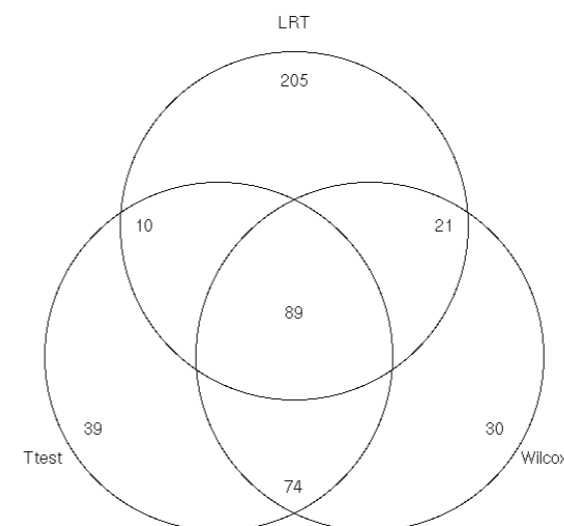
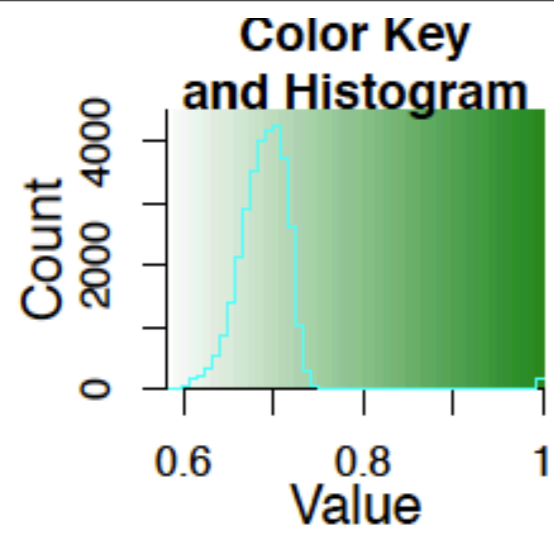


Local event-based analysis : pipeline

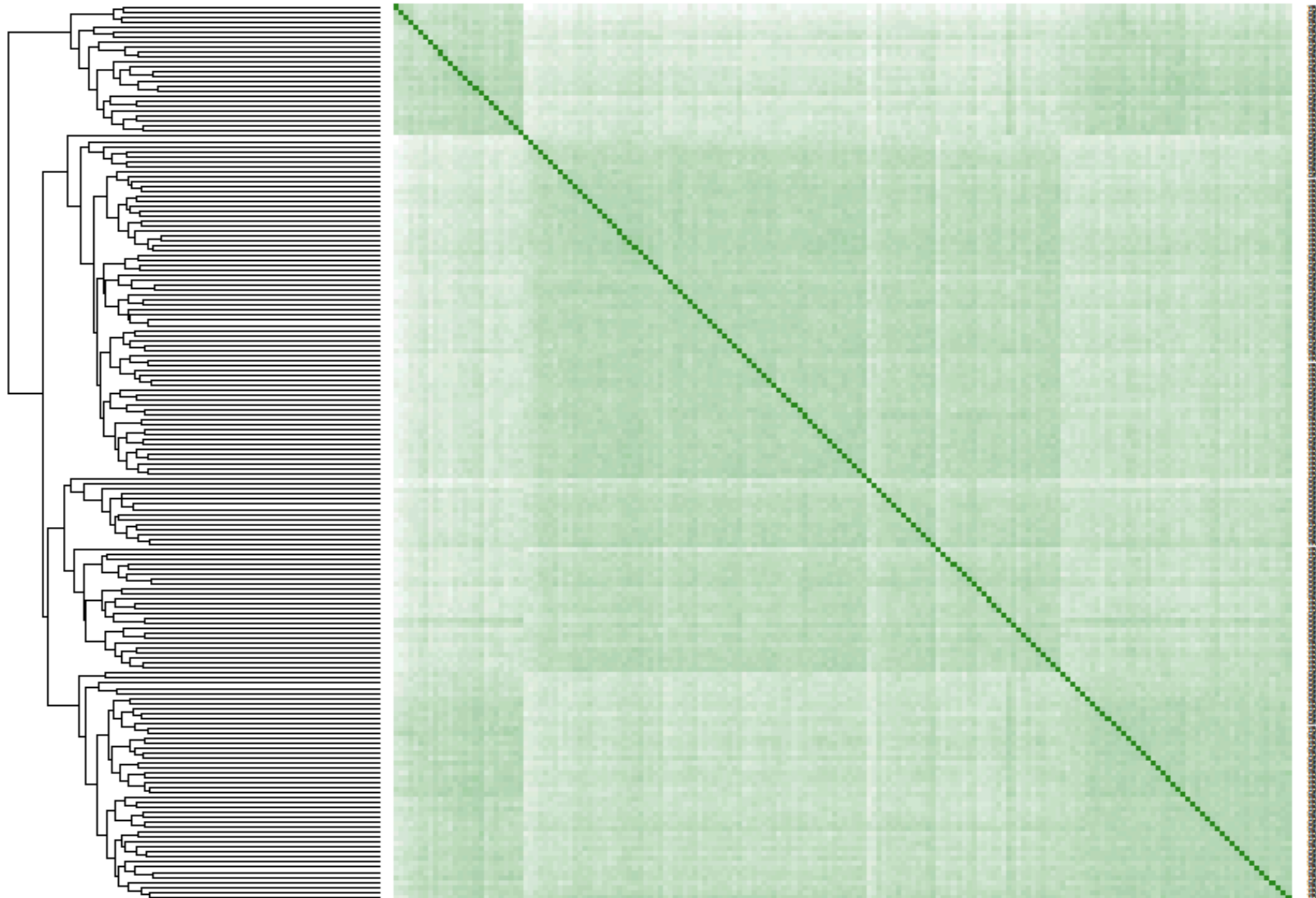
0. Refine transcript models using RNA-seq
1. Get orthologous gene annotation for each species, match exon/splice
2. Build composite gene models and splicing graphs, define local events
3. Count reads compatible with either event, estimate relative expression levels
4. Test for differential alternative transcript usage
 - T test/Wilcoxon test of exon inclusion levels [CEU VS YRI 212/214 (BHP \leq 0.05)]
 - Generalized linear model on exon inclusion reads, normalized for total reads at each locus [CEU VS YRI 325 (BHP \leq 0.05)]

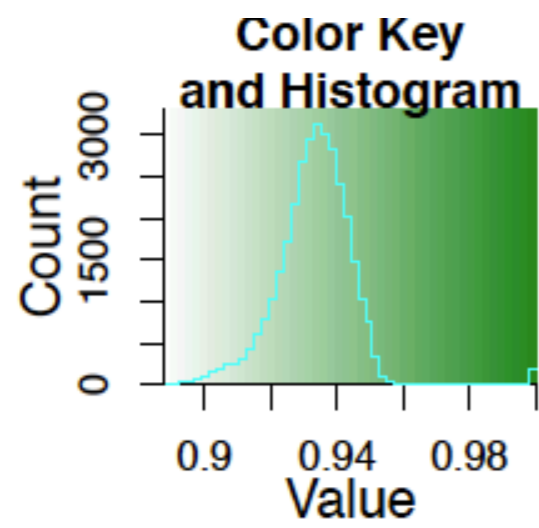




Spearman_cor dist=1-cor

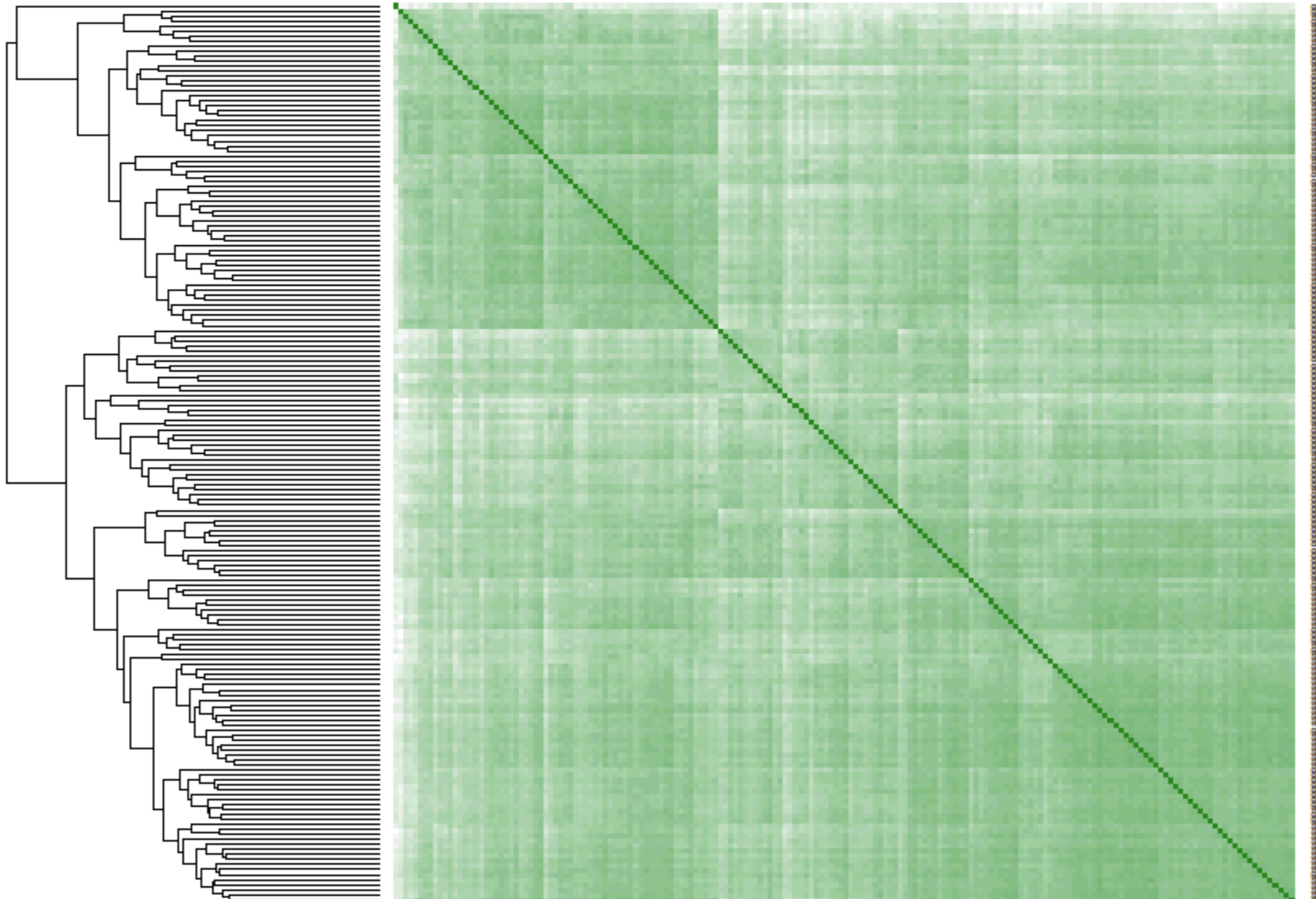
