Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:02:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525185.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_SRR10525185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:02:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	762,341
Mapped reads	708,405 / 92.92%
Unmapped reads	53,936 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,966 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	16,336 / 2.14%
Duplication rate	1.68%
Clipped reads	708,725 / 92.97%

2.2. ACGT Content

Number/percentage of A's	10,734,764 / 25.35%
Number/percentage of C's	7,871,515 / 18.59%
Number/percentage of T's	12,889,966 / 30.44%
Number/percentage of G's	10,846,175 / 25.61%
Number/percentage of N's	1,077 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0137

Standard Deviation	0.1626

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

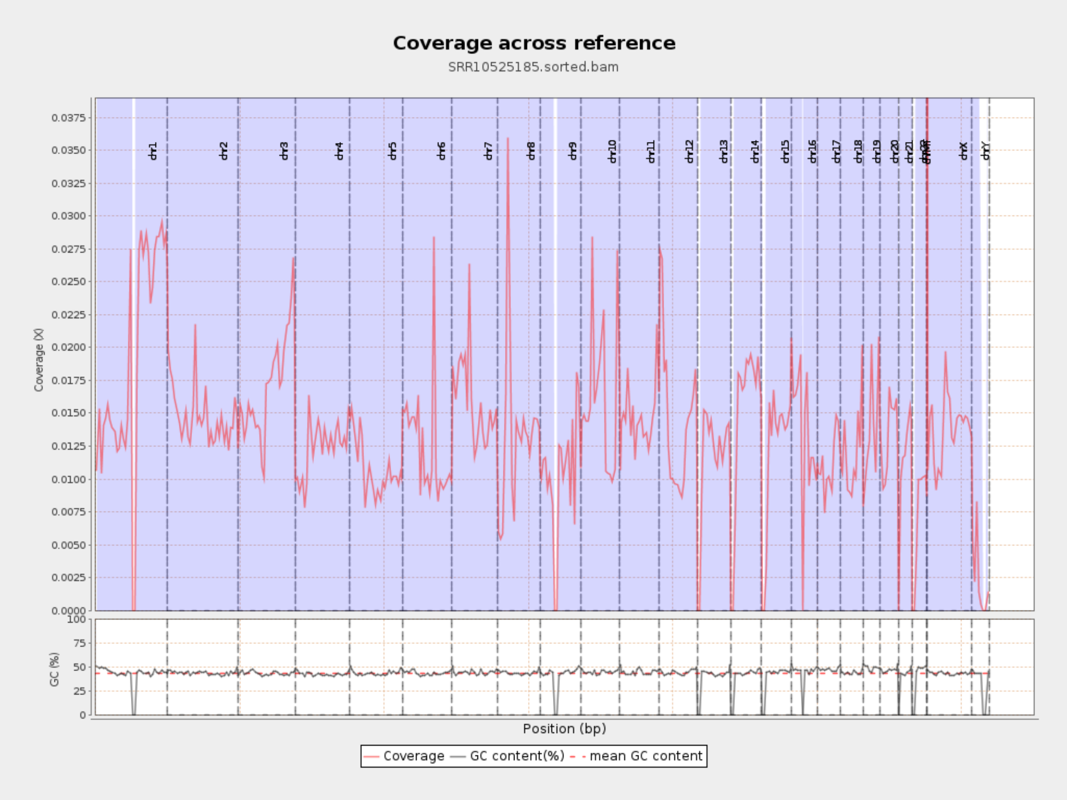
General error rate	0.51%
Mismatches	209,715
Insertions	3,000
Mapped reads with at least one insertion	0.42%
Deletions	8,599
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.21%

2.6. Chromosome stats

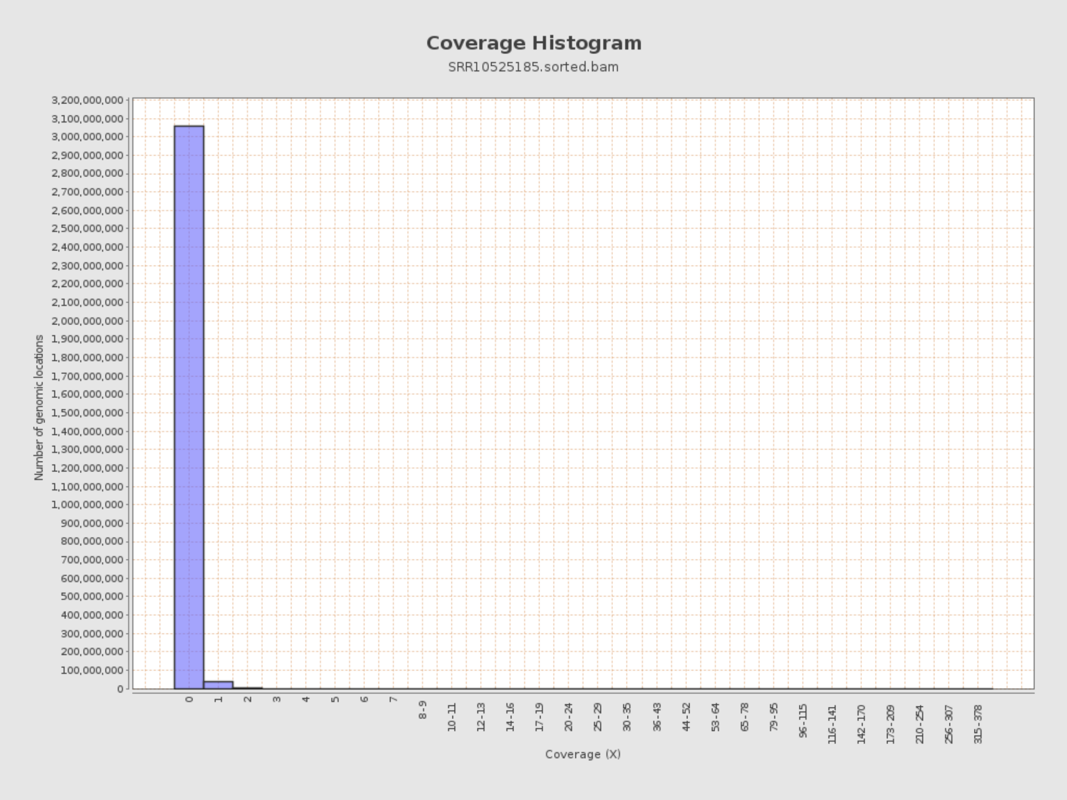
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4720852	0.0189	0.307
chr2	243199373	3589837	0.0148	0.1799
chr3	198022430	3372276	0.017	0.1353
chr4	191154276	2373569	0.0124	0.1197
chr5	180915260	1939829	0.0107	0.1072
chr6	171115067	2147505	0.0126	0.1242
chr7	159138663	2552537	0.016	0.2199

chr8	146364022	1991949	0.0136	0.1406
chr9	141213431	1444124	0.0102	0.1207
chr10	135534747	2216879	0.0164	0.1636
chr11	135006516	1978573	0.0147	0.1404
chr12	133851895	1956748	0.0146	0.1264
chr13	115169878	1322908	0.0115	0.1116
chr14	107349540	1604681	0.0149	0.1285
chr15	102531392	1203626	0.0117	0.1118
chr16	90354753	1227188	0.0136	0.1279
chr17	81195210	909530	0.0112	0.1125
chr18	78077248	912322	0.0117	0.2187
chr19	59128983	827748	0.014	0.2063
chr20	63025520	834366	0.0132	0.1204
chr21	48129895	555081	0.0115	0.1182
chr22	51304566	360809	0.007	0.0868
chrMT	16571	20797	1.255	1.238
chrX	155270560	2158982	0.0139	0.1284
chrY	59373566	134260	0.0023	0.0853

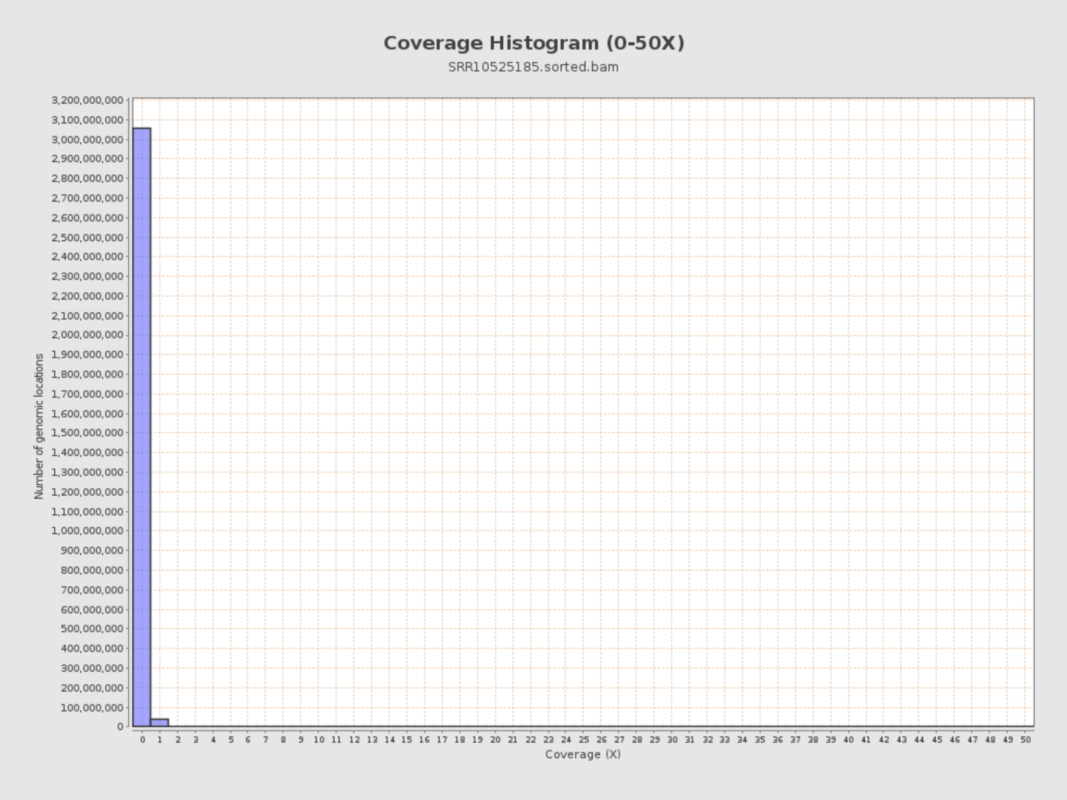
3. Results : Coverage across reference



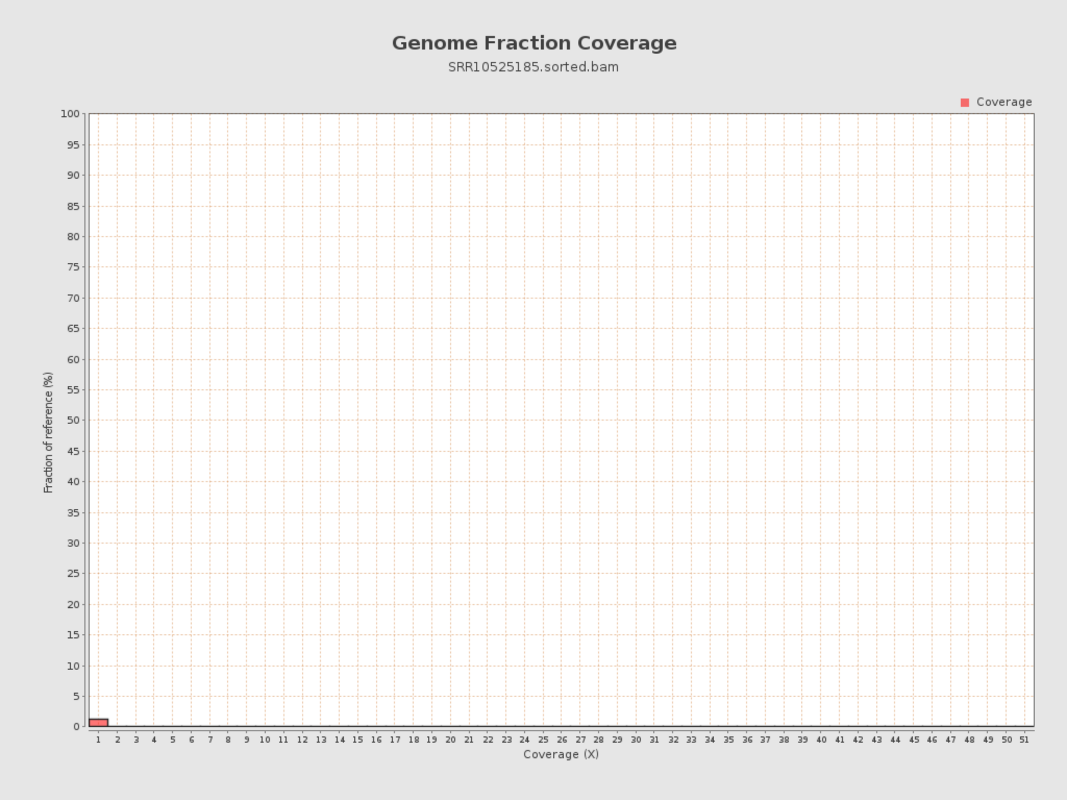
4. Results : Coverage Histogram



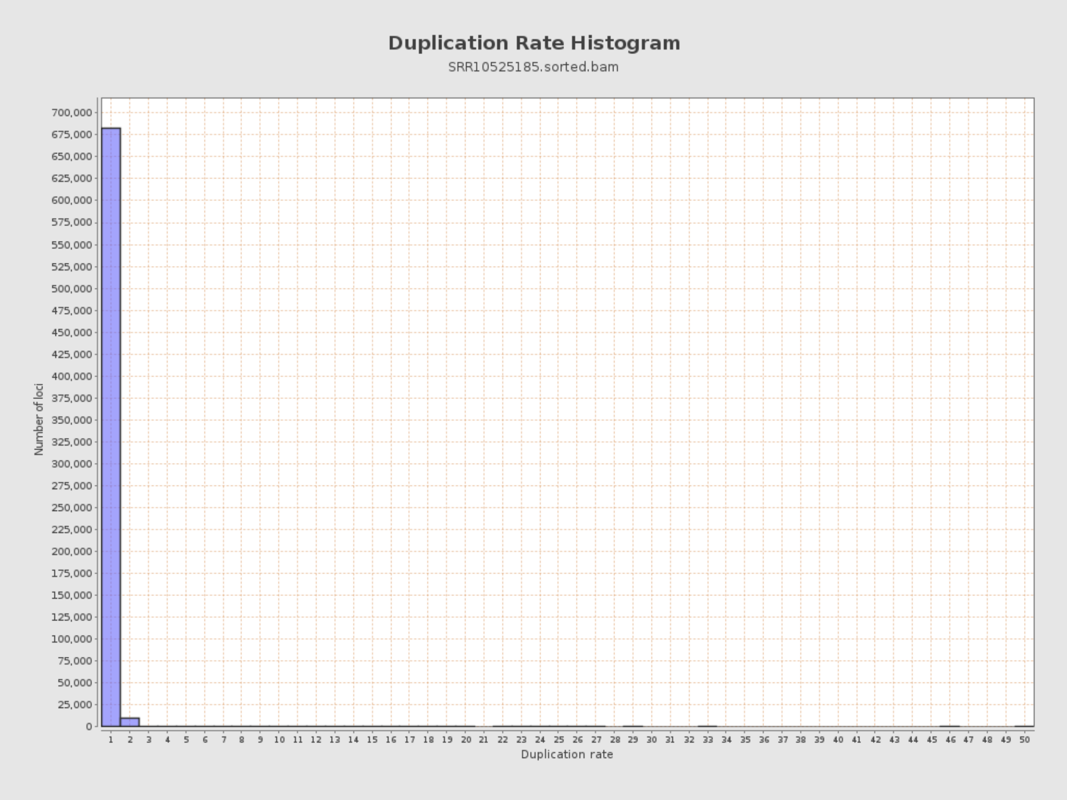
5. Results : Coverage Histogram (0-50X)



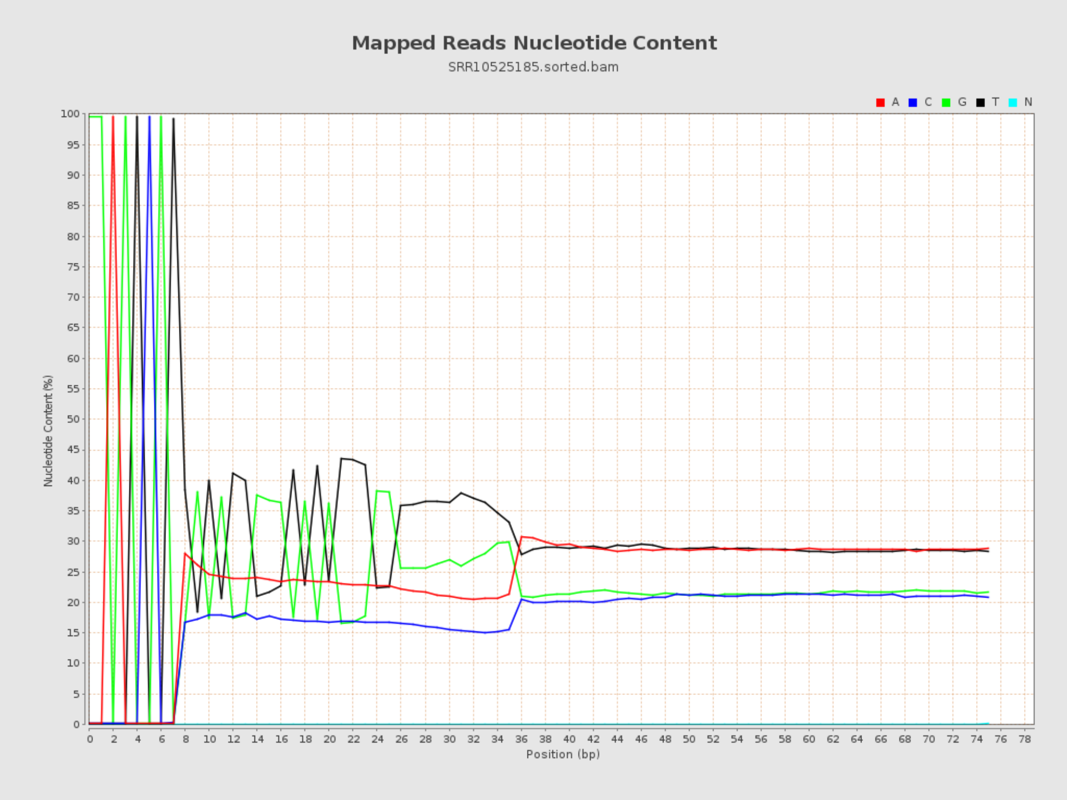
6. Results : Genome Fraction Coverage



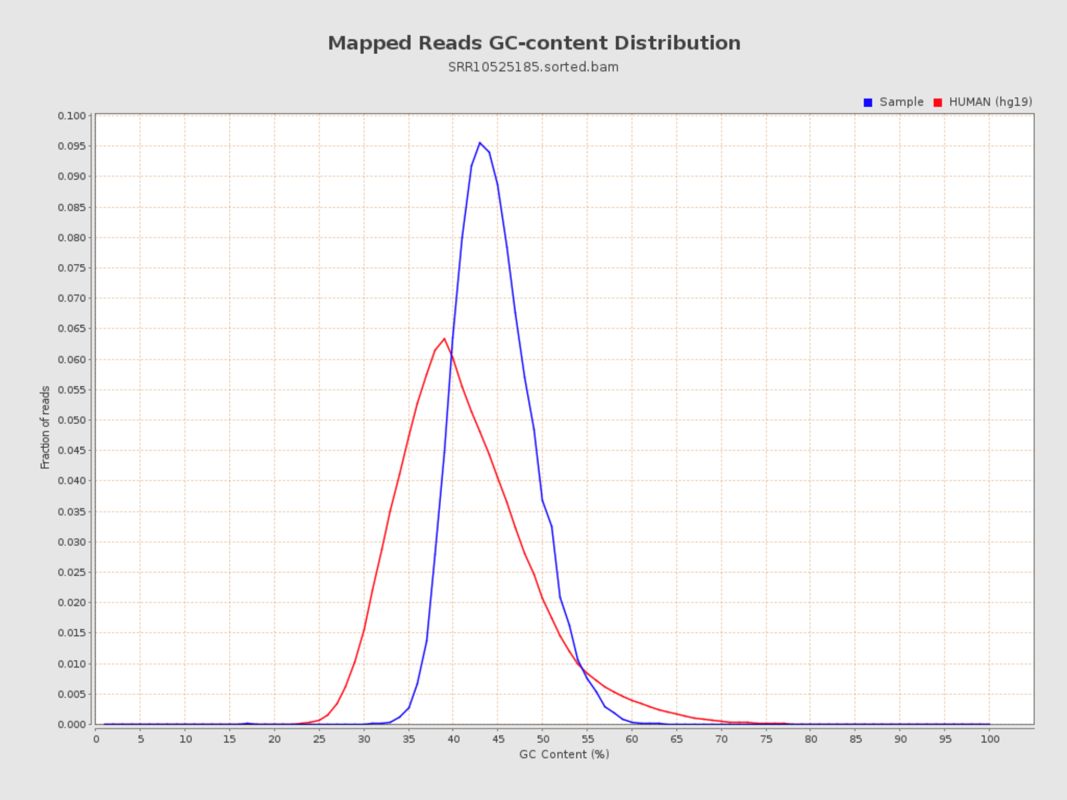
7. Results : Duplication Rate Histogram



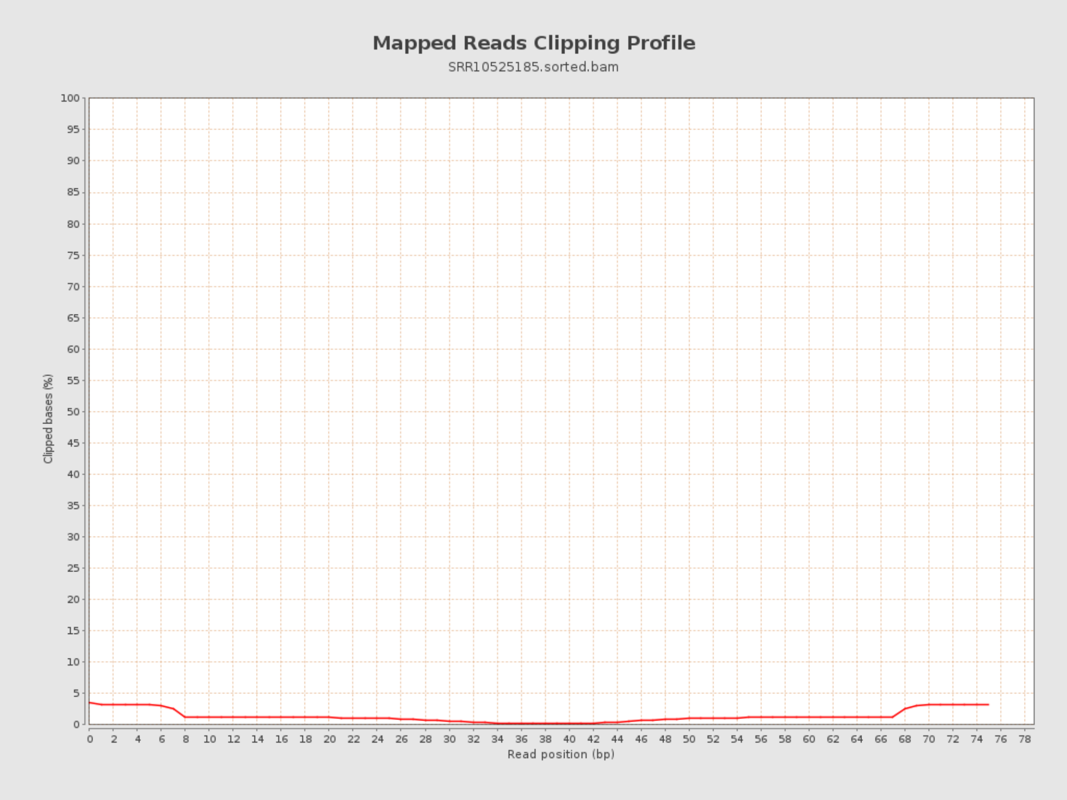
8. Results : Mapped Reads Nucleotide Content



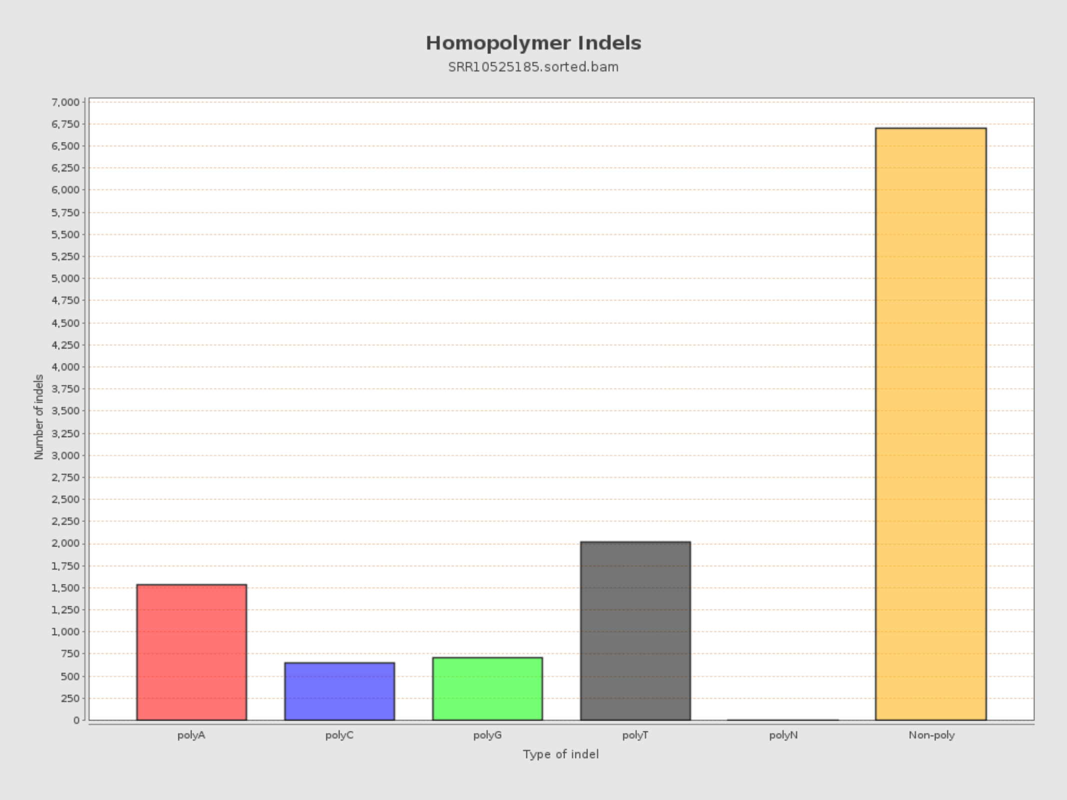
9. Results : Mapped Reads GC-content Distribution



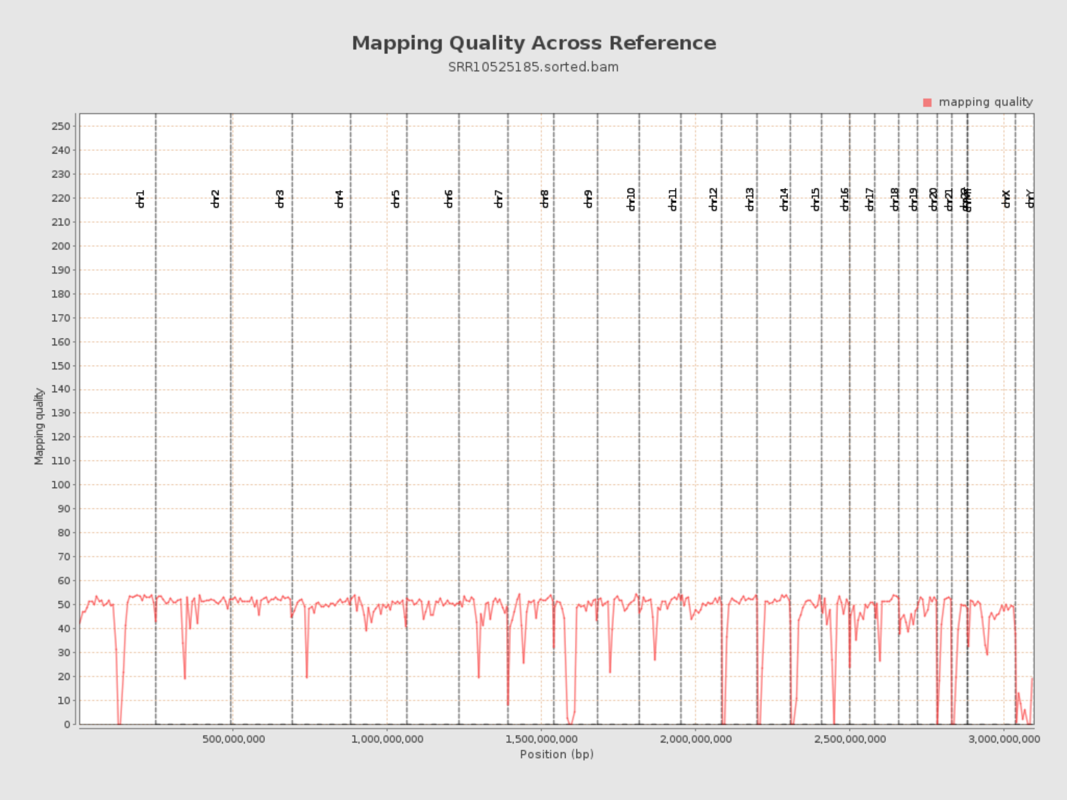
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram