Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:22:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525275.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_SRR10525275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:22:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	806,423
Mapped reads	735,974 / 91.26%
Unmapped reads	70,449 / 8.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,150 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	17,370 / 2.15%
Duplication rate	1.7%
Clipped reads	737,092 / 91.4%

2.2. ACGT Content

Number/percentage of A's	10,667,103 / 25.02%
Number/percentage of C's	7,360,171 / 17.27%
Number/percentage of T's	14,358,215 / 33.68%
Number/percentage of G's	10,243,079 / 24.03%
Number/percentage of N's	757 / 0%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.1648

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

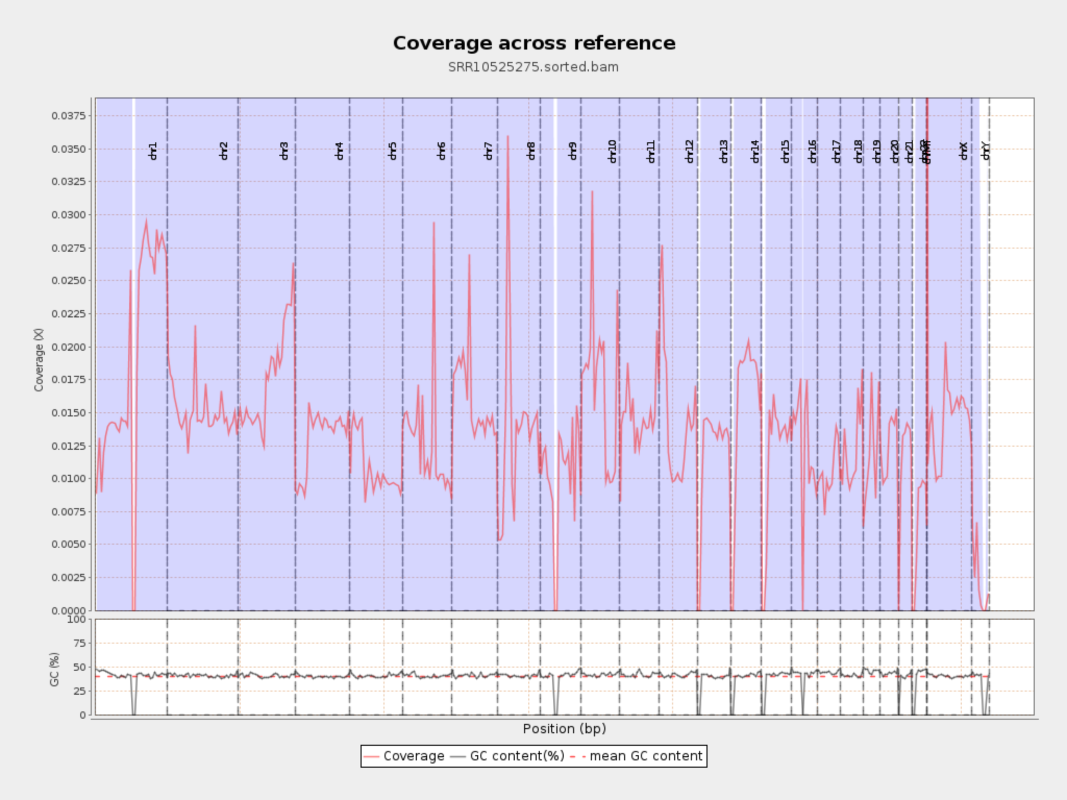
General error rate	0.52%
Mismatches	217,501
Insertions	3,081
Mapped reads with at least one insertion	0.42%
Deletions	9,020
Mapped reads with at least one deletion	1.22%
Homopolymer indels	44.46%

2.6. Chromosome stats

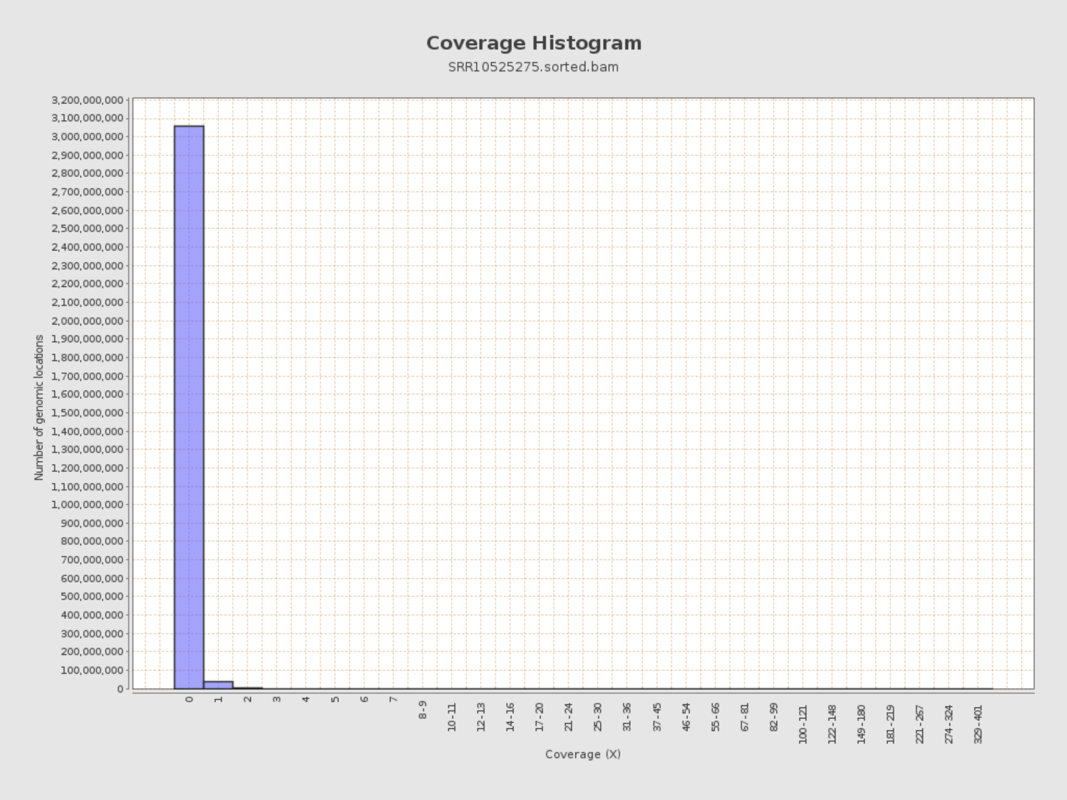
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4670087	0.0187	0.2978
chr2	243199373	3669454	0.0151	0.1986
chr3	198022430	3476963	0.0176	0.1394
chr4	191154276	2513276	0.0131	0.1229
chr5	180915260	1963183	0.0109	0.1086
chr6	171115067	2203179	0.0129	0.1275
chr7	159138663	2562807	0.0161	0.2197

chr8	146364022	2013779	0.0138	0.1611
chr9	141213431	1438150	0.0102	0.123
chr10	135534747	2334859	0.0172	0.1834
chr11	135006516	1984959	0.0147	0.1417
chr12	133851895	1949194	0.0146	0.1264
chr13	115169878	1363763	0.0118	0.1135
chr14	107349540	1663751	0.0155	0.1316
chr15	102531392	1164896	0.0114	0.1118
chr16	90354753	1110036	0.0123	0.1232
chr17	81195210	854552	0.0105	0.1099
chr18	78077248	936479	0.012	0.2056
chr19	59128983	716862	0.0121	0.2076
chr20	63025520	778453	0.0124	0.1157
chr21	48129895	556519	0.0116	0.1143
chr22	51304566	335659	0.0065	0.0837
chrMT	16571	4901	0.2958	0.6241
chrX	155270560	2252489	0.0145	0.1315
chrY	59373566	125395	0.0021	0.0692

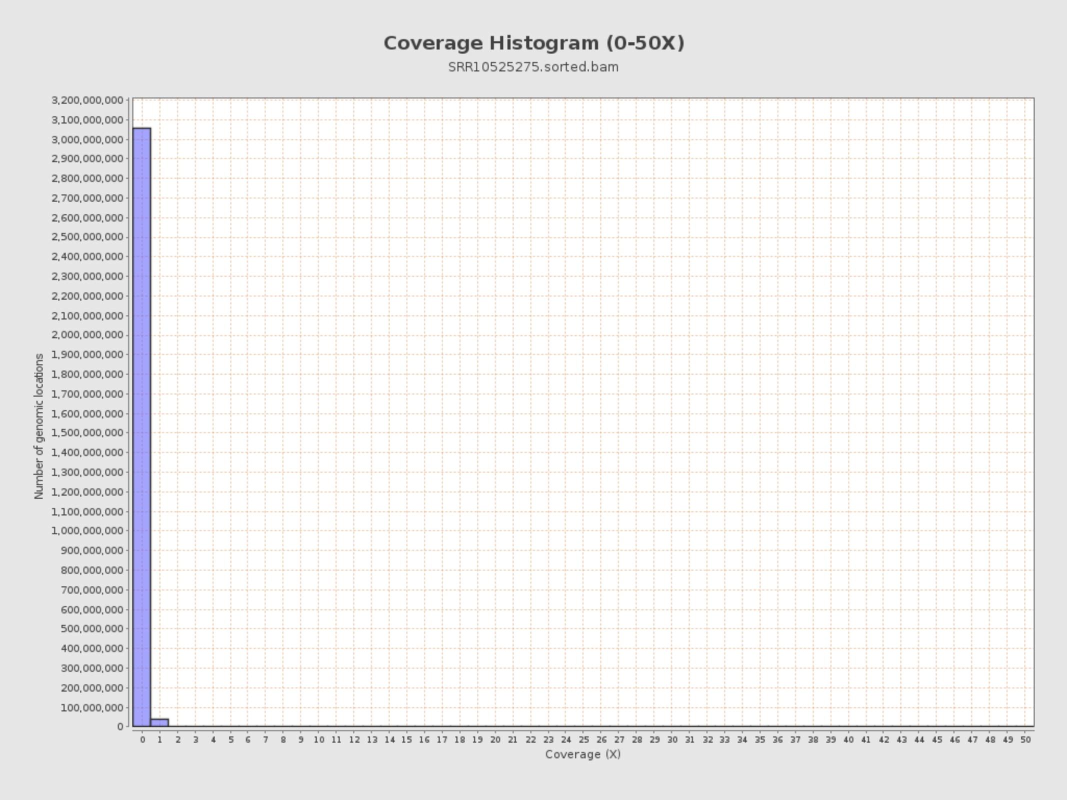
3. Results : Coverage across reference



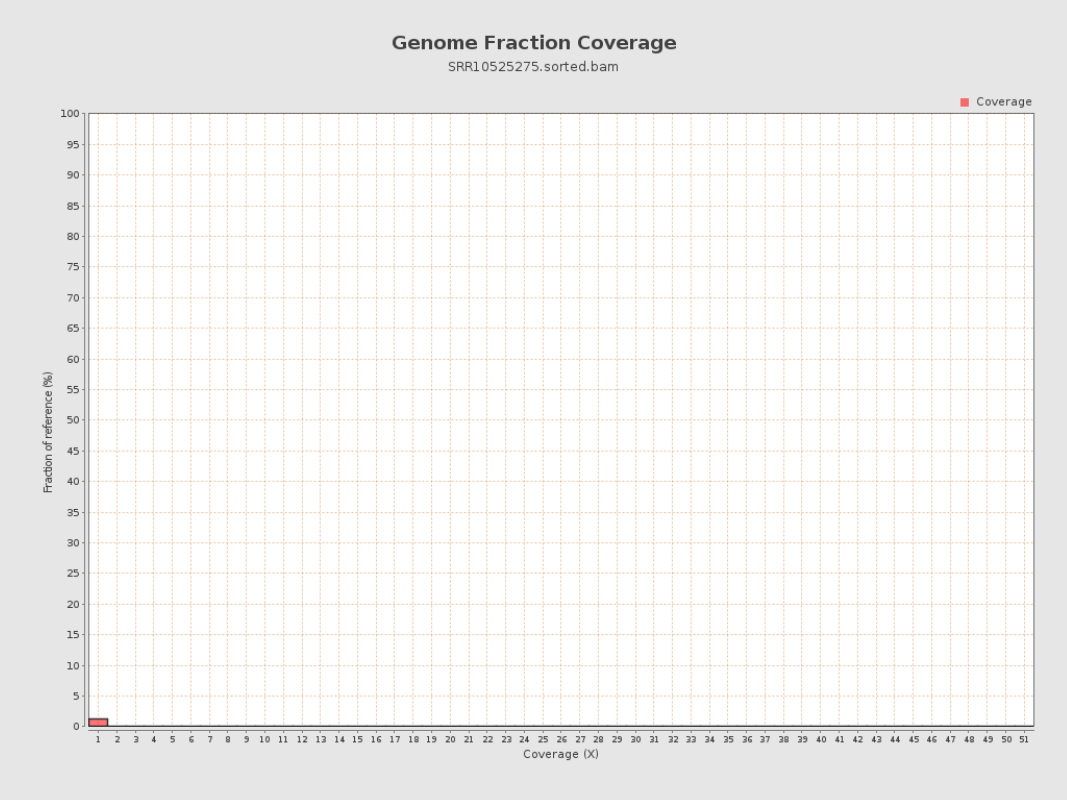
4. Results : Coverage Histogram



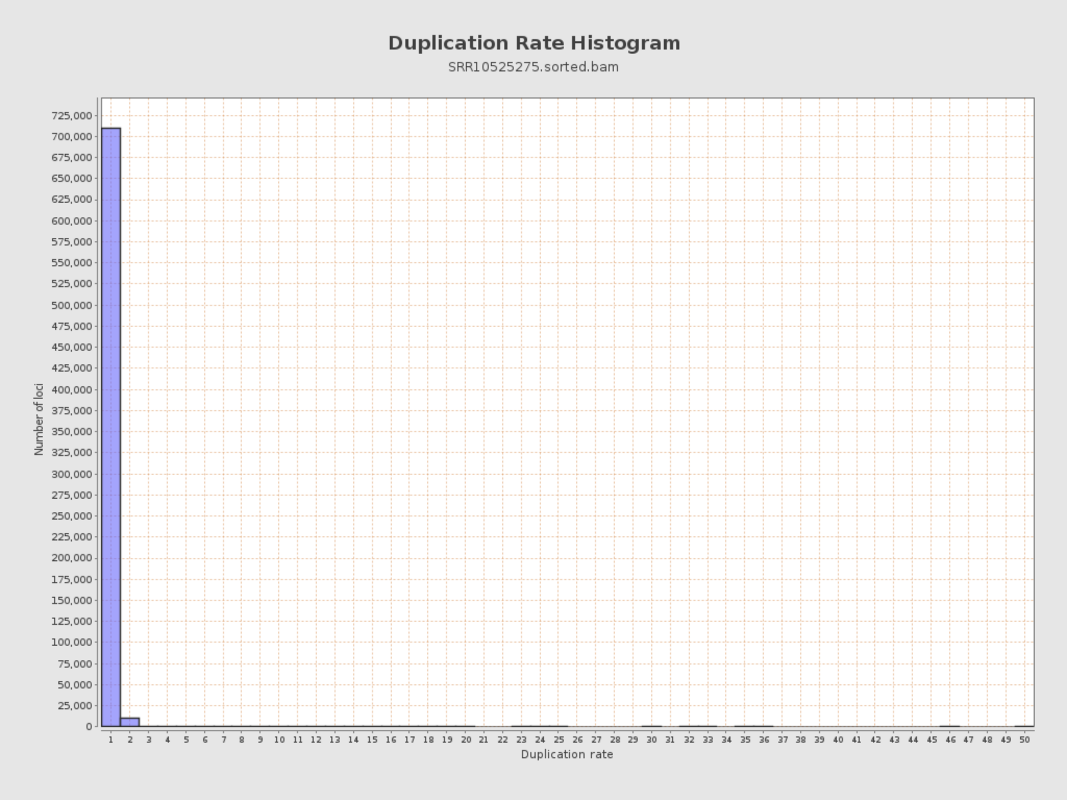
5. Results : Coverage Histogram (0-50X)



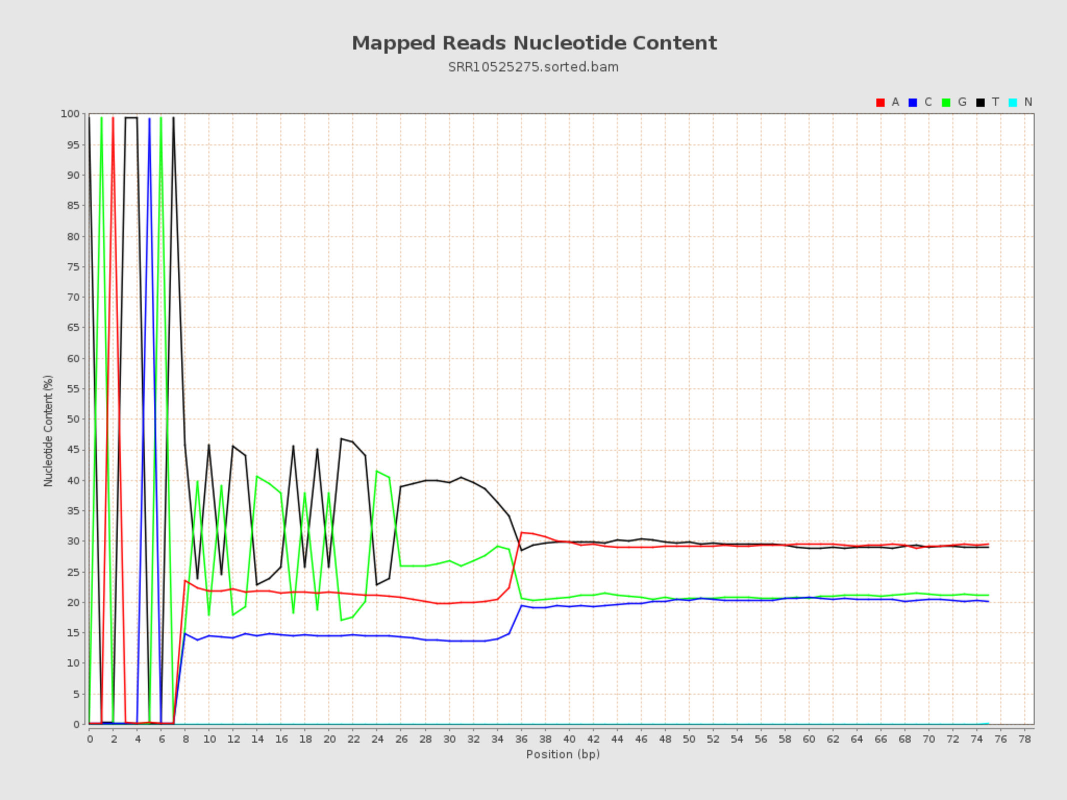
6. Results : Genome Fraction Coverage



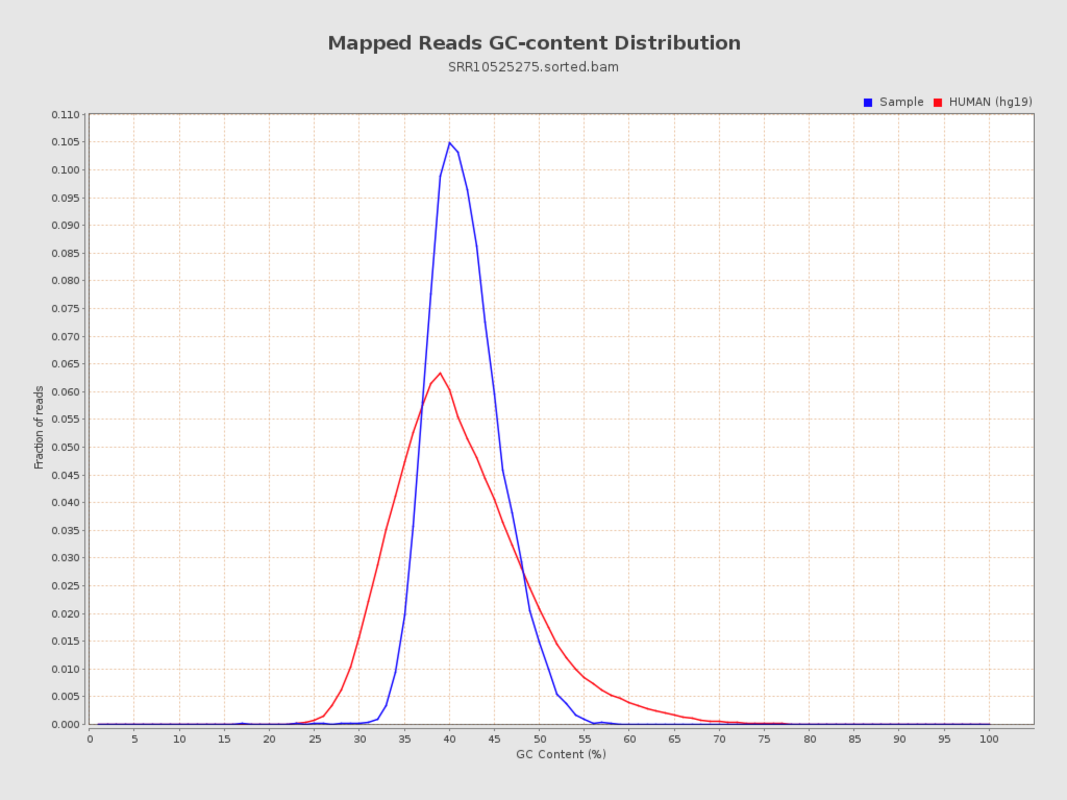
7. Results : Duplication Rate Histogram



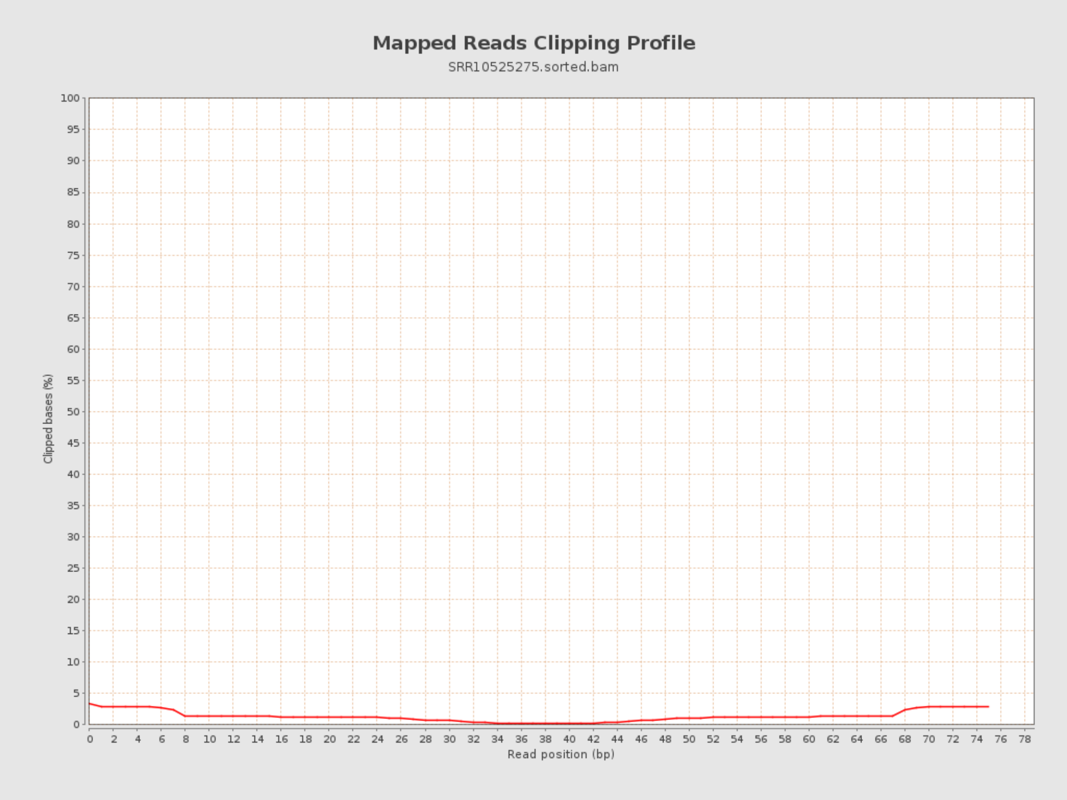
8. Results : Mapped Reads Nucleotide Content



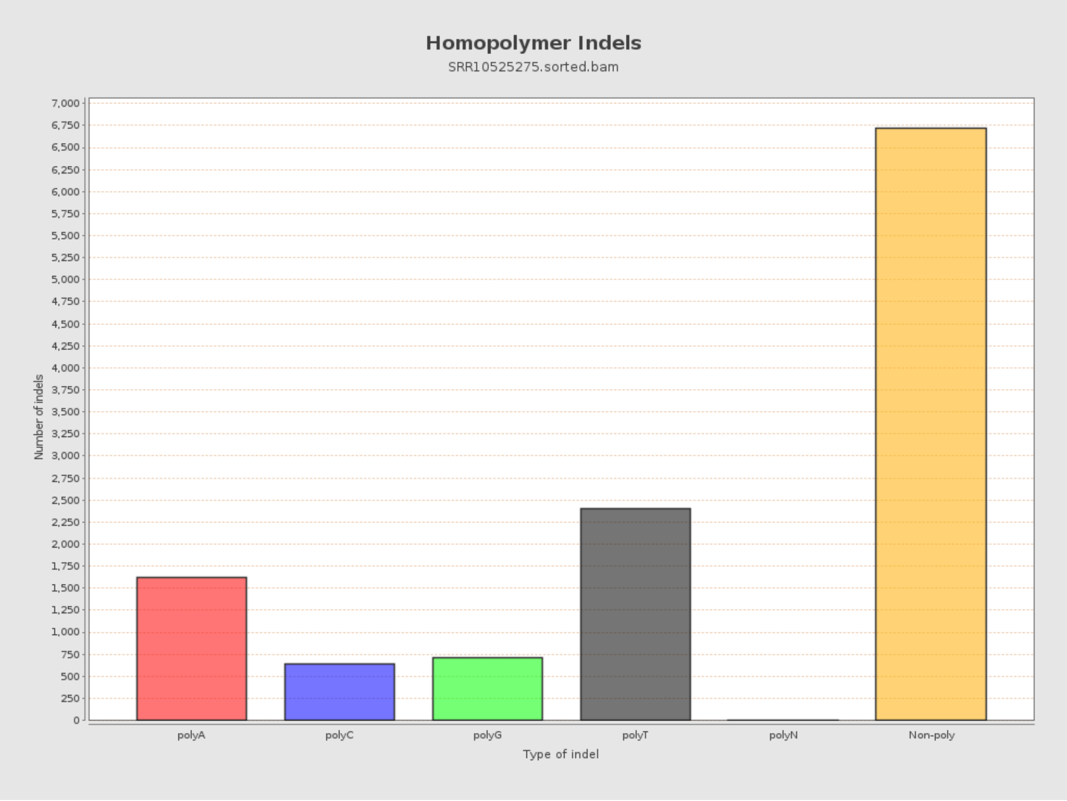
9. Results : Mapped Reads GC-content Distribution



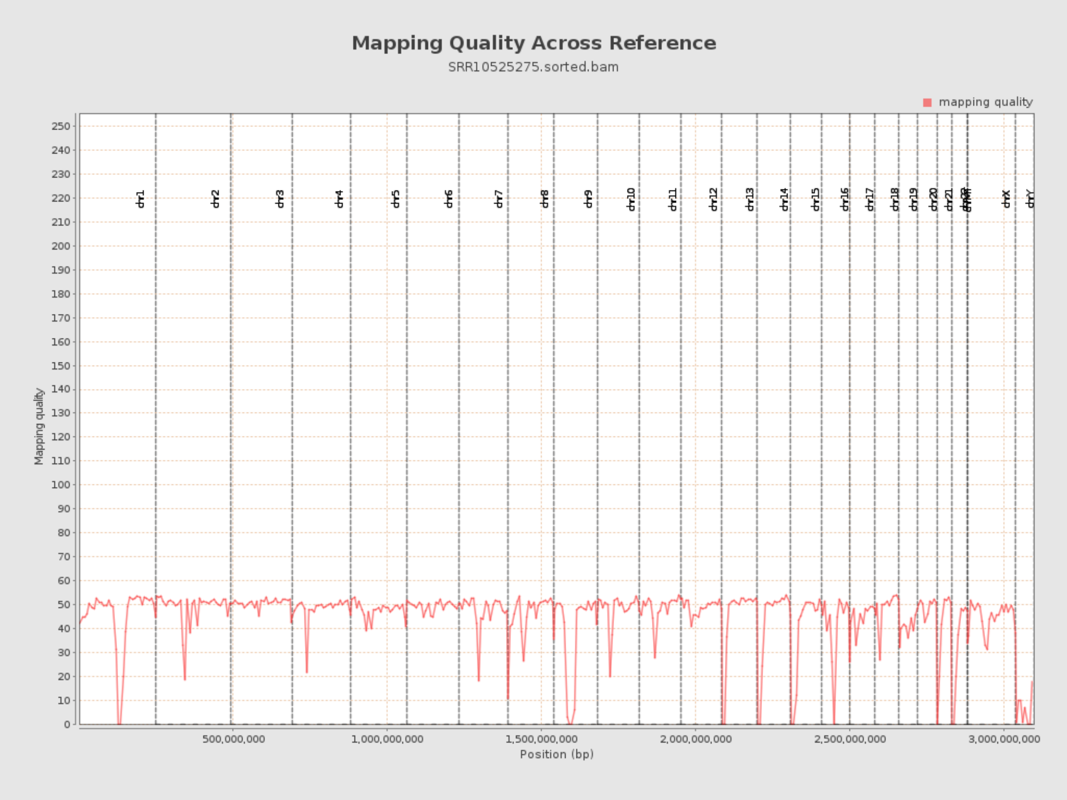
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram