Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:05:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708546.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_SRR1708546 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708546.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:05:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708546.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,114,104
Mapped reads	3,376,532 / 82.07%
Unmapped reads	737,572 / 17.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	106 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	17,750 / 0.43%
Duplication rate	0.52%
Clipped reads	47,385 / 1.15%

2.2. ACGT Content

Number/percentage of A's	52,322,954 / 31.08%
Number/percentage of C's	31,862,624 / 18.93%
Number/percentage of T's	51,944,515 / 30.85%
Number/percentage of G's	32,221,532 / 19.14%
Number/percentage of N's	5,987 / 0%
GC Percentage	38.06%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.2407

2.4. Mapping Quality

Mean Mapping Quality	46.53

2.5. Mismatches and indels

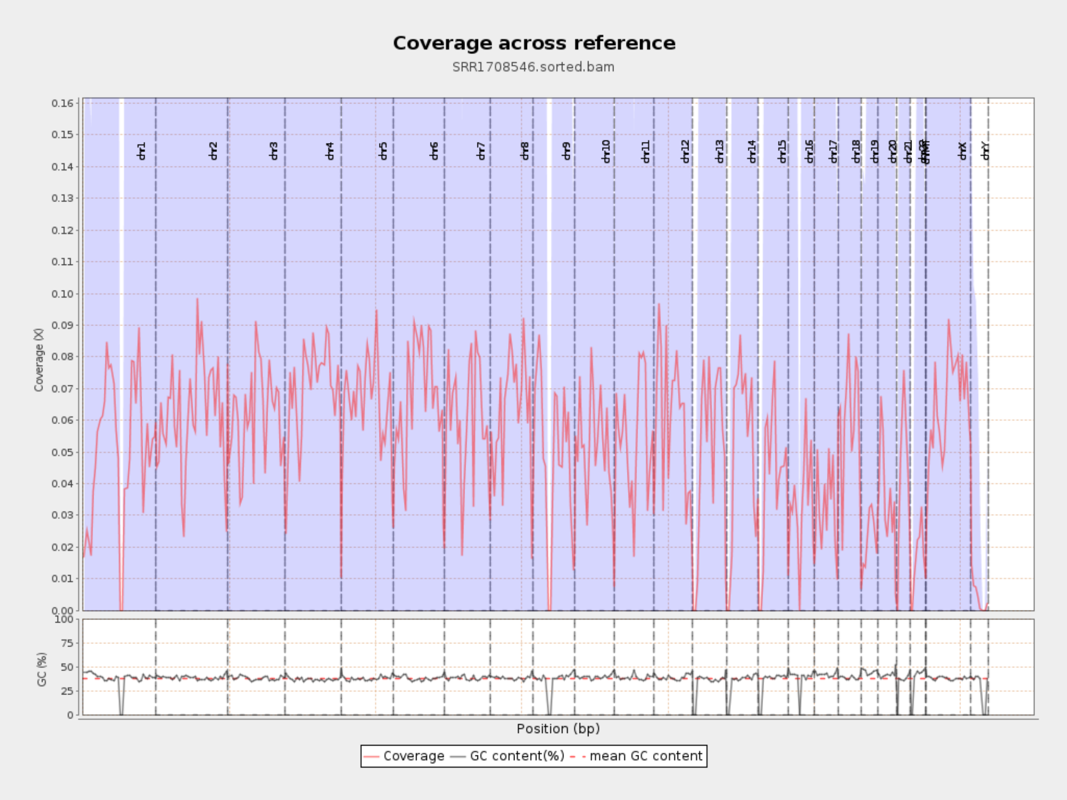
General error rate	0.17%
Mismatches	271,148
Insertions	11,341
Mapped reads with at least one insertion	0.34%
Deletions	9,083
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.25%

2.6. Chromosome stats

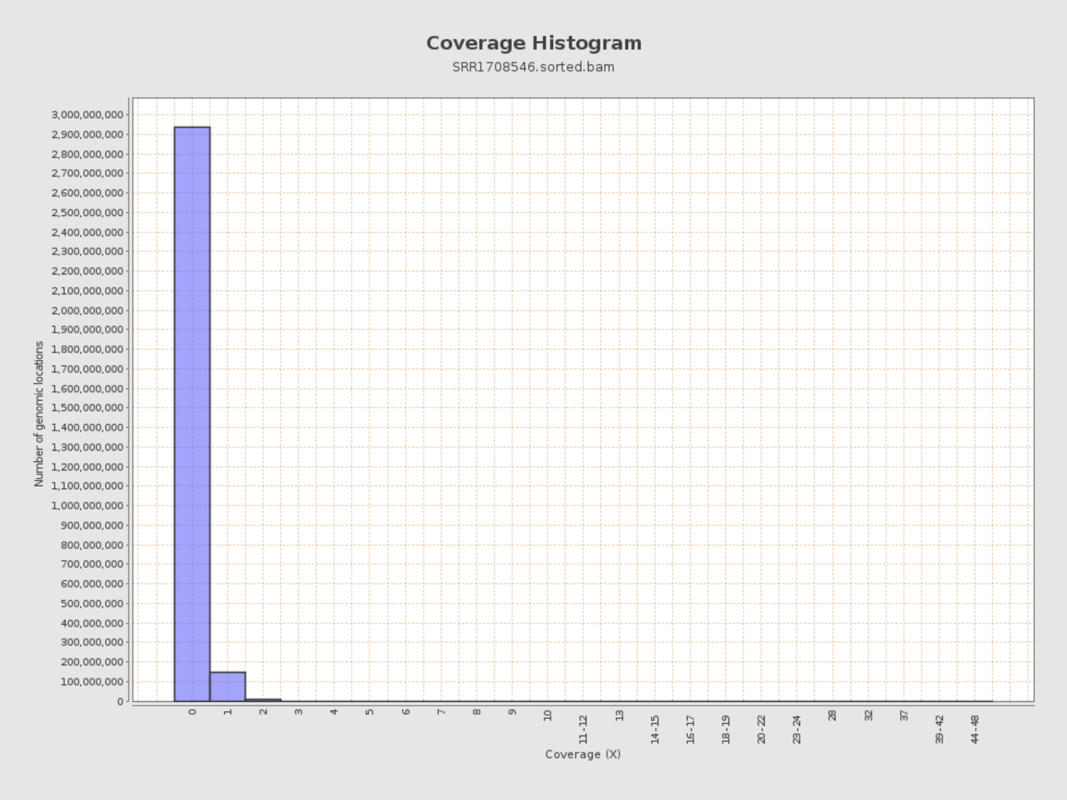
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12594287	0.0505	0.2327
chr2	243199373	15087606	0.062	0.256
chr3	198022430	12209935	0.0617	0.255
chr4	191154276	13428695	0.0703	0.2724
chr5	180915260	11843089	0.0655	0.2628
chr6	171115067	11643075	0.068	0.2687
chr7	159138663	9485264	0.0596	0.252

chr8	146364022	9394774	0.0642	0.2609
chr9	141213431	7040957	0.0499	0.231
chr10	135534747	7199566	0.0531	0.2369
chr11	135006516	7297891	0.0541	0.2403
chr12	133851895	8086455	0.0604	0.2534
chr13	115169878	5835724	0.0507	0.232
chr14	107349540	5539173	0.0516	0.2352
chr15	102531392	4257127	0.0415	0.2103
chr16	90354753	2993459	0.0331	0.1875
chr17	81195210	2676582	0.033	0.1871
chr18	78077248	4760932	0.061	0.2537
chr19	59128983	1359348	0.023	0.1551
chr20	63025520	2343046	0.0372	0.1986
chr21	48129895	2037885	0.0423	0.2135
chr22	51304566	840622	0.0164	0.131
chrMT	16571	250	0.0151	0.1219
chrX	155270560	10169035	0.0655	0.2637
chrY	59373566	248294	0.0042	0.0673

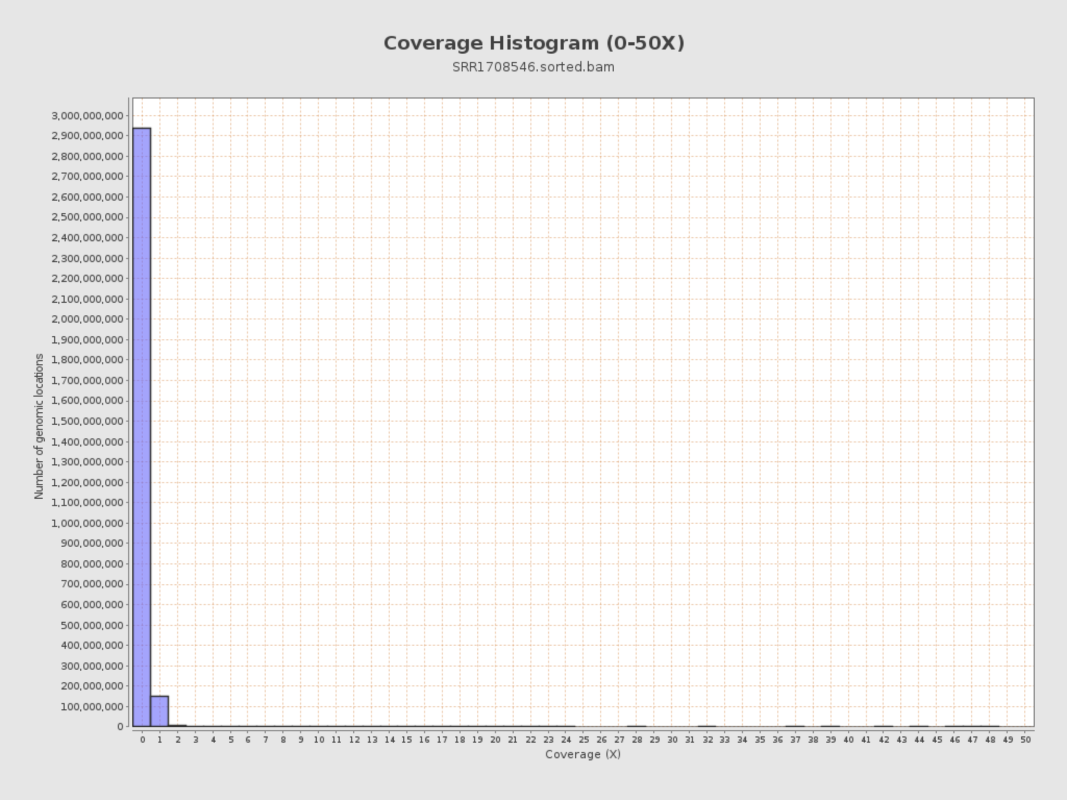
3. Results : Coverage across reference



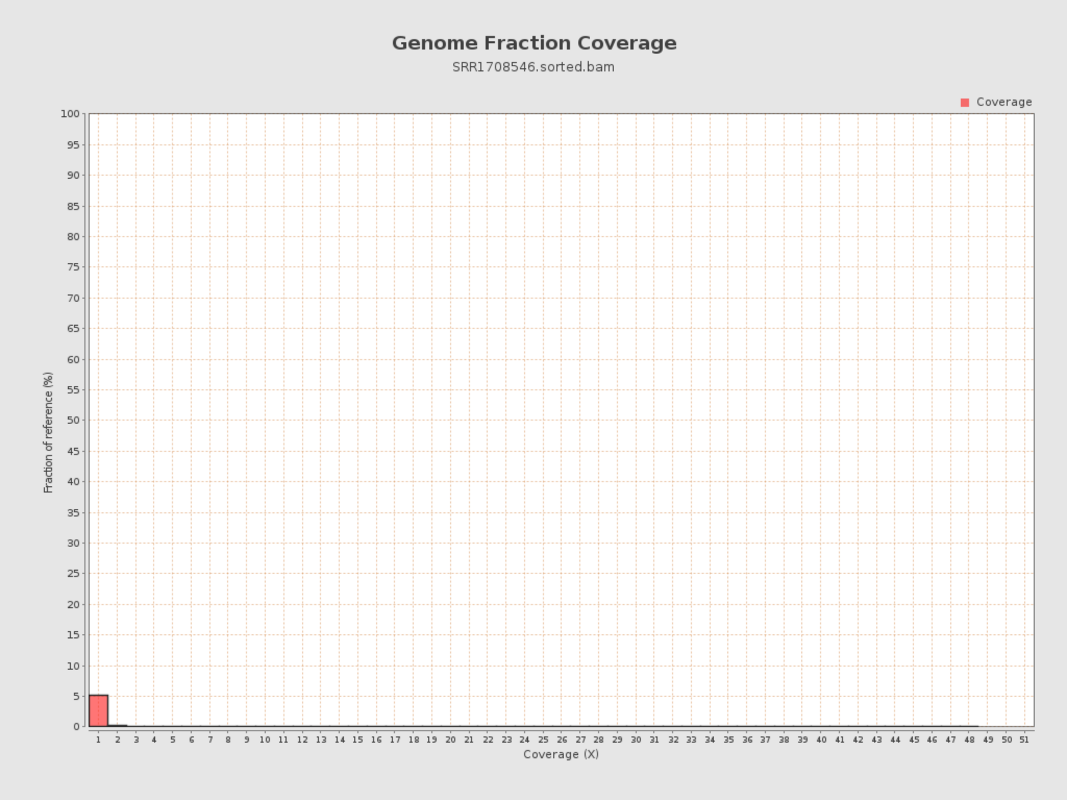
4. Results : Coverage Histogram



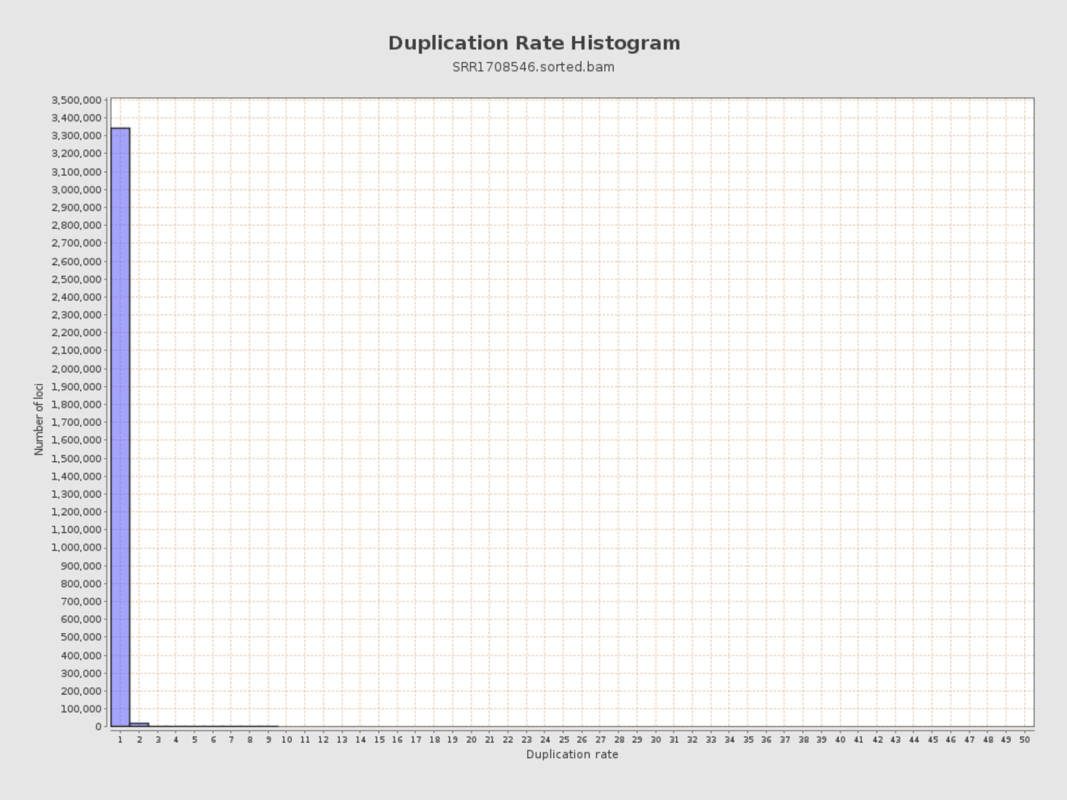
5. Results : Coverage Histogram (0-50X)



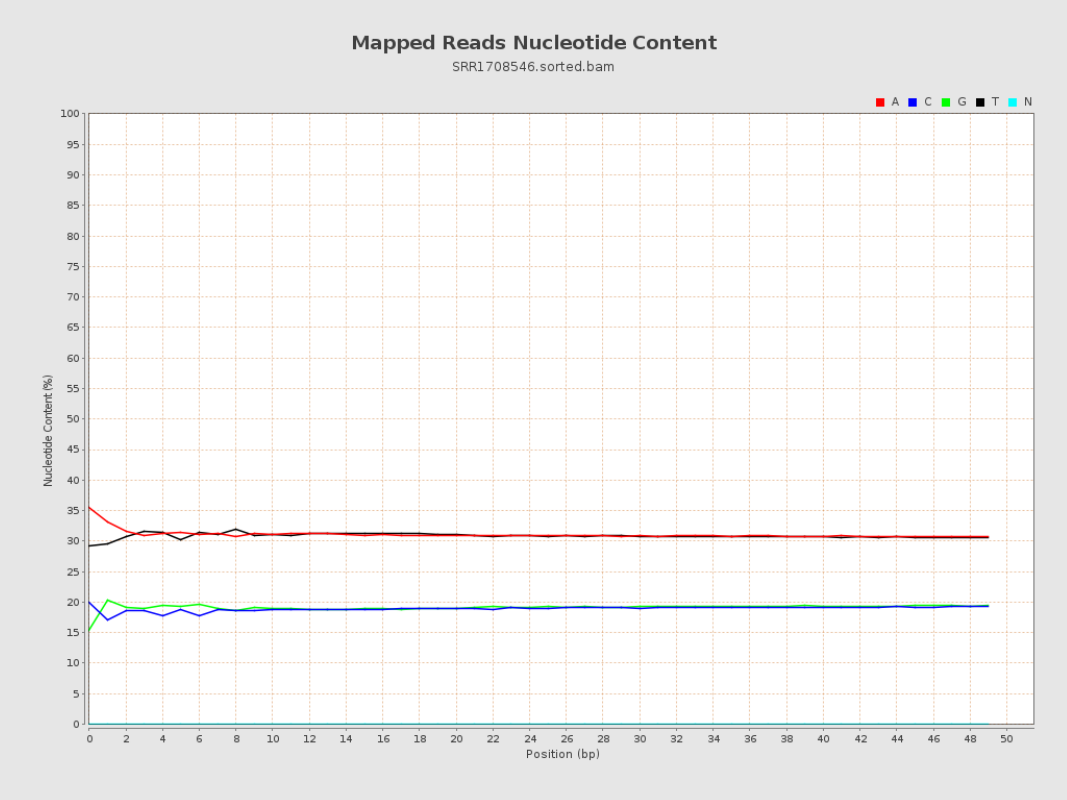
6. Results : Genome Fraction Coverage



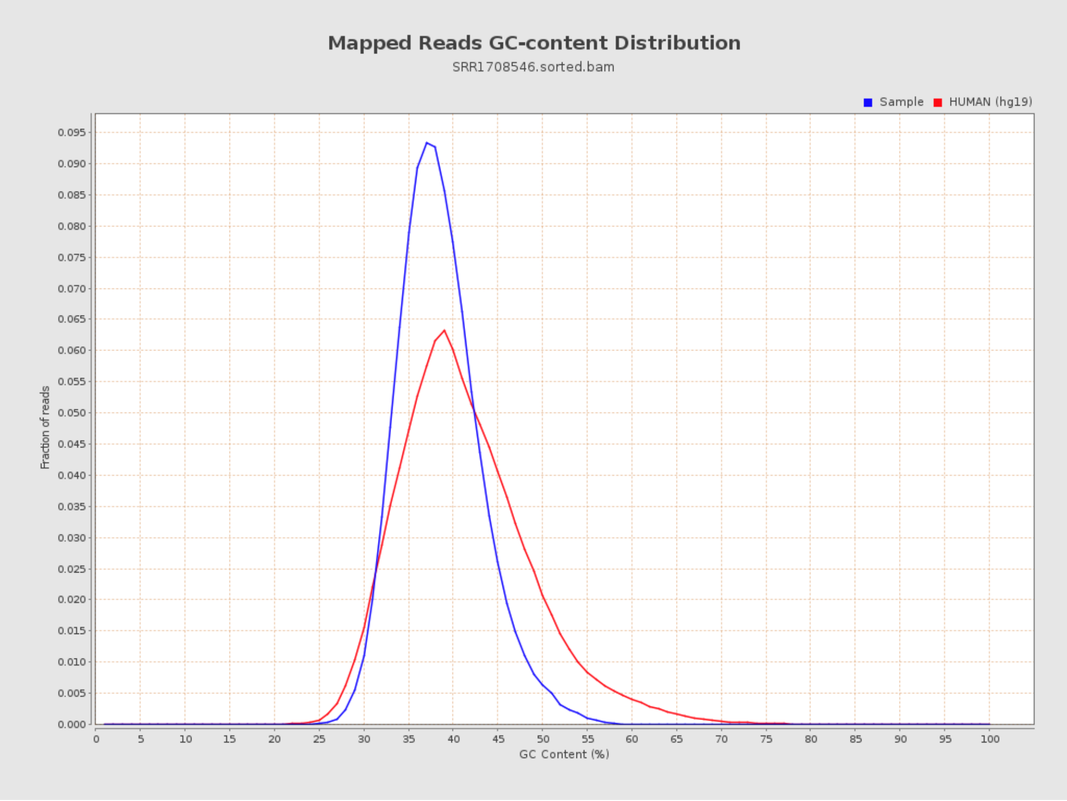
7. Results : Duplication Rate Histogram



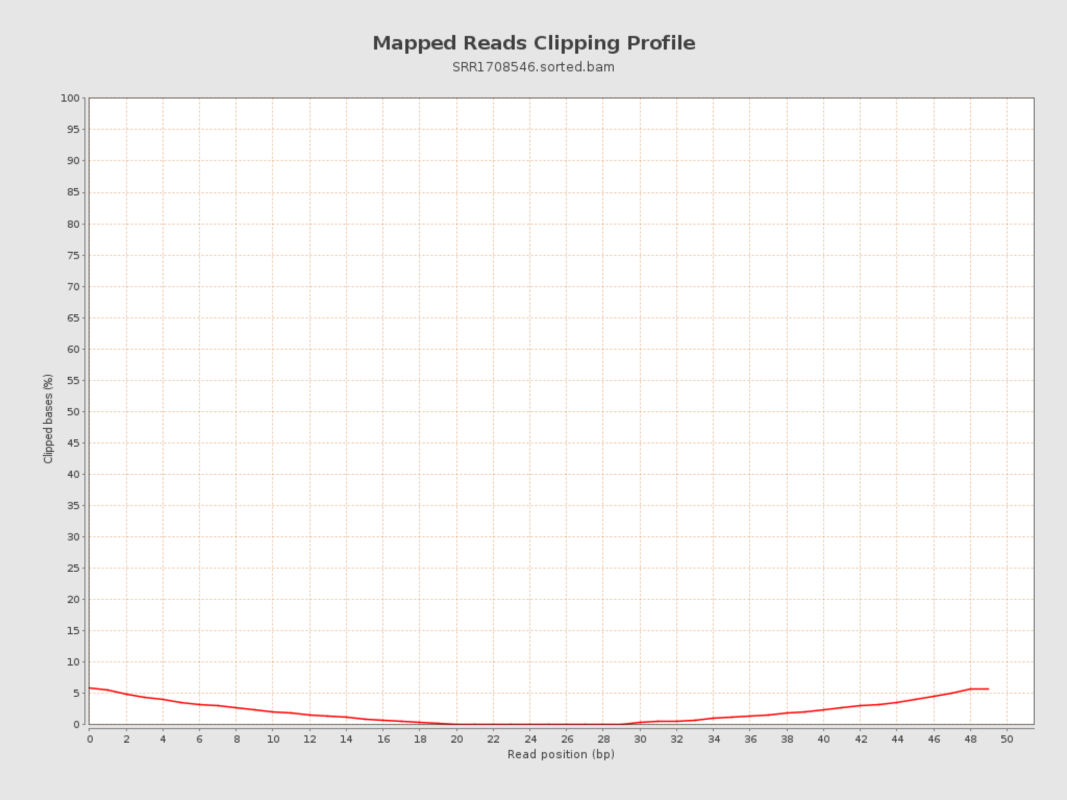
8. Results : Mapped Reads Nucleotide Content



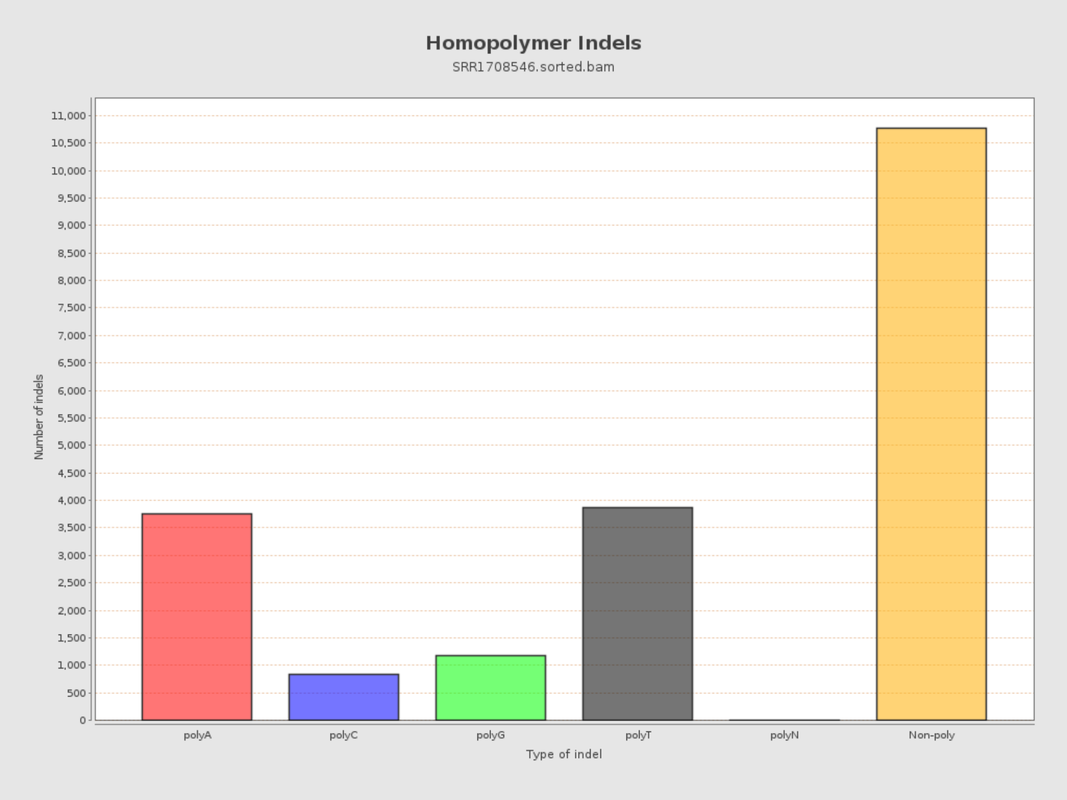
9. Results : Mapped Reads GC-content Distribution



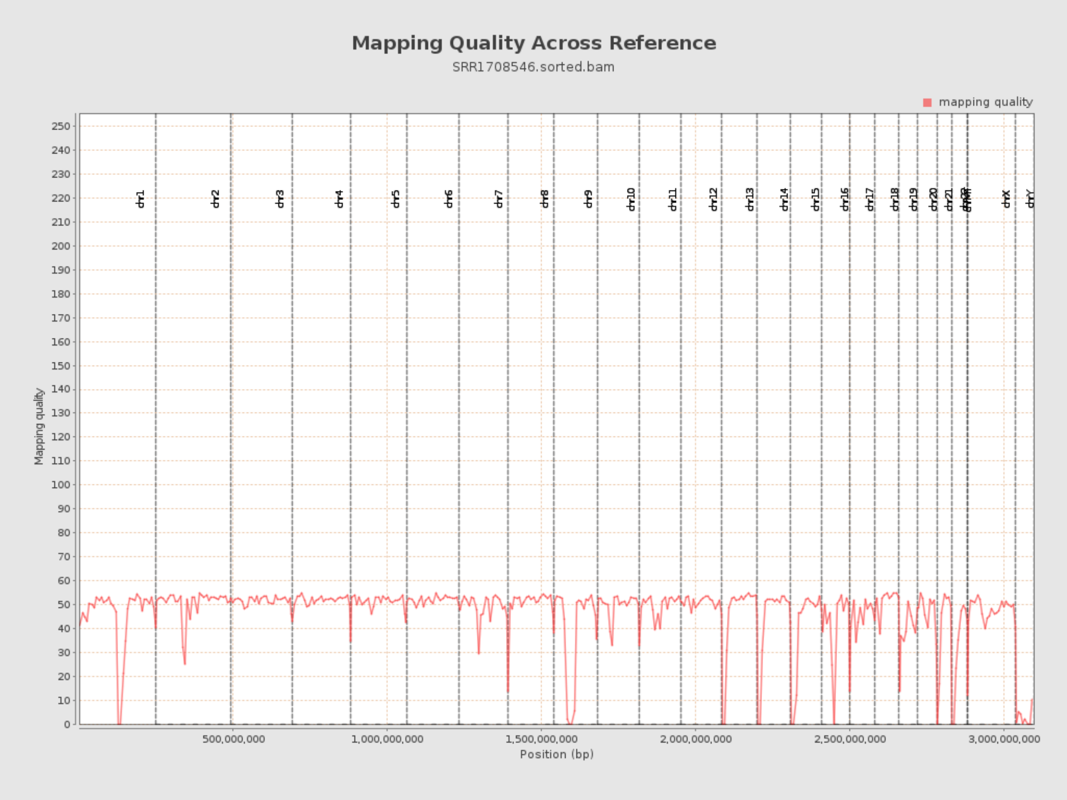
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram