Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:21:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525258.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_SRR10525258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:21:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	620,143
Mapped reads	564,253 / 90.99%
Unmapped reads	55,890 / 9.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,707 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	11,484 / 1.85%
Duplication rate	1.5%
Clipped reads	564,131 / 90.97%

2.2. ACGT Content

Number/percentage of A's	8,252,765 / 25.52%
Number/percentage of C's	5,766,853 / 17.83%
Number/percentage of T's	10,710,476 / 33.12%
Number/percentage of G's	7,612,405 / 23.54%
Number/percentage of N's	678 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1321

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

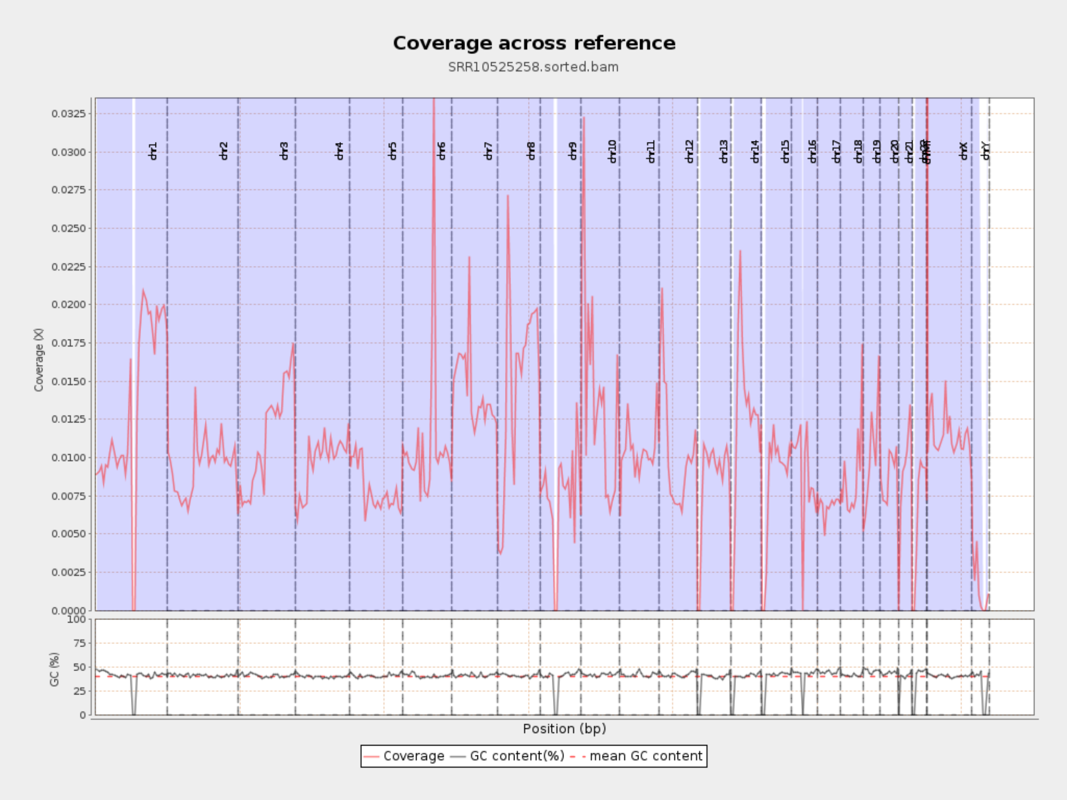
General error rate	0.52%
Mismatches	163,841
Insertions	2,374
Mapped reads with at least one insertion	0.42%
Deletions	6,582
Mapped reads with at least one deletion	1.16%
Homopolymer indels	44.43%

2.6. Chromosome stats

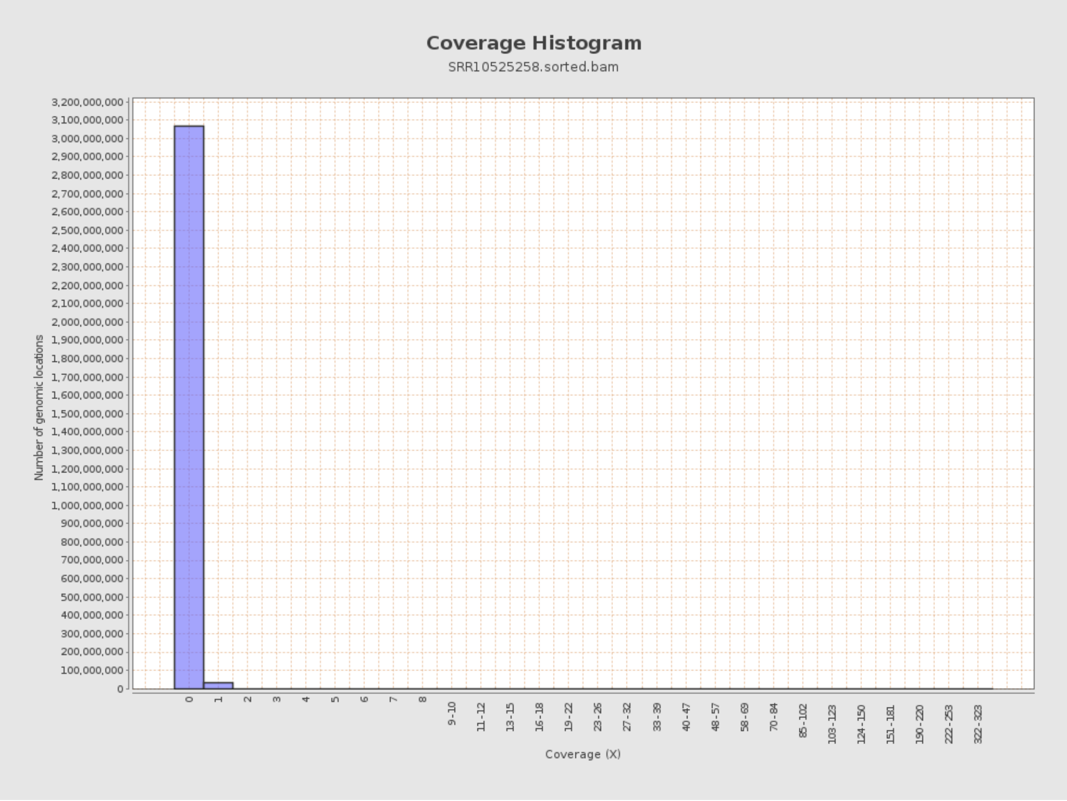
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3308926	0.0133	0.1984
chr2	243199373	2305152	0.0095	0.1621
chr3	198022430	2236189	0.0113	0.1102
chr4	191154276	1857664	0.0097	0.1042
chr5	180915260	1428896	0.0079	0.0921
chr6	171115067	1906324	0.0111	0.1151
chr7	159138663	2297243	0.0144	0.2113

chr8	146364022	2204390	0.0151	0.1453
chr9	141213431	1054020	0.0075	0.0993
chr10	135534747	1898520	0.014	0.1419
chr11	135006516	1406231	0.0104	0.1156
chr12	133851895	1406349	0.0105	0.1067
chr13	115169878	984593	0.0085	0.0963
chr14	107349540	1321442	0.0123	0.1158
chr15	102531392	841806	0.0082	0.0945
chr16	90354753	804417	0.0089	0.1003
chr17	81195210	553083	0.0068	0.0864
chr18	78077248	671247	0.0086	0.1445
chr19	59128983	606500	0.0103	0.1468
chr20	63025520	550470	0.0087	0.0978
chr21	48129895	438348	0.0091	0.1009
chr22	51304566	329932	0.0064	0.0829
chrMT	16571	62281	3.7584	2.7571
chrX	155270560	1789024	0.0115	0.1151
chrY	59373566	90376	0.0015	0.0491

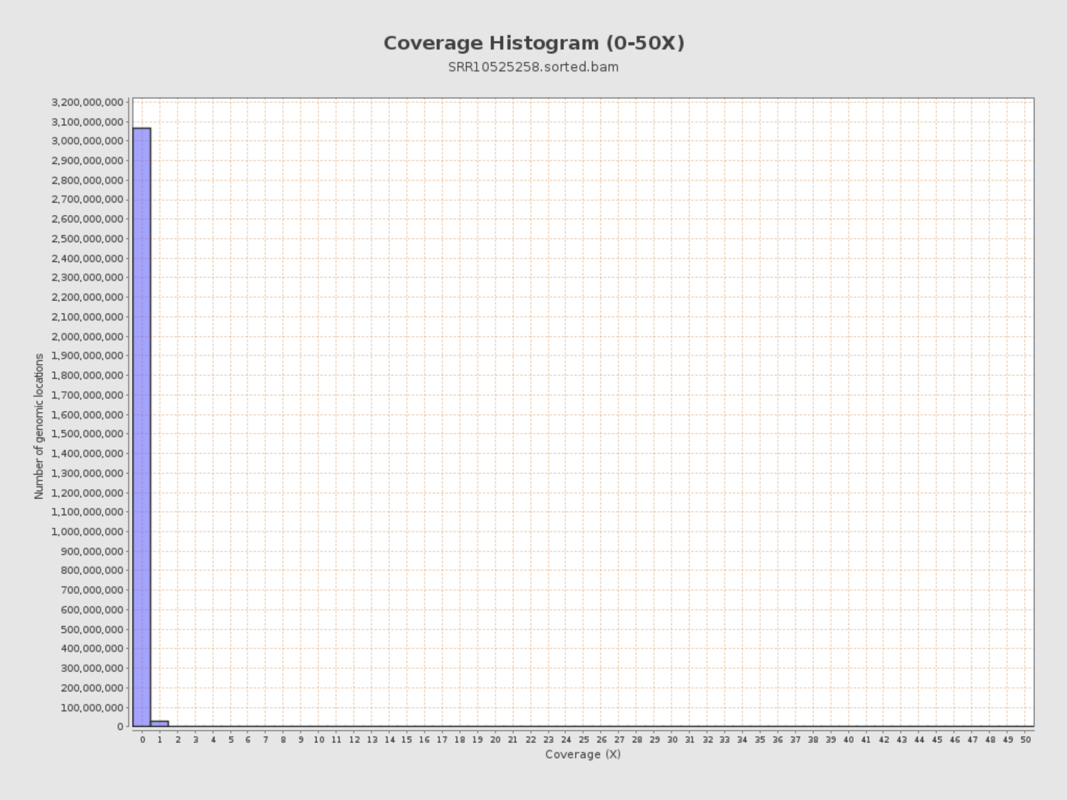
3. Results : Coverage across reference



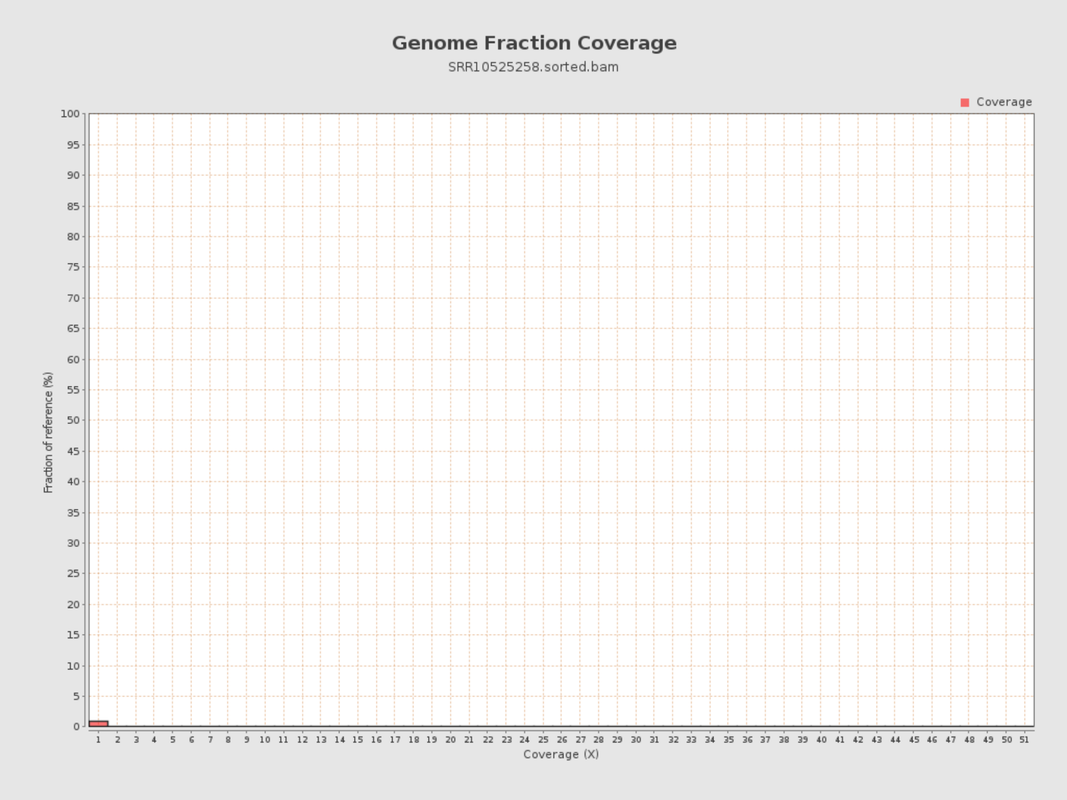
4. Results : Coverage Histogram



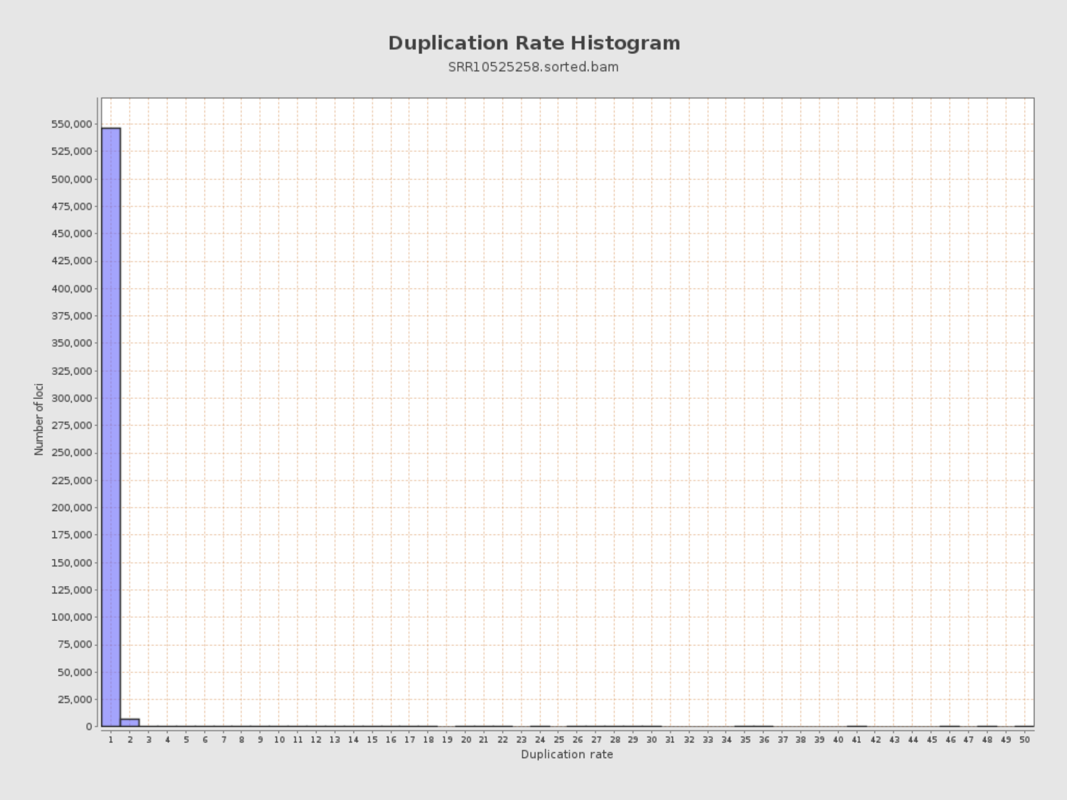
5. Results : Coverage Histogram (0-50X)



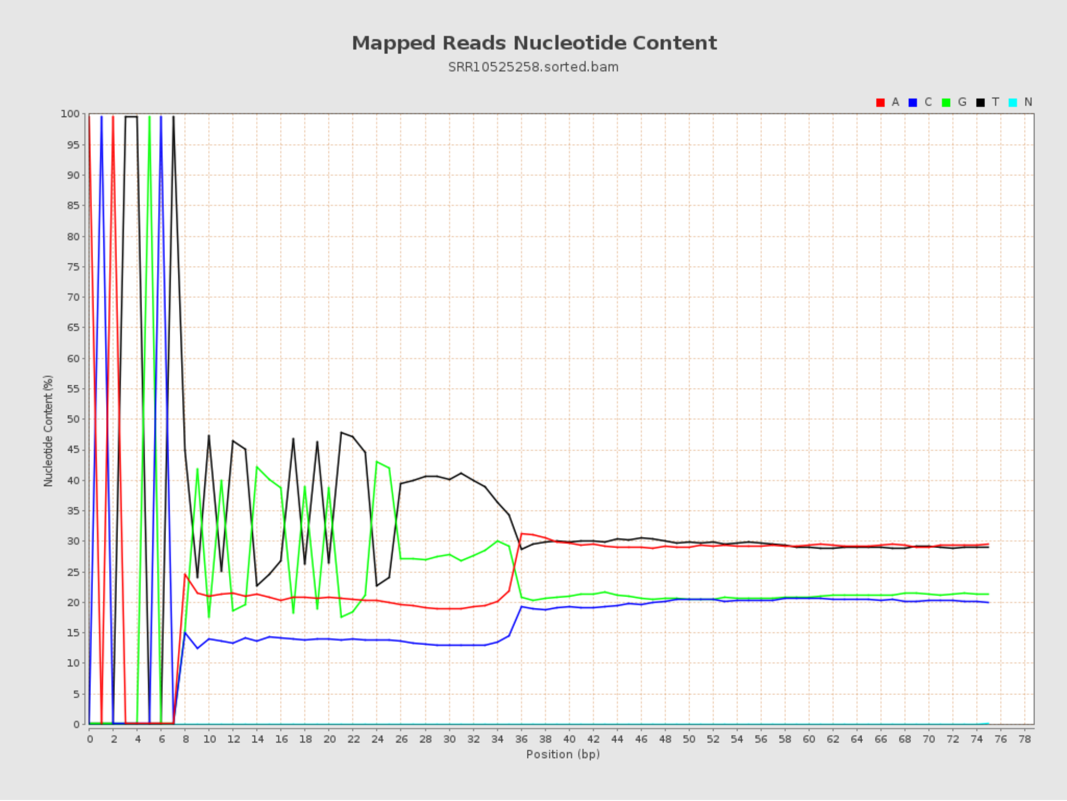
6. Results : Genome Fraction Coverage



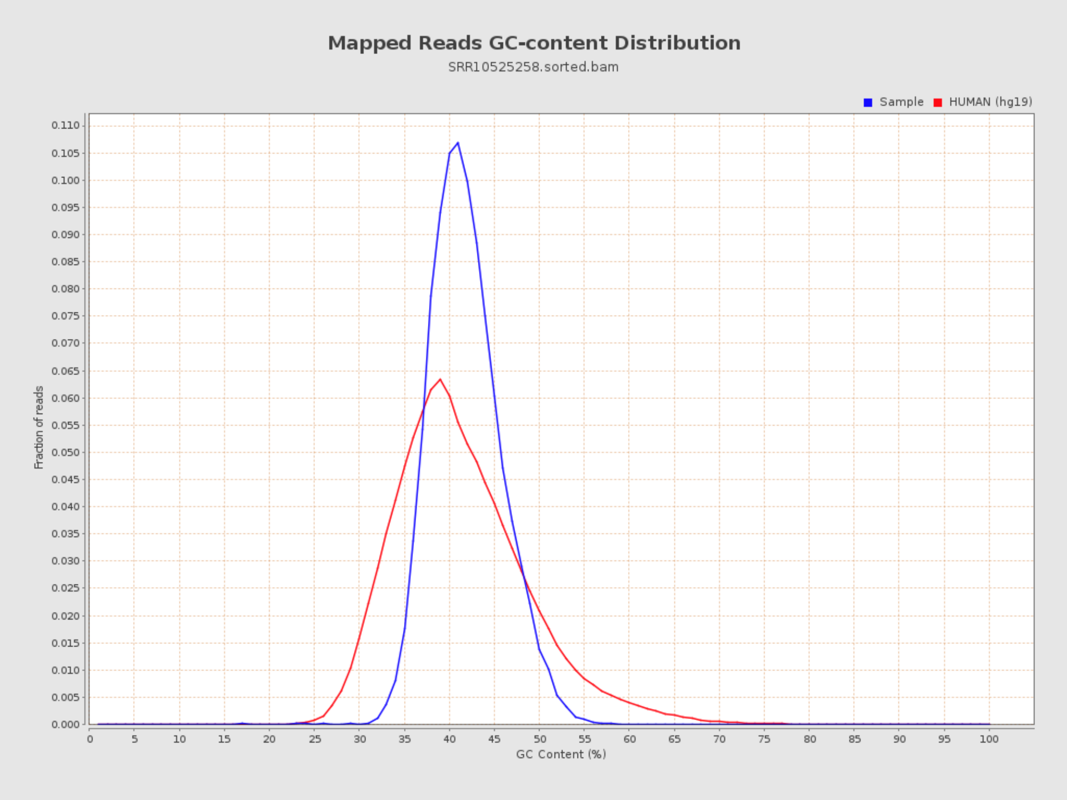
7. Results : Duplication Rate Histogram



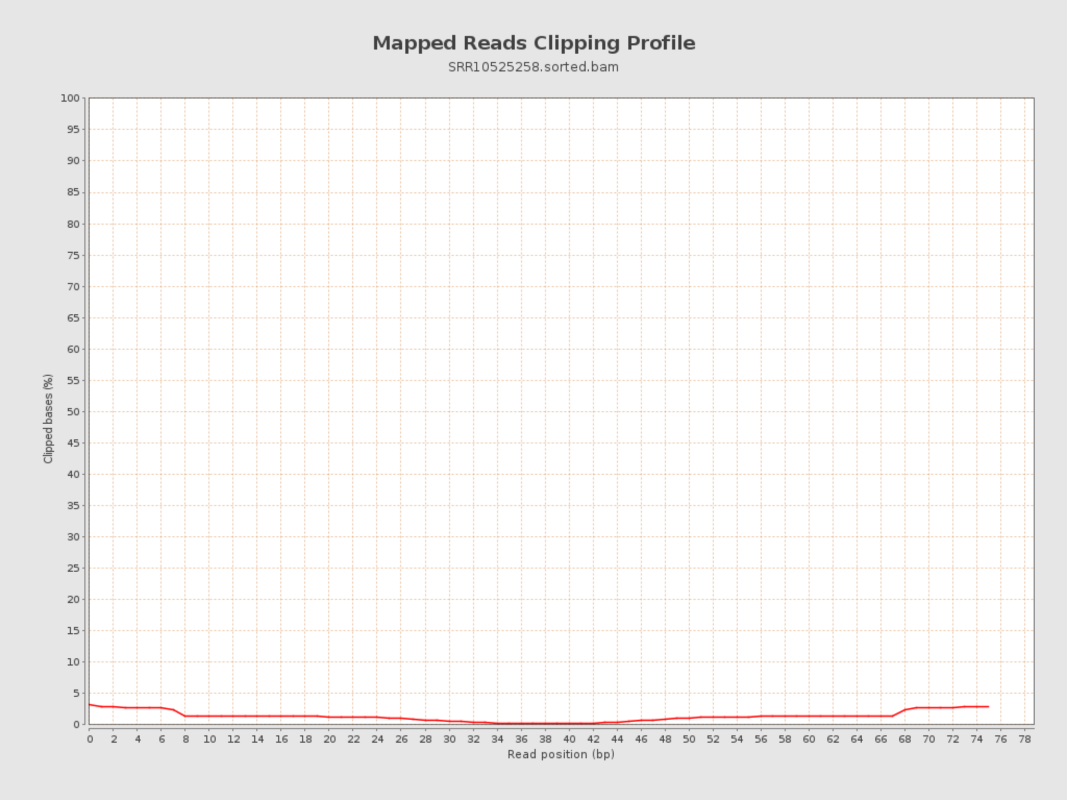
8. Results : Mapped Reads Nucleotide Content



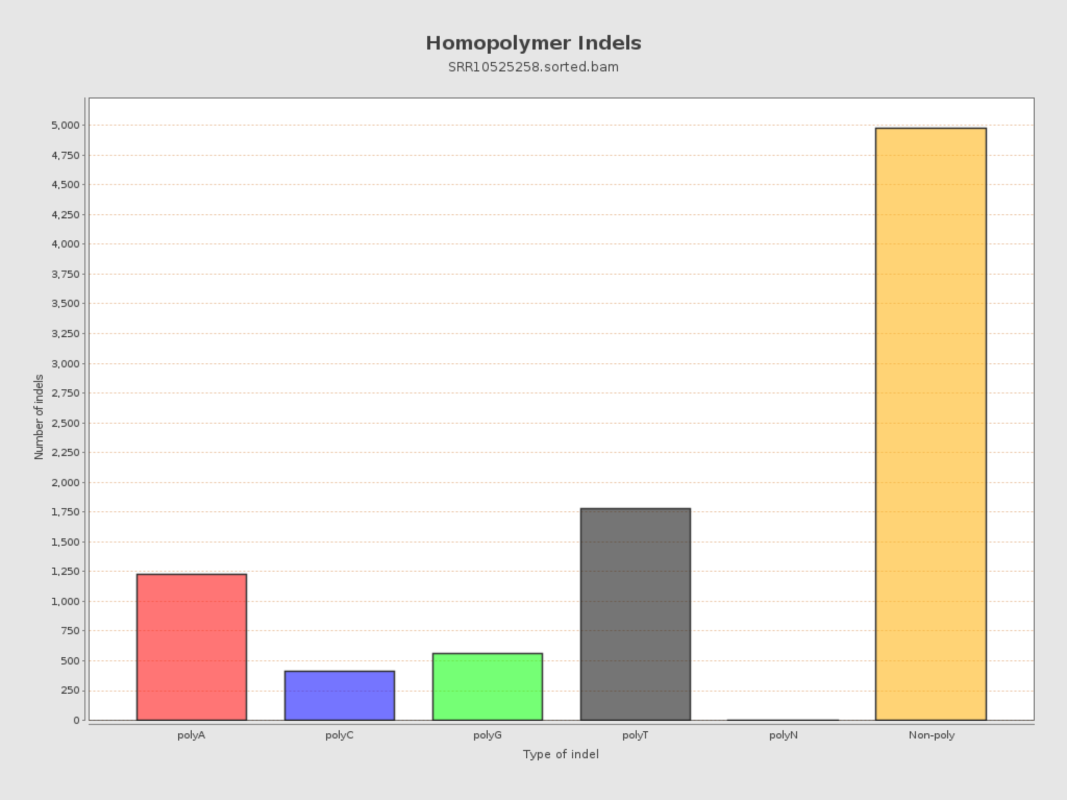
9. Results : Mapped Reads GC-content Distribution



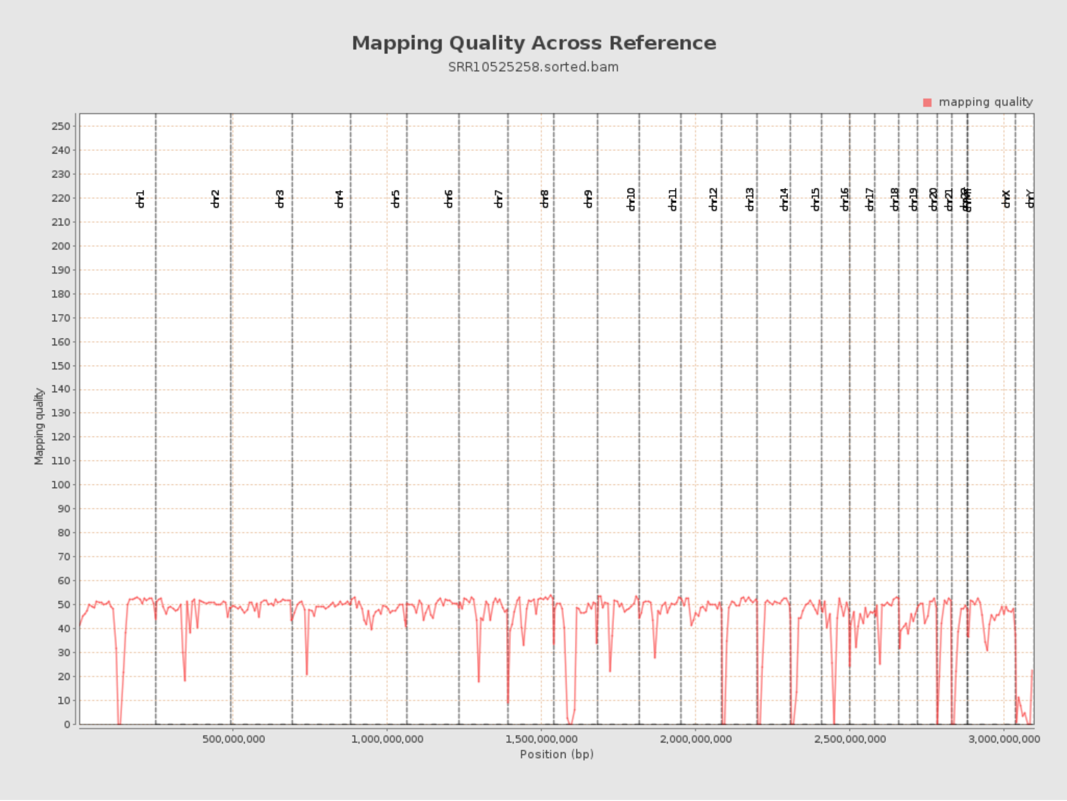
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram