Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:42:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525243.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_SRR10525243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525243.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:42:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,277,351
Mapped reads	1,167,137 / 91.37%
Unmapped reads	110,214 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,142 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	36,557 / 2.86%
Duplication rate	2.34%
Clipped reads	1,168,040 / 91.44%

2.2. ACGT Content

Number/percentage of A's	16,594,638 / 24.64%
Number/percentage of C's	13,330,099 / 19.79%
Number/percentage of T's	22,117,066 / 32.83%
Number/percentage of G's	15,317,378 / 22.74%
Number/percentage of N's	1,377 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.22

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

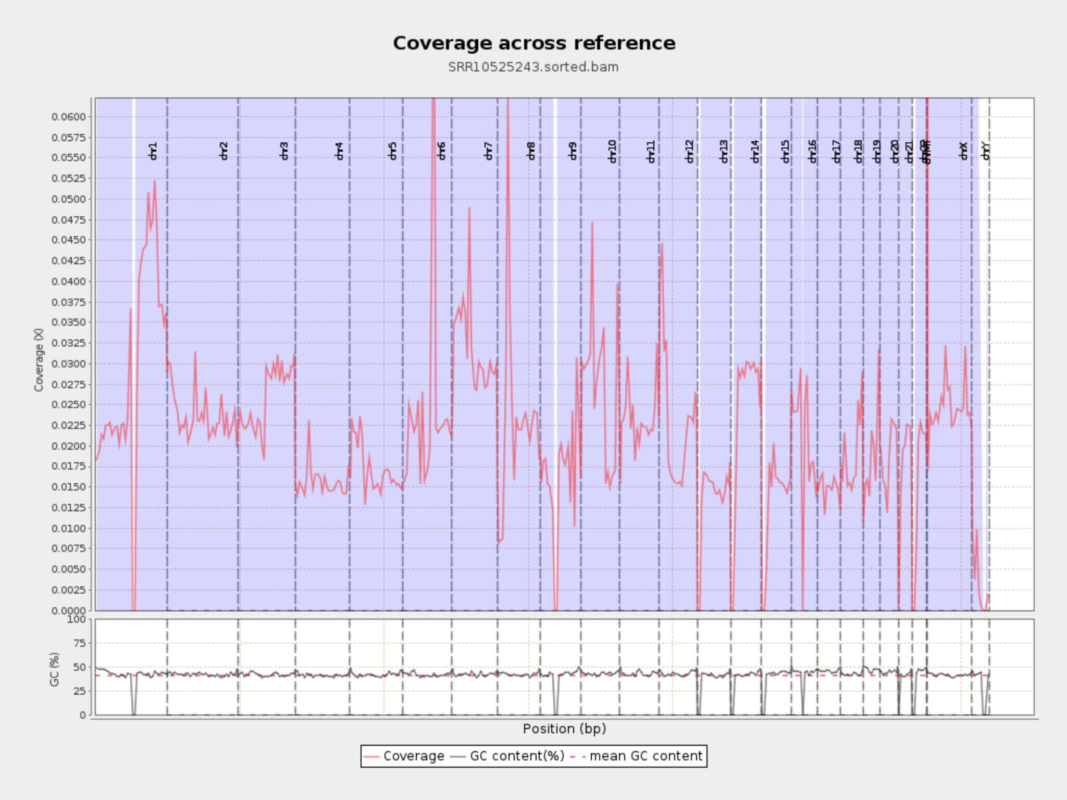
General error rate	0.51%
Mismatches	337,696
Insertions	4,687
Mapped reads with at least one insertion	0.4%
Deletions	13,386
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.99%

2.6. Chromosome stats

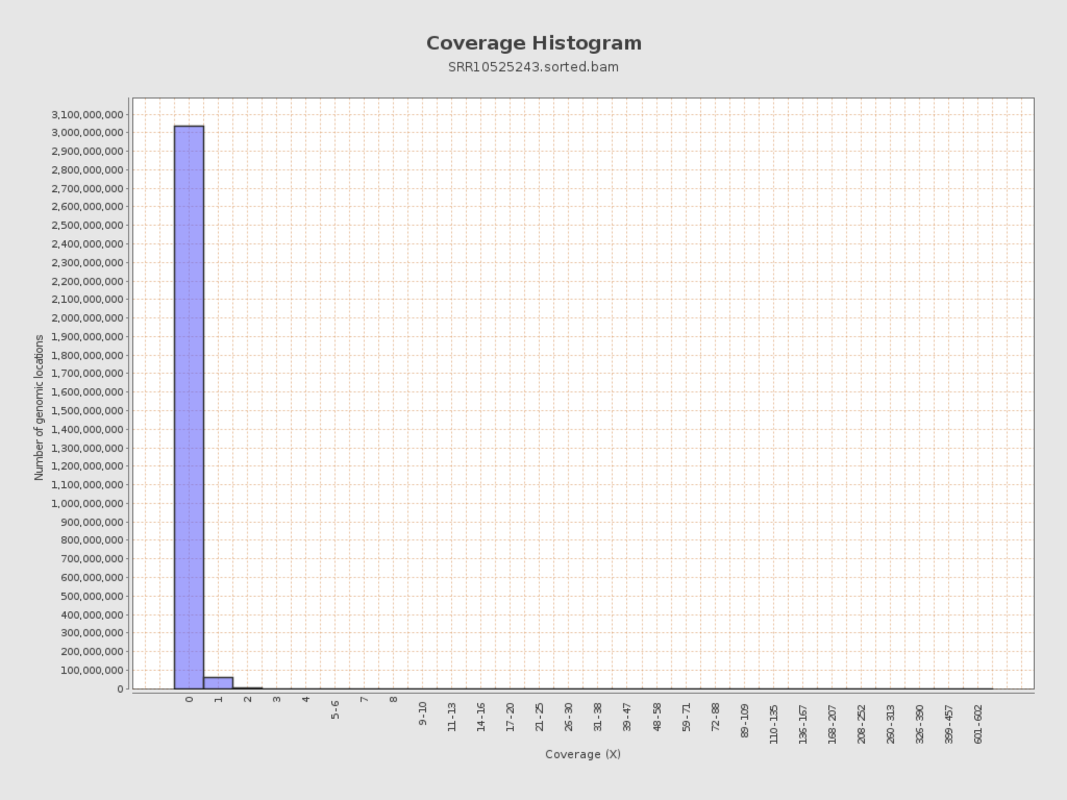
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7372437	0.0296	0.3544
chr2	243199373	5758147	0.0237	0.2899
chr3	198022430	5106309	0.0258	0.172
chr4	191154276	2986277	0.0156	0.1399
chr5	180915260	3141771	0.0174	0.1403
chr6	171115067	4281168	0.025	0.1849
chr7	159138663	5087736	0.032	0.3684

chr8	146364022	3393984	0.0232	0.202
chr9	141213431	2296510	0.0163	0.1616
chr10	135534747	3716439	0.0274	0.2462
chr11	135006516	3147580	0.0233	0.1907
chr12	133851895	3120694	0.0233	0.1646
chr13	115169878	1551702	0.0135	0.1272
chr14	107349540	2578411	0.024	0.1673
chr15	102531392	1329768	0.013	0.126
chr16	90354753	1845588	0.0204	0.1665
chr17	81195210	1210065	0.0149	0.1345
chr18	78077248	1467597	0.0188	0.3063
chr19	59128983	1115379	0.0189	0.2645
chr20	63025520	1162649	0.0184	0.1467
chr21	48129895	864952	0.018	0.1503
chr22	51304566	766193	0.0149	0.1297
chrMT	16571	45844	2.7665	2.114
chrX	155270560	3844055	0.0248	0.1803
chrY	59373566	190485	0.0032	0.093

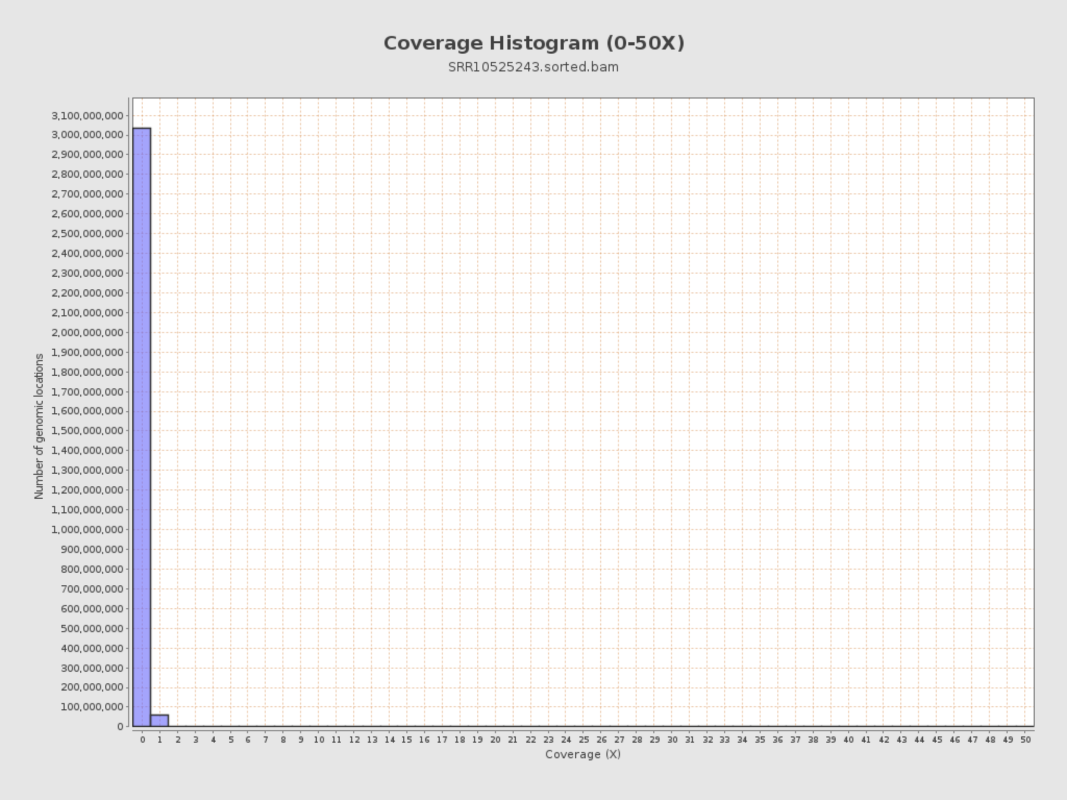
3. Results : Coverage across reference



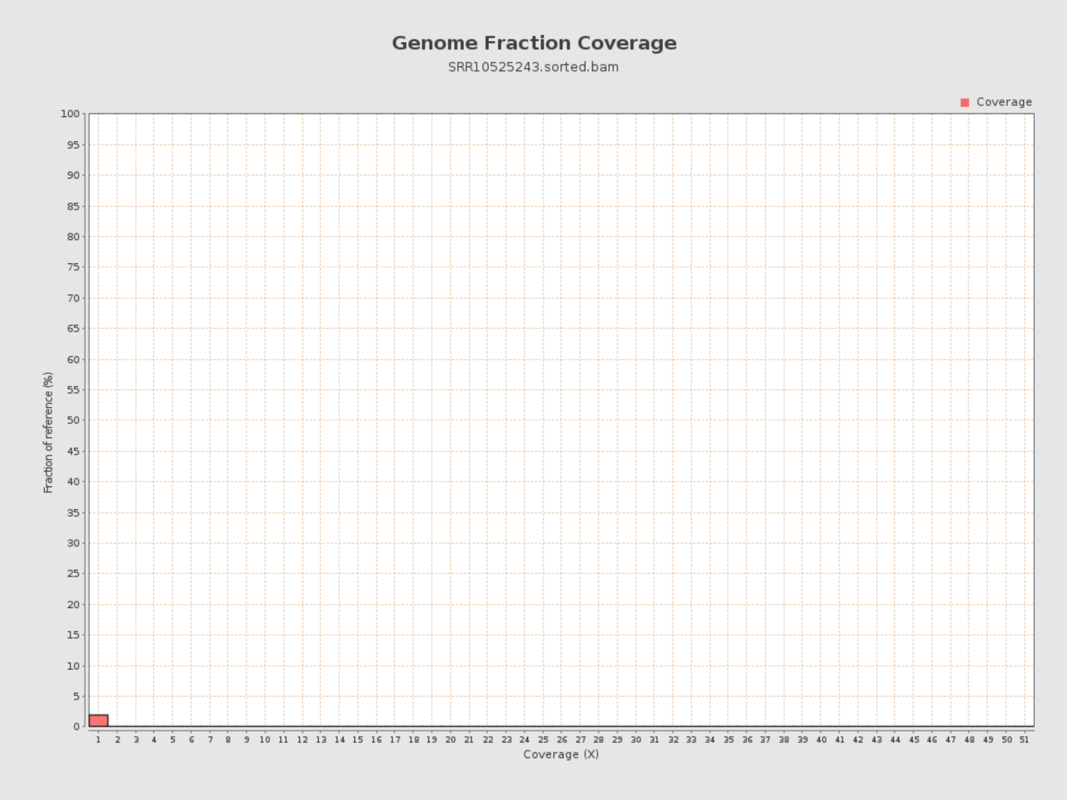
4. Results : Coverage Histogram



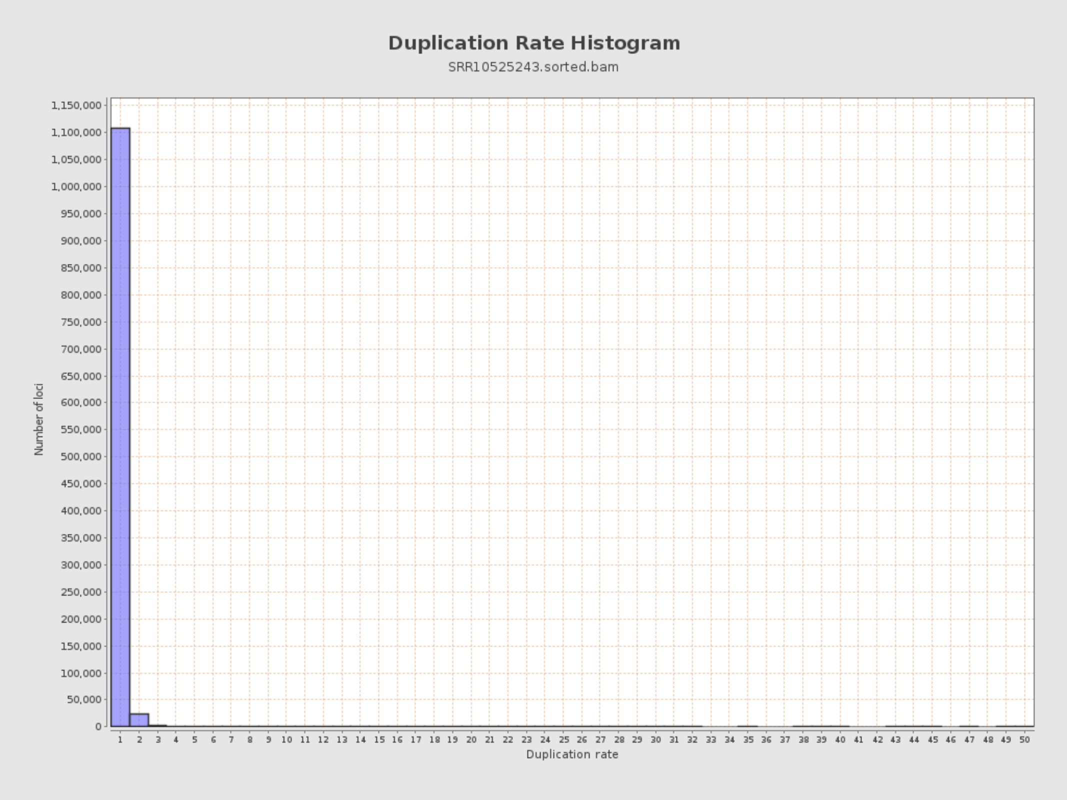
5. Results : Coverage Histogram (0-50X)



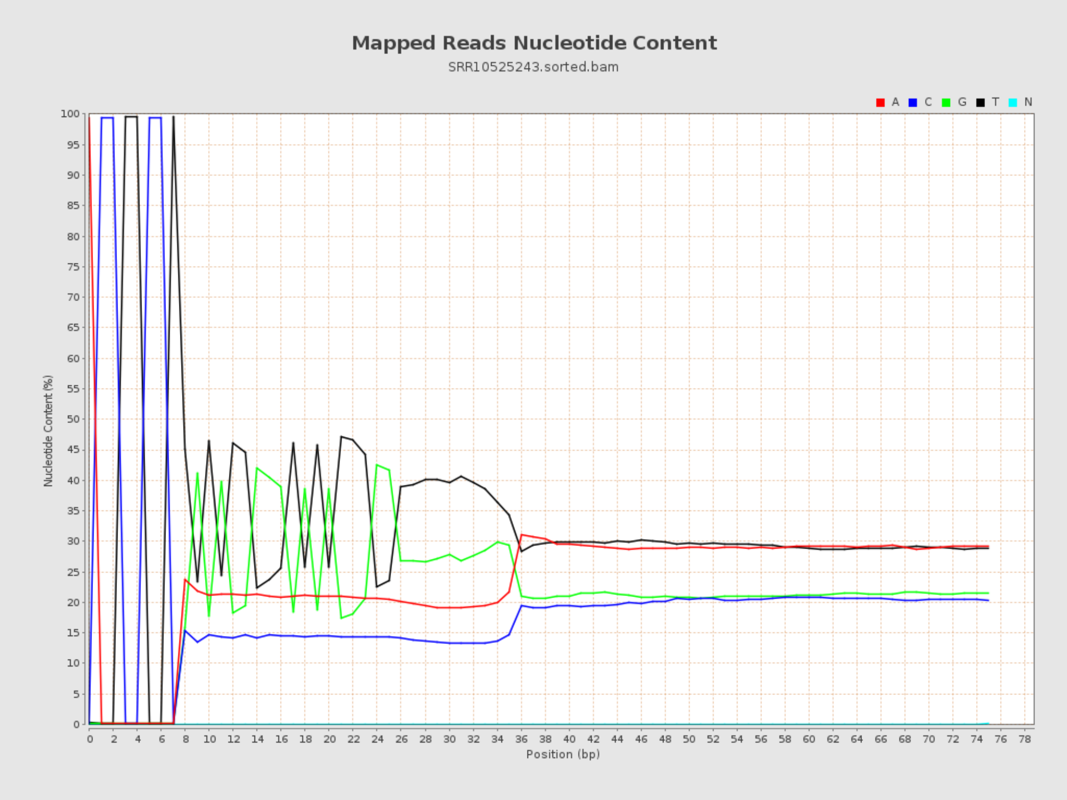
6. Results : Genome Fraction Coverage



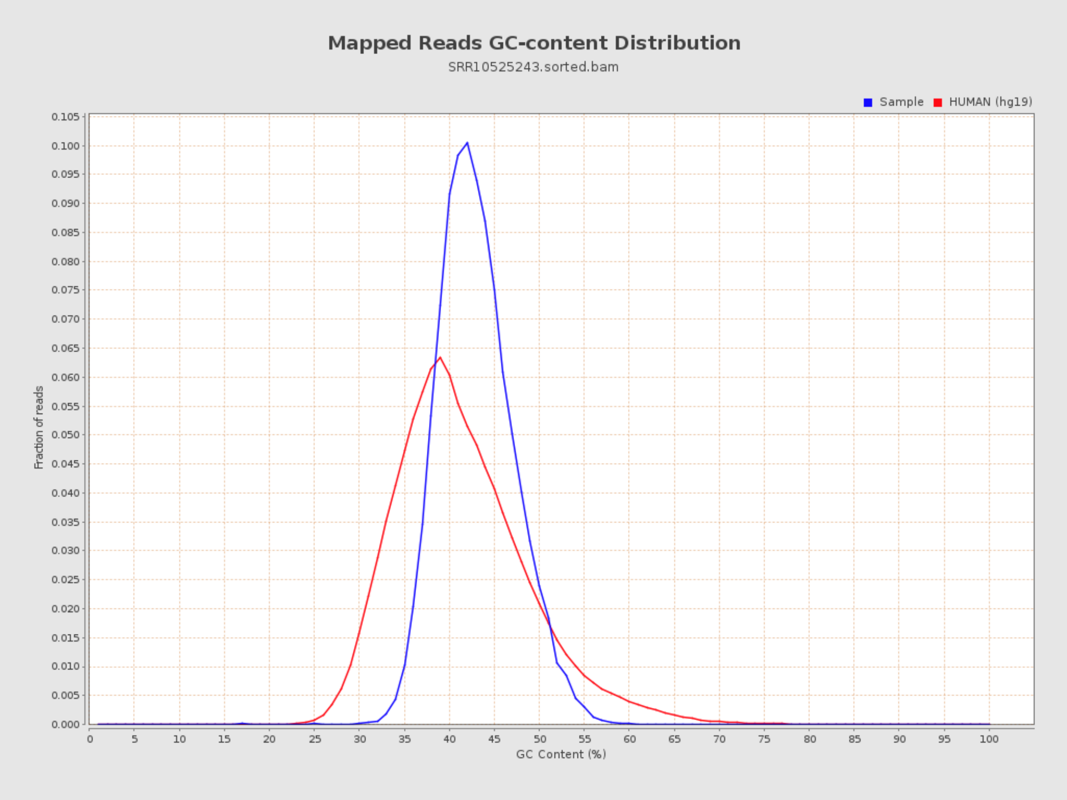
7. Results : Duplication Rate Histogram



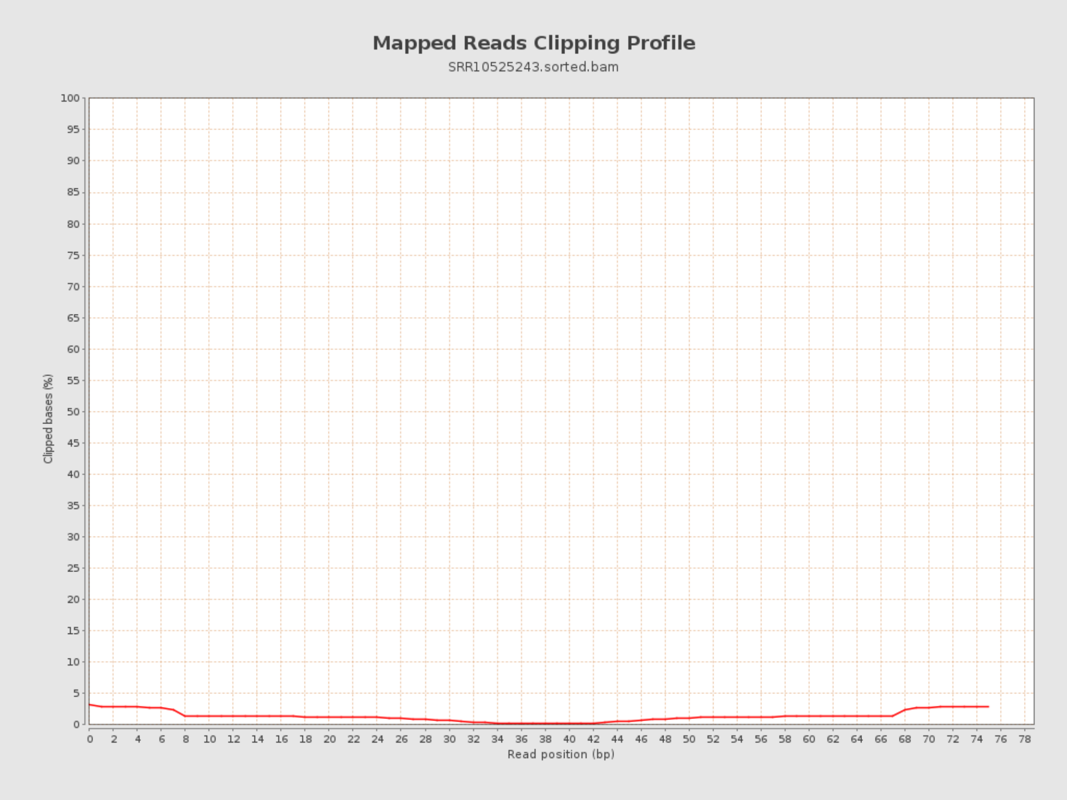
8. Results : Mapped Reads Nucleotide Content



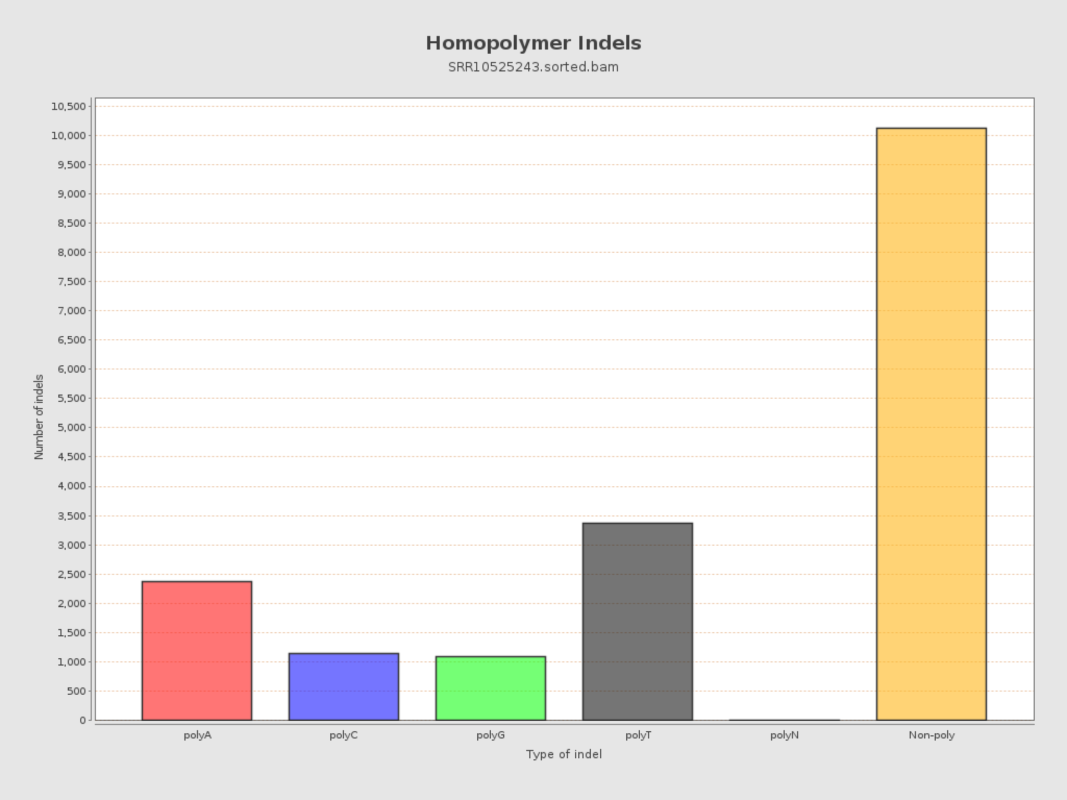
9. Results : Mapped Reads GC-content Distribution



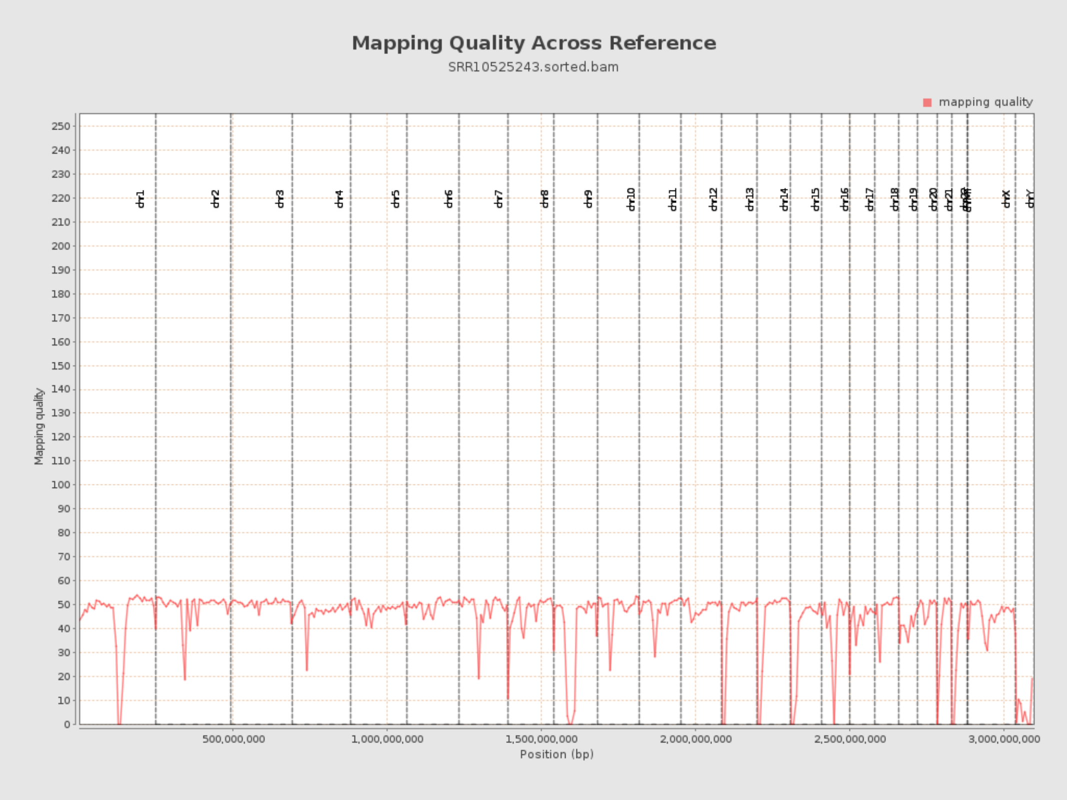
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram