Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:59:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525101.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_SRR10525101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:59:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	628,230
Mapped reads	567,337 / 90.31%
Unmapped reads	60,893 / 9.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,123 / 2.41%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	12,325 / 1.96%
Duplication rate	1.29%
Clipped reads	581,466 / 92.56%

2.2. ACGT Content

Number/percentage of A's	11,362,145 / 26.09%
Number/percentage of C's	8,107,904 / 18.62%
Number/percentage of T's	13,797,165 / 31.69%
Number/percentage of G's	10,275,795 / 23.6%
Number/percentage of N's	1,454 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1856

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

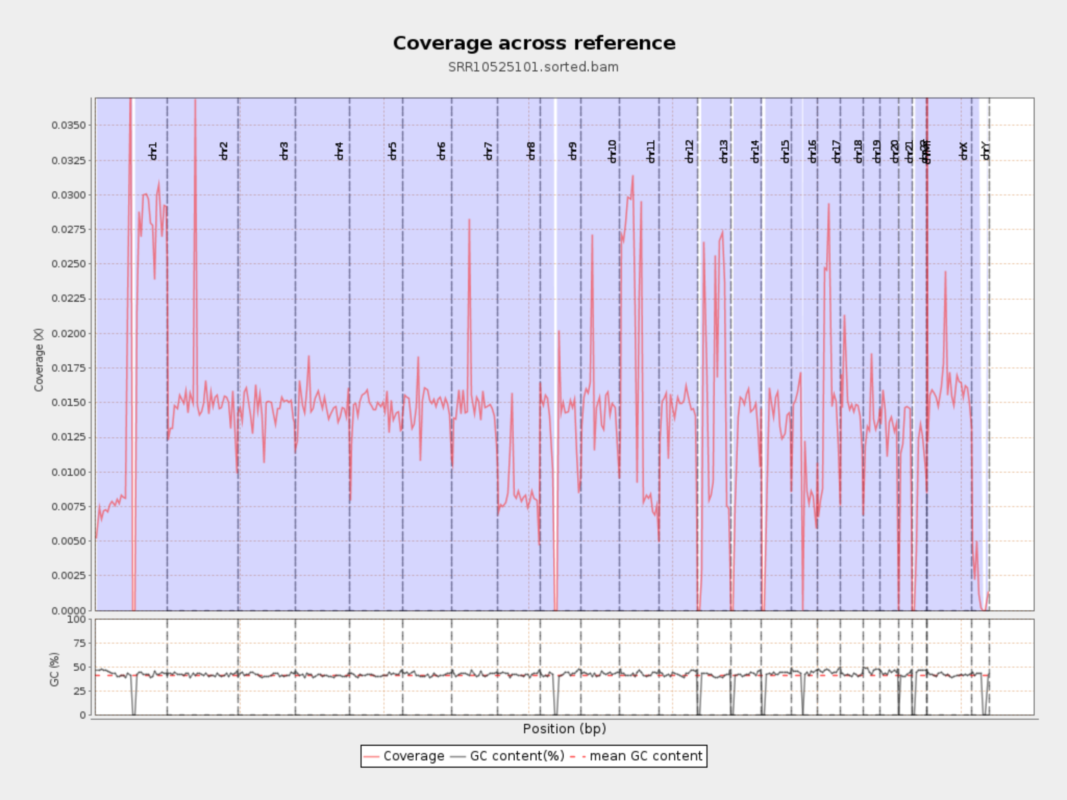
General error rate	0.76%
Mismatches	325,192
Insertions	3,704
Mapped reads with at least one insertion	0.65%
Deletions	9,858
Mapped reads with at least one deletion	1.71%
Homopolymer indels	43.63%

2.6. Chromosome stats

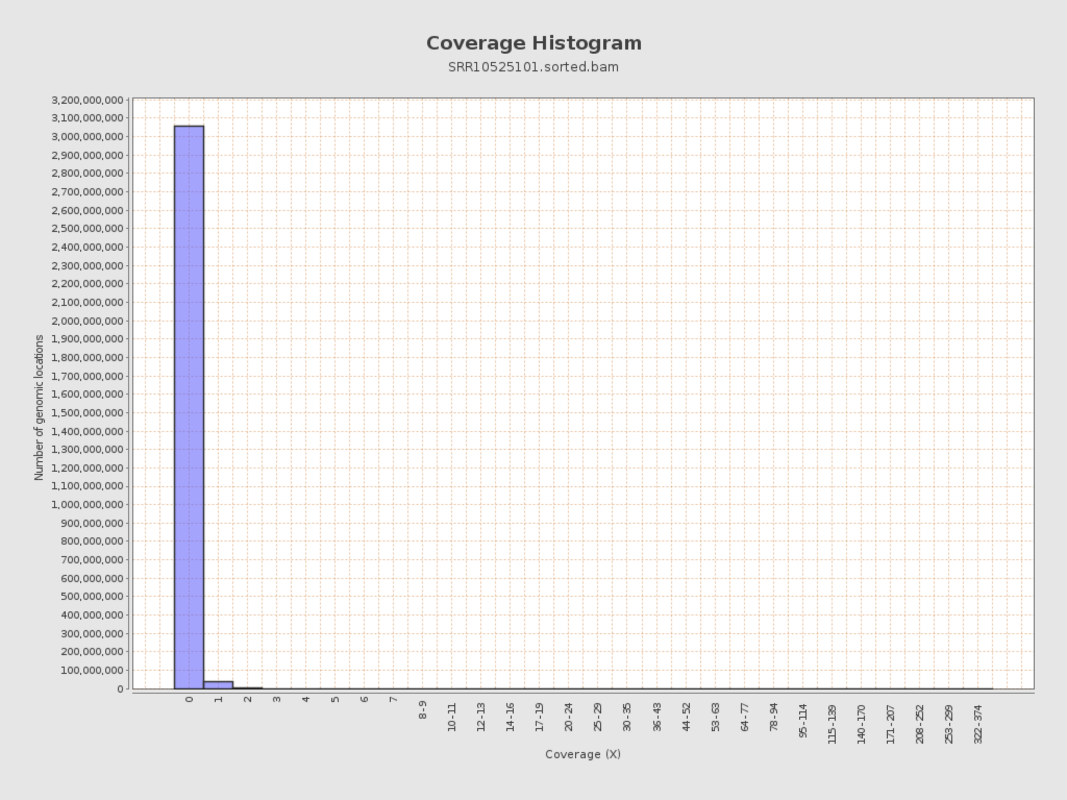
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4364604	0.0175	0.3295
chr2	243199373	3735843	0.0154	0.2262
chr3	198022430	2887454	0.0146	0.1256
chr4	191154276	2818031	0.0147	0.1291
chr5	180915260	2630081	0.0145	0.1267
chr6	171115067	2537562	0.0148	0.1356
chr7	159138663	2408703	0.0151	0.2394

chr8	146364022	1234327	0.0084	0.2024
chr9	141213431	1791638	0.0127	0.1752
chr10	135534747	2039061	0.015	0.1862
chr11	135006516	2441048	0.0181	0.2167
chr12	133851895	1941861	0.0145	0.1257
chr13	115169878	1607263	0.014	0.1228
chr14	107349540	1297798	0.0121	0.1258
chr15	102531392	1195009	0.0117	0.1115
chr16	90354753	930748	0.0103	0.112
chr17	81195210	1265093	0.0156	0.1421
chr18	78077248	1190027	0.0152	0.2789
chr19	59128983	804944	0.0136	0.215
chr20	63025520	836579	0.0133	0.1219
chr21	48129895	566079	0.0118	0.1169
chr22	51304566	423569	0.0083	0.094
chrMT	16571	1048	0.0632	0.2898
chrX	155270560	2512519	0.0162	0.1547
chrY	59373566	100303	0.0017	0.05

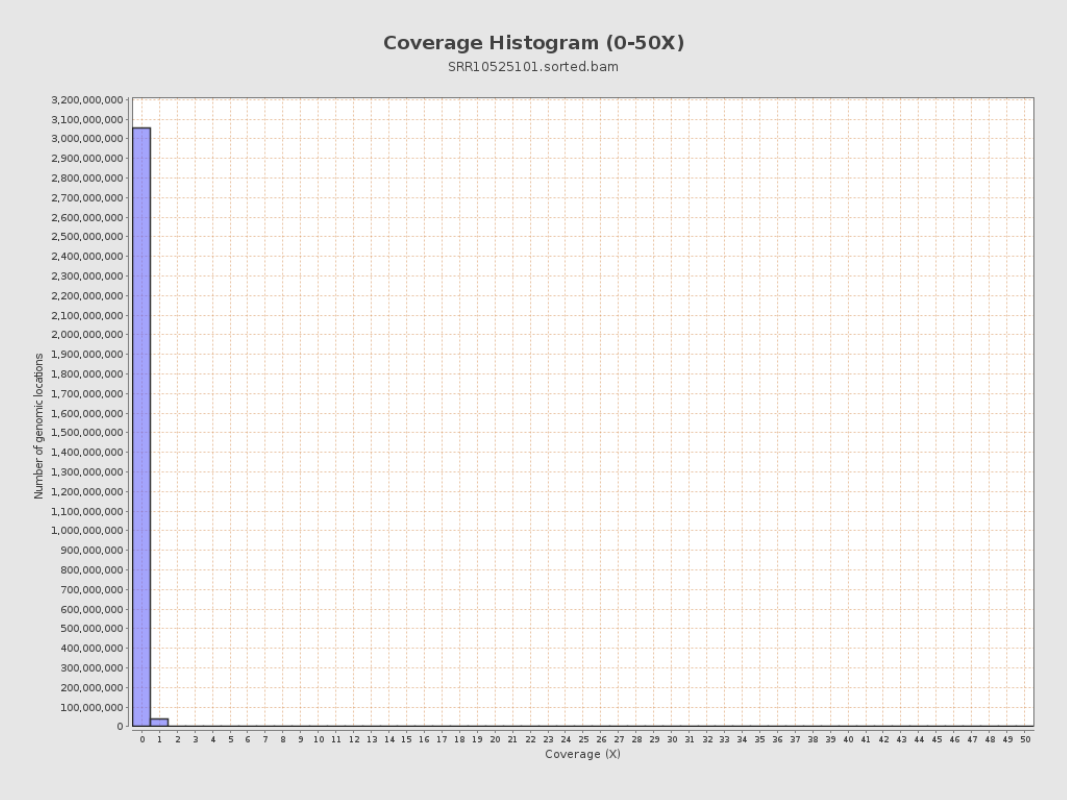
3. Results : Coverage across reference



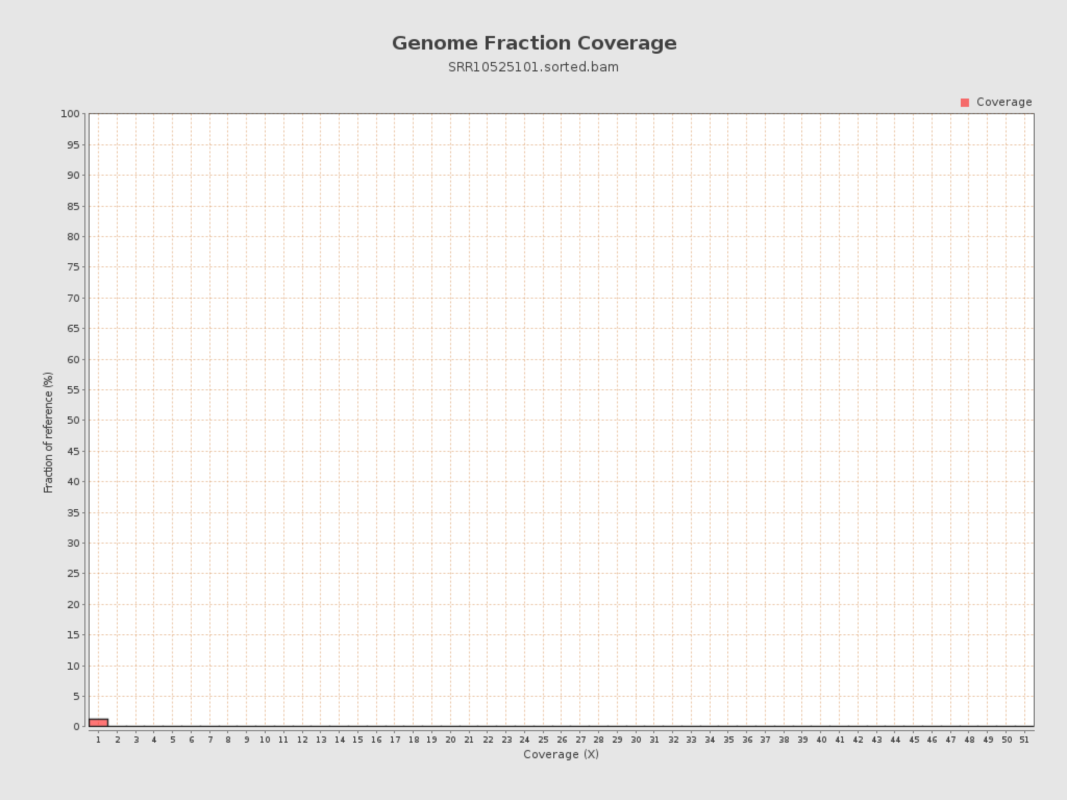
4. Results : Coverage Histogram



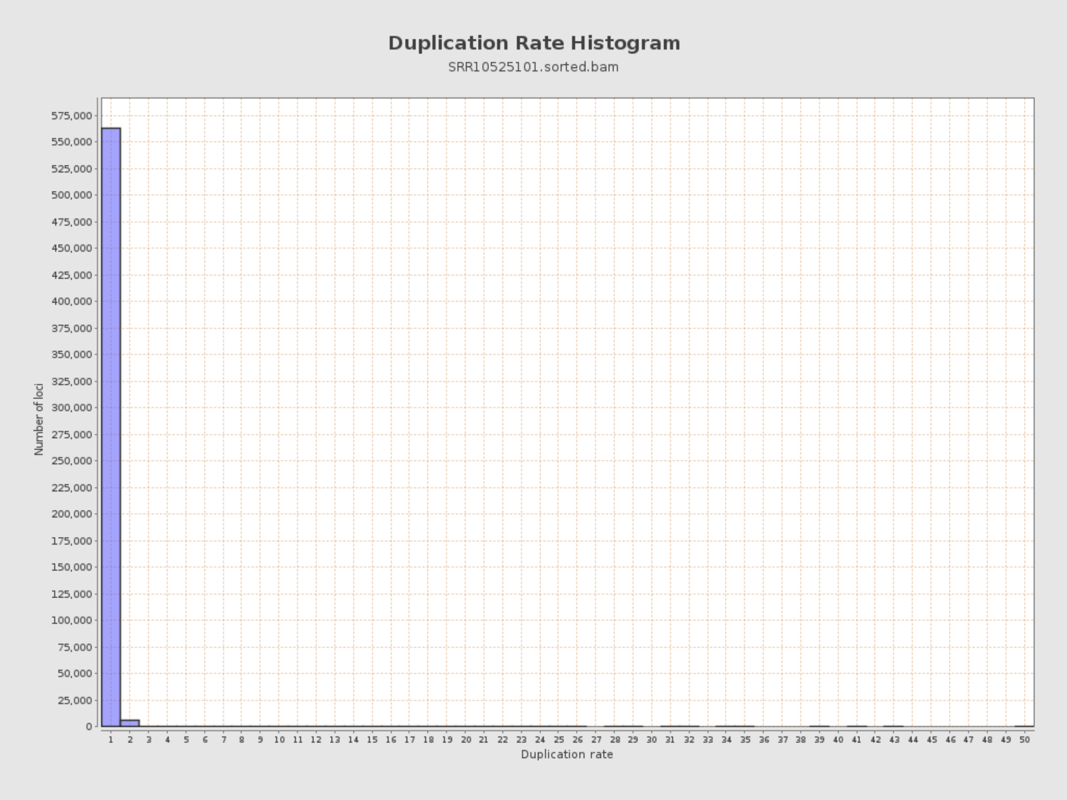
5. Results : Coverage Histogram (0-50X)



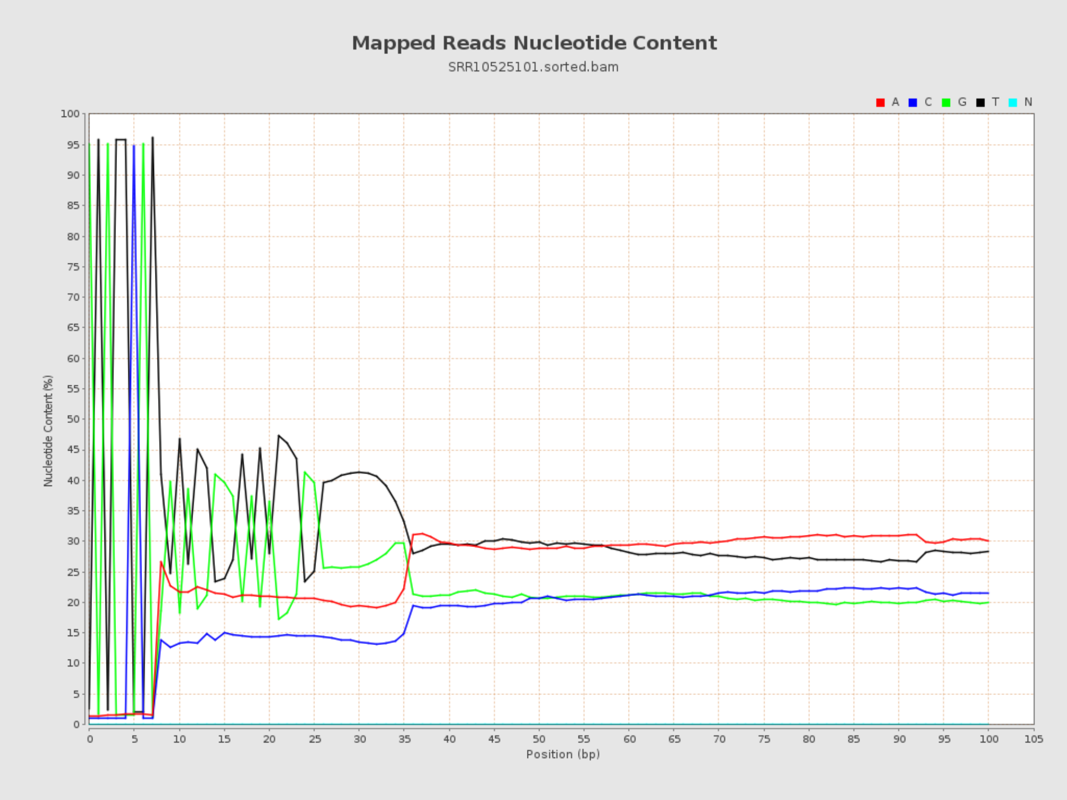
6. Results : Genome Fraction Coverage



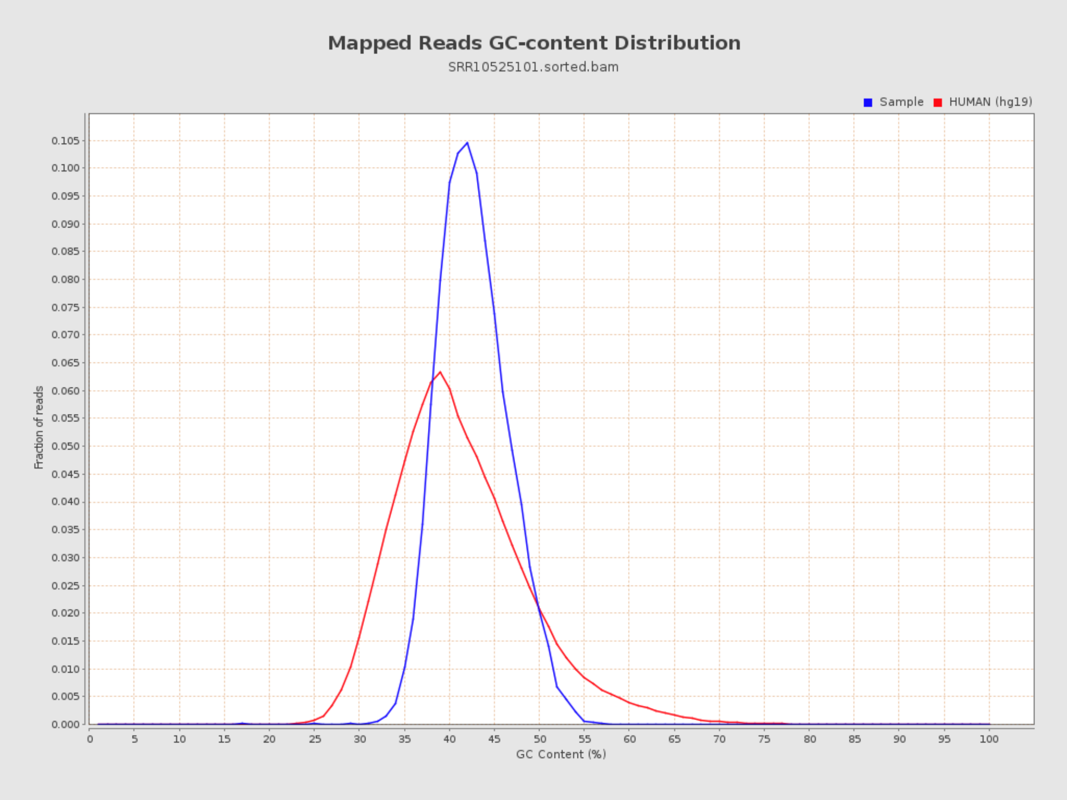
7. Results : Duplication Rate Histogram



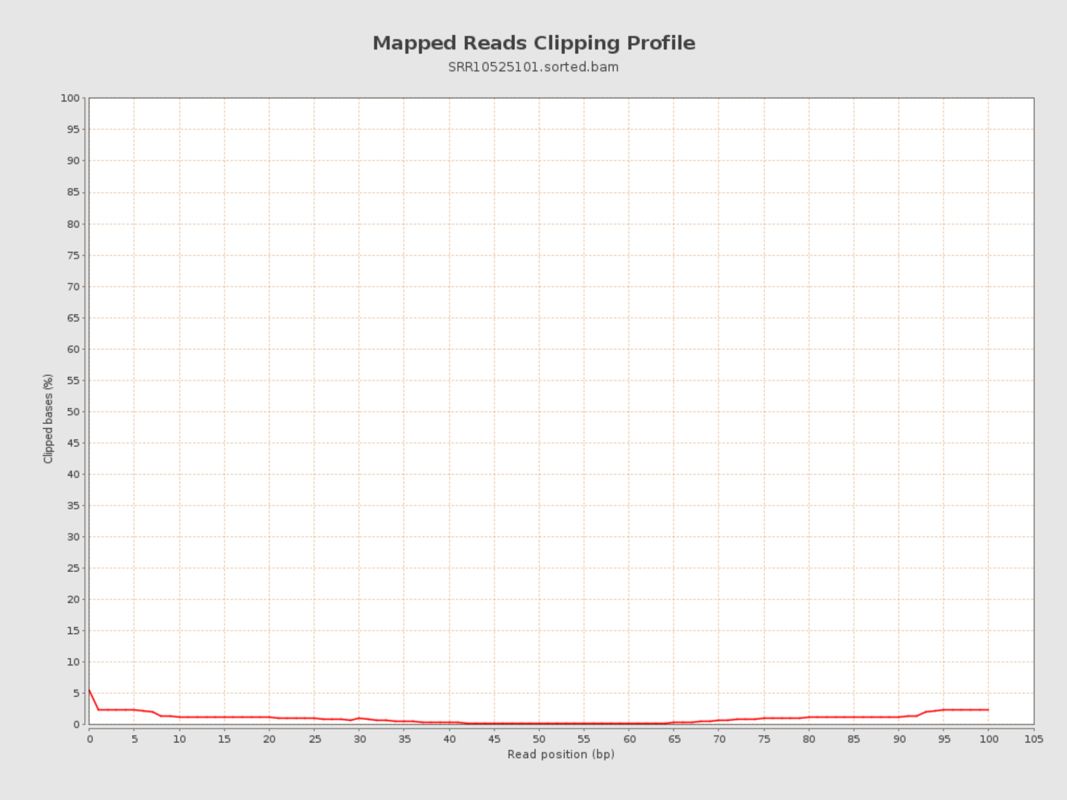
8. Results : Mapped Reads Nucleotide Content



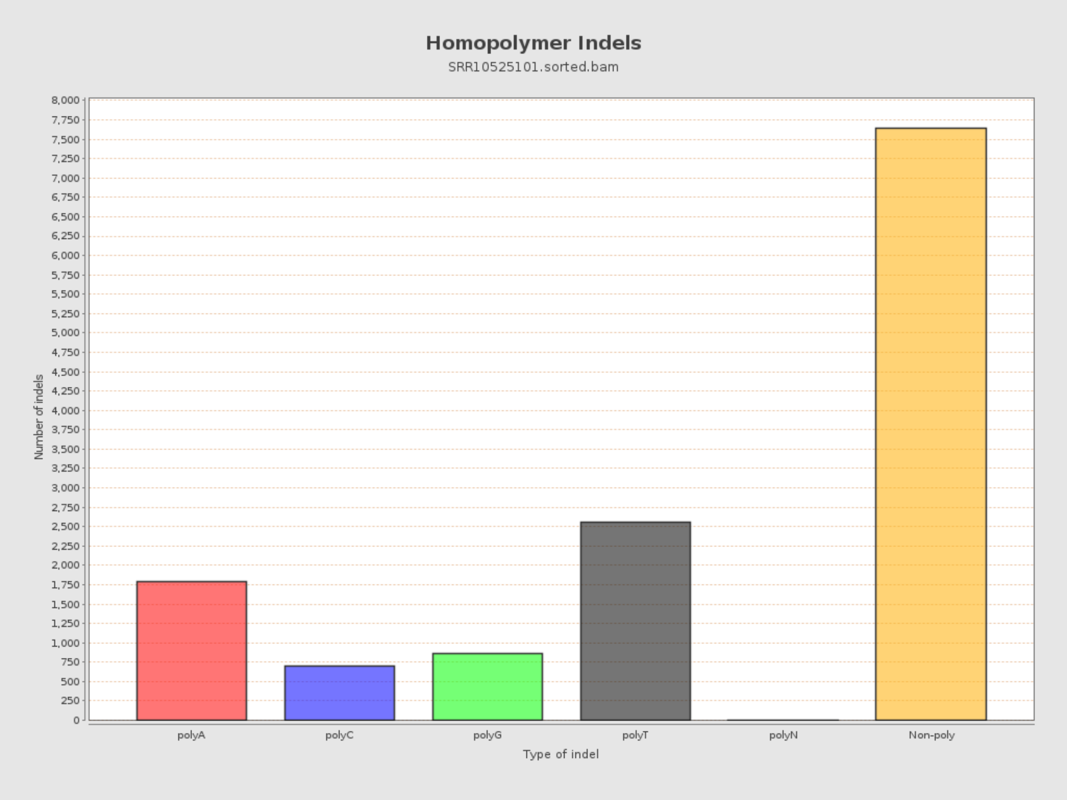
9. Results : Mapped Reads GC-content Distribution



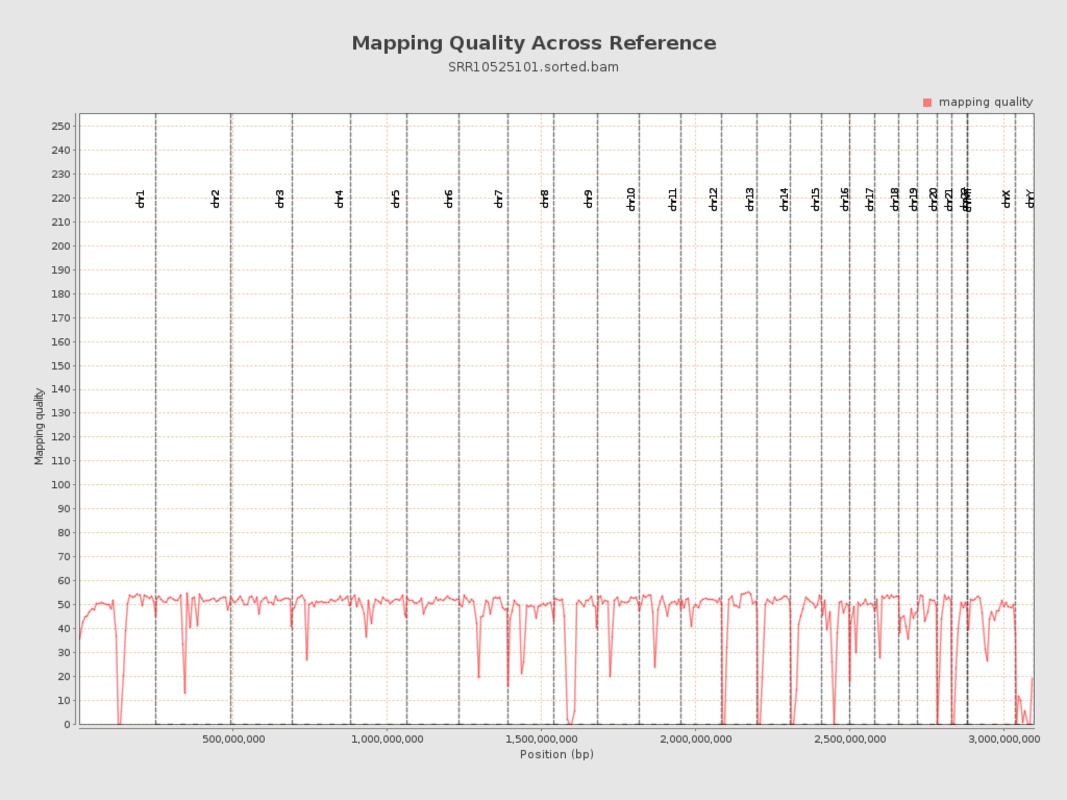
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram