

Illumina reads from eight flax genotypes



Alignment parameters optimisation by mapping CDC Bethune Illumina GA IIx reads against CDC Bethune whole genome shotgun sequence assembly using BWA and Bowtie



Align (map) sequences from eight genotypes onto CDC Bethune reference scaffolds individually using BWA



Eight genotype#.SAM files



Convert .SAM to .BAM; sort .BAM; Merge .BAM files using SAMtools



SNP calling from individual genotypes using SAMtools



Merge SNPs from all eight genotypes, filter low quality SNPs pipeline with criteria described in Table 2 and compile SNPs



High quality SNPs and sequences information available for genotyping