Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:39:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525022.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_SRR10525022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525022.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:39:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525022.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,854,707
Mapped reads	1,696,941 / 91.49%
Unmapped reads	157,766 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,016 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	59,291 / 3.2%
Duplication rate	2.56%
Clipped reads	1,698,387 / 91.57%

2.2. ACGT Content

Number/percentage of A's	25,003,033 / 25.72%
Number/percentage of C's	19,849,982 / 20.42%
Number/percentage of T's	29,454,074 / 30.3%
Number/percentage of G's	22,889,380 / 23.55%
Number/percentage of N's	2,936 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2835

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

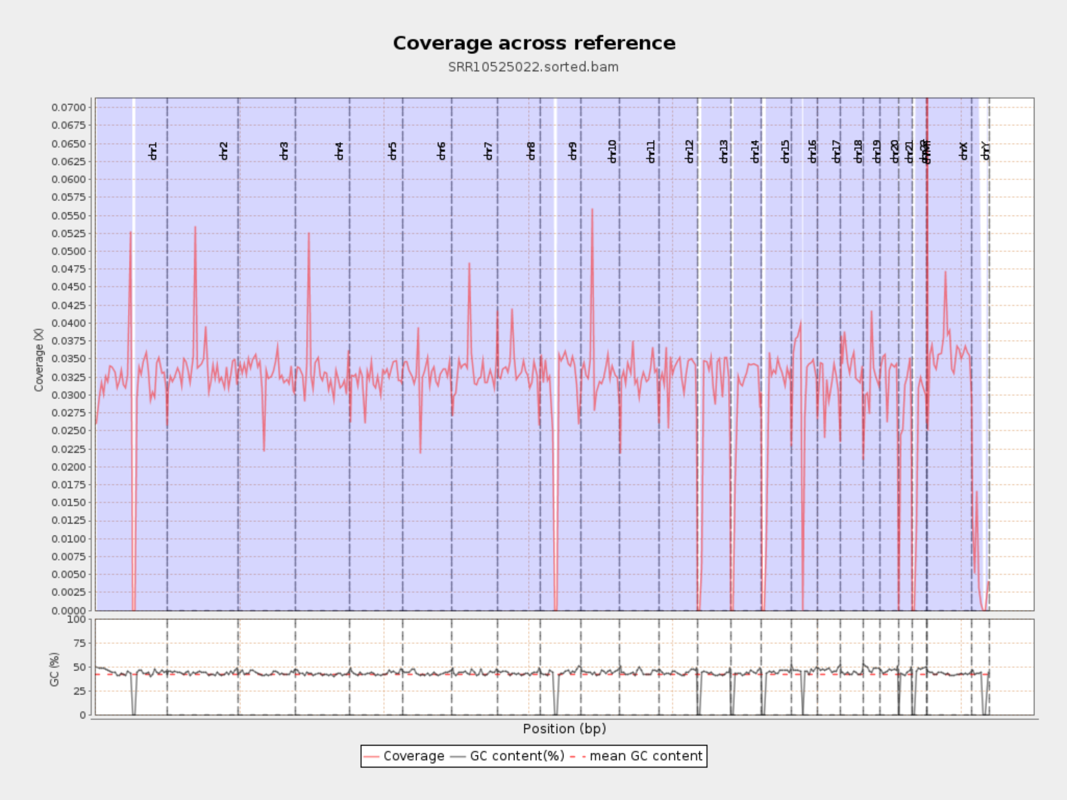
General error rate	0.49%
Mismatches	466,267
Insertions	6,800
Mapped reads with at least one insertion	0.4%
Deletions	15,827
Mapped reads with at least one deletion	0.93%
Homopolymer indels	41.91%

2.6. Chromosome stats

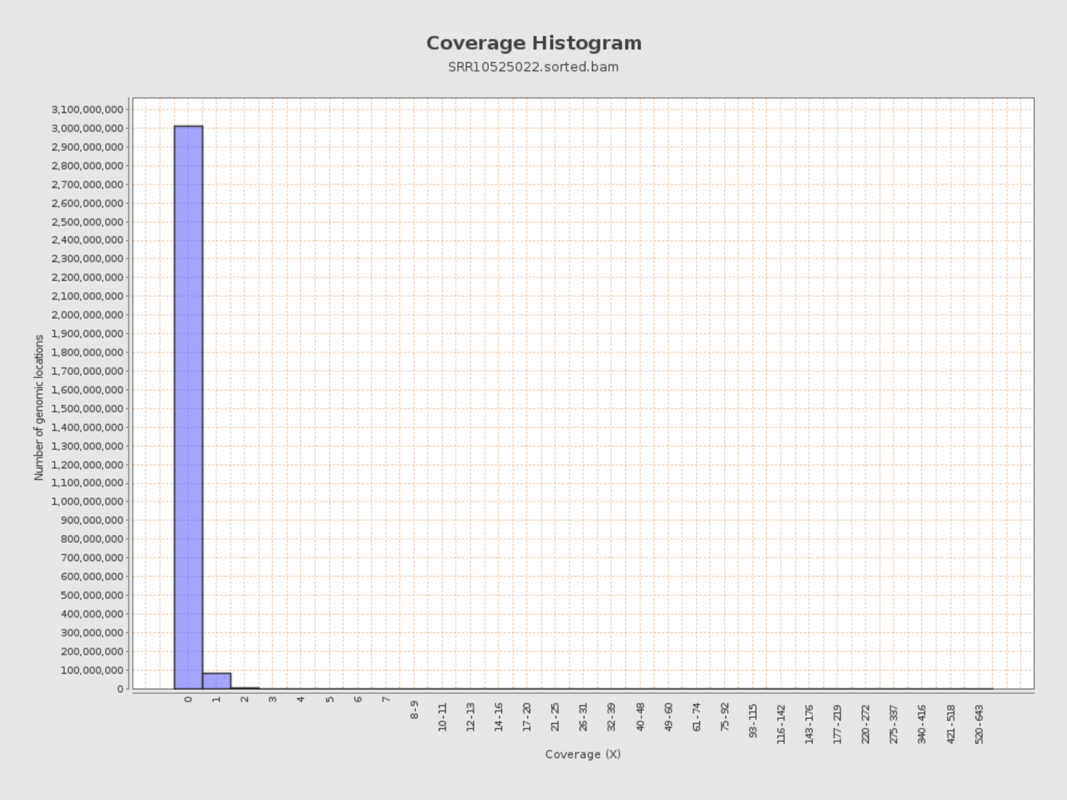
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7654374	0.0307	0.5212
chr2	243199373	8249969	0.0339	0.3006
chr3	198022430	6521449	0.0329	0.1984
chr4	191154276	6350653	0.0332	0.2178
chr5	180915260	5868270	0.0324	0.1983
chr6	171115067	5625582	0.0329	0.2183
chr7	159138663	5324465	0.0335	0.3144

chr8	146364022	4879735	0.0333	0.3026
chr9	141213431	4156003	0.0294	0.2781
chr10	135534747	4590983	0.0339	0.2816
chr11	135006516	4430736	0.0328	0.2634
chr12	133851895	4427607	0.0331	0.2055
chr13	115169878	3191529	0.0277	0.1808
chr14	107349540	2951484	0.0275	0.1945
chr15	102531392	2761563	0.0269	0.1795
chr16	90354753	2818850	0.0312	0.2069
chr17	81195210	2513785	0.031	0.205
chr18	78077248	2681796	0.0343	0.4817
chr19	59128983	1885473	0.0319	0.3831
chr20	63025520	2073710	0.0329	0.2075
chr21	48129895	1286710	0.0267	0.2034
chr22	51304566	1101399	0.0215	0.1603
chrMT	16571	3167	0.1911	0.4637
chrX	155270560	5581263	0.0359	0.2391
chrY	59373566	295021	0.005	0.125

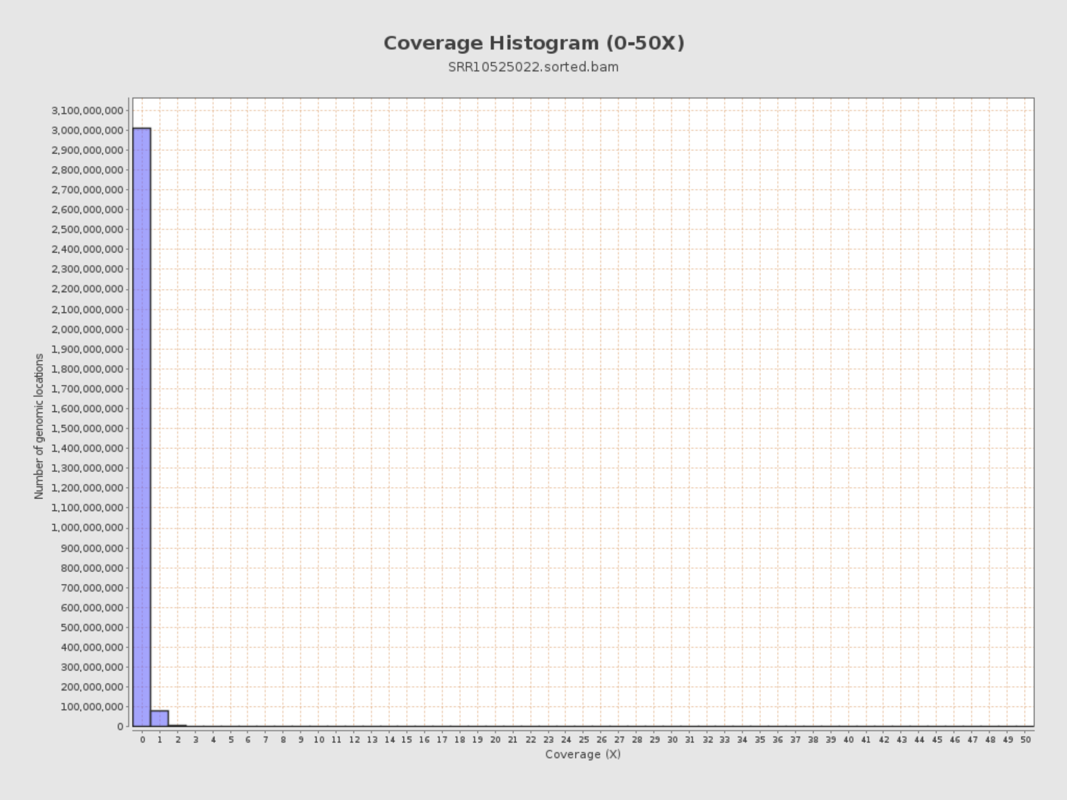
3. Results : Coverage across reference



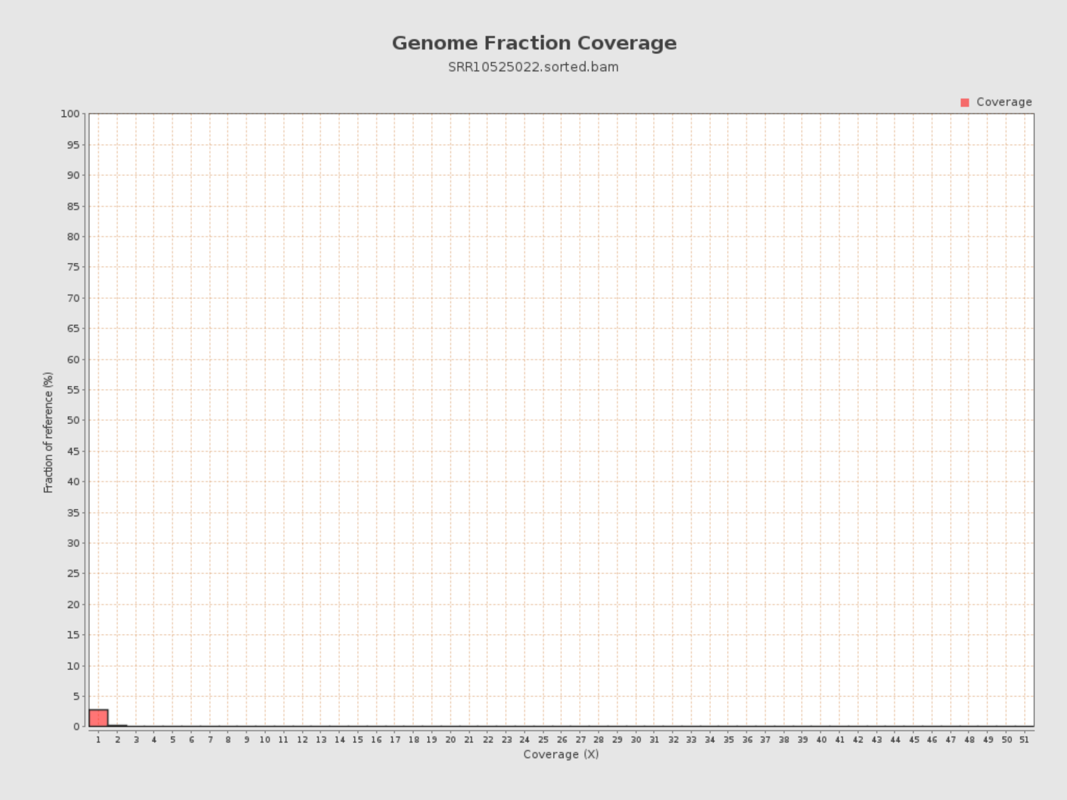
4. Results : Coverage Histogram



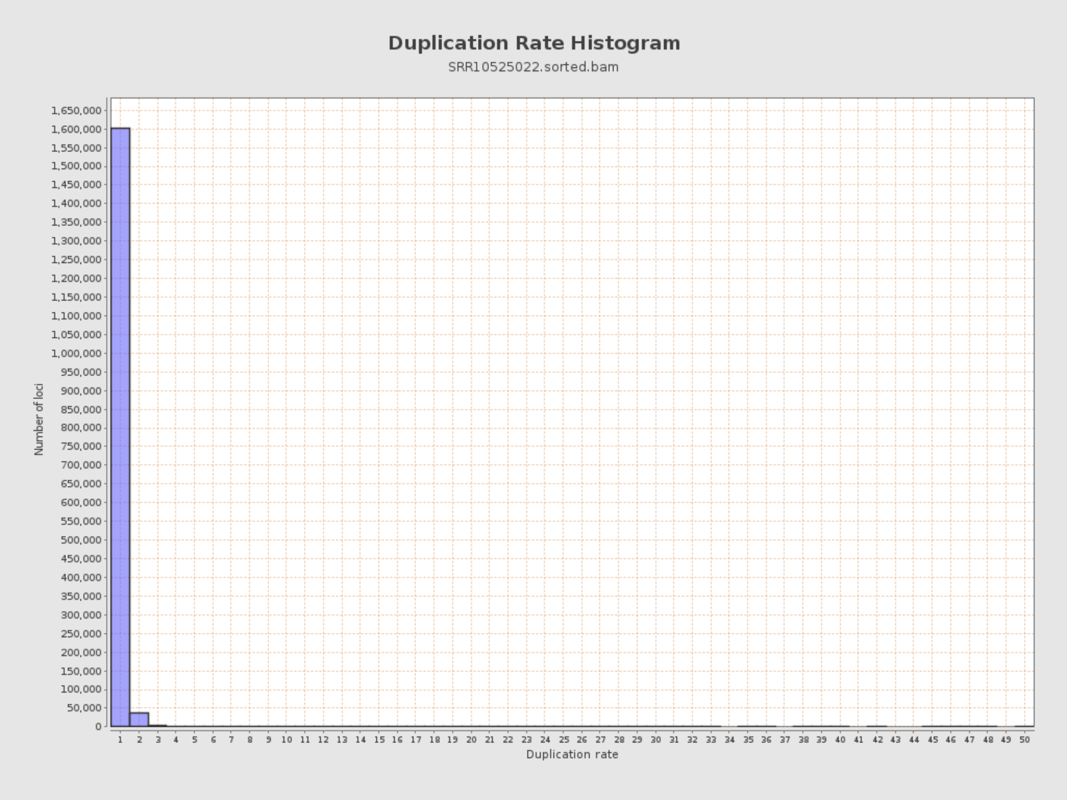
5. Results : Coverage Histogram (0-50X)



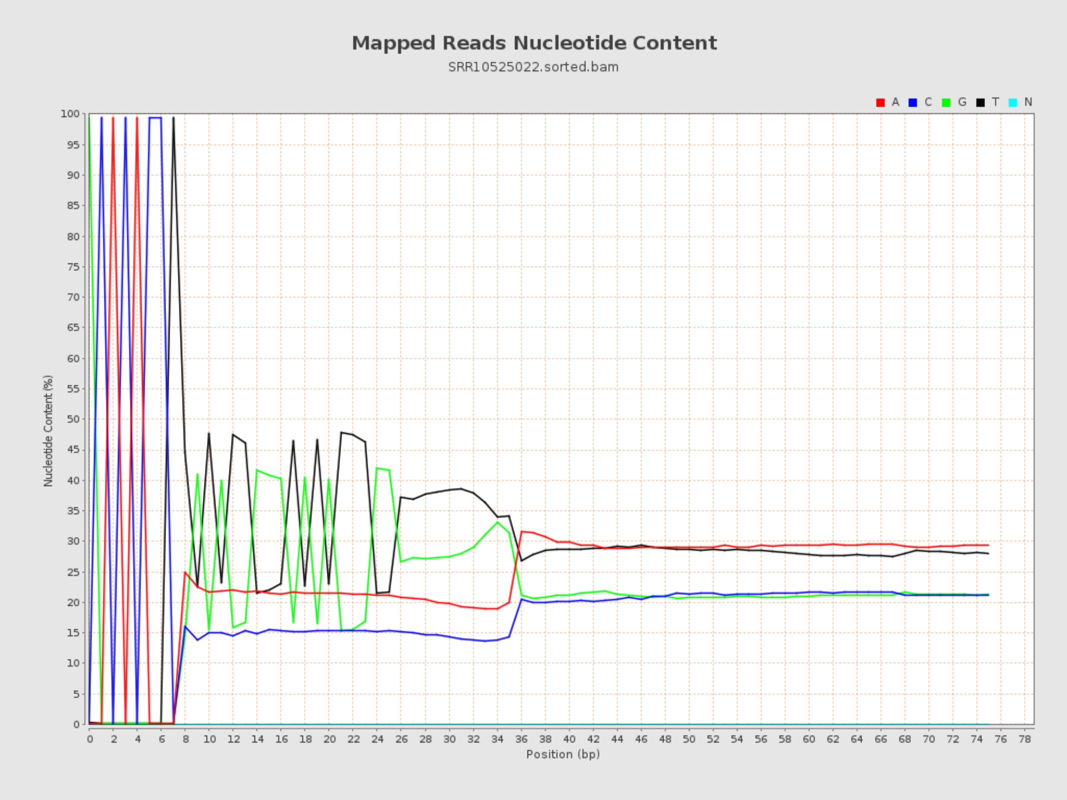
6. Results : Genome Fraction Coverage



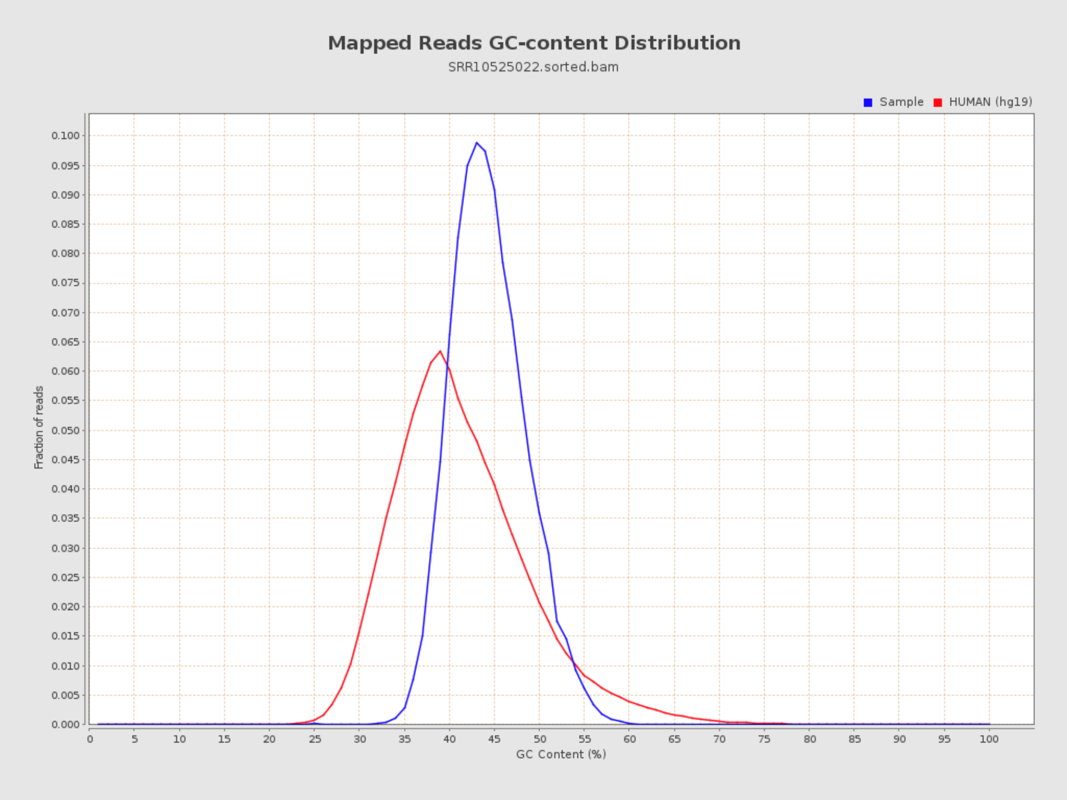
7. Results : Duplication Rate Histogram



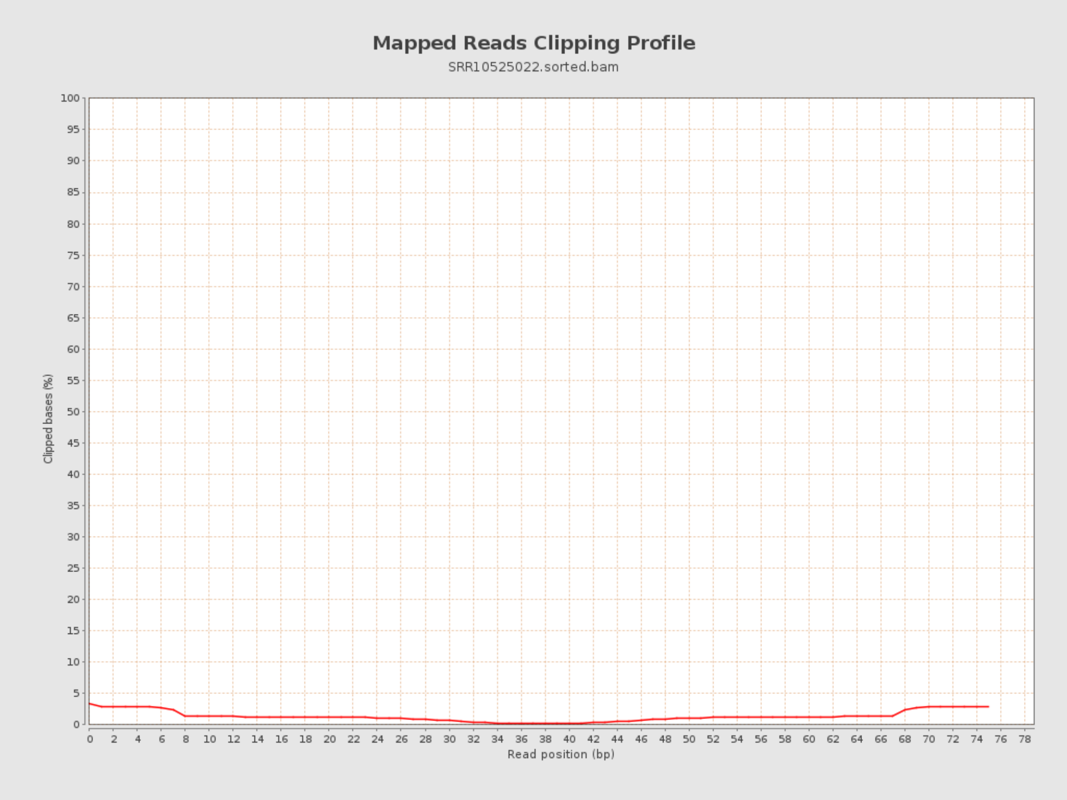
8. Results : Mapped Reads Nucleotide Content



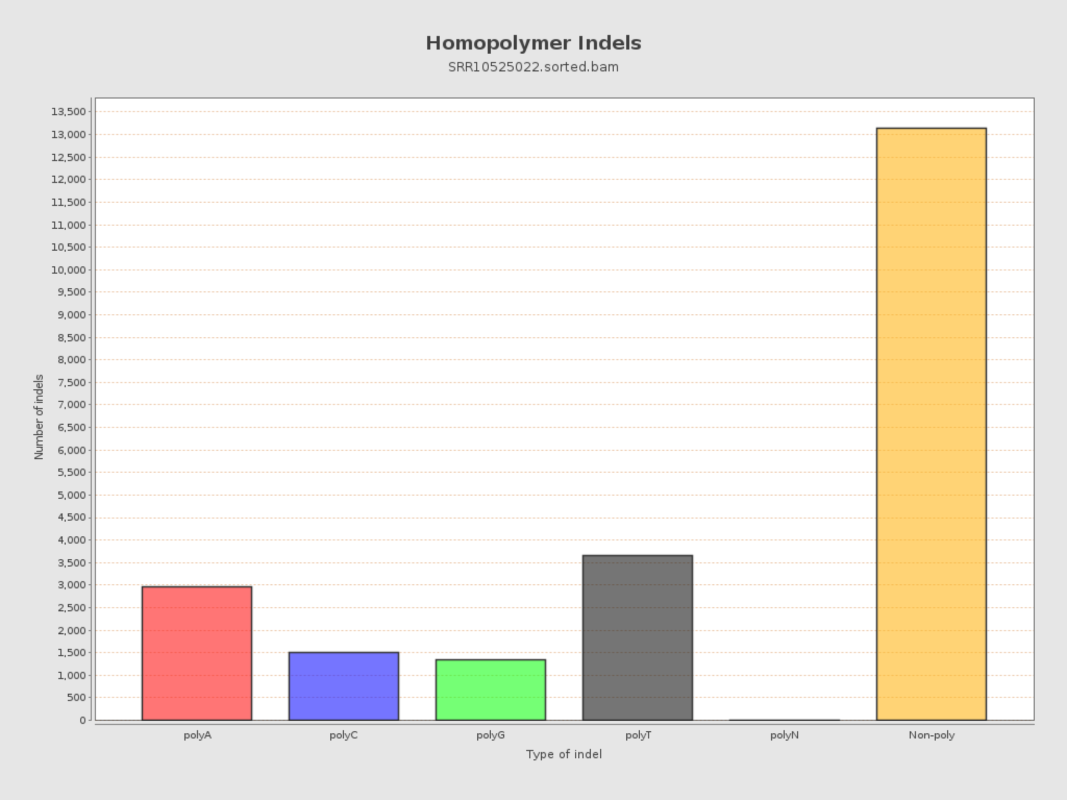
9. Results : Mapped Reads GC-content Distribution



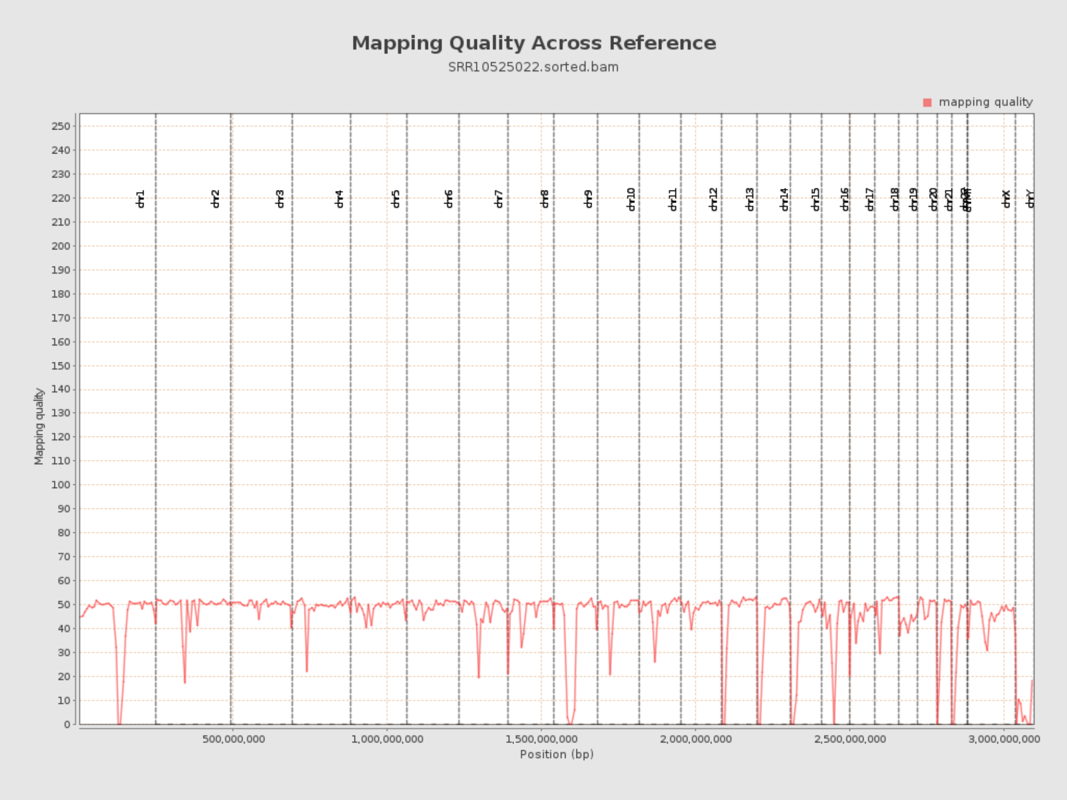
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram