Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:36:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525215.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_SRR10525215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525215.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:36:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525215.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,651,331
Mapped reads	1,506,006 / 91.2%
Unmapped reads	145,325 / 8.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,425 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	46,093 / 2.79%
Duplication rate	2.22%
Clipped reads	1,509,715 / 91.42%

2.2. ACGT Content

Number/percentage of A's	23,157,272 / 26.39%
Number/percentage of C's	15,919,490 / 18.14%
Number/percentage of T's	27,118,161 / 30.9%
Number/percentage of G's	21,551,327 / 24.56%
Number/percentage of N's	2,424 / 0%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2644

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

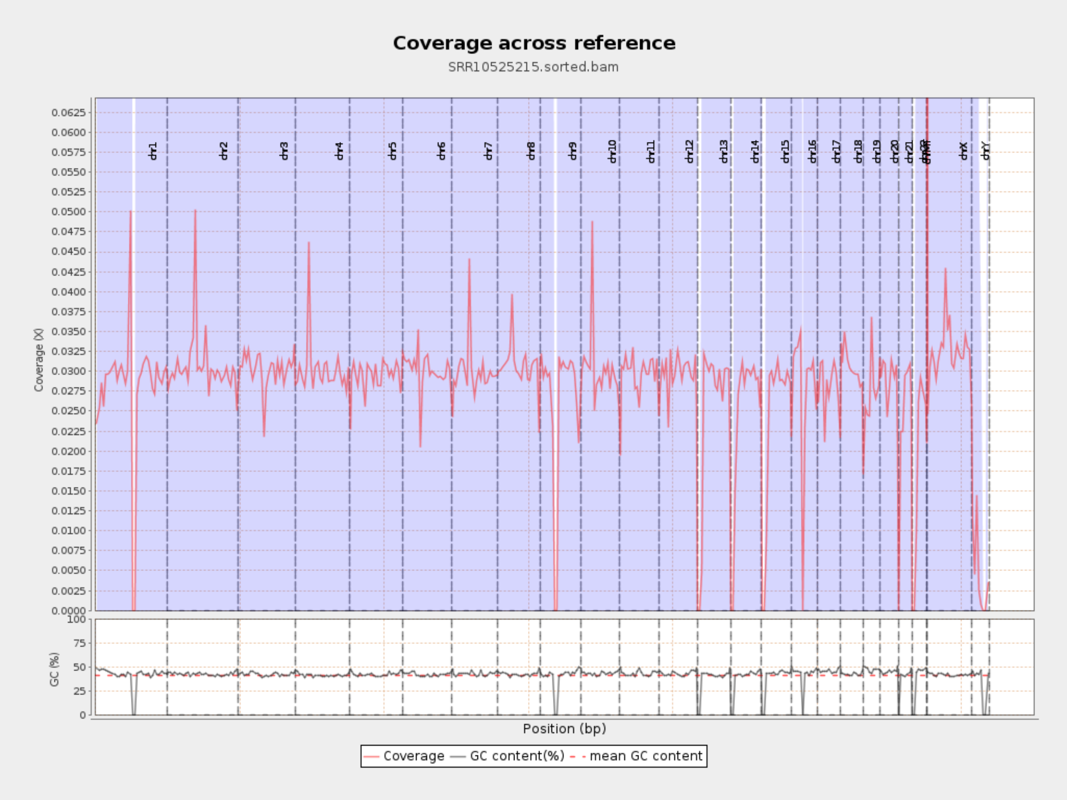
General error rate	0.49%
Mismatches	418,326
Insertions	5,997
Mapped reads with at least one insertion	0.4%
Deletions	14,473
Mapped reads with at least one deletion	0.96%
Homopolymer indels	41.41%

2.6. Chromosome stats

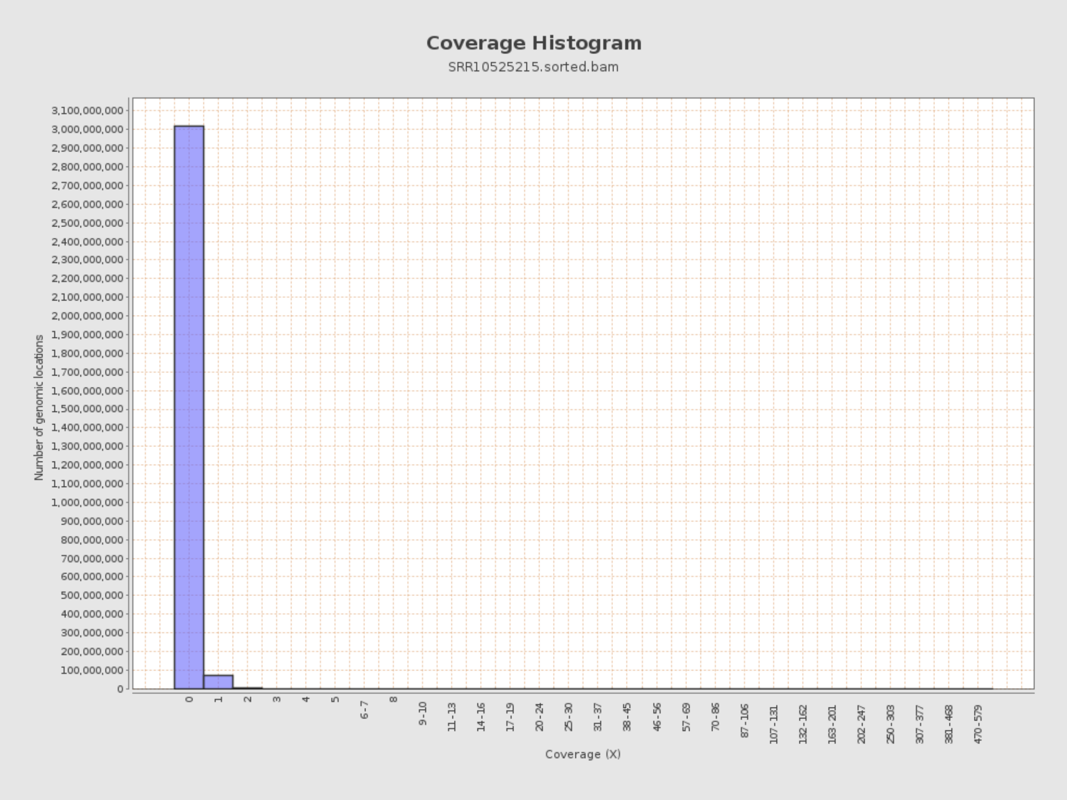
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6983766	0.028	0.4931
chr2	243199373	7455531	0.0307	0.268
chr3	198022430	5983331	0.0302	0.188
chr4	191154276	5784665	0.0303	0.2058
chr5	180915260	5367453	0.0297	0.1874
chr6	171115067	5144251	0.0301	0.2057
chr7	159138663	4788117	0.0301	0.294

chr8	146364022	4497892	0.0307	0.3106
chr9	141213431	3675770	0.026	0.2447
chr10	135534747	4123574	0.0304	0.2518
chr11	135006516	4030704	0.0299	0.2417
chr12	133851895	3996230	0.0299	0.1926
chr13	115169878	2850785	0.0248	0.1696
chr14	107349540	2626481	0.0245	0.183
chr15	102531392	2428565	0.0237	0.1673
chr16	90354753	2463720	0.0273	0.1893
chr17	81195210	2273009	0.028	0.1949
chr18	78077248	2387240	0.0306	0.4404
chr19	59128983	1617240	0.0274	0.3503
chr20	63025520	1822380	0.0289	0.1908
chr21	48129895	1177872	0.0245	0.1847
chr22	51304566	961990	0.0188	0.1474
chrMT	16571	12168	0.7343	0.9424
chrX	155270560	5060968	0.0326	0.2181
chrY	59373566	258788	0.0044	0.1178

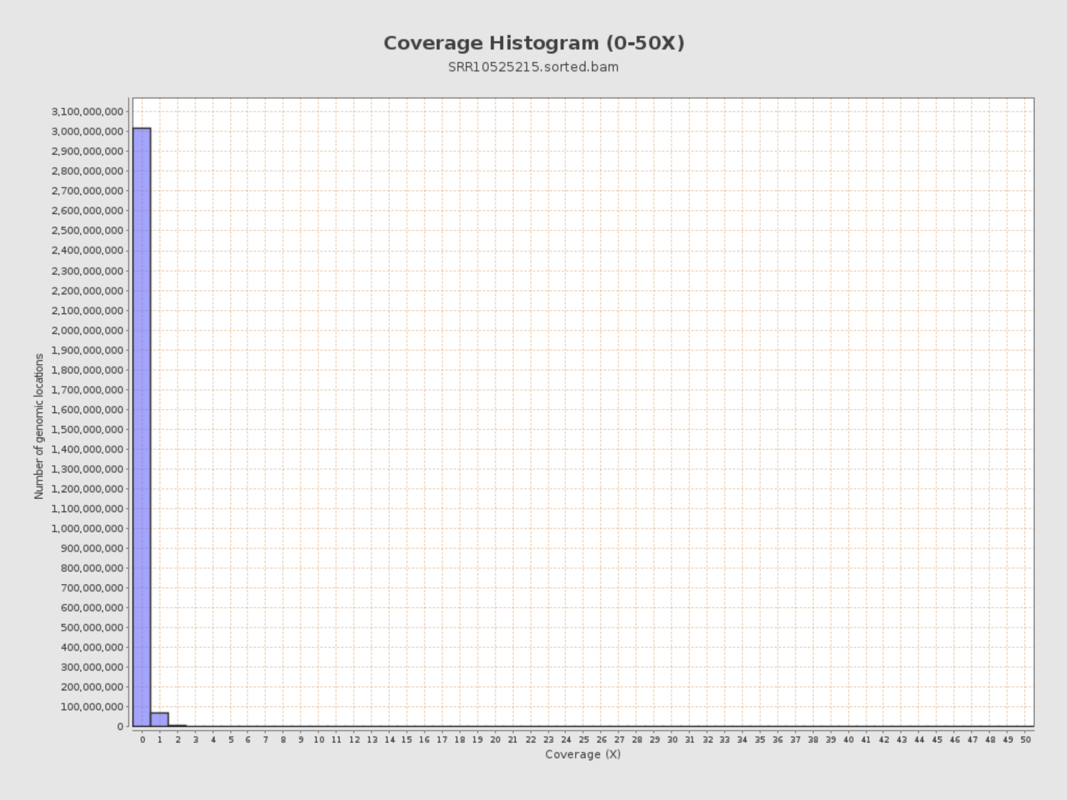
3. Results : Coverage across reference



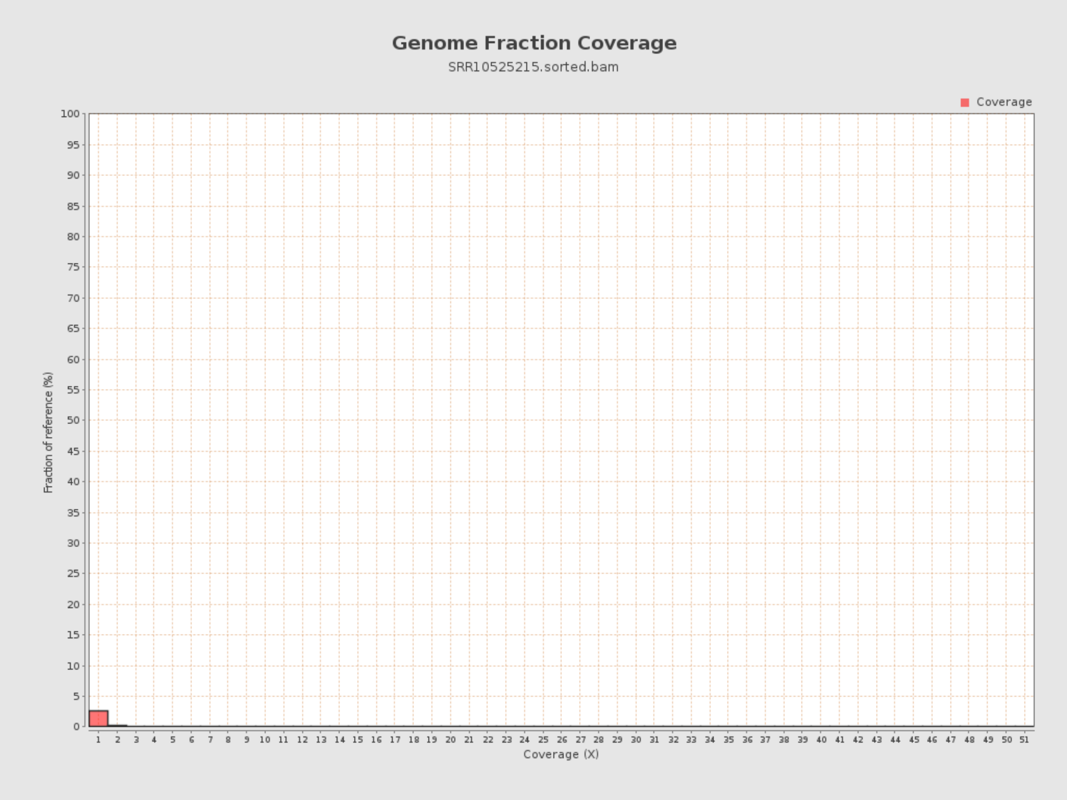
4. Results : Coverage Histogram



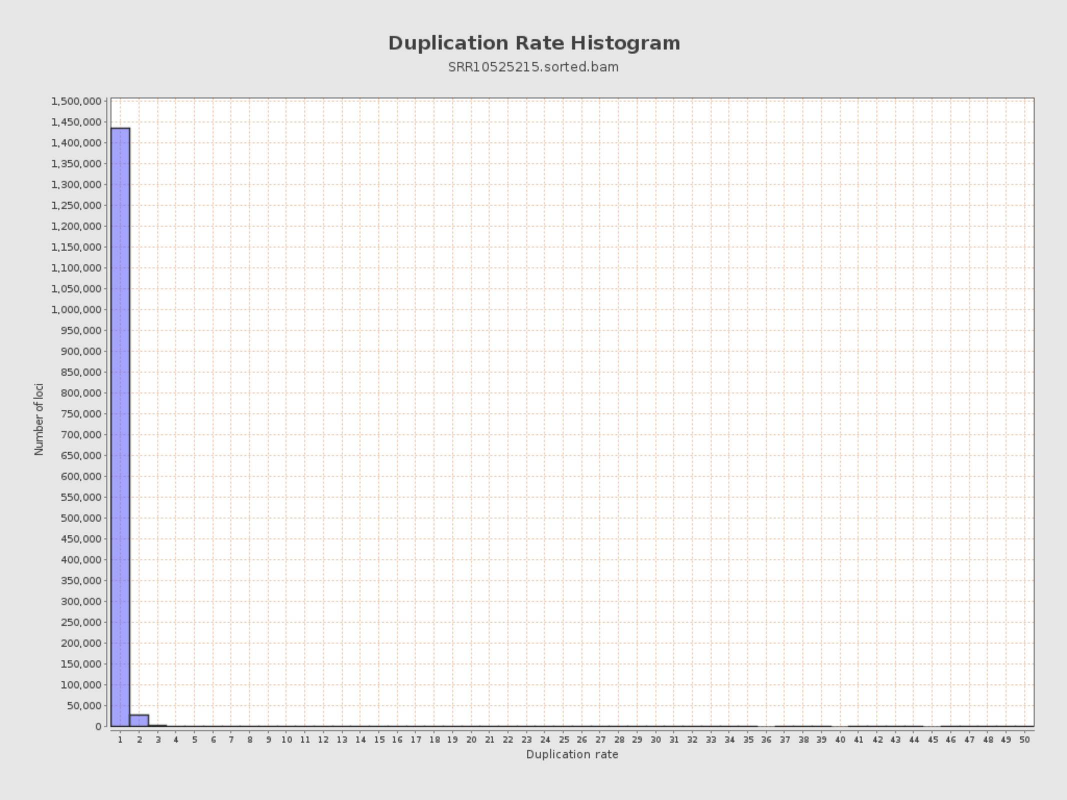
5. Results : Coverage Histogram (0-50X)



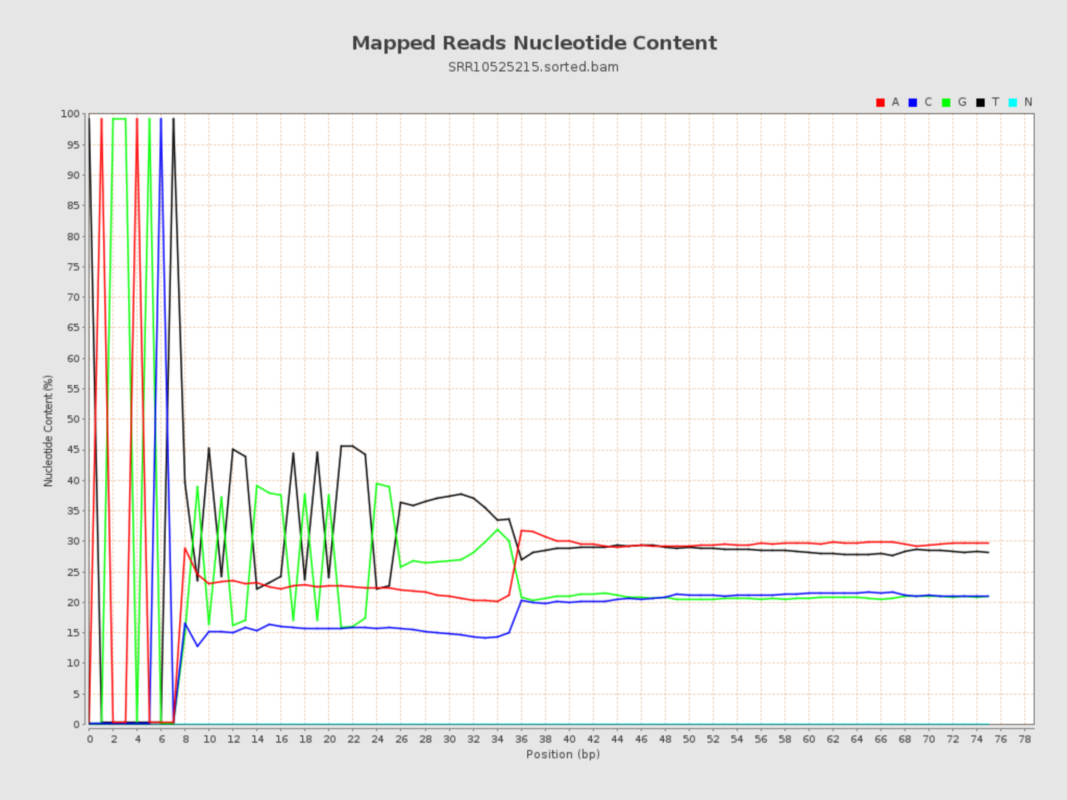
6. Results : Genome Fraction Coverage



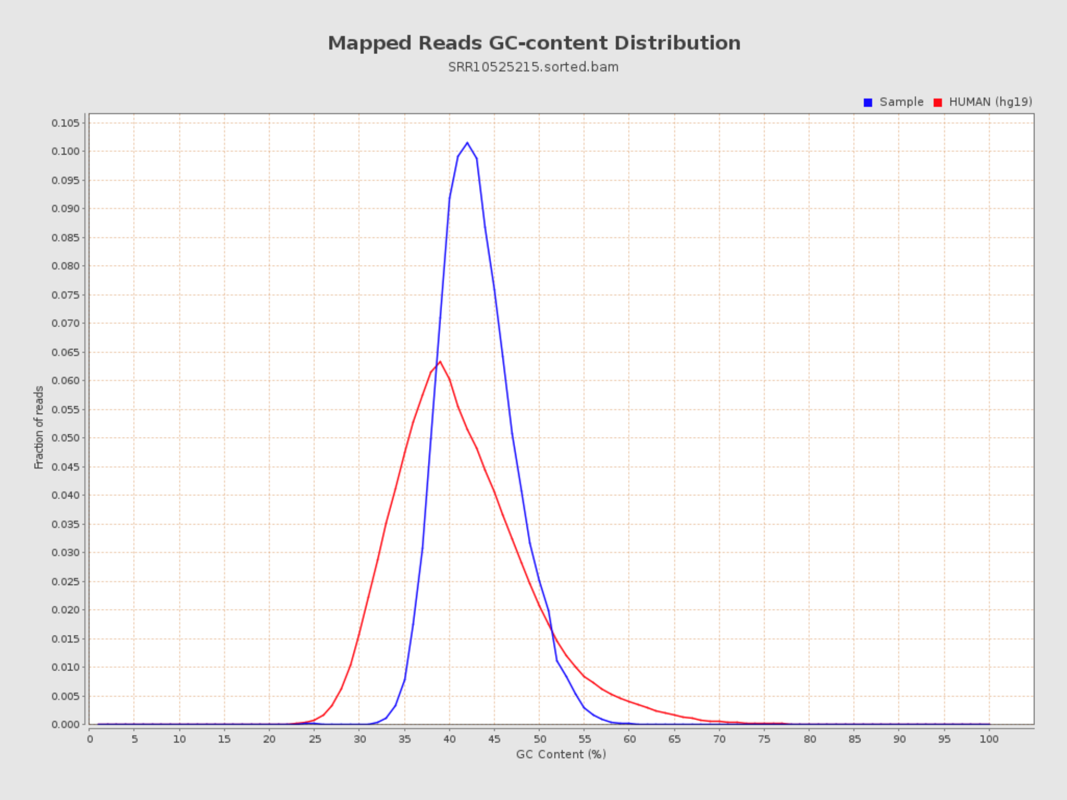
7. Results : Duplication Rate Histogram



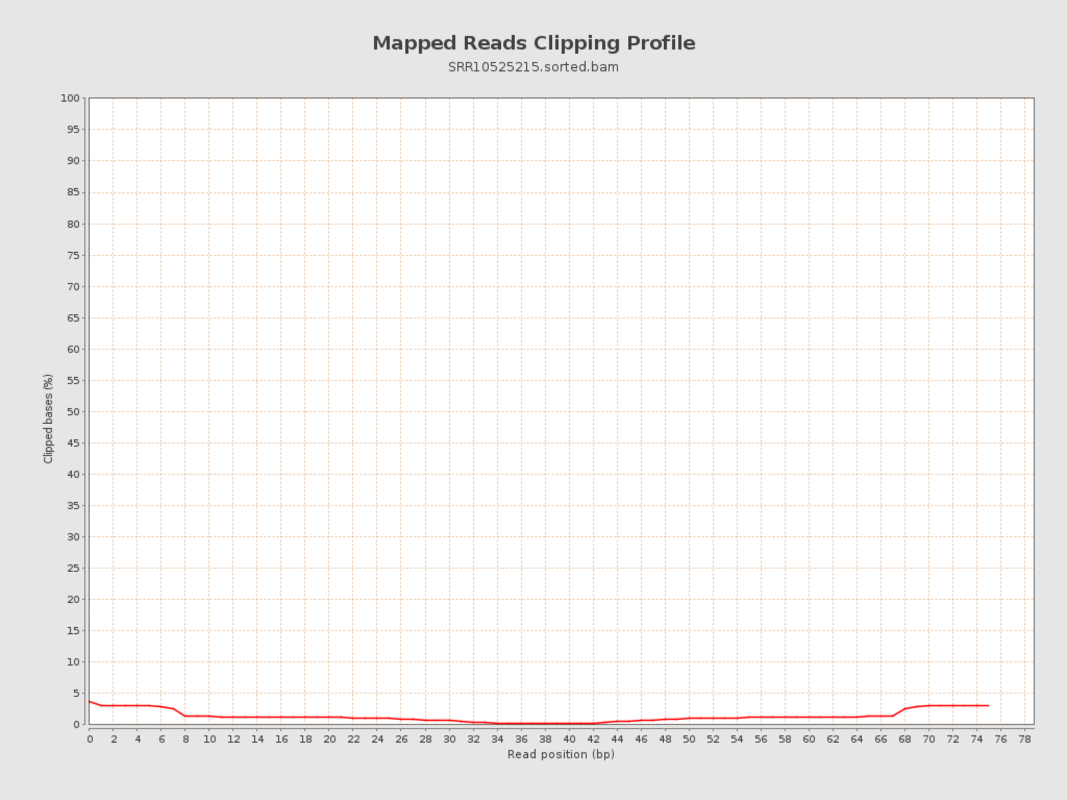
8. Results : Mapped Reads Nucleotide Content



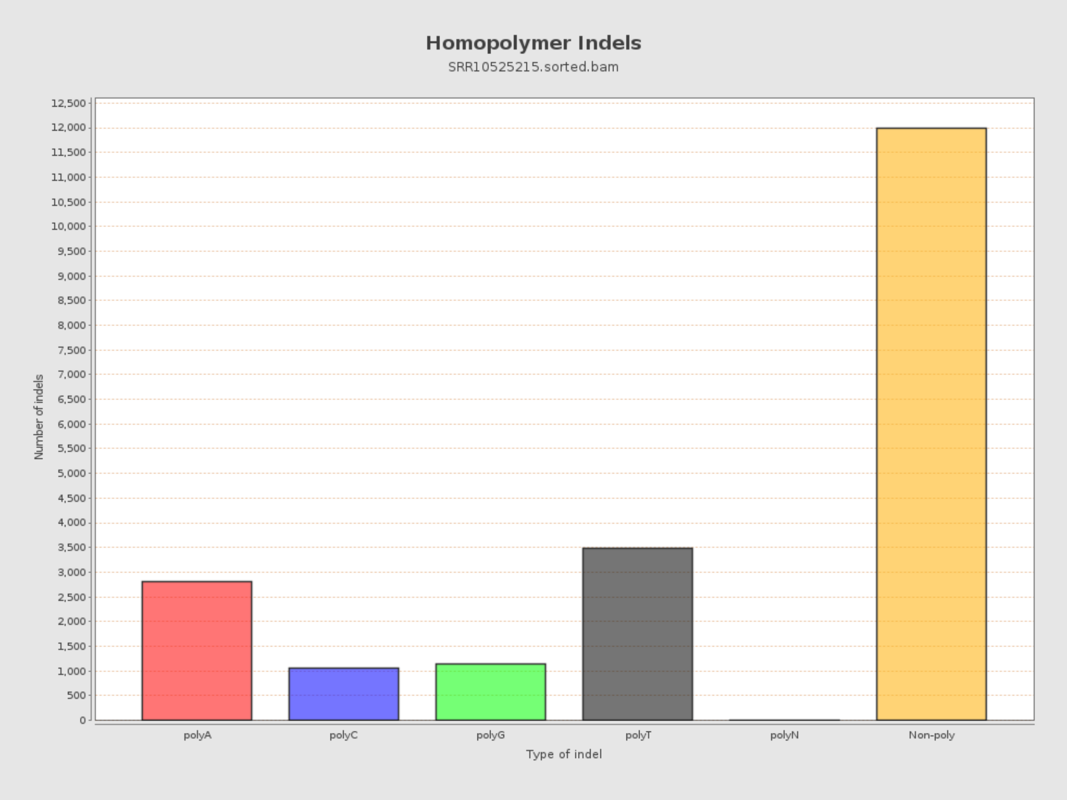
9. Results : Mapped Reads GC-content Distribution



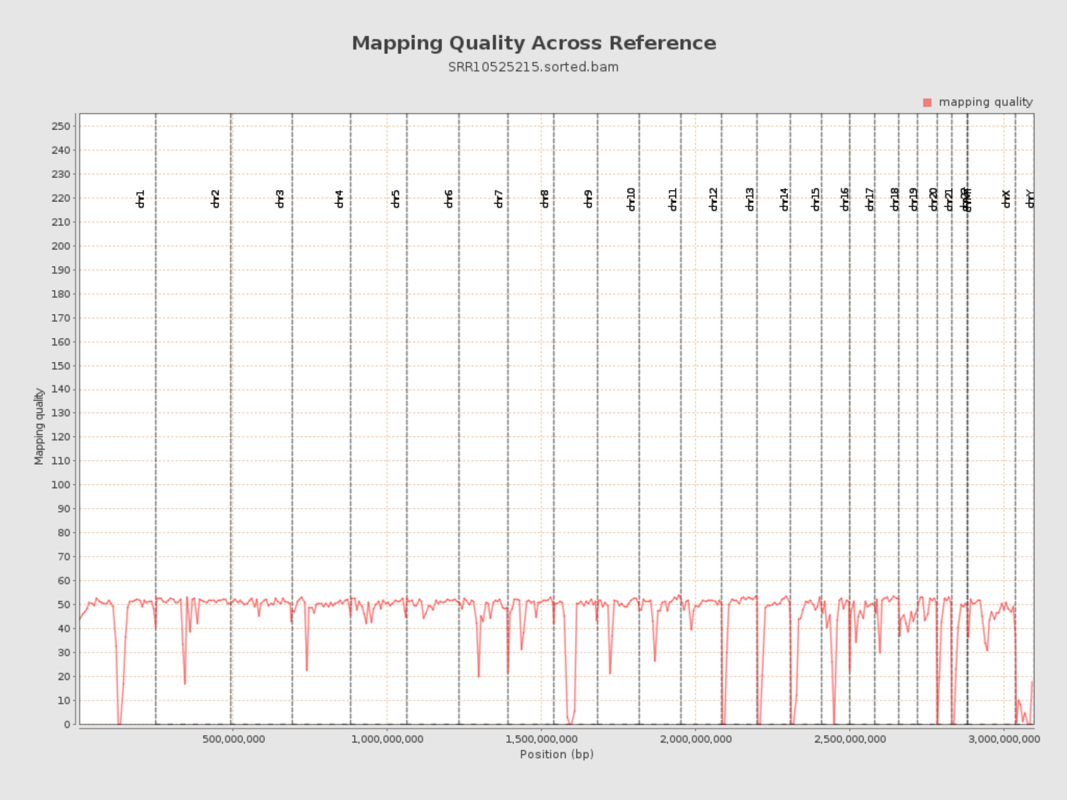
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram