# FSTs in hybrid poplars

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#### 1. Create a Fst Density Plot

• Import libraries and data into R

```
library(ggplot2)
library(reshape2)

sig.fst <- read.table("sig.fst", header=F)
neu.fst <- read.table("neu.fst", header=F)</pre>
```

• Format and merge data

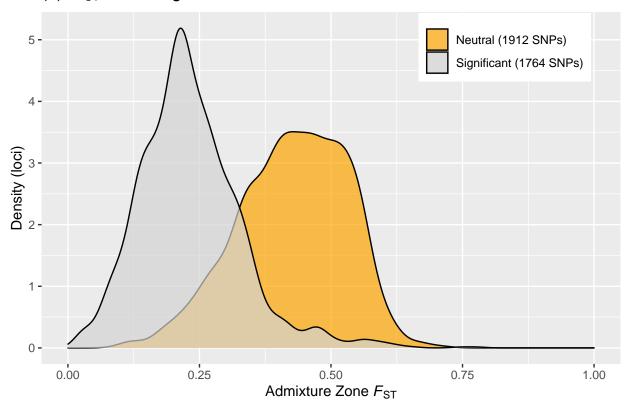
```
sig <- data.frame(x=sig.fst$V2, label=rep("Significant (1764 SNPs)", 1764))
neu <- data.frame(x=neu.fst$V2, label=rep("Neutral (1912 SNPs)", 1912))
fst <- rbind(sig, neu)</pre>
```

• Make density plot

```
ggplot(fst, aes(x, y=..density.., fill=label)) + xlim(0,1) +
    geom_density(color="black", alpha=0.7) +
    scale_fill_manual(values=c("orange", "lightgray")) +
    labs(x=expression(paste("Admixture Zone"~italic(F)[ST])), y="Density (loci)",
        title=expression(paste("(b) "~italic(F)[ST]~" in "~italic("P. angustifolia")~" derived alleles"
    theme(legend.position=c(0.8,0.9), legend.title=element_blank())
```

## Warning: Removed 49 rows containing non-finite values (stat\_density).

## (b) F<sub>ST</sub> in P. angustifolia derived alleles



### 2. Reproducibility of results

• Read the data file

```
pct <- read.table("pval_counts.txt", header=T)</pre>
```

• Assign colors to numbers

• Draw a histogram to show reproducibility

