Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525058.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_SRR10525058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:16:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,710,185
Mapped reads	1,349,689 / 78.92%
Unmapped reads	360,496 / 21.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,123 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	74,873 / 4.38%
Duplication rate	4.57%
Clipped reads	1,350,100 / 78.94%

2.2. ACGT Content

Number/percentage of A's	18,705,898 / 23.99%
Number/percentage of C's	13,506,064 / 17.32%
Number/percentage of T's	26,174,820 / 33.57%
Number/percentage of G's	19,588,254 / 25.12%
Number/percentage of N's	7,226 / 0.01%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.2455

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

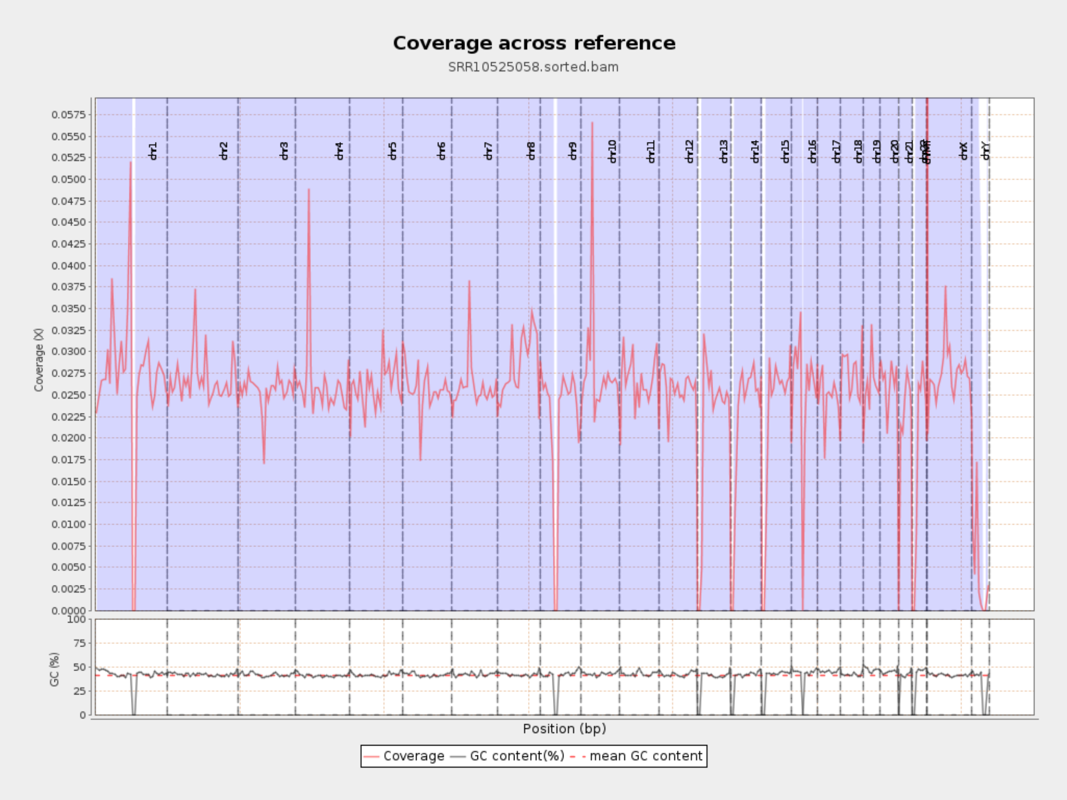
General error rate	0.5%
Mismatches	378,639
Insertions	5,480
Mapped reads with at least one insertion	0.4%
Deletions	15,273
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.62%

2.6. Chromosome stats

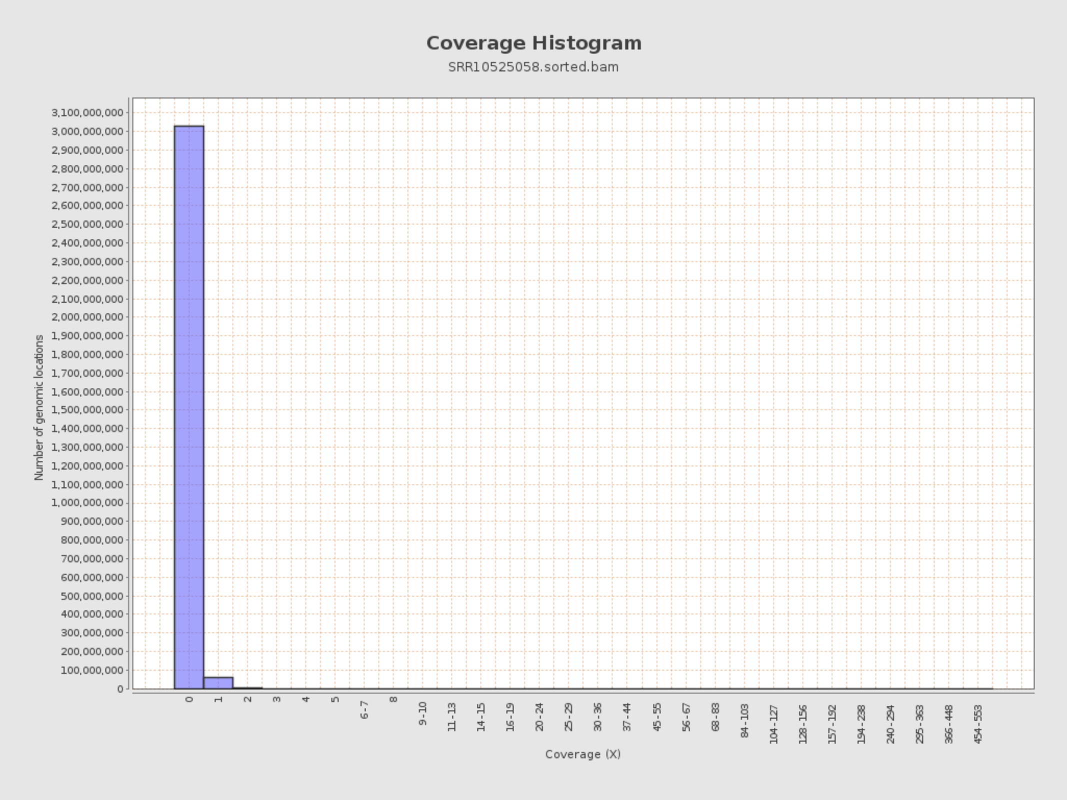
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6717631	0.027	0.4374
chr2	243199373	6517591	0.0268	0.3079
chr3	198022430	5050854	0.0255	0.1768
chr4	191154276	5047799	0.0264	0.2049
chr5	180915260	4743470	0.0262	0.18
chr6	171115067	4395260	0.0257	0.1913
chr7	159138663	4141577	0.026	0.2715

chr8	146364022	4189940	0.0286	0.2518
chr9	141213431	3127146	0.0221	0.1984
chr10	135534747	3797605	0.028	0.2769
chr11	135006516	3624740	0.0268	0.2072
chr12	133851895	3462126	0.0259	0.1821
chr13	115169878	2487628	0.0216	0.1631
chr14	107349540	2328203	0.0217	0.1661
chr15	102531392	2245225	0.0219	0.1658
chr16	90354753	2251665	0.0249	0.1896
chr17	81195210	1990761	0.0245	0.1799
chr18	78077248	2156734	0.0276	0.3253
chr19	59128983	1557121	0.0263	0.329
chr20	63025520	1647191	0.0261	0.185
chr21	48129895	1045438	0.0217	0.1883
chr22	51304566	923040	0.018	0.1487
chrMT	16571	25087	1.5139	1.5779
chrX	155270560	4272392	0.0275	0.202
chrY	59373566	260755	0.0044	0.1549

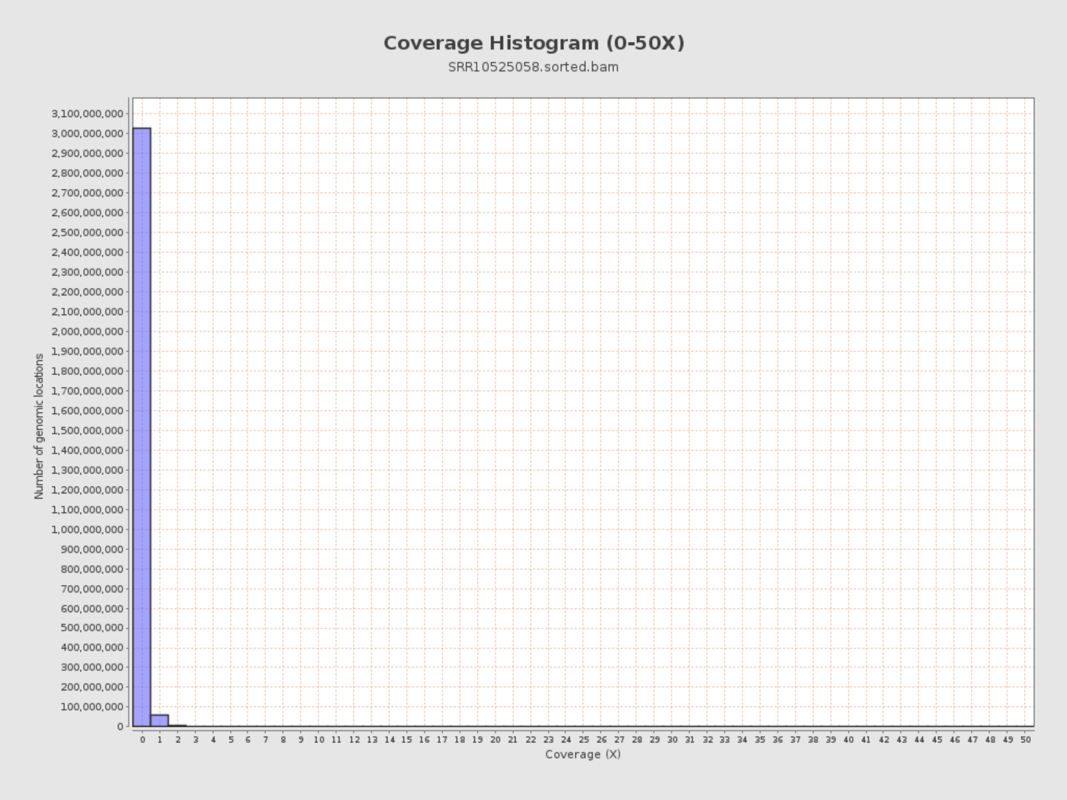
3. Results : Coverage across reference



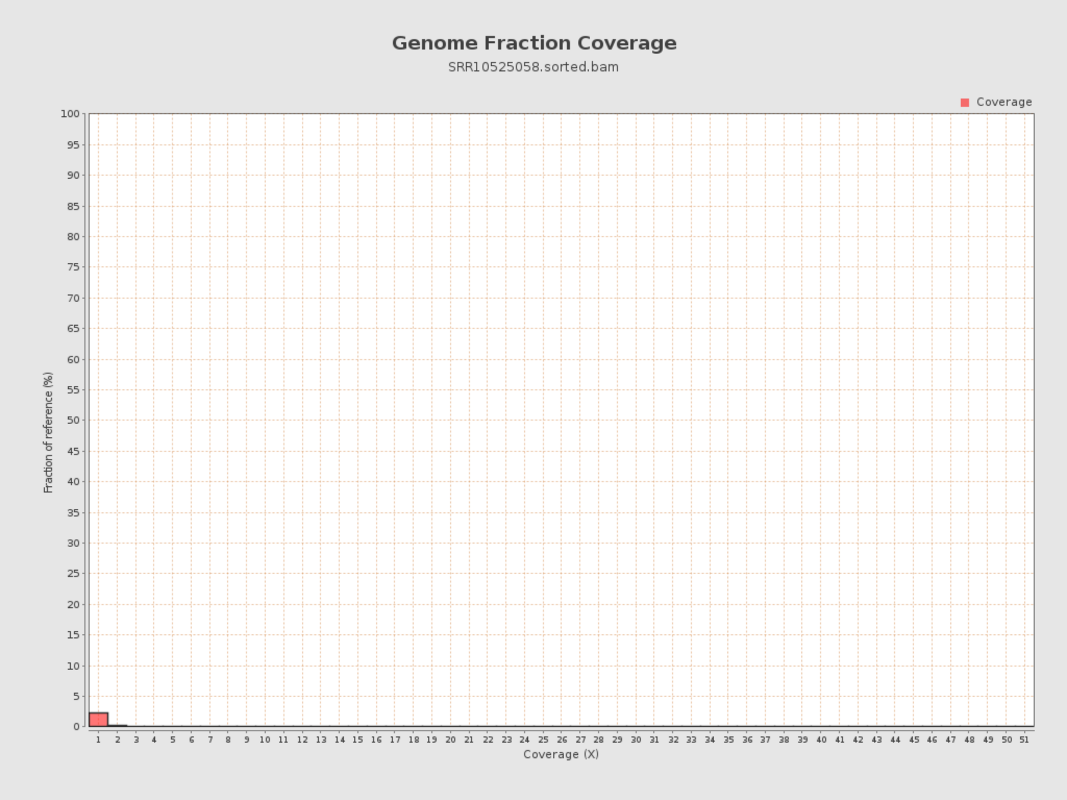
4. Results : Coverage Histogram



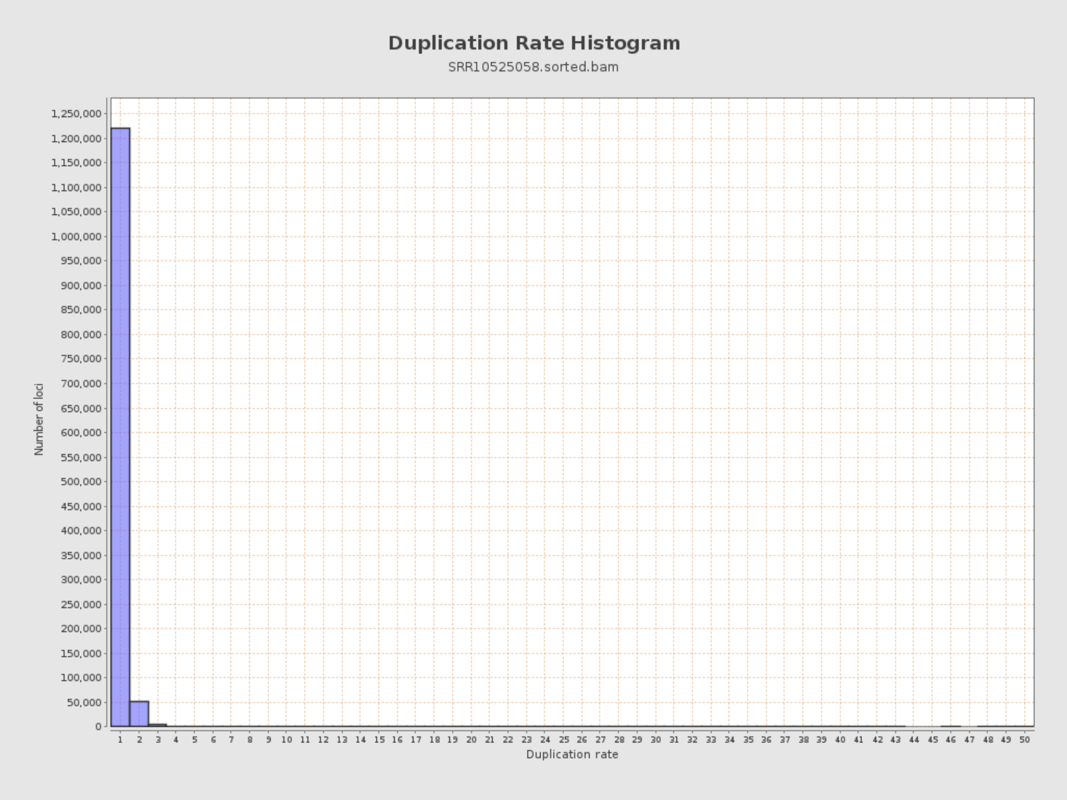
5. Results : Coverage Histogram (0-50X)



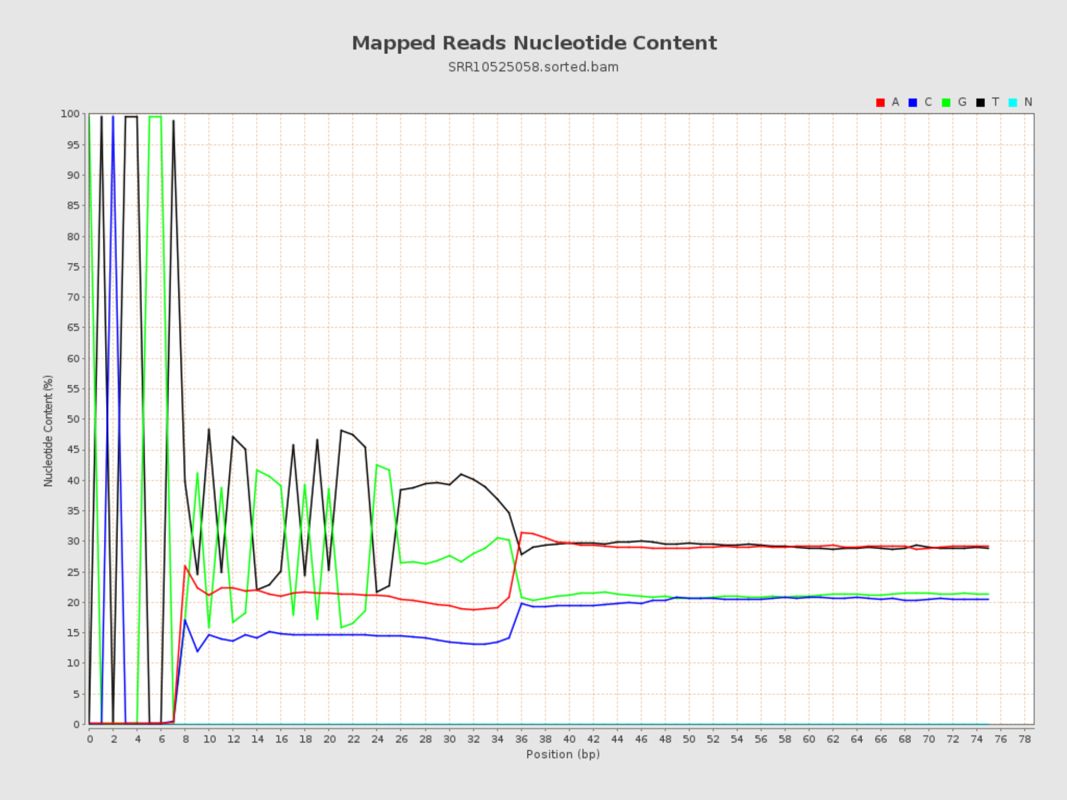
6. Results : Genome Fraction Coverage



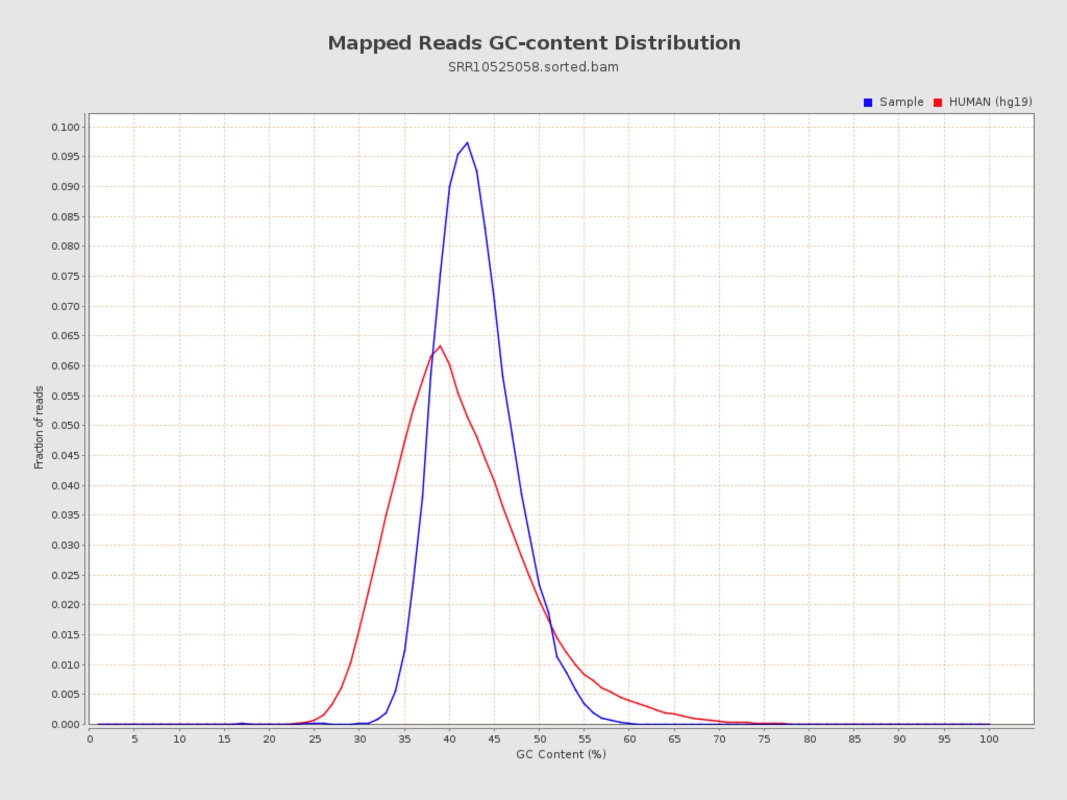
7. Results : Duplication Rate Histogram



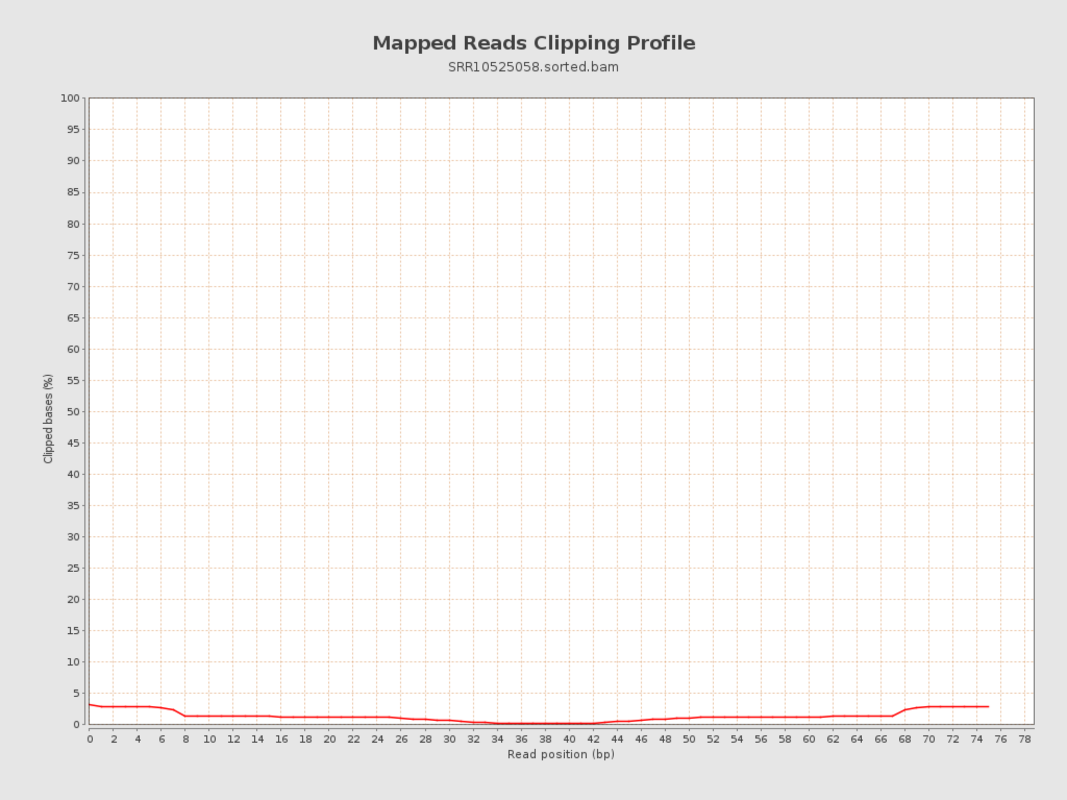
8. Results : Mapped Reads Nucleotide Content



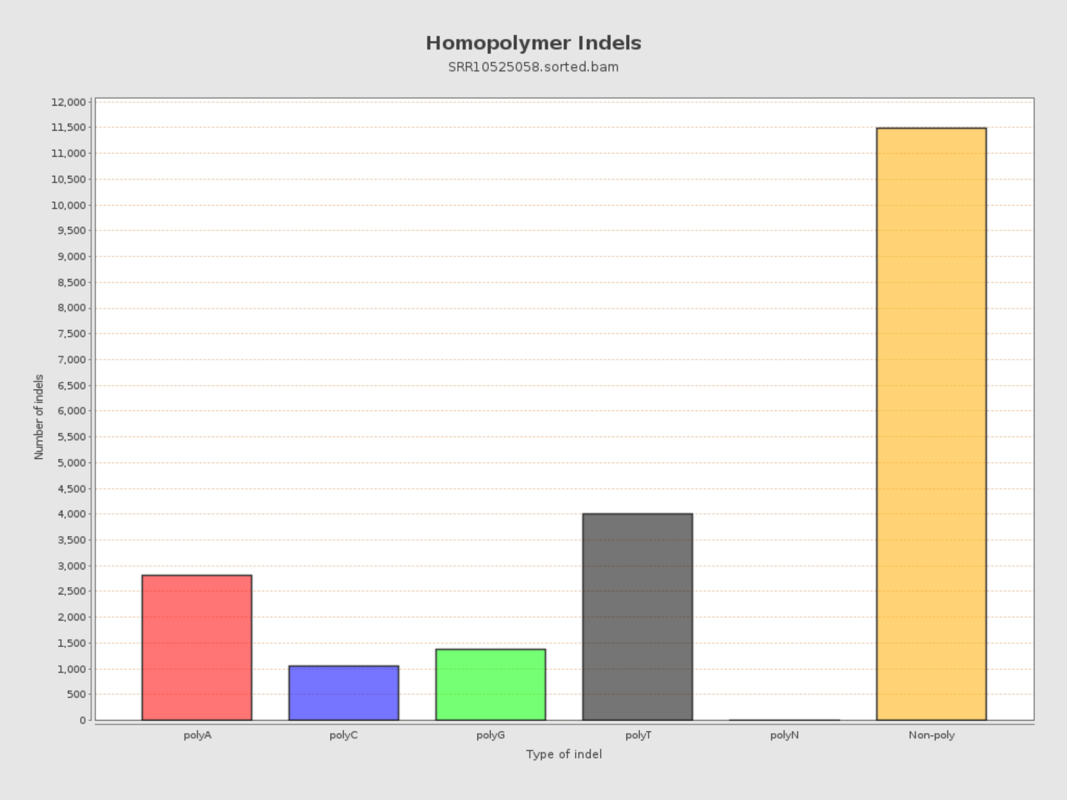
9. Results : Mapped Reads GC-content Distribution



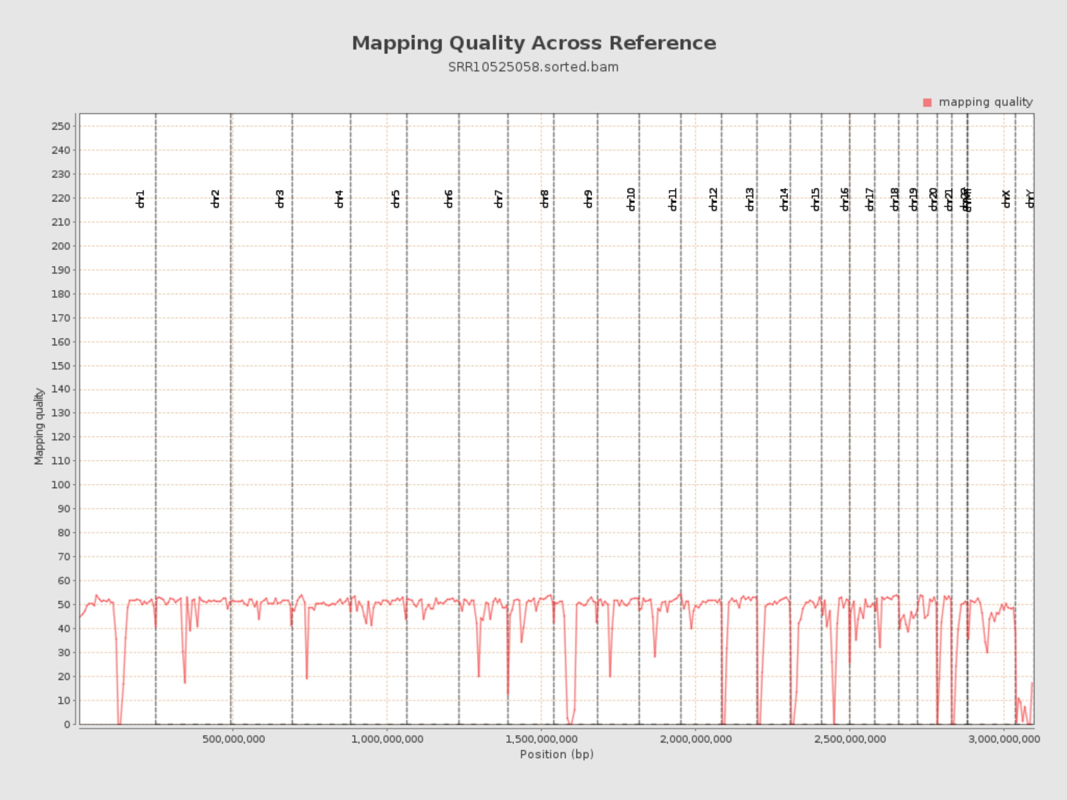
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram