Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:11:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708599.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_SRR1708599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708599.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:11:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,285,480
Mapped reads	5,166,487 / 97.75%
Unmapped reads	118,993 / 2.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	147 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	50,016 / 0.95%
Duplication rate	0.97%
Clipped reads	67,183 / 1.27%

2.2. ACGT Content

Number/percentage of A's	79,830,827 / 30.98%
Number/percentage of C's	48,863,387 / 18.96%
Number/percentage of T's	79,431,396 / 30.82%
Number/percentage of G's	49,562,417 / 19.23%
Number/percentage of N's	5,750 / 0%
GC Percentage	38.19%

2.3. Coverage

Mean	0.0832

Standard Deviation	0.3011

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

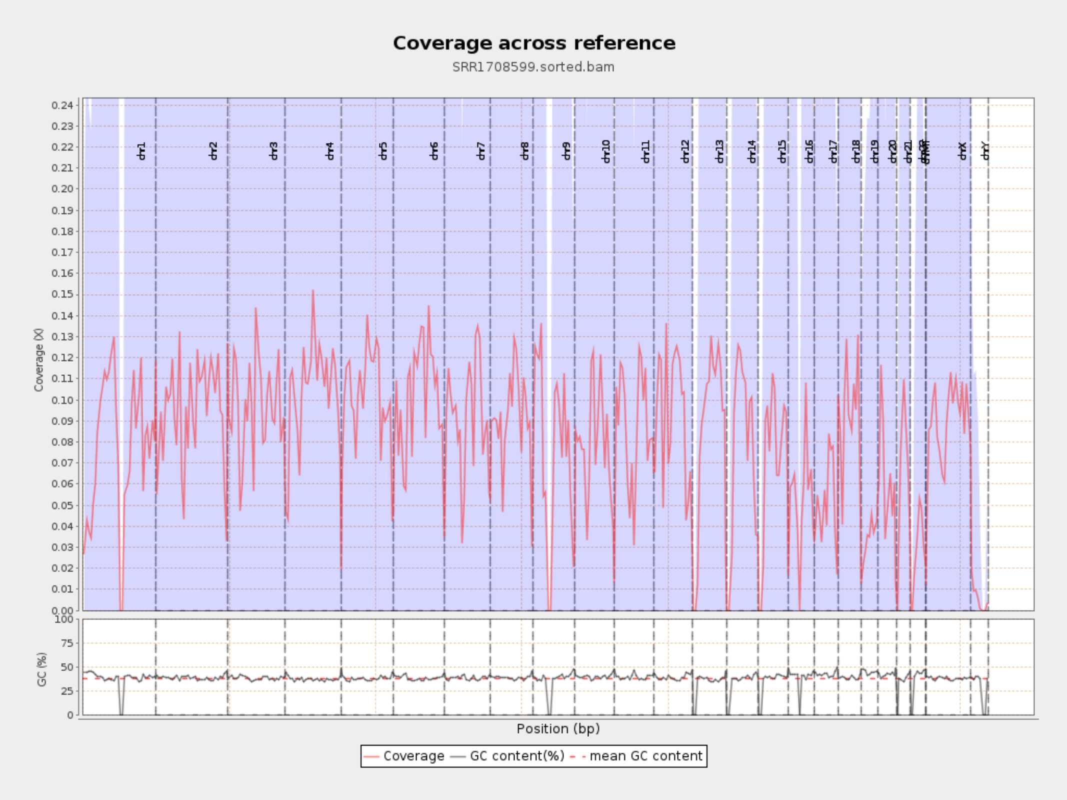
General error rate	0.15%
Mismatches	375,875
Insertions	16,208
Mapped reads with at least one insertion	0.31%
Deletions	13,103
Mapped reads with at least one deletion	0.25%
Homopolymer indels	48.88%

2.6. Chromosome stats

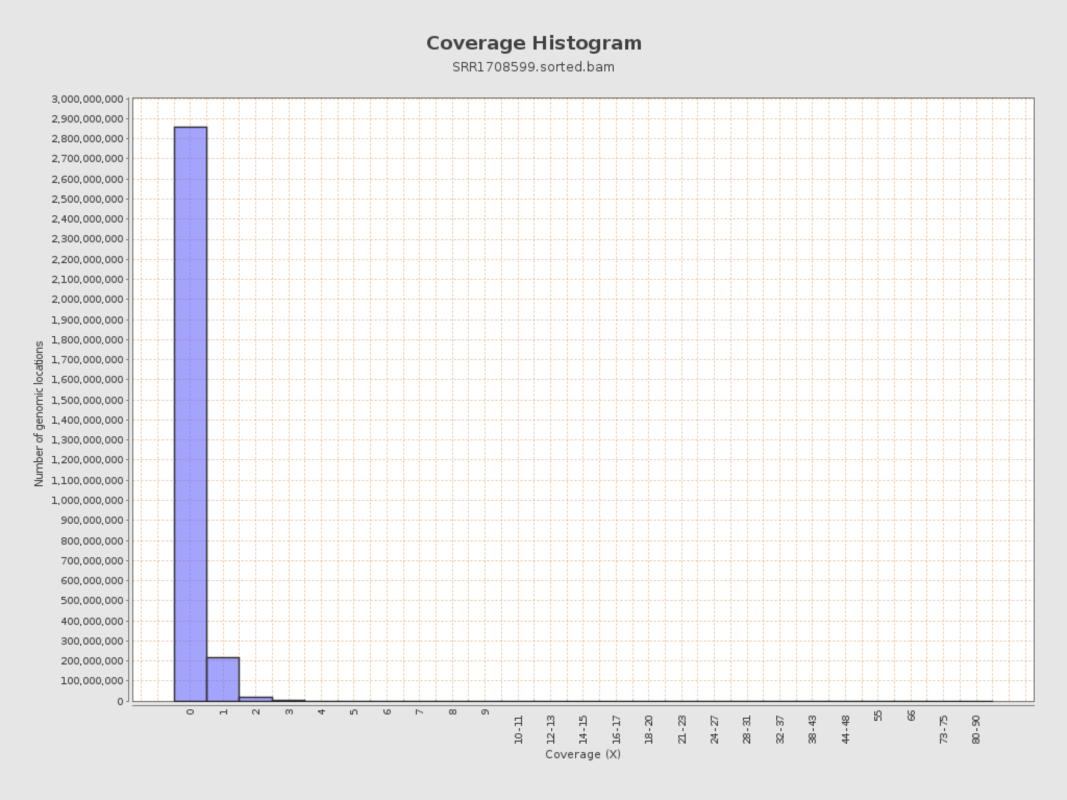
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19297540	0.0774	0.2923
chr2	243199373	22955342	0.0944	0.3191
chr3	198022430	19254810	0.0972	0.3238
chr4	191154276	20055385	0.1049	0.3359
chr5	180915260	18222017	0.1007	0.329
chr6	171115067	17564074	0.1026	0.3331
chr7	159138663	14440285	0.0907	0.3141

chr8	146364022	13424624	0.0917	0.3142
chr9	141213431	10890256	0.0771	0.2907
chr10	135534747	10876290	0.0802	0.2937
chr11	135006516	11667689	0.0864	0.3078
chr12	133851895	12342959	0.0922	0.3166
chr13	115169878	9938995	0.0863	0.3066
chr14	107349540	8345965	0.0777	0.2921
chr15	102531392	7185747	0.0701	0.277
chr16	90354753	4732094	0.0524	0.2375
chr17	81195210	4272303	0.0526	0.2395
chr18	78077248	7369263	0.0944	0.3197
chr19	59128983	2060107	0.0348	0.1925
chr20	63025520	3938970	0.0625	0.2603
chr21	48129895	3038573	0.0631	0.2633
chr22	51304566	1482584	0.0289	0.1766
chrMT	16571	200	0.0121	0.1092
chrX	155270560	14031585	0.0904	0.312
chrY	59373566	328780	0.0055	0.0781

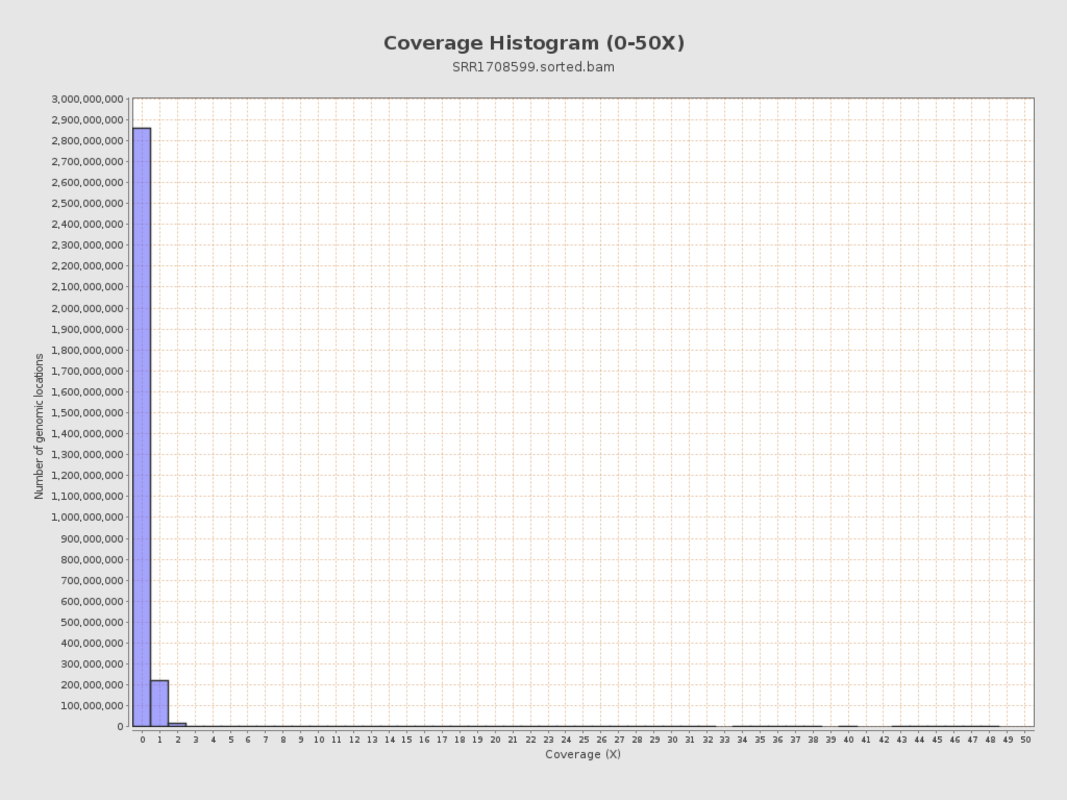
3. Results : Coverage across reference



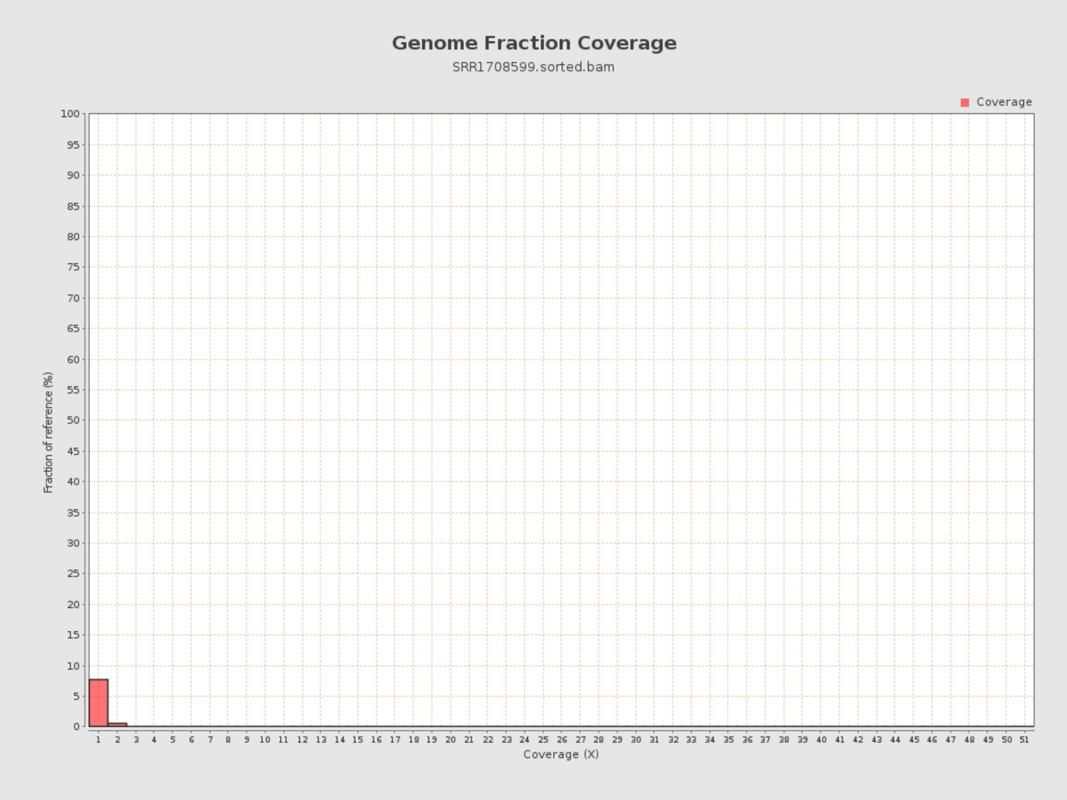
4. Results : Coverage Histogram



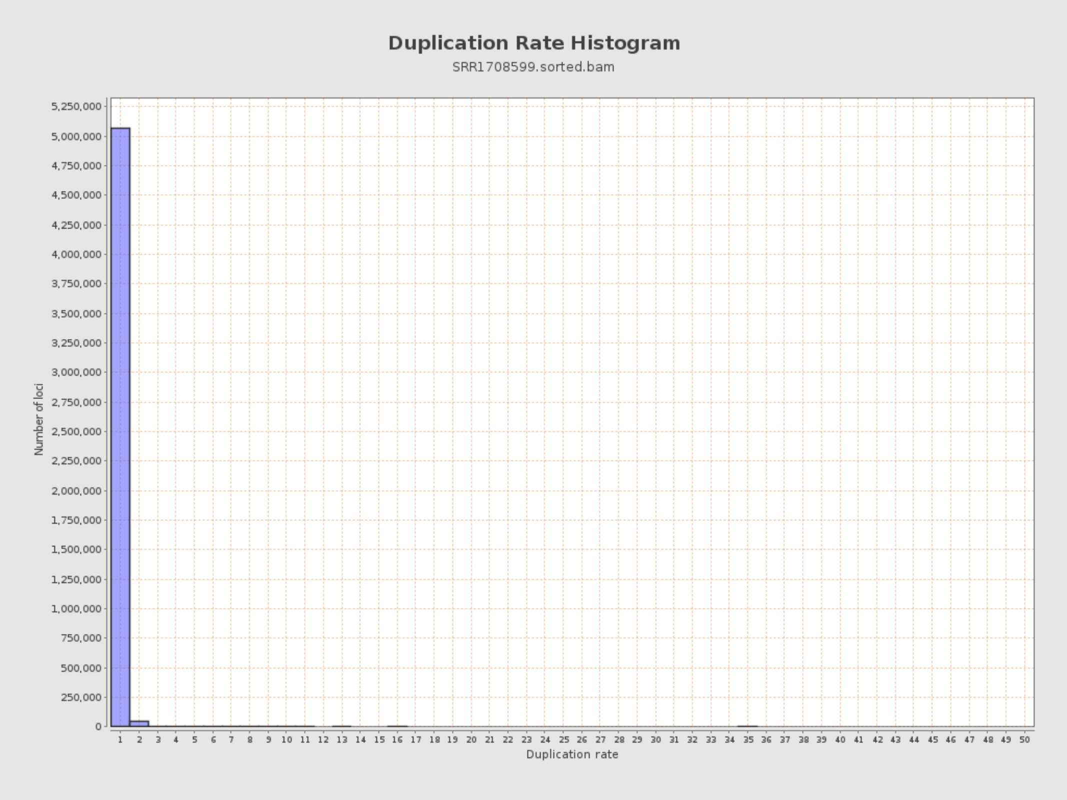
5. Results : Coverage Histogram (0-50X)



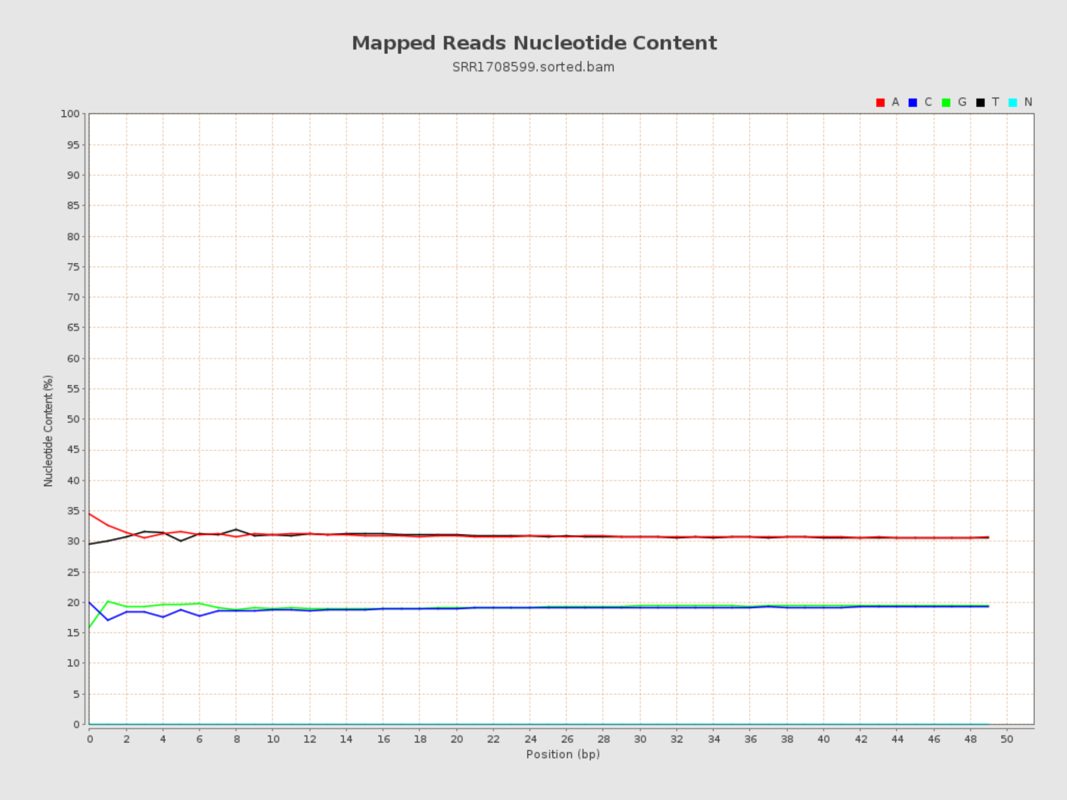
6. Results : Genome Fraction Coverage



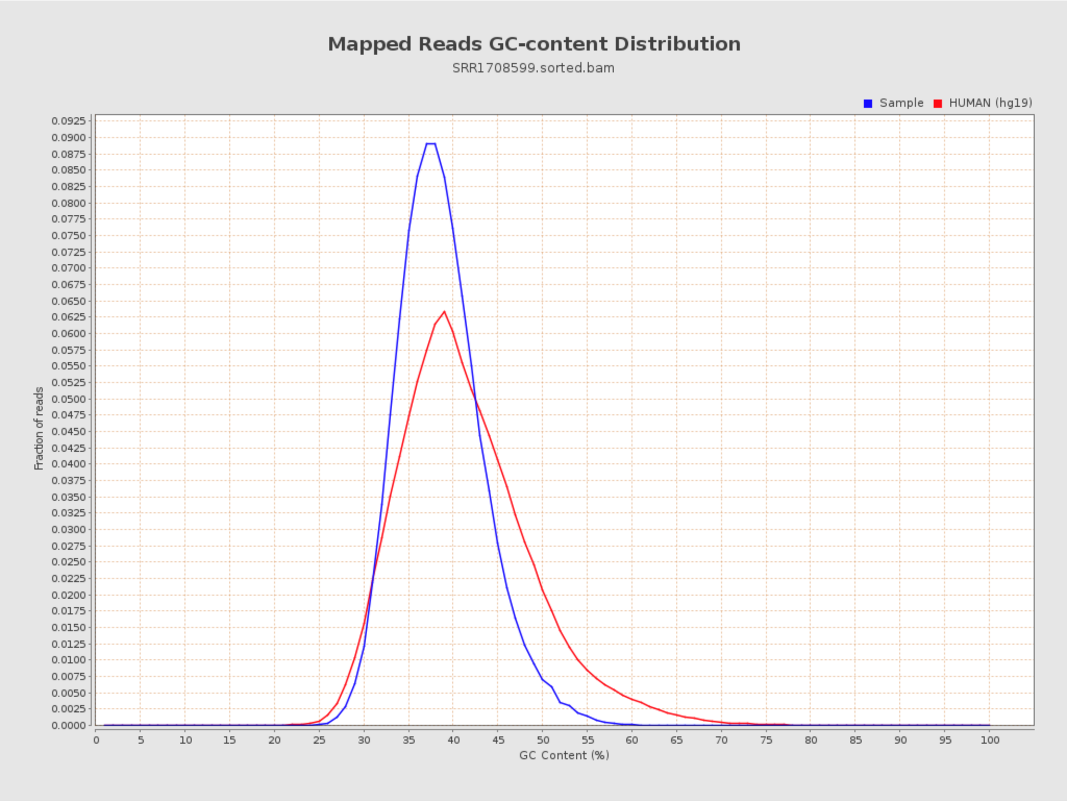
7. Results : Duplication Rate Histogram



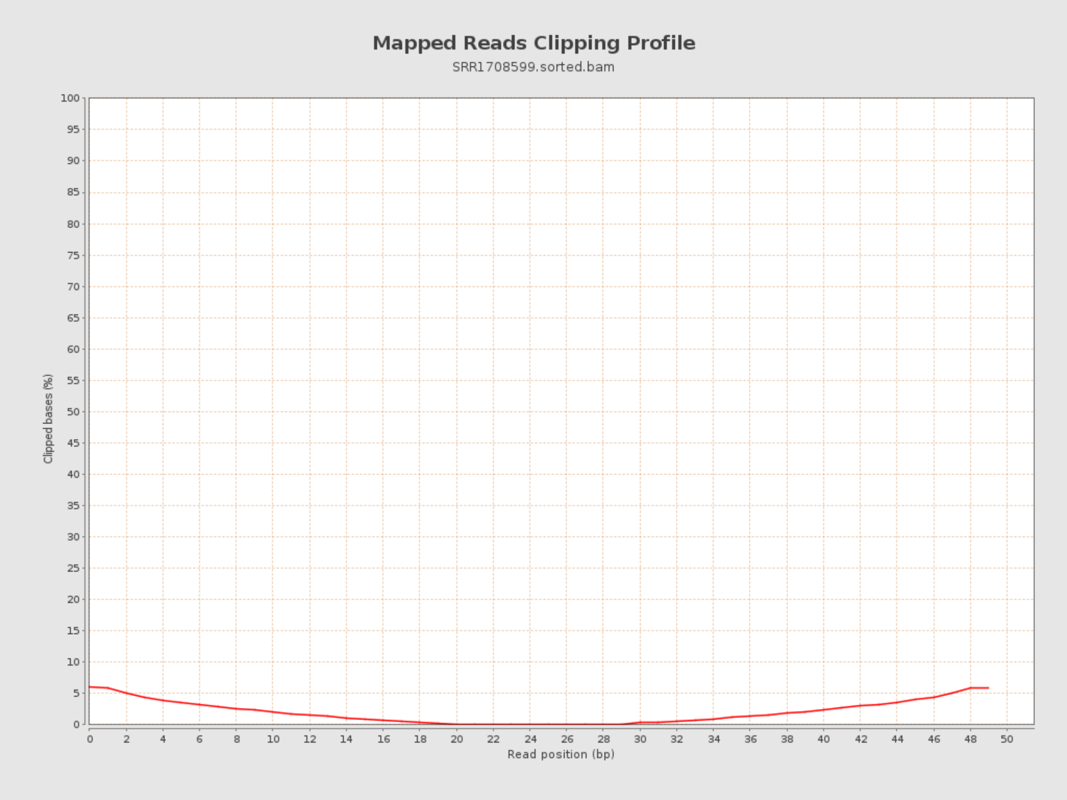
8. Results : Mapped Reads Nucleotide Content



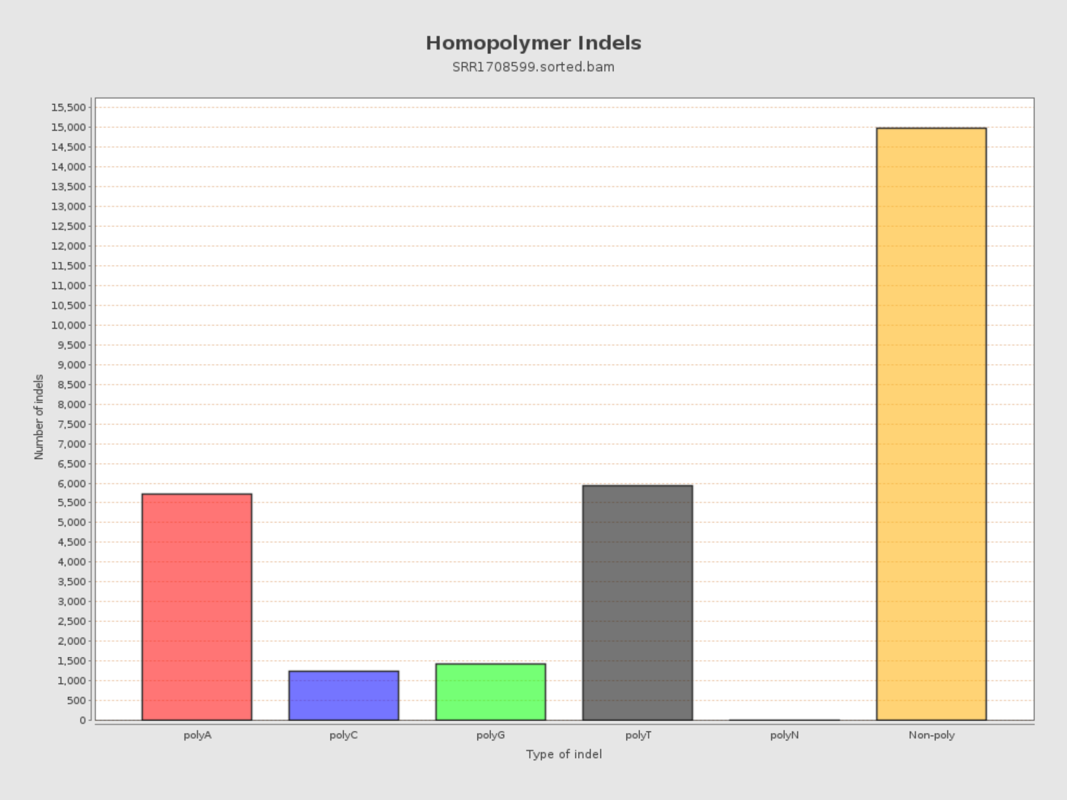
9. Results : Mapped Reads GC-content Distribution



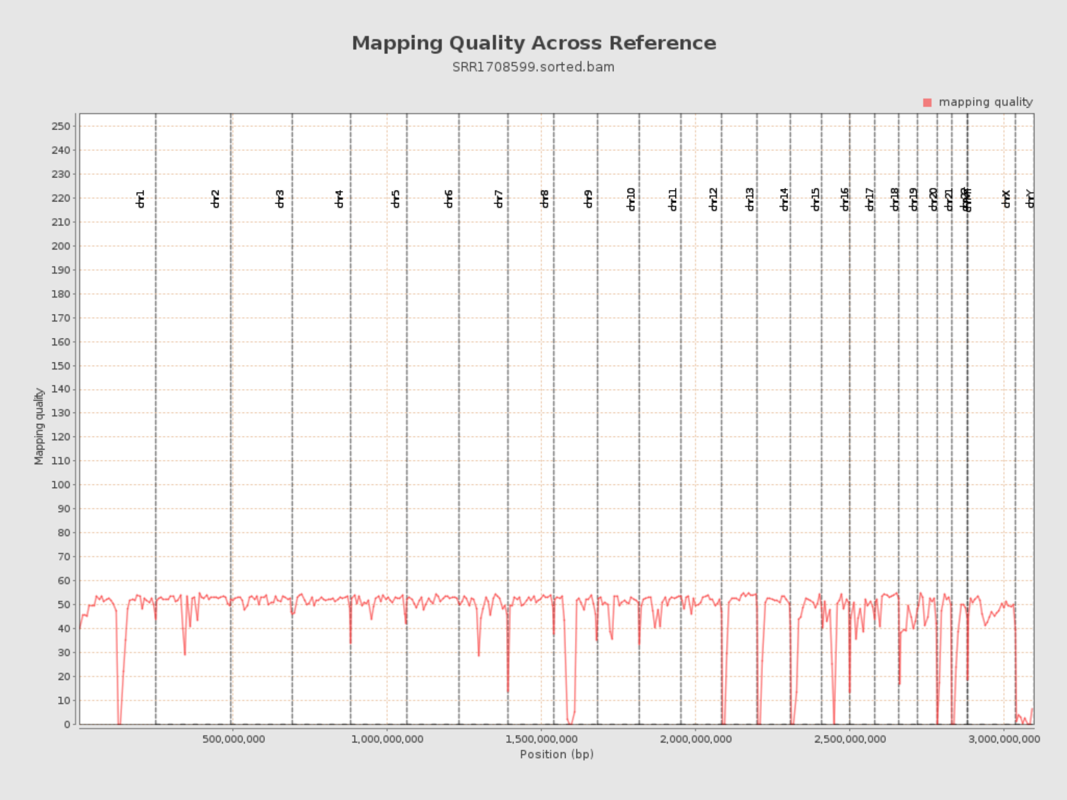
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram