Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:44:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525002.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_SRR10525002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525002.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:44:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	977,859
Mapped reads	891,845 / 91.2%
Unmapped reads	86,014 / 8.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,808 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	18,865 / 1.93%
Duplication rate	1.42%
Clipped reads	891,964 / 91.22%

2.2. ACGT Content

Number/percentage of A's	12,106,293 / 23.57%
Number/percentage of C's	9,604,382 / 18.7%
Number/percentage of T's	16,457,473 / 32.04%
Number/percentage of G's	13,200,885 / 25.7%
Number/percentage of N's	554 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.1756

2.4. Mapping Quality

Mean Mapping Quality	43.58

2.5. Mismatches and indels

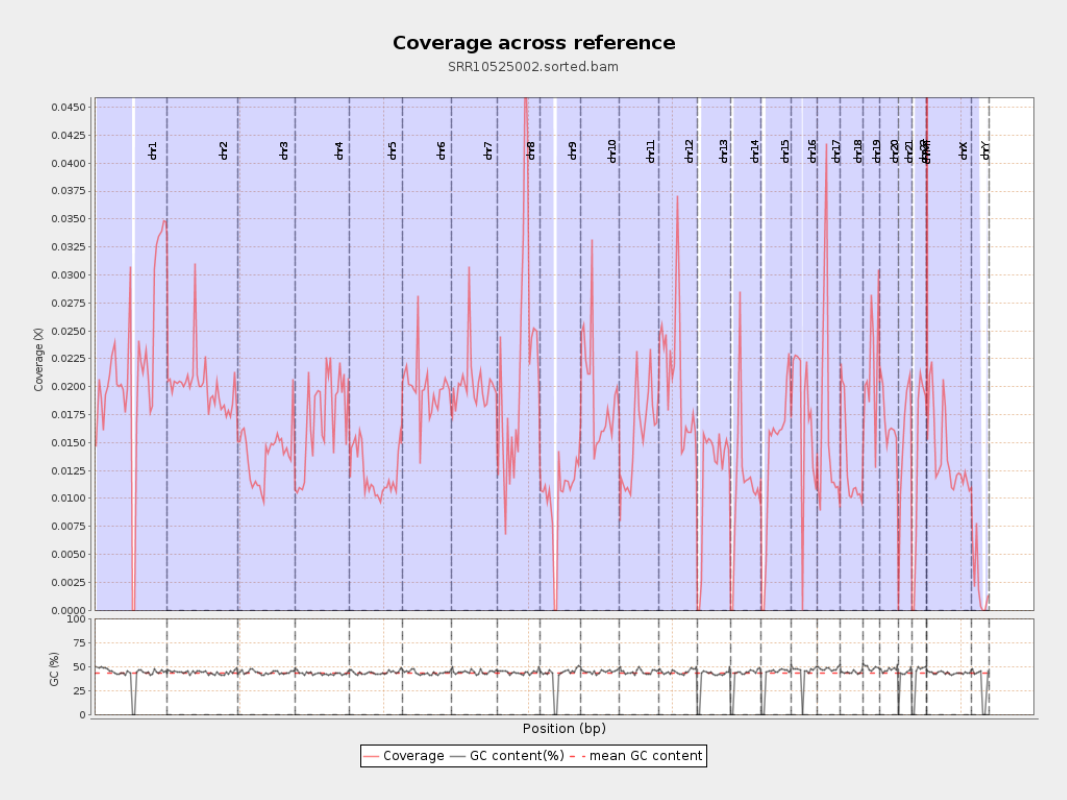
General error rate	0.51%
Mismatches	254,653
Insertions	3,330
Mapped reads with at least one insertion	0.37%
Deletions	10,098
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.64%

2.6. Chromosome stats

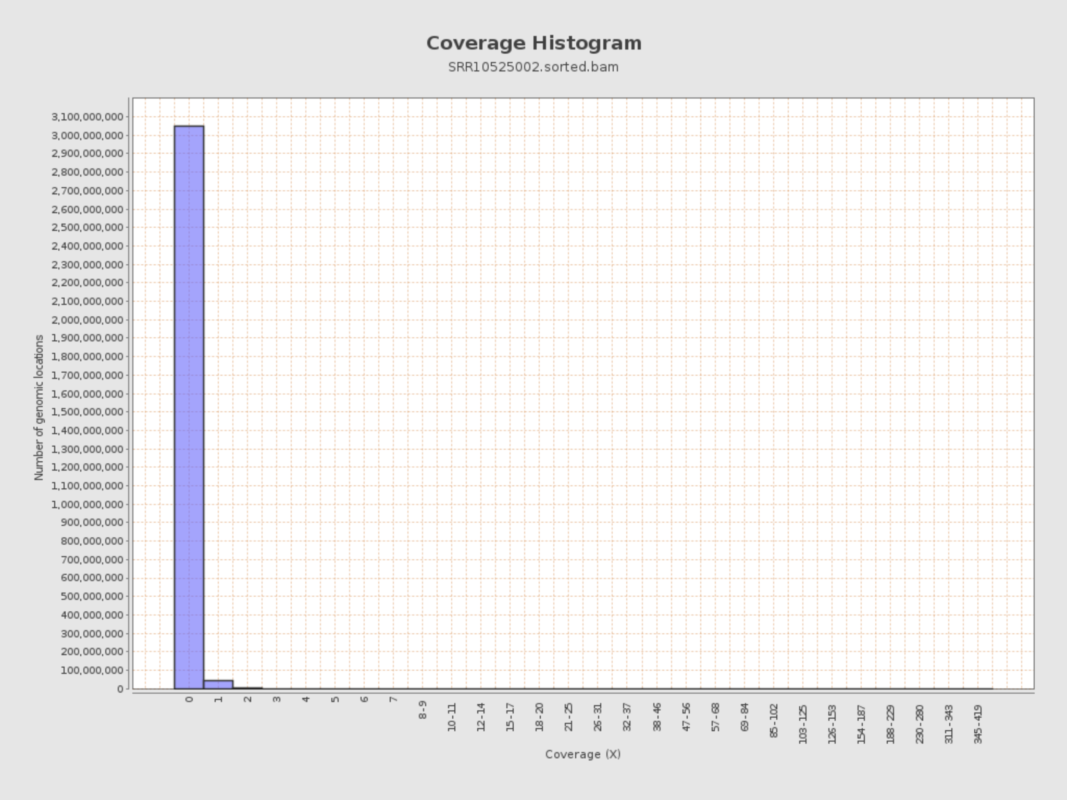
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5397203	0.0217	0.309
chr2	243199373	4870142	0.02	0.1987
chr3	198022430	2766147	0.014	0.1258
chr4	191154276	3282240	0.0172	0.1443
chr5	180915260	2229430	0.0123	0.1172
chr6	171115067	3380708	0.0198	0.178
chr7	159138663	3225942	0.0203	0.2259

chr8	146364022	3197443	0.0218	0.1776
chr9	141213431	1420531	0.0101	0.136
chr10	135534747	2614696	0.0193	0.1834
chr11	135006516	2138067	0.0158	0.1589
chr12	133851895	2783223	0.0208	0.1518
chr13	115169878	1397475	0.0121	0.1144
chr14	107349540	1191464	0.0111	0.112
chr15	102531392	1431555	0.014	0.127
chr16	90354753	1562332	0.0173	0.1442
chr17	81195210	1384227	0.017	0.1663
chr18	78077248	1020247	0.0131	0.2117
chr19	59128983	1283525	0.0217	0.2027
chr20	63025520	1053973	0.0167	0.1363
chr21	48129895	728470	0.0151	0.133
chr22	51304566	701545	0.0137	0.1214
chrMT	16571	3078	0.1857	0.4296
chrX	155270560	2185664	0.0141	0.1372
chrY	59373566	137232	0.0023	0.07

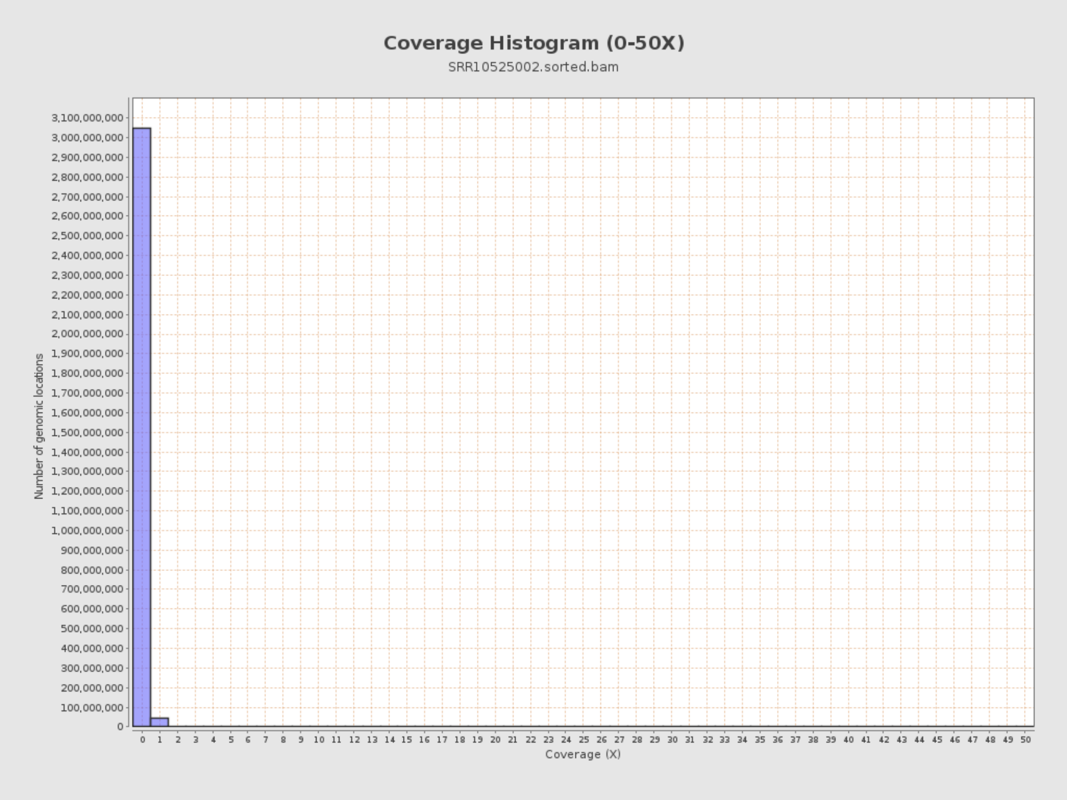
3. Results : Coverage across reference



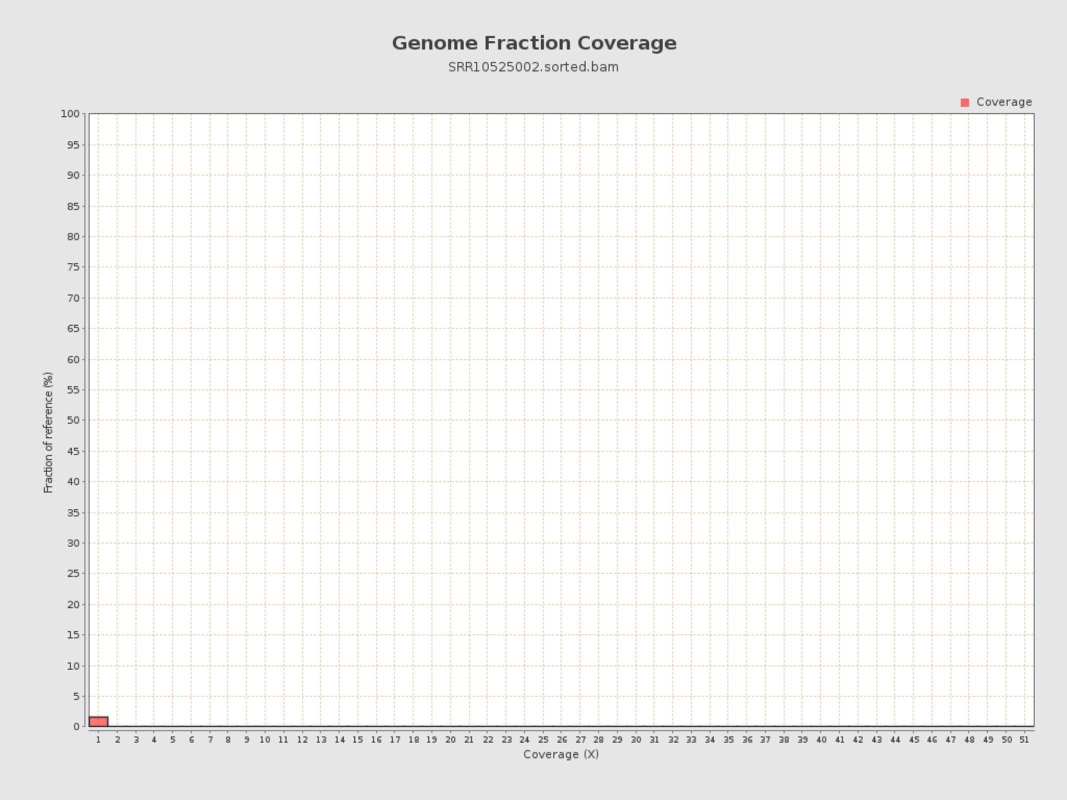
4. Results : Coverage Histogram



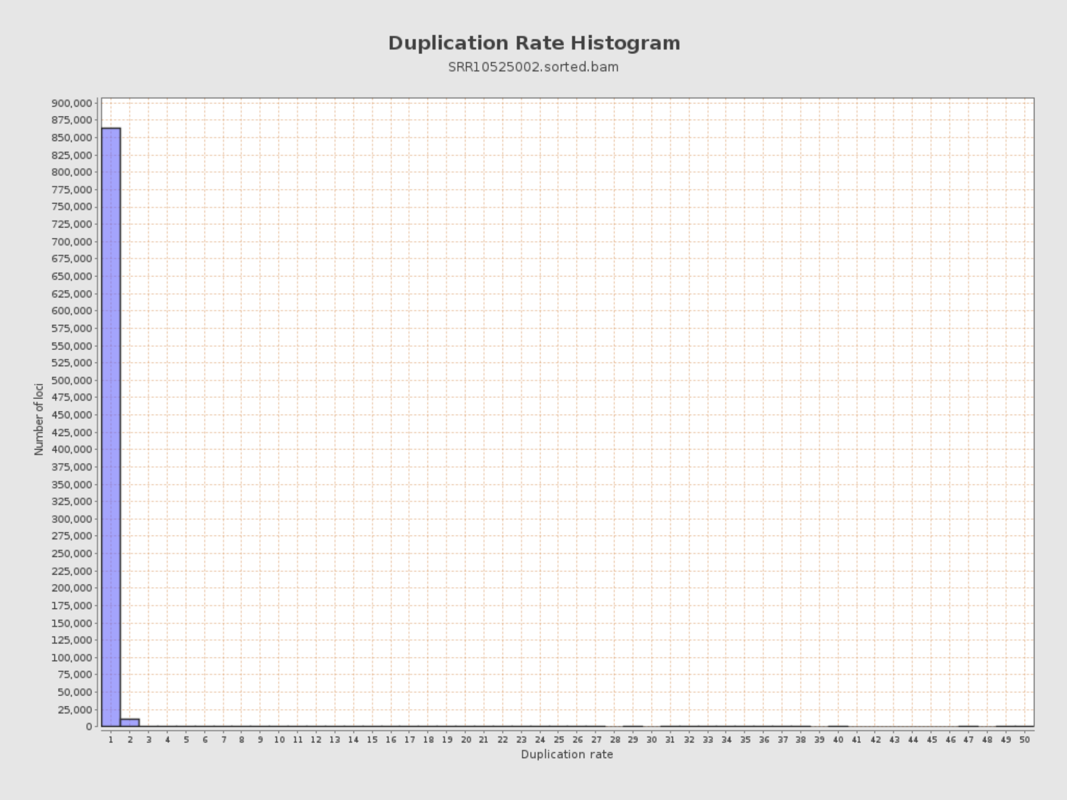
5. Results : Coverage Histogram (0-50X)



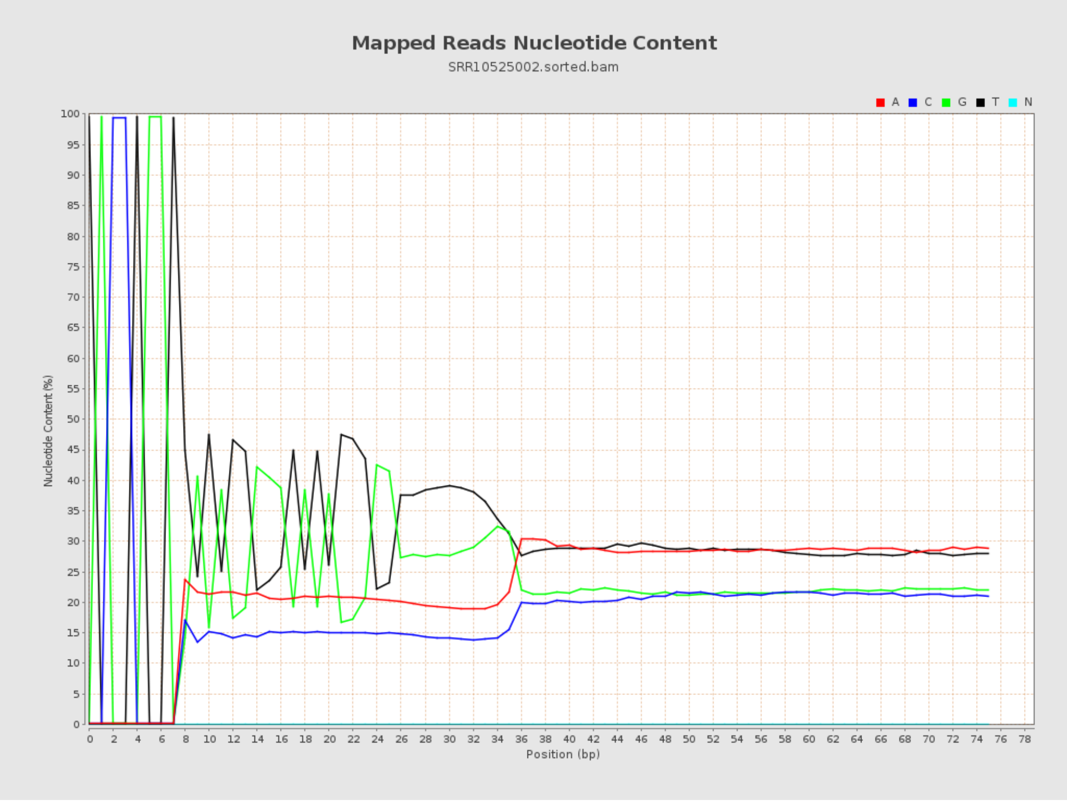
6. Results : Genome Fraction Coverage



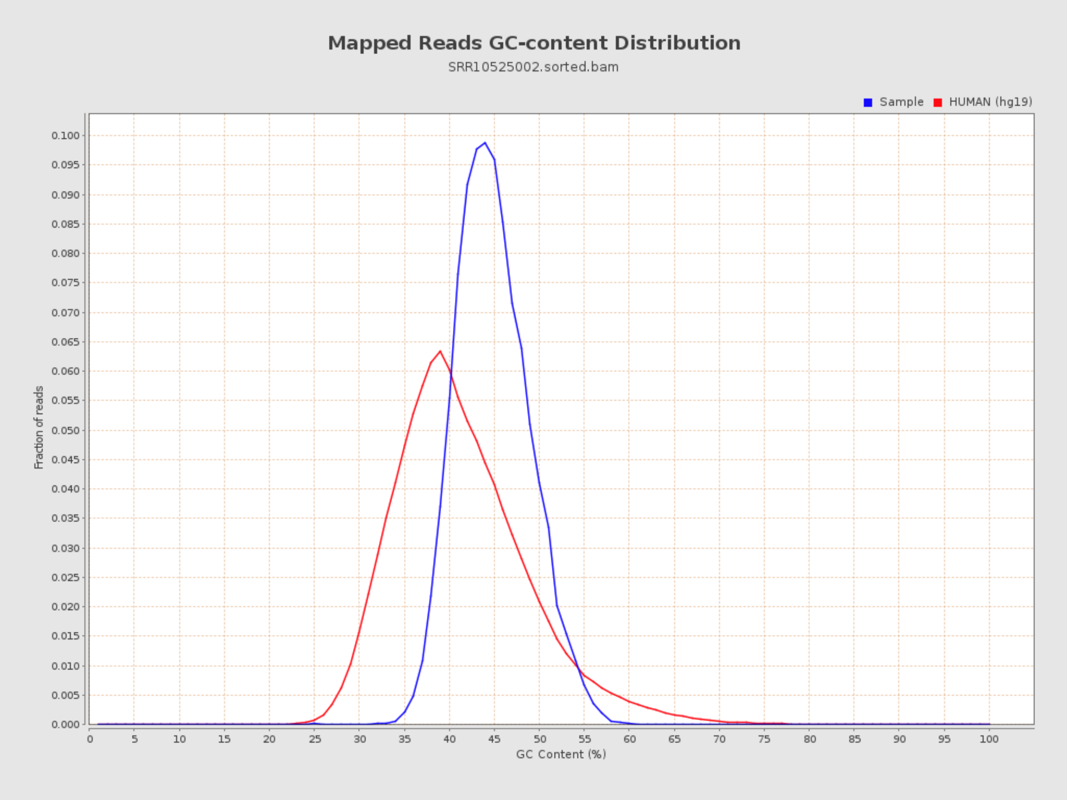
7. Results : Duplication Rate Histogram



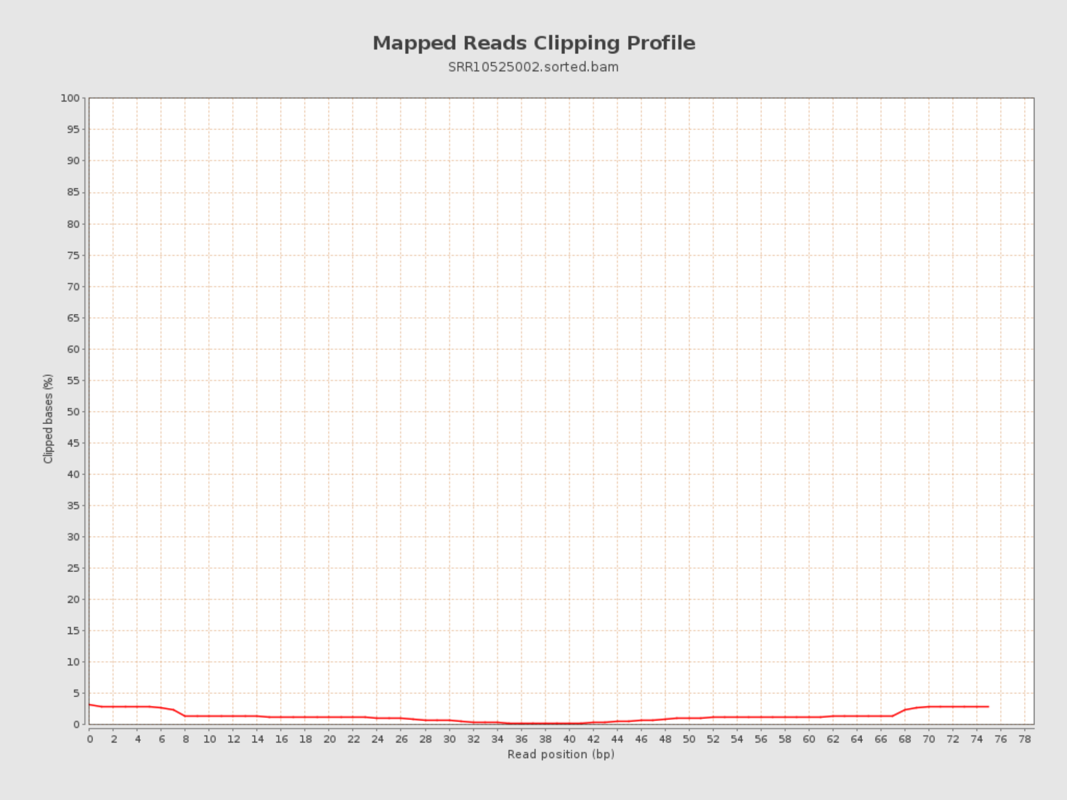
8. Results : Mapped Reads Nucleotide Content



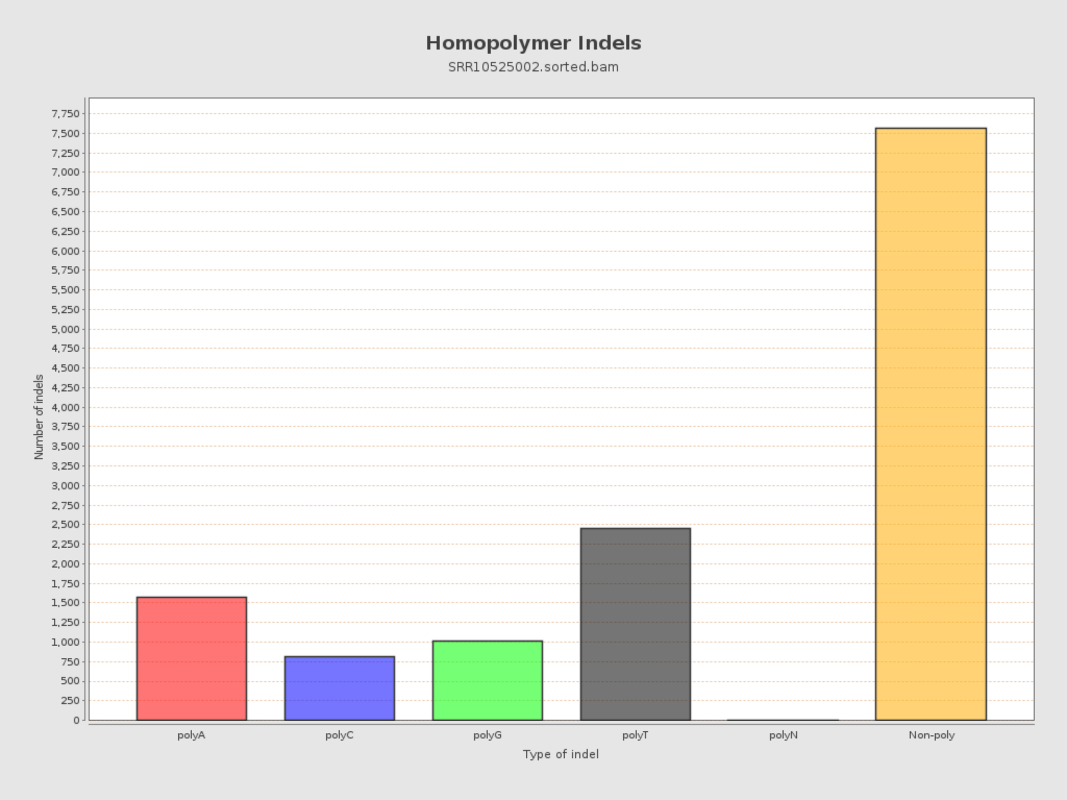
9. Results : Mapped Reads GC-content Distribution



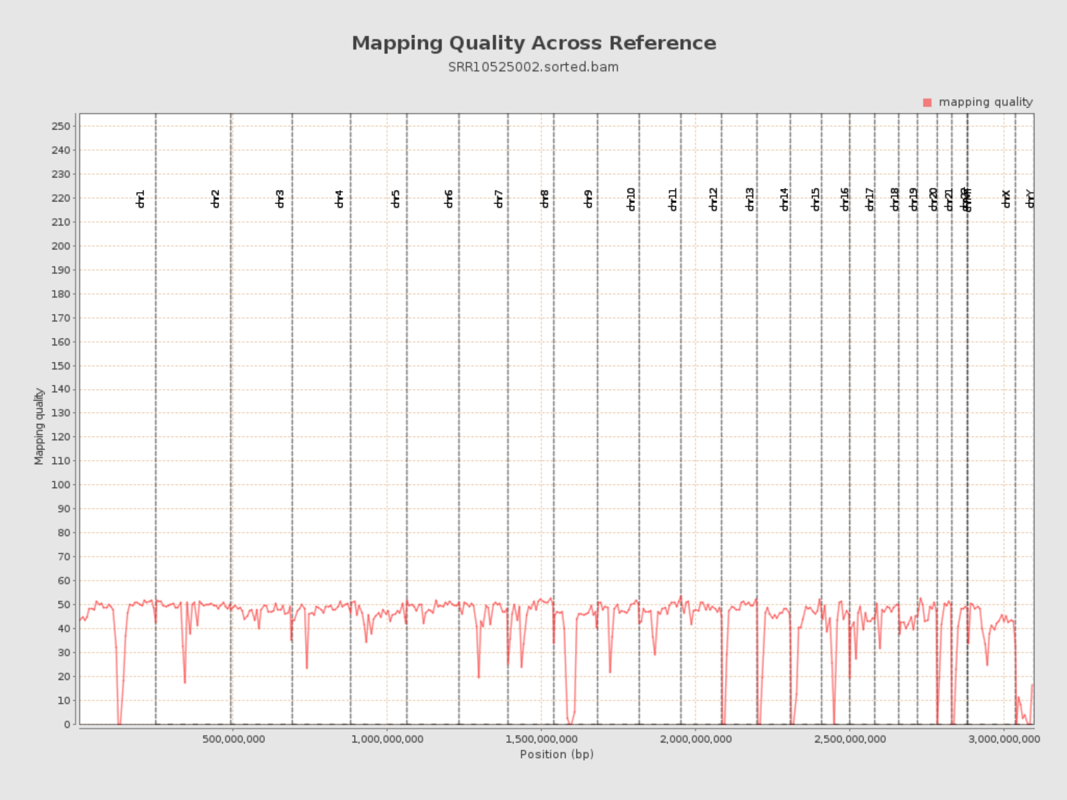
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram