

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:55:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068068.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_SRR6068068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:55:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,672,675
Mapped reads	4,488,725 / 96.06%
Unmapped reads	183,950 / 3.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,773 / 0.94%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,392,390 / 29.8%
Duplication rate	16.69%
Clipped reads	2,064,465 / 44.18%

2.2. ACGT Content

Number/percentage of A's	79,459,614 / 26.8%
Number/percentage of C's	53,788,189 / 18.14%
Number/percentage of T's	96,006,073 / 32.38%
Number/percentage of G's	67,251,528 / 22.68%
Number/percentage of N's	35,063 / 0.01%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0958

Standard Deviation	1.1084
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2.4. Mapping Quality

Mean Mapping Quality	46.18
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2.5. Mismatches and indels

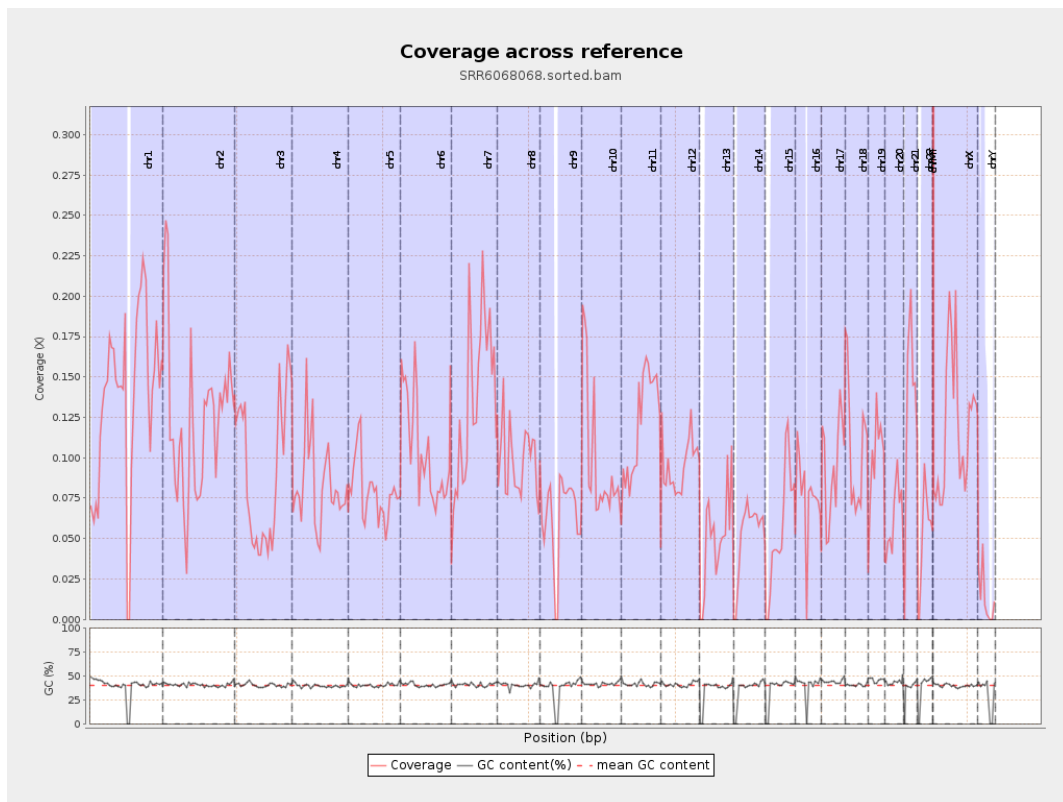
General error rate	0.49%
Mismatches	1,402,890
Insertions	20,784
Mapped reads with at least one insertion	0.46%
Deletions	54,128
Mapped reads with at least one deletion	1.19%
Homopolymer indels	45.98%

2.6. Chromosome stats

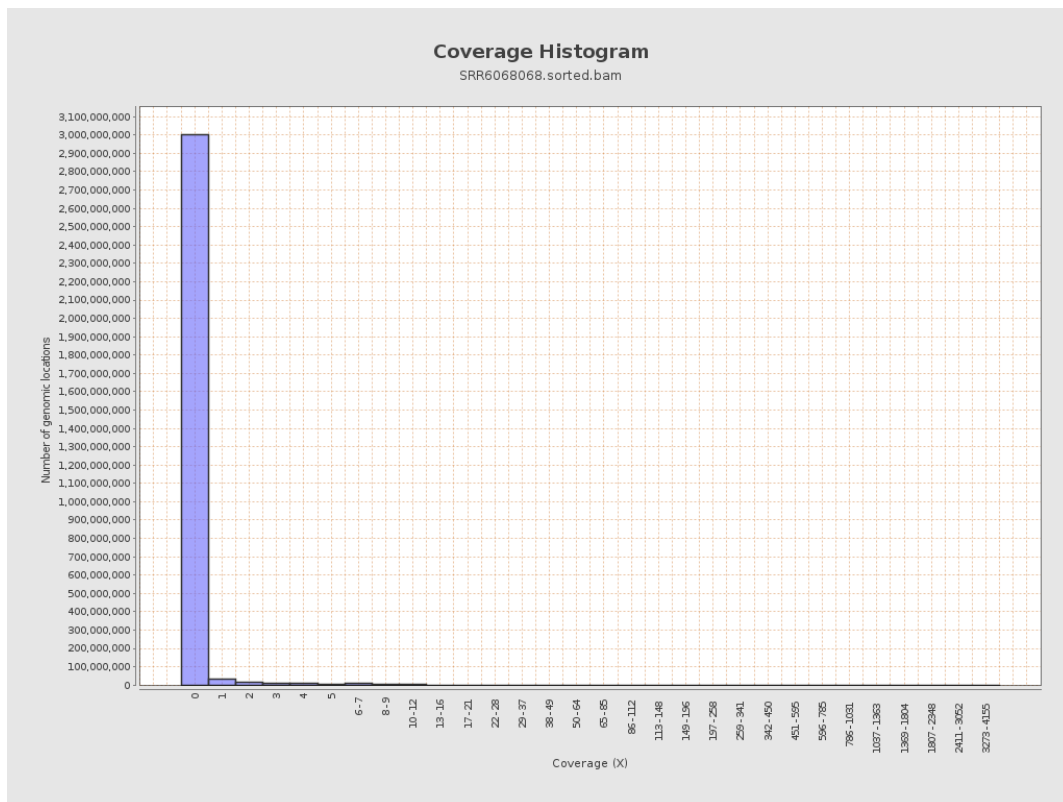
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34151682	0.137	1.8103
chr2	243199373	30223757	0.1243	1.1726
chr3	198022430	17999307	0.0909	0.7139
chr4	191154276	16062208	0.084	0.7499
chr5	180915260	14313807	0.0791	0.6491
chr6	171115067	18043246	0.1054	0.8059
chr7	159138663	21791197	0.1369	1.5726

chr8	146364022	14328417	0.0979	2.4632
chr9	141213431	8992358	0.0637	0.7309
chr10	135534747	13335737	0.0984	0.9334
chr11	135006516	16344160	0.1211	0.8611
chr12	133851895	12799109	0.0956	0.7347
chr13	115169878	5880078	0.0511	0.5468
chr14	107349540	5673309	0.0528	0.5712
chr15	102531392	5643783	0.055	0.5368
chr16	90354753	6754683	0.0748	0.6647
chr17	81195210	7807272	0.0962	0.7376
chr18	78077248	8253965	0.1057	1.3379
chr19	59128983	5897573	0.0997	1.1586
chr20	63025520	3994124	0.0634	0.6436
chr21	48129895	6180804	0.1284	0.8692
chr22	51304566	2661113	0.0519	0.5137
chrMT	16571	239321	14.4422	14.2744
chrX	155270560	18475136	0.119	0.844
chrY	59373566	790768	0.0133	0.425

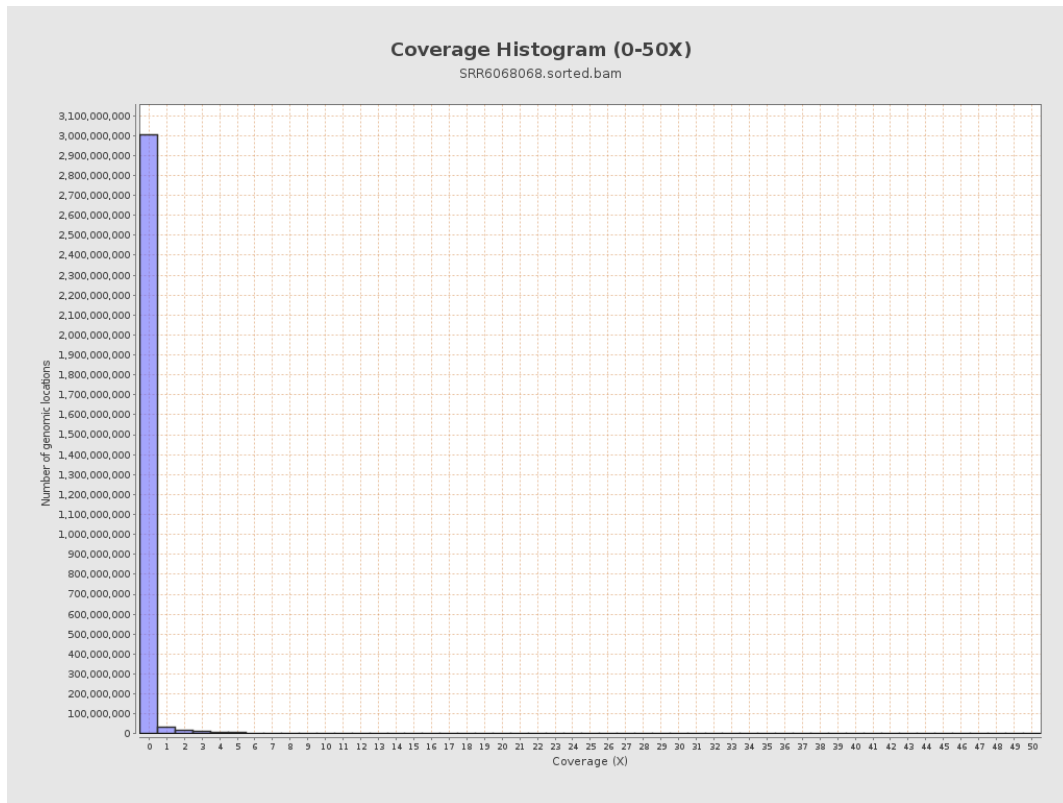
3. Results : Coverage across reference



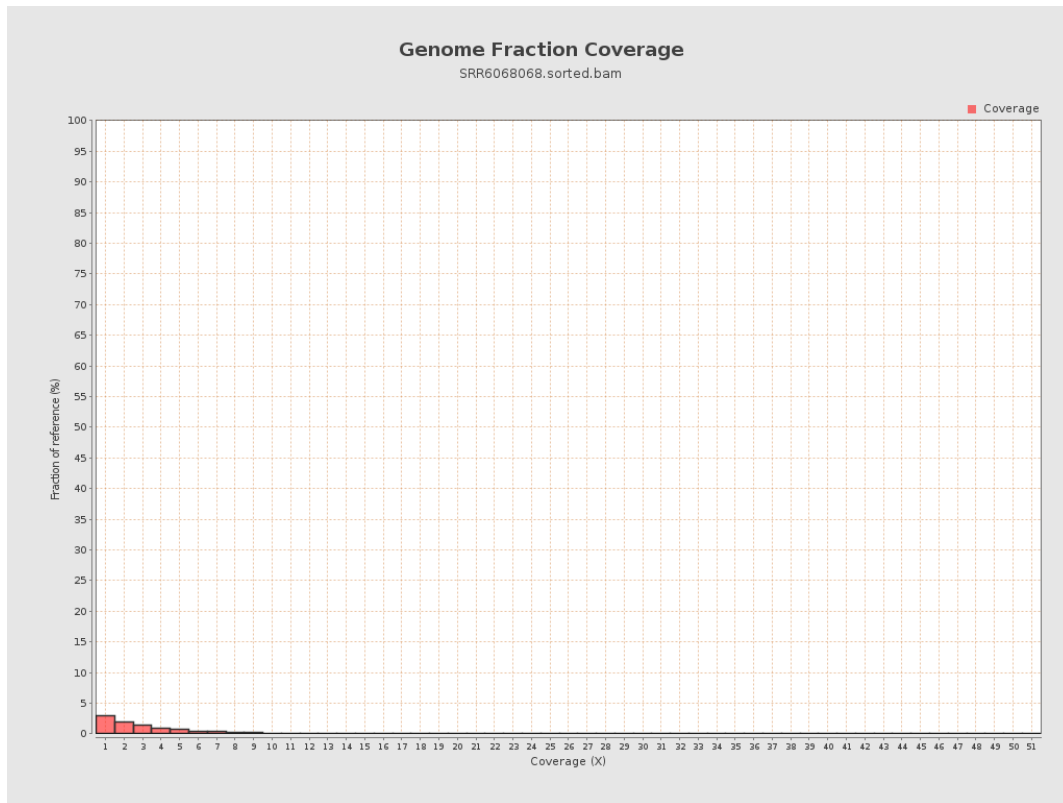
4. Results : Coverage Histogram



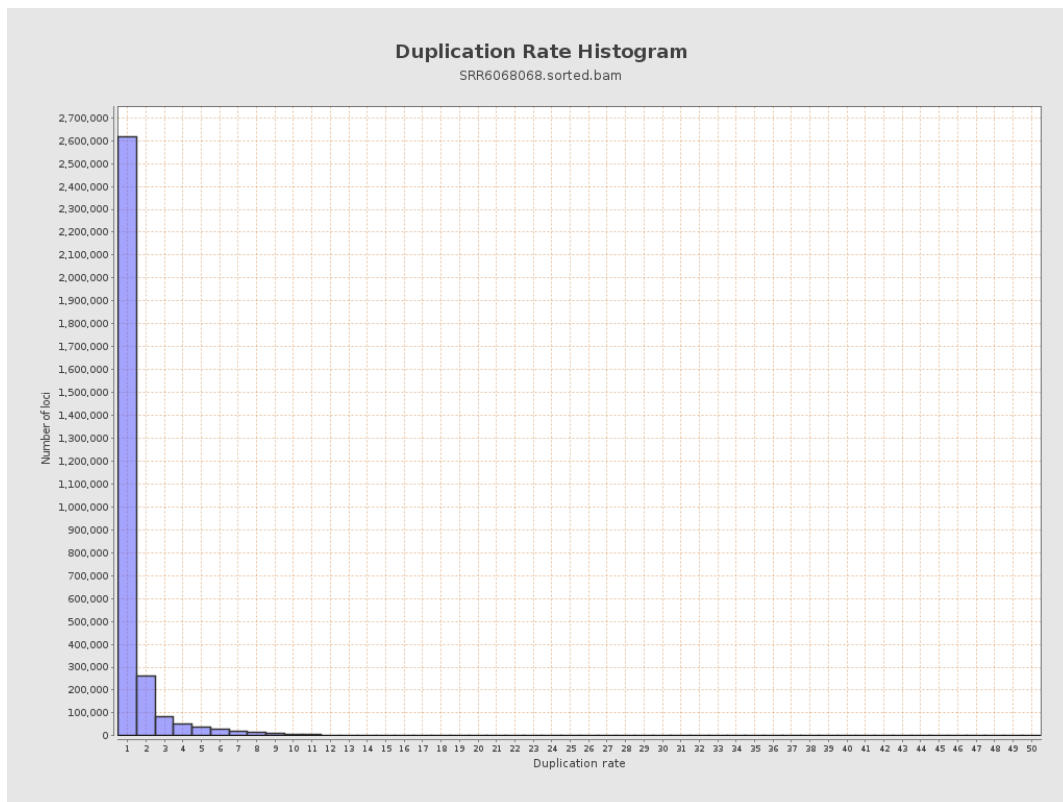
5. Results : Coverage Histogram (0-50X)



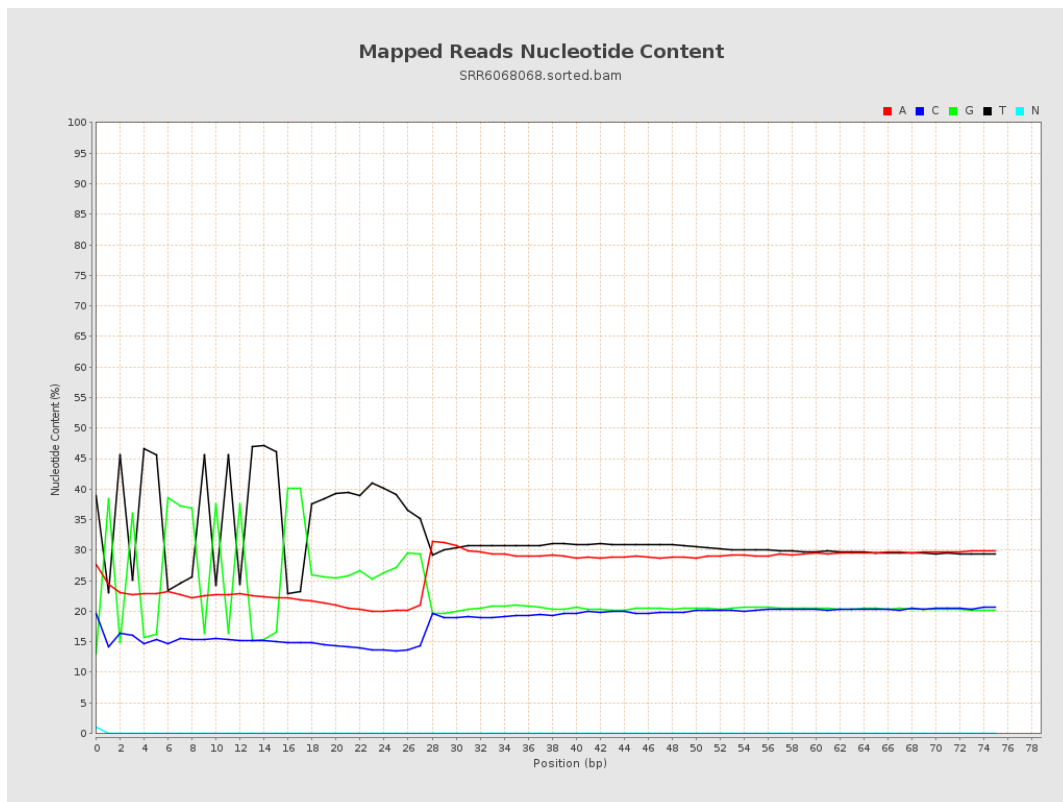
6. Results : Genome Fraction Coverage



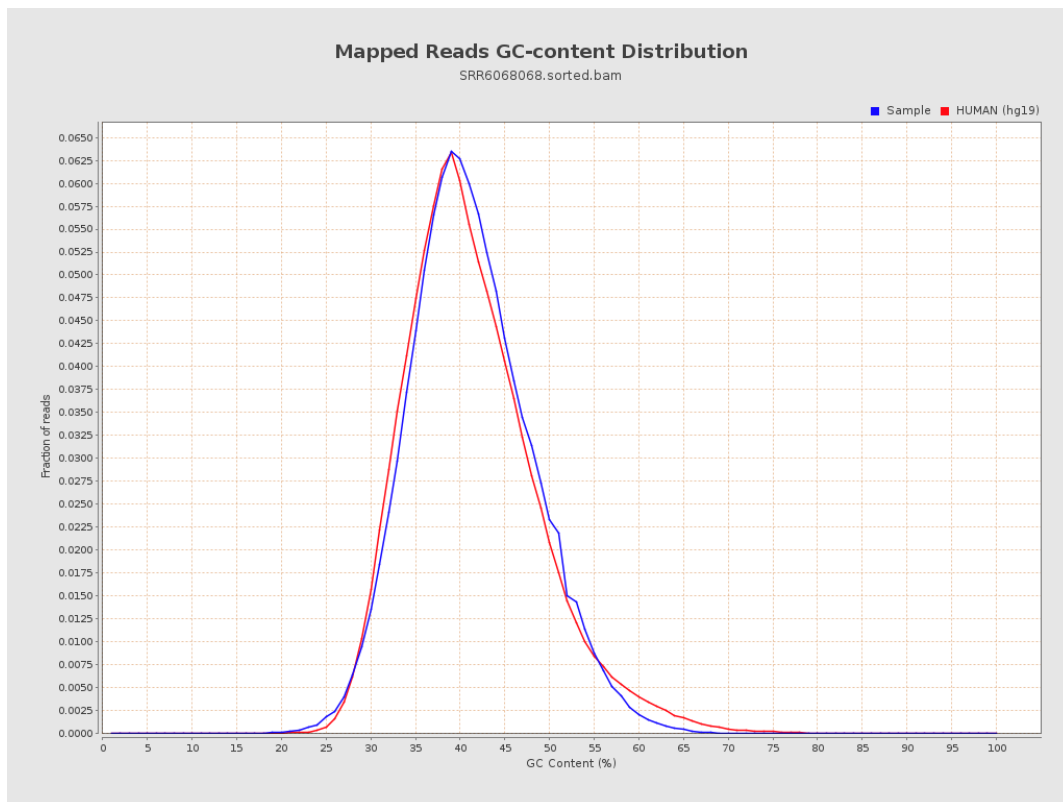
7. Results : Duplication Rate Histogram



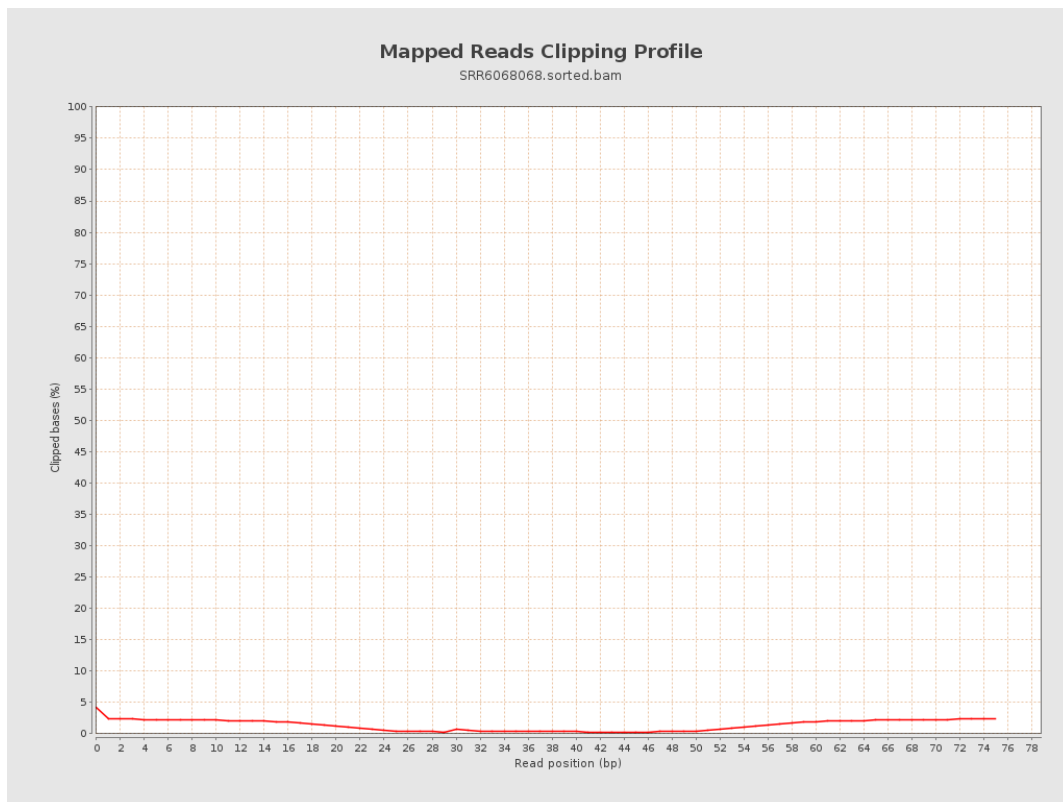
8. Results : Mapped Reads Nucleotide Content



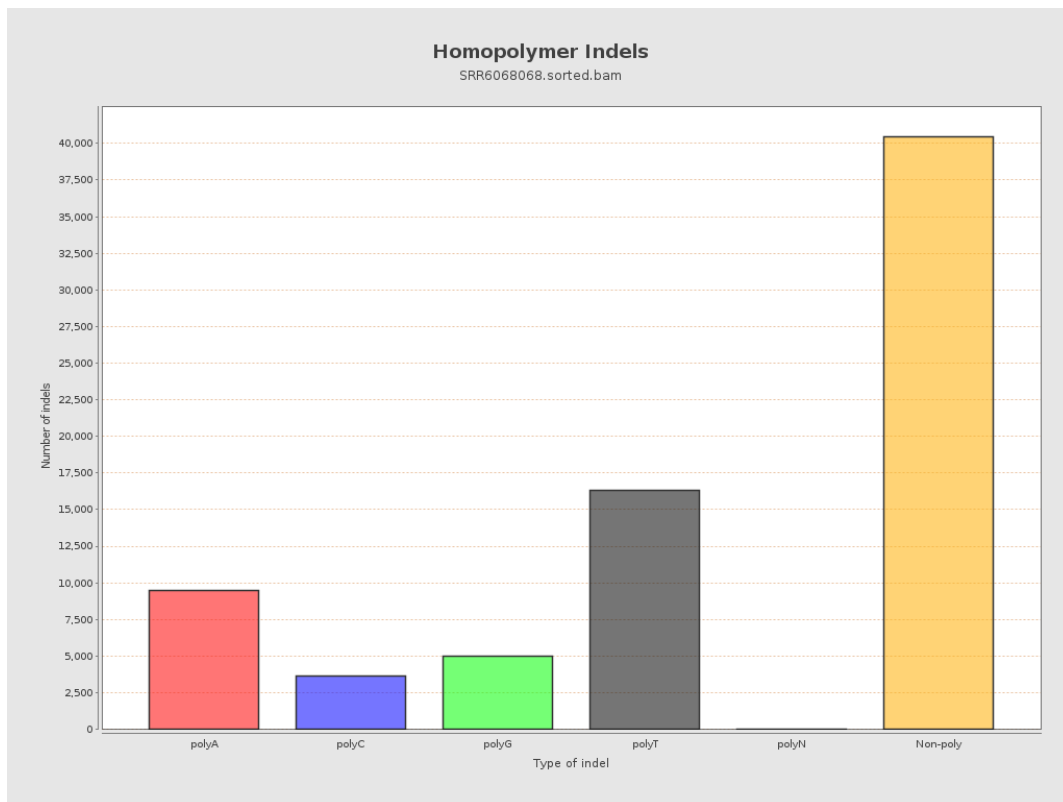
9. Results : Mapped Reads GC-content Distribution



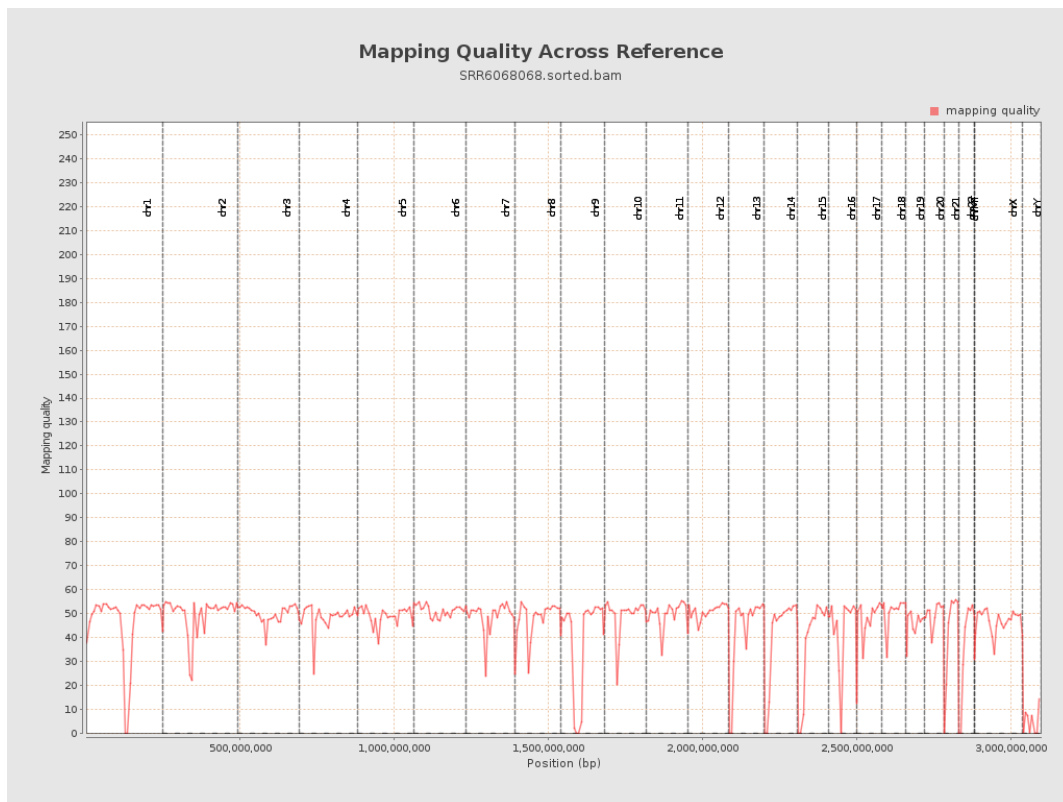
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

