

## Supplemental Figure legends

**Supplemental Figure 1.** Schematic overview of the WGP pipeline leading from a BAC clone library to a WGP physical map. Indicated are the six subsequent processing units with their individual laboratory or computational activities.

**Supplemental Figure 2.** Effect of WGP tag length on the uniqueness of WGP tags for both *in silico* derived WGP tags and the WGP tags derived from the actual sequencing experiment. On the x-axis the length of the WGP tag, including the restriction site is shown and on the y axis the number of WGP tags. The dashed line indicates the theoretical maximum number of WGP tags, as determined by the number of different *EcoRI/MseI in silico* predicted restriction fragments in the Arabidopsis ecotype Colombia genome sequence.

**Supplemental Figure 3.** Contig size distribution of the initial physical BAC map (solid bars) and after filtering problematic BACs (hatched bars); at the x-axis the number of BACs per contig and at the y-axis the number of contigs (left: purple) and the number of BACs represented by these contigs (right: blue) are shown.