Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:32:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525159.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_SRR10525159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:32:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	709,077
Mapped reads	635,594 / 89.64%
Unmapped reads	73,483 / 10.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,279 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,348 / 1.6%
Duplication rate	1.32%
Clipped reads	636,793 / 89.81%

2.2. ACGT Content

Number/percentage of A's	9,126,108 / 25.02%
Number/percentage of C's	6,793,878 / 18.63%
Number/percentage of T's	11,669,495 / 31.99%
Number/percentage of G's	8,884,077 / 24.36%
Number/percentage of N's	1,019 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.1337

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

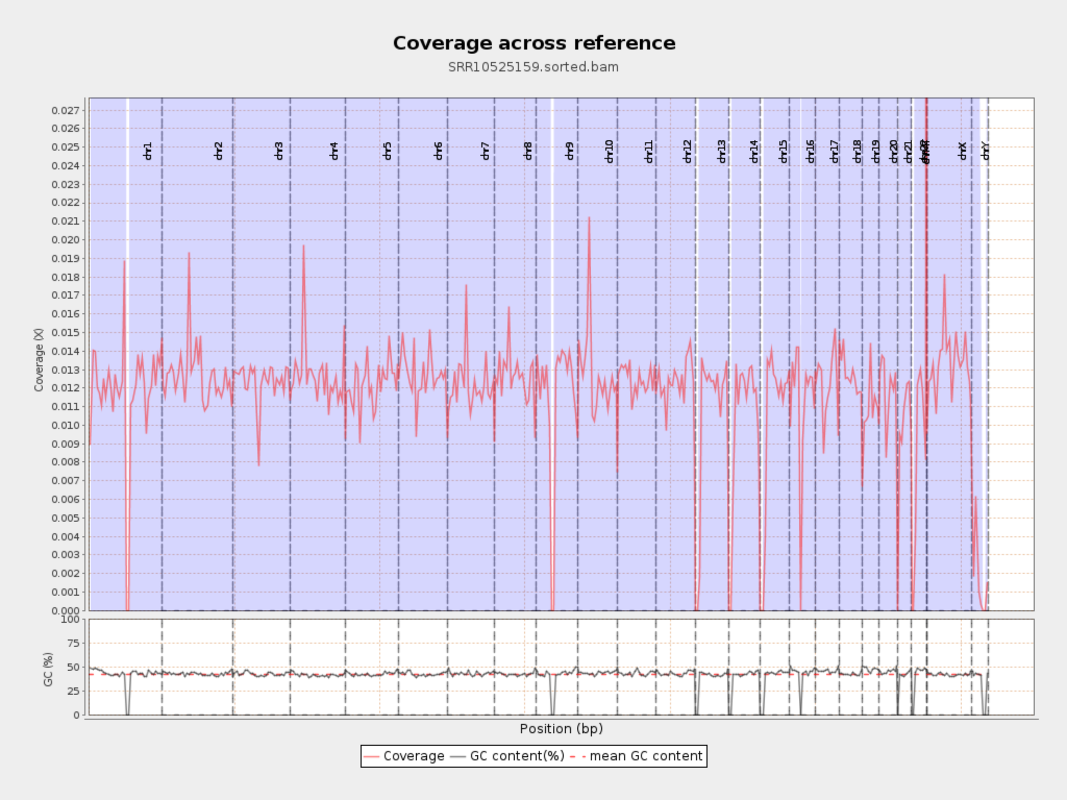
General error rate	0.49%
Mismatches	173,290
Insertions	2,405
Mapped reads with at least one insertion	0.38%
Deletions	5,729
Mapped reads with at least one deletion	0.89%
Homopolymer indels	42.48%

2.6. Chromosome stats

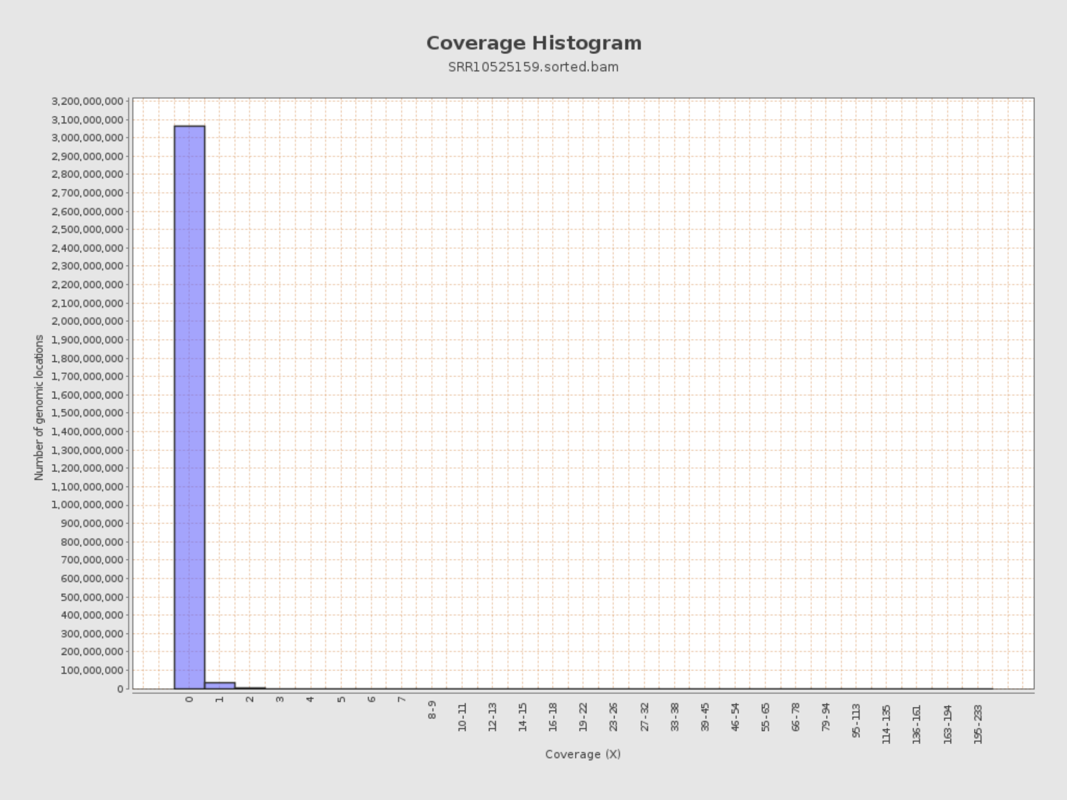
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2904890	0.0117	0.2064
chr2	243199373	3095401	0.0127	0.14
chr3	198022430	2444796	0.0123	0.1152
chr4	191154276	2430359	0.0127	0.1221
chr5	180915260	2205080	0.0122	0.1148
chr6	171115067	2181041	0.0127	0.1207
chr7	159138663	1950165	0.0123	0.1442

chr8	146364022	1850107	0.0126	0.1415
chr9	141213431	1597145	0.0113	0.1302
chr10	135534747	1733566	0.0128	0.1352
chr11	135006516	1675056	0.0124	0.1294
chr12	133851895	1650155	0.0123	0.1165
chr13	115169878	1190824	0.0103	0.1053
chr14	107349540	1090097	0.0102	0.1077
chr15	102531392	1042296	0.0102	0.1045
chr16	90354753	1013850	0.0112	0.1117
chr17	81195210	978776	0.0121	0.1171
chr18	78077248	996533	0.0128	0.1862
chr19	59128983	646192	0.0109	0.1511
chr20	63025520	747498	0.0119	0.1149
chr21	48129895	465269	0.0097	0.1067
chr22	51304566	405456	0.0079	0.0921
chrMT	16571	3749	0.2262	0.4673
chrX	155270560	2076379	0.0134	0.1258
chrY	59373566	109521	0.0018	0.0574

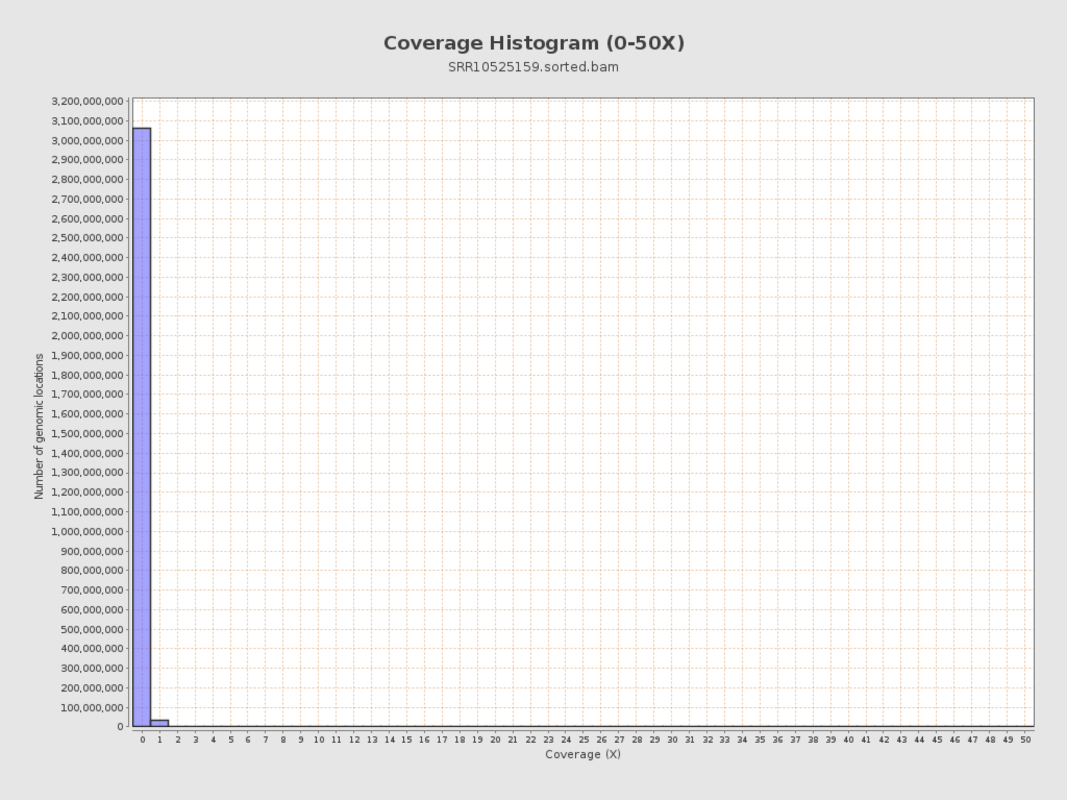
3. Results : Coverage across reference



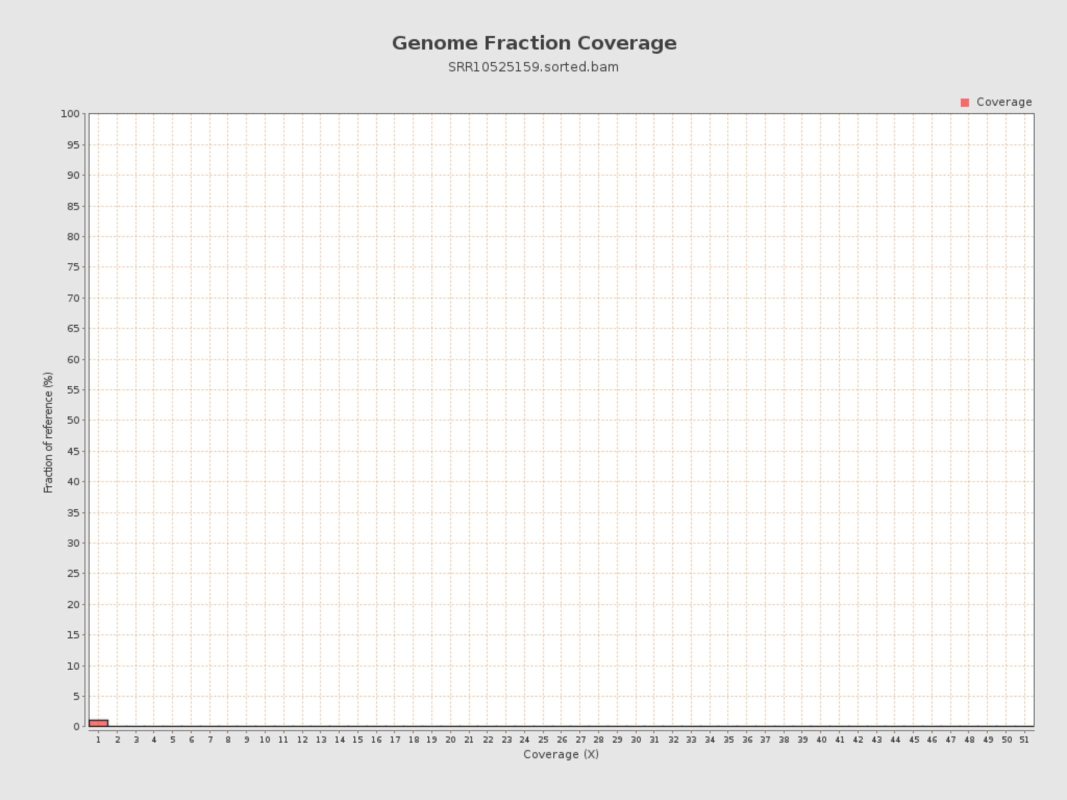
4. Results : Coverage Histogram



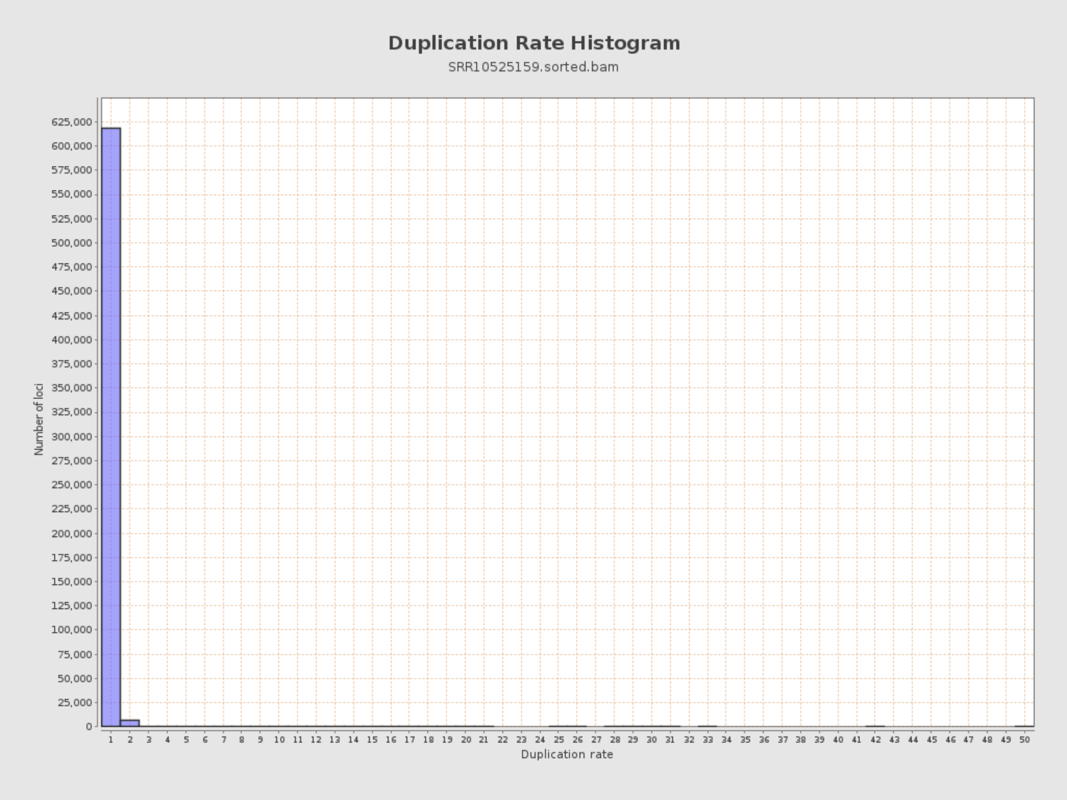
5. Results : Coverage Histogram (0-50X)



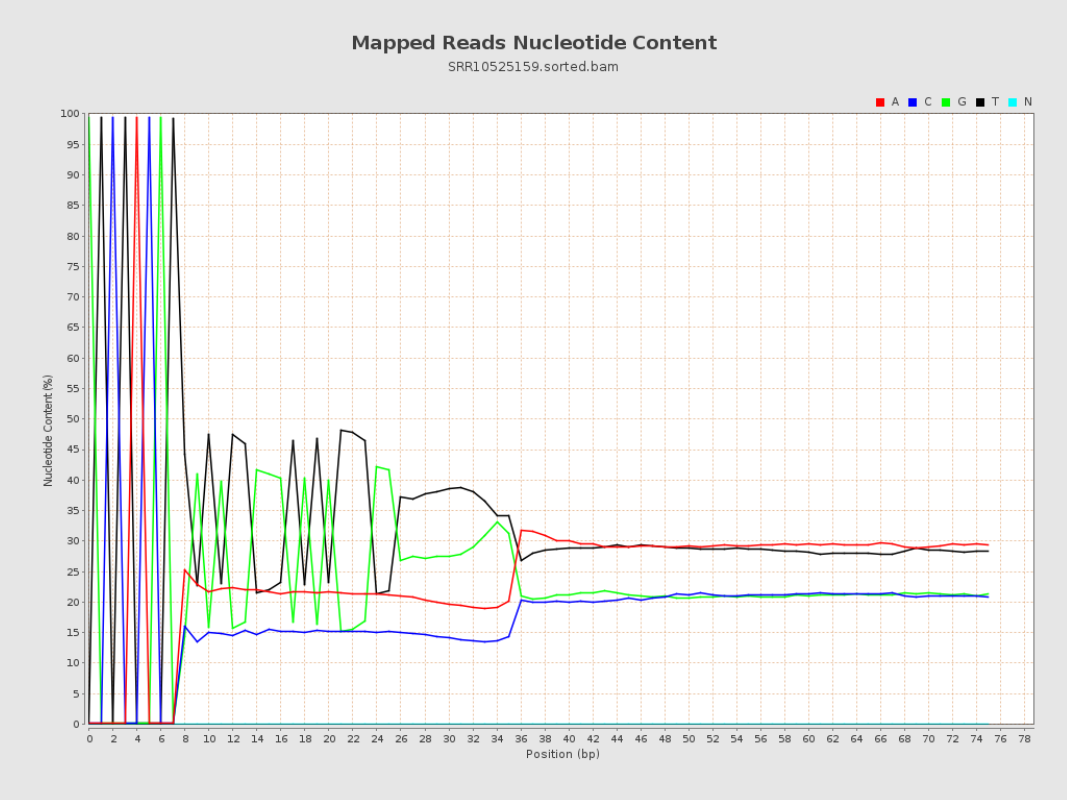
6. Results : Genome Fraction Coverage



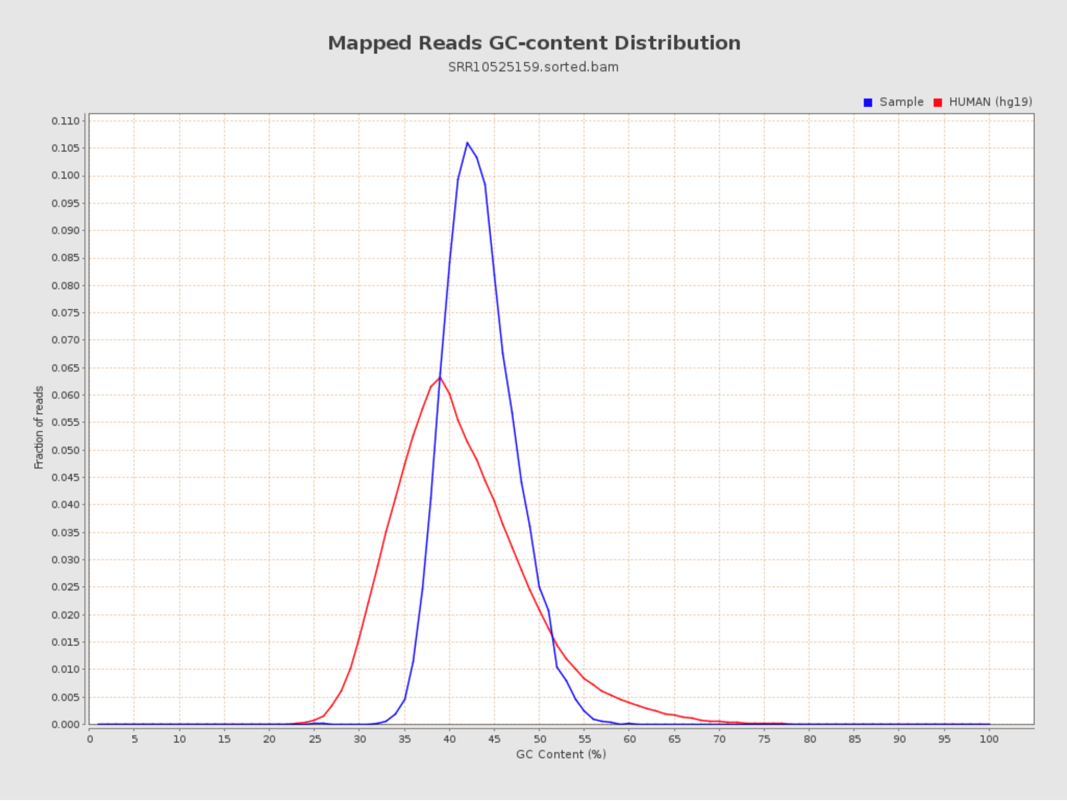
7. Results : Duplication Rate Histogram



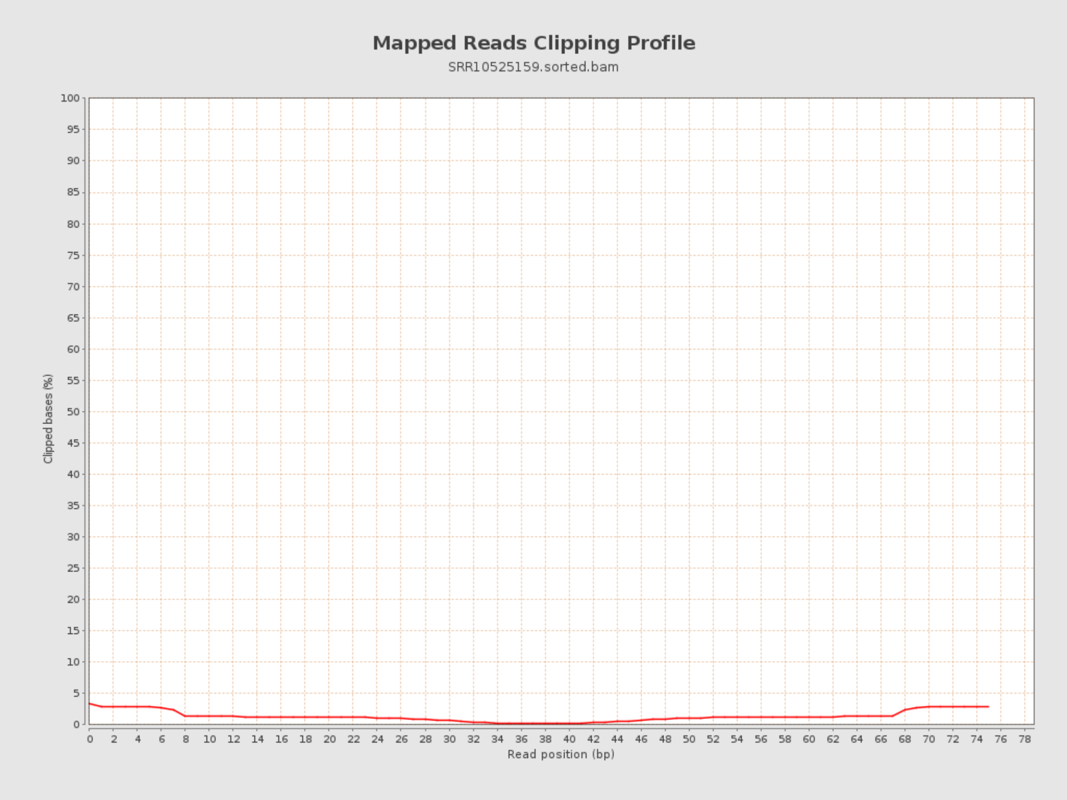
8. Results : Mapped Reads Nucleotide Content



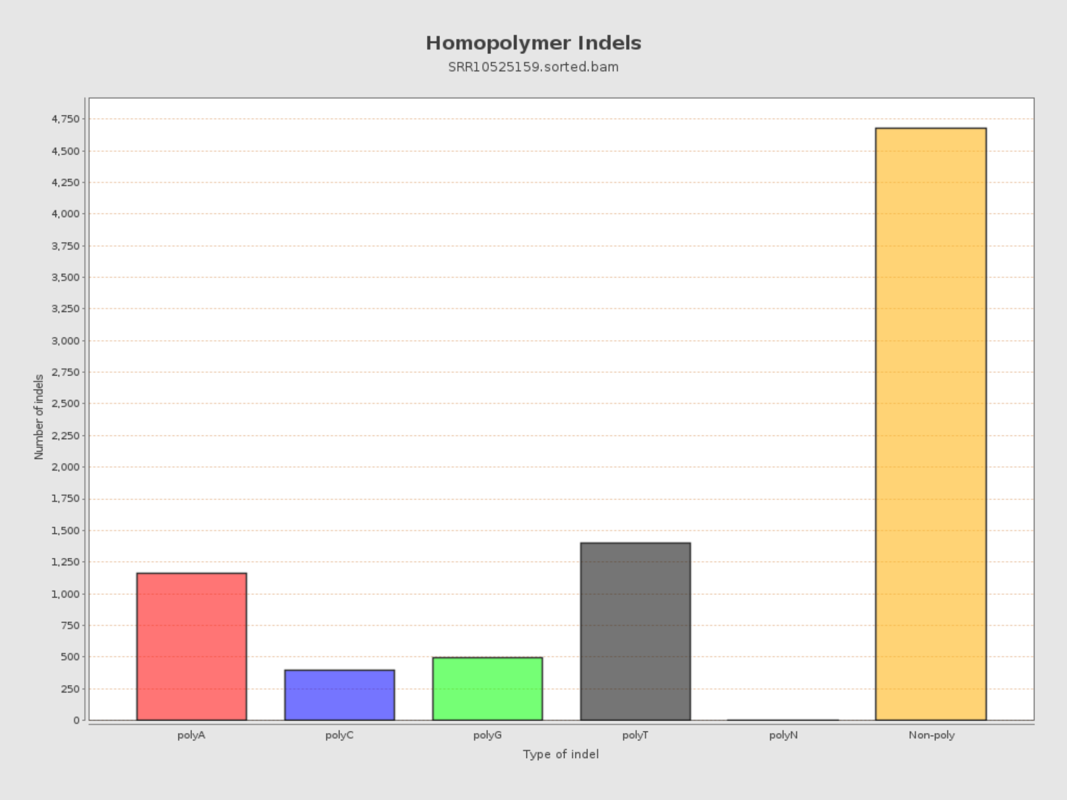
9. Results : Mapped Reads GC-content Distribution



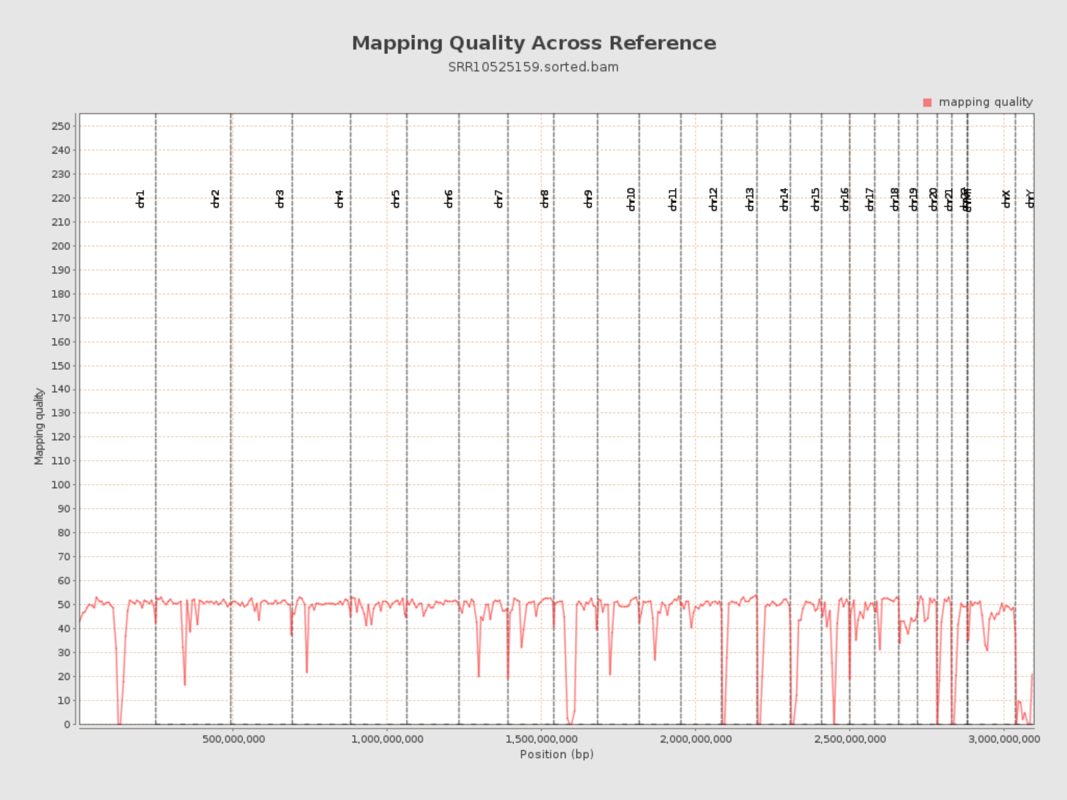
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram