

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:27:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013178.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013178 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013178.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:27:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013178.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,719,431
Mapped reads	1,476,115 / 85.85%
Unmapped reads	243,316 / 14.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,104 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	74,917 / 4.36%
Duplication rate	3.97%
Clipped reads	785,816 / 45.7%

2.2. ACGT Content

Number/percentage of A's	25,989,324 / 27.21%
Number/percentage of C's	17,892,279 / 18.73%
Number/percentage of T's	30,029,850 / 31.44%
Number/percentage of G's	21,594,826 / 22.61%
Number/percentage of N's	23,382 / 0.02%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.3368
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2.4. Mapping Quality

Mean Mapping Quality	42.81
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2.5. Mismatches and indels

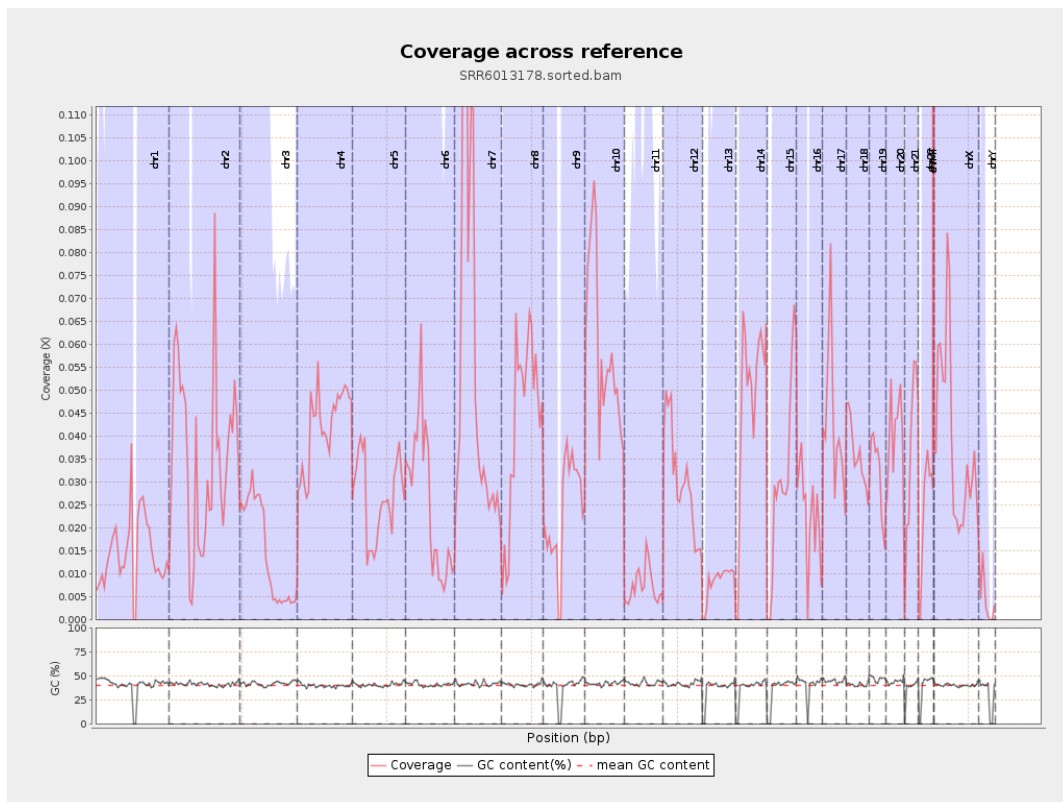
General error rate	0.95%
Mismatches	892,224
Insertions	6,848
Mapped reads with at least one insertion	0.46%
Deletions	42,136
Mapped reads with at least one deletion	2.81%
Homopolymer indels	42.88%

2.6. Chromosome stats

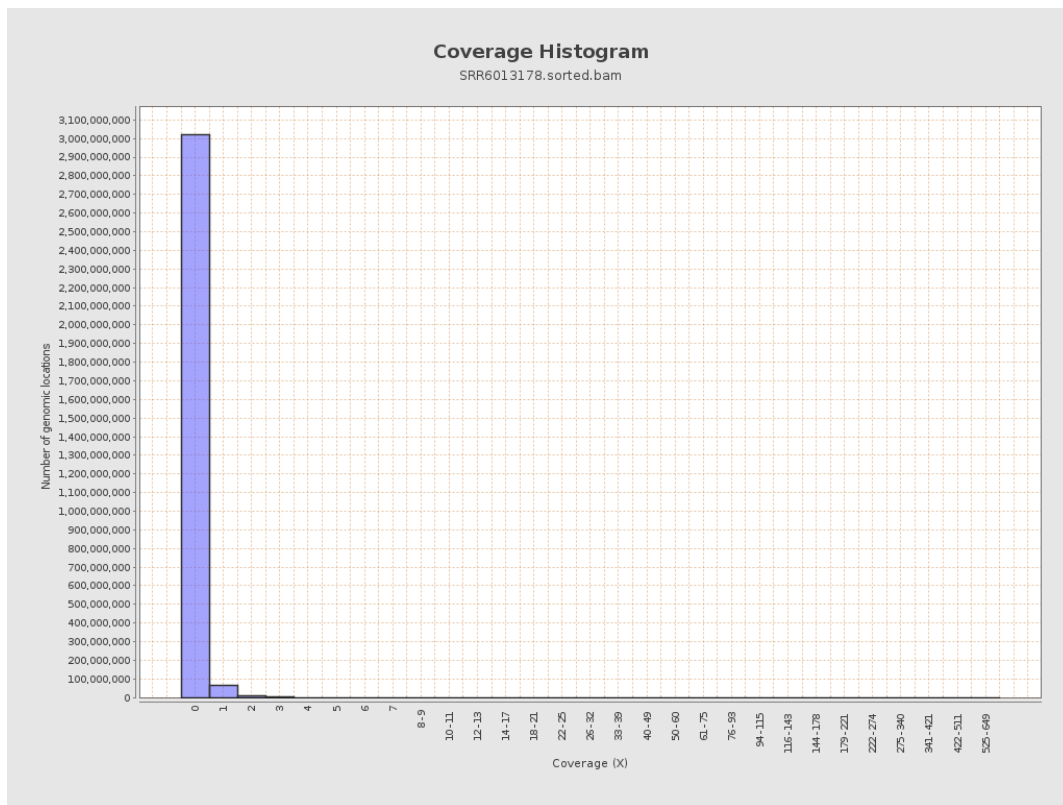
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3585696	0.0144	0.3614
chr2	243199373	8523790	0.035	0.3776
chr3	198022430	2922586	0.0148	0.1425
chr4	191154276	8066307	0.0422	0.2592
chr5	180915260	4822759	0.0267	0.192
chr6	171115067	4343762	0.0254	0.2841
chr7	159138663	9379071	0.0589	0.8825

chr8	146364022	6266916	0.0428	0.3712
chr9	141213431	3323185	0.0235	0.2497
chr10	135534747	8135985	0.06	0.4005
chr11	135006516	1015462	0.0075	0.1509
chr12	133851895	4042940	0.0302	0.2052
chr13	115169878	933915	0.0081	0.1062
chr14	107349540	5091639	0.0474	0.2651
chr15	102531392	3143713	0.0307	0.2073
chr16	90354753	2025752	0.0224	0.1864
chr17	81195210	3477602	0.0428	0.2937
chr18	78077248	2832534	0.0363	0.4353
chr19	59128983	1881988	0.0318	0.3043
chr20	63025520	2550914	0.0405	0.241
chr21	48129895	1741701	0.0362	0.2396
chr22	51304566	1182760	0.0231	0.1788
chrMT	16571	13824	0.8342	1.114
chrX	155270560	6041246	0.0389	0.2495
chrY	59373566	256859	0.0043	0.1323

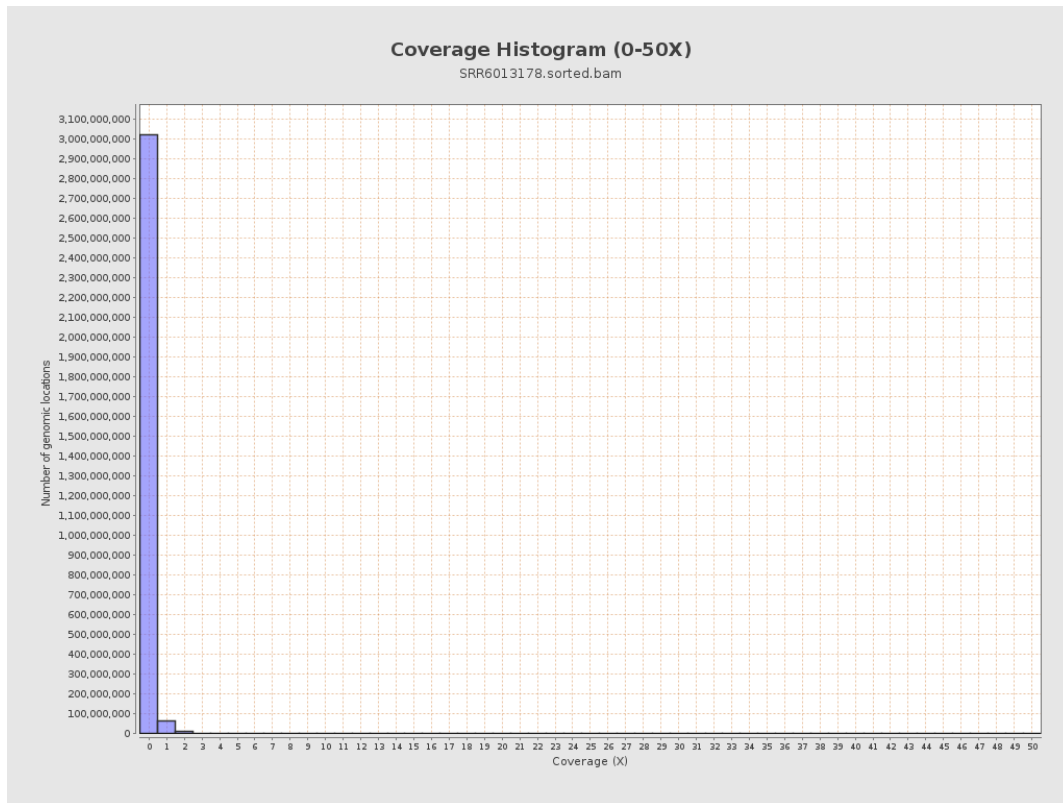
3. Results : Coverage across reference



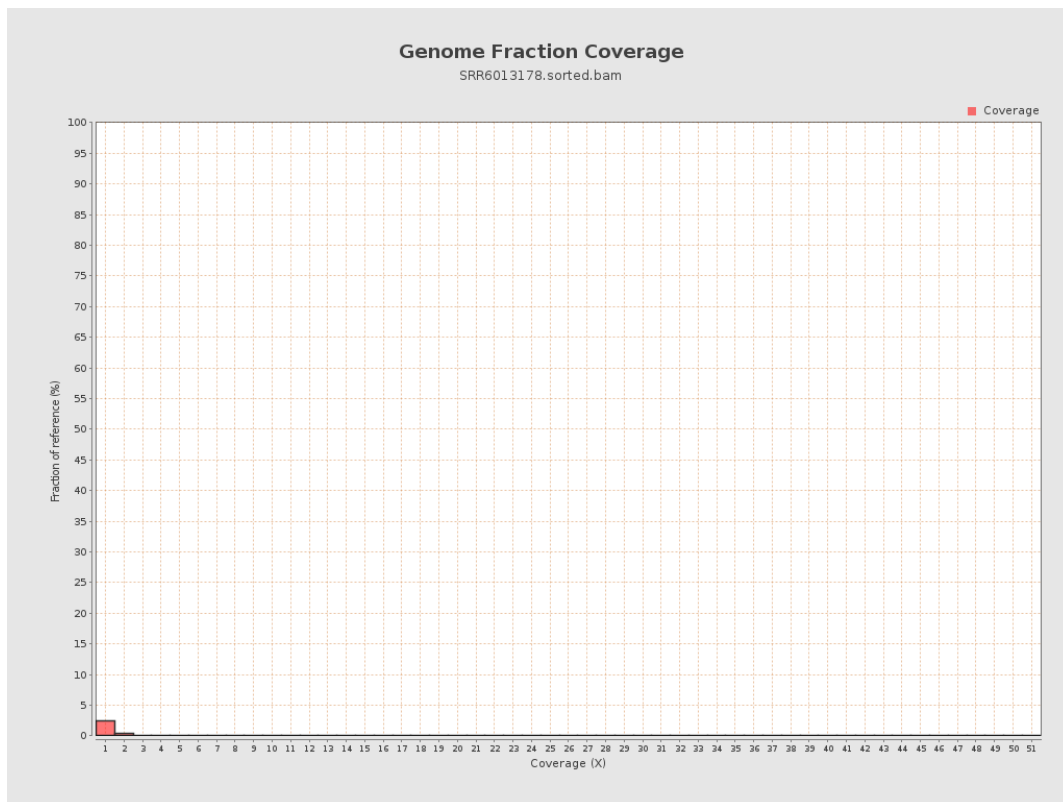
4. Results : Coverage Histogram



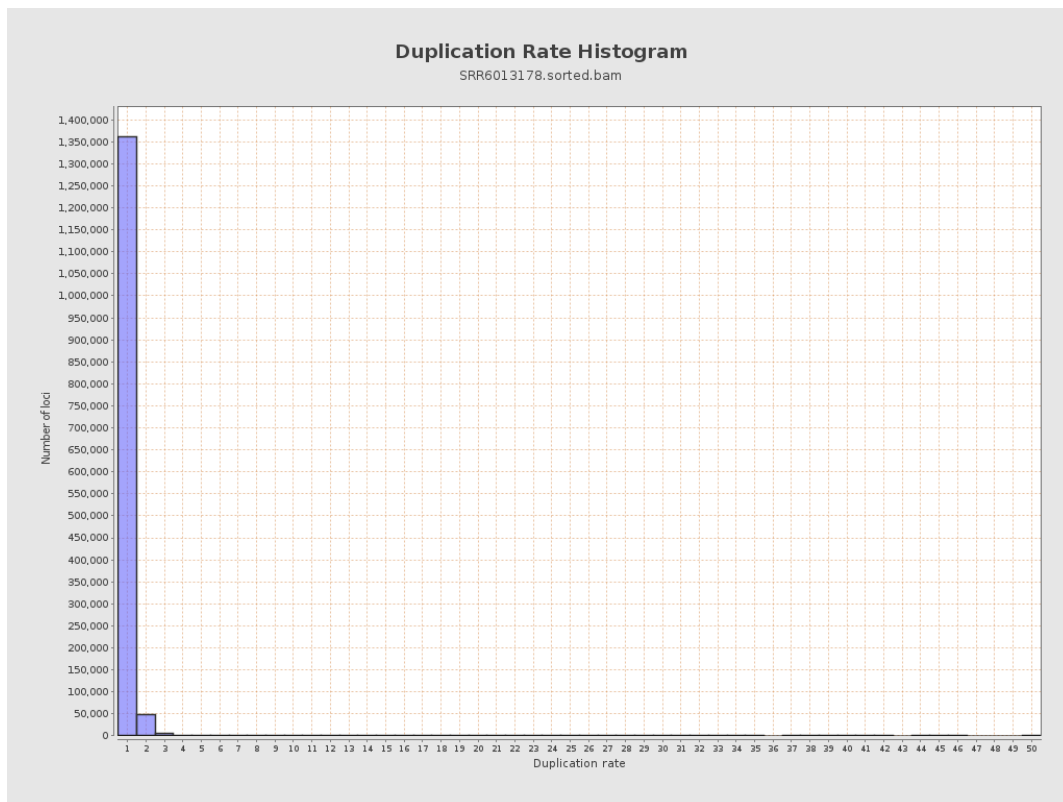
5. Results : Coverage Histogram (0-50X)



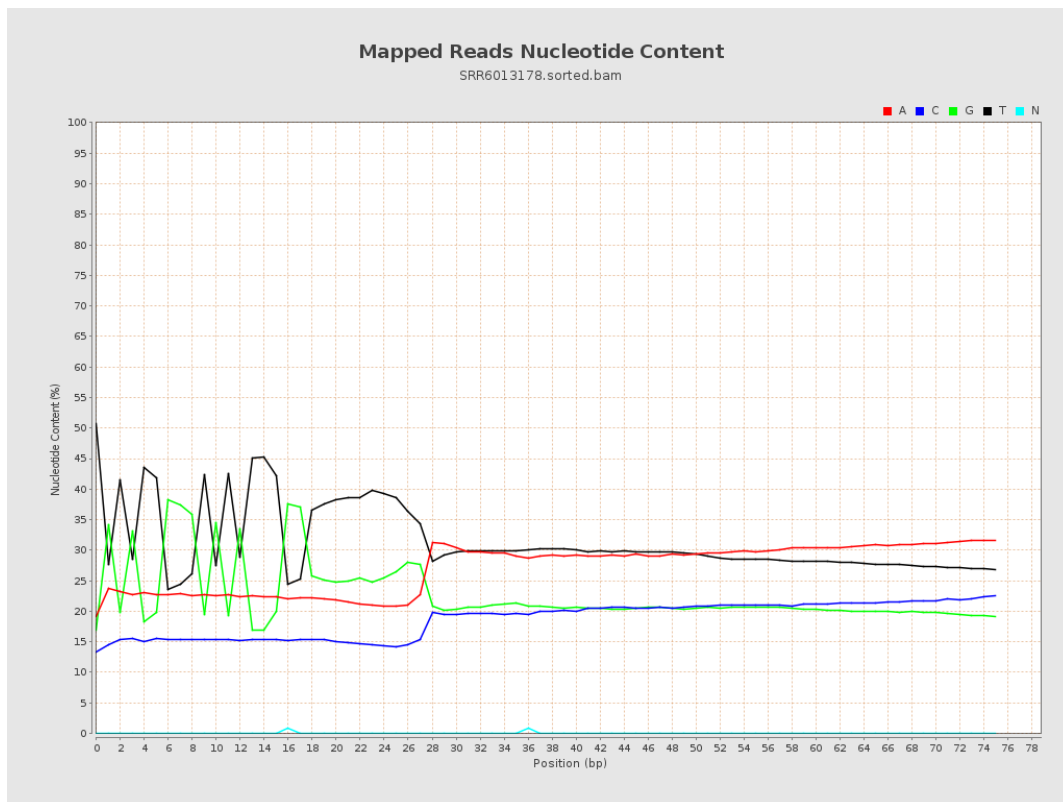
6. Results : Genome Fraction Coverage



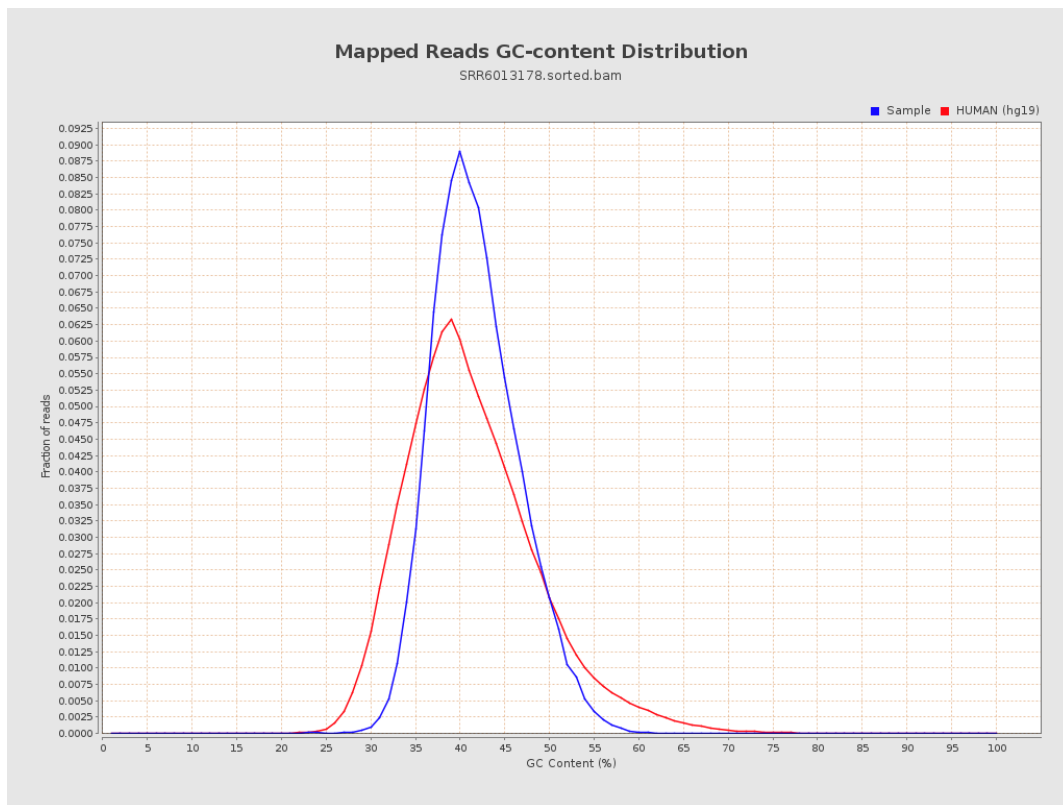
7. Results : Duplication Rate Histogram



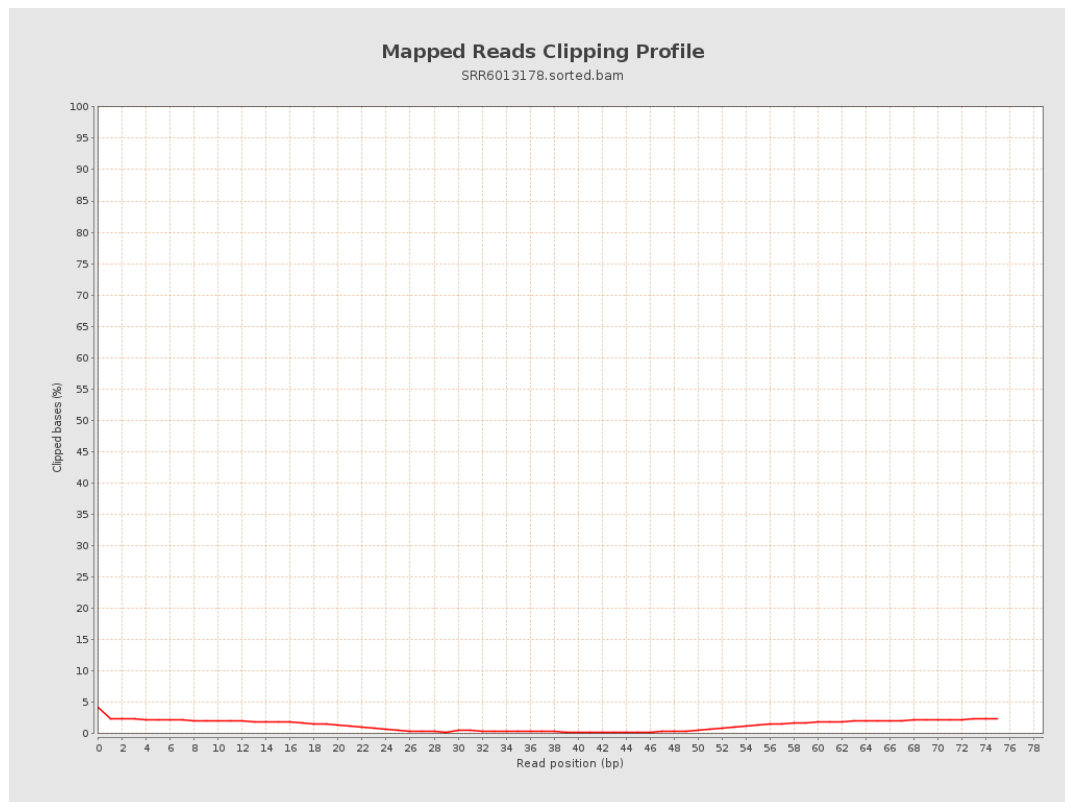
8. Results : Mapped Reads Nucleotide Content



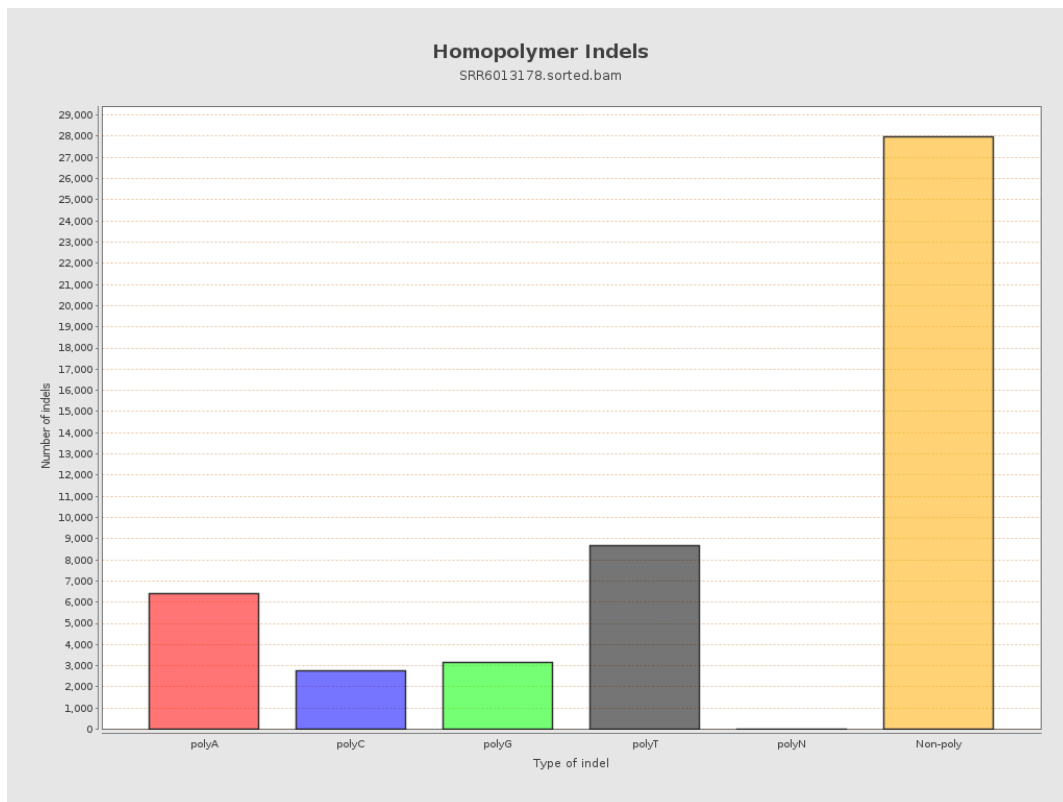
9. Results : Mapped Reads GC-content Distribution



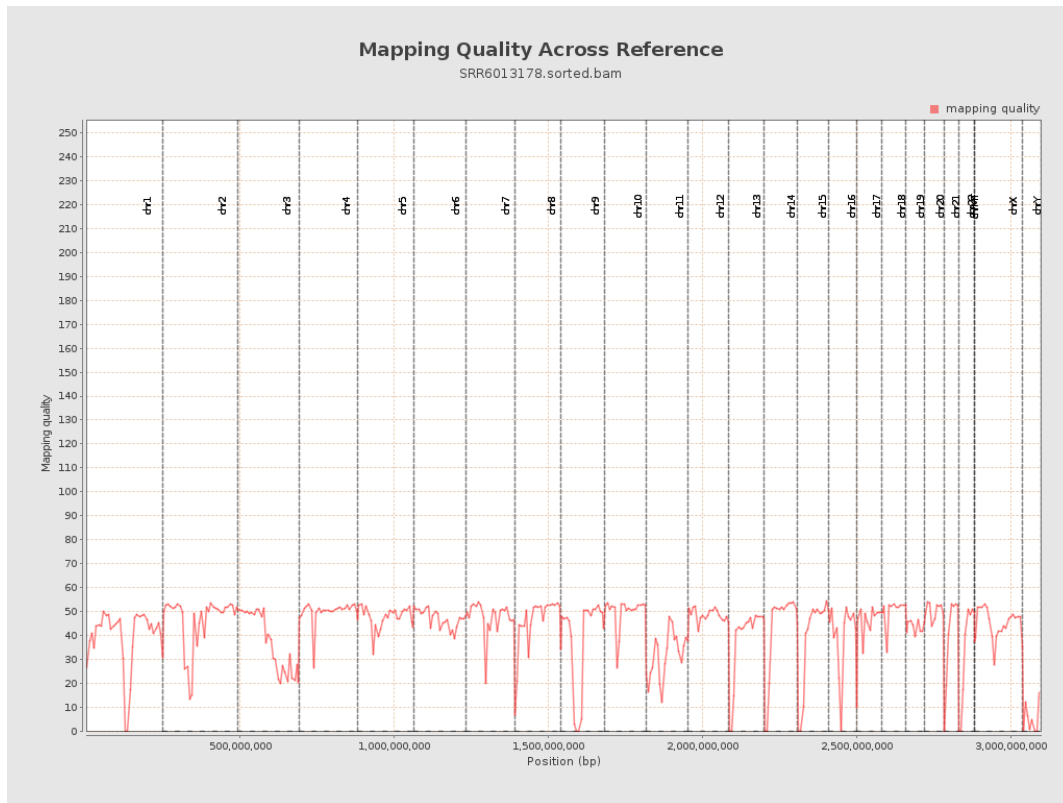
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

