Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:05:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525169.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_SRR10525169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	943,881
Mapped reads	867,463 / 91.9%
Unmapped reads	76,418 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,074 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	19,284 / 2.04%
Duplication rate	1.59%
Clipped reads	869,394 / 92.11%

2.2. ACGT Content

Number/percentage of A's	13,256,852 / 25.52%
Number/percentage of C's	9,932,621 / 19.12%
Number/percentage of T's	16,293,647 / 31.37%
Number/percentage of G's	12,461,418 / 23.99%
Number/percentage of N's	1,291 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1845

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

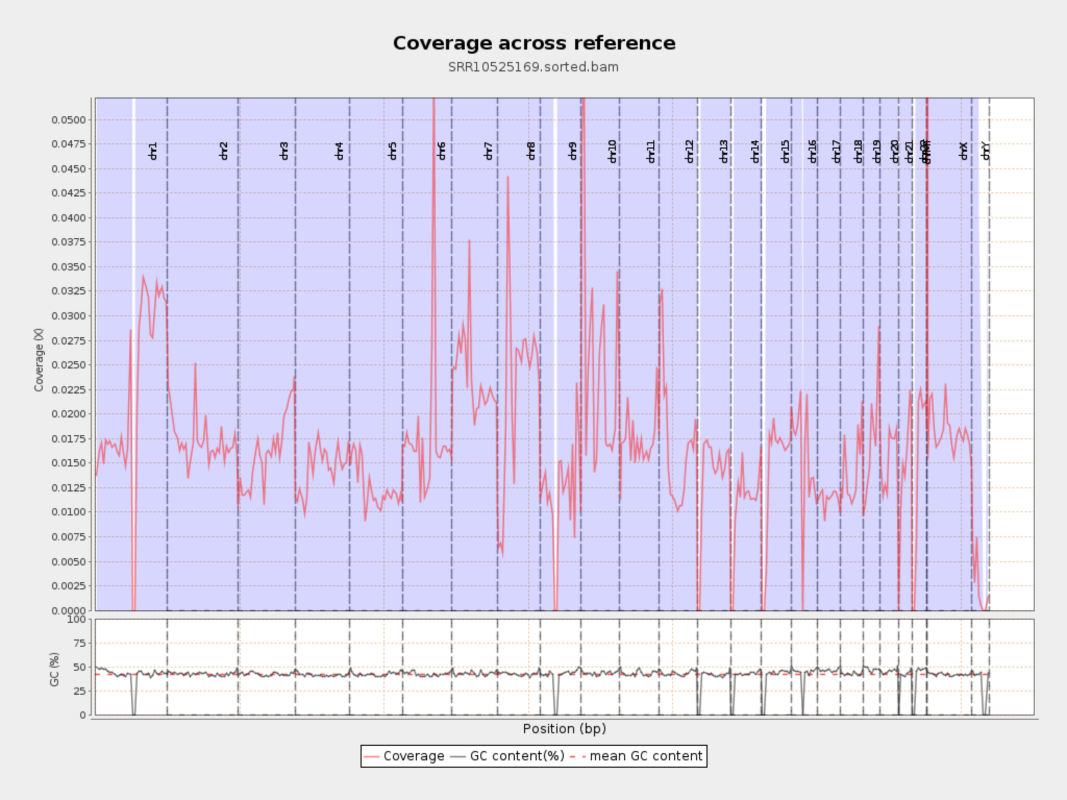
General error rate	0.5%
Mismatches	256,410
Insertions	2,946
Mapped reads with at least one insertion	0.34%
Deletions	10,340
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.75%

2.6. Chromosome stats

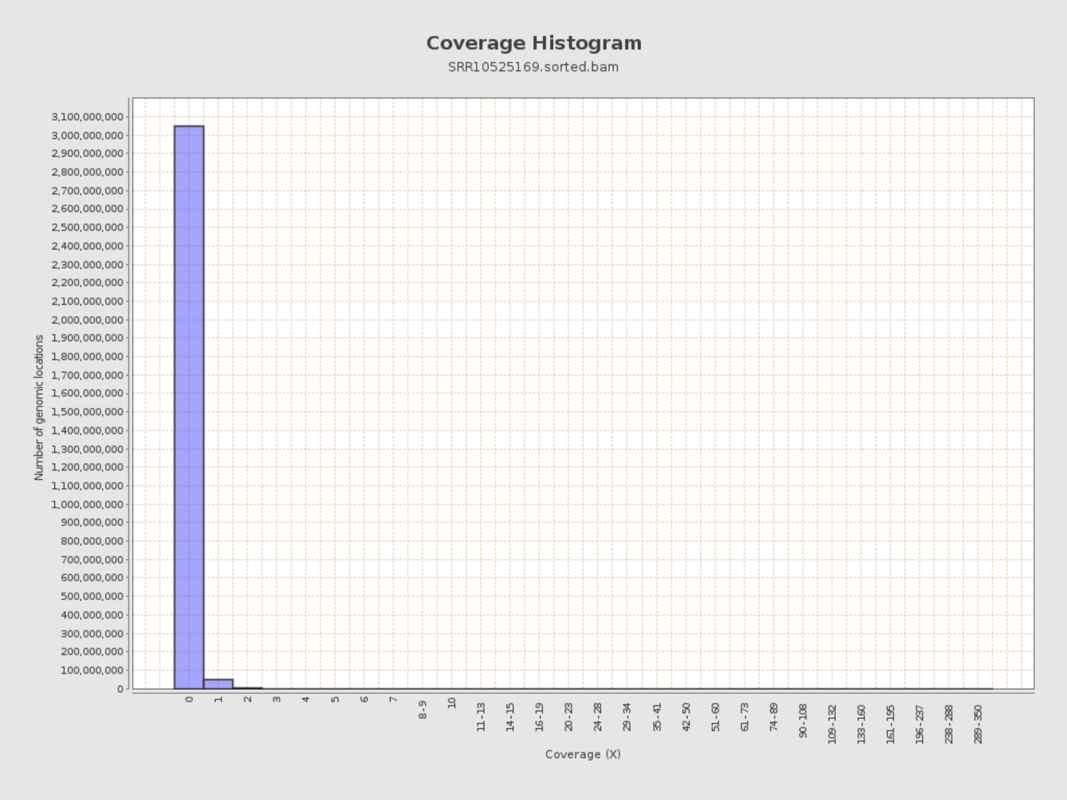
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5460111	0.0219	0.3173
chr2	243199373	4210796	0.0173	0.2069
chr3	198022430	3177921	0.016	0.1343
chr4	191154276	2790873	0.0146	0.1288
chr5	180915260	2274473	0.0126	0.117
chr6	171115067	3105819	0.0182	0.1477
chr7	159138663	3812569	0.024	0.3127

chr8	146364022	3357475	0.0229	0.1815
chr9	141213431	1700792	0.012	0.1391
chr10	135534747	3497531	0.0258	0.2063
chr11	135006516	2343862	0.0174	0.1644
chr12	133851895	2257060	0.0169	0.1364
chr13	115169878	1553072	0.0135	0.122
chr14	107349540	1155606	0.0108	0.1133
chr15	102531392	1426133	0.0139	0.1238
chr16	90354753	1391459	0.0154	0.1389
chr17	81195210	926723	0.0114	0.1148
chr18	78077248	1096377	0.014	0.2516
chr19	59128983	1023409	0.0173	0.2261
chr20	63025520	962539	0.0153	0.1302
chr21	48129895	702850	0.0146	0.1308
chr22	51304566	752361	0.0147	0.1262
chrMT	16571	5109	0.3083	0.5479
chrX	155270560	2834438	0.0183	0.1484
chrY	59373566	142995	0.0024	0.0705

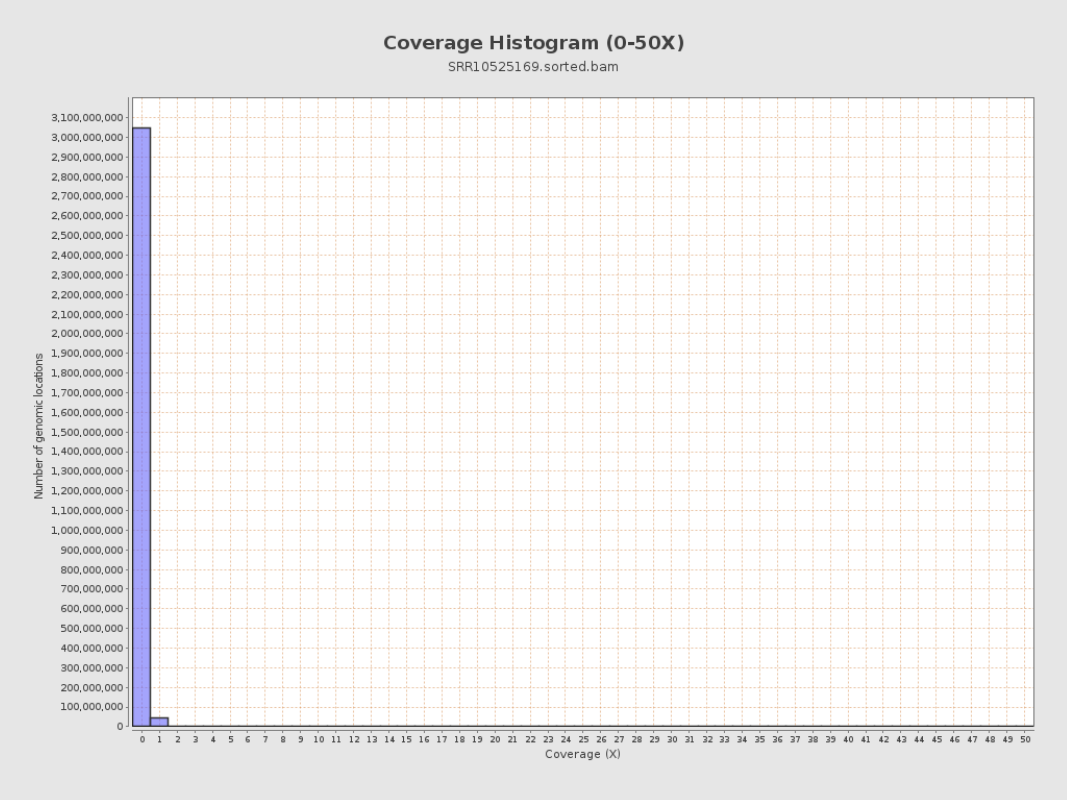
3. Results : Coverage across reference



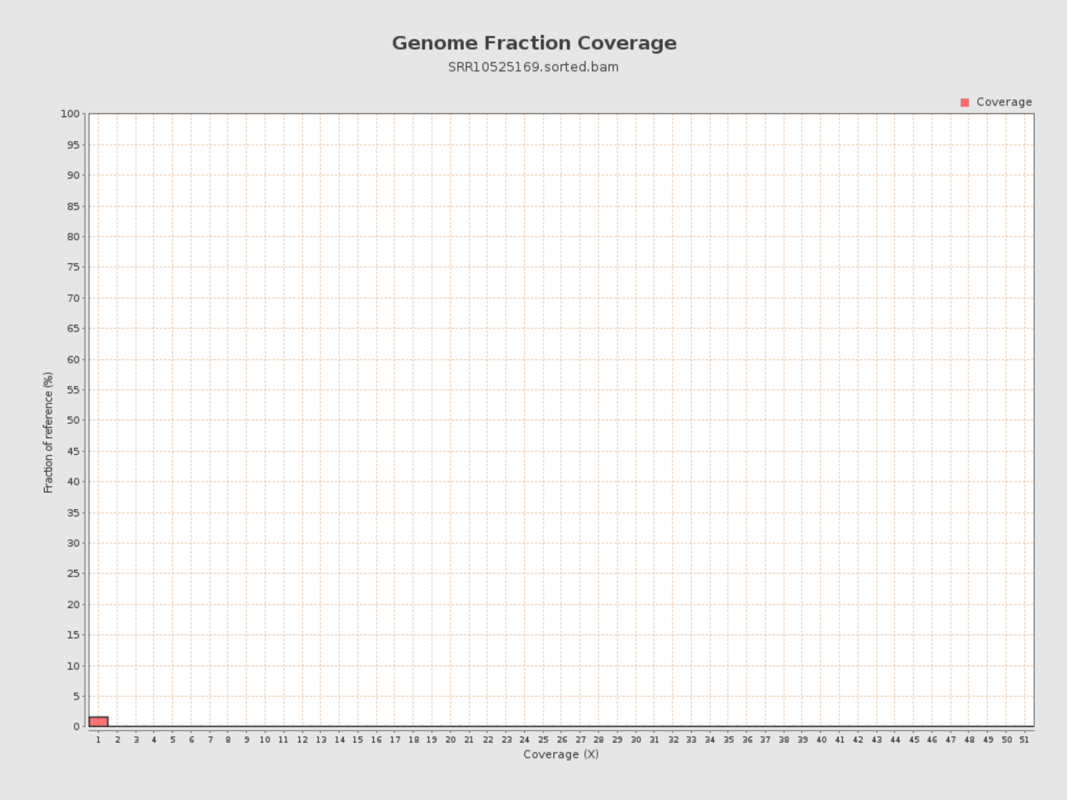
4. Results : Coverage Histogram



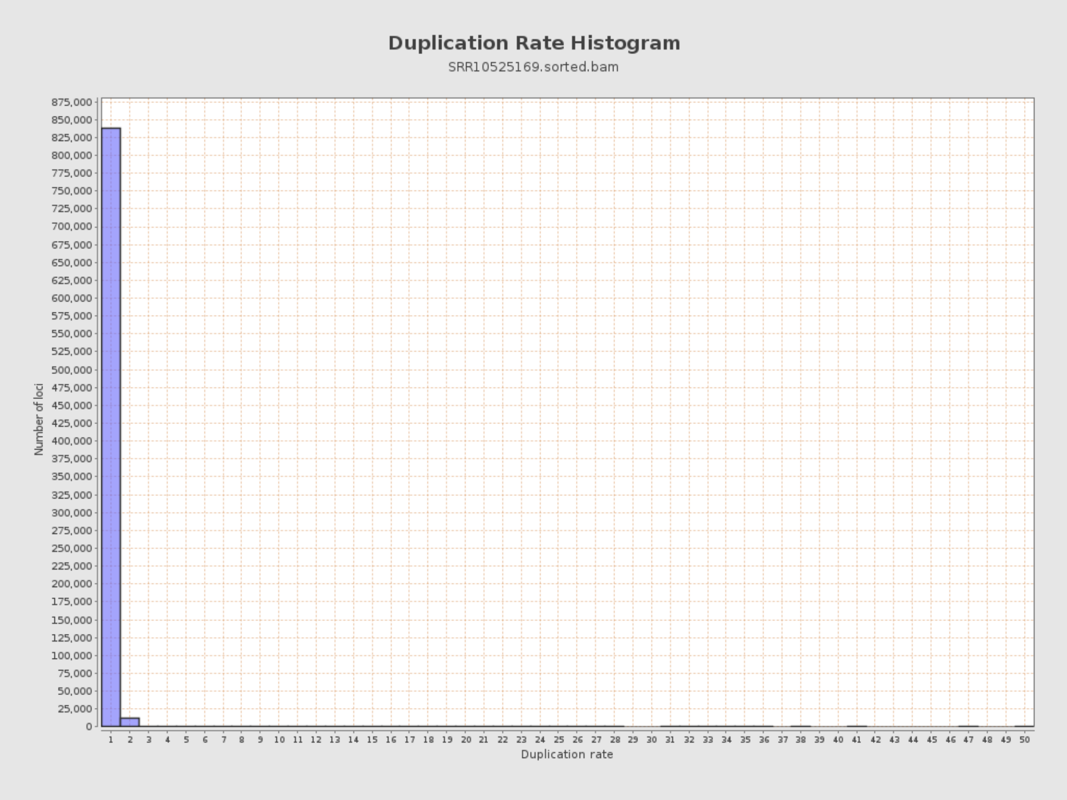
5. Results : Coverage Histogram (0-50X)



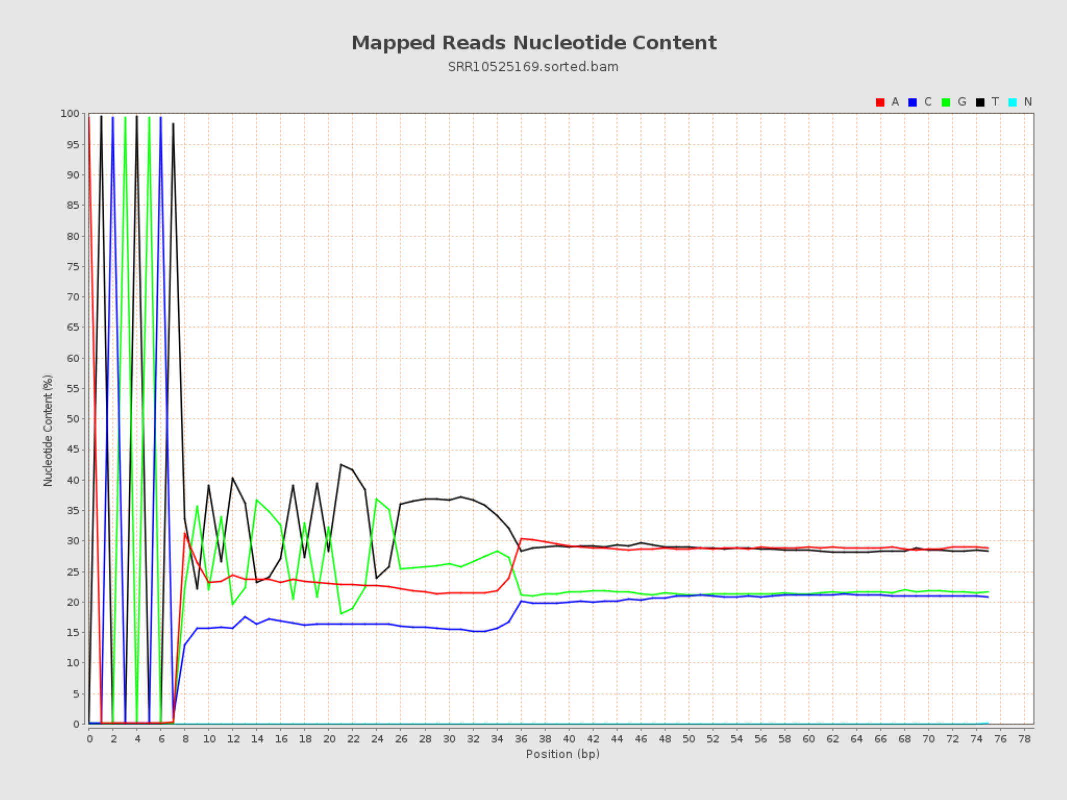
6. Results : Genome Fraction Coverage



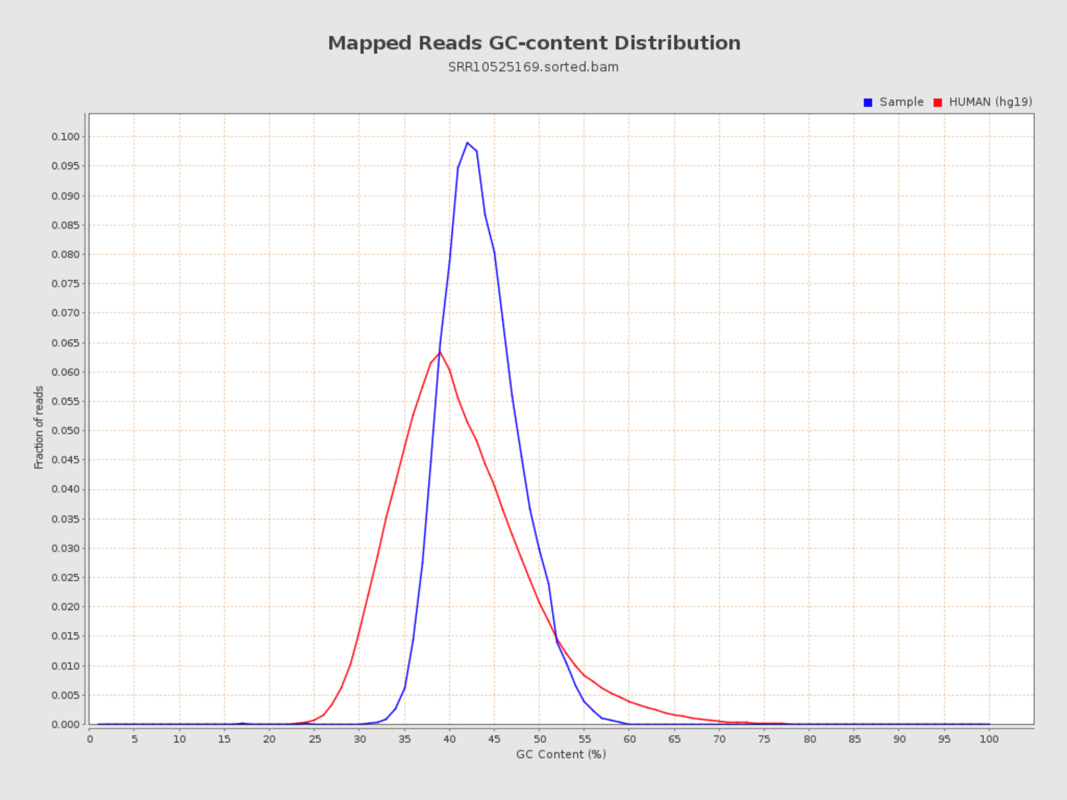
7. Results : Duplication Rate Histogram



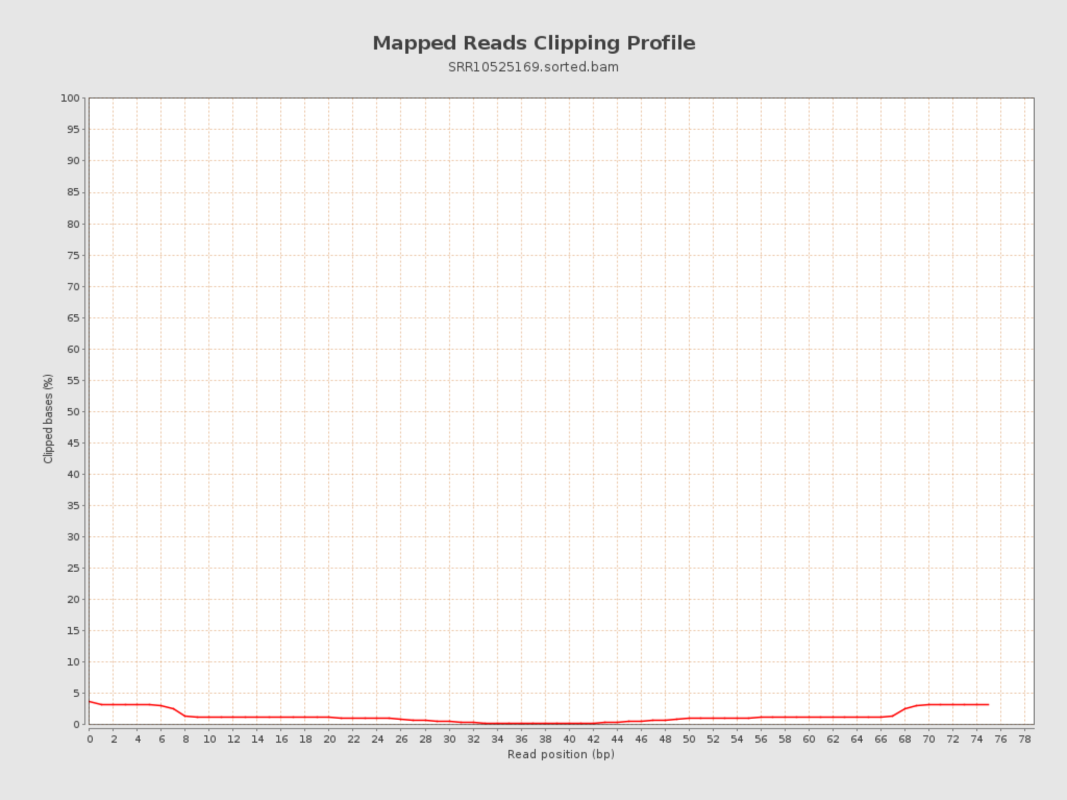
8. Results : Mapped Reads Nucleotide Content



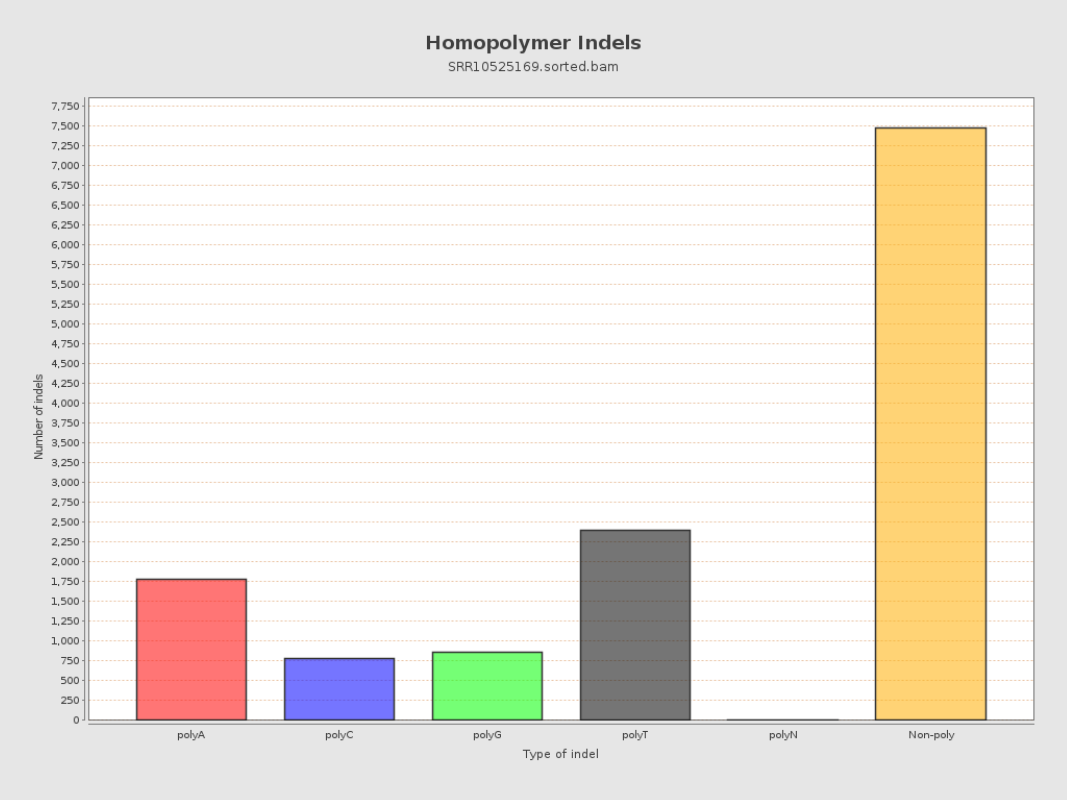
9. Results : Mapped Reads GC-content Distribution



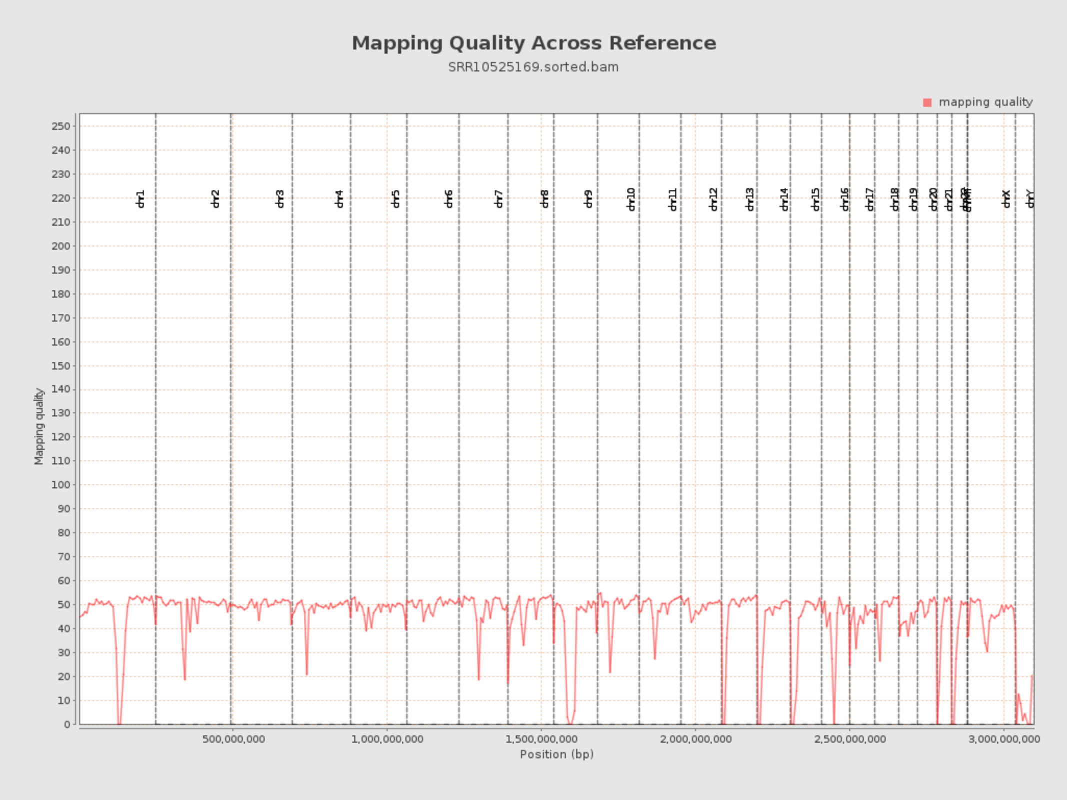
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram