Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:56:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708532.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_SRR1708532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708532.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:56:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,243,614
Mapped reads	2,058,043 / 91.73%
Unmapped reads	185,571 / 8.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	103 / 0%
Read min/max/mean length	30 / 51 / 51
Duplicated reads (estimated)	62,770 / 2.8%
Duplication rate	2.3%
Clipped reads	104,409 / 4.65%

2.2. ACGT Content

Number/percentage of A's	30,921,091 / 29.72%
Number/percentage of C's	20,895,249 / 20.09%
Number/percentage of T's	31,348,156 / 30.14%
Number/percentage of G's	20,859,174 / 20.05%
Number/percentage of N's	1,514 / 0%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0336

Standard Deviation	0.3172

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

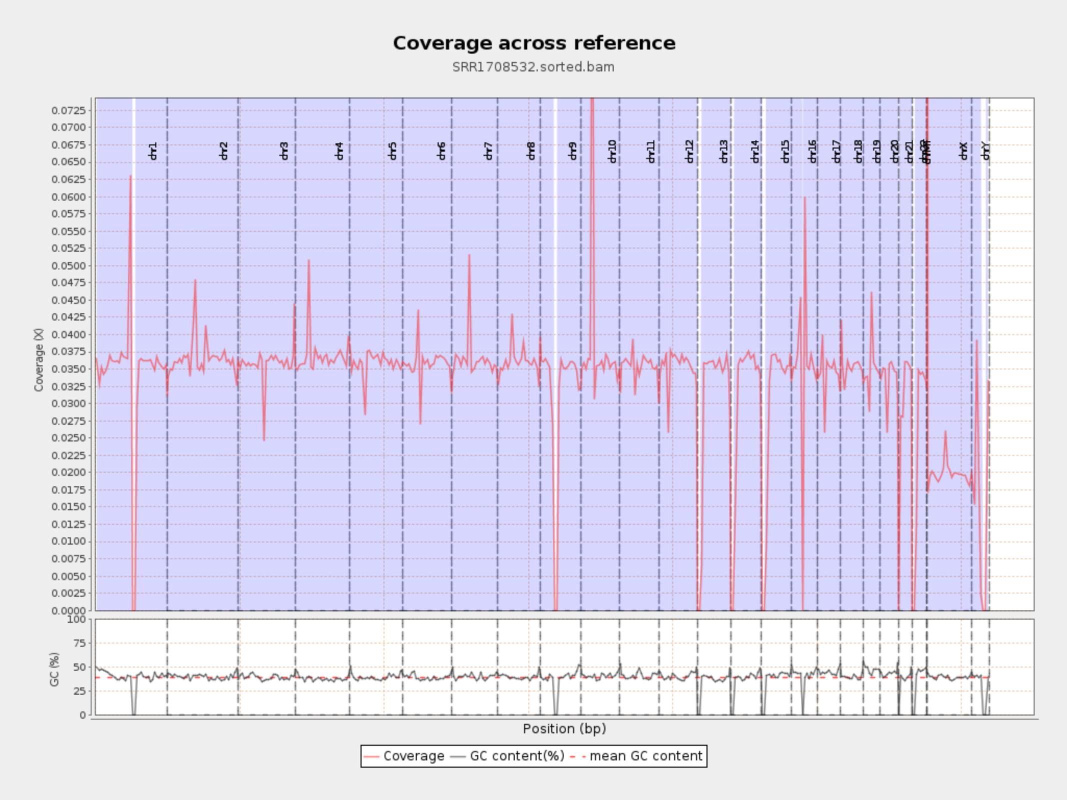
General error rate	0.47%
Mismatches	480,649
Insertions	4,860
Mapped reads with at least one insertion	0.24%
Deletions	6,586
Mapped reads with at least one deletion	0.32%
Homopolymer indels	43.47%

2.6. Chromosome stats

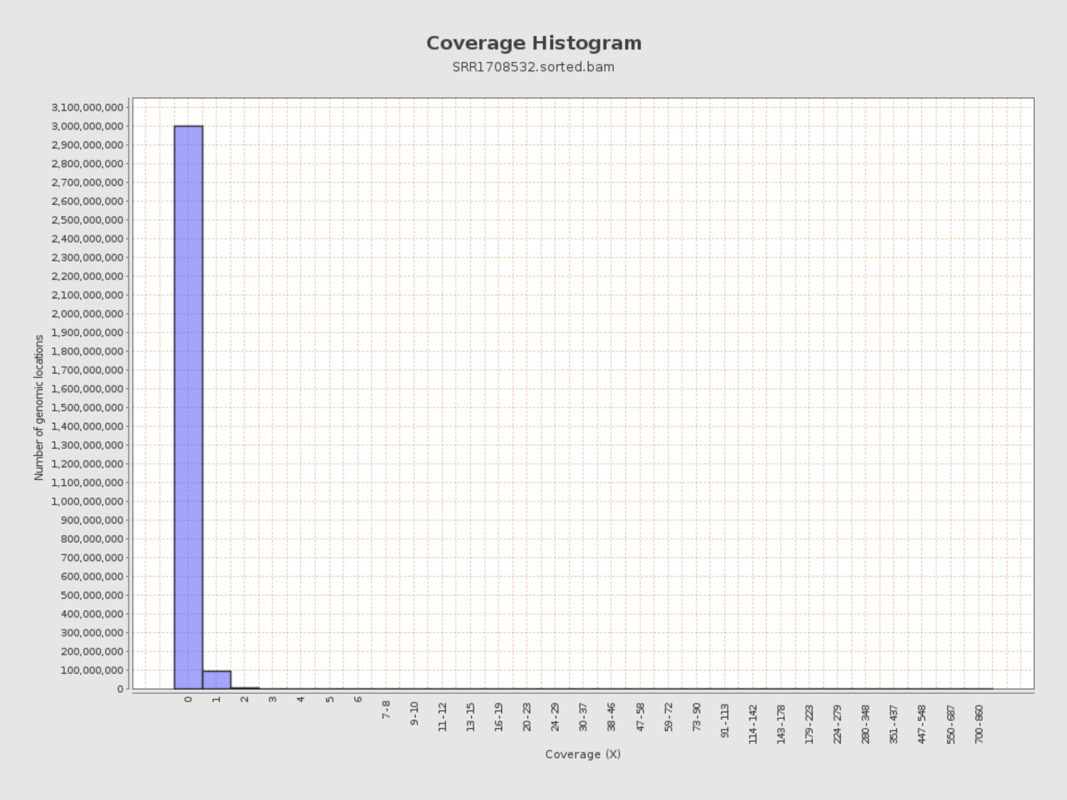
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8551517	0.0343	0.6534
chr2	243199373	8912110	0.0366	0.2499
chr3	198022430	7060742	0.0357	0.2055
chr4	191154276	7072598	0.037	0.2229
chr5	180915260	6486374	0.0359	0.1969
chr6	171115067	6130347	0.0358	0.2152
chr7	159138663	5819595	0.0366	0.3095

chr8	146364022	5283447	0.0361	0.3458
chr9	141213431	4376778	0.031	0.2
chr10	135534747	5343799	0.0394	0.5806
chr11	135006516	4806781	0.0356	0.2311
chr12	133851895	4744469	0.0354	0.1962
chr13	115169878	3424636	0.0297	0.1772
chr14	107349540	3208785	0.0299	0.181
chr15	102531392	2946896	0.0287	0.1741
chr16	90354753	3189424	0.0353	0.2929
chr17	81195210	2793484	0.0344	0.2124
chr18	78077248	2772847	0.0355	0.3021
chr19	59128983	2088858	0.0353	0.4996
chr20	63025520	2125970	0.0337	0.1932
chr21	48129895	1437168	0.0299	0.2204
chr22	51304566	1217666	0.0237	0.1884
chrMT	16571	214896	12.9682	4.9823
chrX	155270560	3084702	0.0199	0.1594
chrY	59373566	942353	0.0159	0.2407

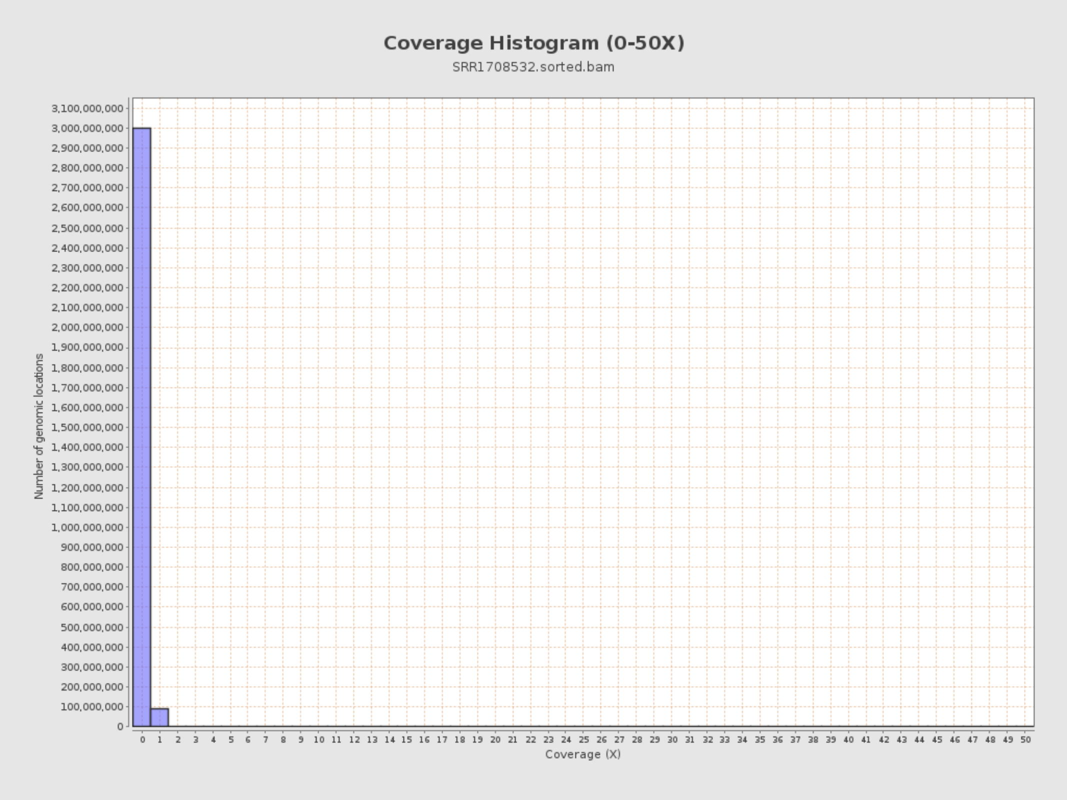
3. Results : Coverage across reference



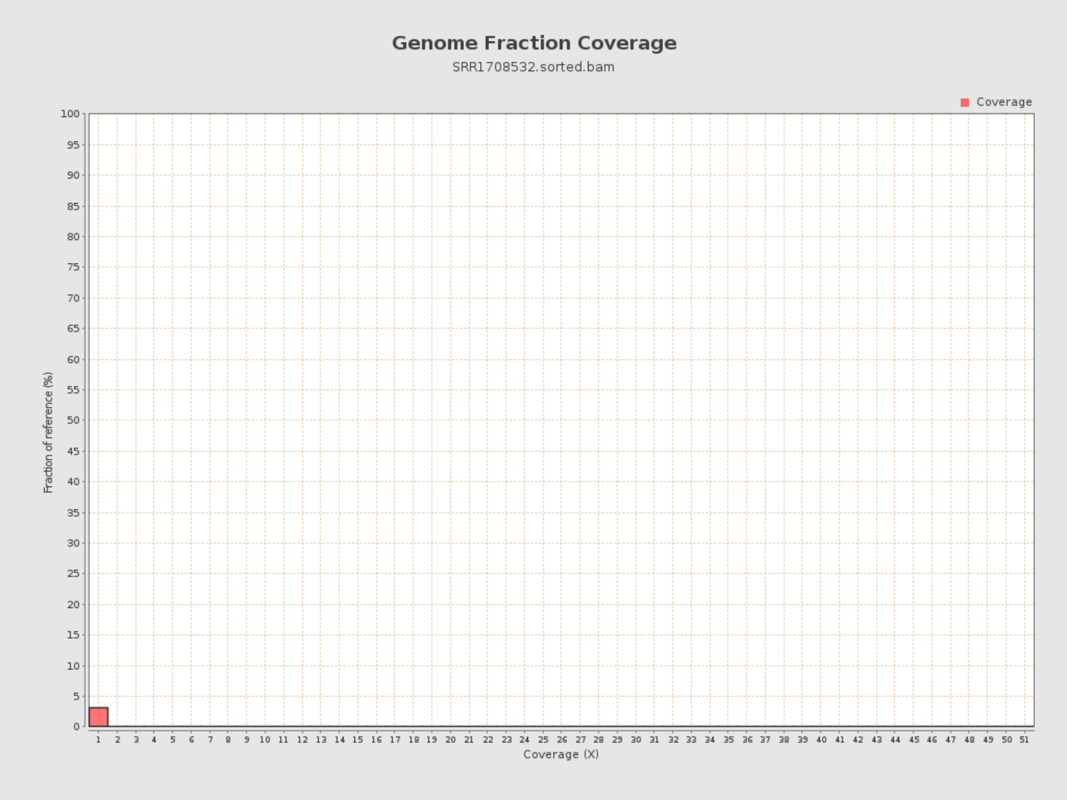
4. Results : Coverage Histogram



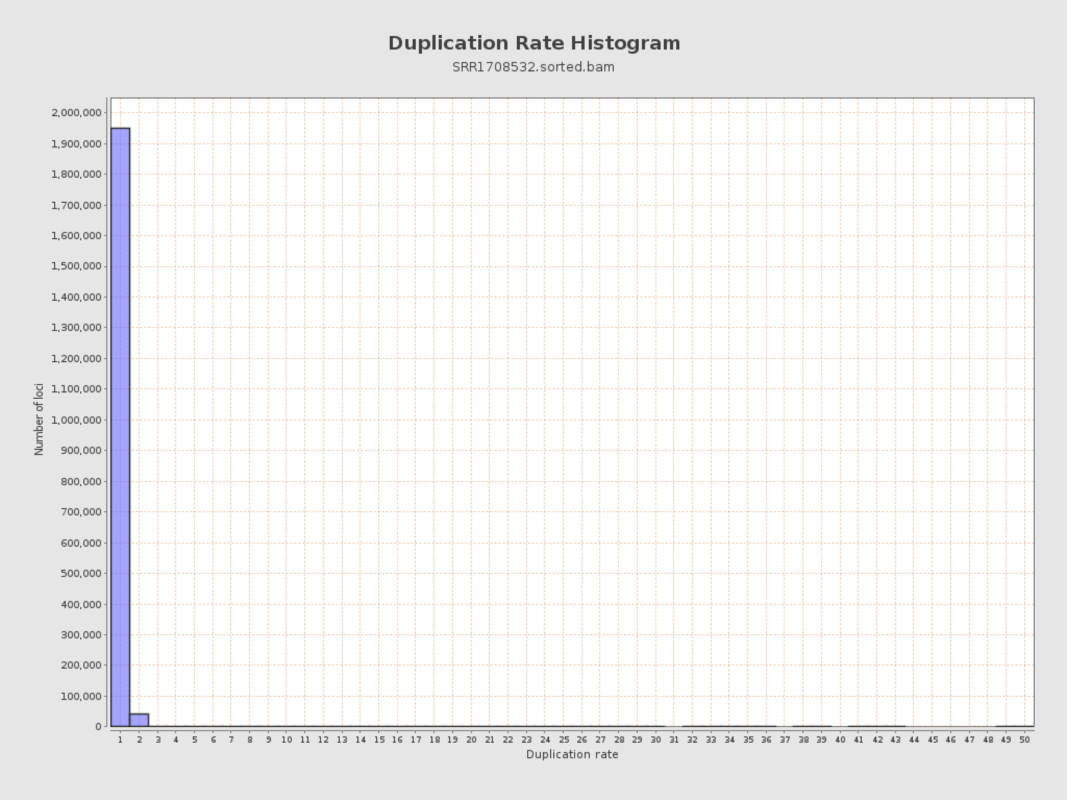
5. Results : Coverage Histogram (0-50X)



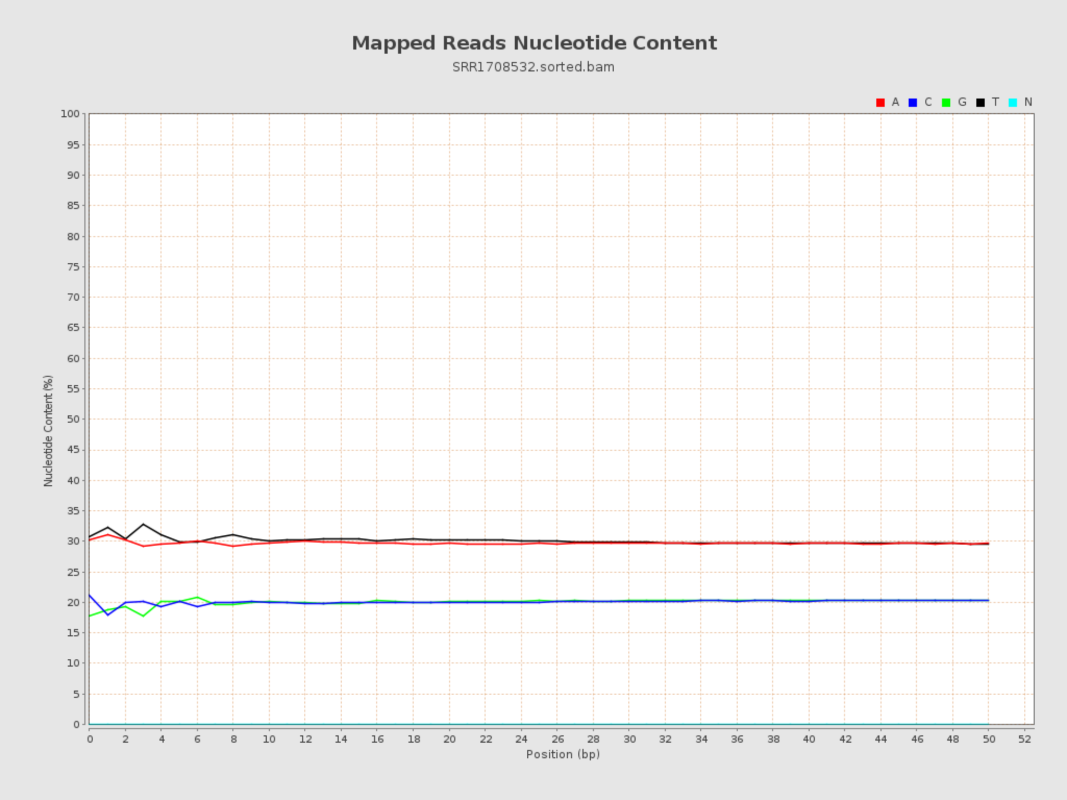
6. Results : Genome Fraction Coverage



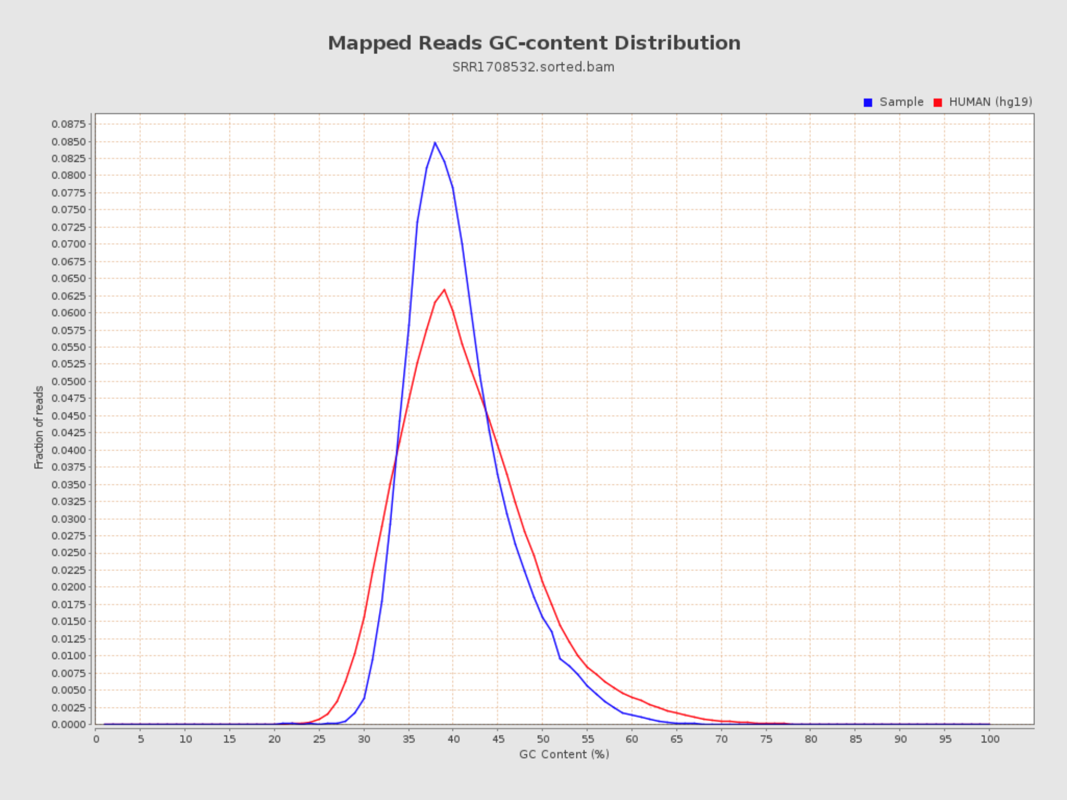
7. Results : Duplication Rate Histogram



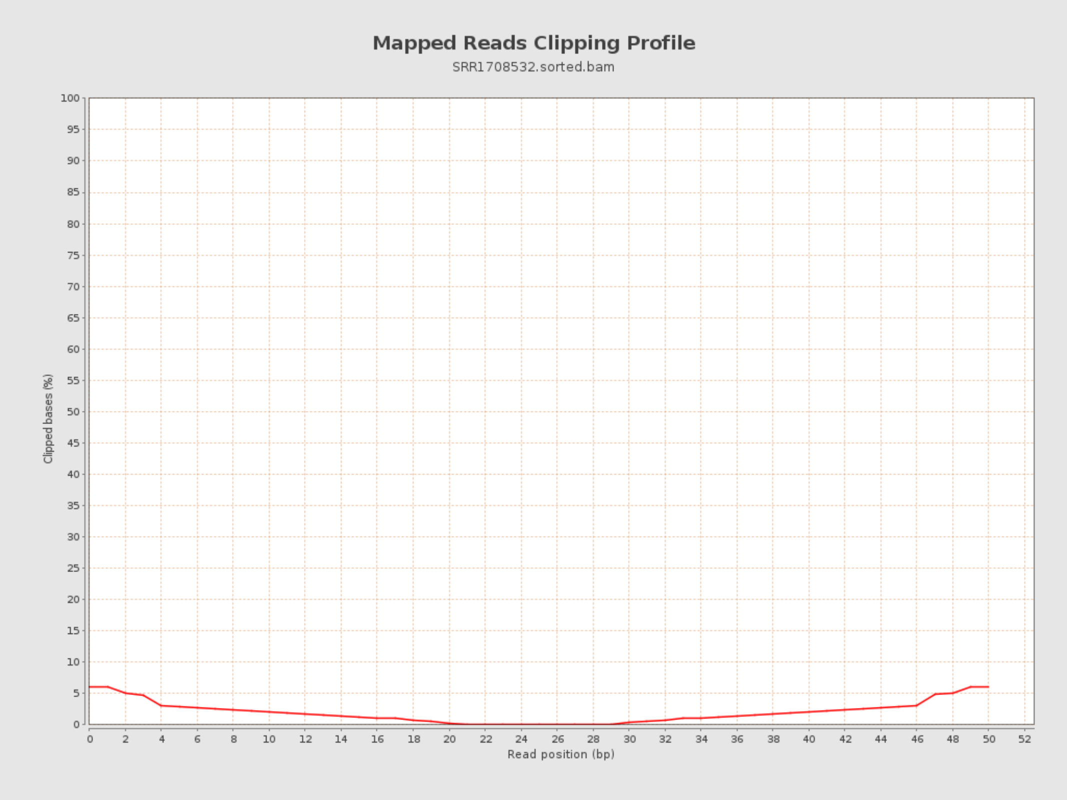
8. Results : Mapped Reads Nucleotide Content



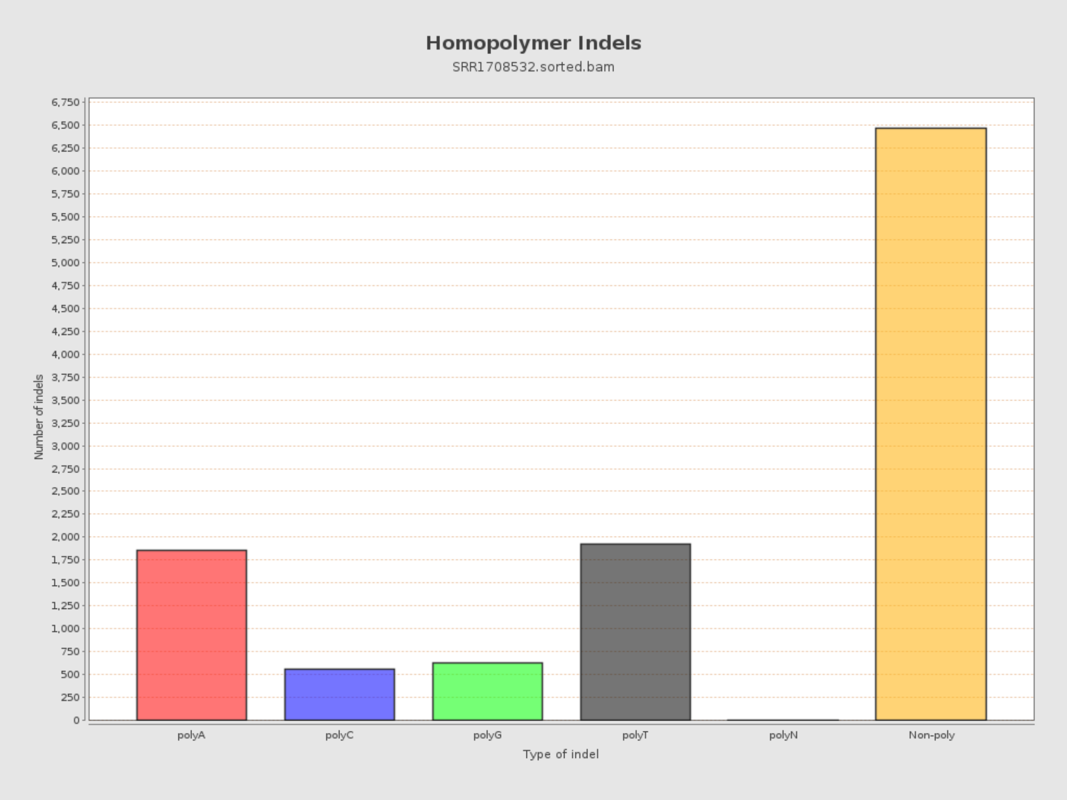
9. Results : Mapped Reads GC-content Distribution



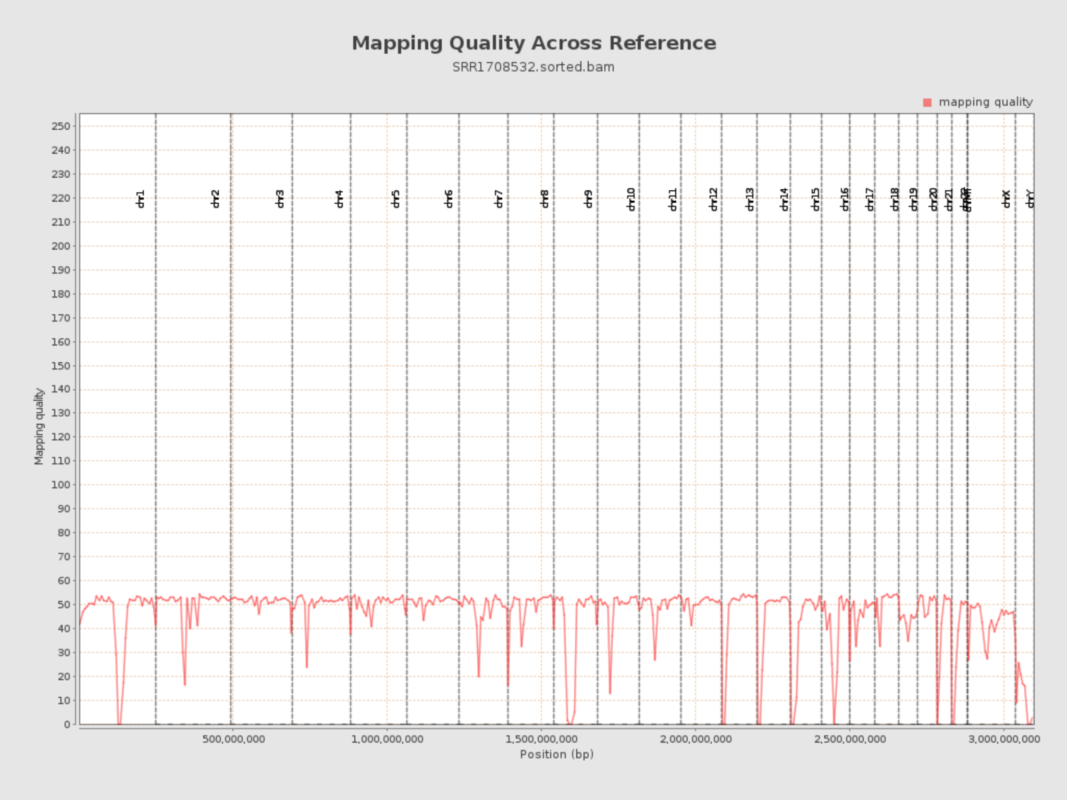
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram