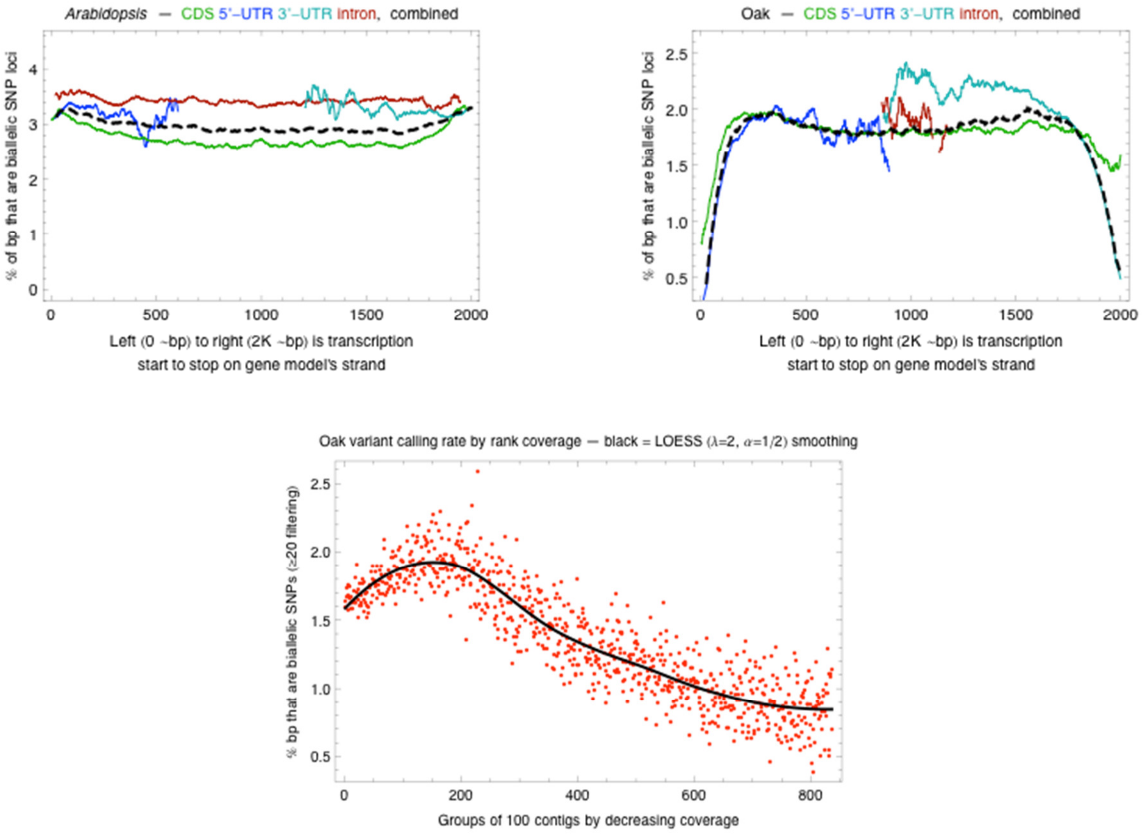

Additional file 11: **SNP locus rate in oak versus *Arabidopsis***.
Comparison of called SNP locus rate per base pair in **(a)** *Arabidopsis* and **(b)** oak by model-relative position averaged over gene models (stretching/compressing each transcription start to stop span to a nominal length of 2 kbp), including breakdown by coding (green), 5′-UTR (blue), 3′-UTR (light blue), intron (red), and all types combined (black, dashed); and **(c)** called SNP locus rate per oak base pair as a function of descending coverage, consistent with the low SNP locus rates at the edges of oak in (a) and (b) originating from low coverage at contig edges (and thus lower power to detect variants).