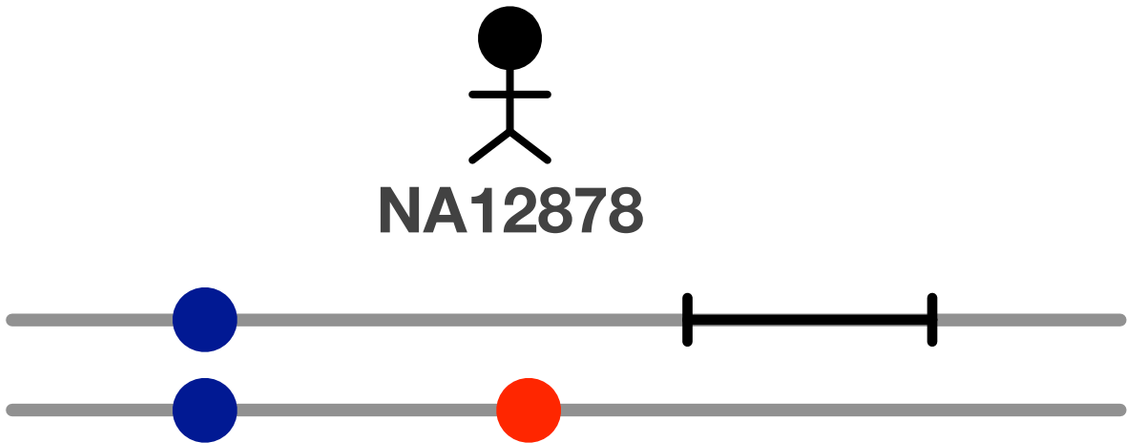
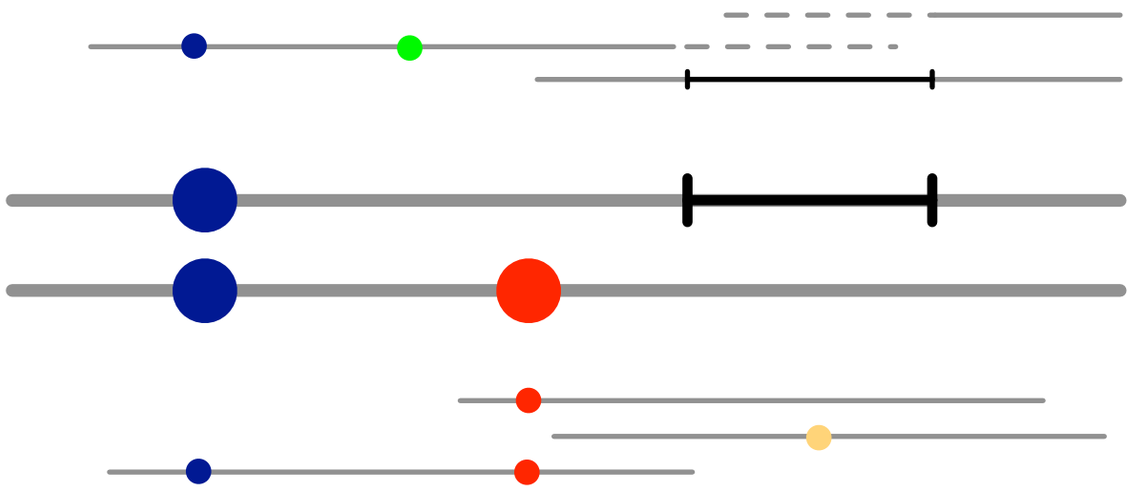
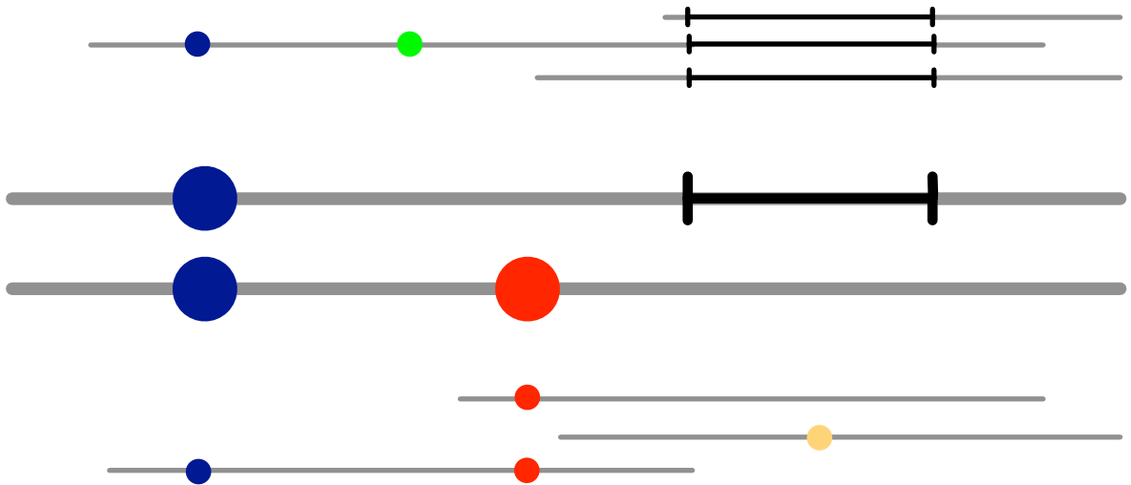
1. Select sample with known germline



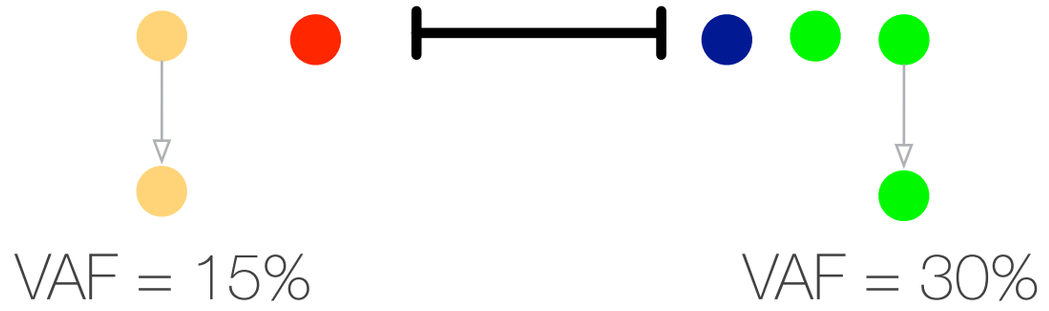
2. Assign reads to germline haplotypes



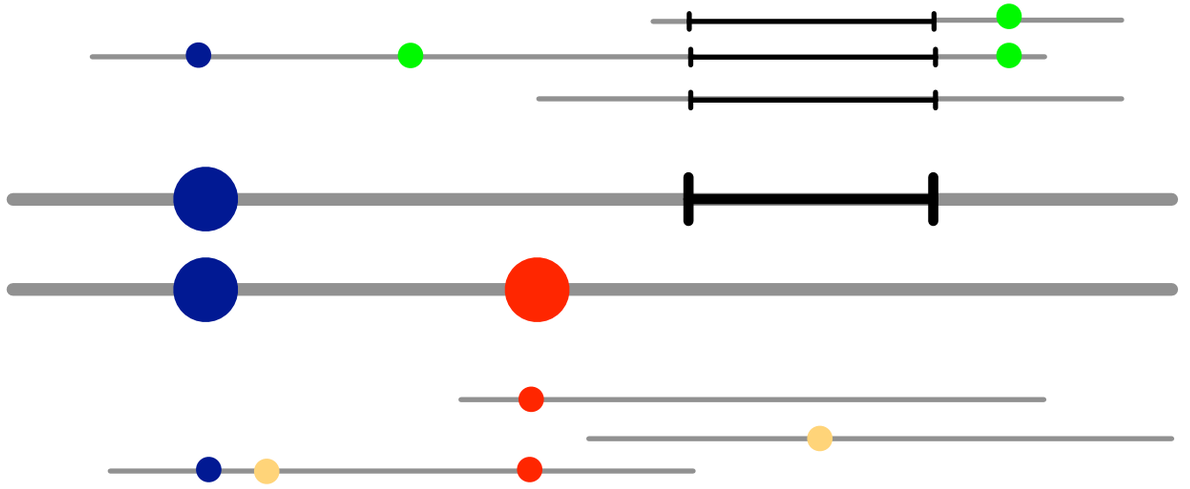
3. Realign reads to germline haplotypes



4. Sample PCAWG tumour-specific calls



5. Spike PCAWG mutations onto reads



6. Remap spiked reads