

Figure 1.

Figure S1.

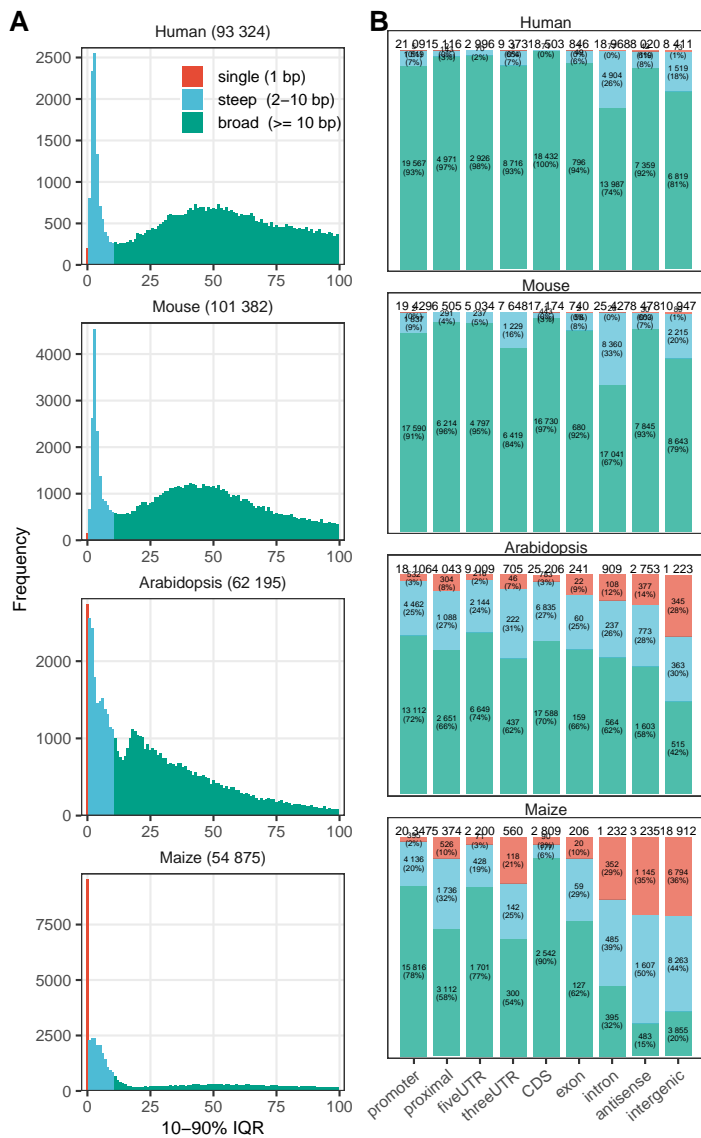


Figure S2. TSS shape comparison between maize and three other species.

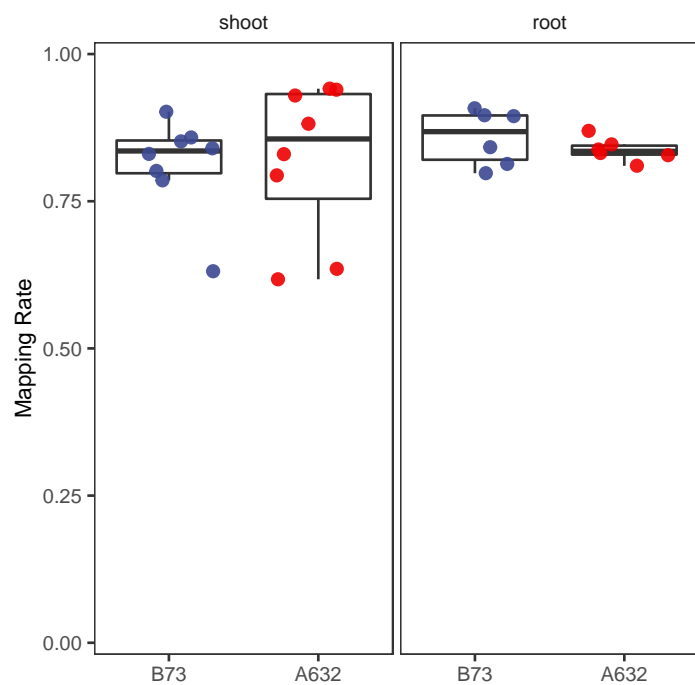


Figure S3. CAGE tag mapping rates for B73 and A632 samples.

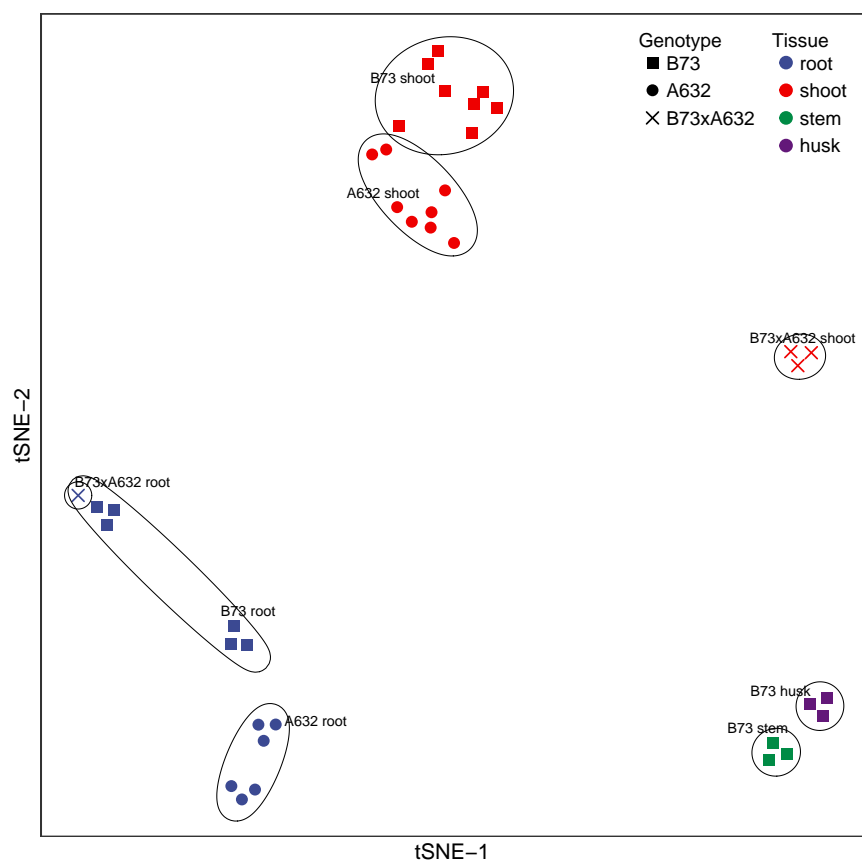


Figure S3b. t-SNE clustering of all samples.

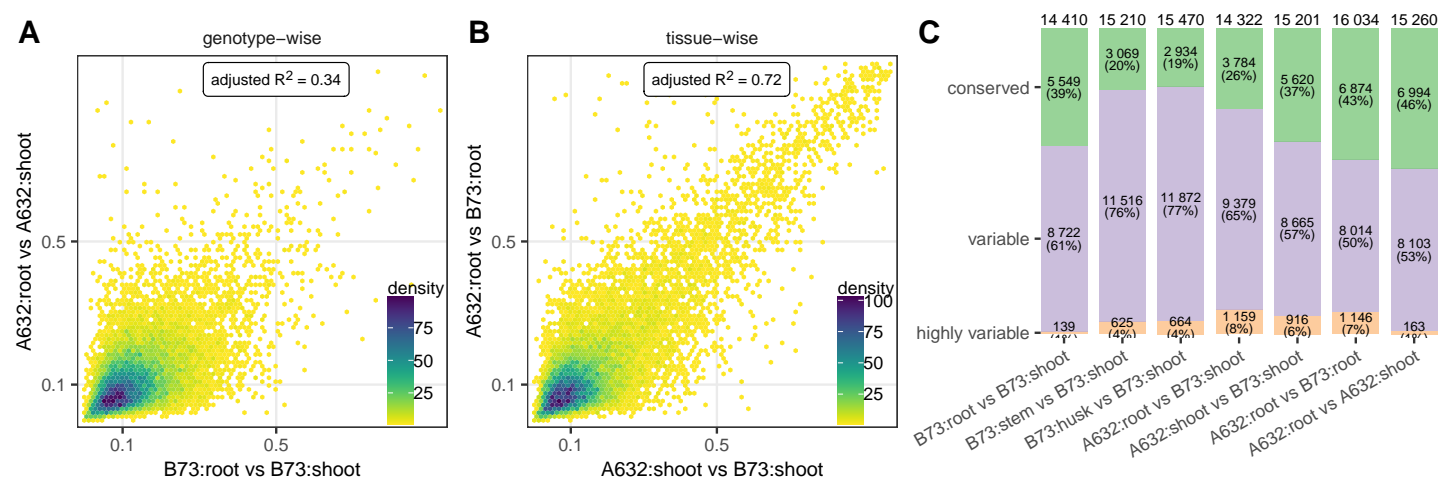


Figure 2. Shifting scores.

Table 1. TSSs identified in the study.

| Genotype | Tissue | # TCs | # Genes w. TCs | # novel TCs | # Genes w. novel TCs | # Genes w. Alternate TCs |
|----------|--------|--------|----------------|-------------|----------------------|--------------------------|
| B73 | shoot | 42,736 | 18,203 | 0 | 0 | 0 |
| B73 | root | 37,236 | 18,205 | 4,890 | 2,085 | 1,132 |
| B73 | stem | 29,022 | 19,878 | 8,336 | 2,958 | 2,254 |
| B73 | husk | 30,296 | 20,518 | 8,934 | 3,264 | 2,500 |
| A632 | shoot | 40,090 | 18,681 | 5,979 | 1,650 | 1,252 |
| A632 | root | 40,778 | 18,718 | 7,436 | 2,733 | 1,528 |
| B73xA632 | shoot | 34,535 | 16,366 | 3,981 | 930 | 648 |
| B73xA632 | root | 29,020 | 12,978 | 3,243 | 917 | 521 |