Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:13:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525151.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_SRR10525151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:13:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,415,070
Mapped reads	510,649 / 36.09%
Unmapped reads	904,421 / 63.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,725 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	8,500 / 0.6%
Duplication rate	1.26%
Clipped reads	510,258 / 36.06%

2.2. ACGT Content

Number/percentage of A's	8,045,958 / 25.55%
Number/percentage of C's	6,066,595 / 19.27%
Number/percentage of T's	9,711,599 / 30.84%
Number/percentage of G's	7,663,969 / 24.34%
Number/percentage of N's	712 / 0%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0102

Standard Deviation	0.127

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

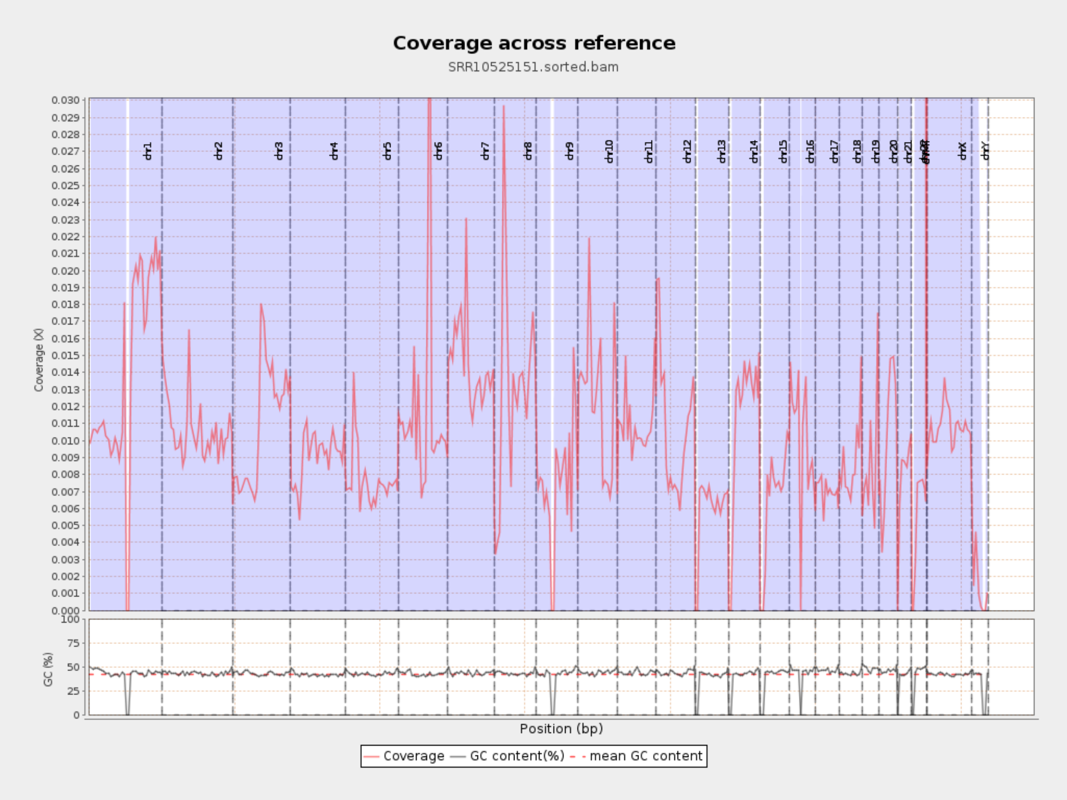
General error rate	0.49%
Mismatches	150,164
Insertions	2,359
Mapped reads with at least one insertion	0.46%
Deletions	6,231
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.07%

2.6. Chromosome stats

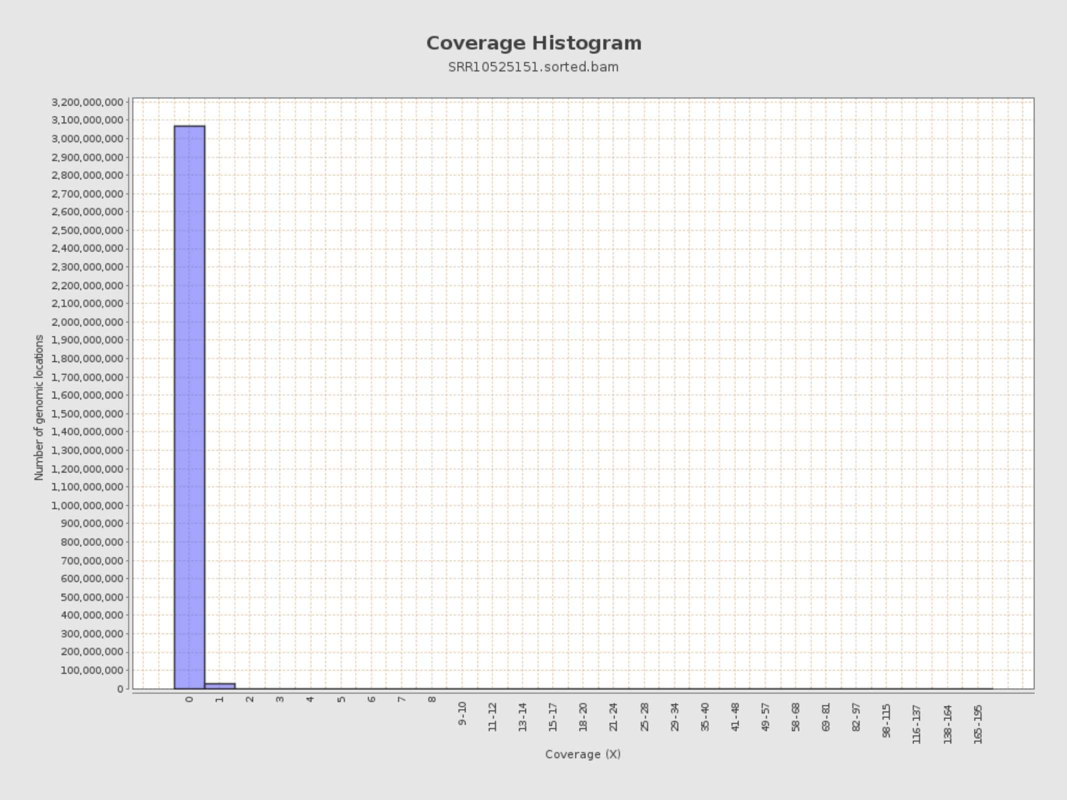
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3441300	0.0138	0.2004
chr2	243199373	2595619	0.0107	0.1336
chr3	198022430	2158104	0.0109	0.1078
chr4	191154276	1730134	0.0091	0.0996
chr5	180915260	1391510	0.0077	0.0902
chr6	171115067	2066490	0.0121	0.1196
chr7	159138663	2324446	0.0146	0.2026

chr8	146364022	1888750	0.0129	0.1261
chr9	141213431	1046959	0.0074	0.0992
chr10	135534747	1691003	0.0125	0.1396
chr11	135006516	1476534	0.0109	0.1163
chr12	133851895	1428209	0.0107	0.1068
chr13	115169878	684182	0.0059	0.0797
chr14	107349540	1191492	0.0111	0.1111
chr15	102531392	668080	0.0065	0.0838
chr16	90354753	891522	0.0099	0.1067
chr17	81195210	570697	0.007	0.0877
chr18	78077248	678356	0.0087	0.1513
chr19	59128983	509858	0.0086	0.1591
chr20	63025520	646748	0.0103	0.1053
chr21	48129895	375723	0.0078	0.0941
chr22	51304566	266794	0.0052	0.0739
chrMT	16571	15102	0.9114	1.0158
chrX	155270560	1675983	0.0108	0.1097
chrY	59373566	85343	0.0014	0.0522

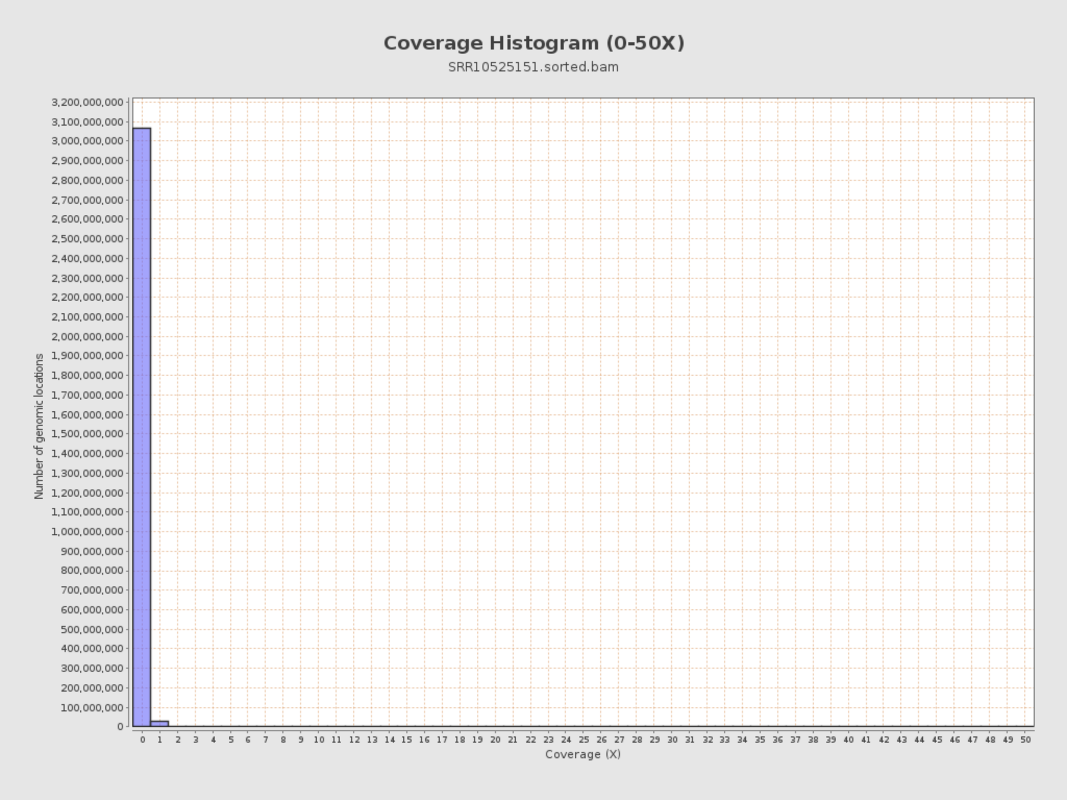
3. Results : Coverage across reference



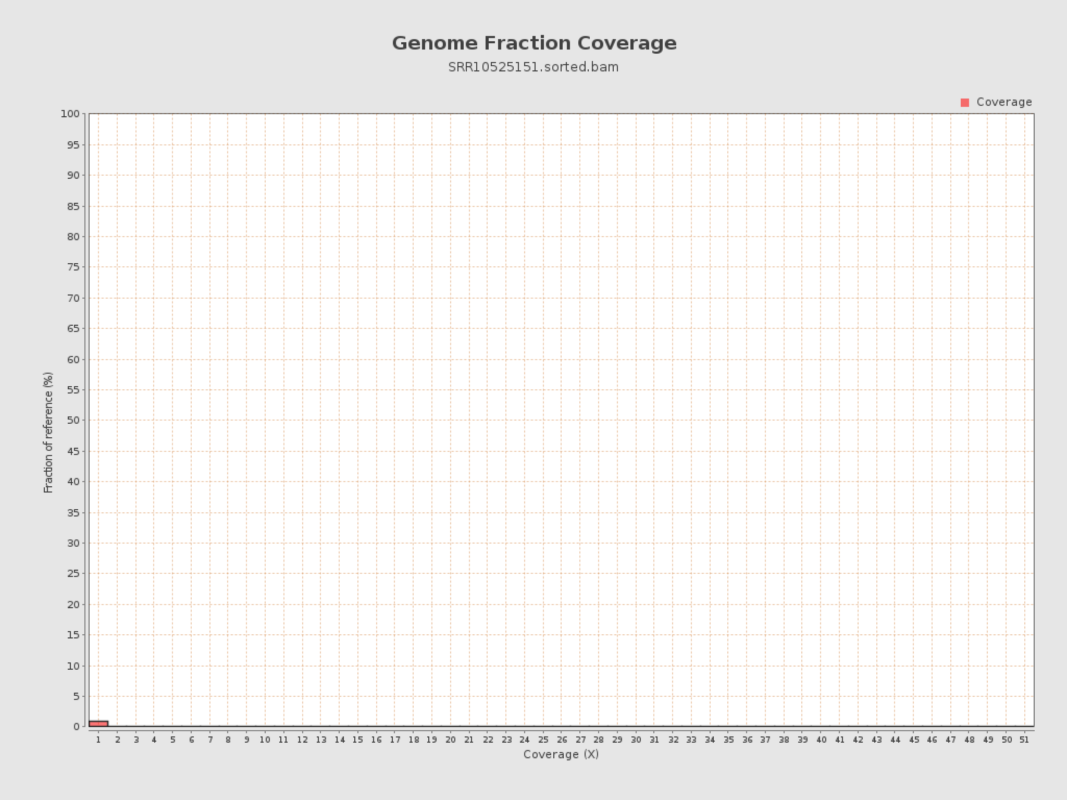
4. Results : Coverage Histogram



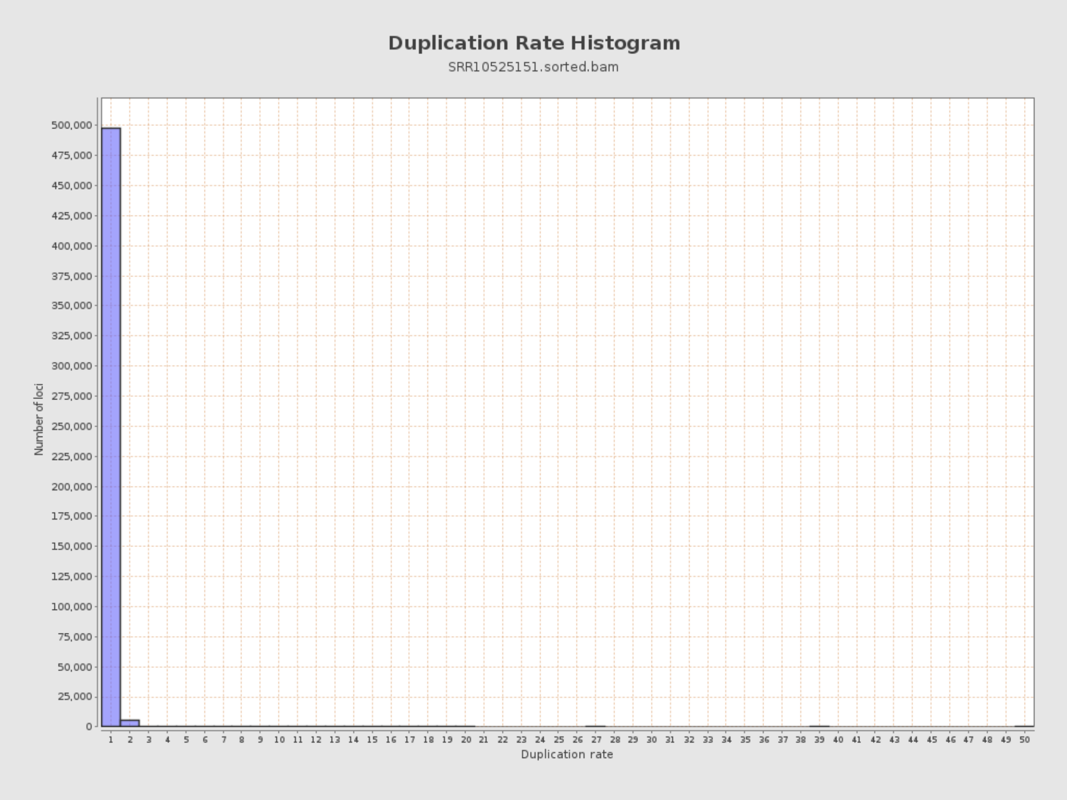
5. Results : Coverage Histogram (0-50X)



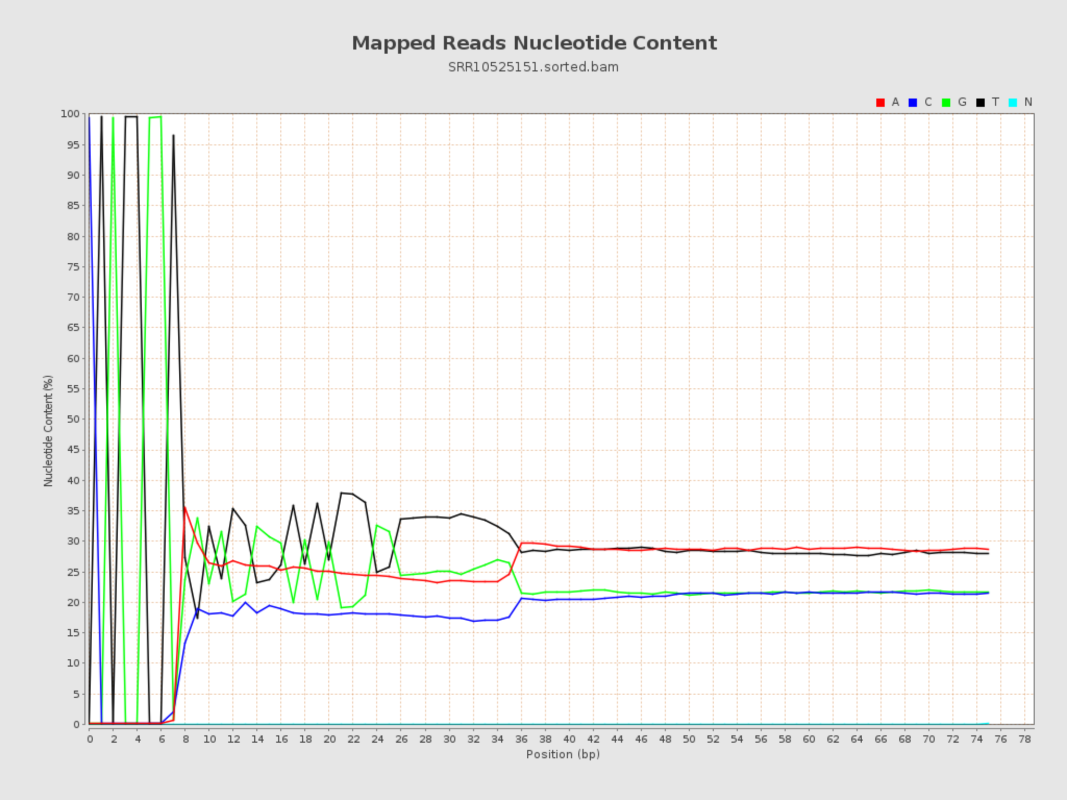
6. Results : Genome Fraction Coverage



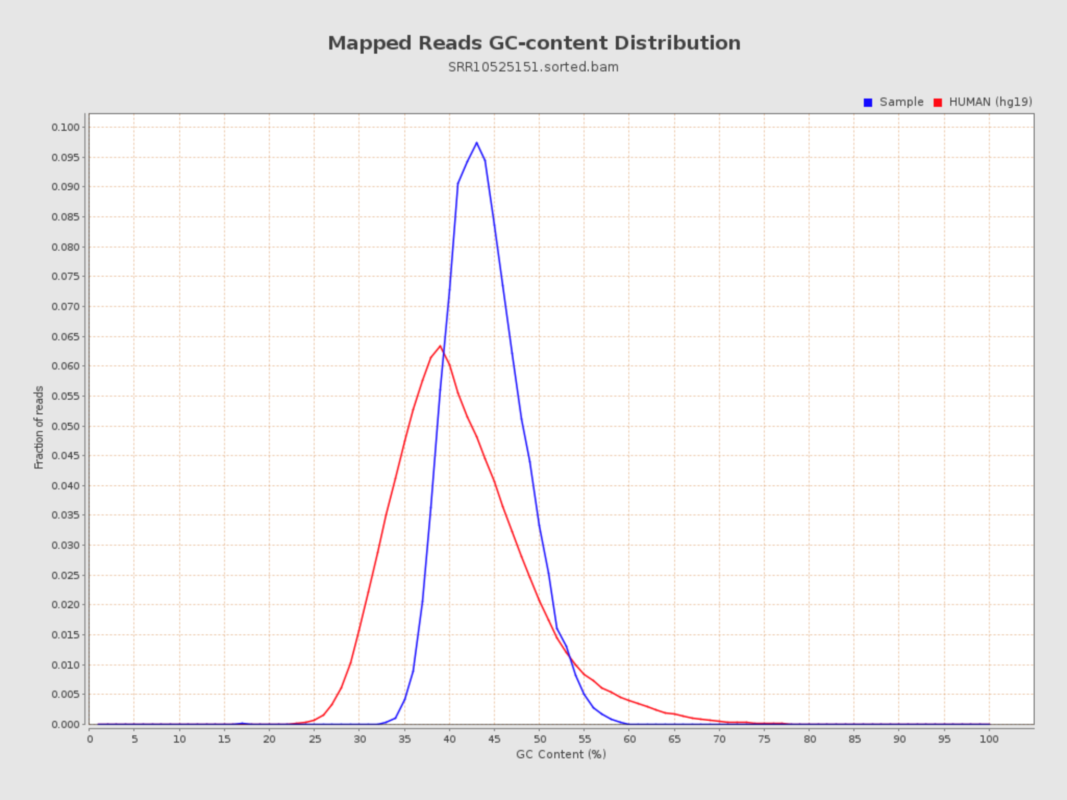
7. Results : Duplication Rate Histogram



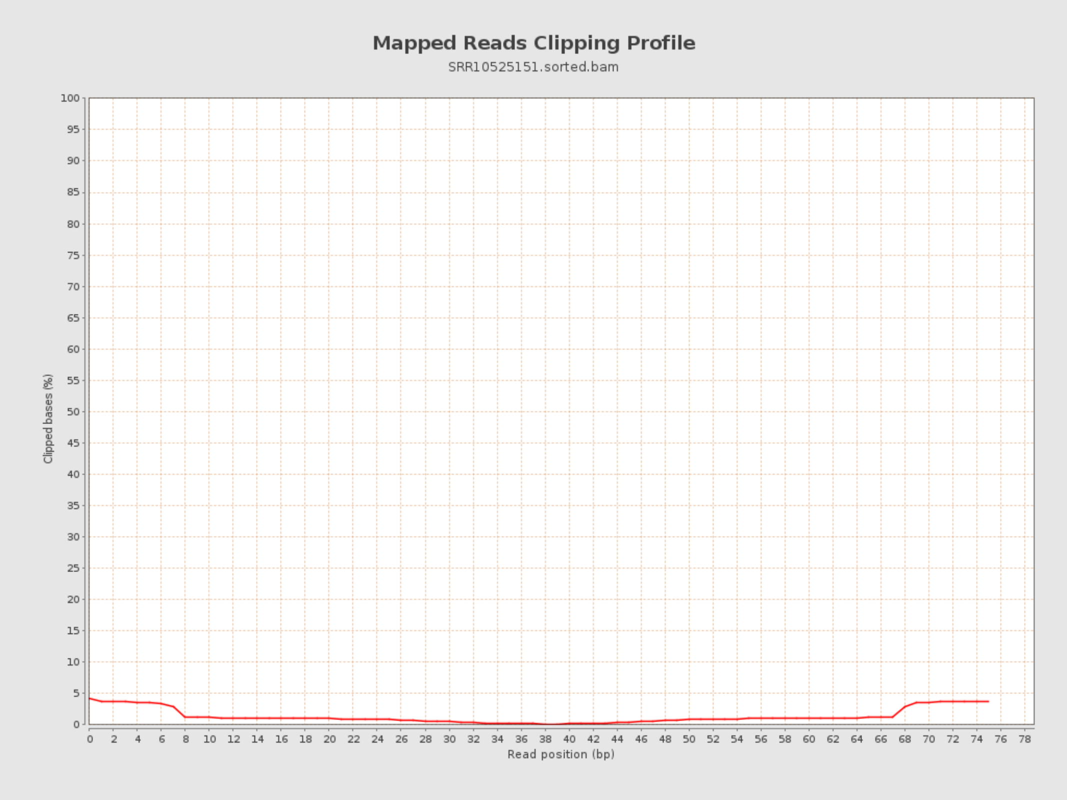
8. Results : Mapped Reads Nucleotide Content



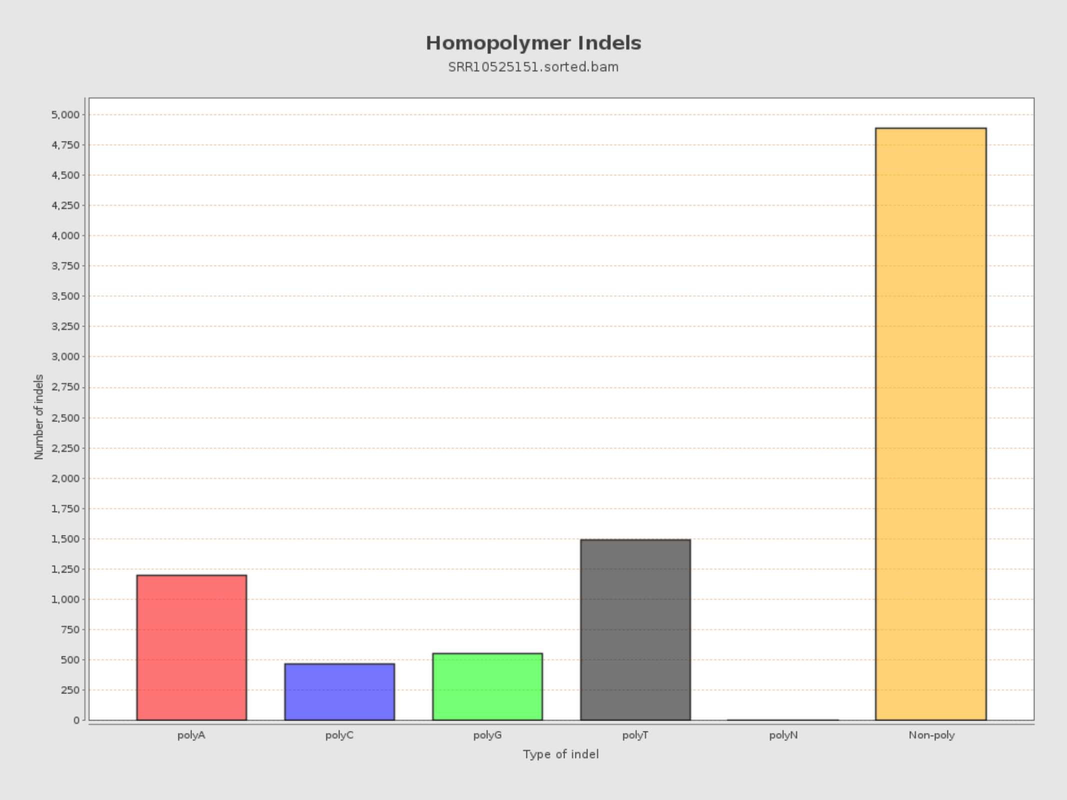
9. Results : Mapped Reads GC-content Distribution



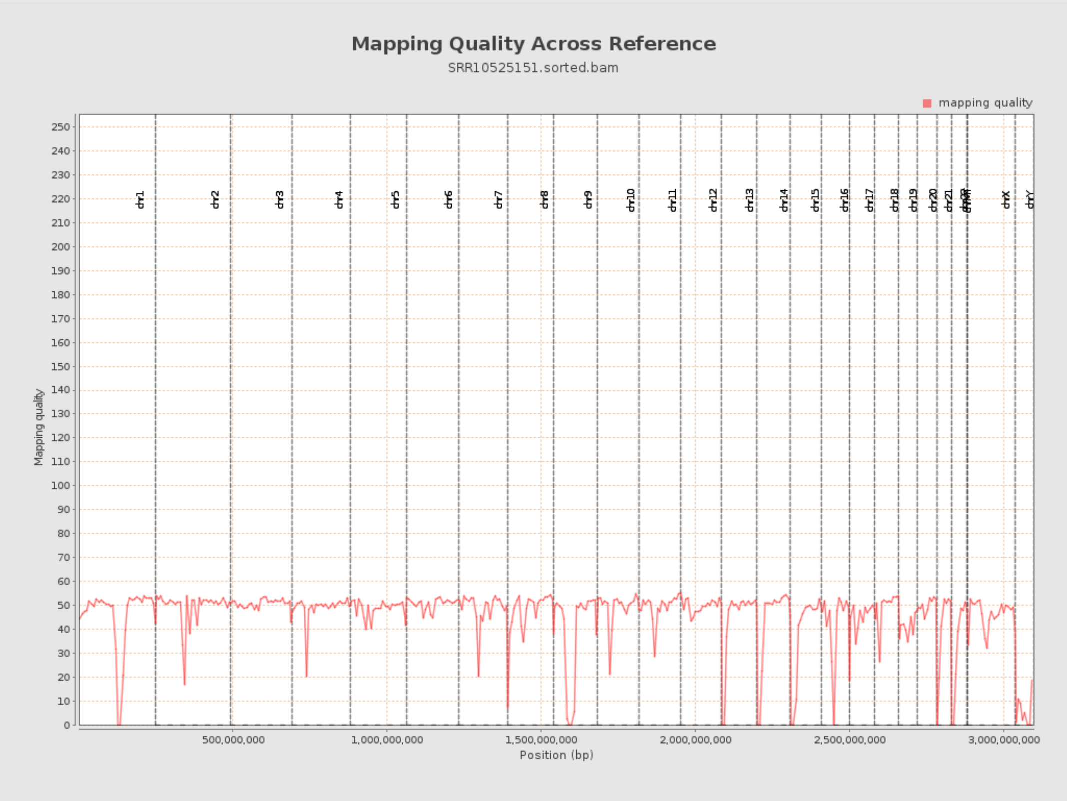
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram