Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:28:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524757.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_SRR10524757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:28:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,401,616
Mapped reads	1,263,453 / 90.14%
Unmapped reads	138,163 / 9.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,508 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	36,961 / 2.64%
Duplication rate	2.18%
Clipped reads	1,266,864 / 90.39%

2.2. ACGT Content

Number/percentage of A's	17,697,980 / 24.61%
Number/percentage of C's	14,003,597 / 19.47%
Number/percentage of T's	22,508,343 / 31.3%
Number/percentage of G's	17,703,621 / 24.62%
Number/percentage of N's	8,388 / 0.01%
GC Percentage	44.09%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2082

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

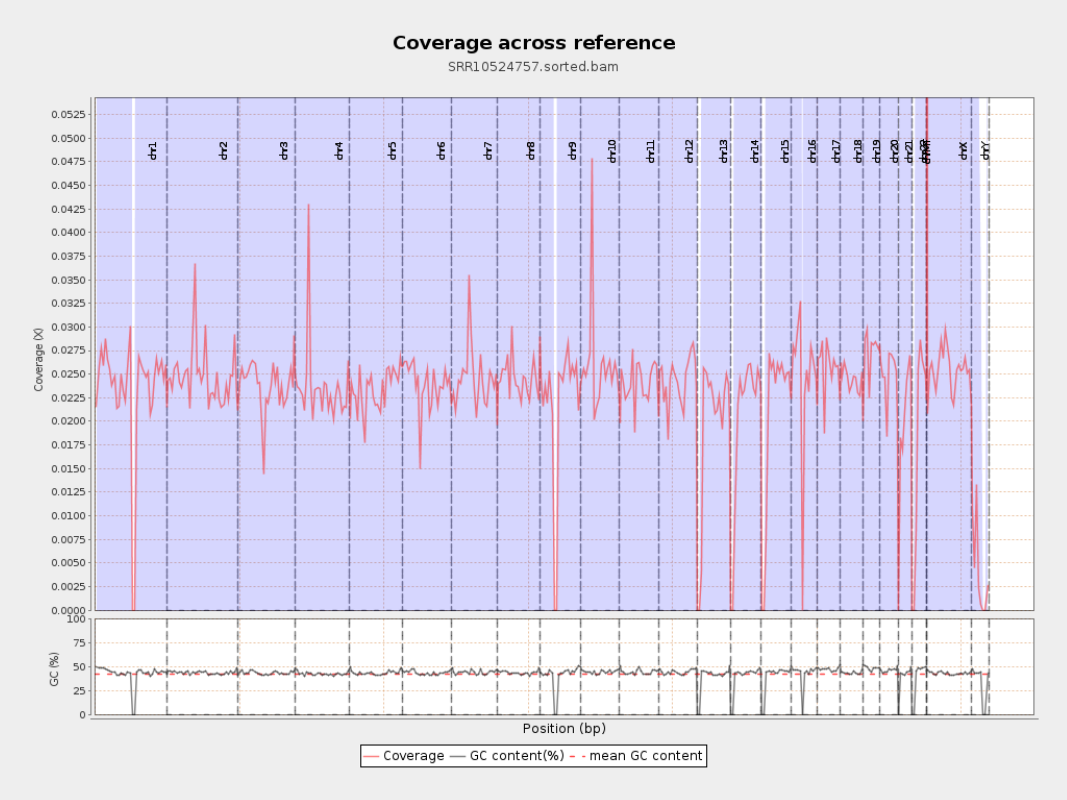
General error rate	0.52%
Mismatches	367,768
Insertions	4,054
Mapped reads with at least one insertion	0.32%
Deletions	13,594
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.01%

2.6. Chromosome stats

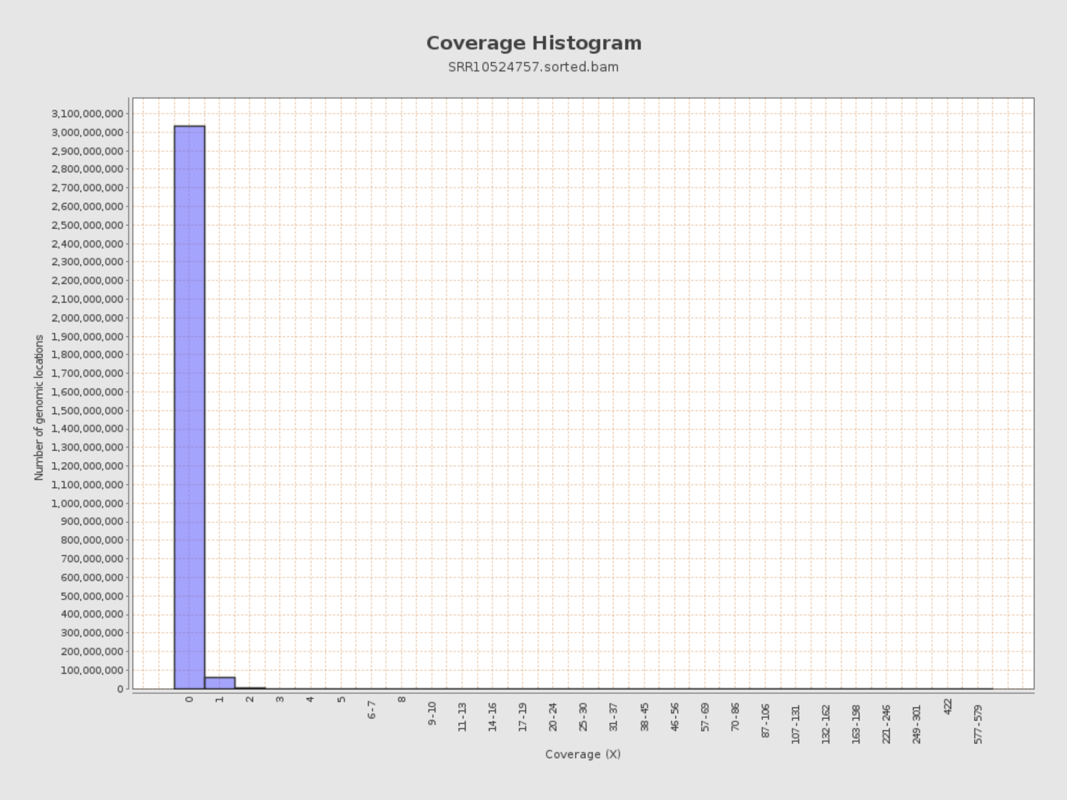
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5800035	0.0233	0.2564
chr2	243199373	6040584	0.0248	0.3122
chr3	198022430	4696813	0.0237	0.168
chr4	191154276	4526224	0.0237	0.1865
chr5	180915260	4244302	0.0235	0.1647
chr6	171115067	4084255	0.0239	0.1767
chr7	159138663	3918712	0.0246	0.2533

chr8	146364022	3587066	0.0245	0.1935
chr9	141213431	3061580	0.0217	0.1837
chr10	135534747	3532865	0.0261	0.2535
chr11	135006516	3267334	0.0242	0.1967
chr12	133851895	3255737	0.0243	0.1702
chr13	115169878	2218290	0.0193	0.1495
chr14	107349540	2153820	0.0201	0.1554
chr15	102531392	2101796	0.0205	0.1584
chr16	90354753	2191534	0.0243	0.1837
chr17	81195210	2094067	0.0258	0.1798
chr18	78077248	1904853	0.0244	0.2821
chr19	59128983	1614188	0.0273	0.2321
chr20	63025520	1559665	0.0247	0.1771
chr21	48129895	953679	0.0198	0.166
chr22	51304566	927004	0.0181	0.1459
chrMT	16571	19293	1.1643	1.2658
chrX	155270560	3953837	0.0255	0.185
chrY	59373566	236103	0.004	0.1095

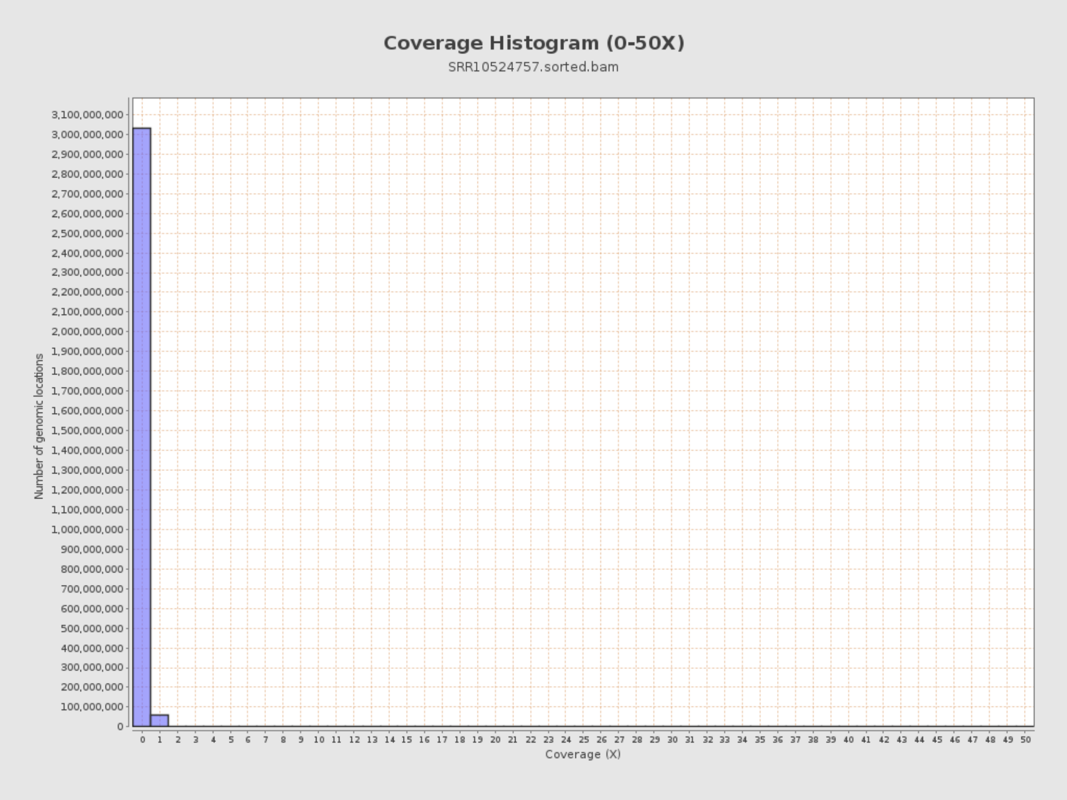
3. Results : Coverage across reference



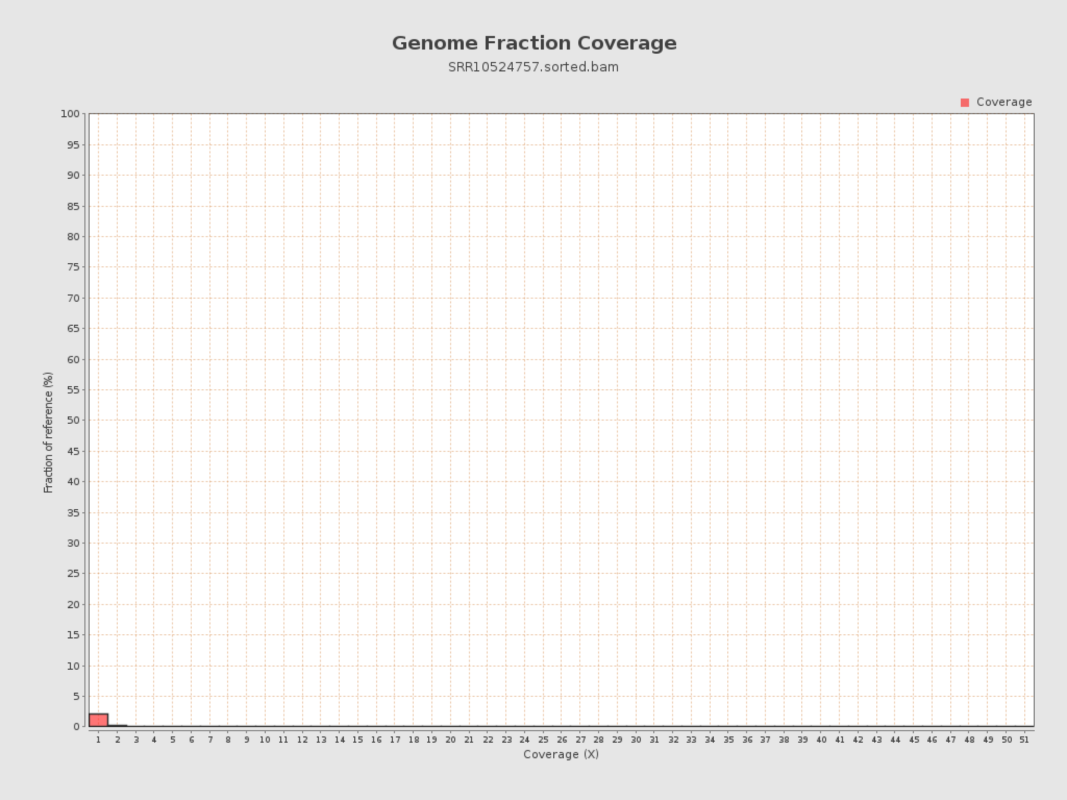
4. Results : Coverage Histogram



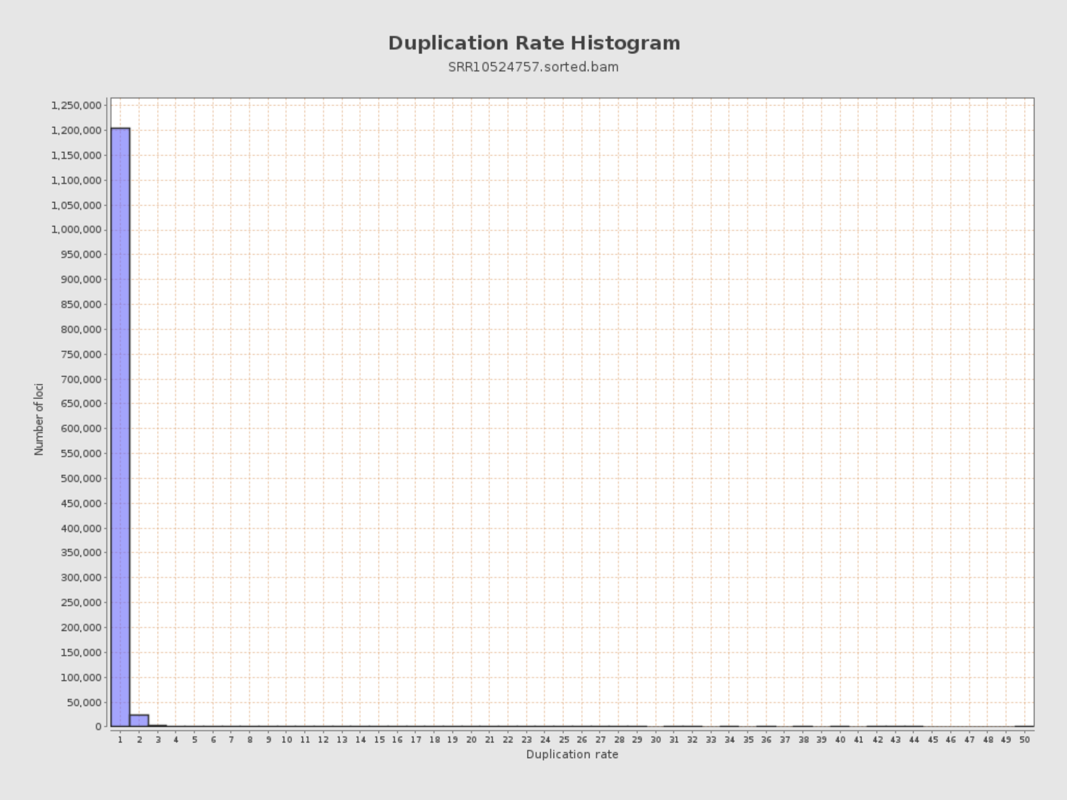
5. Results : Coverage Histogram (0-50X)



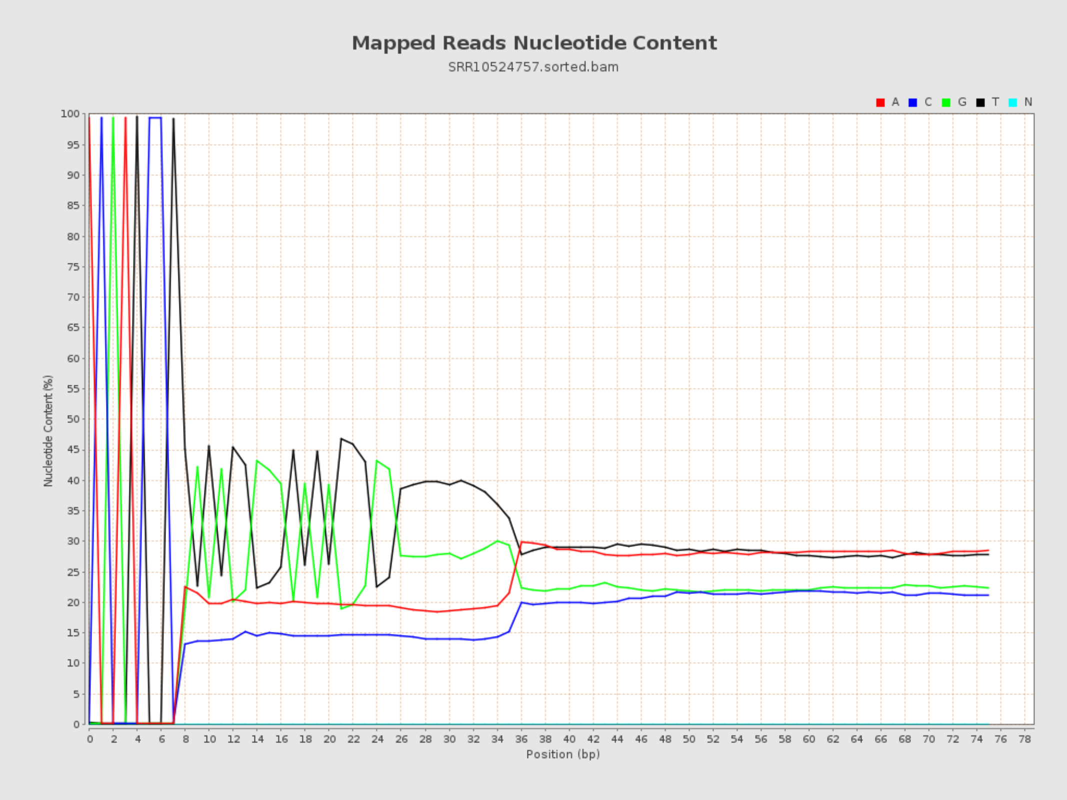
6. Results : Genome Fraction Coverage



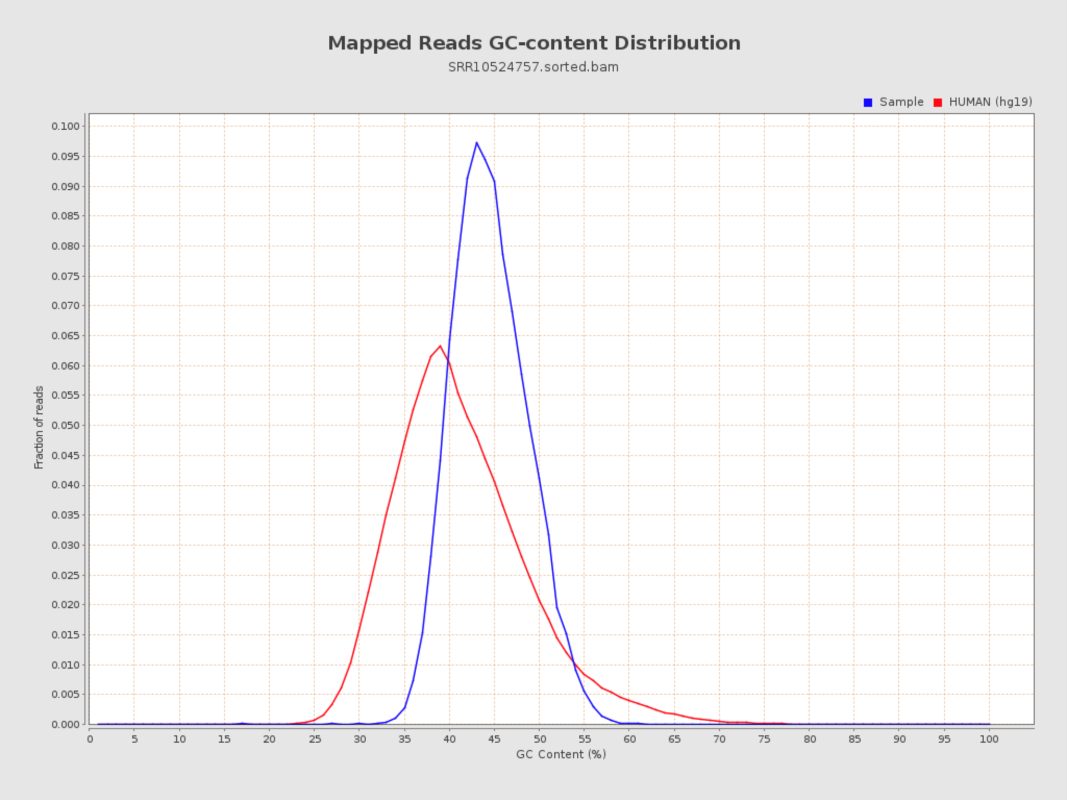
7. Results : Duplication Rate Histogram



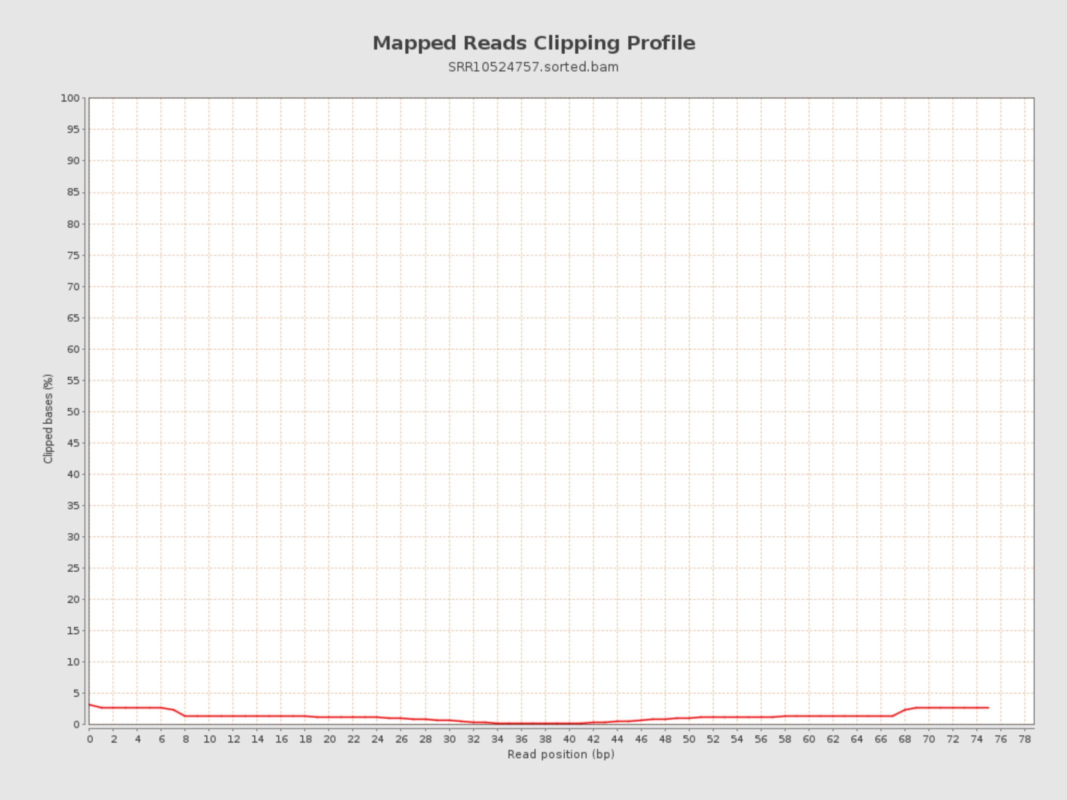
8. Results : Mapped Reads Nucleotide Content



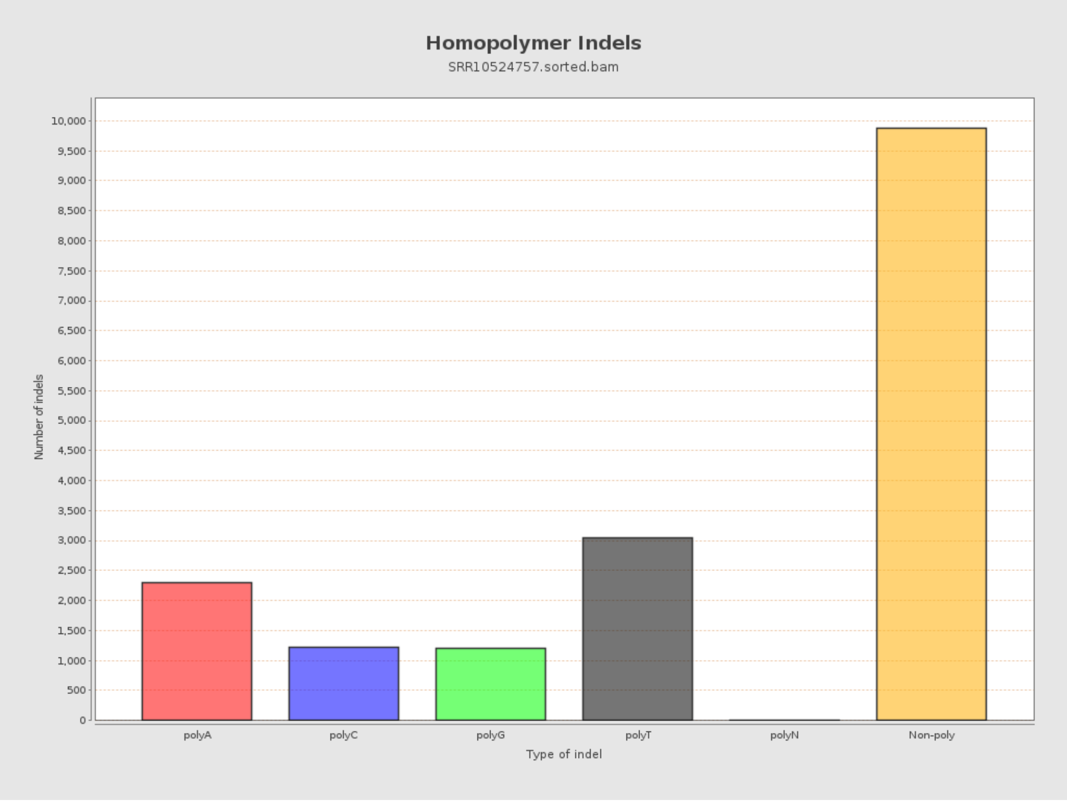
9. Results : Mapped Reads GC-content Distribution



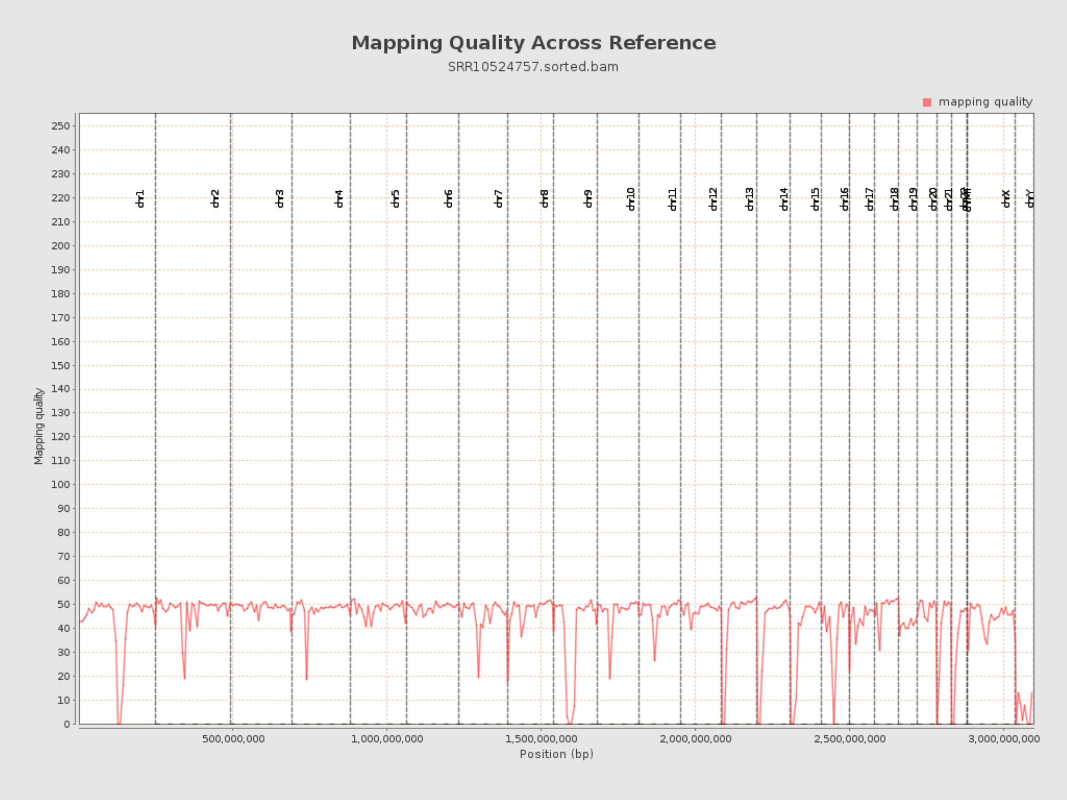
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram