Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:24:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525276.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_SRR10525276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525276.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:24:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	694,941
Mapped reads	642,565 / 92.46%
Unmapped reads	52,376 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,866 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	13,607 / 1.96%
Duplication rate	1.53%
Clipped reads	644,928 / 92.8%

2.2. ACGT Content

Number/percentage of A's	9,145,590 / 24.37%
Number/percentage of C's	7,171,311 / 19.11%
Number/percentage of T's	11,950,922 / 31.84%
Number/percentage of G's	9,264,619 / 24.68%
Number/percentage of N's	743 / 0%
GC Percentage	43.79%

2.3. Coverage

Mean	0.0121

Standard Deviation	0.1474

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

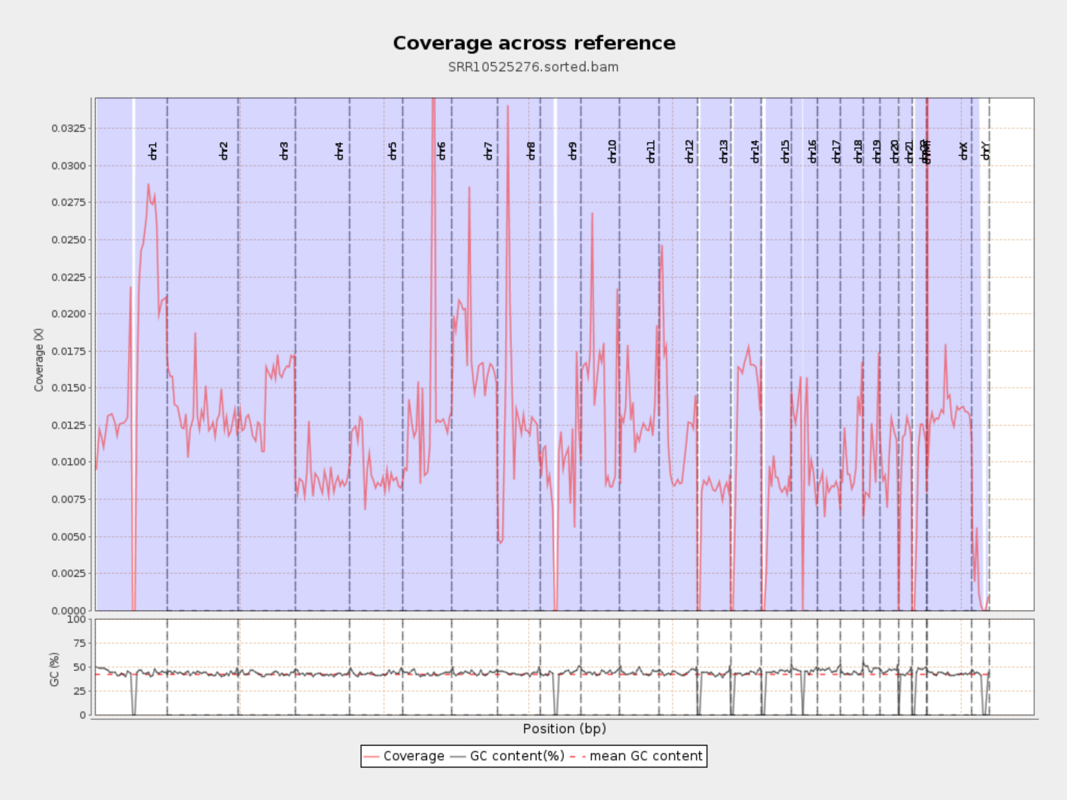
General error rate	0.51%
Mismatches	186,087
Insertions	2,286
Mapped reads with at least one insertion	0.35%
Deletions	8,018
Mapped reads with at least one deletion	1.24%
Homopolymer indels	44.55%

2.6. Chromosome stats

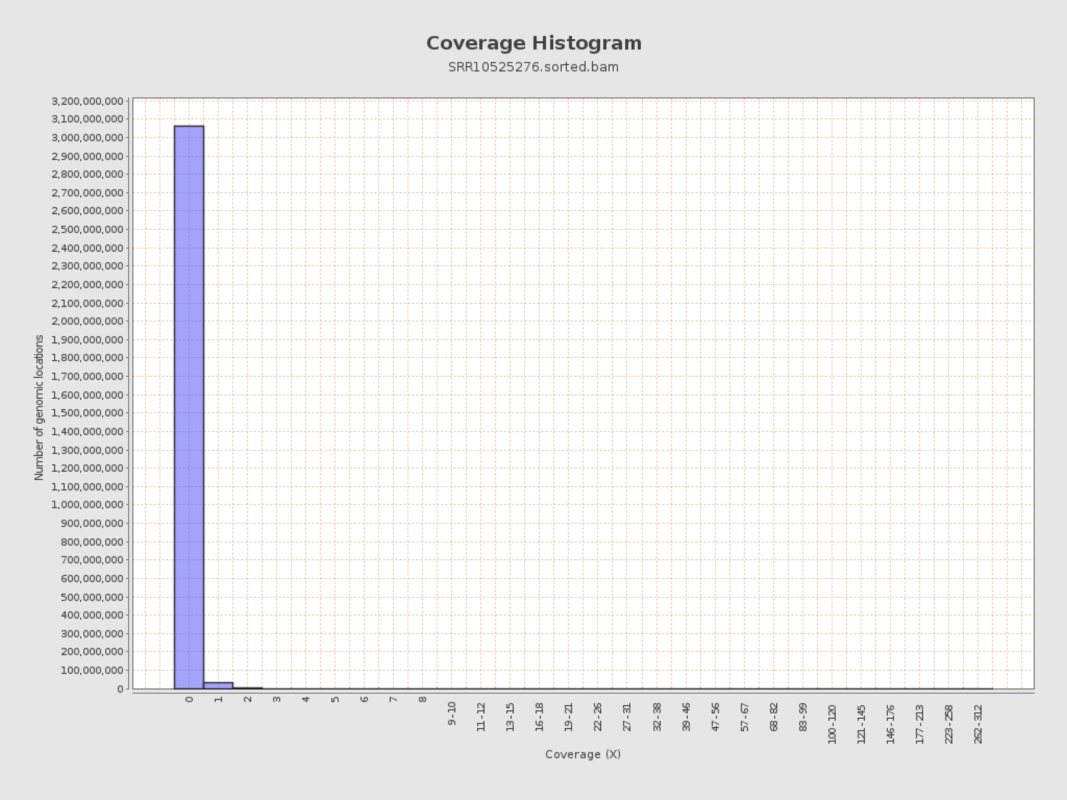
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4200175	0.0169	0.2403
chr2	243199373	3228544	0.0133	0.1757
chr3	198022430	2843258	0.0144	0.1254
chr4	191154276	1685329	0.0088	0.1
chr5	180915260	1749317	0.0097	0.1019
chr6	171115067	2399565	0.014	0.1294
chr7	159138663	2839959	0.0178	0.2417

chr8	146364022	1887941	0.0129	0.137
chr9	141213431	1291646	0.0091	0.1142
chr10	135534747	2034330	0.015	0.1611
chr11	135006516	1773778	0.0131	0.1359
chr12	133851895	1718119	0.0128	0.1177
chr13	115169878	856805	0.0074	0.0897
chr14	107349540	1447576	0.0135	0.1216
chr15	102531392	725177	0.0071	0.0876
chr16	90354753	998902	0.0111	0.1149
chr17	81195210	668767	0.0082	0.0953
chr18	78077248	838235	0.0107	0.1822
chr19	59128983	607544	0.0103	0.1651
chr20	63025520	645136	0.0102	0.1058
chr21	48129895	498738	0.0104	0.1077
chr22	51304566	418105	0.0081	0.0931
chrMT	16571	4193	0.253	0.5612
chrX	155270560	2083299	0.0134	0.1249
chrY	59373566	101641	0.0017	0.0588

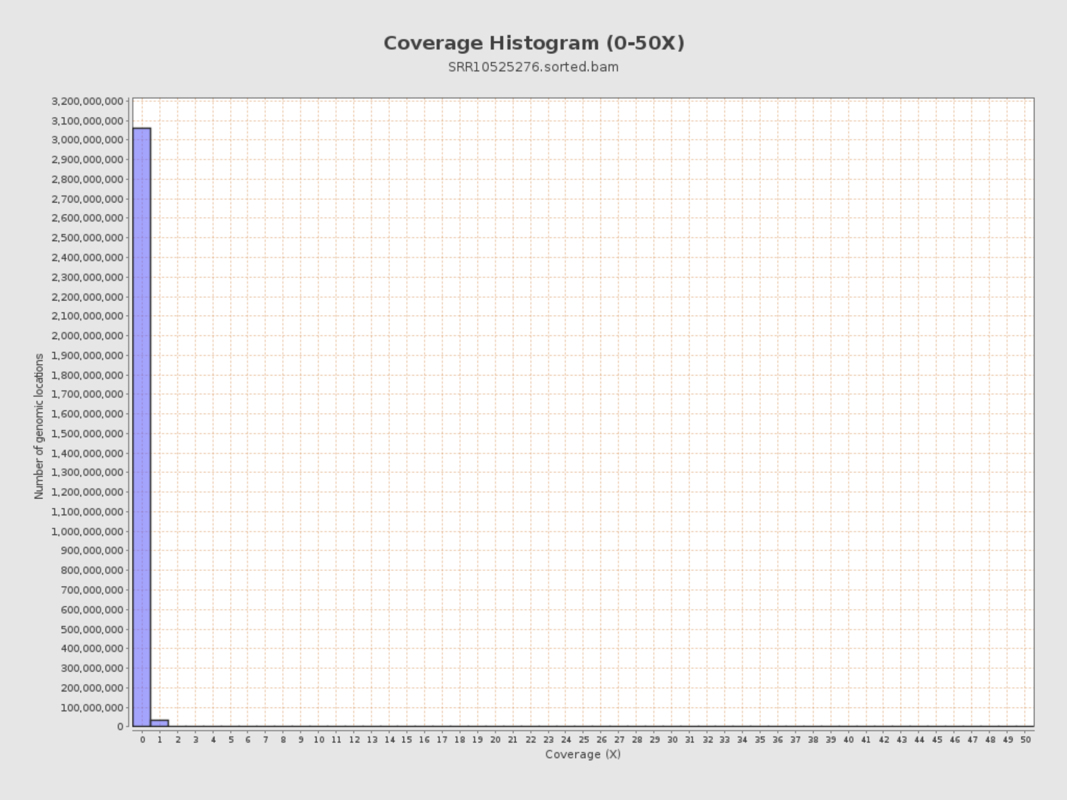
3. Results : Coverage across reference



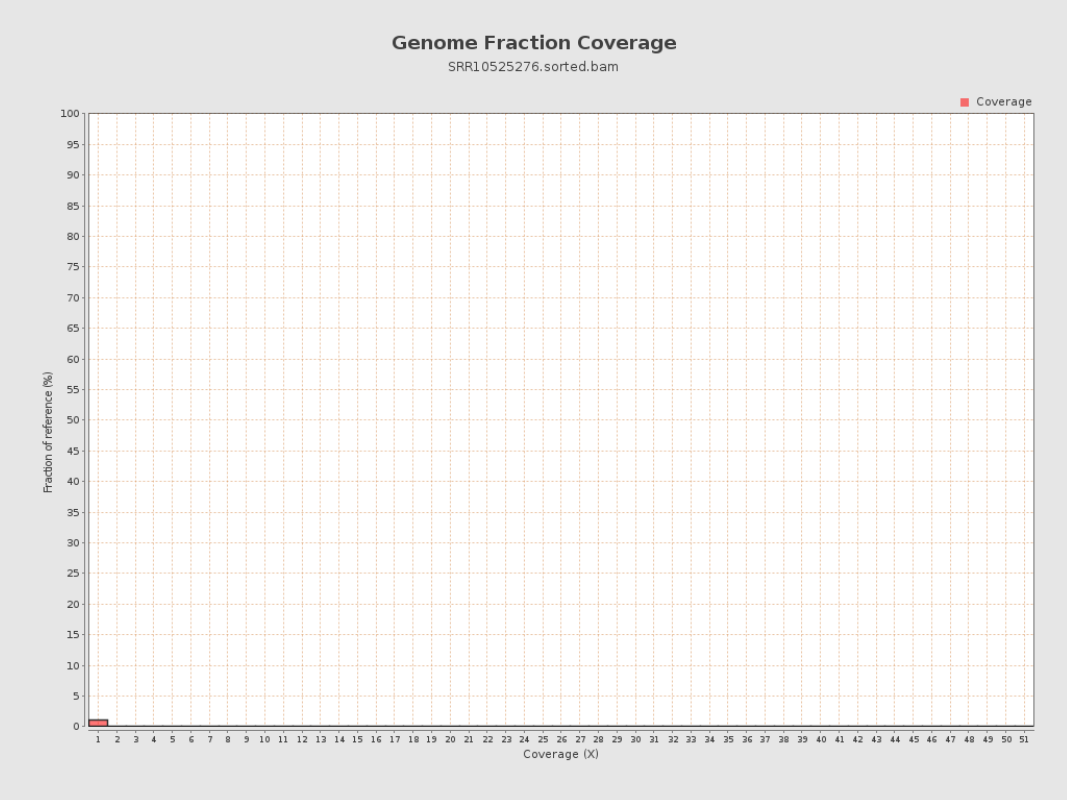
4. Results : Coverage Histogram



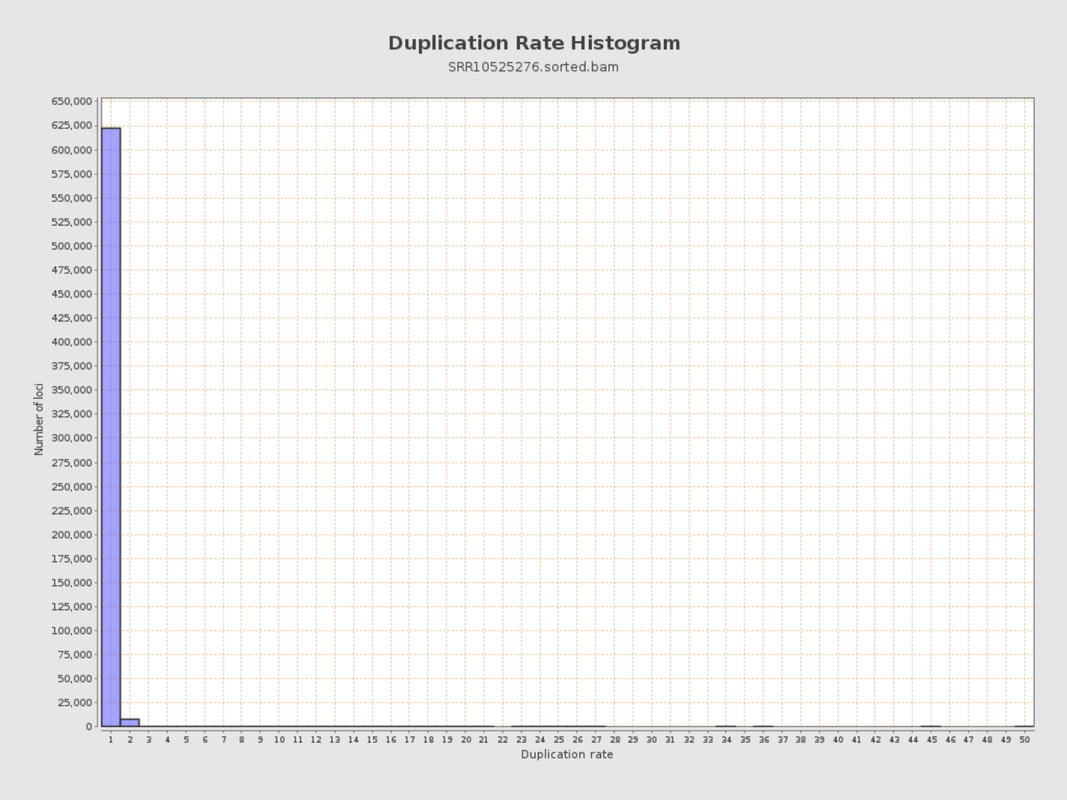
5. Results : Coverage Histogram (0-50X)



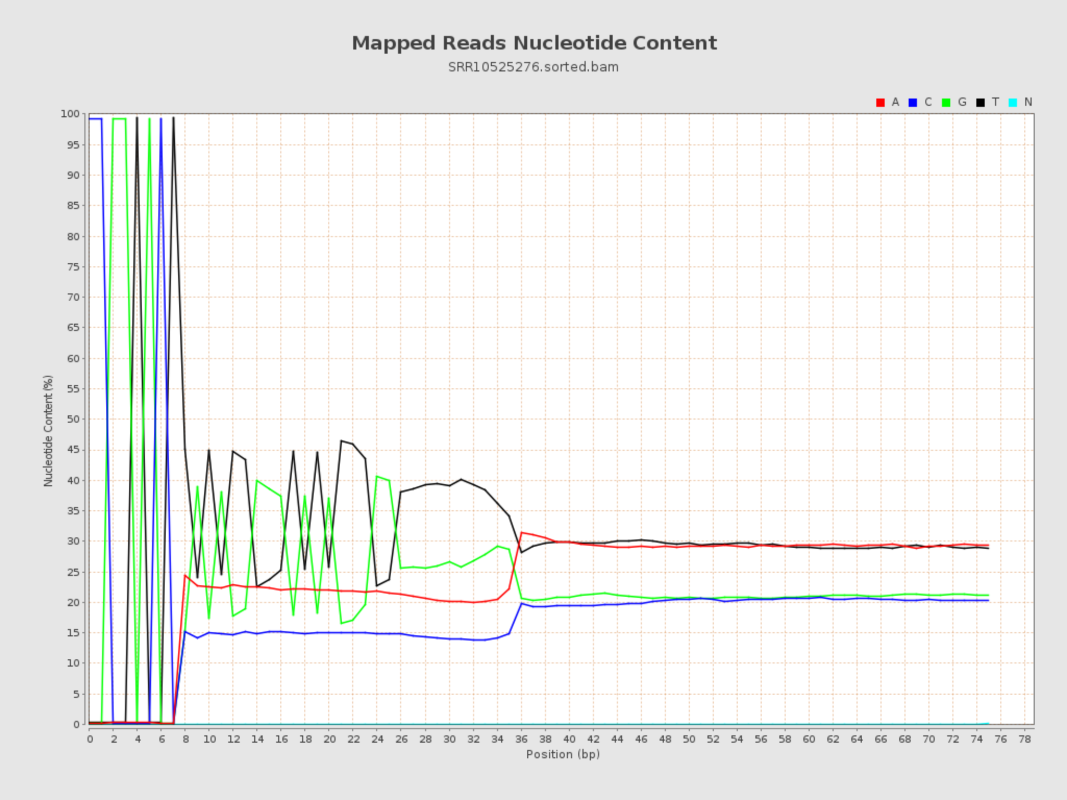
6. Results : Genome Fraction Coverage



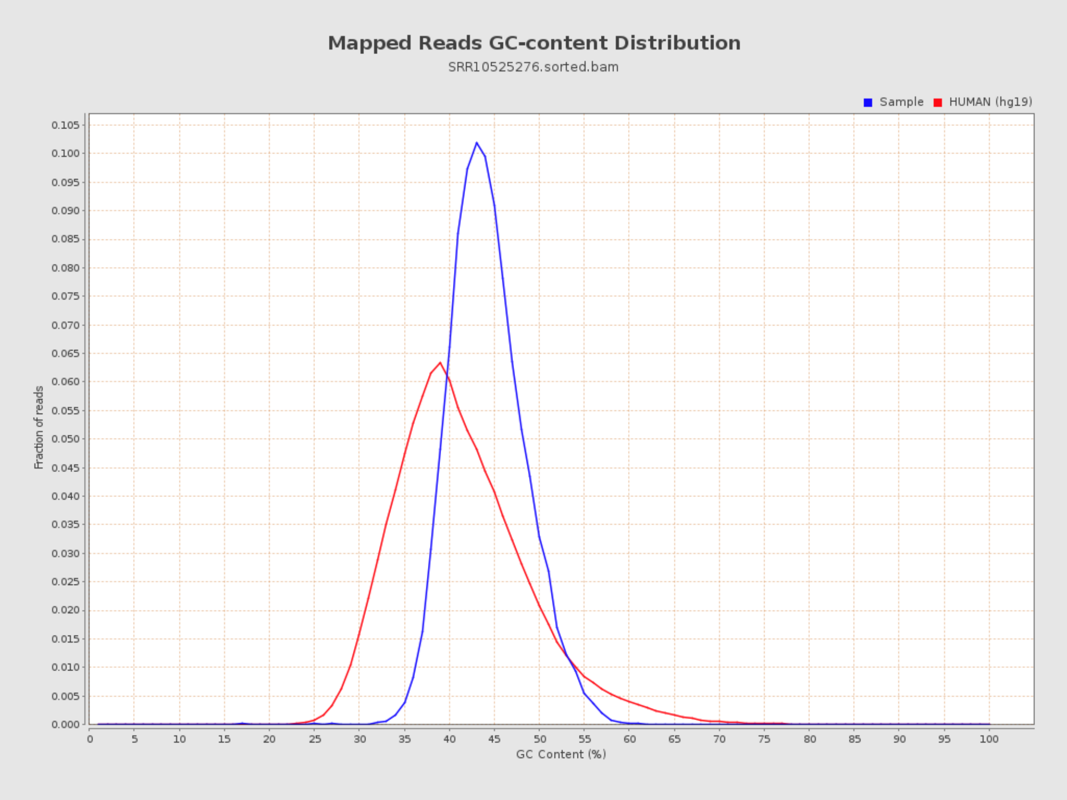
7. Results : Duplication Rate Histogram



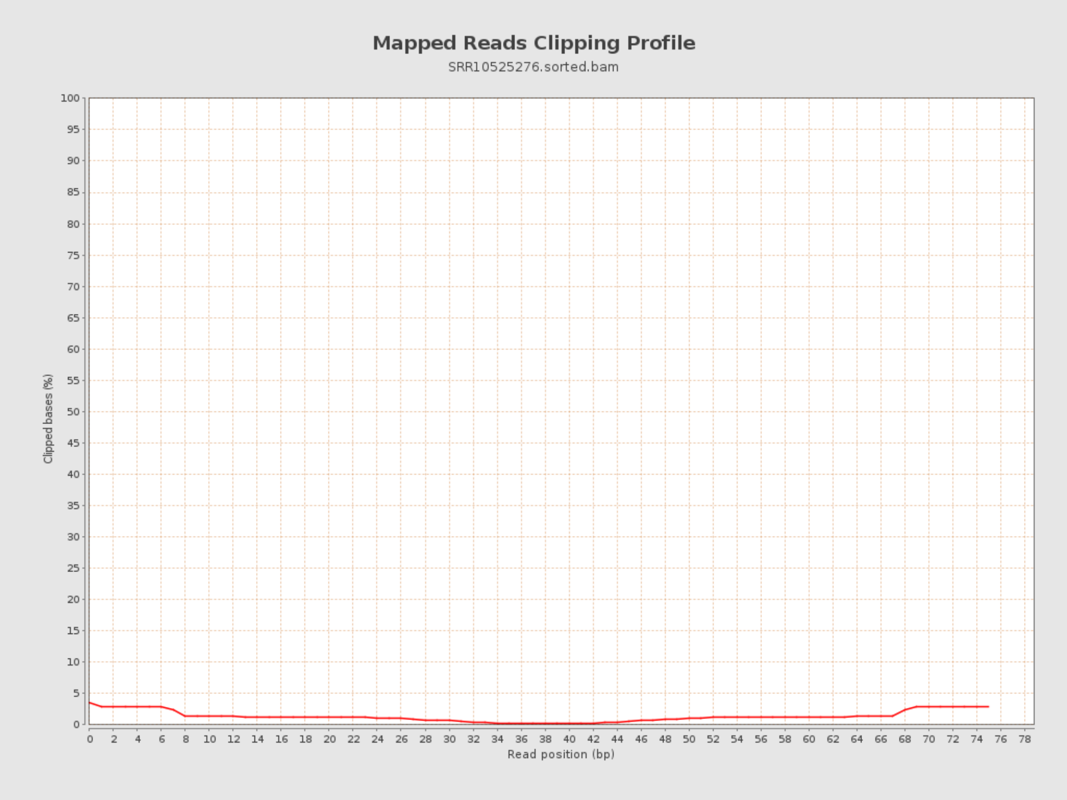
8. Results : Mapped Reads Nucleotide Content



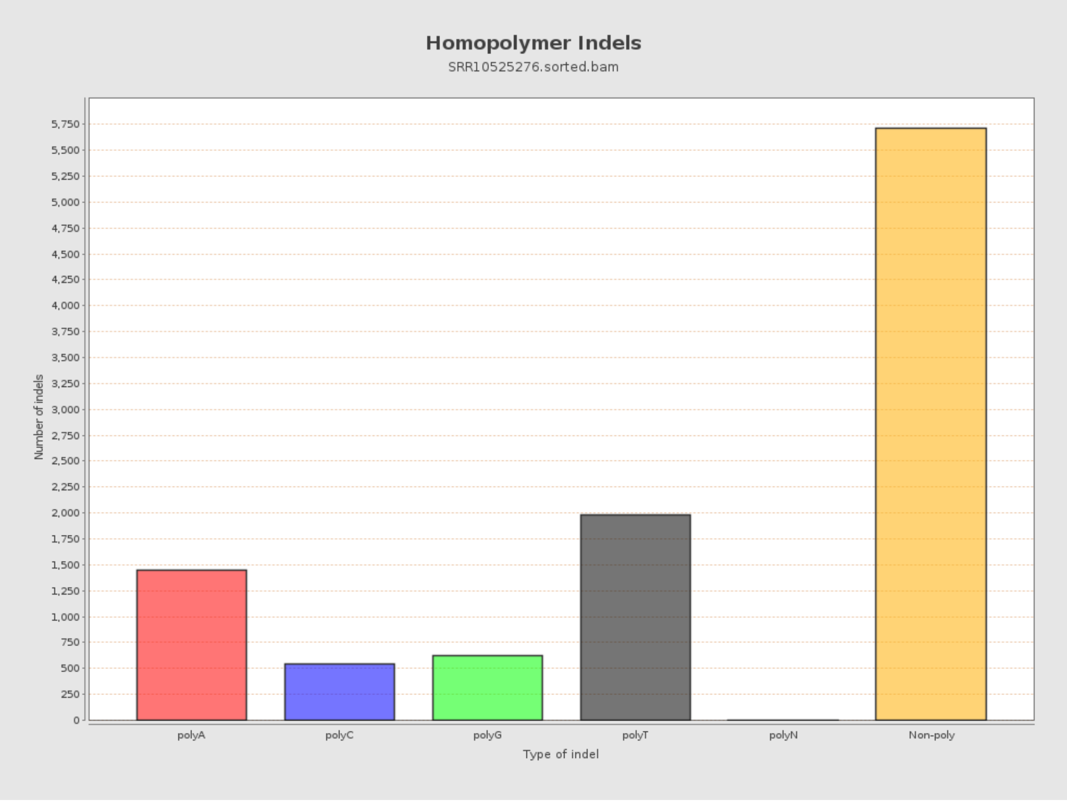
9. Results : Mapped Reads GC-content Distribution



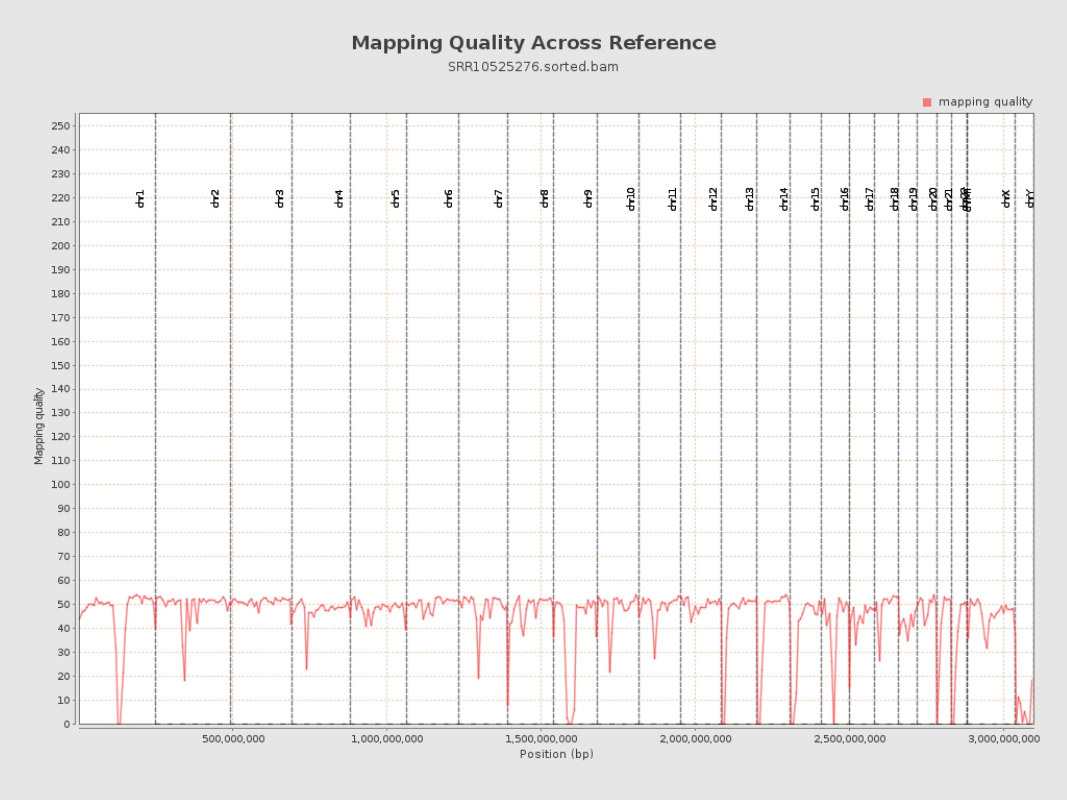
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram