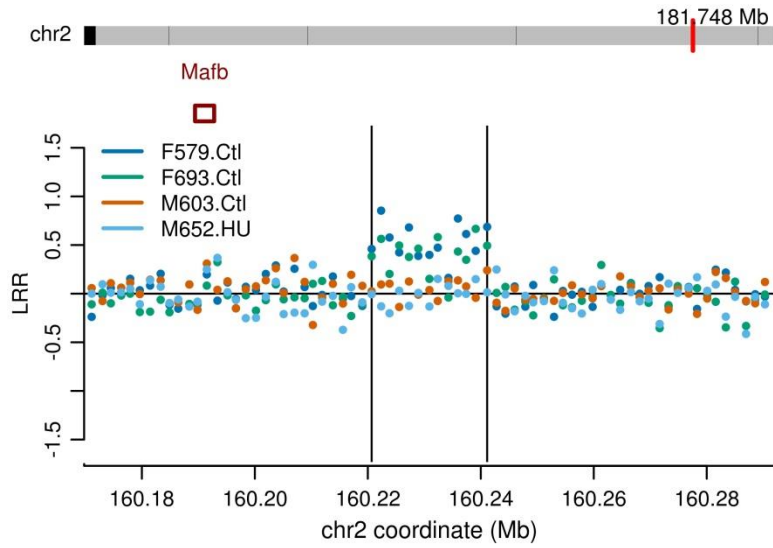
Each panel shows a chromosome bar at the top, with a red hash/box showing the location of the CNV, followed by an Ensembl gene track. Boxes around plots highlight *de novo* CNVs.

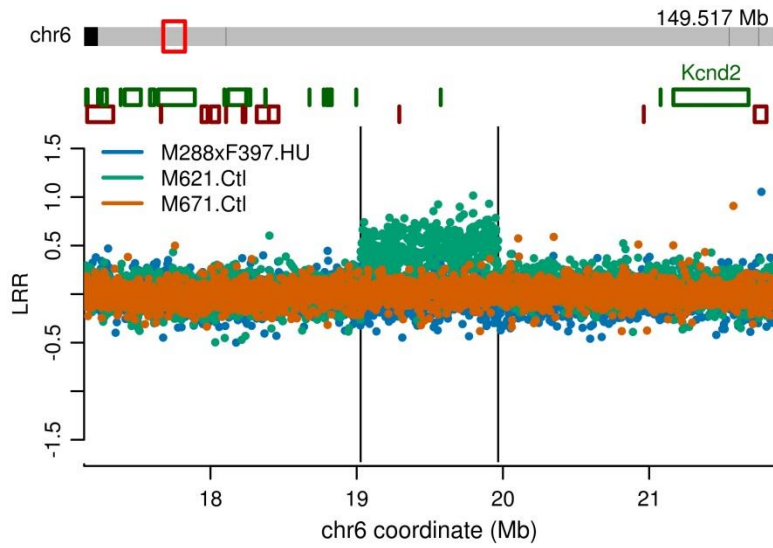
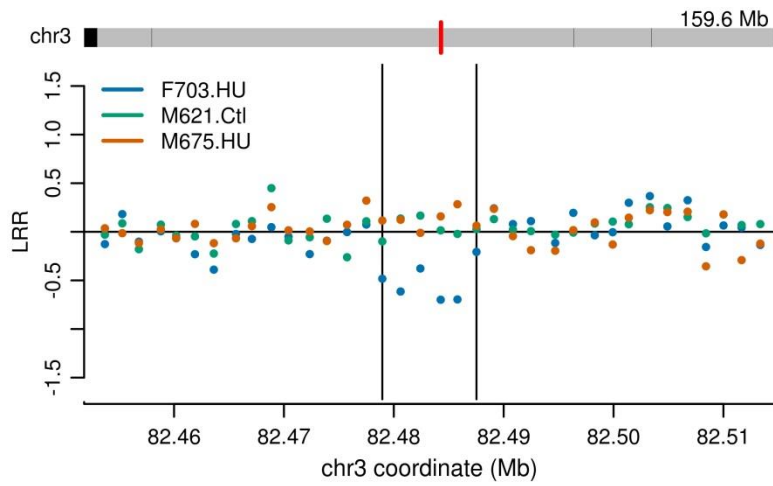
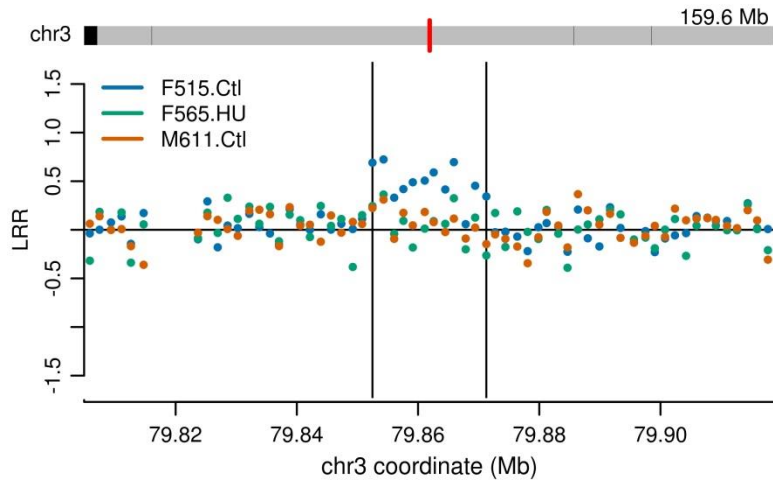
aCGH data use mm9 coordinates and are plotted as the sex-corrected log R Ratio (LRR). A subset of samples are plotted that, when possible, include two pups with and two without the CNV. Vertical lines indicate the span of the CNV region.

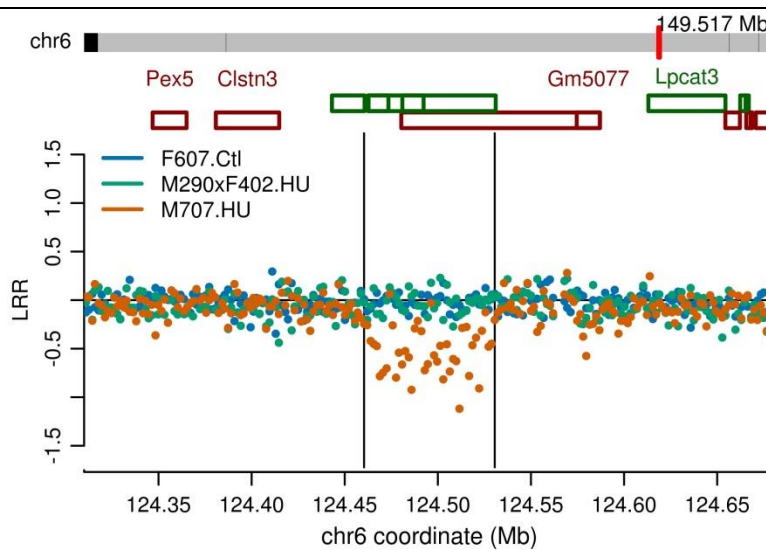
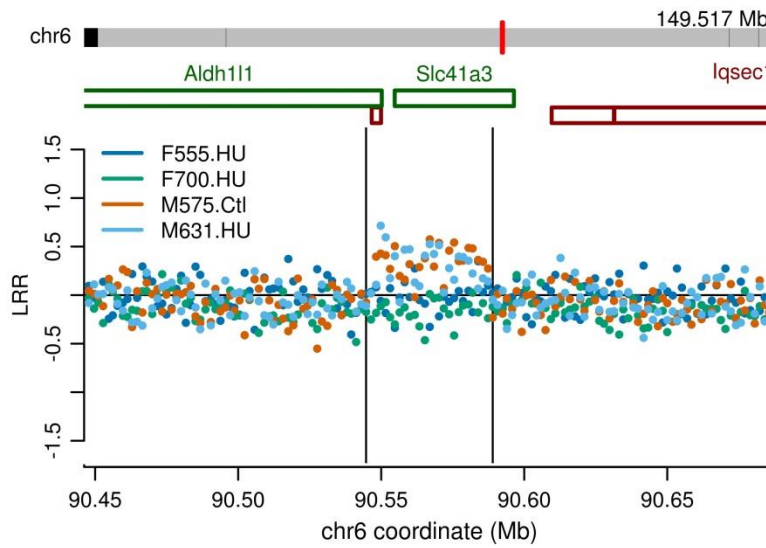
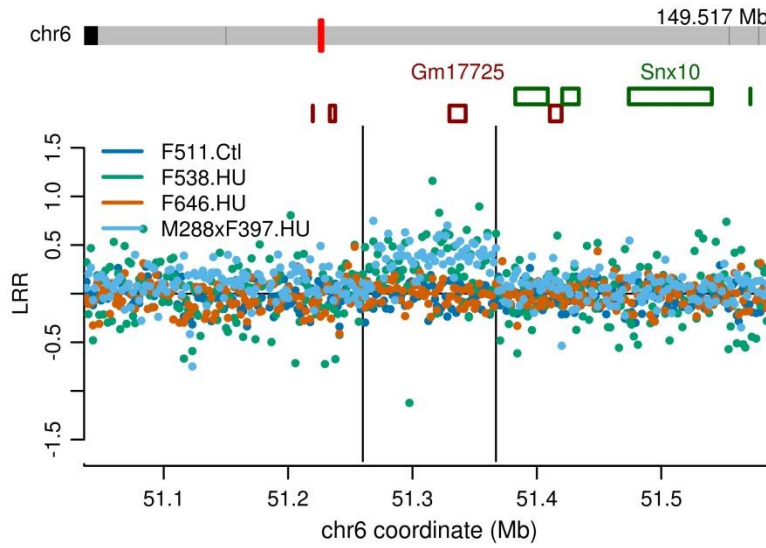
Mate-pair sequencing data use mm10 coordinates and are plotted first as the copy number change determined from fragment coverage depth, and then as the span of anomalous deletion(del) or duplication (dup) pairs, showing one sample with and one without the CNV.

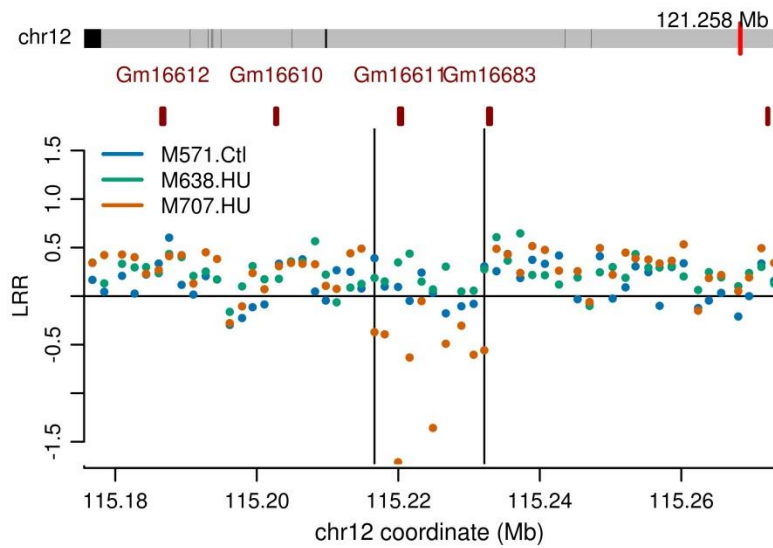
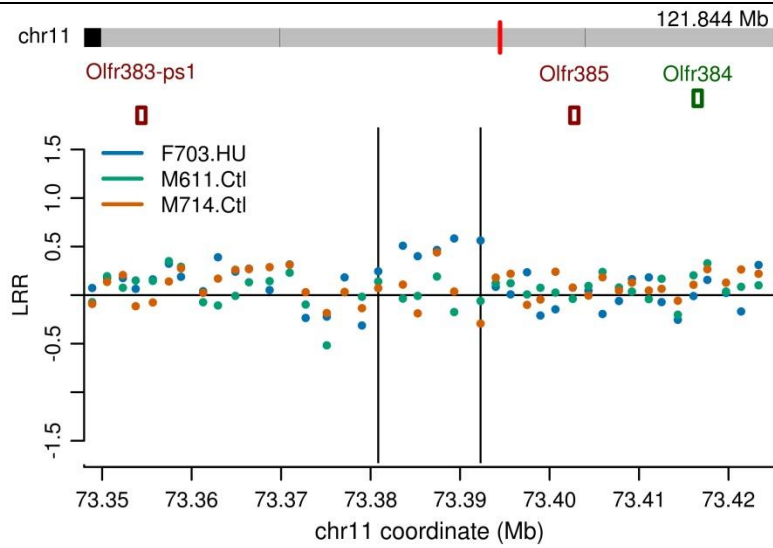
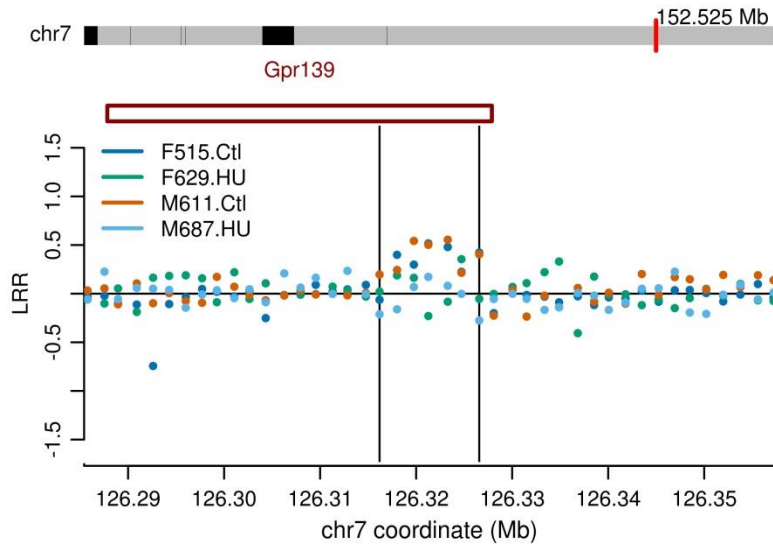
Experiment: Gavage, 60 mg/kg HU (aCGH)

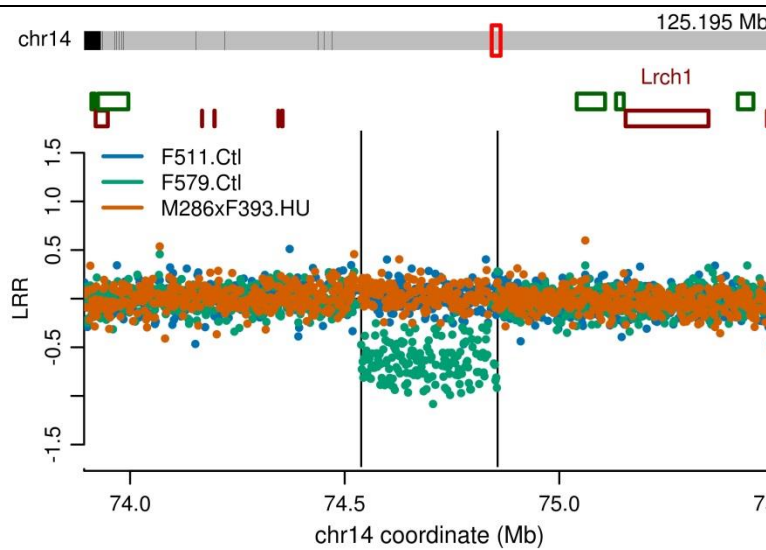
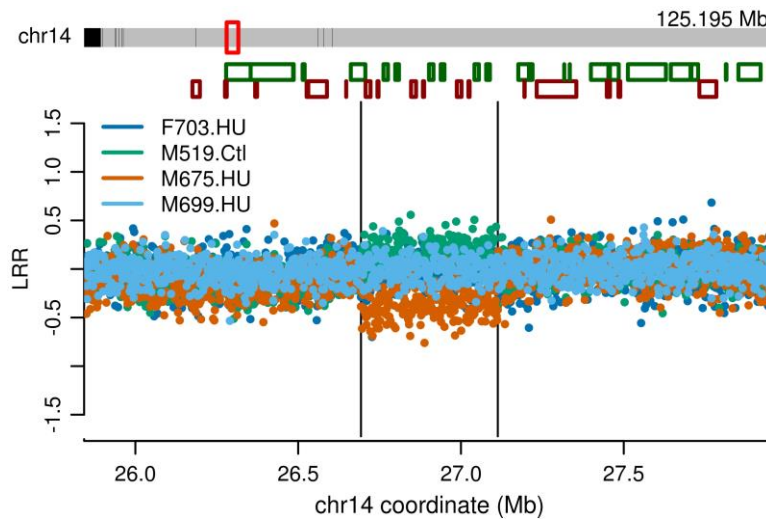
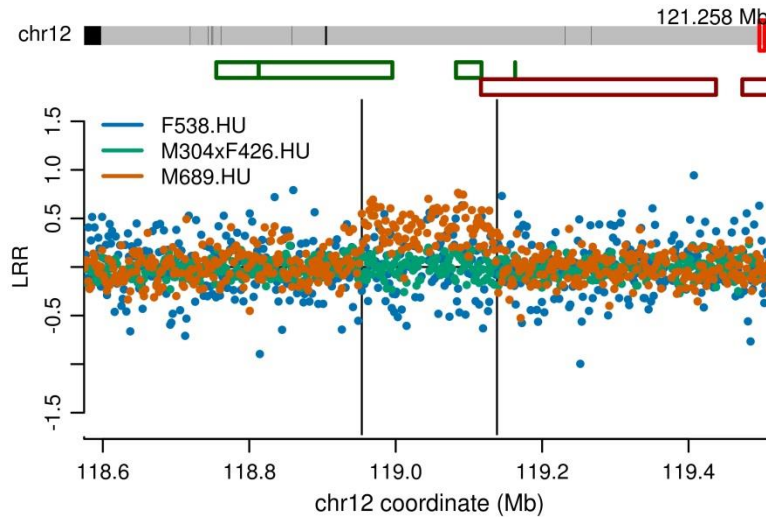


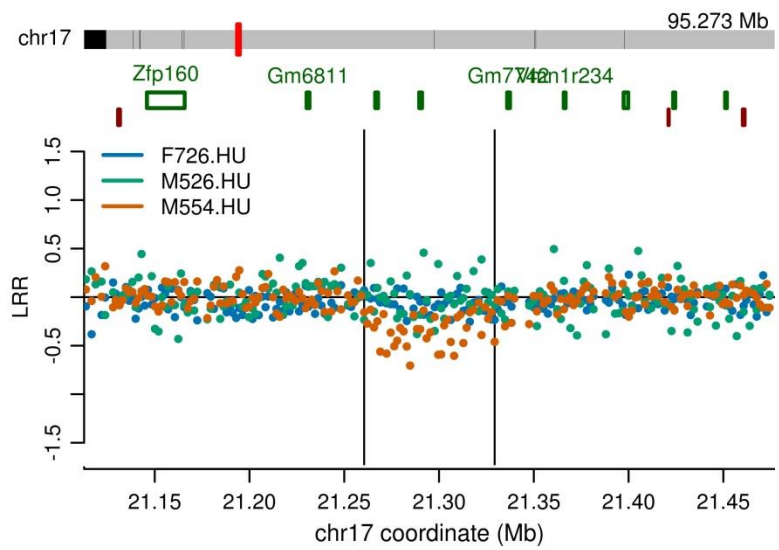
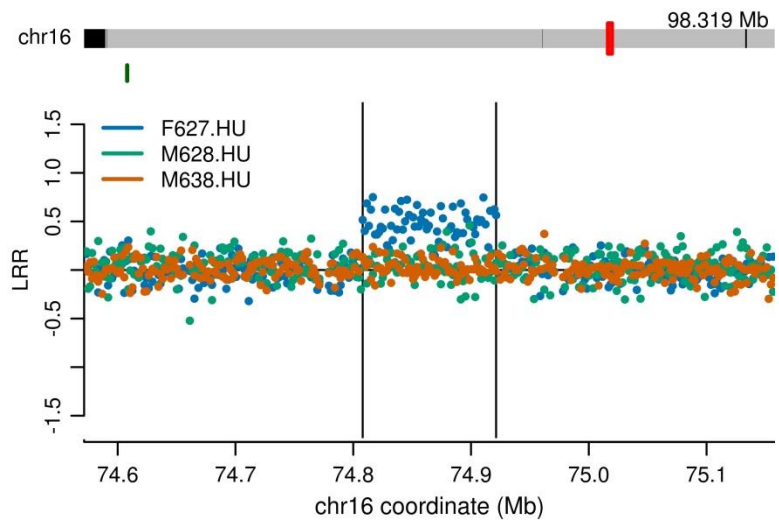
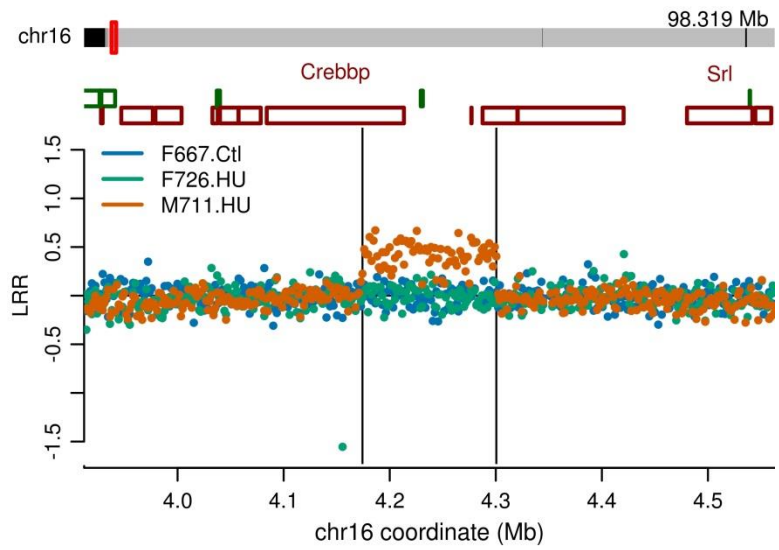


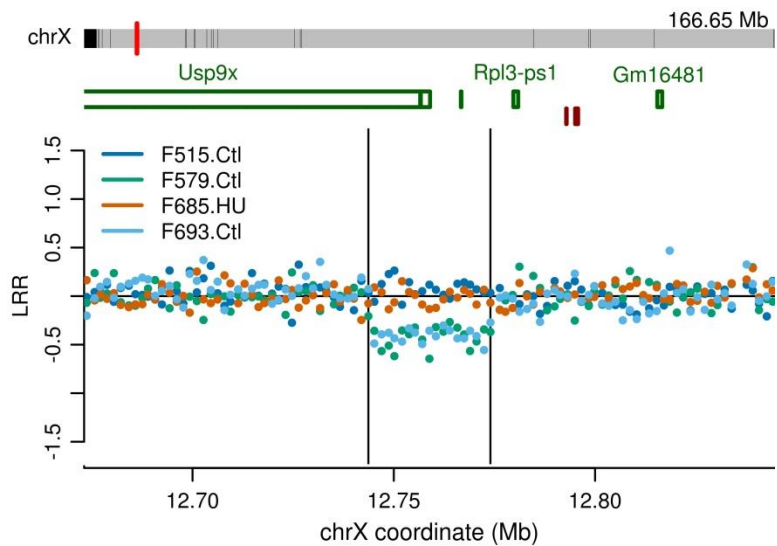
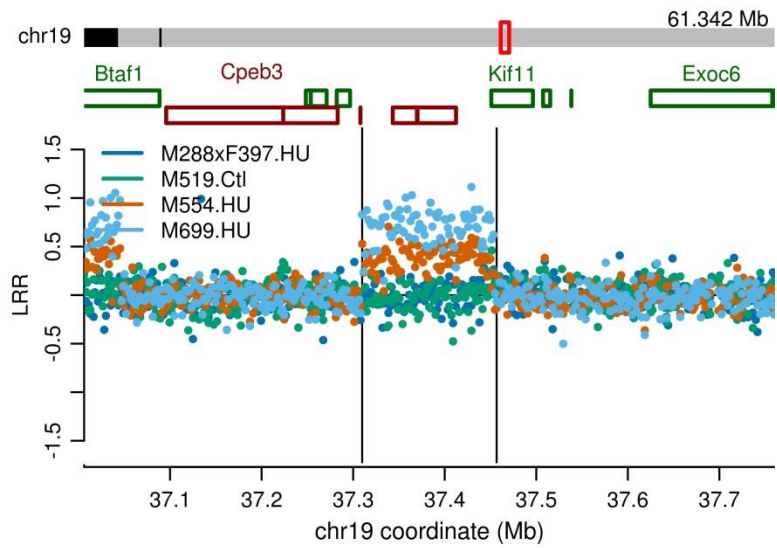
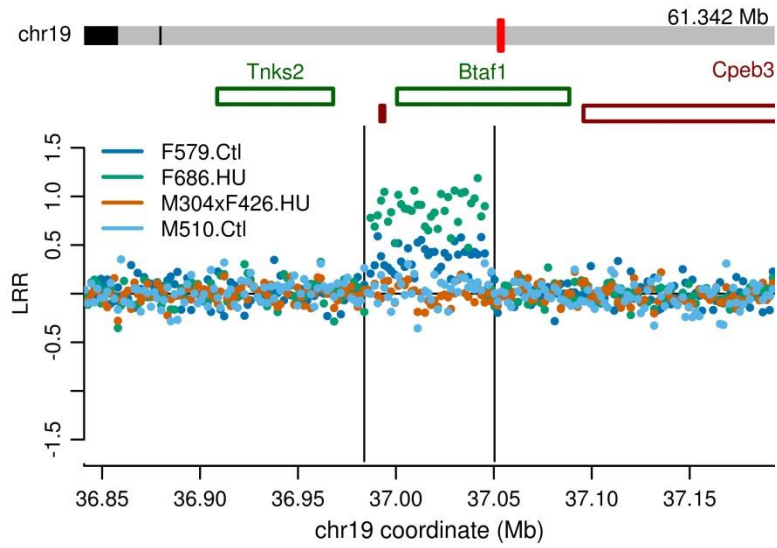


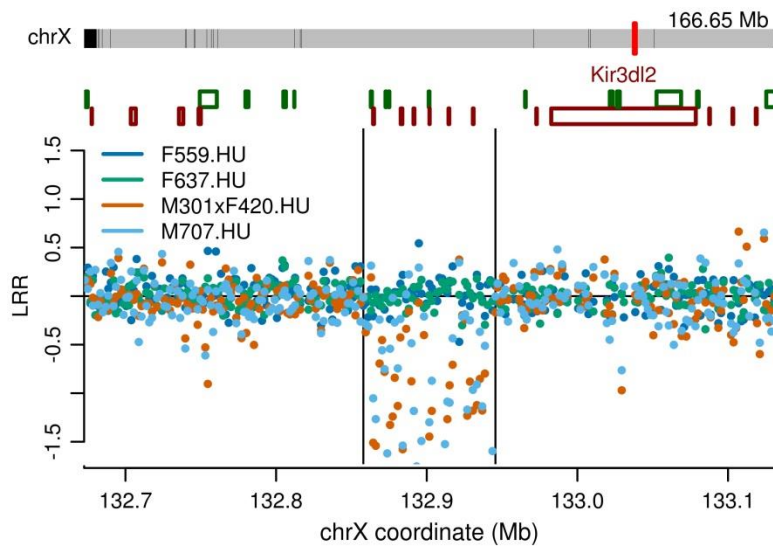
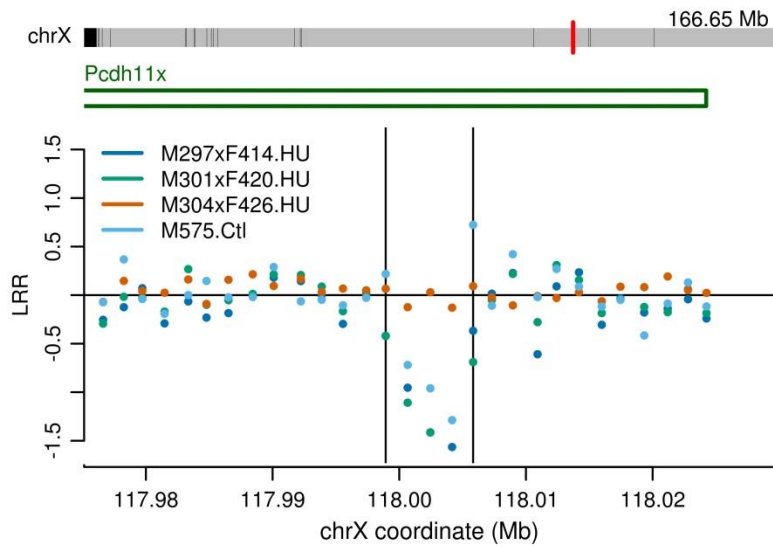
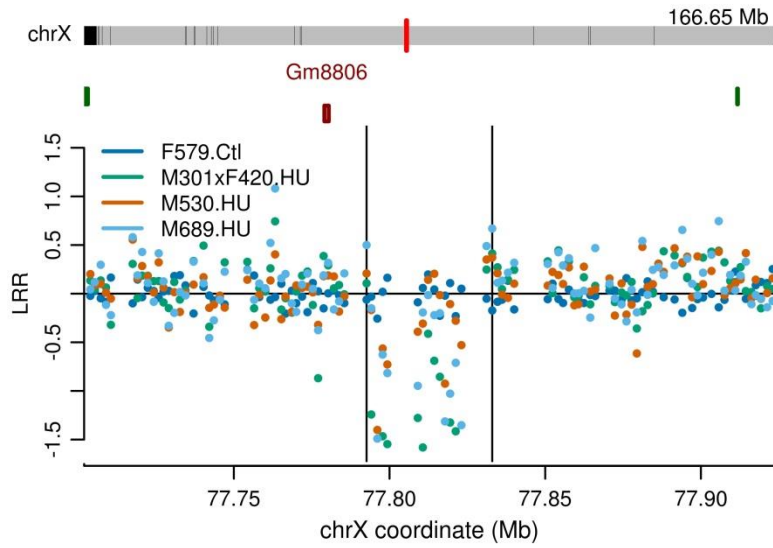




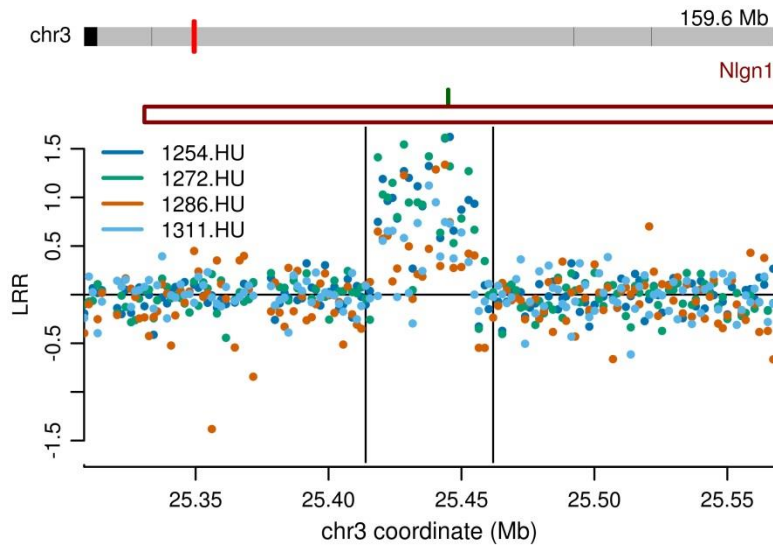
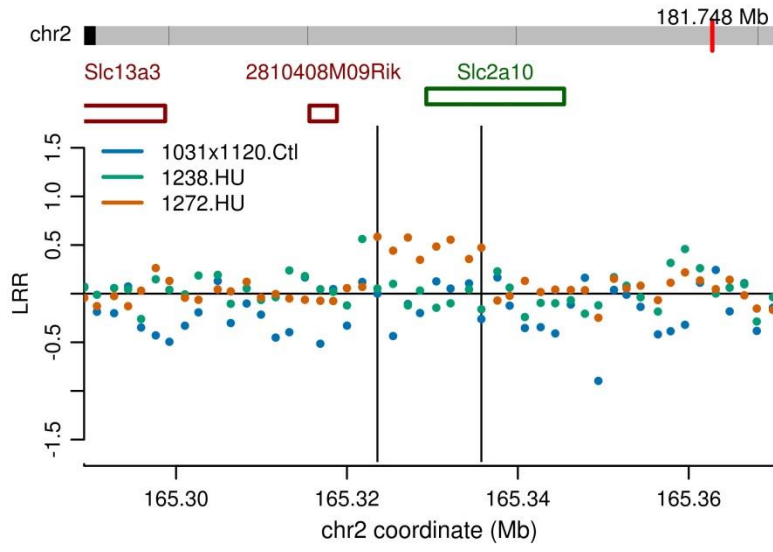


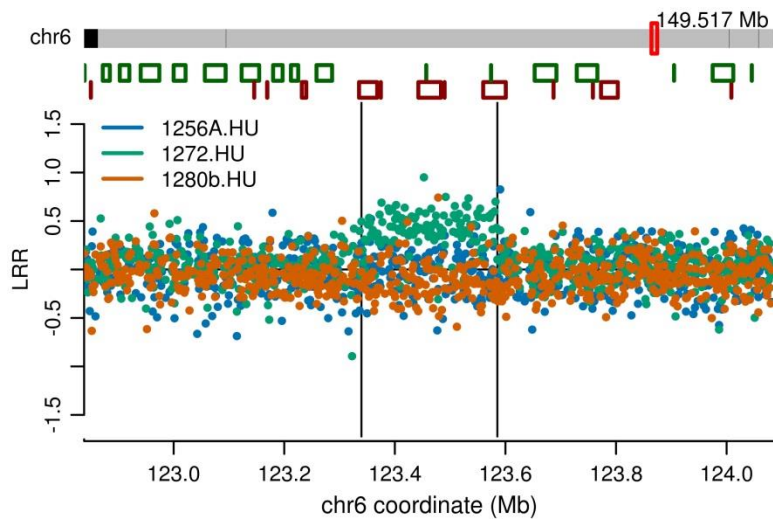
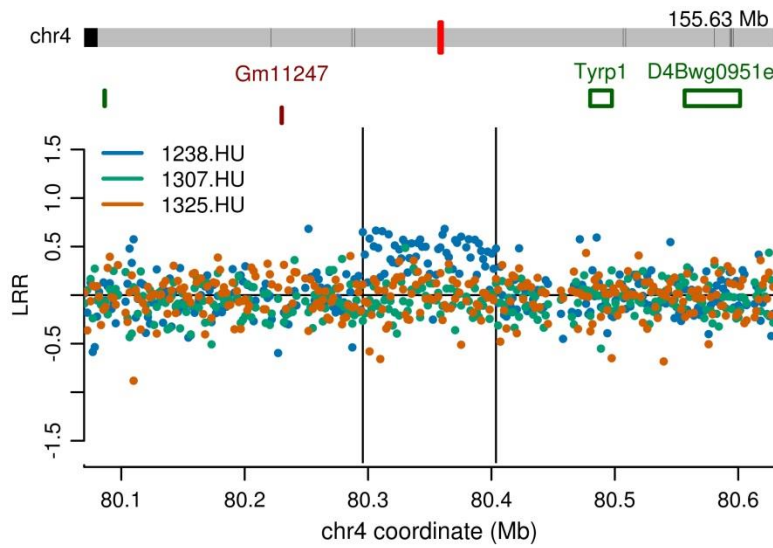
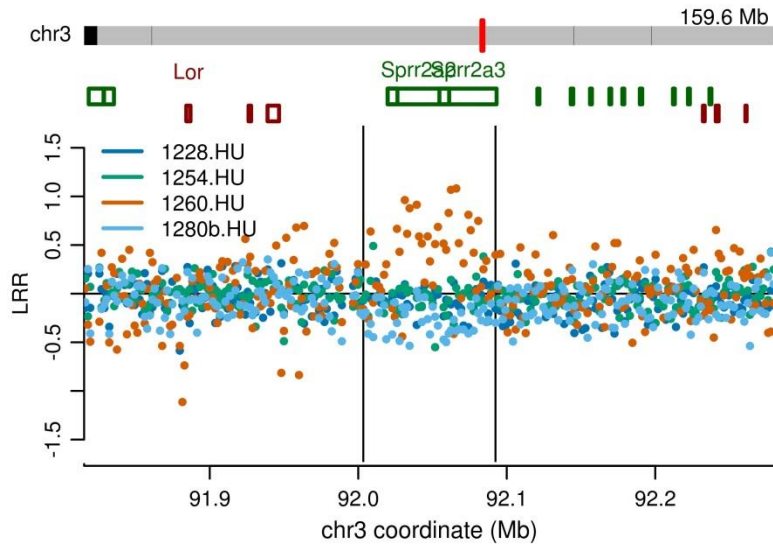


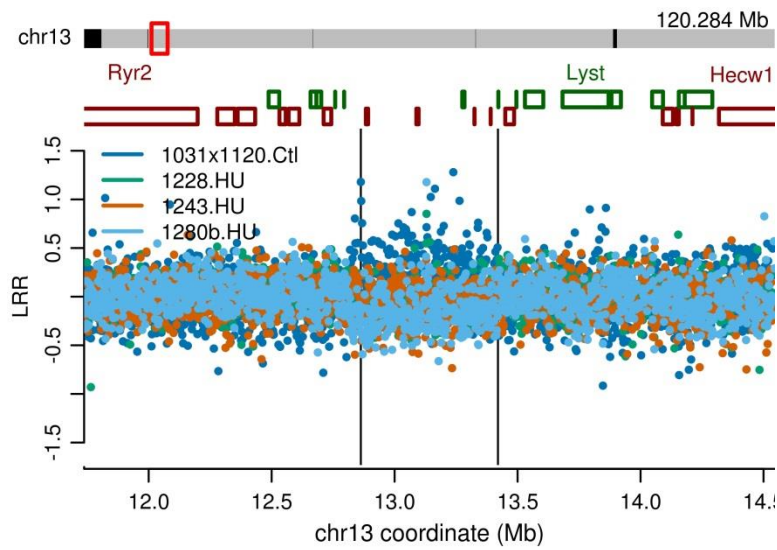
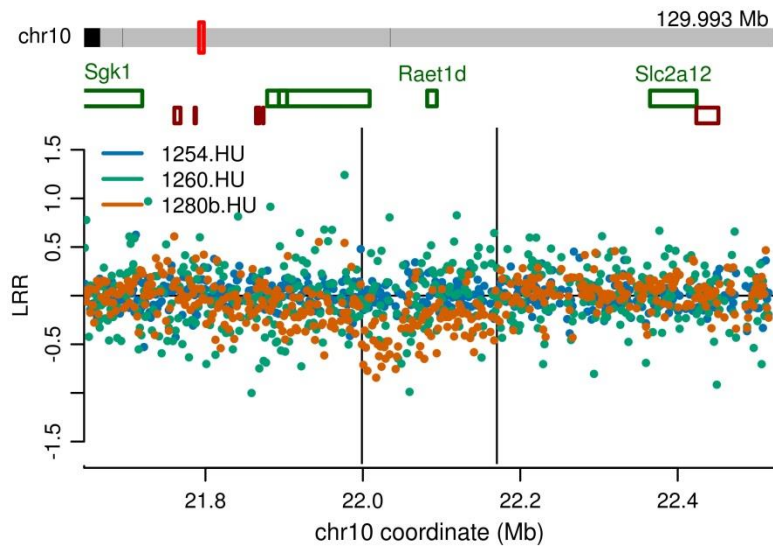


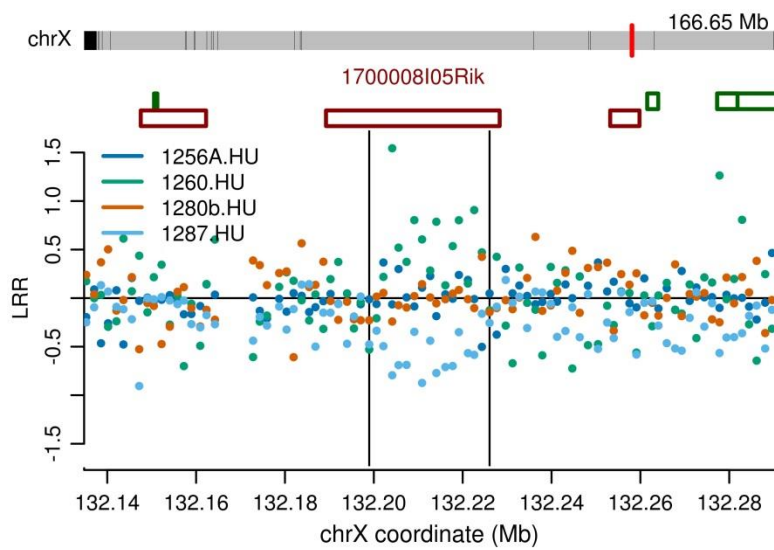
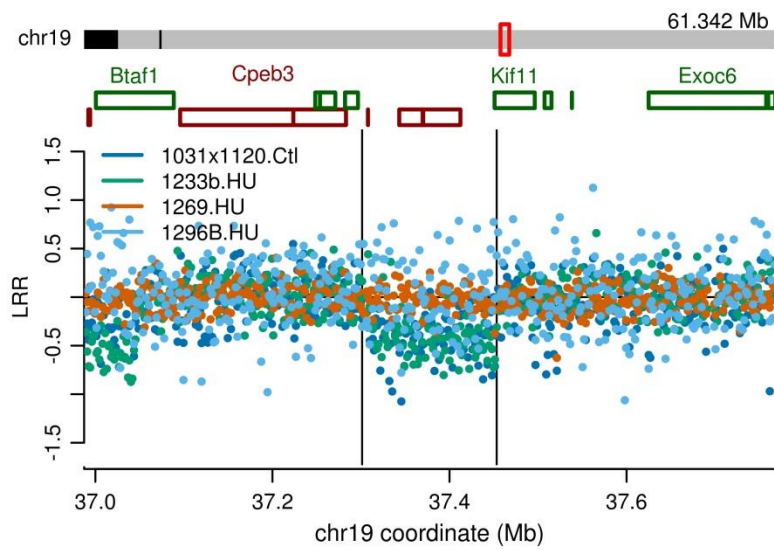
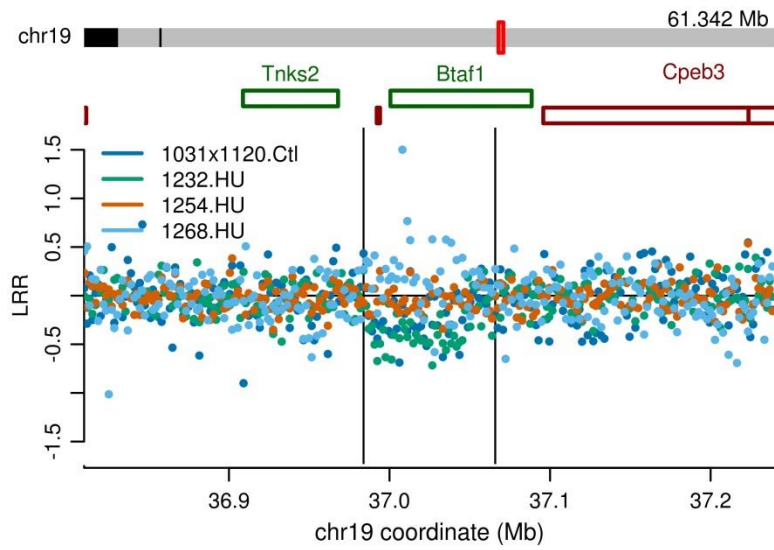


Experiment: Infusion Pump, 19.5 mg/kg/hr (aCGH)









Experiment: Infusion Pump, 17.4 mg/kg/hr HU (mate-pair sequencing)

