Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:51:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008707.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_SRR6008707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:51:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,172,604
Mapped reads	932,581 / 79.53%
Unmapped reads	240,023 / 20.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,386 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,161 / 2.83%
Duplication rate	2.64%
Clipped reads	504,812 / 43.05%

2.2. ACGT Content

Number/percentage of A's	16,731,879 / 28.17%
Number/percentage of C's	9,981,049 / 16.8%
Number/percentage of T's	18,730,641 / 31.53%
Number/percentage of G's	13,958,364 / 23.5%
Number/percentage of N's	2,941 / 0%
GC Percentage	40.3%

2.3. Coverage

Mean	0.0192

Standard Deviation	0.197

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

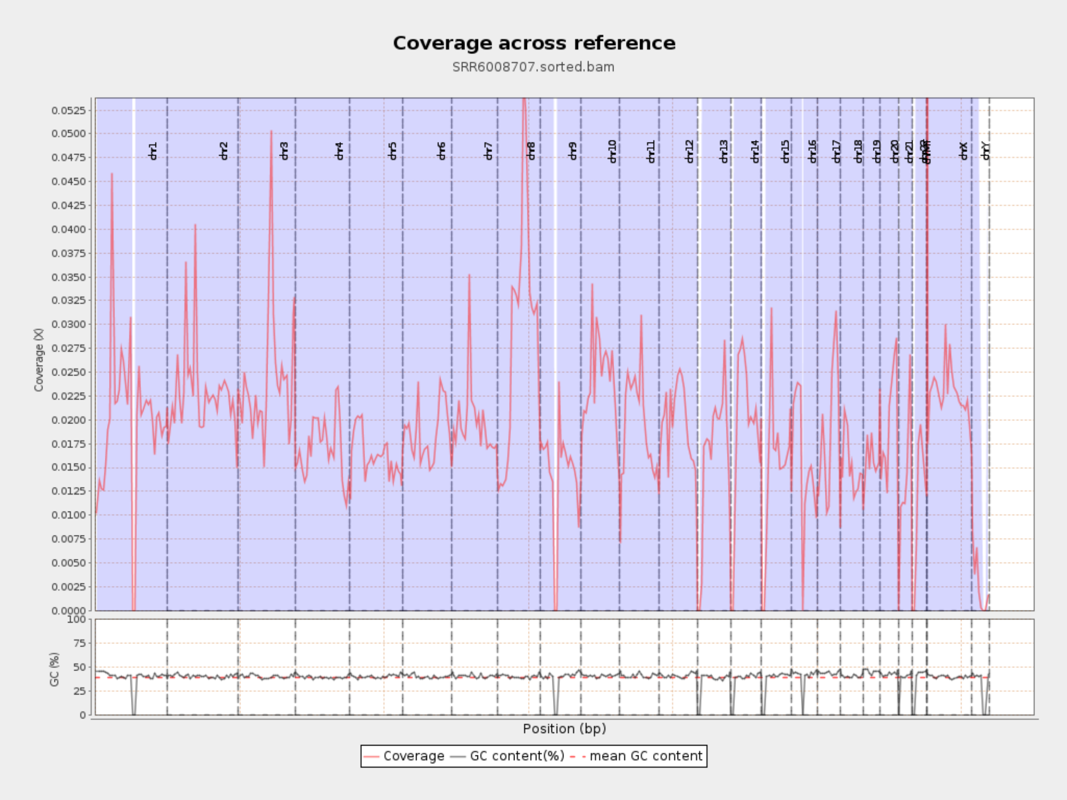
General error rate	0.83%
Mismatches	484,120
Insertions	5,045
Mapped reads with at least one insertion	0.54%
Deletions	19,241
Mapped reads with at least one deletion	2.04%
Homopolymer indels	48.56%

2.6. Chromosome stats

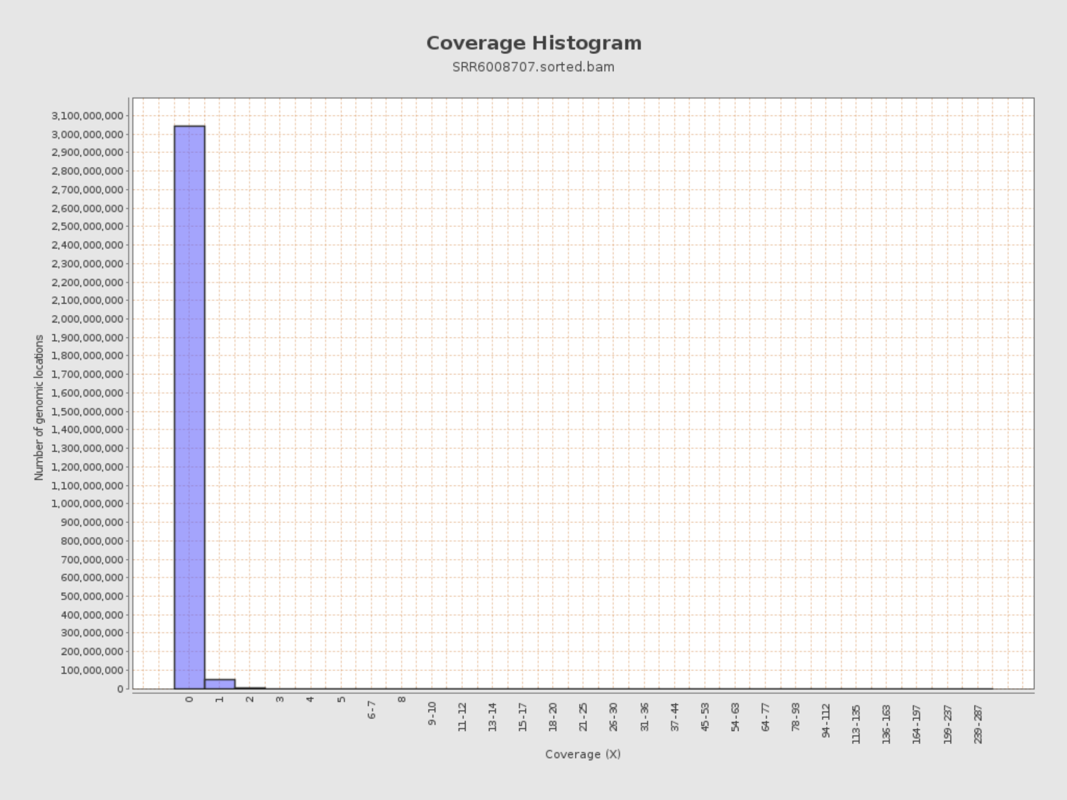
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4942042	0.0198	0.2566
chr2	243199373	5582648	0.023	0.2565
chr3	198022430	4774574	0.0241	0.1683
chr4	191154276	3247292	0.017	0.1434
chr5	180915260	2977923	0.0165	0.1383
chr6	171115067	3177800	0.0186	0.1672
chr7	159138663	3151462	0.0198	0.2815

chr8	146364022	4323038	0.0295	0.2354
chr9	141213431	2005173	0.0142	0.1954
chr10	135534747	3262228	0.0241	0.2056
chr11	135006516	2650751	0.0196	0.2046
chr12	133851895	2654369	0.0198	0.1542
chr13	115169878	1862051	0.0162	0.1381
chr14	107349540	2033648	0.0189	0.1532
chr15	102531392	1527090	0.0149	0.1346
chr16	90354753	1378547	0.0153	0.1418
chr17	81195210	1537789	0.0189	0.1702
chr18	78077248	1175287	0.0151	0.3218
chr19	59128983	946150	0.016	0.1927
chr20	63025520	1249266	0.0198	0.153
chr21	48129895	661201	0.0137	0.1284
chr22	51304566	593014	0.0116	0.1143
chrMT	16571	14839	0.8955	1.1927
chrX	155270560	3555264	0.0229	0.1778
chrY	59373566	152607	0.0026	0.0649

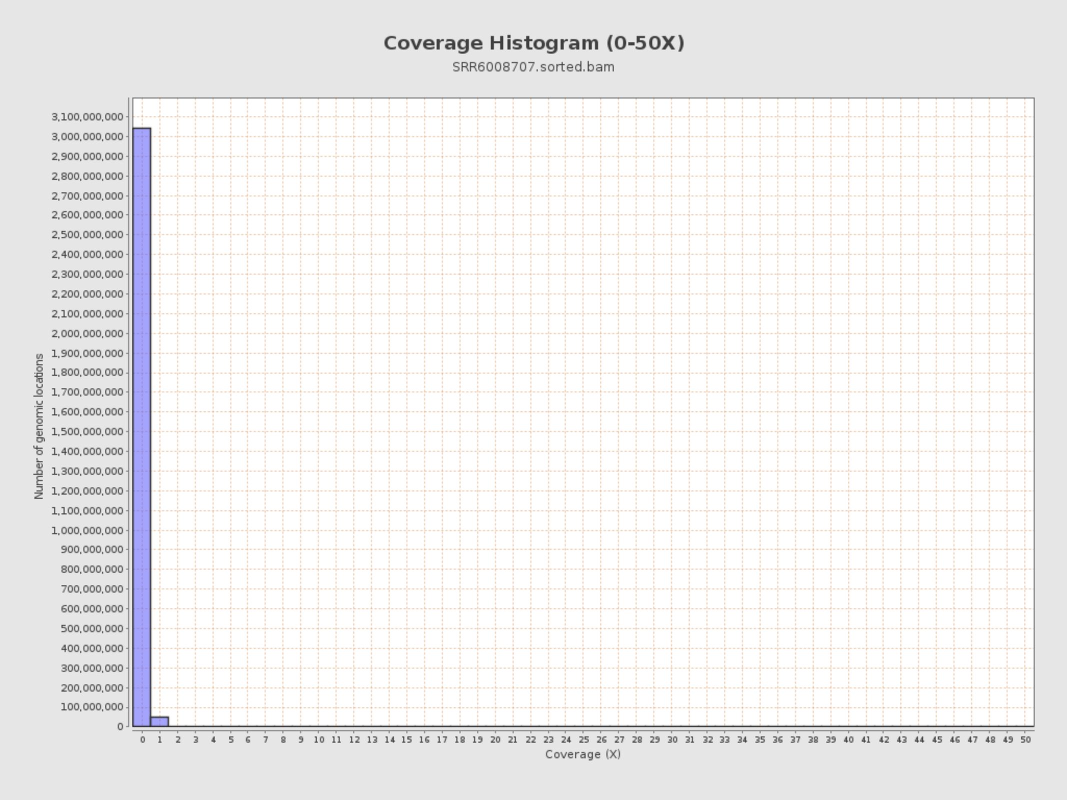
3. Results : Coverage across reference



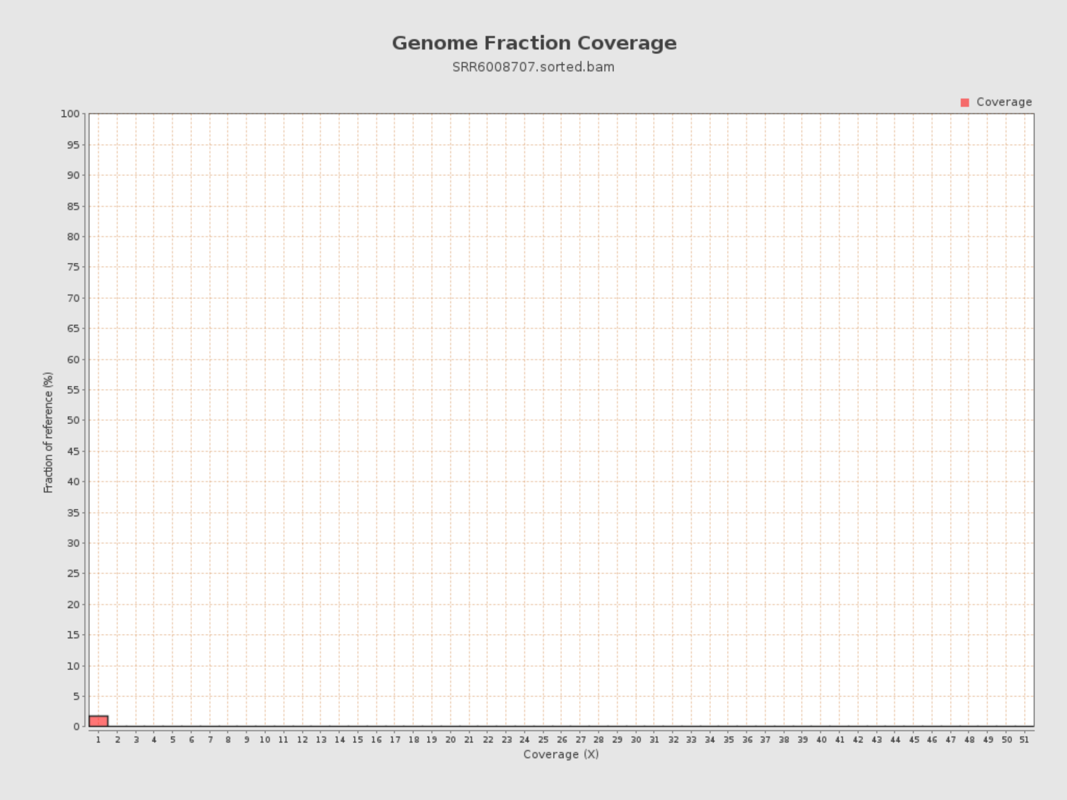
4. Results : Coverage Histogram



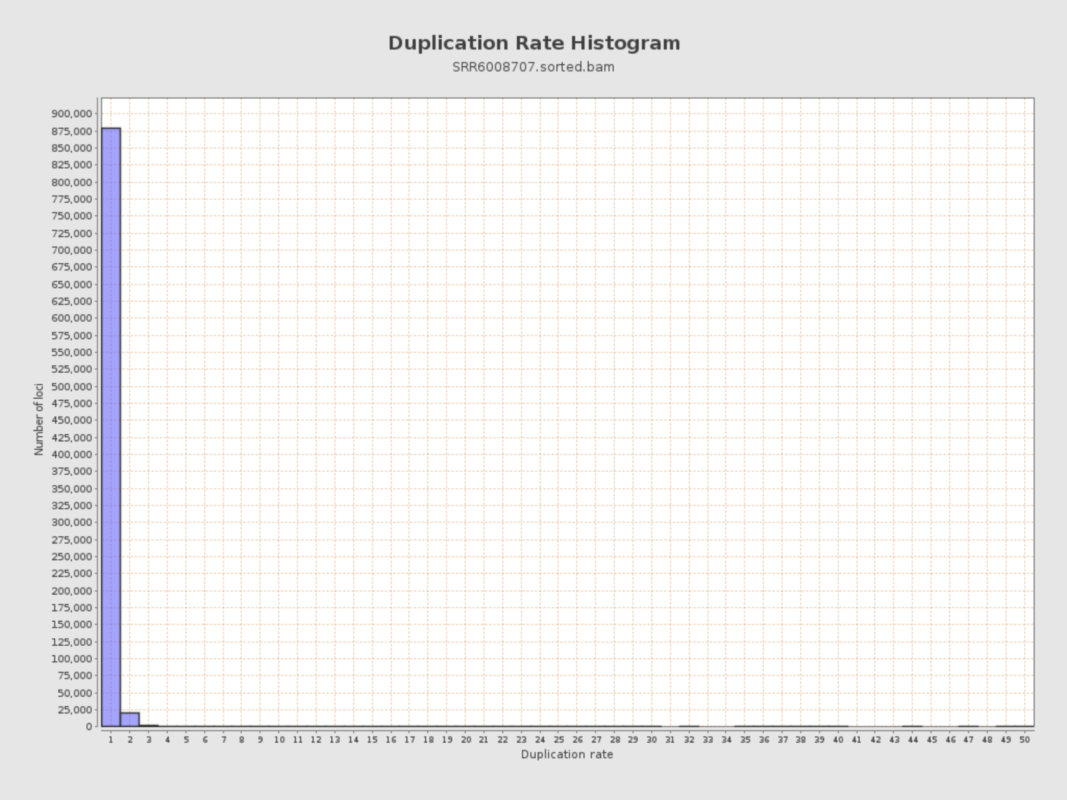
5. Results : Coverage Histogram (0-50X)



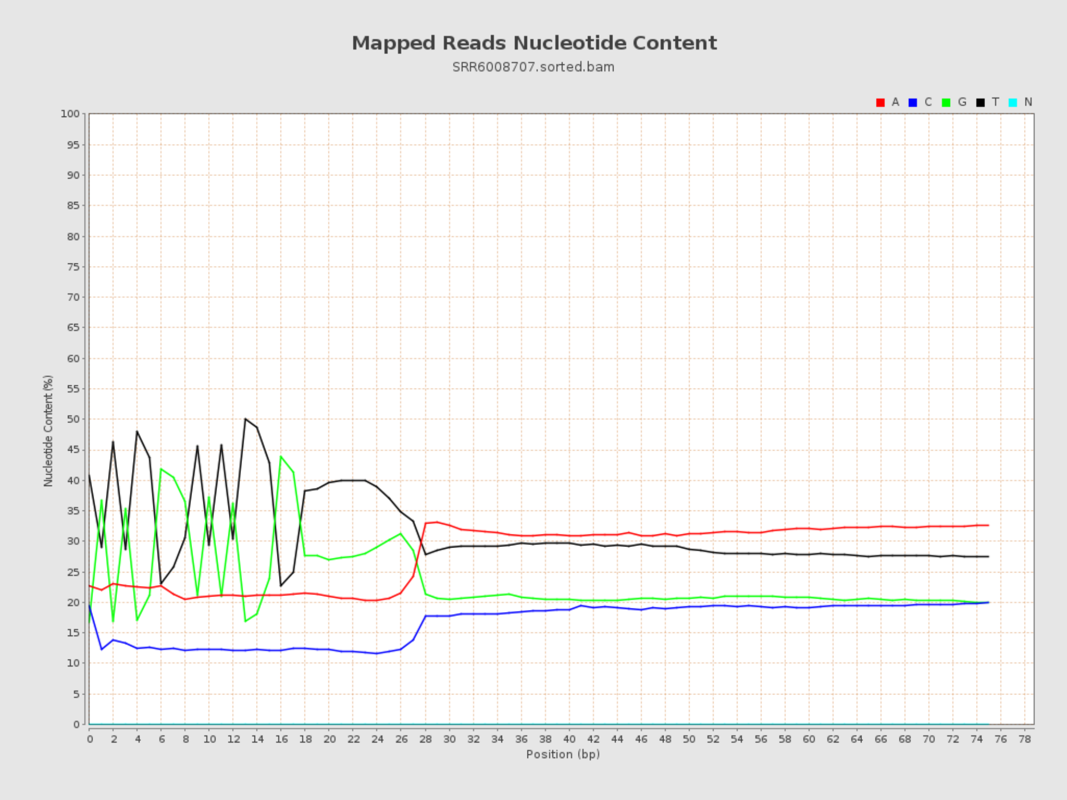
6. Results : Genome Fraction Coverage



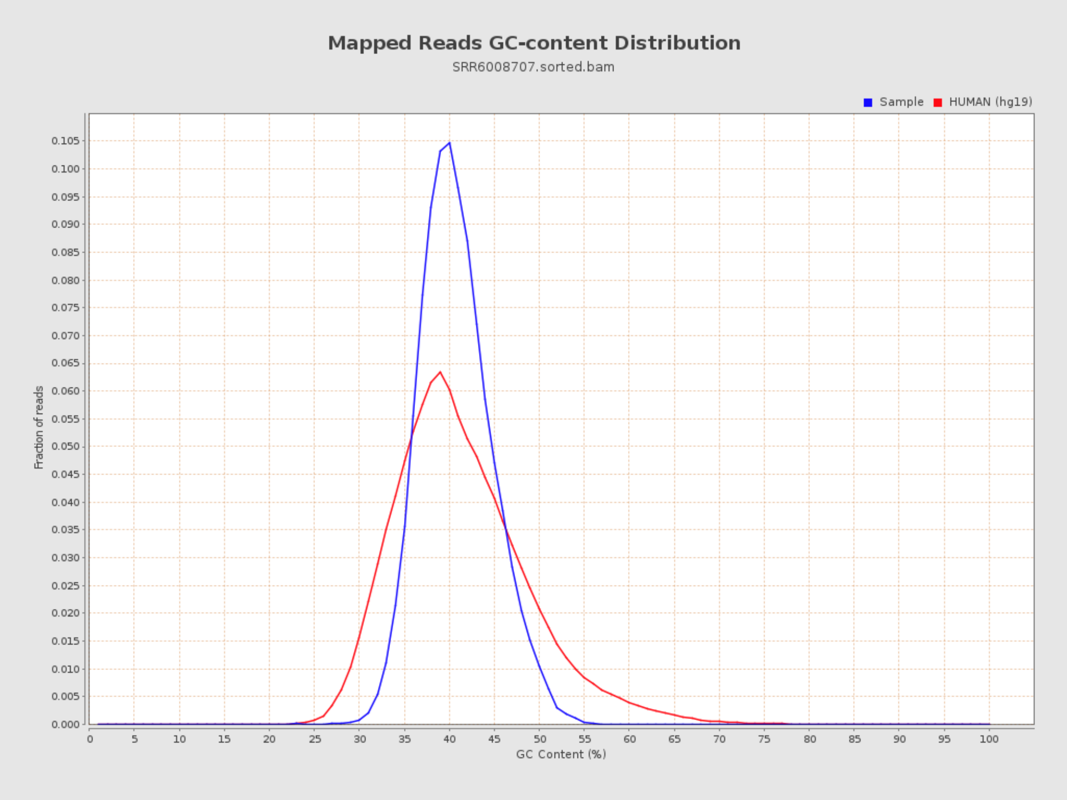
7. Results : Duplication Rate Histogram



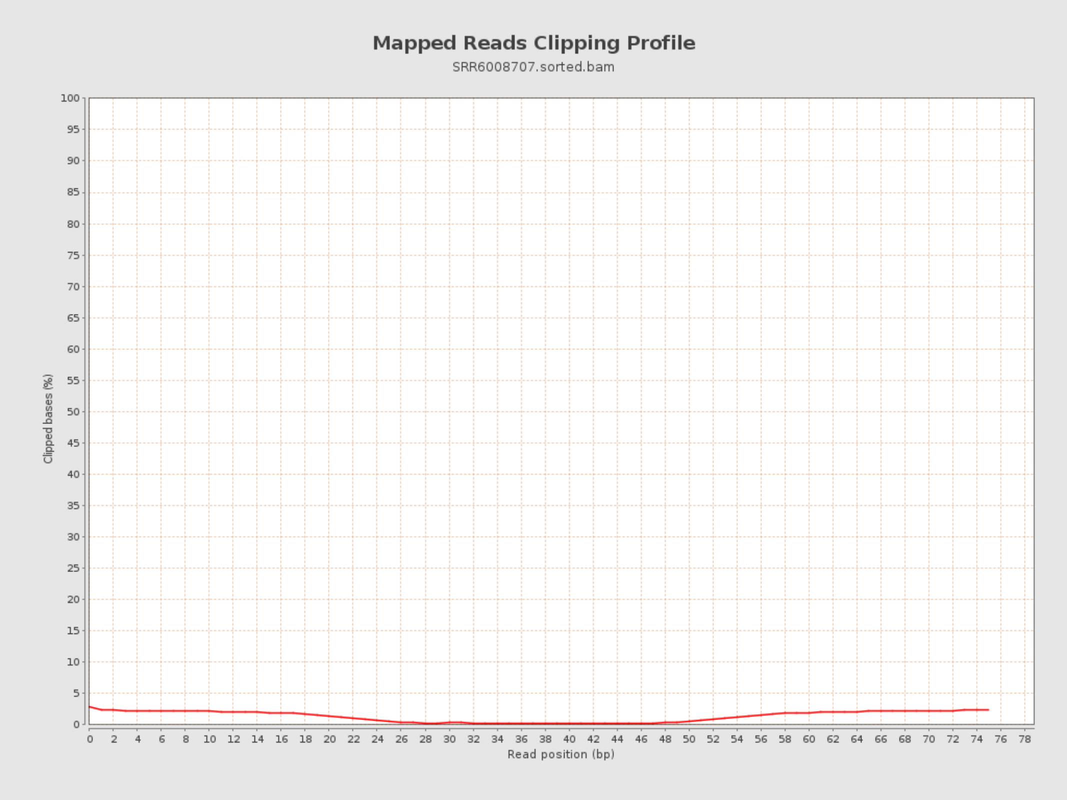
8. Results : Mapped Reads Nucleotide Content



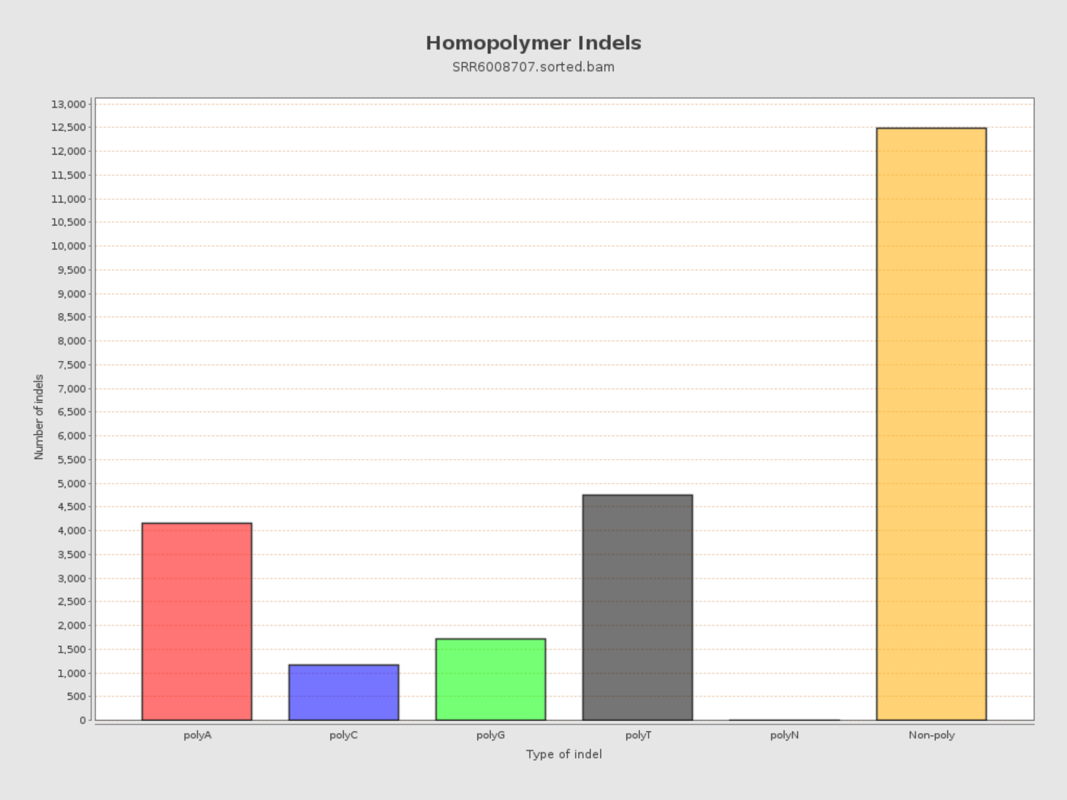
9. Results : Mapped Reads GC-content Distribution



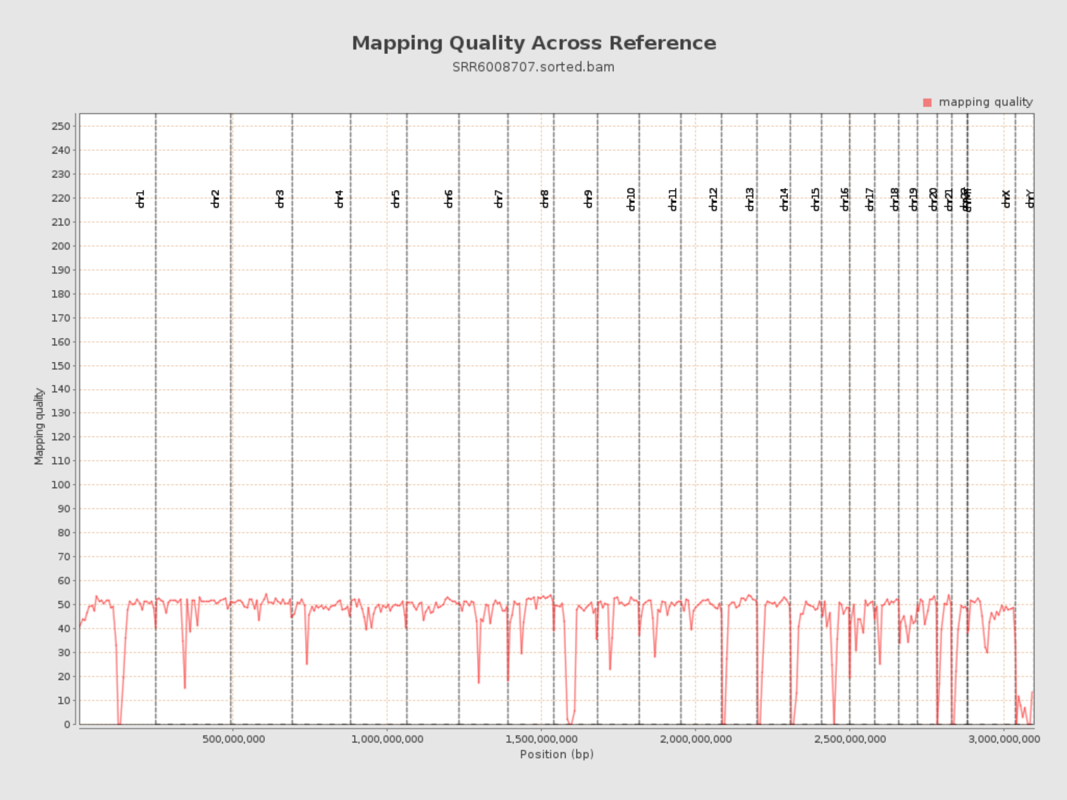
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram