Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:17:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068121.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_SRR6068121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:17:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,446,339
Mapped reads	721,167 / 49.86%
Unmapped reads	725,172 / 50.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,637 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	128,811 / 8.91%
Duplication rate	12.11%
Clipped reads	396,874 / 27.44%

2.2. ACGT Content

Number/percentage of A's	12,246,460 / 26.64%
Number/percentage of C's	8,227,529 / 17.9%
Number/percentage of T's	14,796,328 / 32.19%
Number/percentage of G's	10,655,404 / 23.18%
Number/percentage of N's	46,078 / 0.1%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0149

Standard Deviation	0.2756

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

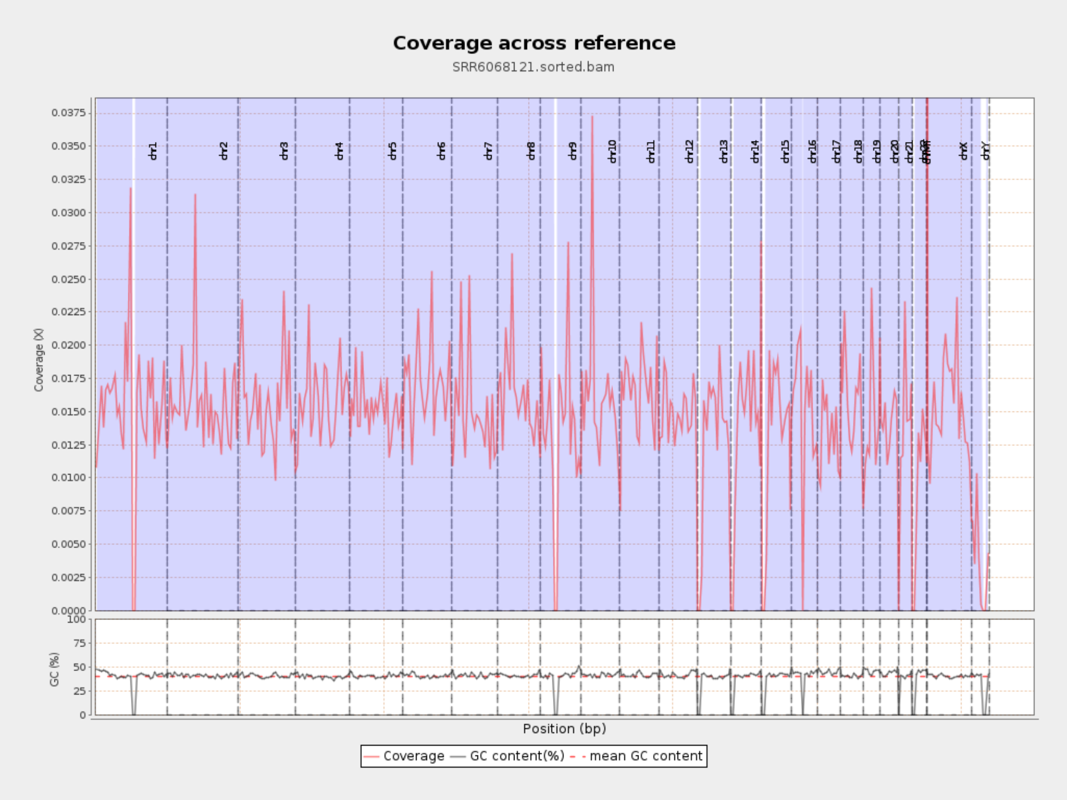
General error rate	0.96%
Mismatches	437,273
Insertions	3,447
Mapped reads with at least one insertion	0.47%
Deletions	11,395
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.18%

2.6. Chromosome stats

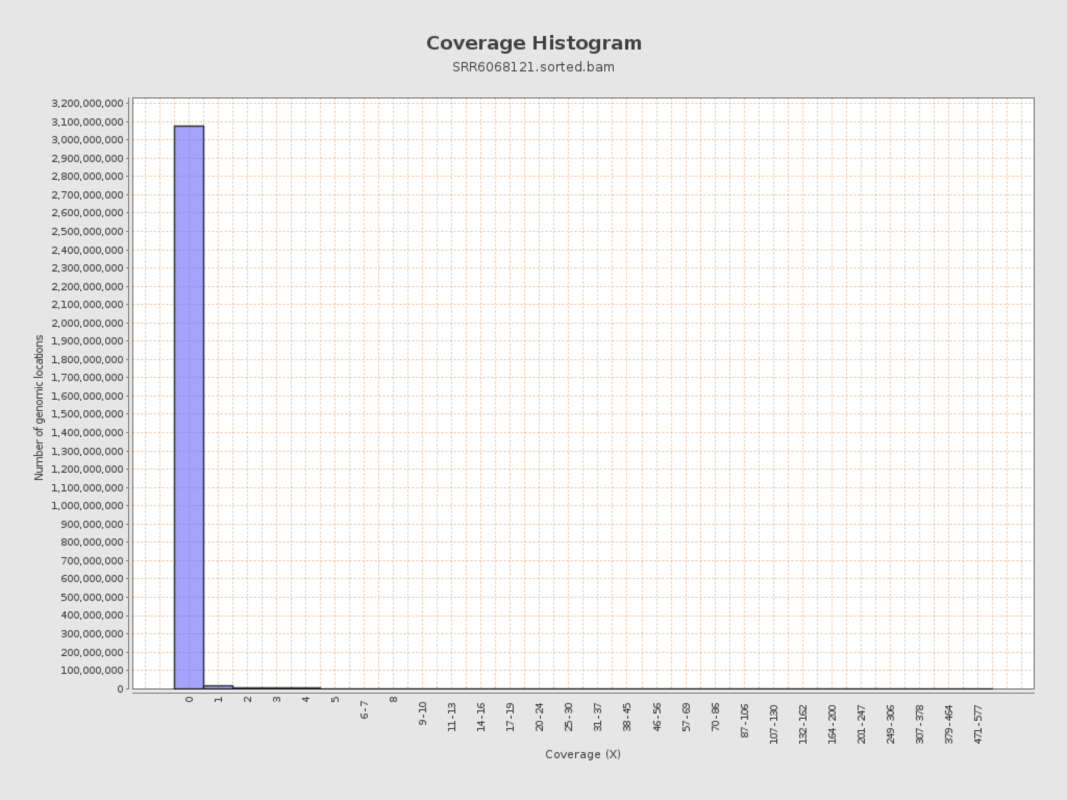
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3778470	0.0152	0.4589
chr2	243199373	3825367	0.0157	0.2805
chr3	198022430	3122230	0.0158	0.2458
chr4	191154276	3017726	0.0158	0.262
chr5	180915260	2761587	0.0153	0.2399
chr6	171115067	2938255	0.0172	0.2574
chr7	159138663	2379083	0.0149	0.2616

chr8	146364022	2402459	0.0164	0.2654
chr9	141213431	1896386	0.0134	0.2311
chr10	135534747	2224474	0.0164	0.3033
chr11	135006516	2247954	0.0167	0.2712
chr12	133851895	2003458	0.015	0.2267
chr13	115169878	1445221	0.0125	0.2197
chr14	107349540	1444220	0.0135	0.2225
chr15	102531392	1312476	0.0128	0.252
chr16	90354753	1361979	0.0151	0.2339
chr17	81195210	1058955	0.013	0.2142
chr18	78077248	1249547	0.016	0.3417
chr19	59128983	855067	0.0145	0.3054
chr20	63025520	884415	0.014	0.227
chr21	48129895	666633	0.0139	0.2355
chr22	51304566	477616	0.0093	0.1743
chrMT	16571	42472	2.563	3.0921
chrX	155270560	2385318	0.0154	0.2465
chrY	59373566	209272	0.0035	0.1182

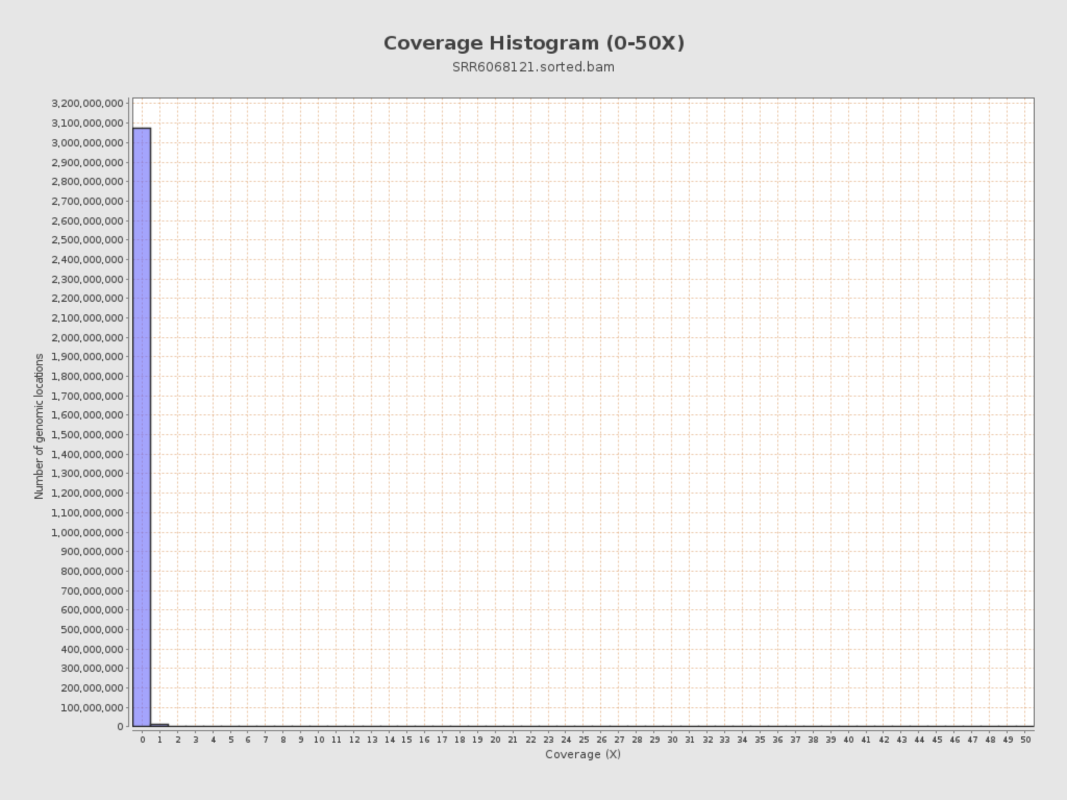
3. Results : Coverage across reference



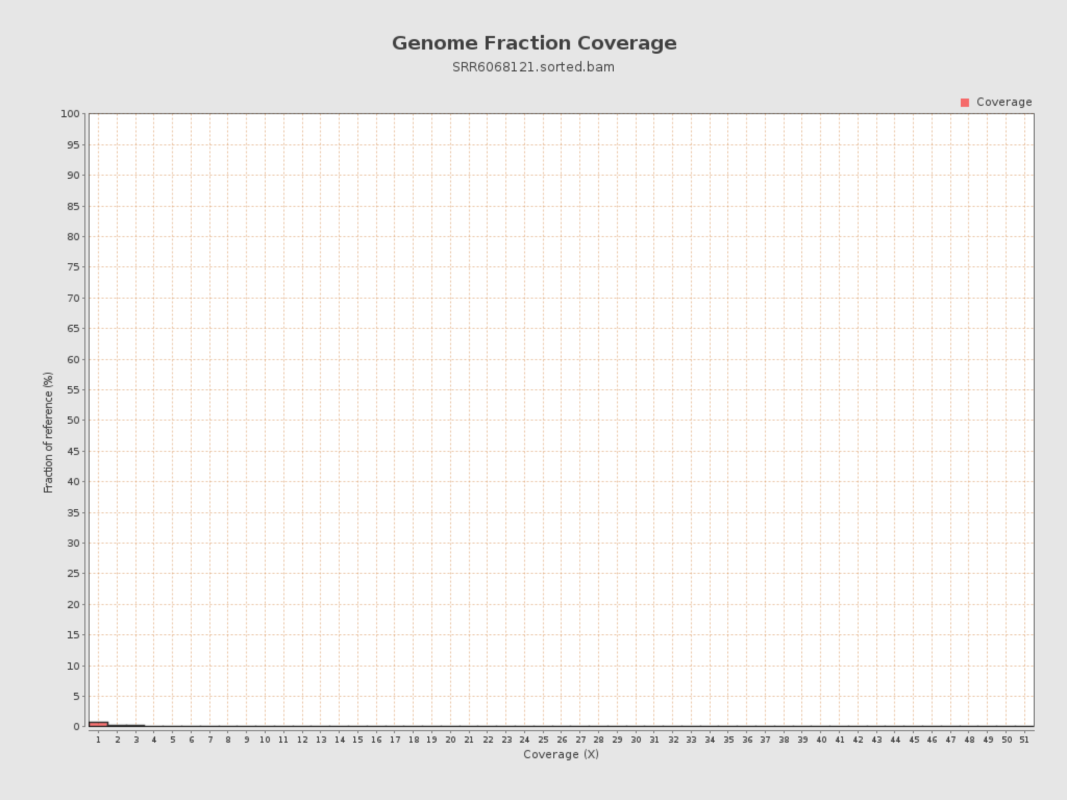
4. Results : Coverage Histogram



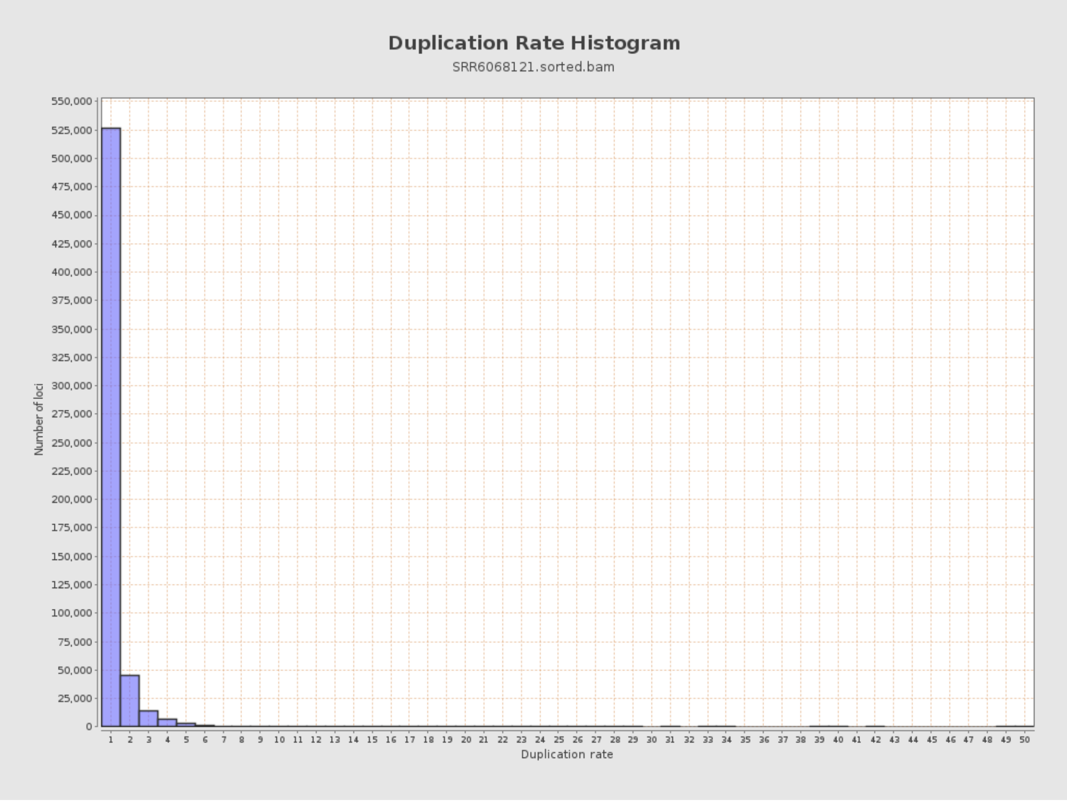
5. Results : Coverage Histogram (0-50X)



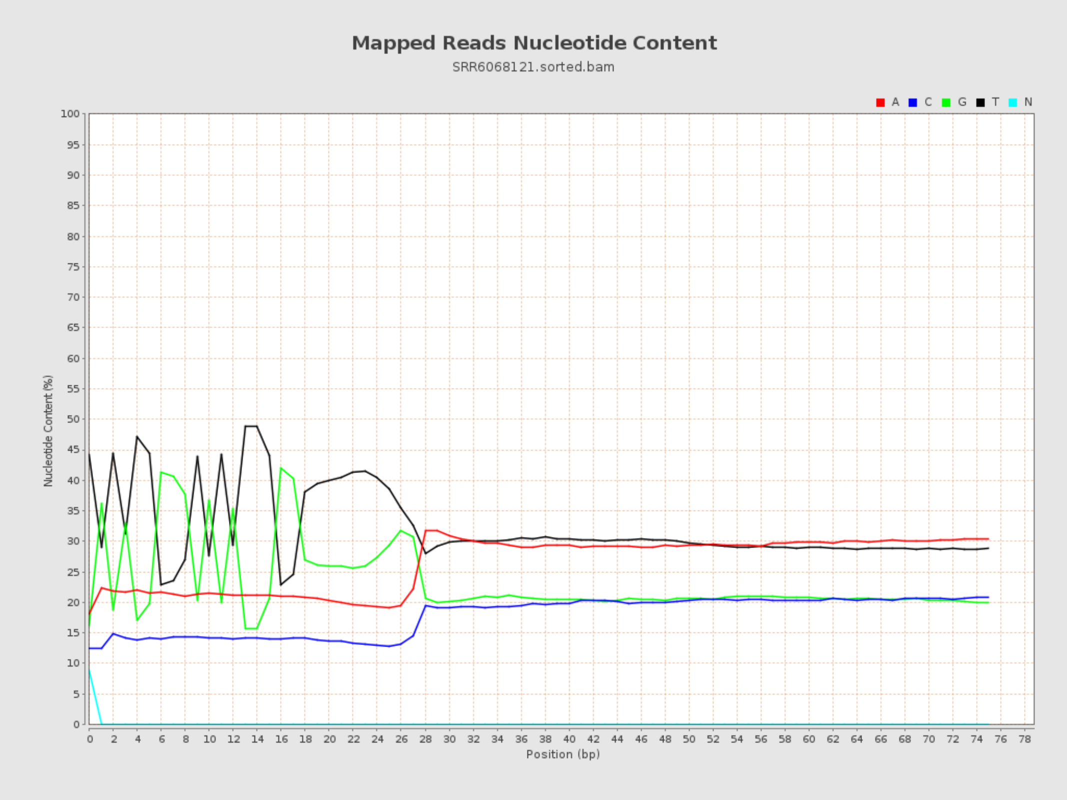
6. Results : Genome Fraction Coverage



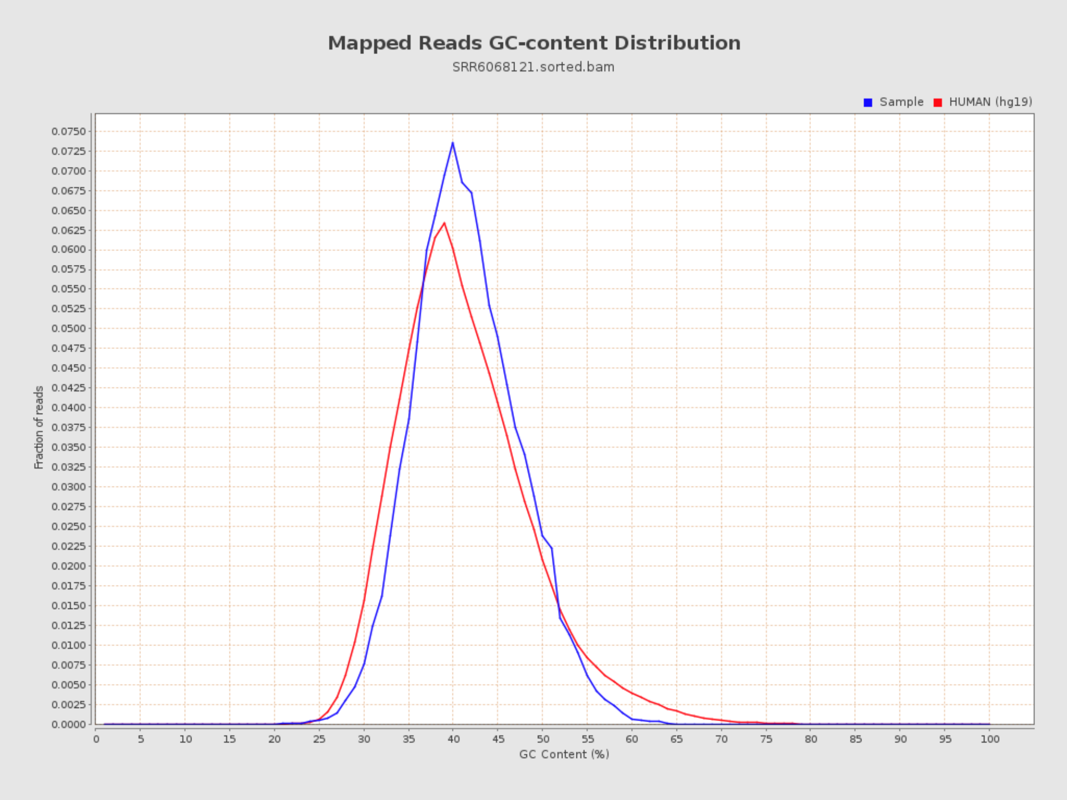
7. Results : Duplication Rate Histogram



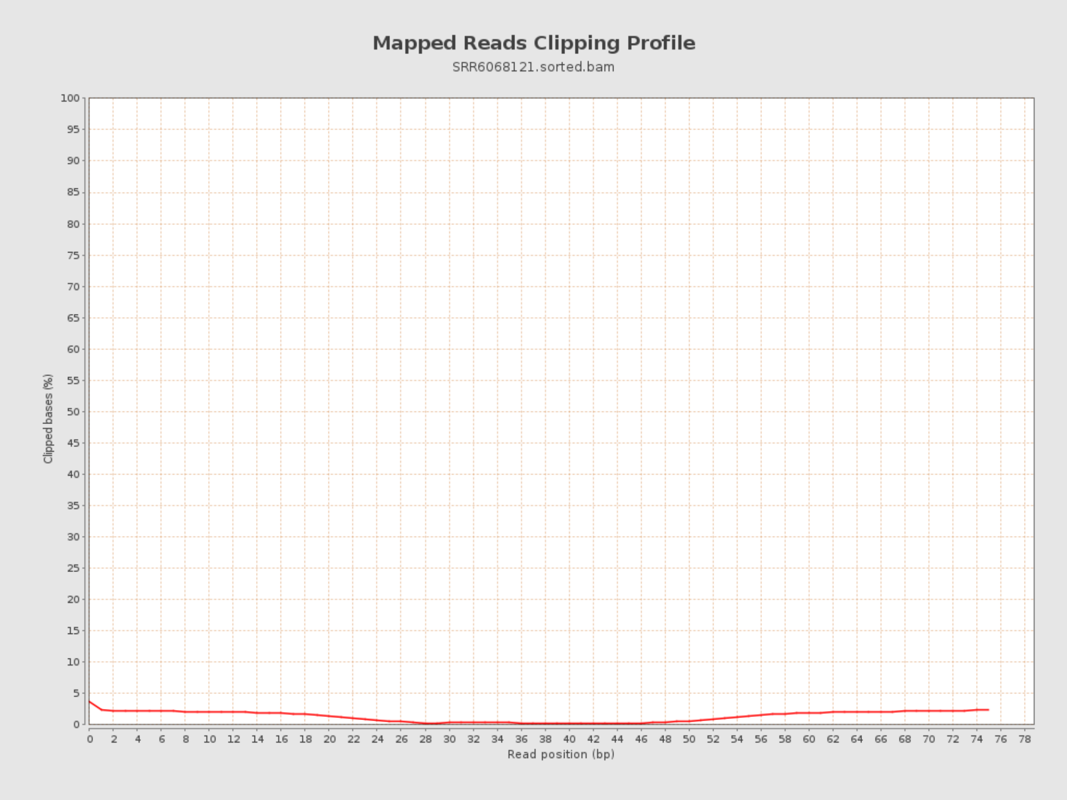
8. Results : Mapped Reads Nucleotide Content



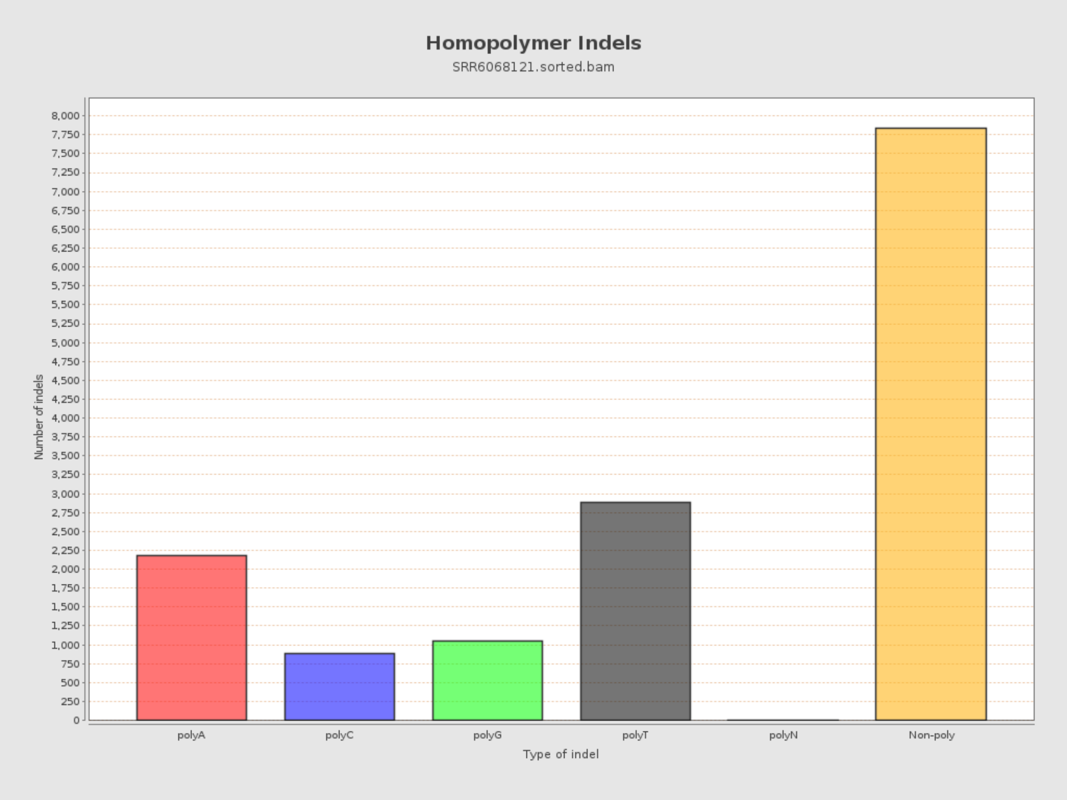
9. Results : Mapped Reads GC-content Distribution



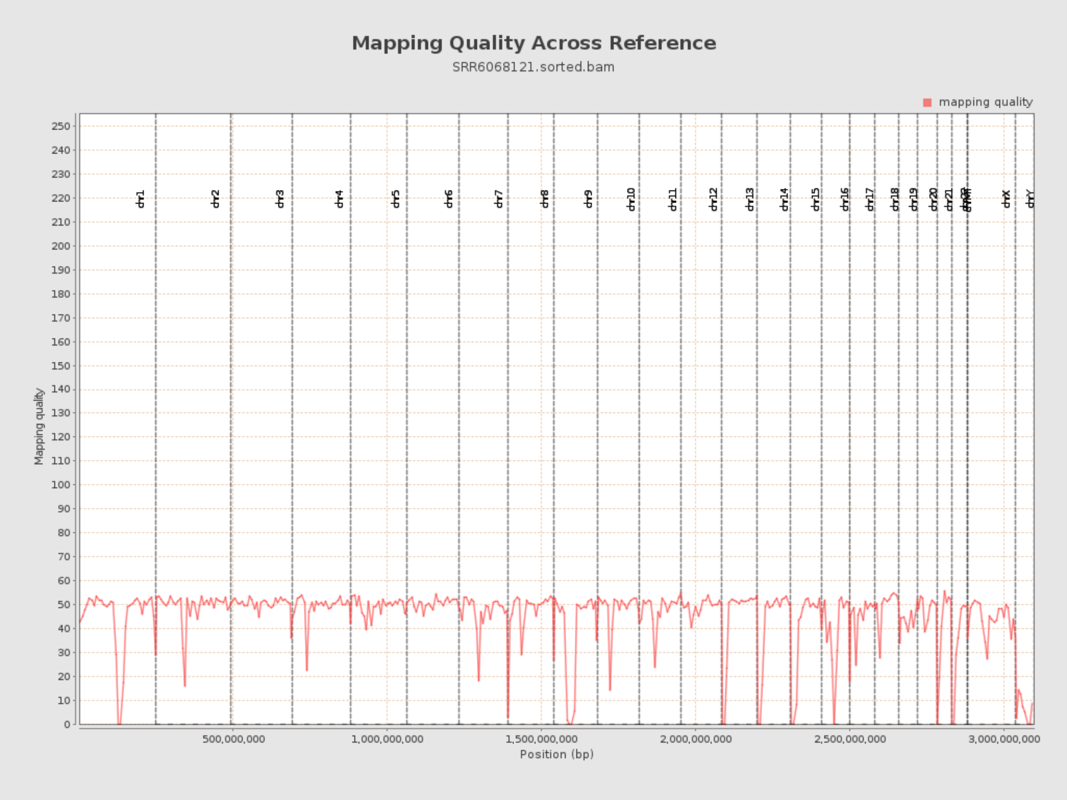
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram