

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.