Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:11:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008669.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_SRR6008669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:11:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,149
Mapped reads	677,363 / 38.61%
Unmapped reads	1,076,786 / 61.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,408 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	57,076 / 3.25%
Duplication rate	6.82%
Clipped reads	332,480 / 18.95%

2.2. ACGT Content

Number/percentage of A's	12,108,784 / 27.31%
Number/percentage of C's	8,392,754 / 18.93%
Number/percentage of T's	13,806,310 / 31.14%
Number/percentage of G's	9,964,316 / 22.47%
Number/percentage of N's	63,207 / 0.14%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.207

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

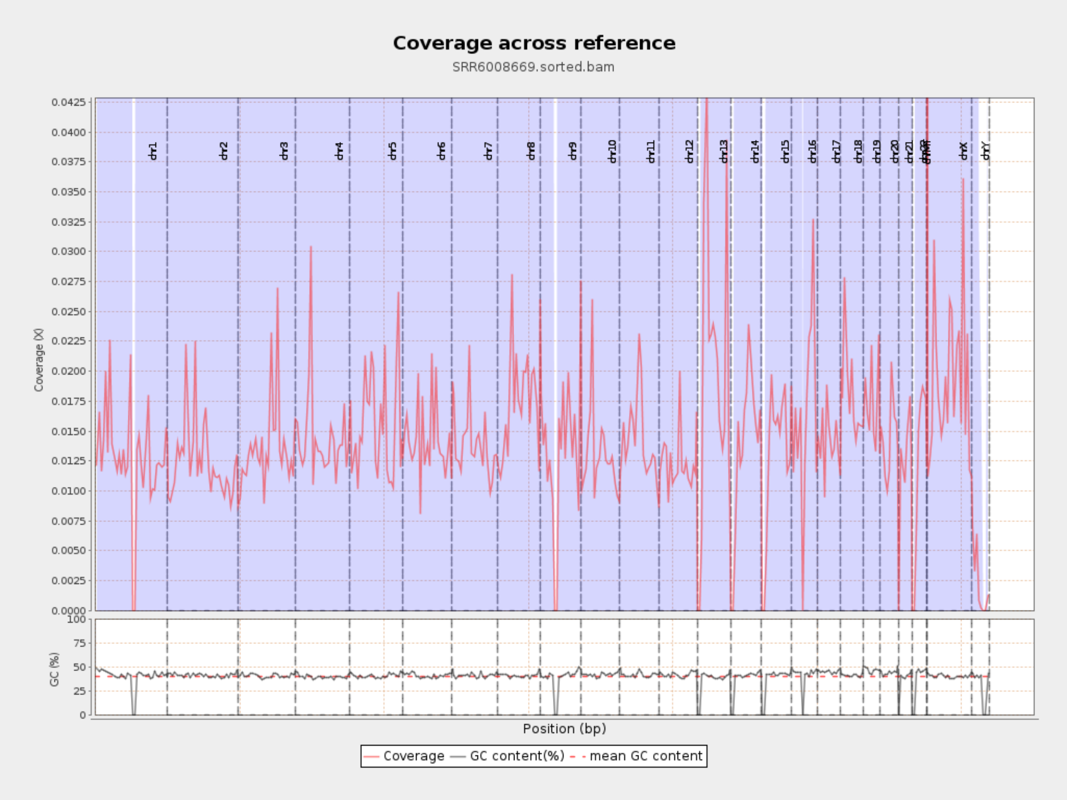
General error rate	0.84%
Mismatches	368,236
Insertions	3,130
Mapped reads with at least one insertion	0.46%
Deletions	10,986
Mapped reads with at least one deletion	1.61%
Homopolymer indels	46.87%

2.6. Chromosome stats

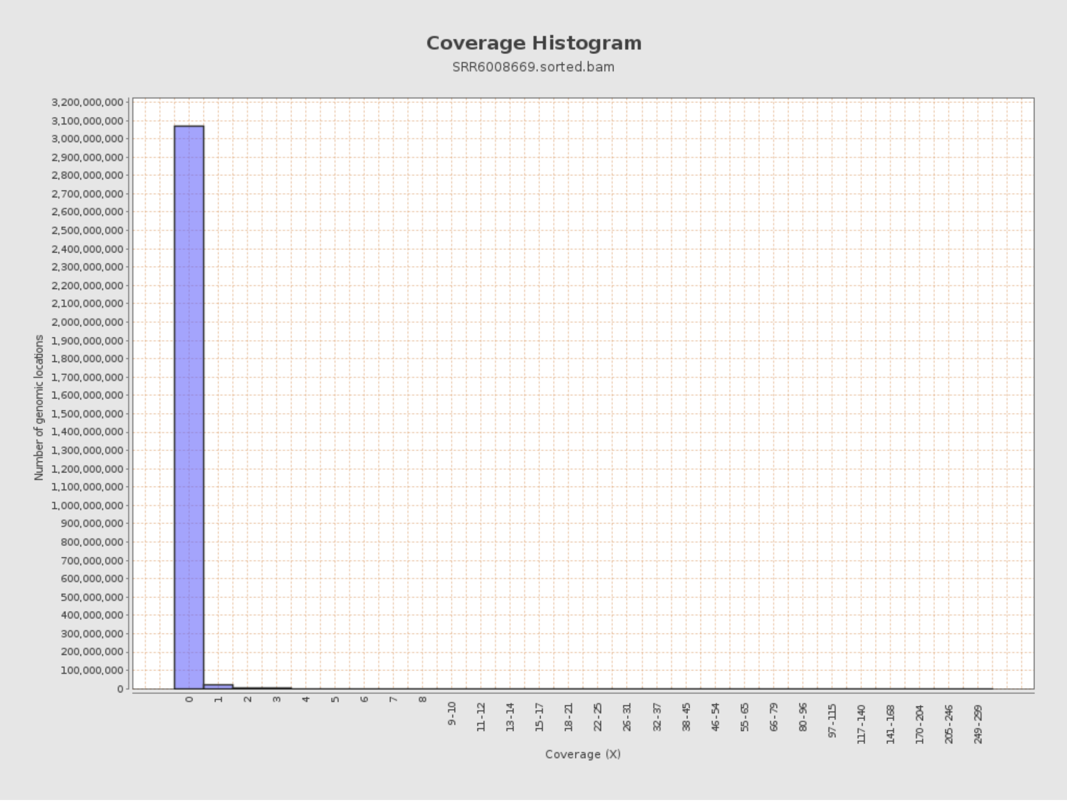
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3179727	0.0128	0.3072
chr2	243199373	3041428	0.0125	0.2213
chr3	198022430	2675288	0.0135	0.1673
chr4	191154276	2764813	0.0145	0.1843
chr5	180915260	2796468	0.0155	0.1809
chr6	171115067	2457212	0.0144	0.1865
chr7	159138663	2242259	0.0141	0.1937

chr8	146364022	2545970	0.0174	0.2605
chr9	141213431	1811898	0.0128	0.18
chr10	135534747	1773275	0.0131	0.1902
chr11	135006516	1959835	0.0145	0.1918
chr12	133851895	1654156	0.0124	0.1646
chr13	115169878	2302144	0.02	0.2123
chr14	107349540	1487545	0.0139	0.1841
chr15	102531392	1293427	0.0126	0.1687
chr16	90354753	1486190	0.0164	0.2008
chr17	81195210	1149709	0.0142	0.1741
chr18	78077248	1416814	0.0181	0.2694
chr19	59128983	1034383	0.0175	0.2465
chr20	63025520	900764	0.0143	0.1756
chr21	48129895	598790	0.0124	0.1905
chr22	51304566	608972	0.0119	0.1569
chrMT	16571	23256	1.4034	1.8381
chrX	155270560	3020998	0.0195	0.211
chrY	59373566	129805	0.0022	0.0711

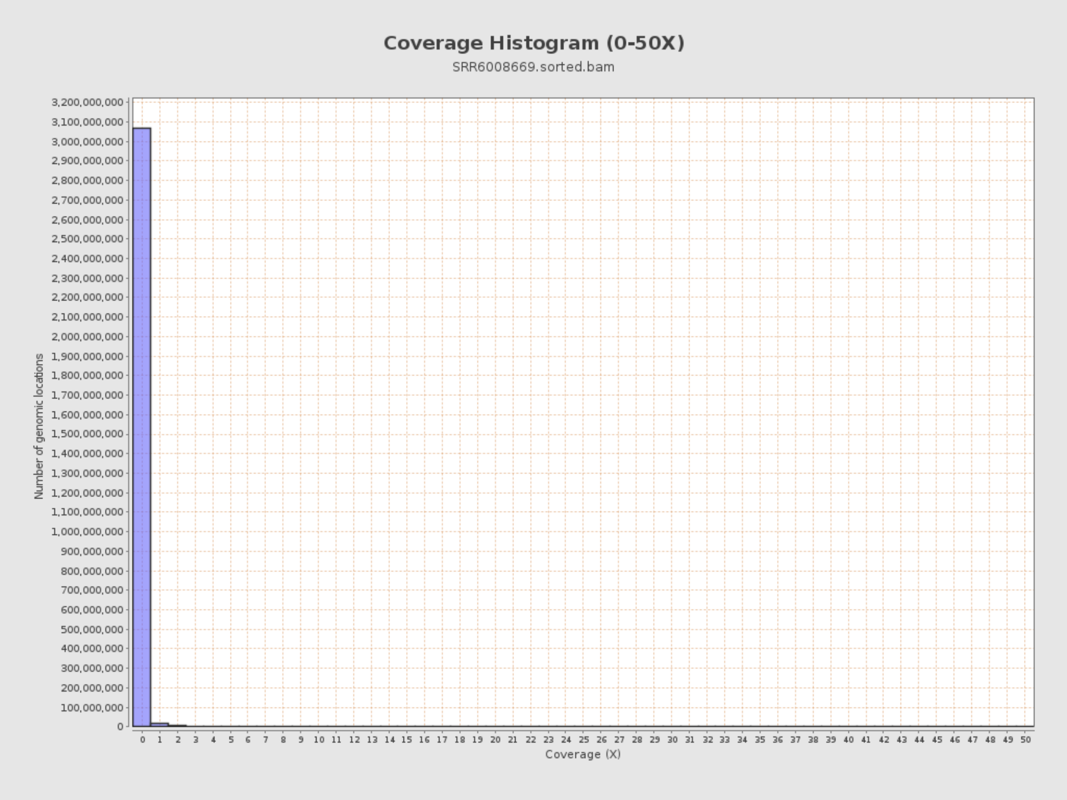
3. Results : Coverage across reference



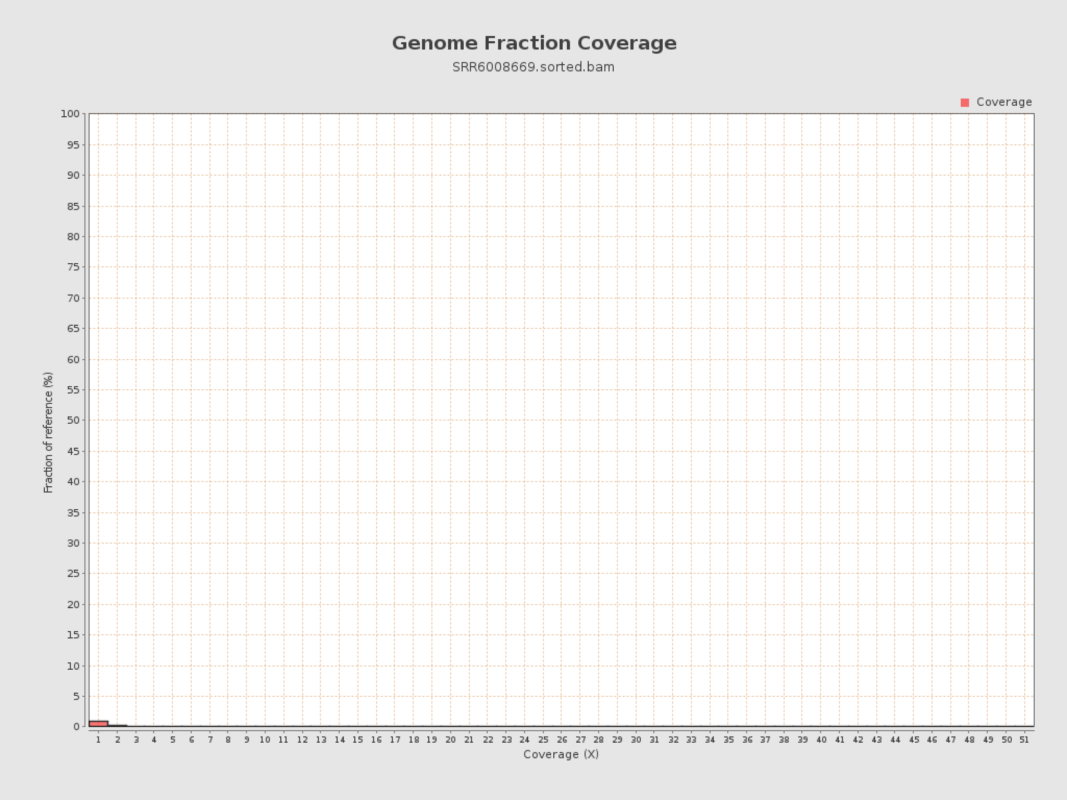
4. Results : Coverage Histogram



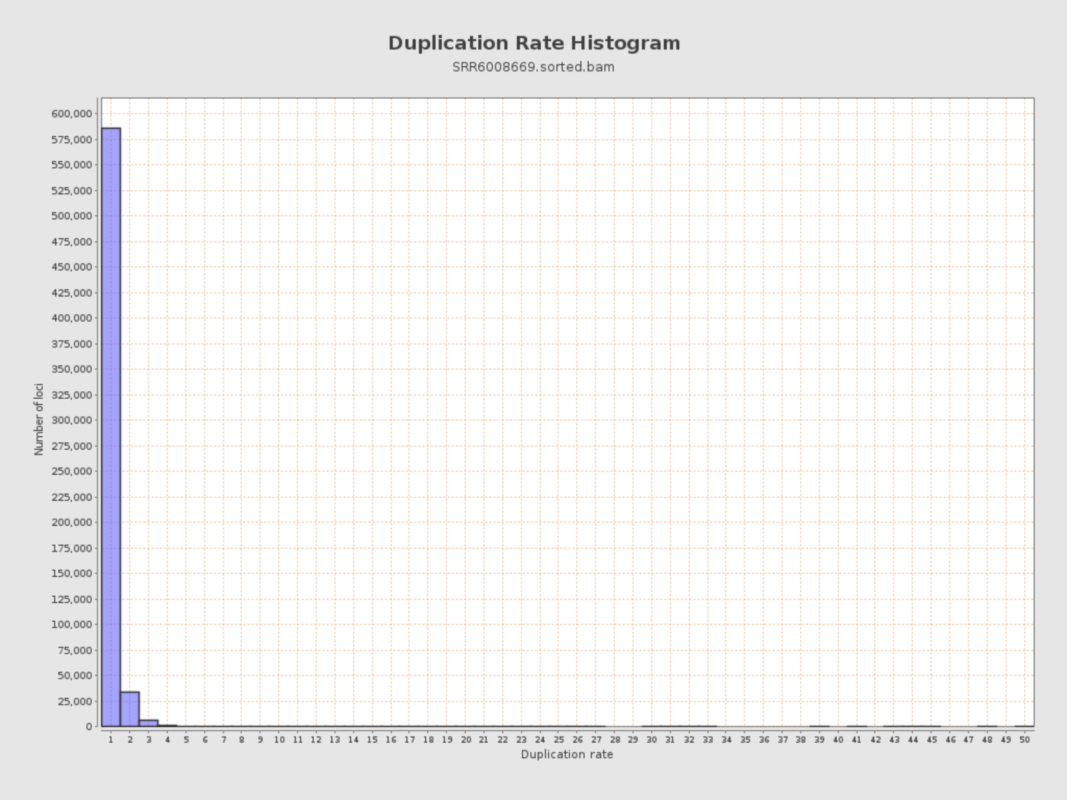
5. Results : Coverage Histogram (0-50X)



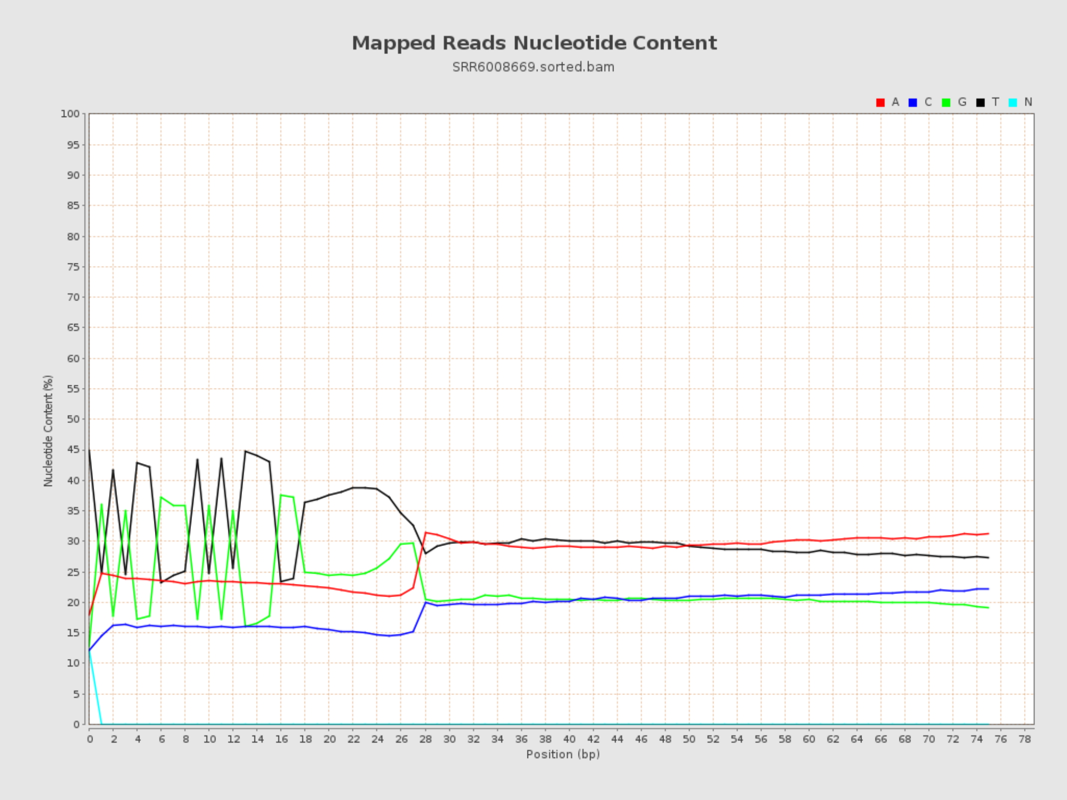
6. Results : Genome Fraction Coverage



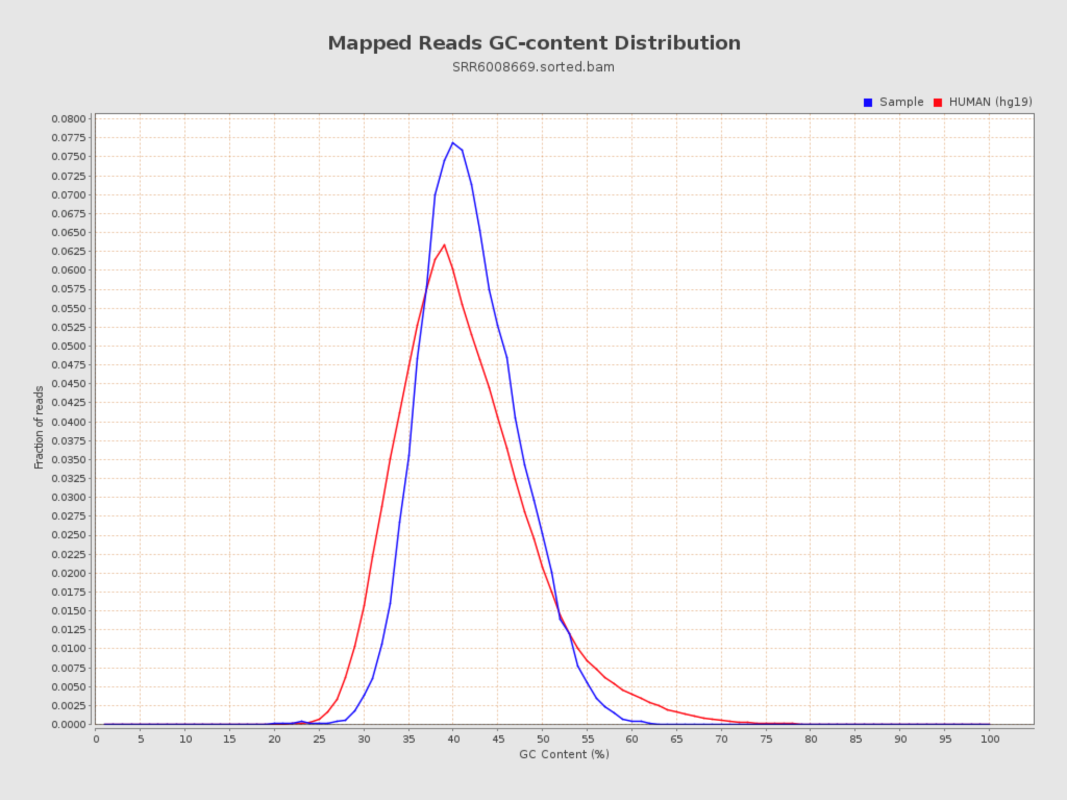
7. Results : Duplication Rate Histogram



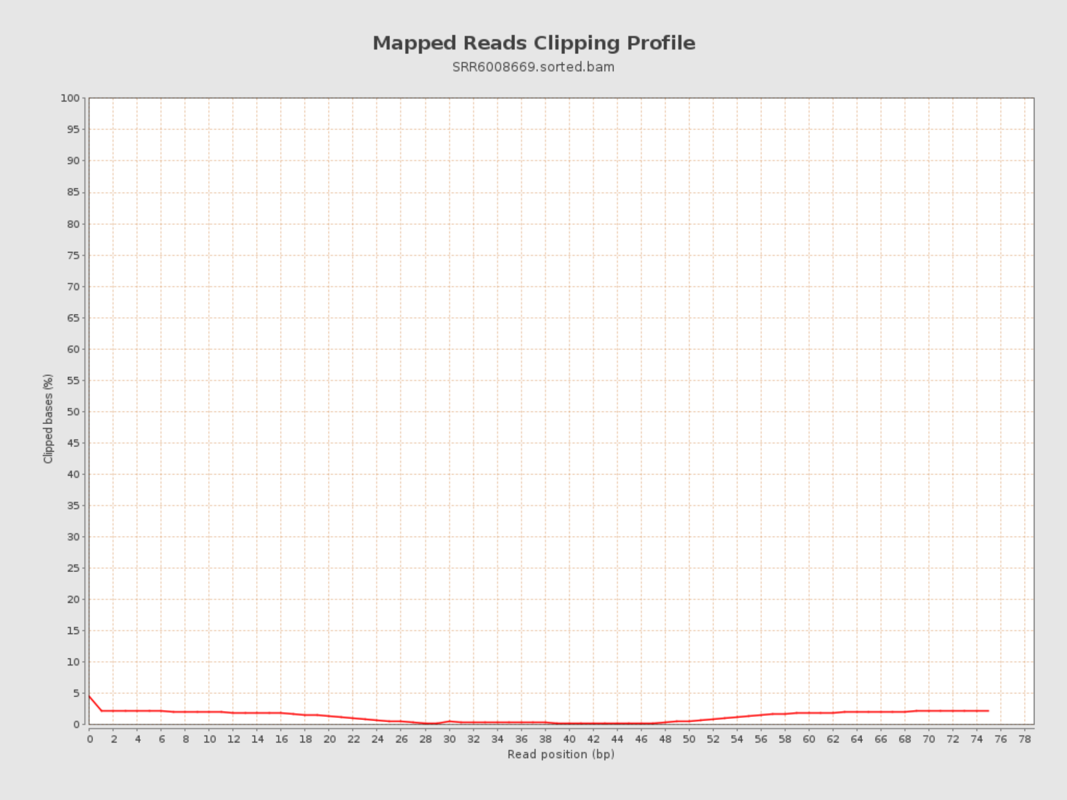
8. Results : Mapped Reads Nucleotide Content



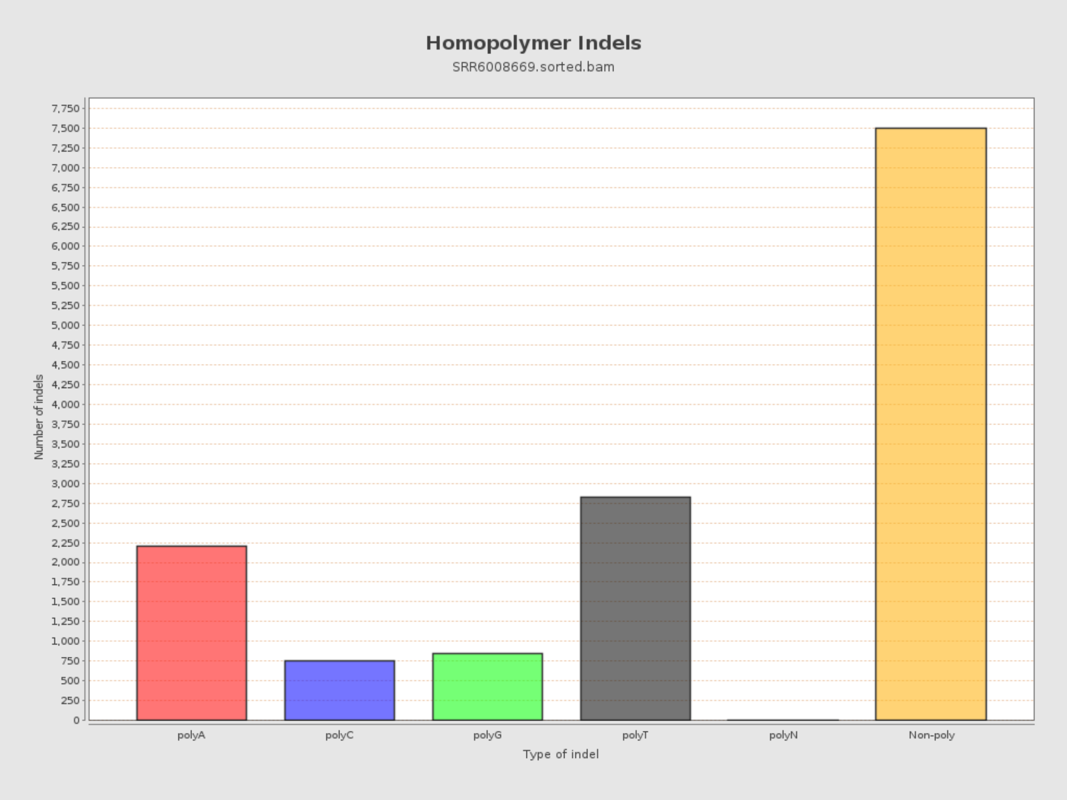
9. Results : Mapped Reads GC-content Distribution



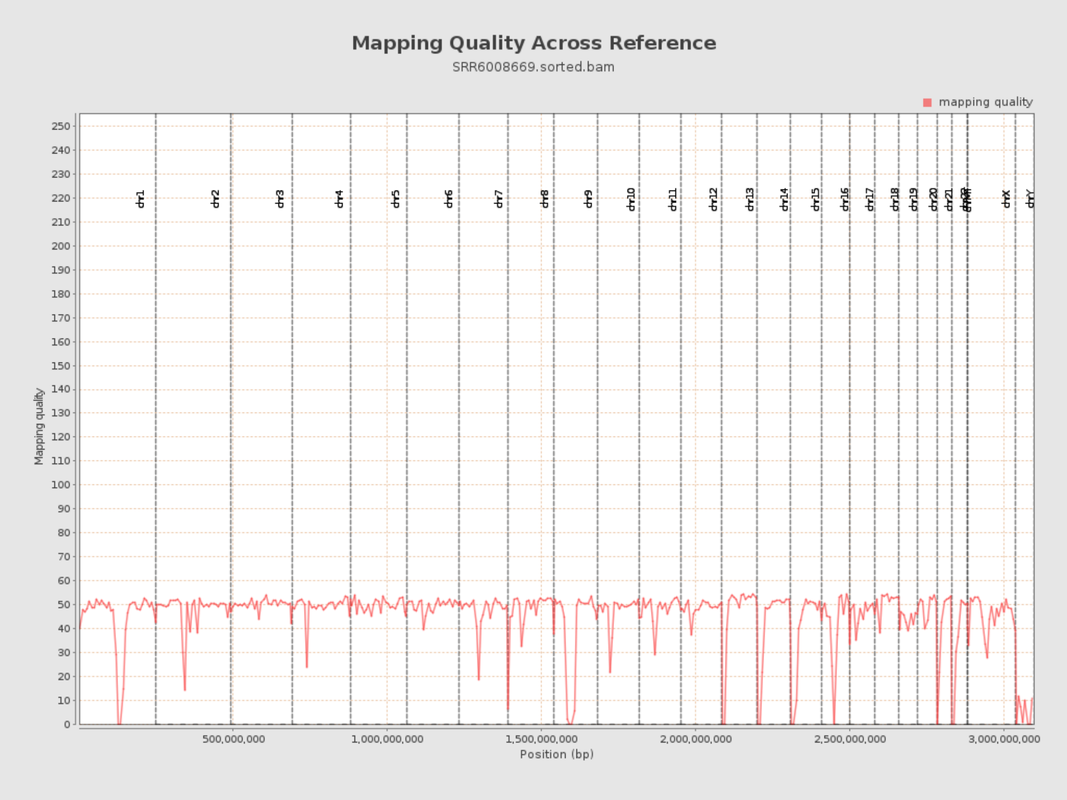
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram