Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:19:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525257.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_SRR10525257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:19:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	711,884
Mapped reads	645,444 / 90.67%
Unmapped reads	66,440 / 9.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,160 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,202 / 1.99%
Duplication rate	1.63%
Clipped reads	646,887 / 90.87%

2.2. ACGT Content

Number/percentage of A's	9,266,769 / 24.83%
Number/percentage of C's	6,771,496 / 18.14%
Number/percentage of T's	12,235,718 / 32.78%
Number/percentage of G's	9,047,872 / 24.24%
Number/percentage of N's	693 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0121

Standard Deviation	0.1434

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

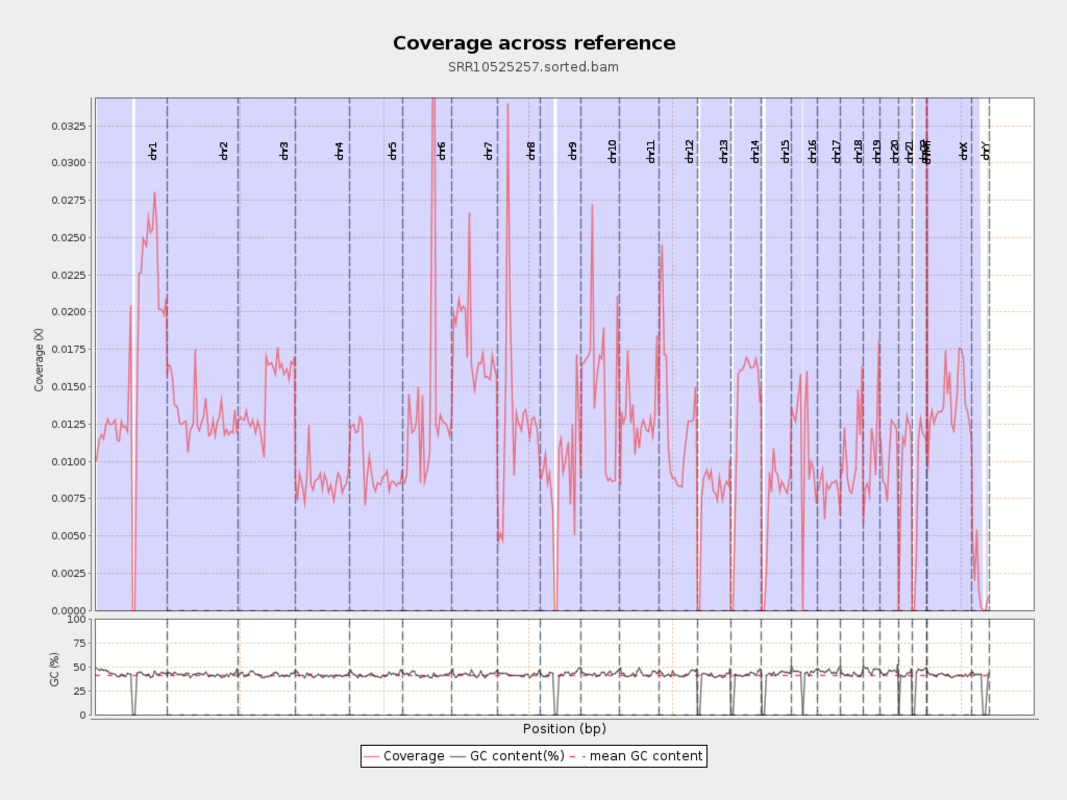
General error rate	0.51%
Mismatches	187,778
Insertions	2,138
Mapped reads with at least one insertion	0.33%
Deletions	7,439
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.26%

2.6. Chromosome stats

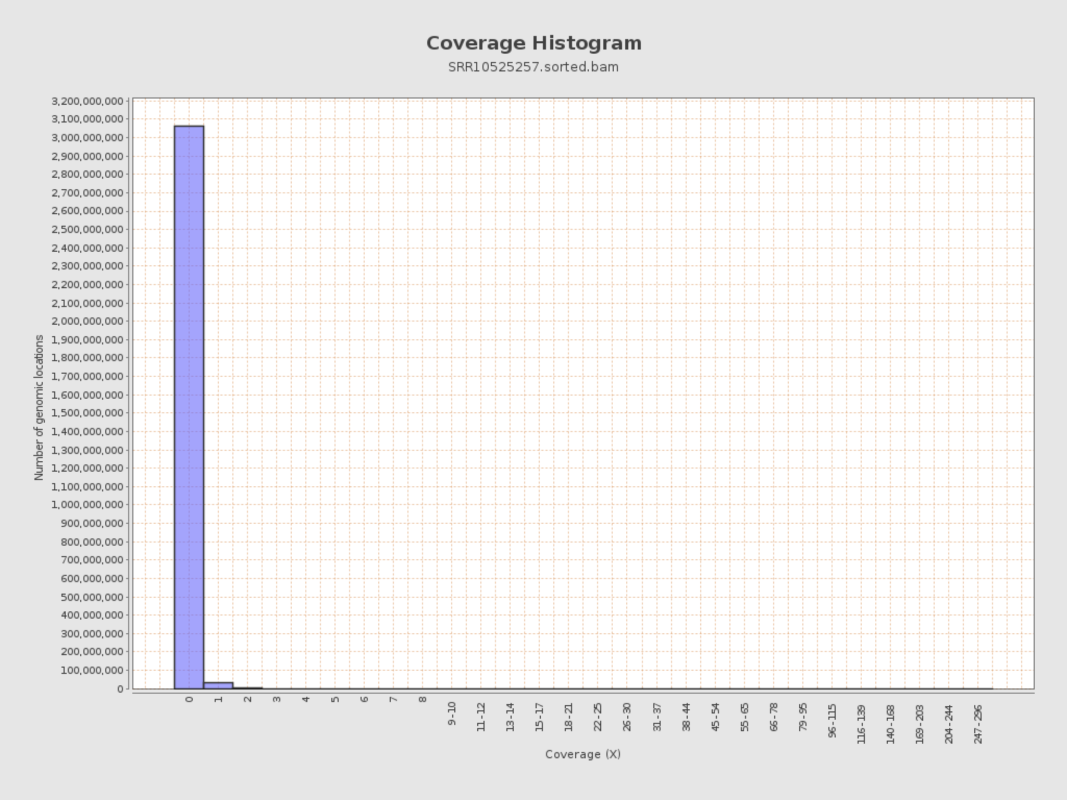
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4058898	0.0163	0.2231
chr2	243199373	3159410	0.013	0.1694
chr3	198022430	2861828	0.0145	0.1256
chr4	191154276	1649620	0.0086	0.0988
chr5	180915260	1742541	0.0096	0.1018
chr6	171115067	2385448	0.0139	0.13
chr7	159138663	2838828	0.0178	0.2295

chr8	146364022	1891335	0.0129	0.1337
chr9	141213431	1266759	0.009	0.1158
chr10	135534747	2052295	0.0151	0.1658
chr11	135006516	1745482	0.0129	0.1327
chr12	133851895	1712437	0.0128	0.118
chr13	115169878	864604	0.0075	0.0908
chr14	107349540	1438720	0.0134	0.1217
chr15	102531392	728217	0.0071	0.0893
chr16	90354753	1000482	0.0111	0.116
chr17	81195210	665452	0.0082	0.096
chr18	78077248	818779	0.0105	0.1773
chr19	59128983	620347	0.0105	0.1578
chr20	63025520	650523	0.0103	0.1066
chr21	48129895	484587	0.0101	0.1056
chr22	51304566	418881	0.0082	0.0933
chrMT	16571	626	0.0378	0.1907
chrX	155270560	2176828	0.014	0.1279
chrY	59373566	101475	0.0017	0.0563

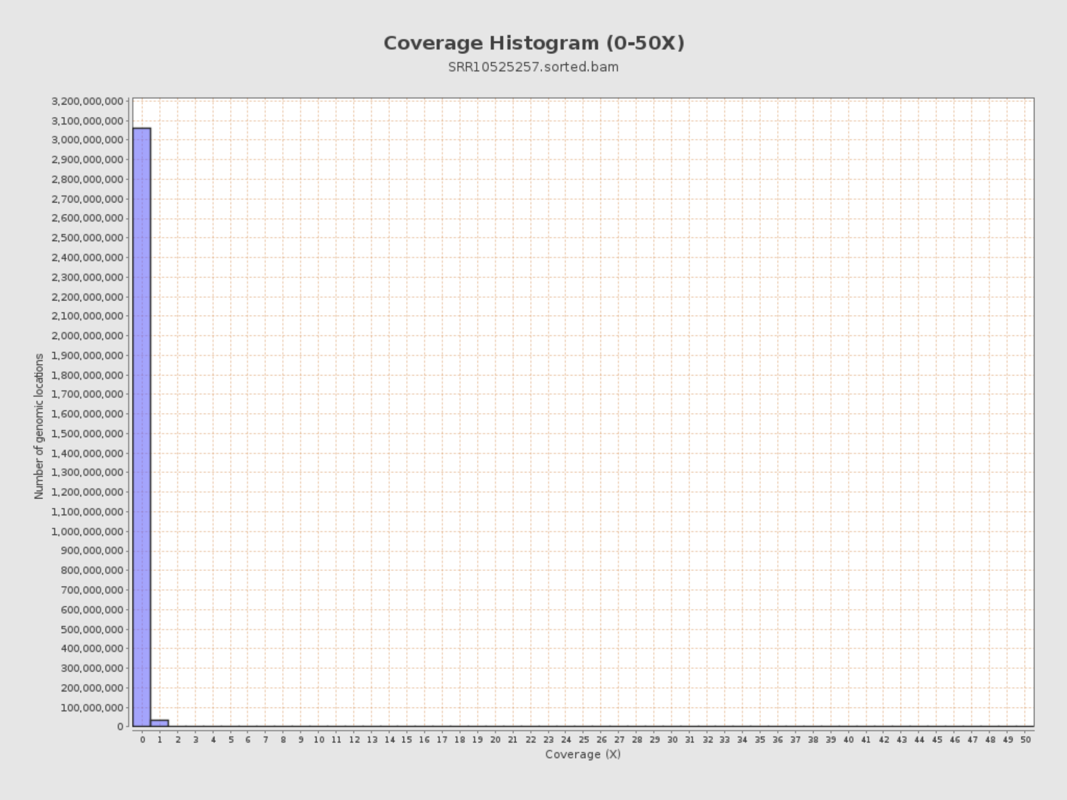
3. Results : Coverage across reference



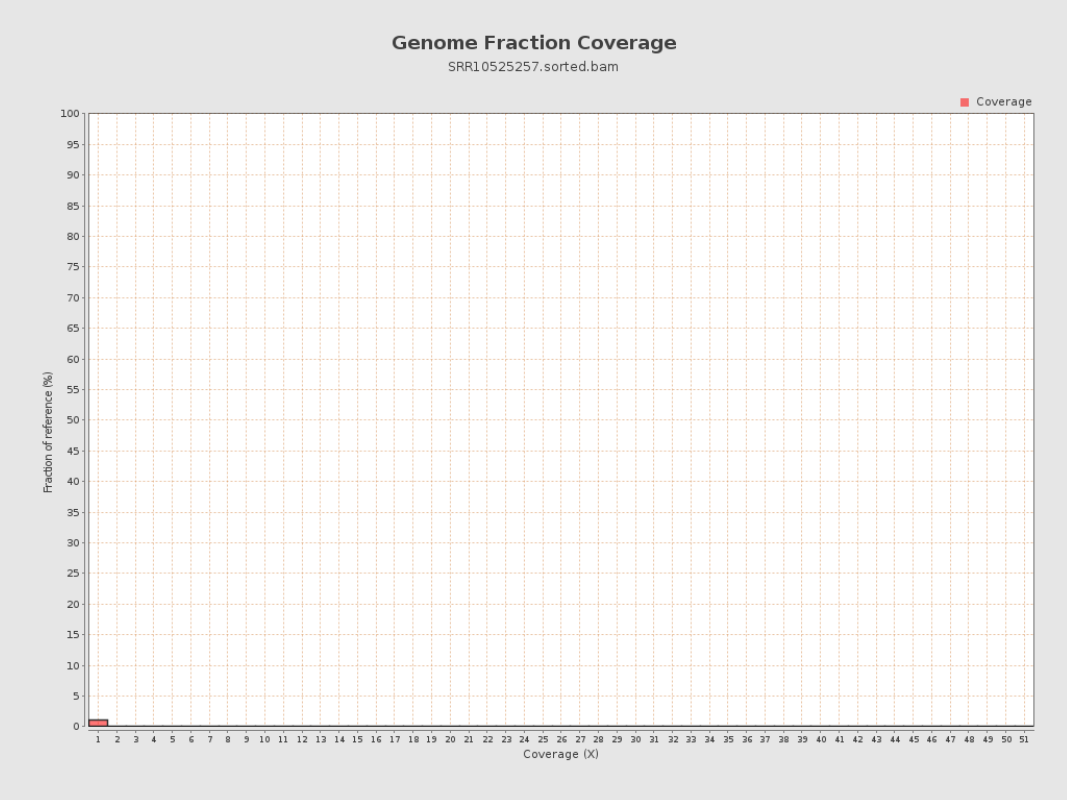
4. Results : Coverage Histogram



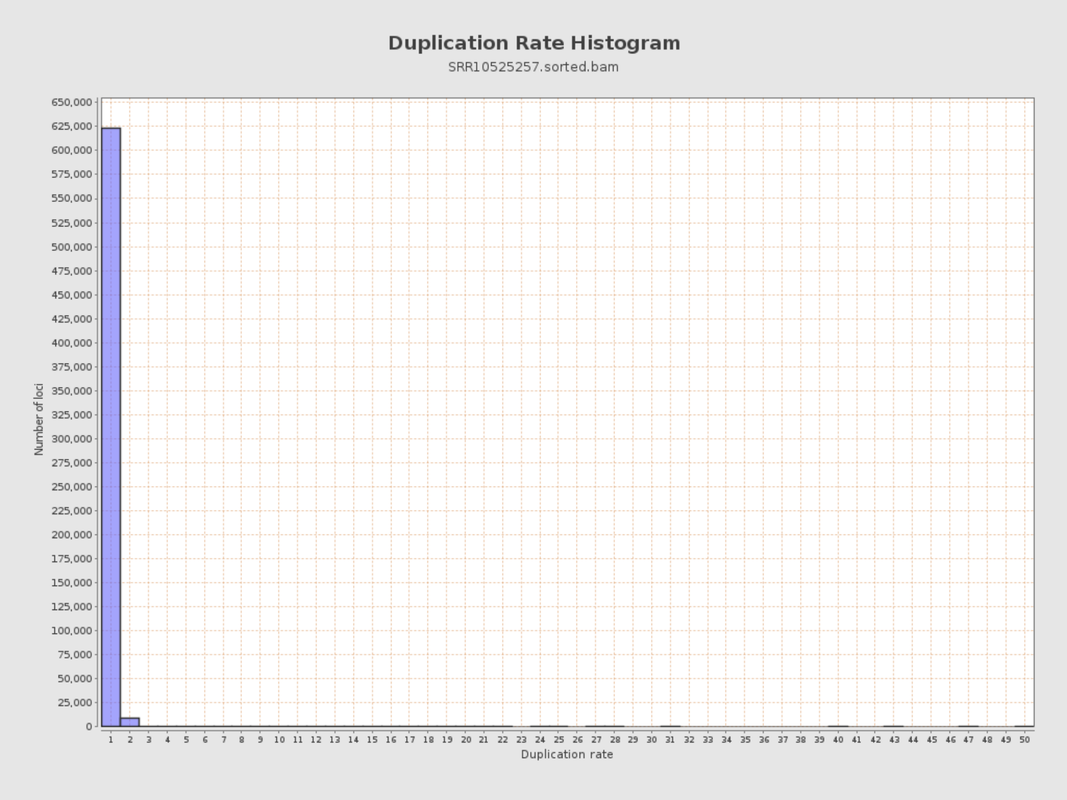
5. Results : Coverage Histogram (0-50X)



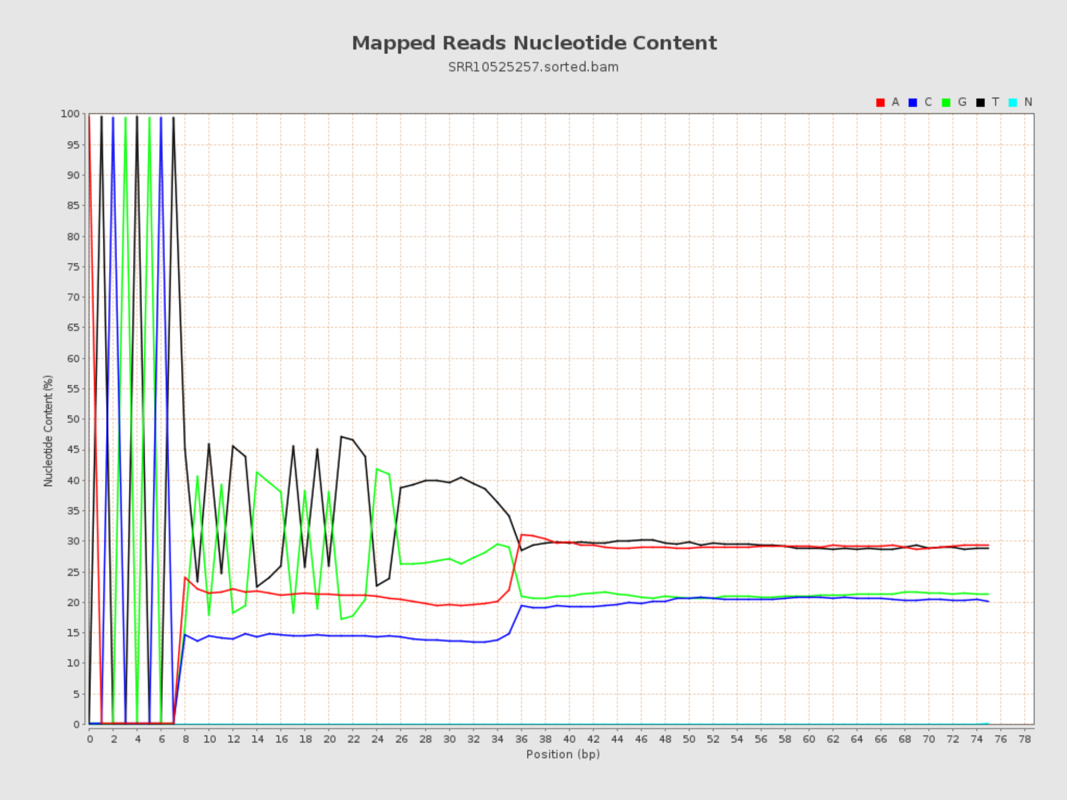
6. Results : Genome Fraction Coverage



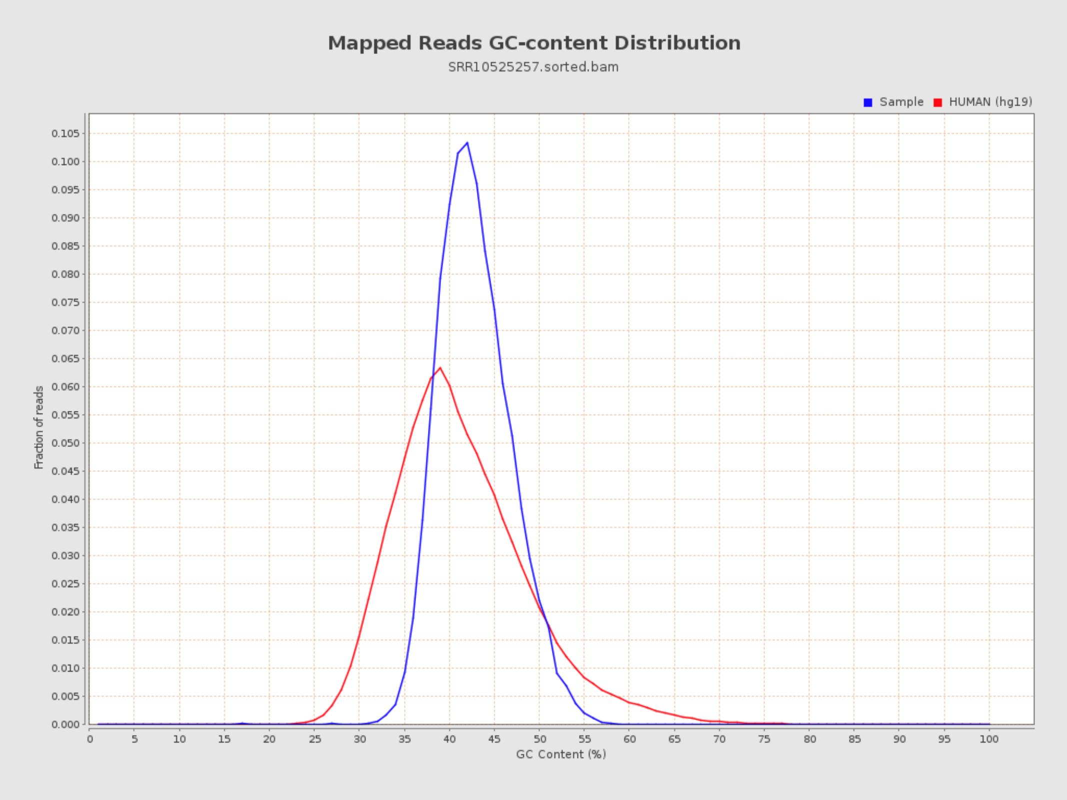
7. Results : Duplication Rate Histogram



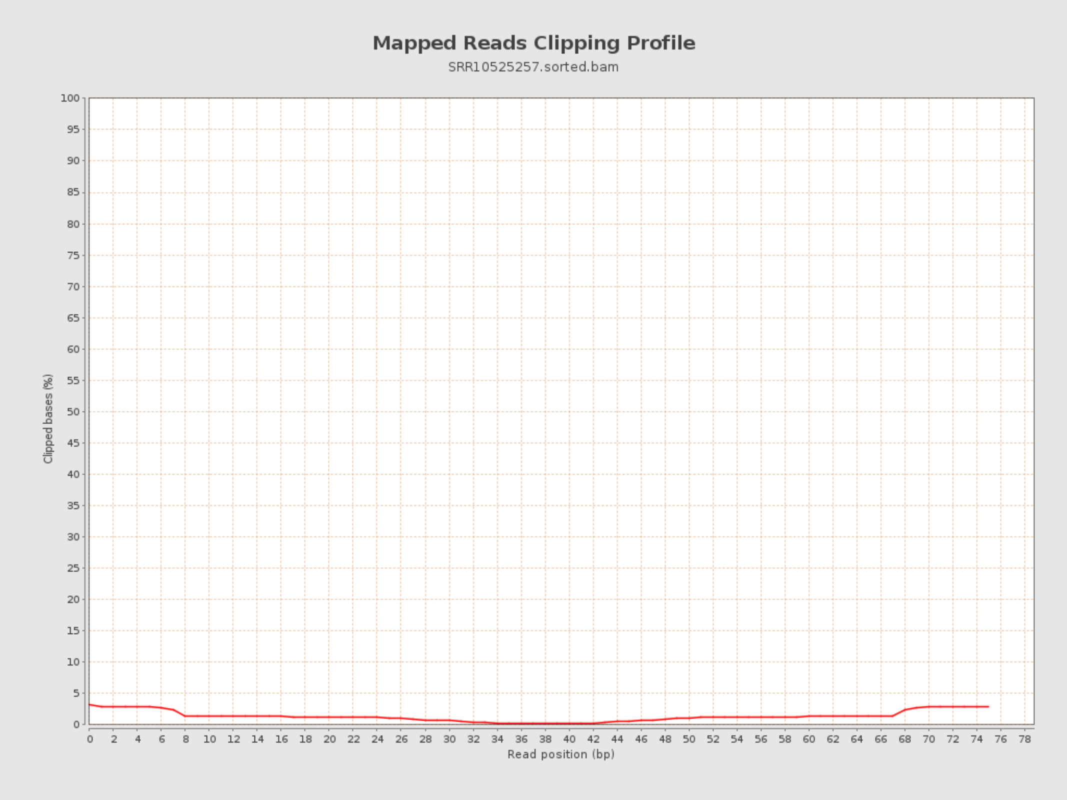
8. Results : Mapped Reads Nucleotide Content



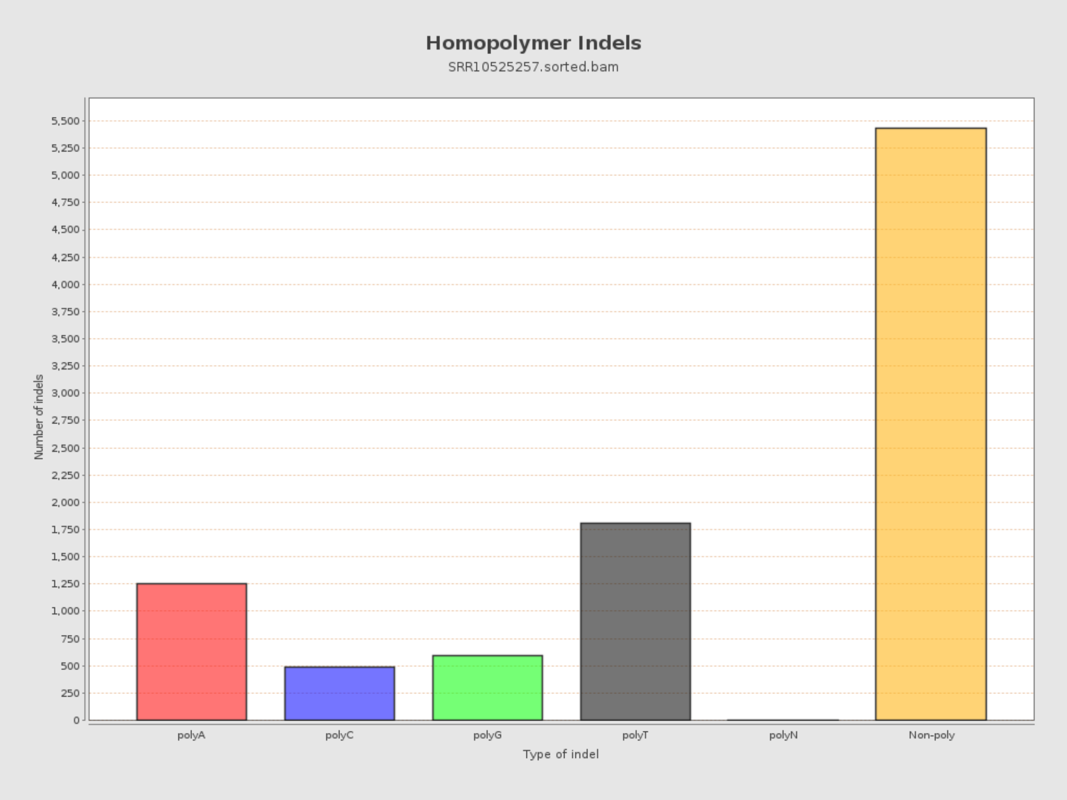
9. Results : Mapped Reads GC-content Distribution



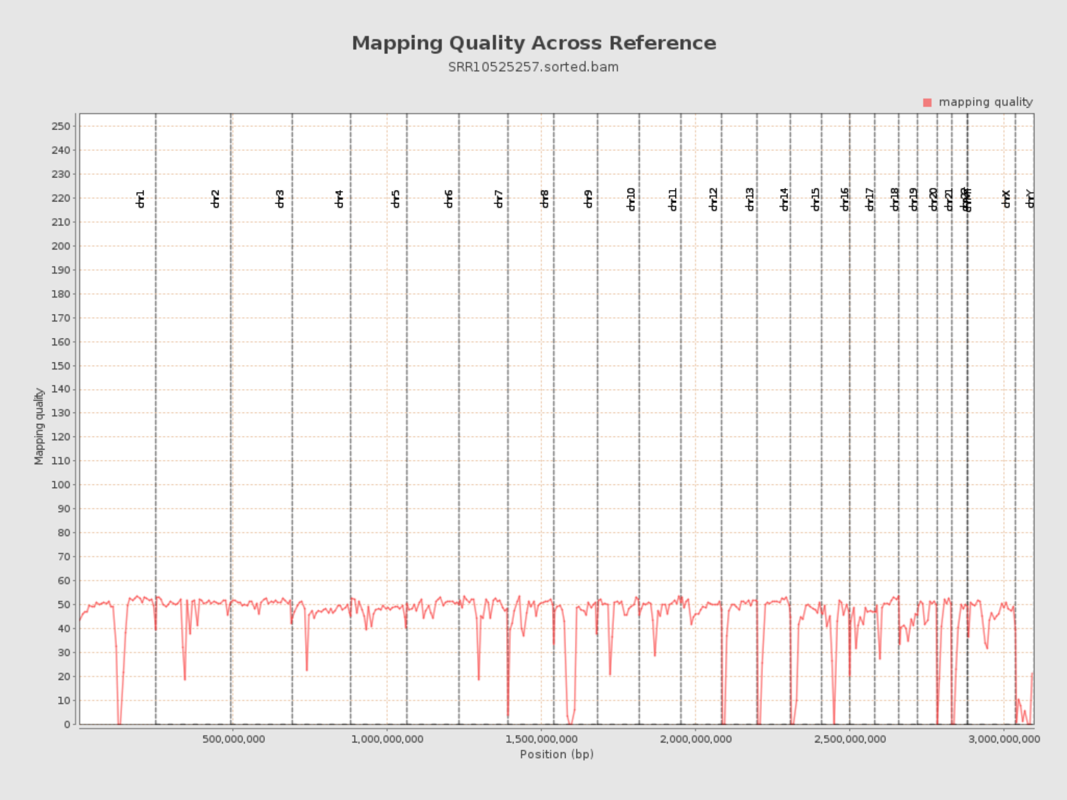
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram