Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:15:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525152.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_SRR10525152 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525152.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:15:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525152.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,279,128
Mapped reads	1,217,320 / 95.17%
Unmapped reads	61,808 / 4.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,780 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	25,893 / 2.02%
Duplication rate	1.42%
Clipped reads	1,220,898 / 95.45%

2.2. ACGT Content

Number/percentage of A's	20,806,335 / 26.71%
Number/percentage of C's	17,395,871 / 22.33%
Number/percentage of T's	22,709,461 / 29.15%
Number/percentage of G's	16,982,449 / 21.8%
Number/percentage of N's	2,108 / 0%
GC Percentage	44.13%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.2539

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

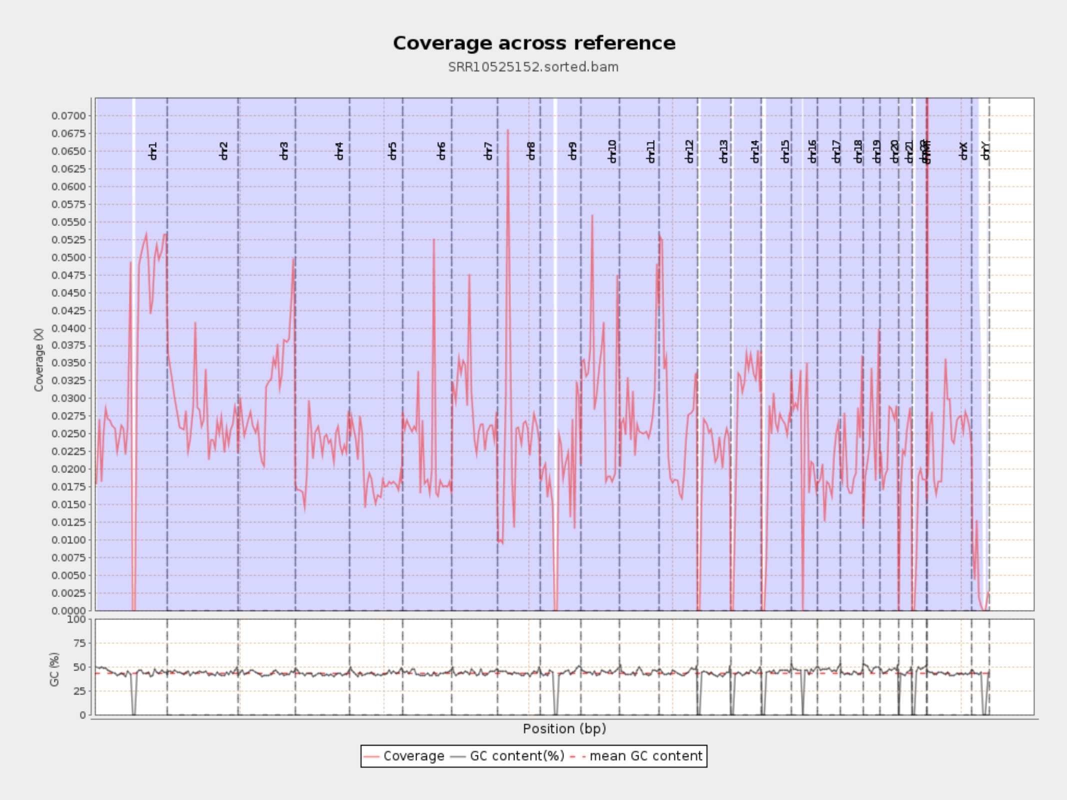
General error rate	0.47%
Mismatches	360,703
Insertions	4,885
Mapped reads with at least one insertion	0.4%
Deletions	15,701
Mapped reads with at least one deletion	1.28%
Homopolymer indels	44.86%

2.6. Chromosome stats

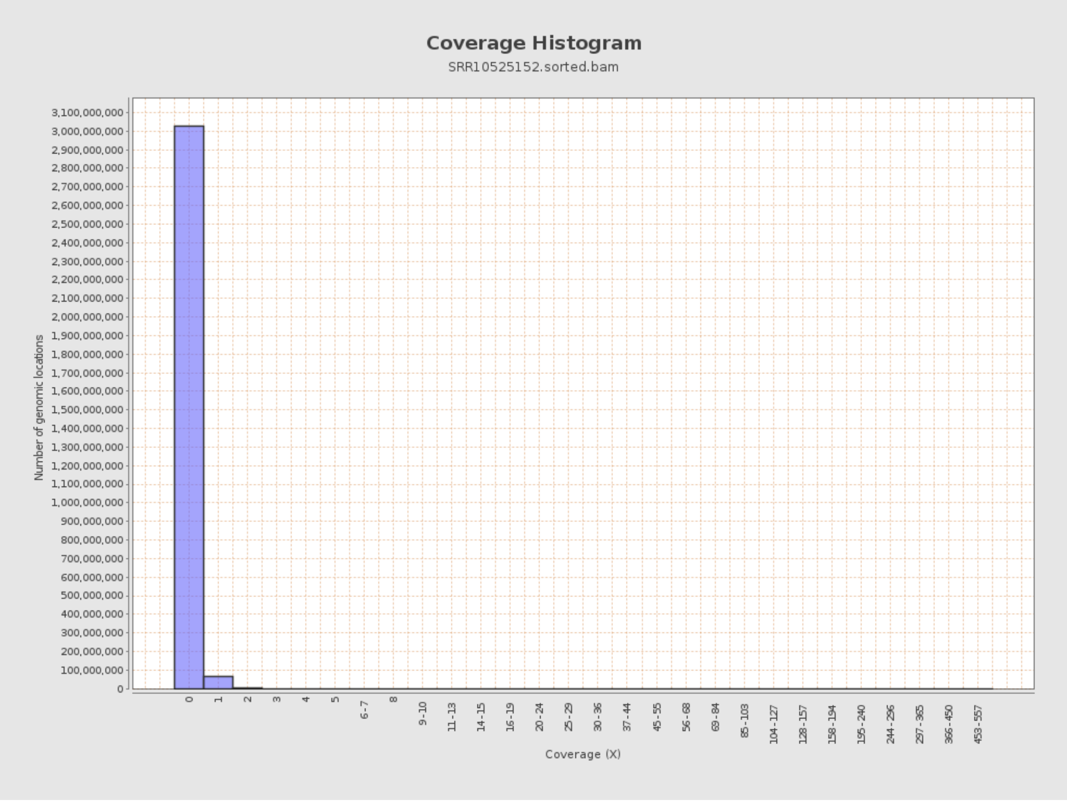
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8582682	0.0344	0.5169
chr2	243199373	6666192	0.0274	0.2373
chr3	198022430	6199084	0.0313	0.1898
chr4	191154276	4339437	0.0227	0.1684
chr5	180915260	3532258	0.0195	0.1484
chr6	171115067	3928083	0.023	0.18
chr7	159138663	4671723	0.0294	0.3833

chr8	146364022	3679716	0.0251	0.202
chr9	141213431	2619569	0.0186	0.1949
chr10	135534747	4332018	0.032	0.2812
chr11	135006516	3752388	0.0278	0.2071
chr12	133851895	3655839	0.0273	0.1773
chr13	115169878	2418090	0.021	0.1529
chr14	107349540	3002512	0.028	0.1836
chr15	102531392	2224534	0.0217	0.1557
chr16	90354753	2173181	0.0241	0.1803
chr17	81195210	1600175	0.0197	0.1562
chr18	78077248	1700652	0.0218	0.372
chr19	59128983	1481903	0.0251	0.352
chr20	63025520	1502013	0.0238	0.167
chr21	48129895	1026999	0.0213	0.162
chr22	51304566	676082	0.0132	0.1208
chrMT	16571	23896	1.442	1.3873
chrX	155270560	3910544	0.0252	0.1775
chrY	59373566	222503	0.0037	0.1303

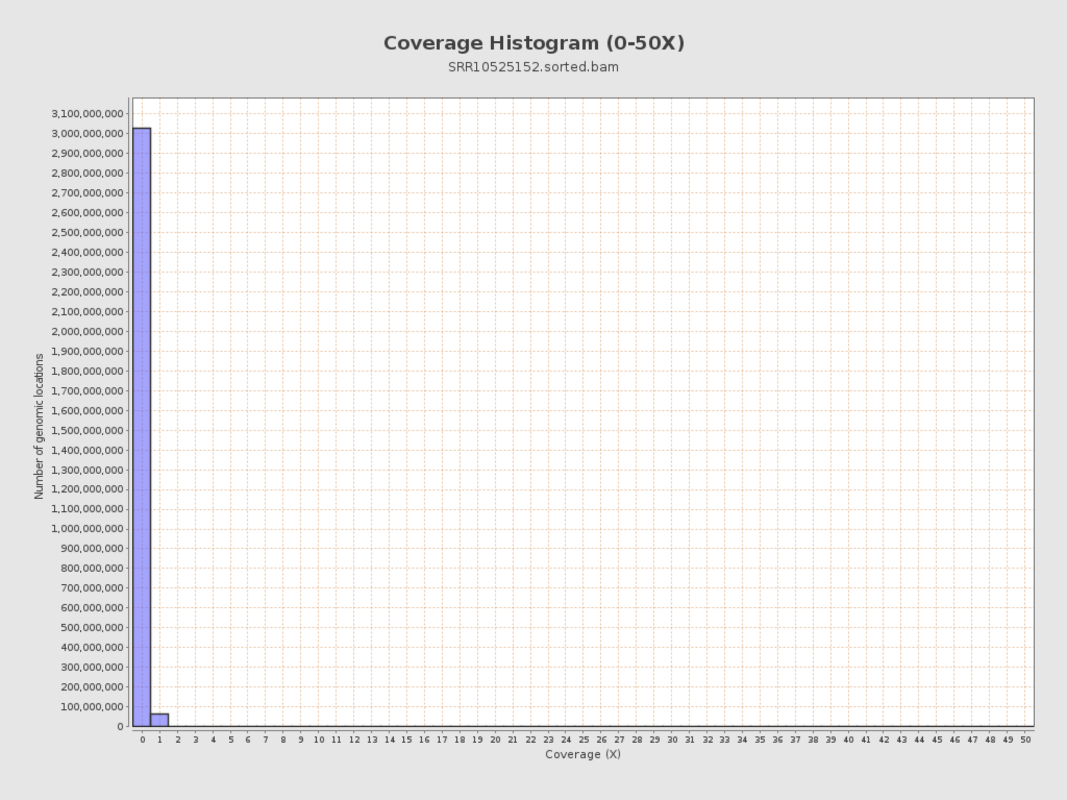
3. Results : Coverage across reference



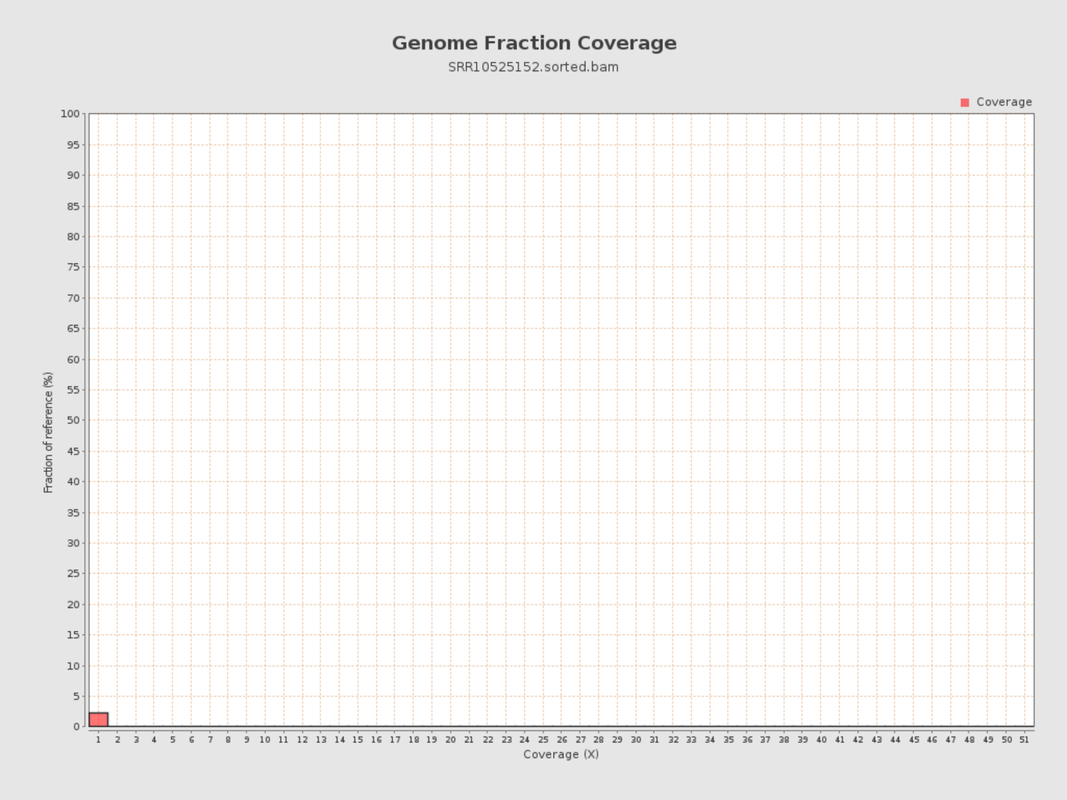
4. Results : Coverage Histogram



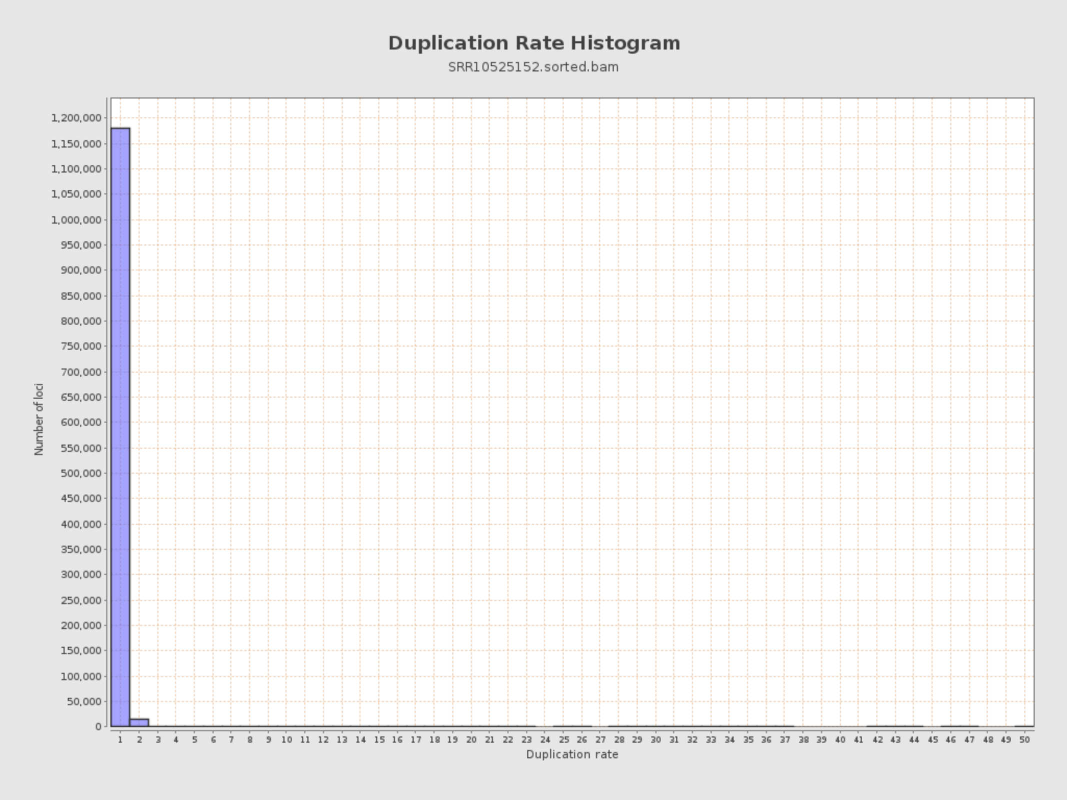
5. Results : Coverage Histogram (0-50X)



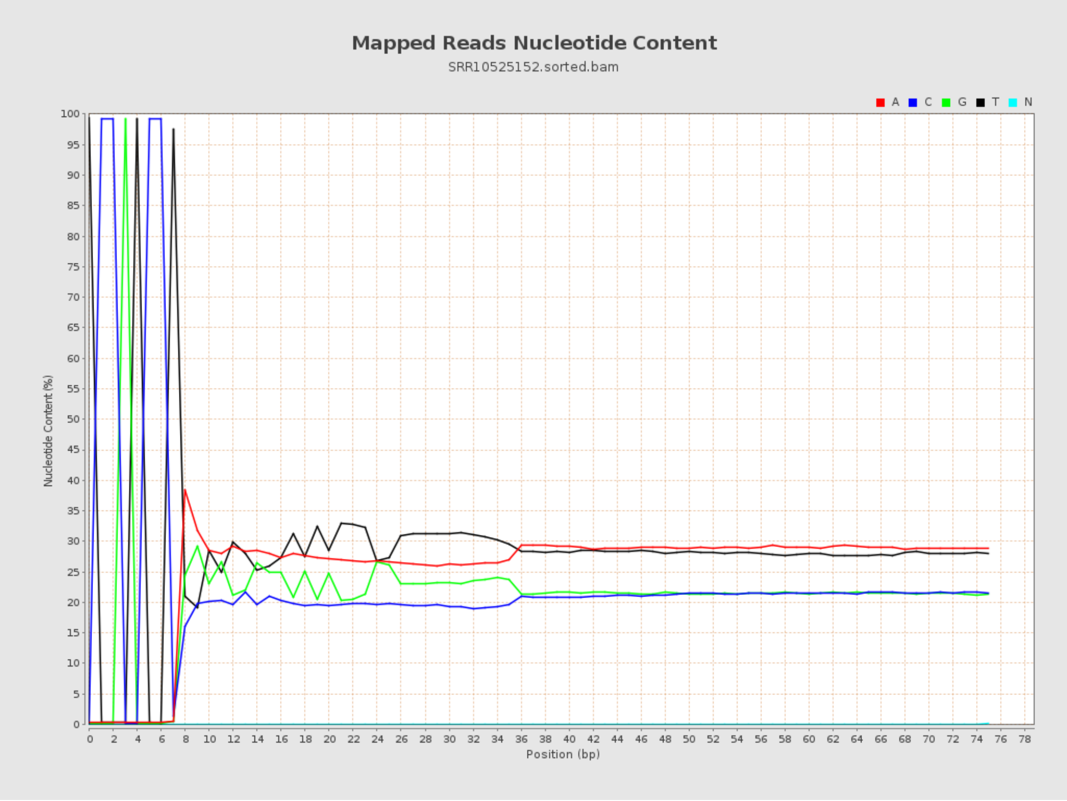
6. Results : Genome Fraction Coverage



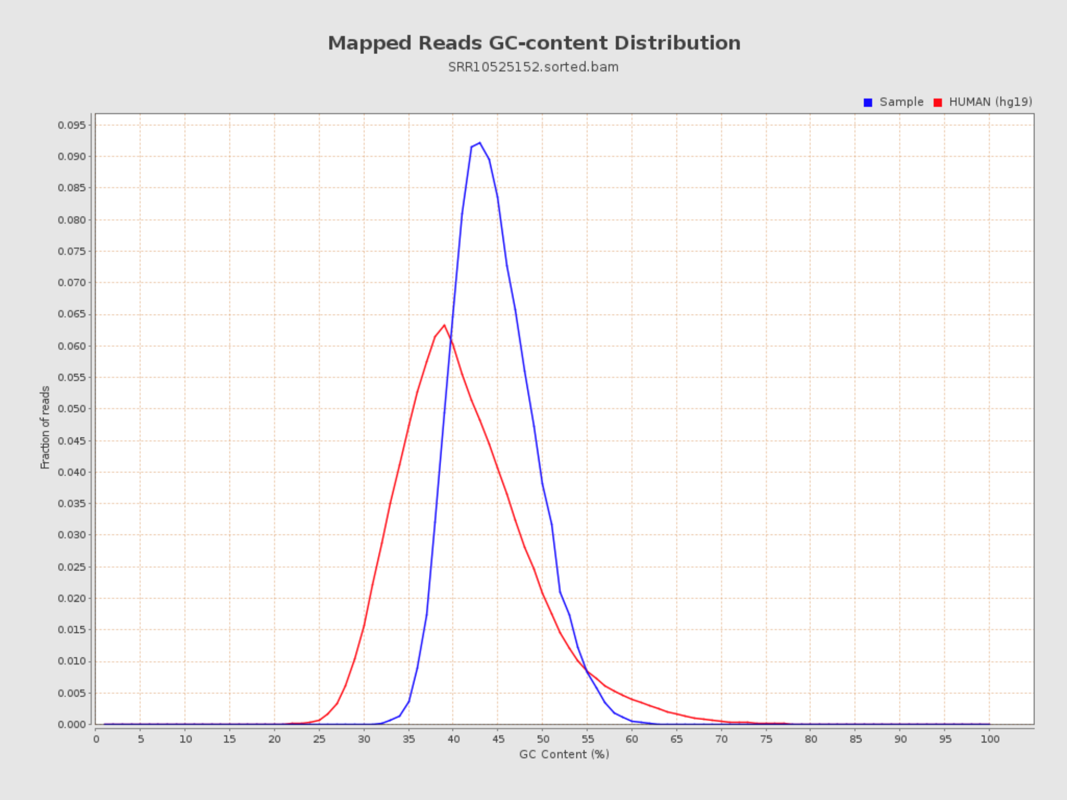
7. Results : Duplication Rate Histogram



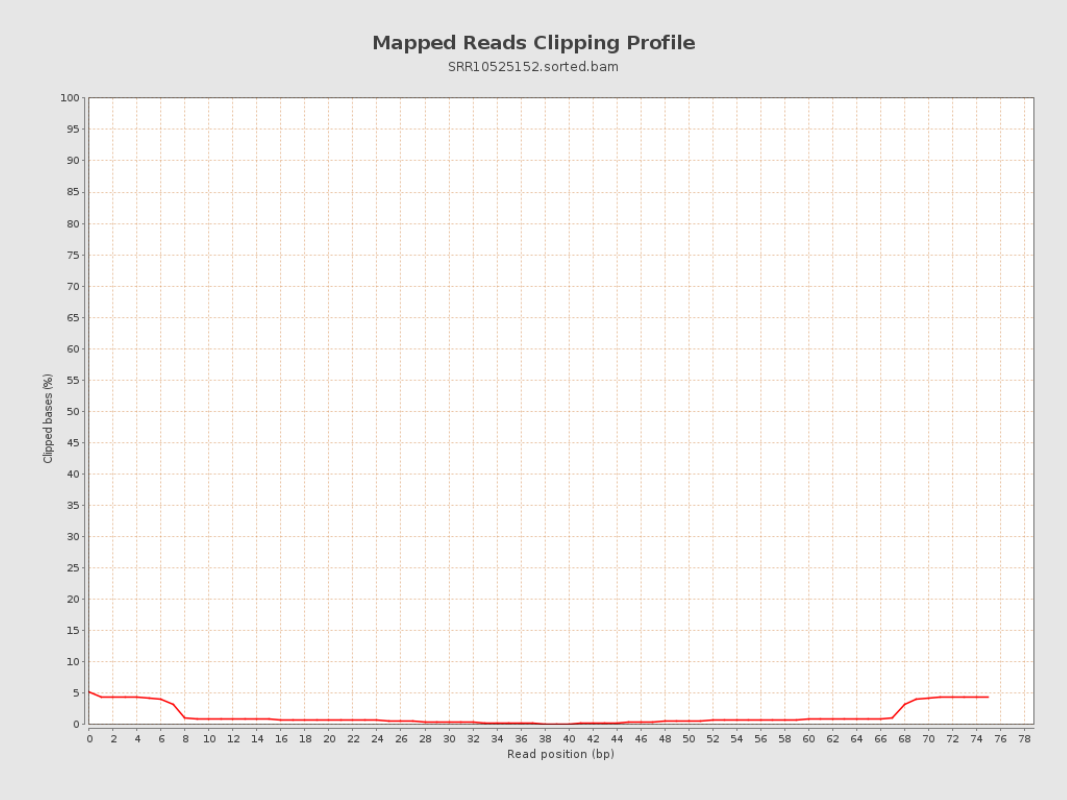
8. Results : Mapped Reads Nucleotide Content



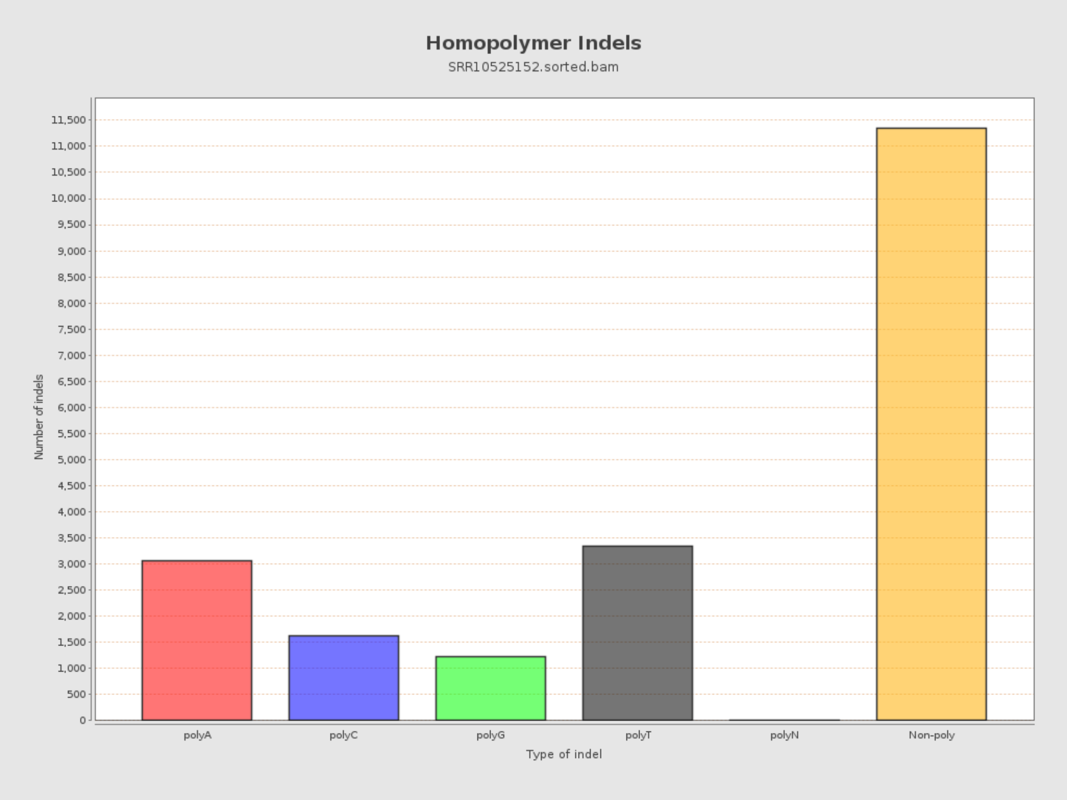
9. Results : Mapped Reads GC-content Distribution



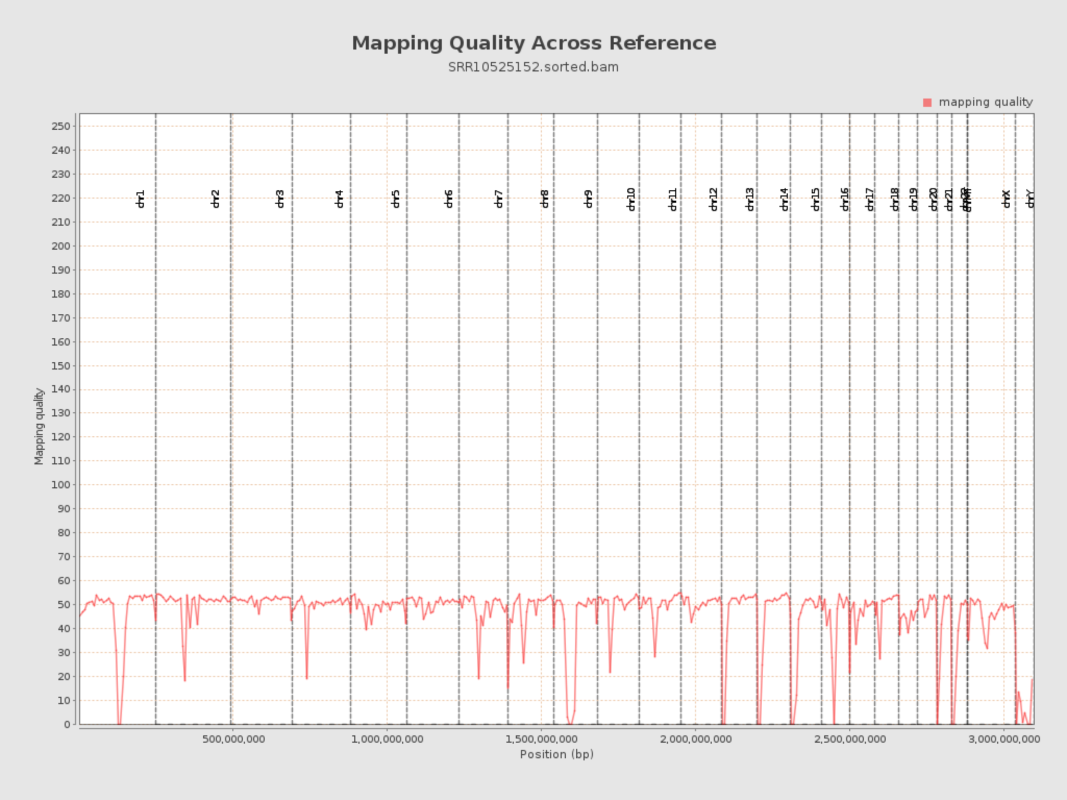
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram