

Figure S1. *Per Base depth and per gene breadth of the coverage for all analysed shotgun sequences.* For each cultivar analysed (aligned and filtered shotgun sequence) there are four plots. Upper left: per base depth of the coverage; lower left: probability density function fitted to the per base depth of coverage; upper right: number of reads per gene, lower right: percentage of the gene covered by at least one read base. Final positive calls and the identity of the alleles are indicated in the lower right panel. For all plots, the x-axis labels (synthetic sequence on the left and genes ids within the synthetic sequence on the right) are plotted at bottom of each page.





















