B A TREAT (Tandem REpeat Annotation Toolkit) Flanking sequence Local re-alignment of flanks Tandem repeat Genome chr10 100 1000 **AAAGAAAGAAAG** Realignment chr12 1250 1500 Reference **AAAGAAAGAAAG** Full read Mapped Consortium reads .bed file .bam file Reference Unmapped Reference Reads spanning the genome with tandem repeat tandem repeat Kernel Pairwise sequence alignment Density (a) **Estimation** (b) Frequency (c) Consensus haplotype I Haplotype I Hap.I: (AAAG)16 Sequence error Hap.II: (AAAG)14 Consensus Haplotype II haplotype II Motif analysis Reads spanning Local assembly Guided clustering Germline allele-seq 1: Consensus allele-seq 2: per cluster Somatic allele-seq 1: allele-seq 3: Analyze Genotypes Visualize D_1