CEU VS YRI
PSI



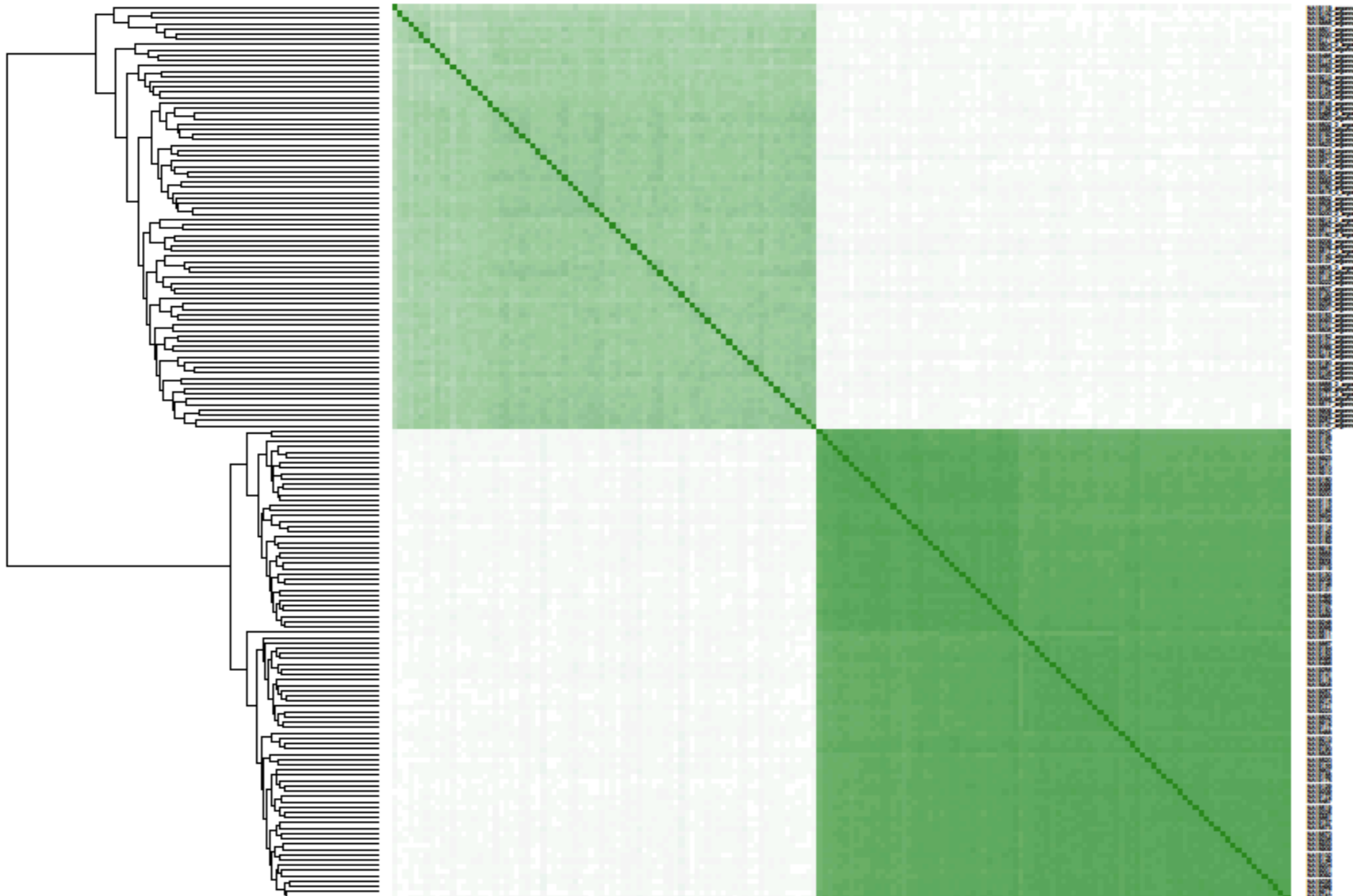
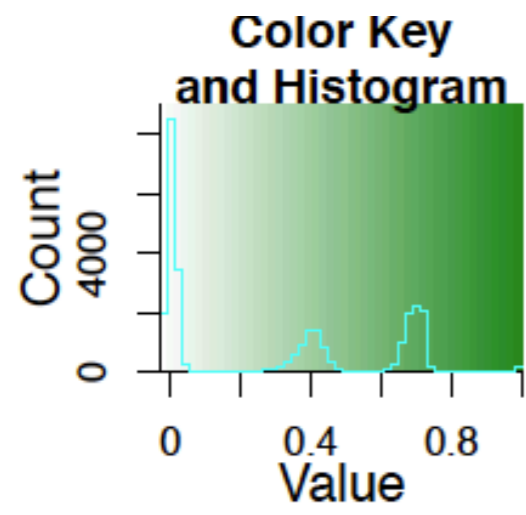


Spearman_cor
dist=1-cor

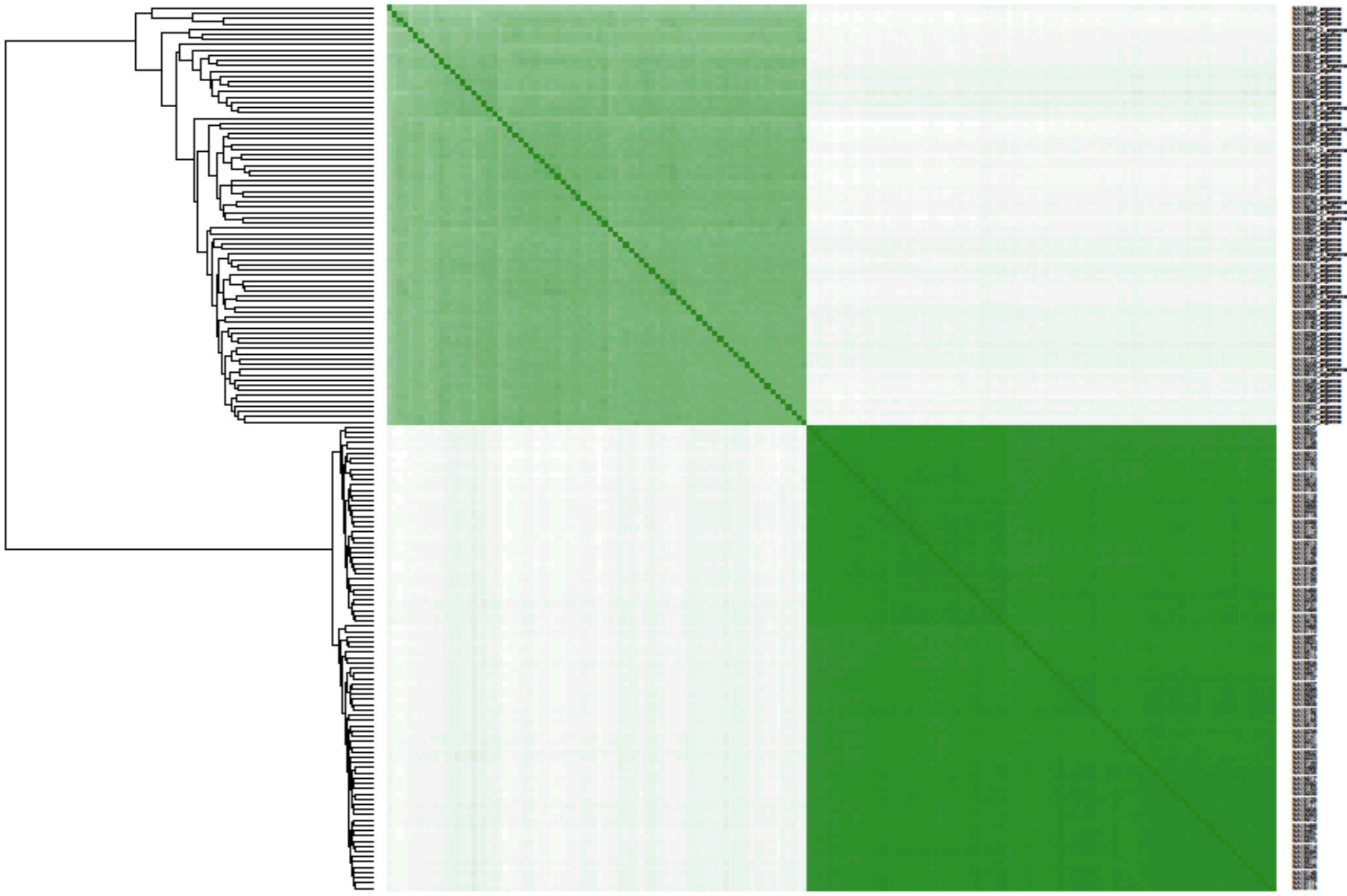
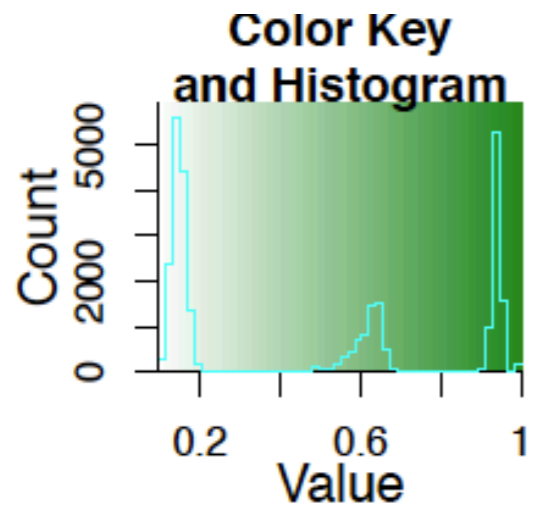
CEU VS YRI
Total read counts



Spearman_cor dist=1-cor

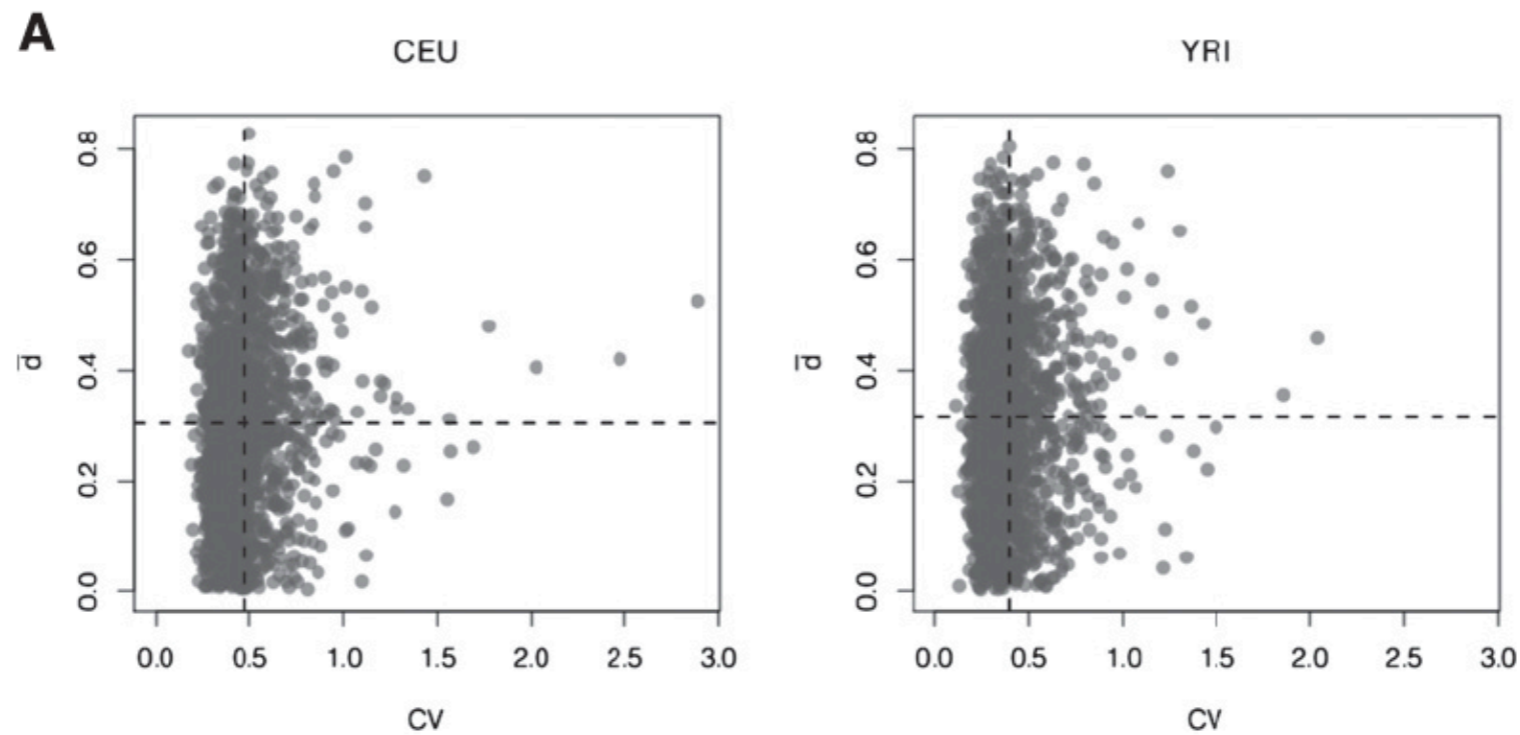


Spearman_cor dist=1-cor



Estimation of alternative splicing variability in human populations

Mar Gonzàlez-Porta,^{1,5} Miquel Calvo,² Michael Sammeth,^{1,3} and Roderic Guigó^{1,4,6}



C

| area | CEU | YRI | common | |
|--------------|------|------|--------|---------|
| 1 | 576 | 587 | 397 | 68.92 % |
| 2 | 276 | 288 | 144 | 52.17 % |
| 3 | 461 | 455 | 282 | 61.98 % |
| 4 | 341 | 324 | 181 | 55.86 % |
| total | 1654 | 1654 | 181 | 60.70 % |