Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:26:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525277.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_SRR10525277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525277.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:26:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	843,049
Mapped reads	753,829 / 89.42%
Unmapped reads	89,220 / 10.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,302 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	18,377 / 2.18%
Duplication rate	1.83%
Clipped reads	755,188 / 89.58%

2.2. ACGT Content

Number/percentage of A's	10,902,109 / 24.95%
Number/percentage of C's	7,951,398 / 18.2%
Number/percentage of T's	14,345,213 / 32.83%
Number/percentage of G's	10,489,957 / 24.01%
Number/percentage of N's	901 / 0%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1617

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

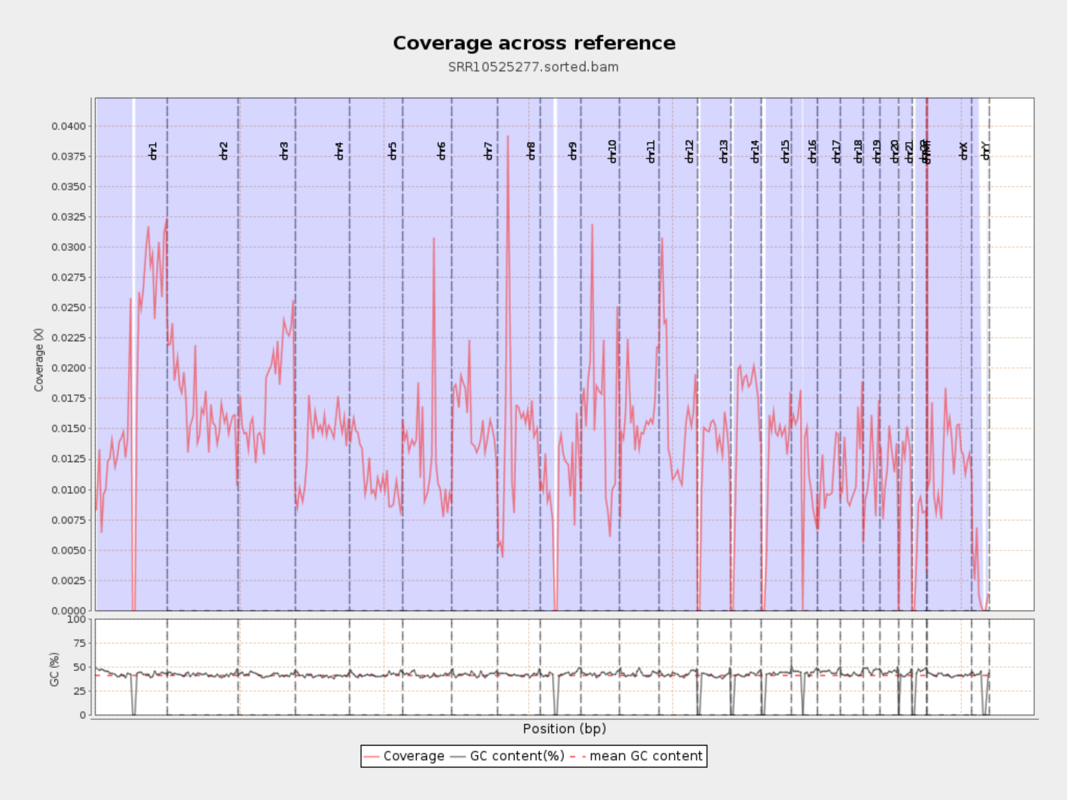
General error rate	0.51%
Mismatches	219,201
Insertions	3,083
Mapped reads with at least one insertion	0.41%
Deletions	8,857
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.91%

2.6. Chromosome stats

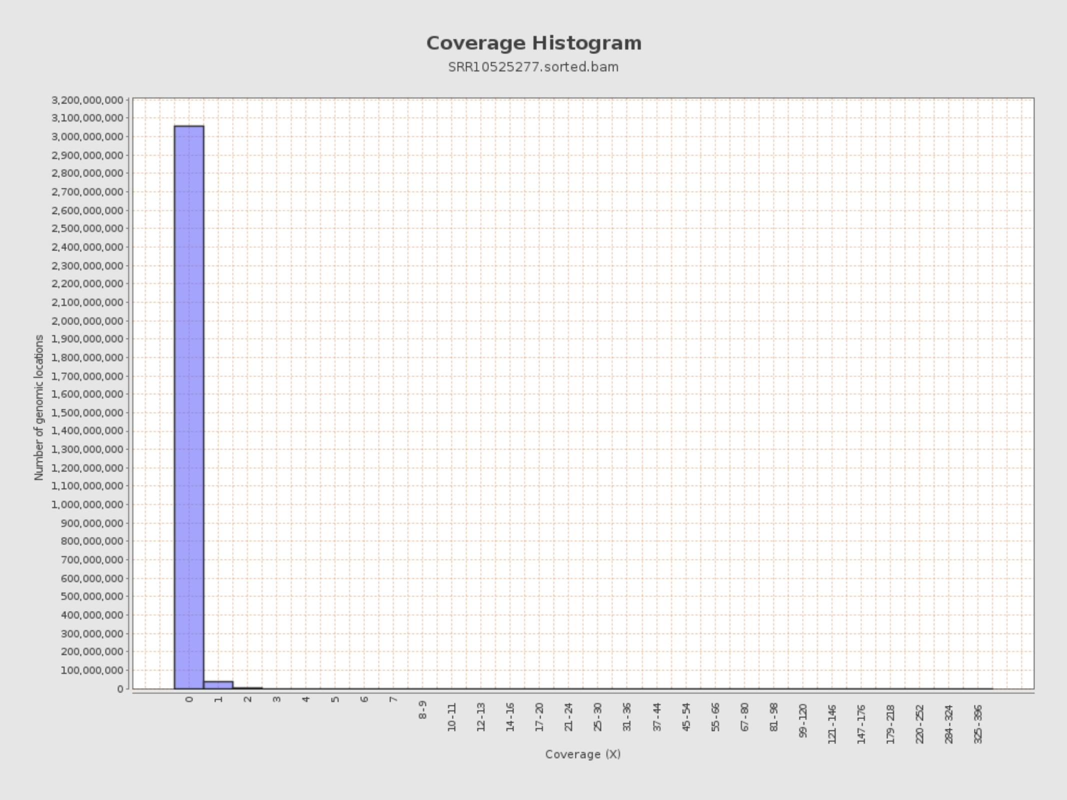
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4628621	0.0186	0.2898
chr2	243199373	4095641	0.0168	0.195
chr3	198022430	3600559	0.0182	0.1414
chr4	191154276	2705005	0.0142	0.1272
chr5	180915260	2018504	0.0112	0.1103
chr6	171115067	2219016	0.013	0.1299
chr7	159138663	2525487	0.0159	0.1898

chr8	146364022	2198345	0.015	0.1583
chr9	141213431	1451702	0.0103	0.1249
chr10	135534747	2256660	0.0167	0.1812
chr11	135006516	2142490	0.0159	0.1453
chr12	133851895	2211227	0.0165	0.1349
chr13	115169878	1467622	0.0127	0.1182
chr14	107349540	1660883	0.0155	0.1313
chr15	102531392	1238803	0.0121	0.1159
chr16	90354753	1094764	0.0121	0.1233
chr17	81195210	879664	0.0108	0.111
chr18	78077248	912187	0.0117	0.2111
chr19	59128983	693587	0.0117	0.1896
chr20	63025520	752438	0.0119	0.1156
chr21	48129895	547357	0.0114	0.1144
chr22	51304566	302964	0.0059	0.08
chrMT	16571	1134	0.0684	0.2568
chrX	155270560	1976341	0.0127	0.1239
chrY	59373566	122836	0.0021	0.0676

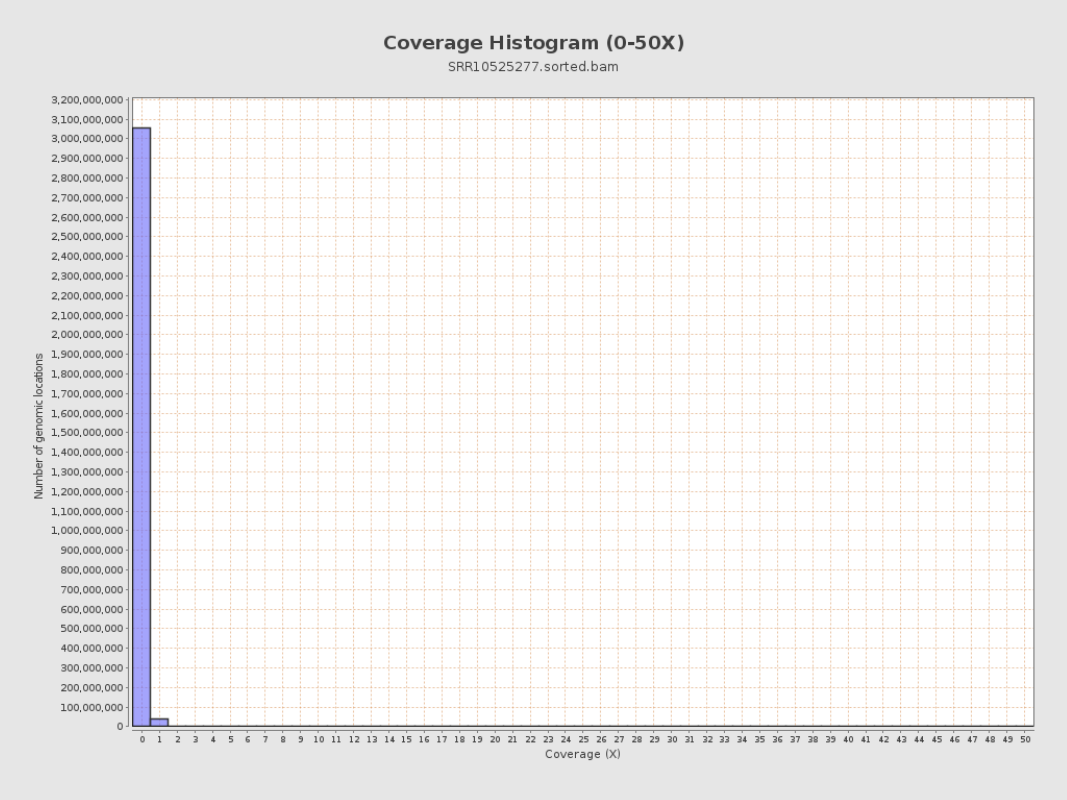
3. Results : Coverage across reference



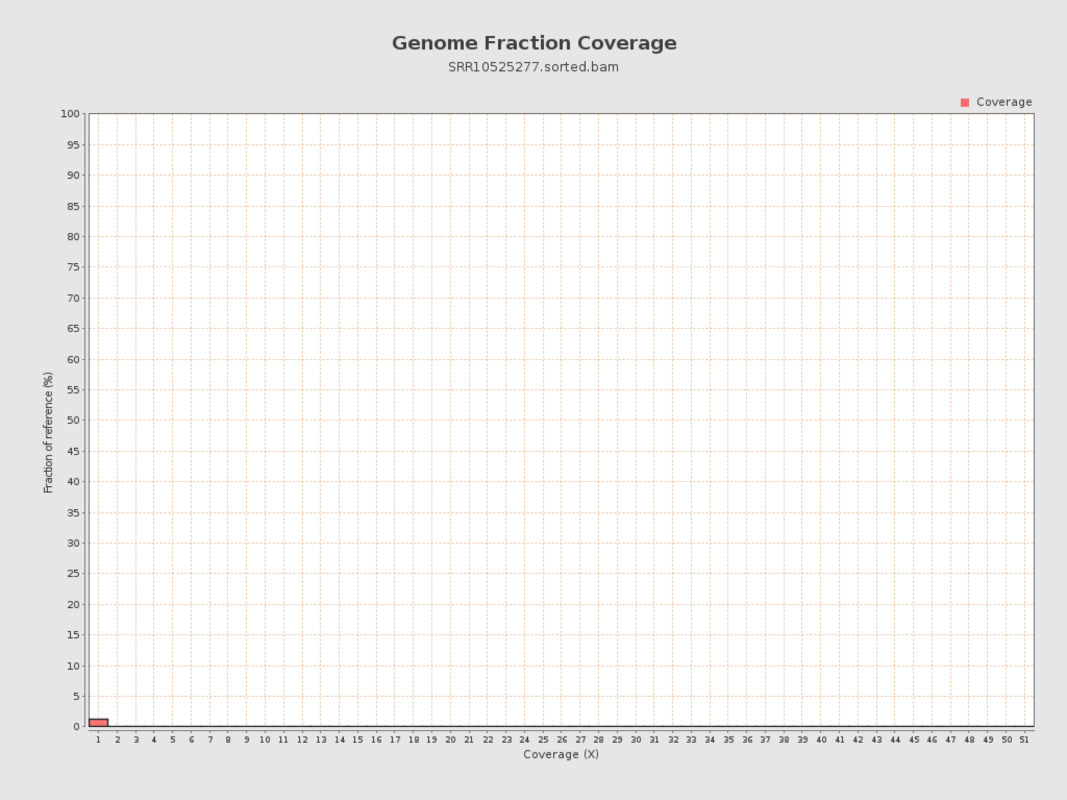
4. Results : Coverage Histogram



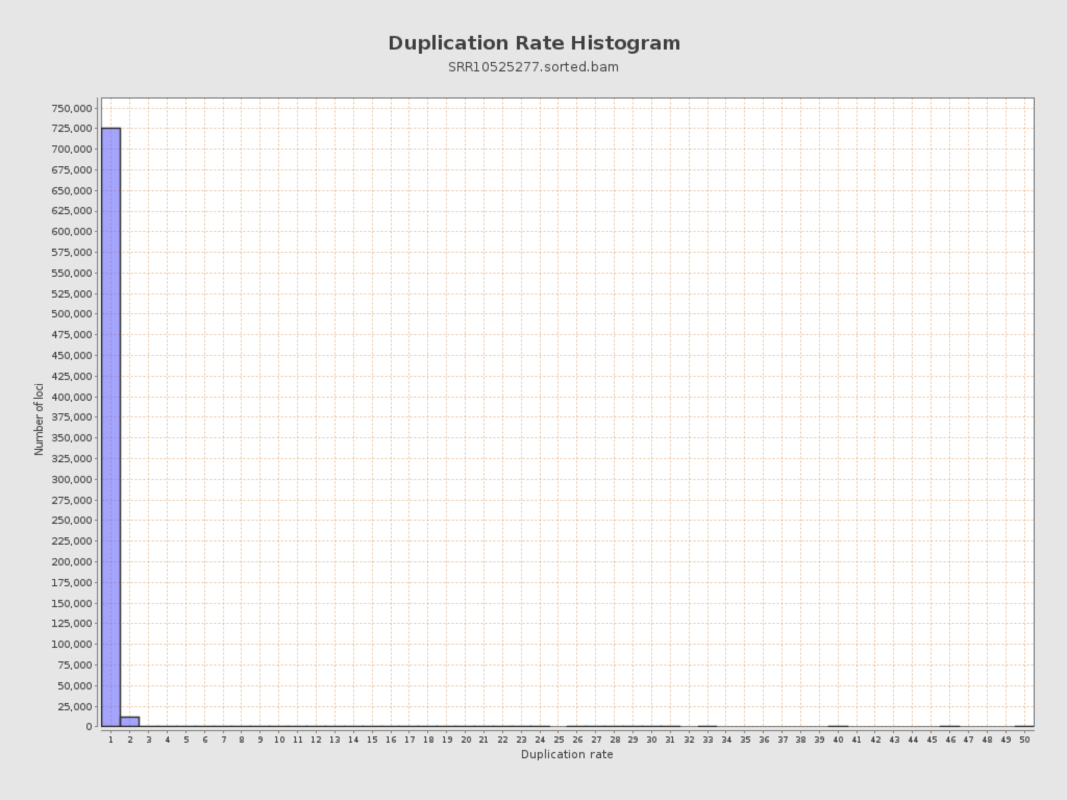
5. Results : Coverage Histogram (0-50X)



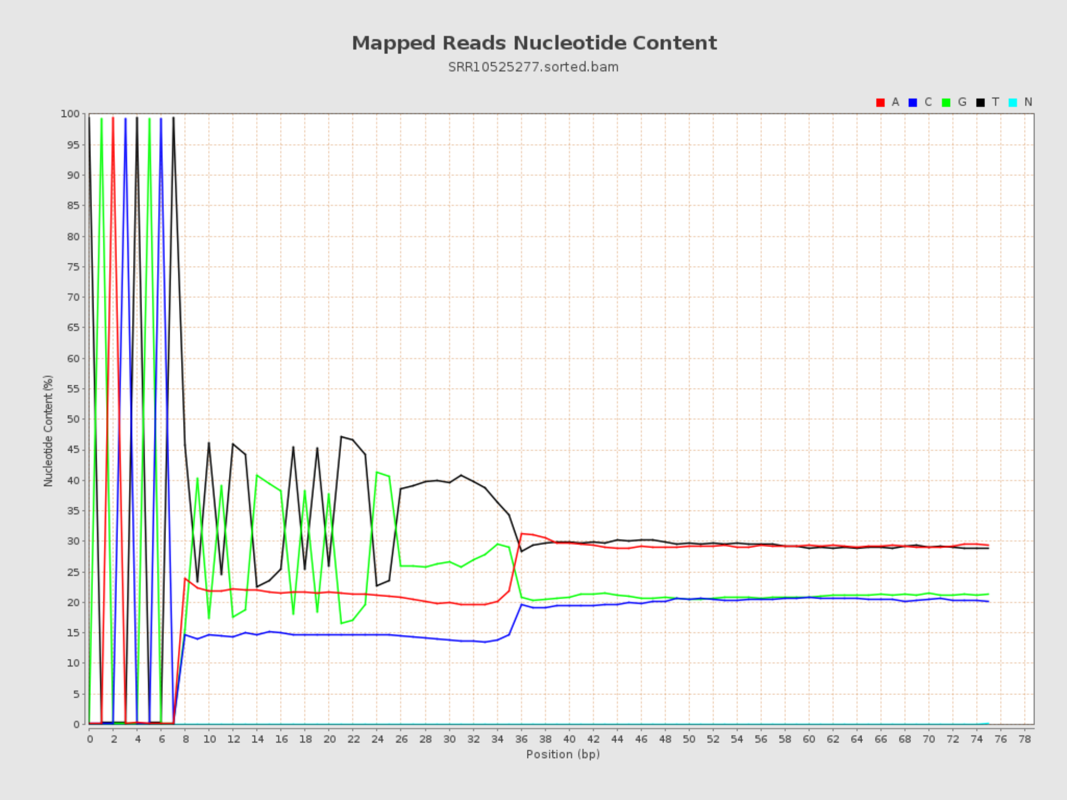
6. Results : Genome Fraction Coverage



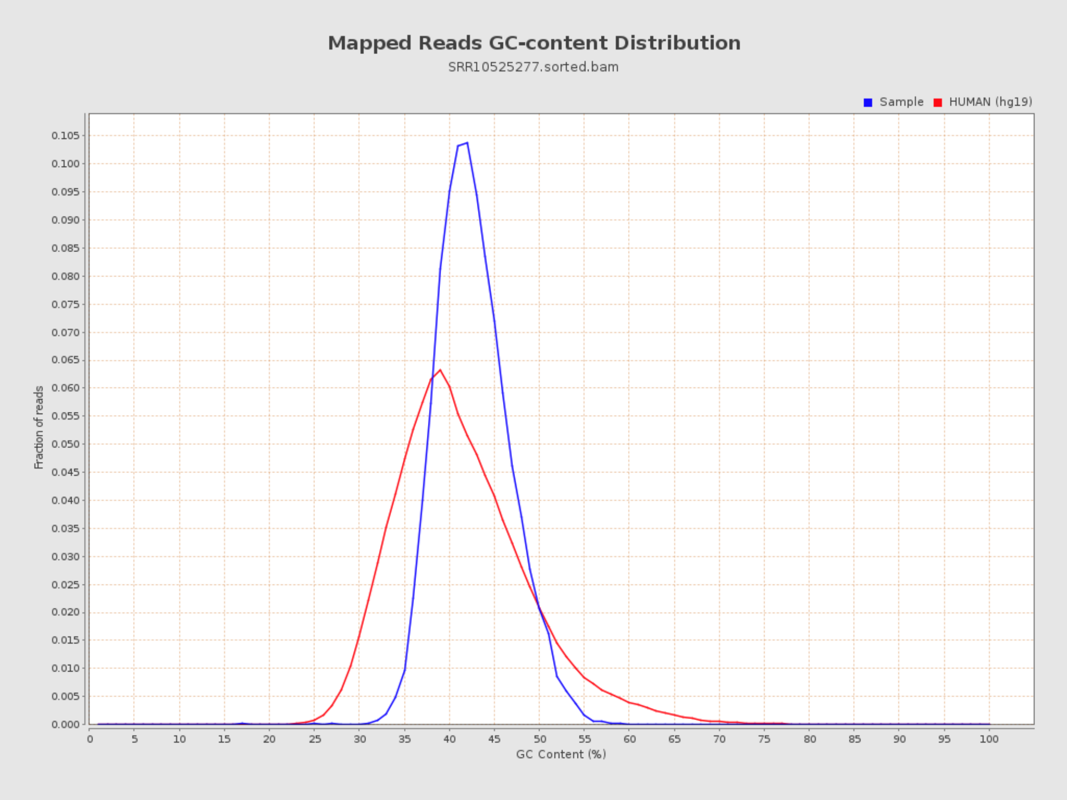
7. Results : Duplication Rate Histogram



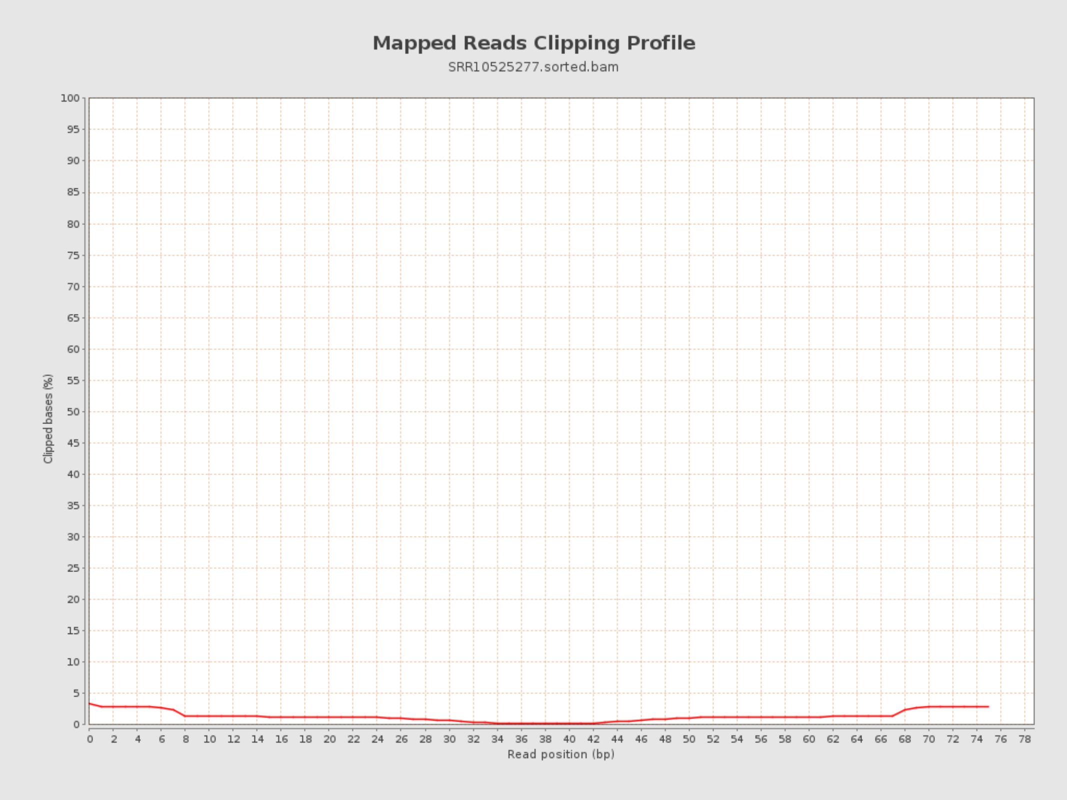
8. Results : Mapped Reads Nucleotide Content



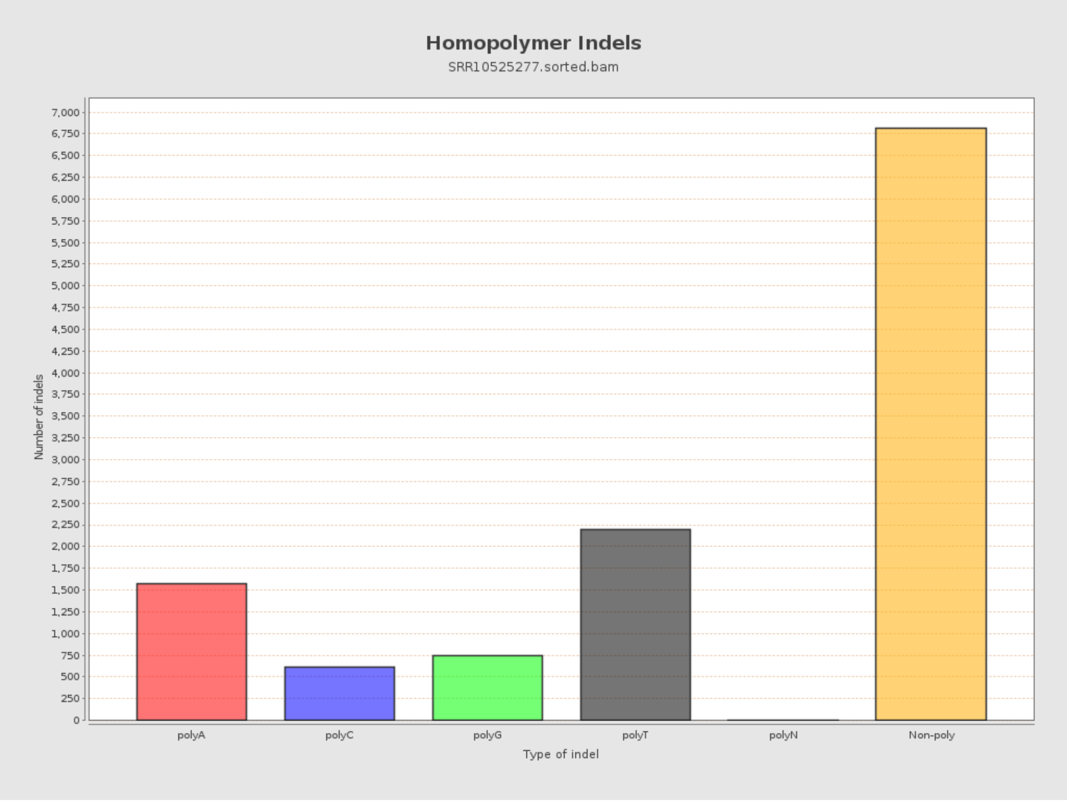
9. Results : Mapped Reads GC-content Distribution



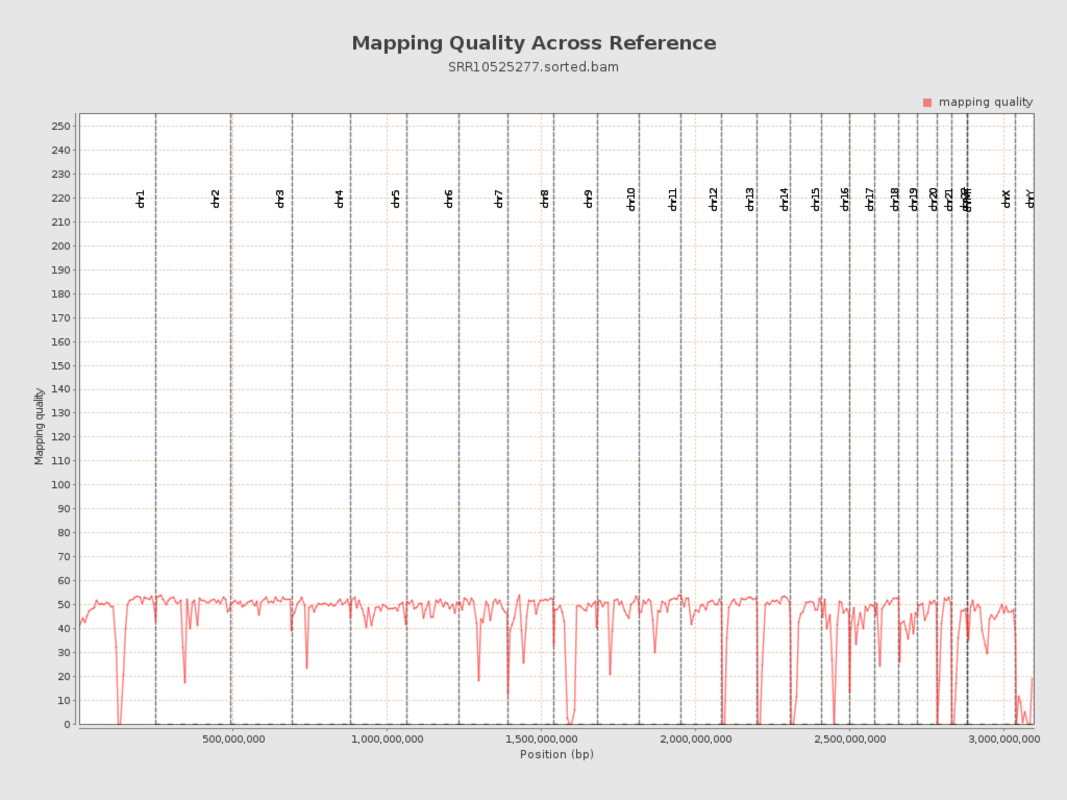
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram