Phase chrX → For each individual:
For each tissue:
Identify positions on chrX where allele balance is equal to 1

PT101159 heart

Allele balance

60624	3.0	13.0	0.230769230769230 78
694619	14.0	26.0	0.53846153846153 84
879465	4.0	13.0	0.30769230769230 77
1314201	19.0	26.0	0.73076923076923 07
1436296	21.0	38.0	0.55263157894736 85
1436503	22.0	40.0	0.55
1436515	22.0	38.0	0.57894736842105 27
1717258	84.0	178.0	0.47191011235955 055
1724510	9.0	46.0	0.19565217391304 35
8720846	5.0	13.0	0.38461538461538 464

Total number of reads

position

Number of reads for the biased allele (biased allele is determined from phasing

Obtain the positions where the allele balance is equal to 1 (completely skewed)

15705225	172.0	172.0	1.0
79147400	26.0	26.0	1.0
79147429	30.0	30.0	1.0
147054400	29.0	29.0	1.0
147054504	29.0	29.0	1.0
147054527	24.0	24.0	1.0
147054535	27.0	27.0	1.0
147054564	24.0	24.0	1.0
147054617	21.0	21.0	1.0

Repeat for all of the tissues within an individual

2

```r
# PT101159
setwd("c://Users/tuyen/Documents/postdoc_asu/projects/Cayo_x_inactivation/whole_X_inactivation/results
/phase_whole_X/minDepth10/PT101159/")

heart = read.table("PT101159_hap1_heart_hardfilter_complete_skewed.tsv")
liver = read.table("PT101159_hap1_liver_hardfilter_complete_skewed.tsv")
lung = read.table("PT101159_hap1_lung_hardfilter_complete_skewed.tsv")
ovary = read.table("PT101159_hap1_gonads_hardfilter_complete_skewed.tsv")
pituitary = read.table("PT101159_hap1_pituitary_hardfilter_complete_skewed.tsv")
adrenal = read.table("PT101159_hap1_adrenal_hardfilter_complete_skewed.tsv")


heart_label = rep("heart", nrow(heart))
liver_label = rep("liver", nrow(liver))
lung_label = rep("lung", nrow(lung))
ovary_label = rep("ovary", nrow(ovary))
pituitary_label = rep("pituitary", nrow(pituitary))
adrenal_label = rep("adrenal", nrow(adrenal))



plot_data = data.frame(tissues=c(heart_label, liver_label, lung_label, ovary_label, pituitary_label,
adrenal_label), allele_balance = 1, positions = c(heart[,1], liver[,1], lung[,1], ovary[,1], pituitary[,1],
adrenal[,1]))

cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2")

png("c://Users/tuyen/Documents/postdoc_asu/projects/Cayo_x_inactivation/whole_X_inactivation/results/phase_wh
ole_X/minDepth10/Plots/PT101159_complete_skewed.png", width = 7, height = 4, units = "in", res = 300)
ggplot(data=plot_data, aes(x=positions, y=allele_balance, fill=tissues)) +
  geom_point(shape=21, size=3, color="black", position="jitter") +
  theme_bw() +
  coord_cartesian(xlim = c(1, 156040895)) +
  # geom_jitter(shape=21, size=4, color="black", aes(fill=tissues)) +
  scale_x_continuous(breaks=c(0, 20000000, 40000000, 60000000, 80000000, 100000000, 120000000, 140000000),
                     labels=c("0", "20", "40", "60", "80", "100", "120", "140")) +
  labs(x="chrX position (Mb)", y="Allele balance", title="PT101159") +
  theme(plot.title = element_text(hjust = 0.5, size=18)) +
  geom_rect(aes(xmin=10001, xmax=2781479, ymin=0, ymax=Inf), fill=NA, color="black") +
  geom_rect(aes(xmin=155701383, xmax=156030895, ymin=0, ymax=Inf), fill=NA, color="black") +
  scale_fill_manual(values=alpha(cbbPalette, 0.7))
dev.off()
```
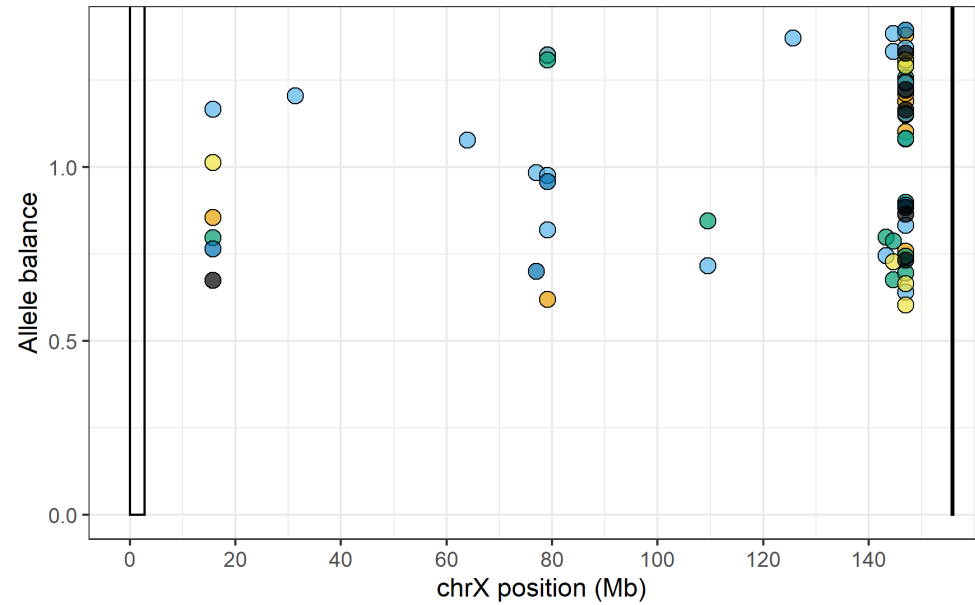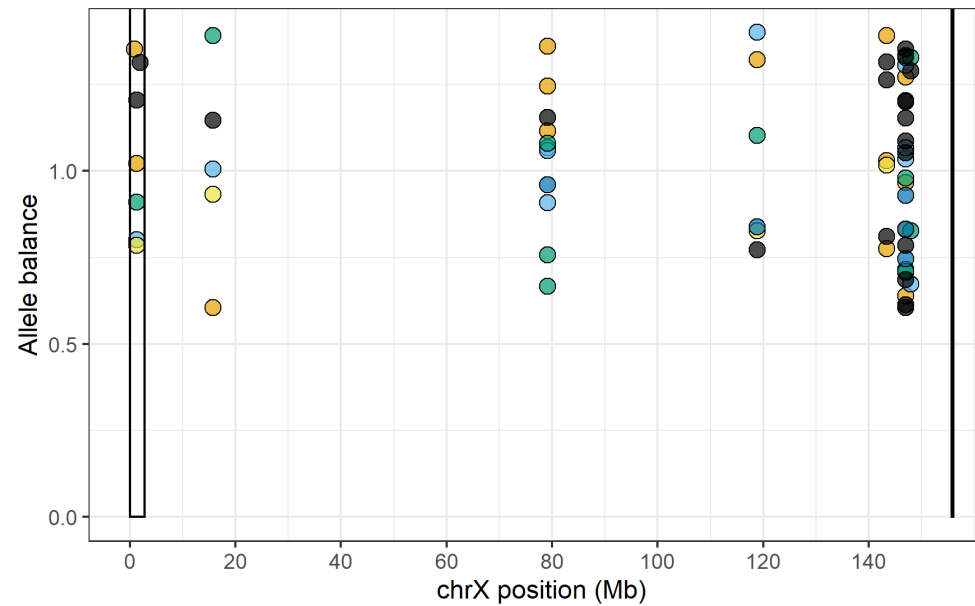
PT101159

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 15,705,225
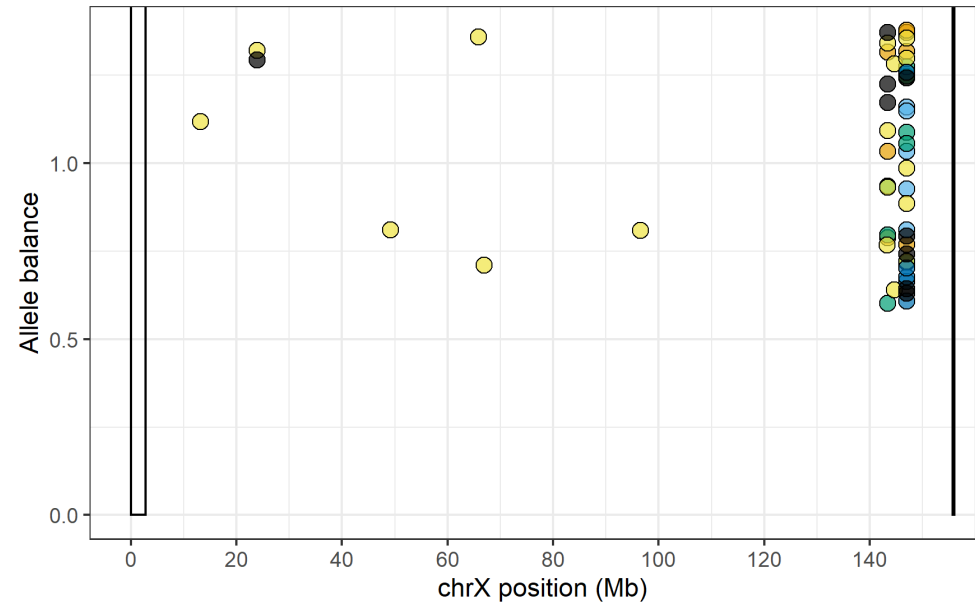- 147,054,504
- 147,054,527
- 147,054,535
- 147,054,564

PT101210

Positions on the X that are completely skewed that are shared across all 6 tissues:
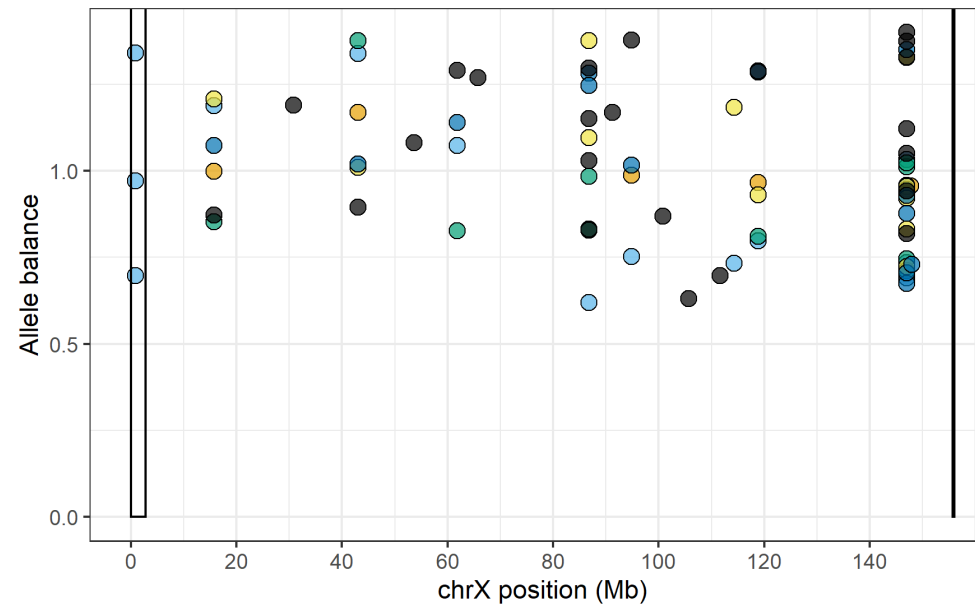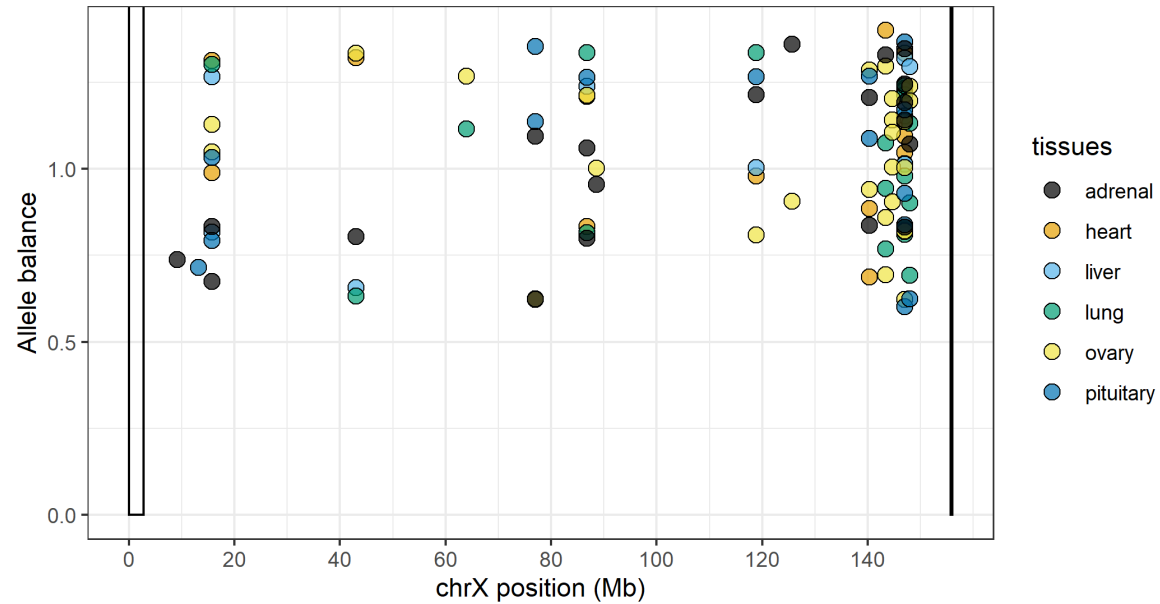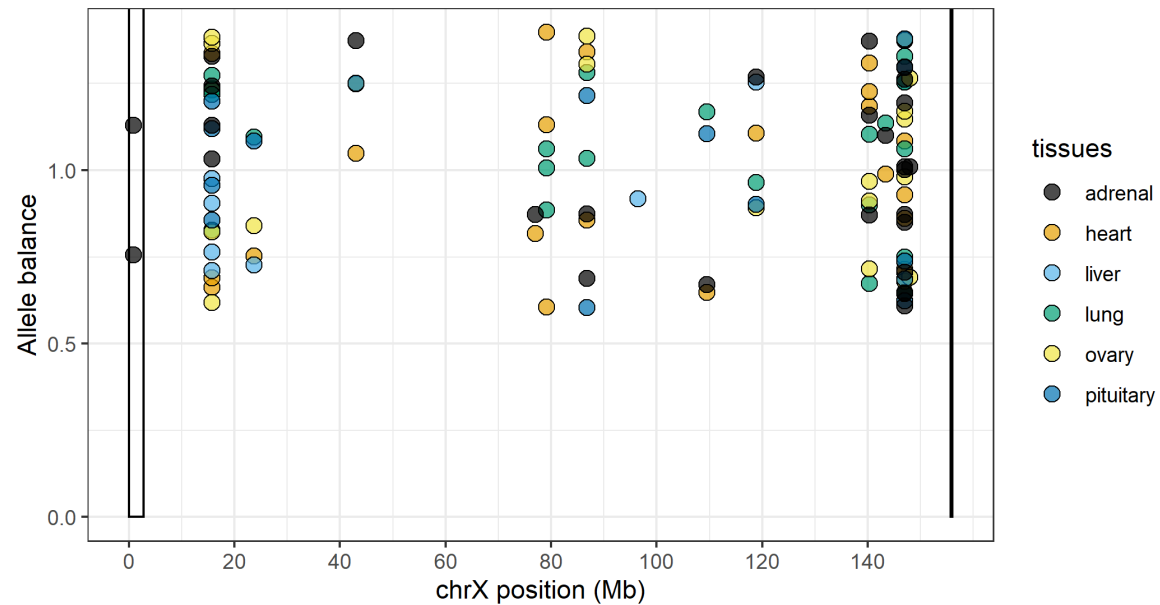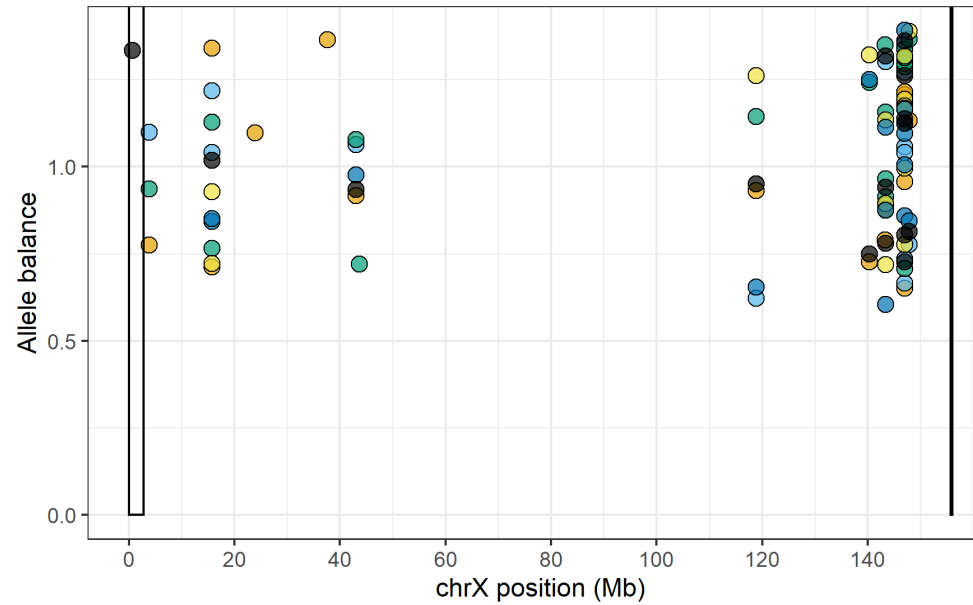- 118,831,364

tissues
- adrenal
- heart
- liver
- lung
- ovary
- pituitary

4

PT102485

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 147,054,504
- 147,054,527
- 147,054,535
- 147,054,564
- 147,054,617

PT102842

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 15,705,200
- 43,034,819
- 118,831,364

PT103352

Positions on the X that are
completely skewed that are
shared across all 6 tissues:
- 15,705,233
- 118,831,364
- 147,054,400
- 147,054,504
- 147,054,527
- 147,054,535
- 147,054,564

PT103811

Positions on the X that are
completely skewed that are
shared across all 6 tissues:
- 15,705,200
- 15,705,225
- 15,705,233
- 15,705,394
- 118,831,364
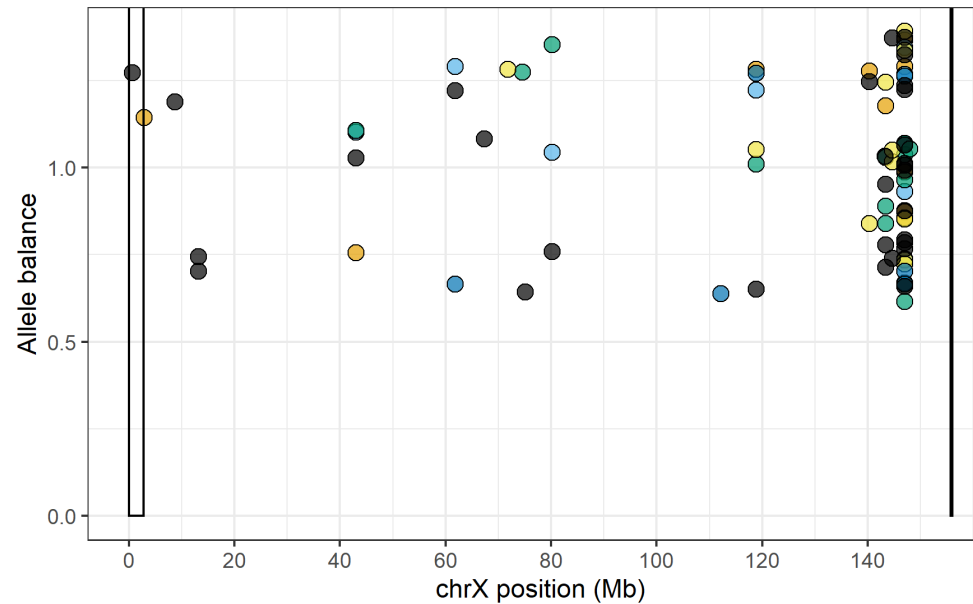- 147,054,504
- 147,054,527
- 147,054,535

PT104219

PT104883

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 15,705,225
- 118,831,364
- 143,373,439
- 147,054,400
- 147,054,504
- 147,054,527
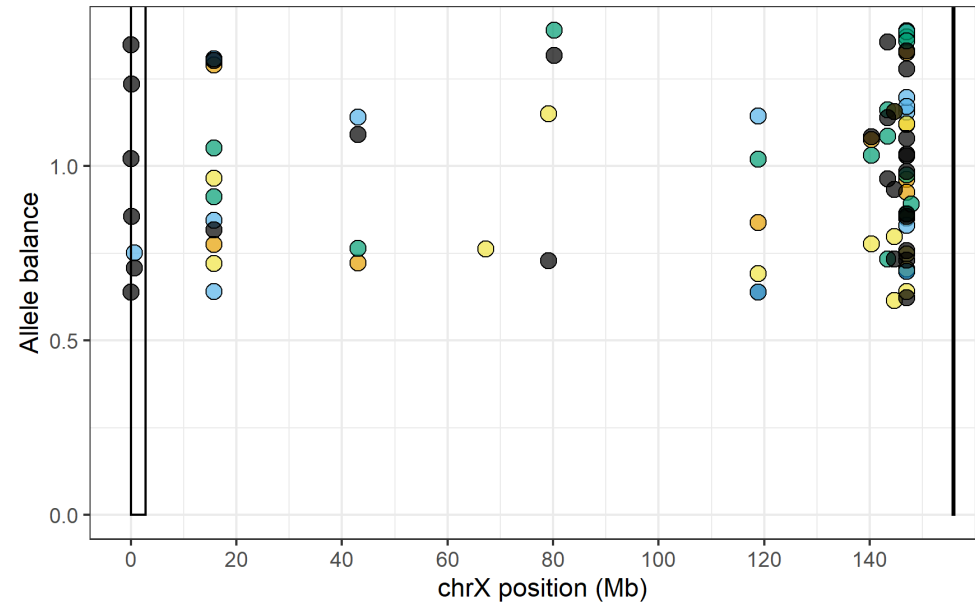- 147,054,535
- 147,054,564
- 147,054,617
- 147,823,222

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 118,831,364
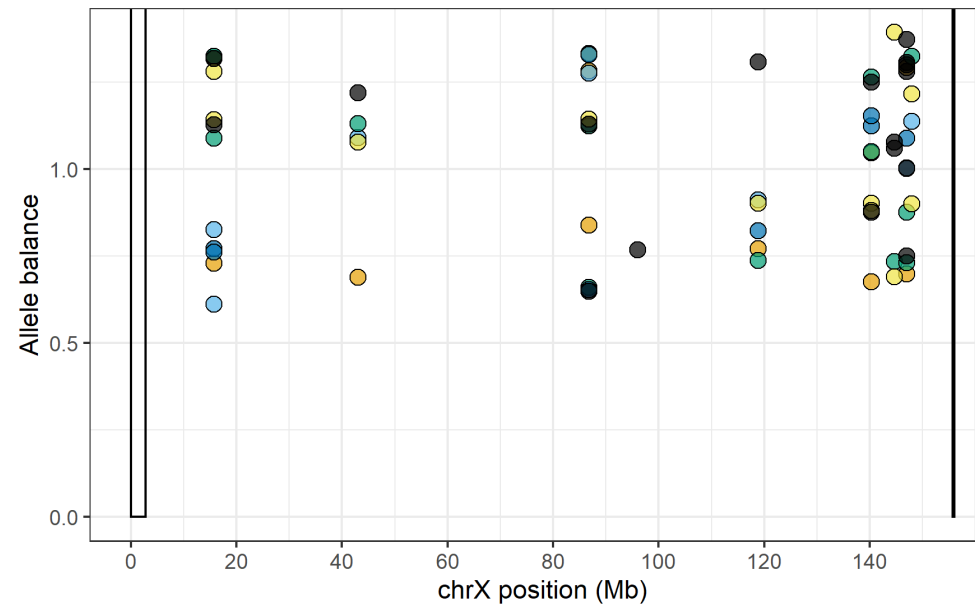- 147,054,527
- 147,054,535
- 147,054,564

PT105239

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 15,705,225
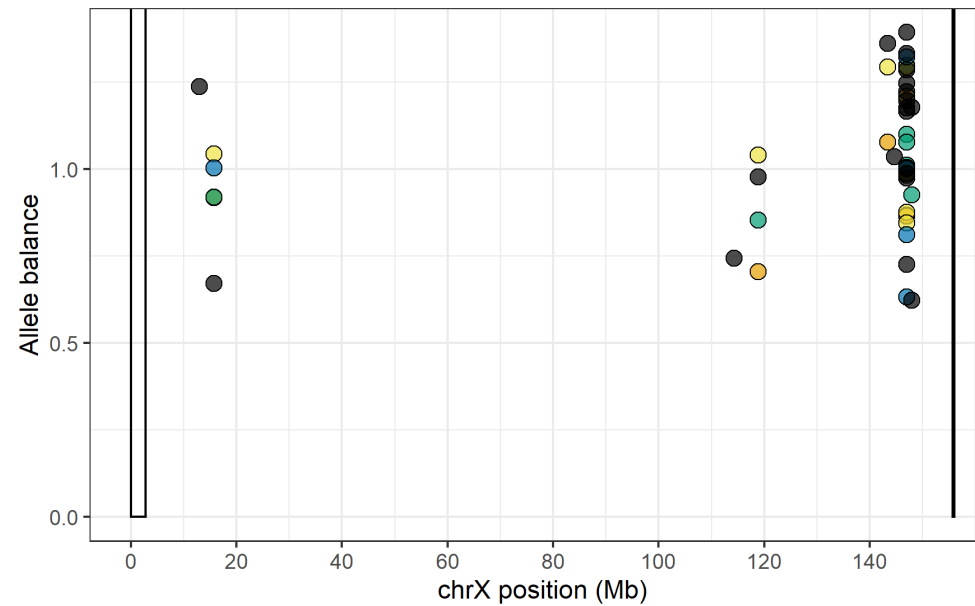- 147,054,504

PT105290

Positions on the X that are completely skewed that are shared across all 6 tissues:
- 15,705,225
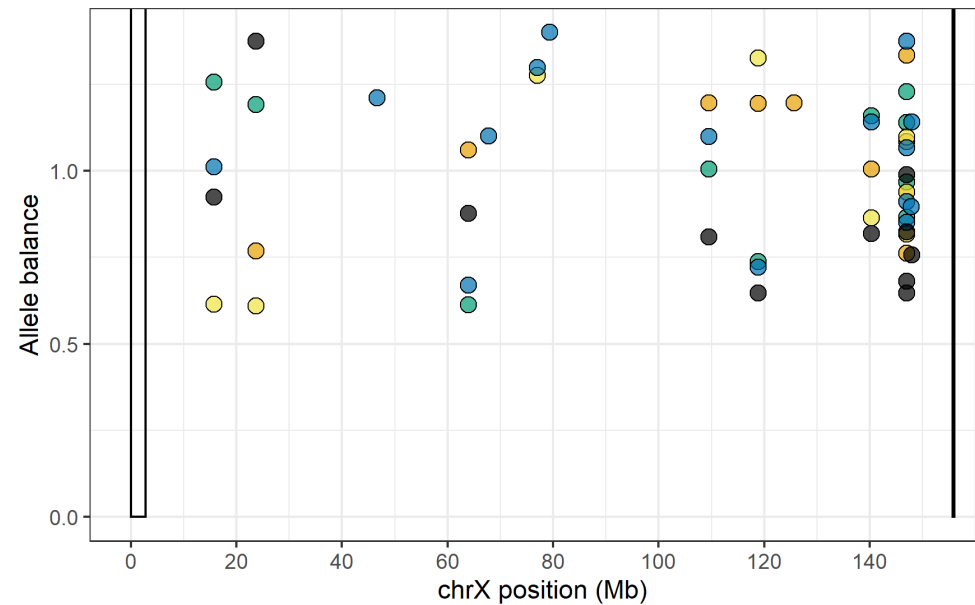- 15,705,233
- 86,750,672
- 118,831,364

PT103046

Positions on the X that are completely skewed that are shared across all 5 tissues:
- 15,705,394
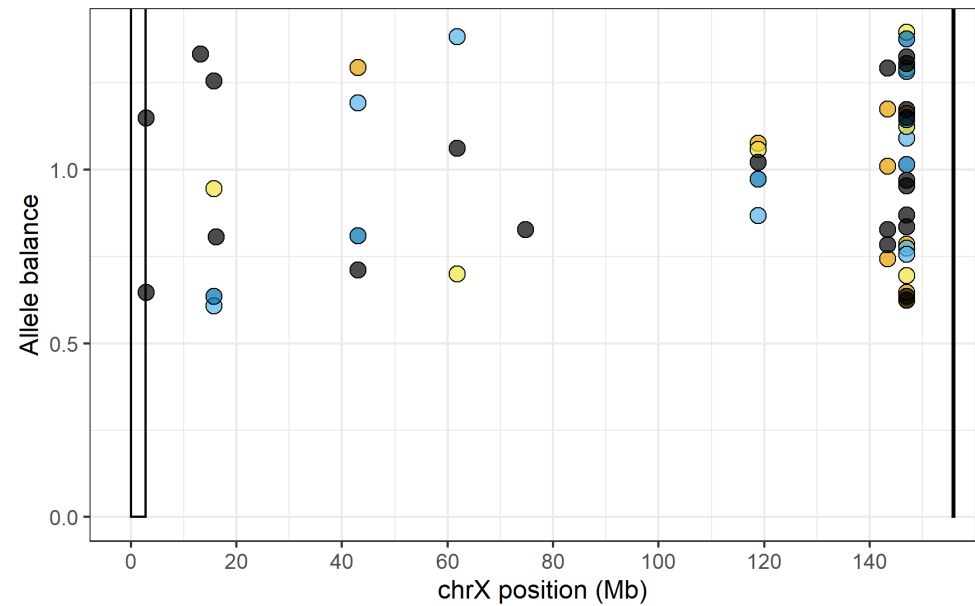- 147,054,527
- 147,054,564

PT104733

Positions on the X that are completely skewed that are shared across all 5 tissues:
- 118,831,364
- 140,353,426
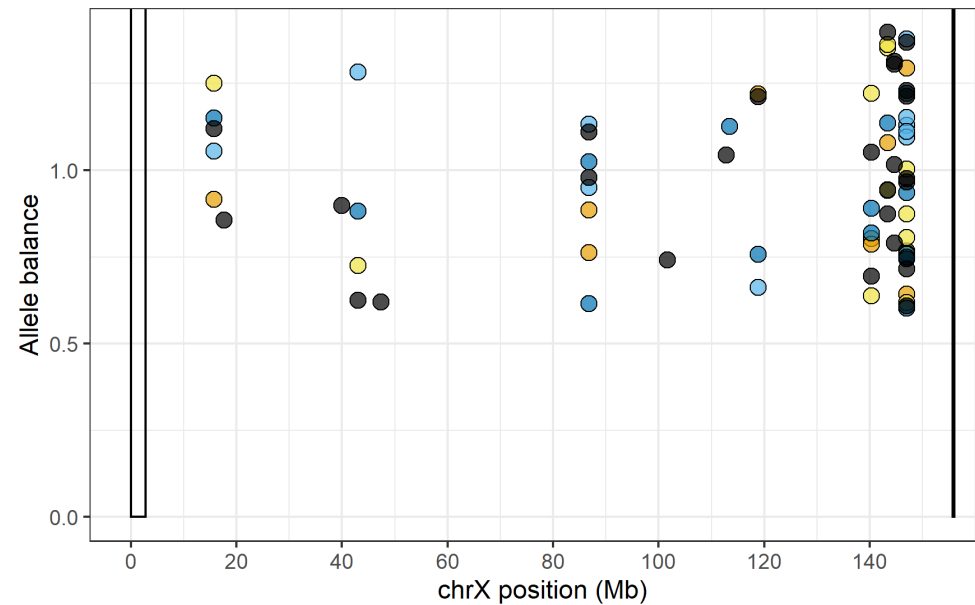- 147,054,504
- 147,054,527
- 147,054,535

PT103760

Positions on the X that are completely skewed that are shared across all 5 tissues:
- 118,831,364
- 147,054,504
- 147,054,527
- 147,054,535
- 147,054,564

PT104270

Positions on the X that are completely skewed that are shared across all 5 tissues:
- 15,705,225
- 147,054,504
- 147,054,535
- 147,054,564