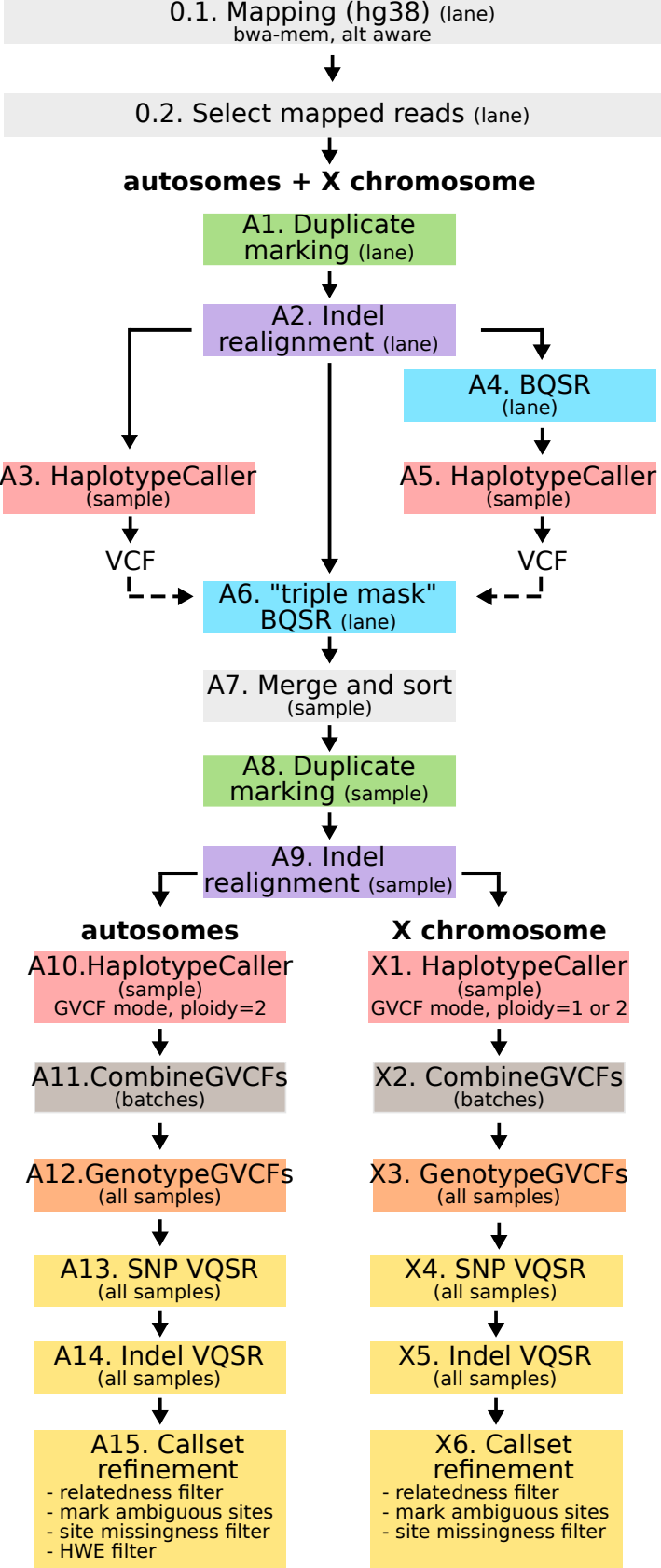
0.1. Mapping (hg38) (lane)
bwa-mem, alt aware
0.2. Select mapped reads (lane)
autosomes + X chromosome
A1. Duplicate marking (lane)
A2. Indel realignment (lane)
A4. BQSR (lane)
A3. HaplotypeCaller (sample)
A5. HaplotypeCaller (sample)
VCF
VCF
A6. "triple mask" BQSR (lane)
A7. Merge and sort (sample)
A8. Duplicate marking (sample)
A9. Indel realignment (sample)
autosomes
X chromosome
A10.HaplotypeCaller (sample) GVCF mode, ploidy=2
X1. HaplotypeCaller (sample) GVCF mode, ploidy=1 or 2
A11.CombineGVCFs (batches)
X2. CombineGVCFs (batches)
A12.GenotypeGVCFs (all samples)
X3. GenotypeGVCFs (all samples)
A13. SNP VQSR (all samples)
X4. SNP VQSR (all samples)
A14. Indel VQSR (all samples)
X5. Indel VQSR (all samples)
A15. Callset refinement
- relatedness filter
- mark ambiguous sites
- site missingness filter
- HWE filter
X6. Callset refinement
- relatedness filter
- mark ambiguous sites
- site missingness filter