**Title:**

**Efficient detection of novel nuclear markers for Brassicaceae by transcriptome sequencing**

**File: "Arabis\_alpina\_and\_Cardamine\_hirsuta\_mapped.zip"**

We provide here the sequence alignment files of two transcriptome sequencing runs on a Genome Sequencer FLX (Roche, Switzerland) for pooled RNA samples of *Arabis alpina* and *Cardamine hirsuta* mapped to *Arabidopsis thaliana* (TAIR9; Swarbreck *et al.* 2007)). Each sample was sequenced twice on half a picotiter plate. The alignments were used to detect conserved regions among the aforementioned species. The reads have been mapped against the five chromosomes of *Arabidopsis thaliana* using samtools (Li *et al.* 2009).

**References**

Li H, Handsaker B, Wysoker A*, et al.* (2009) The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079.

Swarbreck D, Wilks C, Lamesch P*, et al.* (2007) The *Arabidopsis* Information Resource (TAIR): gene structure and function annotation. *Nucleic Acids Research* **36**, D1009-D1014.