Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:36:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008746.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_SRR6008746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:36:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,994,429
Mapped reads	1,496,232 / 75.02%
Unmapped reads	498,197 / 24.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,161 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	142,653 / 7.15%
Duplication rate	7.99%
Clipped reads	919,875 / 46.12%

2.2. ACGT Content

Number/percentage of A's	24,788,764 / 26.79%
Number/percentage of C's	16,032,862 / 17.33%
Number/percentage of T's	30,301,736 / 32.75%
Number/percentage of G's	21,386,217 / 23.11%
Number/percentage of N's	24,410 / 0.03%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0299

Standard Deviation	0.3354

2.4. Mapping Quality

Mean Mapping Quality	42.68

2.5. Mismatches and indels

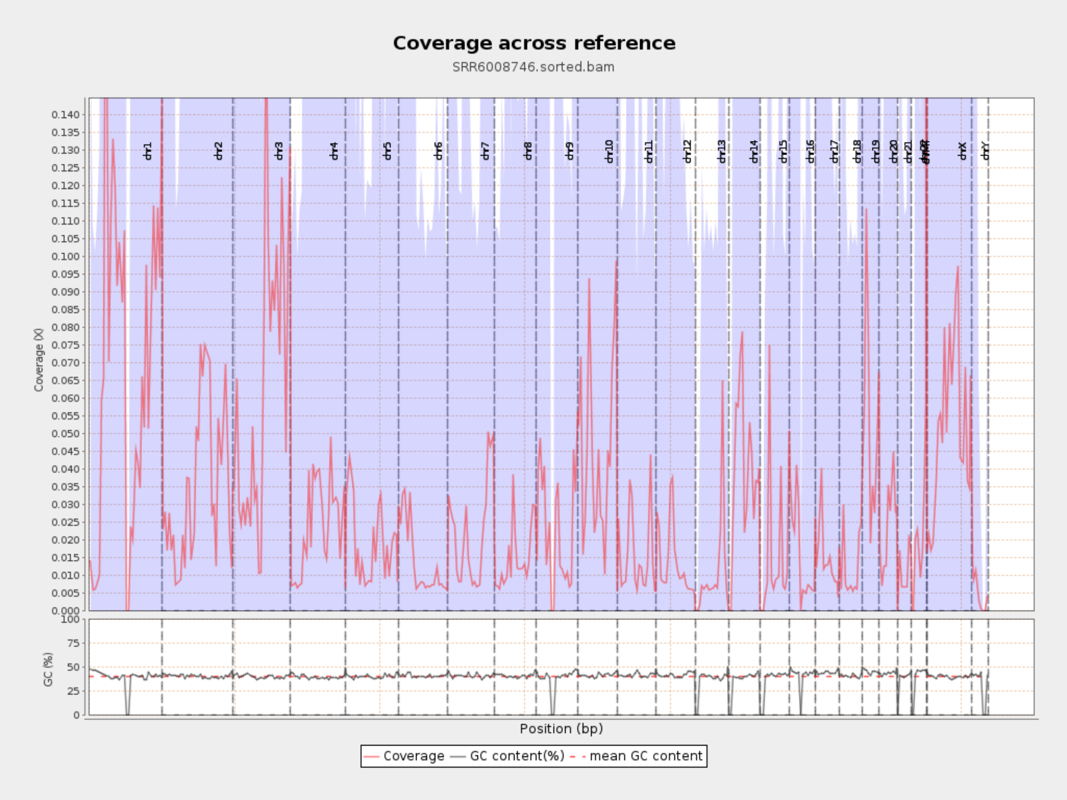
General error rate	0.86%
Mismatches	780,139
Insertions	7,455
Mapped reads with at least one insertion	0.49%
Deletions	29,050
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.06%

2.6. Chromosome stats

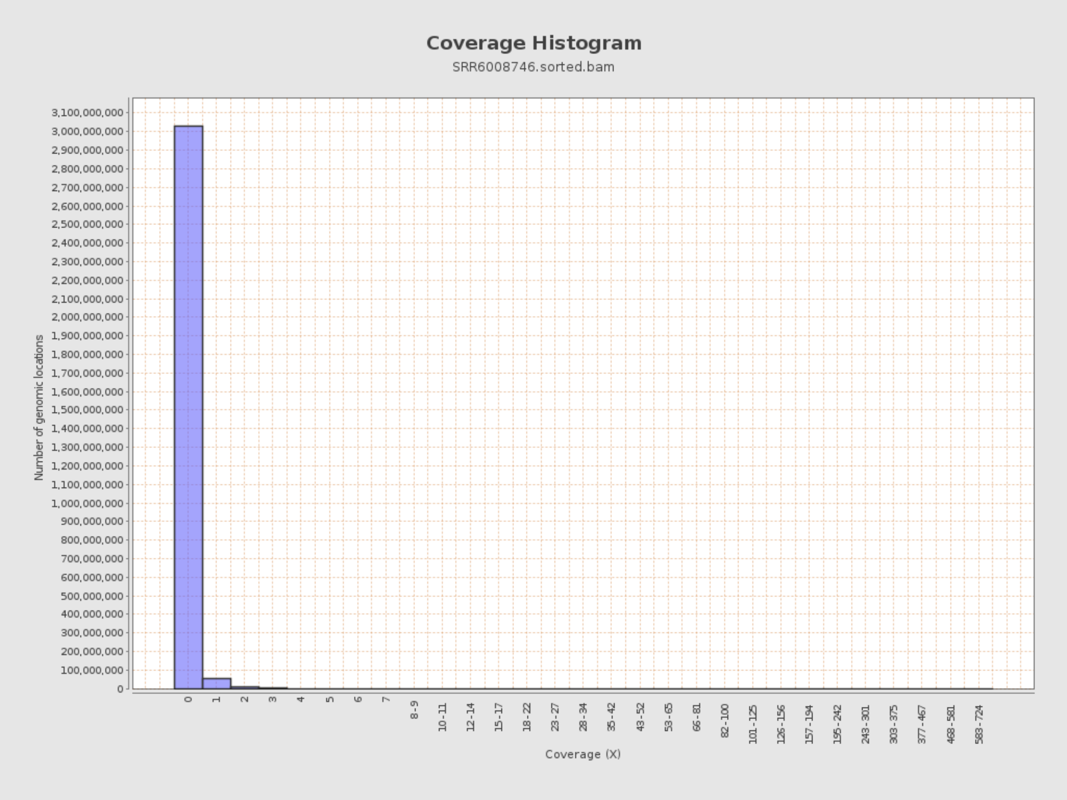
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16784138	0.0673	0.6965
chr2	243199373	8672610	0.0357	0.3193
chr3	198022430	12434682	0.0628	0.3425
chr4	191154276	4598063	0.0241	0.2011
chr5	180915260	3504076	0.0194	0.1793
chr6	171115067	2371370	0.0139	0.1809
chr7	159138663	3468632	0.0218	0.2277

chr8	146364022	2207355	0.0151	0.1734
chr9	141213431	3205321	0.0227	0.2243
chr10	135534747	6146844	0.0454	0.6575
chr11	135006516	2066395	0.0153	0.283
chr12	133851895	1919809	0.0143	0.1574
chr13	115169878	1270603	0.011	0.1357
chr14	107349540	4208656	0.0392	0.2577
chr15	102531392	1568519	0.0153	0.1605
chr16	90354753	1390980	0.0154	0.2589
chr17	81195210	1178560	0.0145	0.1903
chr18	78077248	928792	0.0119	0.3926
chr19	59128983	3214189	0.0544	0.4386
chr20	63025520	1493350	0.0237	0.1979
chr21	48129895	530642	0.011	0.1411
chr22	51304566	980496	0.0191	0.1757
chrMT	16571	46524	2.8076	2.6155
chrX	155270560	8107506	0.0522	0.3211
chrY	59373566	283798	0.0048	0.1296

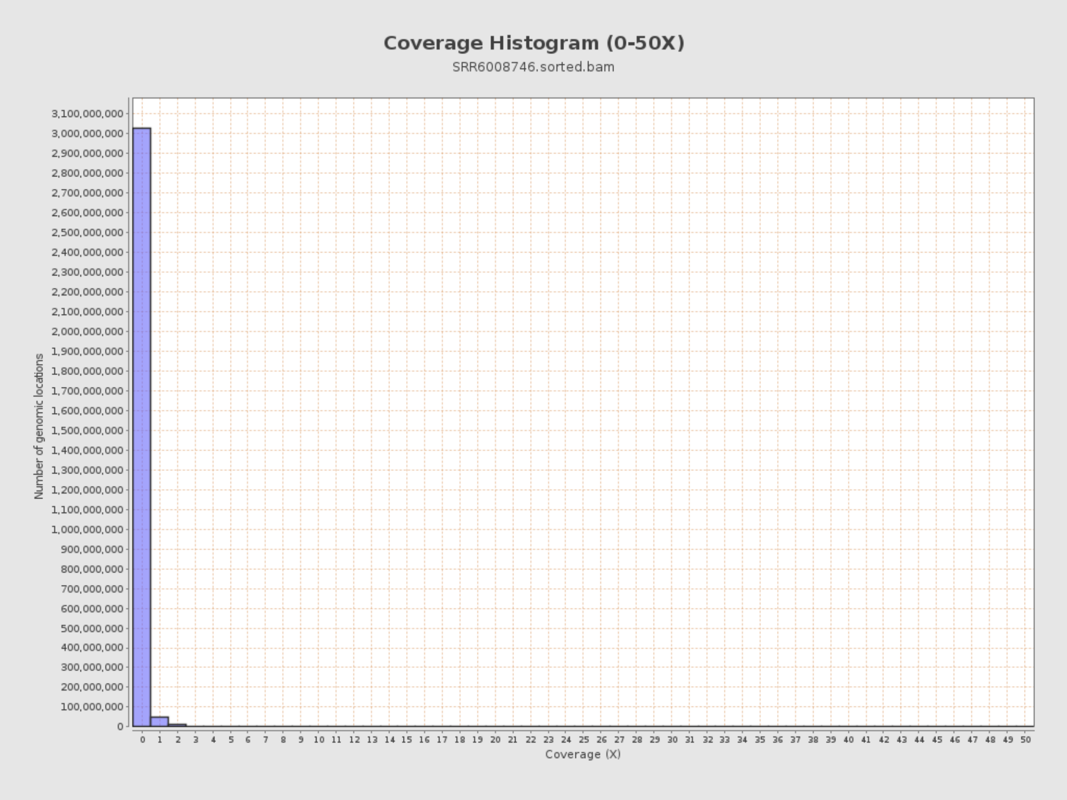
3. Results : Coverage across reference



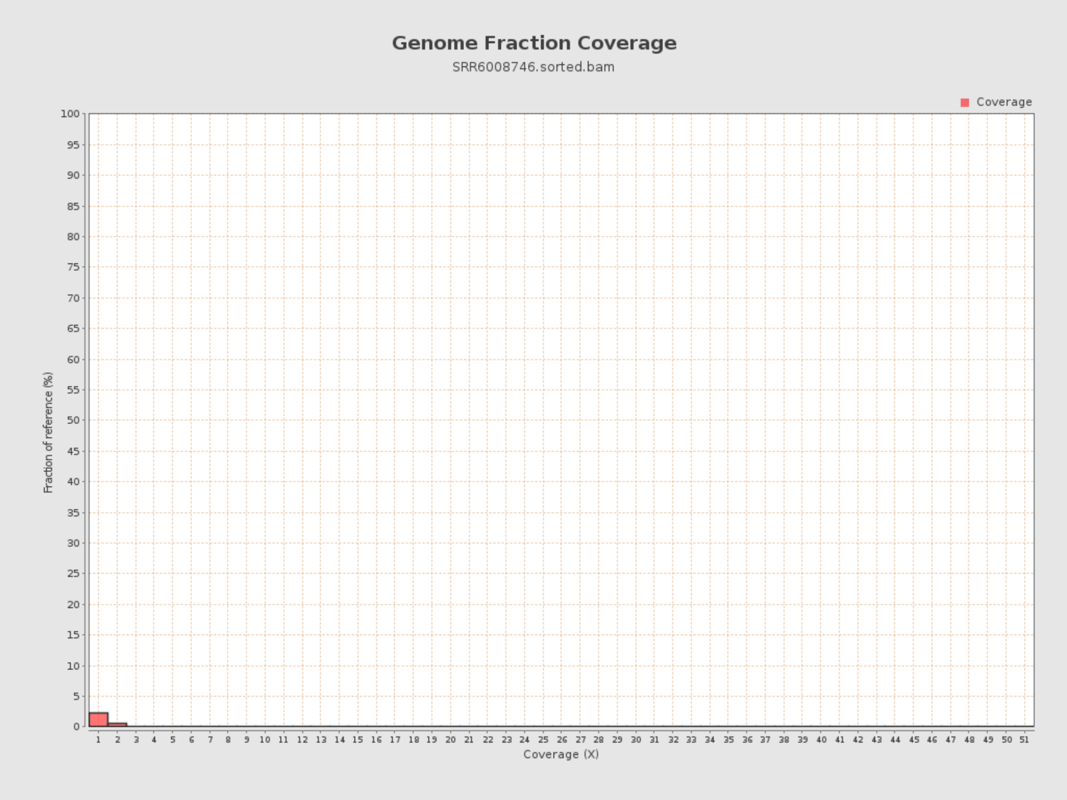
4. Results : Coverage Histogram



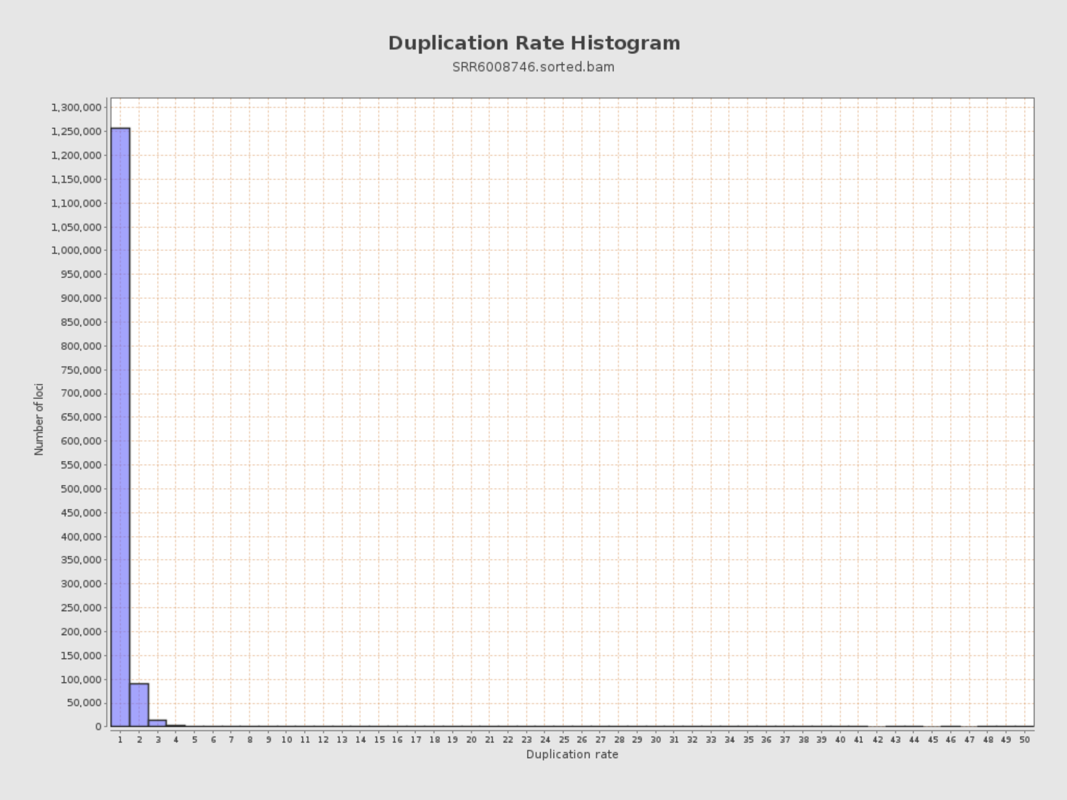
5. Results : Coverage Histogram (0-50X)



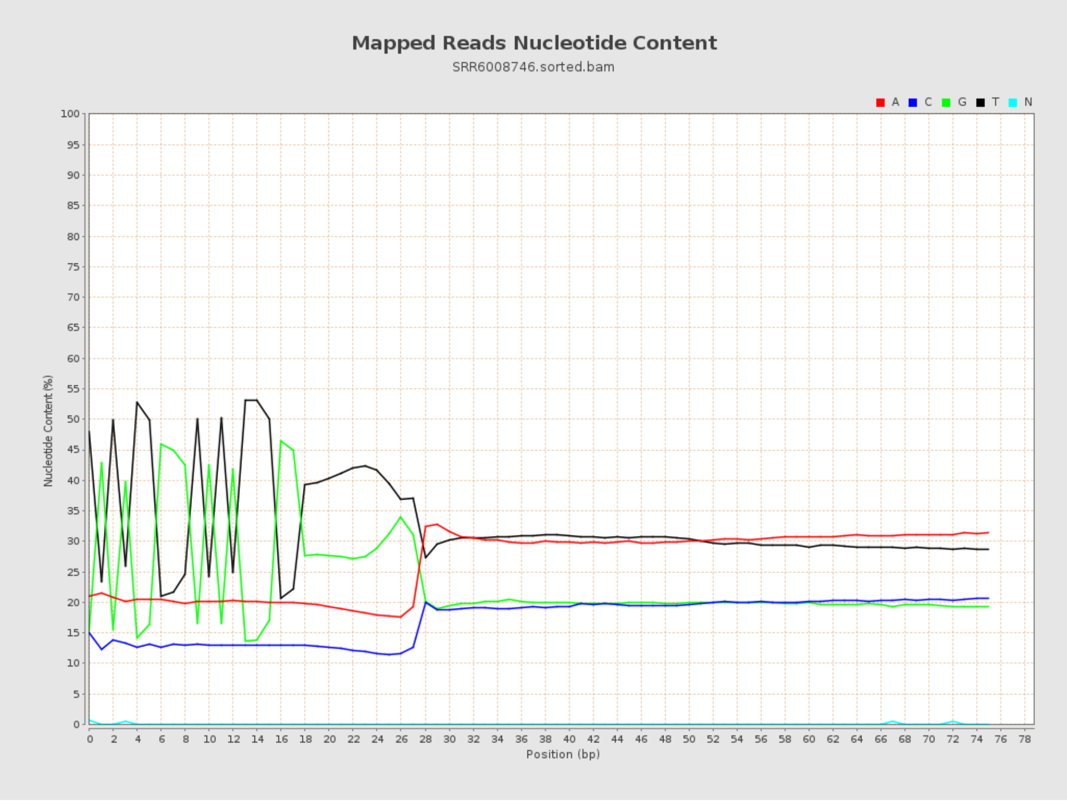
6. Results : Genome Fraction Coverage



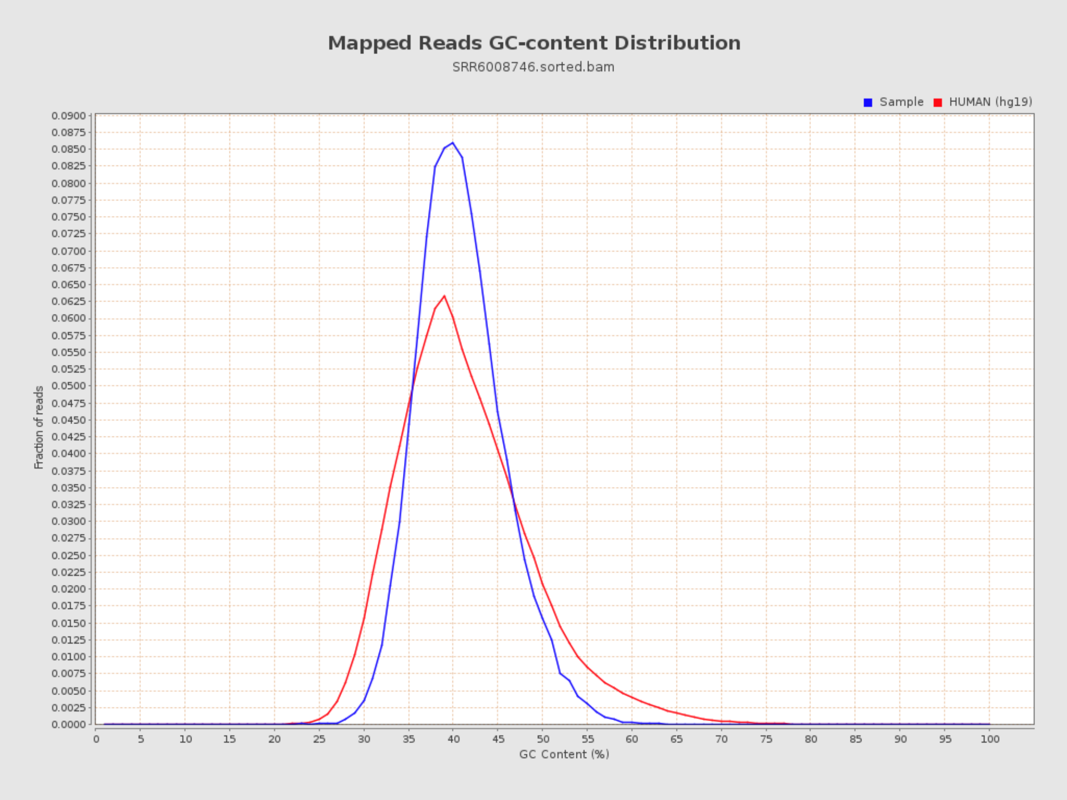
7. Results : Duplication Rate Histogram



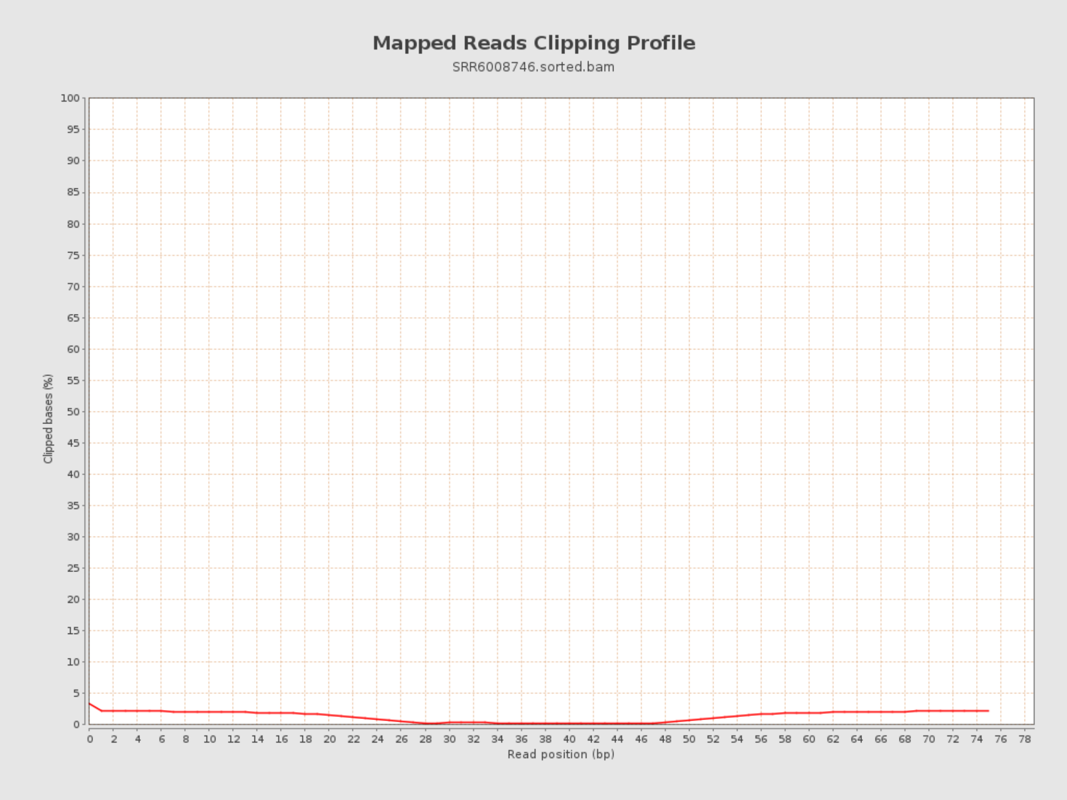
8. Results : Mapped Reads Nucleotide Content



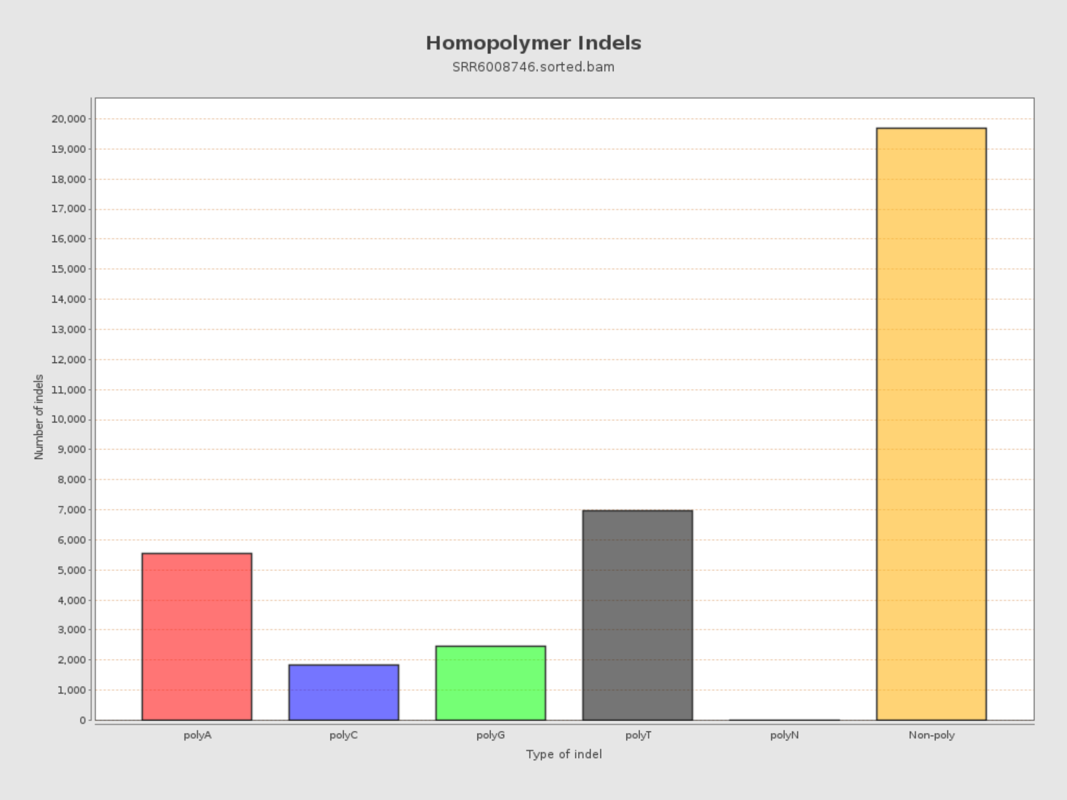
9. Results : Mapped Reads GC-content Distribution



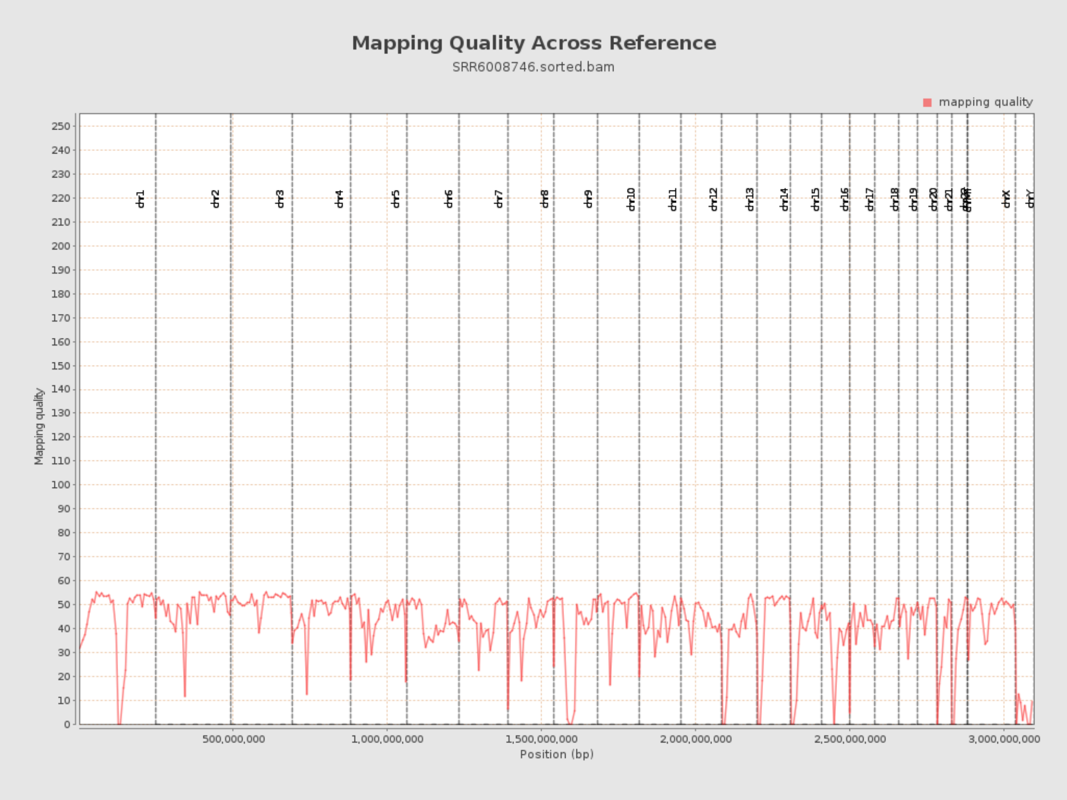
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram