Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524627.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_SRR10524627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524627.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:23:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,418,023
Mapped reads	1,321,263 / 93.18%
Unmapped reads	96,760 / 6.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,731 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	54,846 / 3.87%
Duplication rate	3.3%
Clipped reads	1,319,880 / 93.08%

2.2. ACGT Content

Number/percentage of A's	19,566,250 / 25.53%
Number/percentage of C's	12,714,026 / 16.59%
Number/percentage of T's	24,831,559 / 32.39%
Number/percentage of G's	19,540,807 / 25.49%
Number/percentage of N's	460 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2238

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

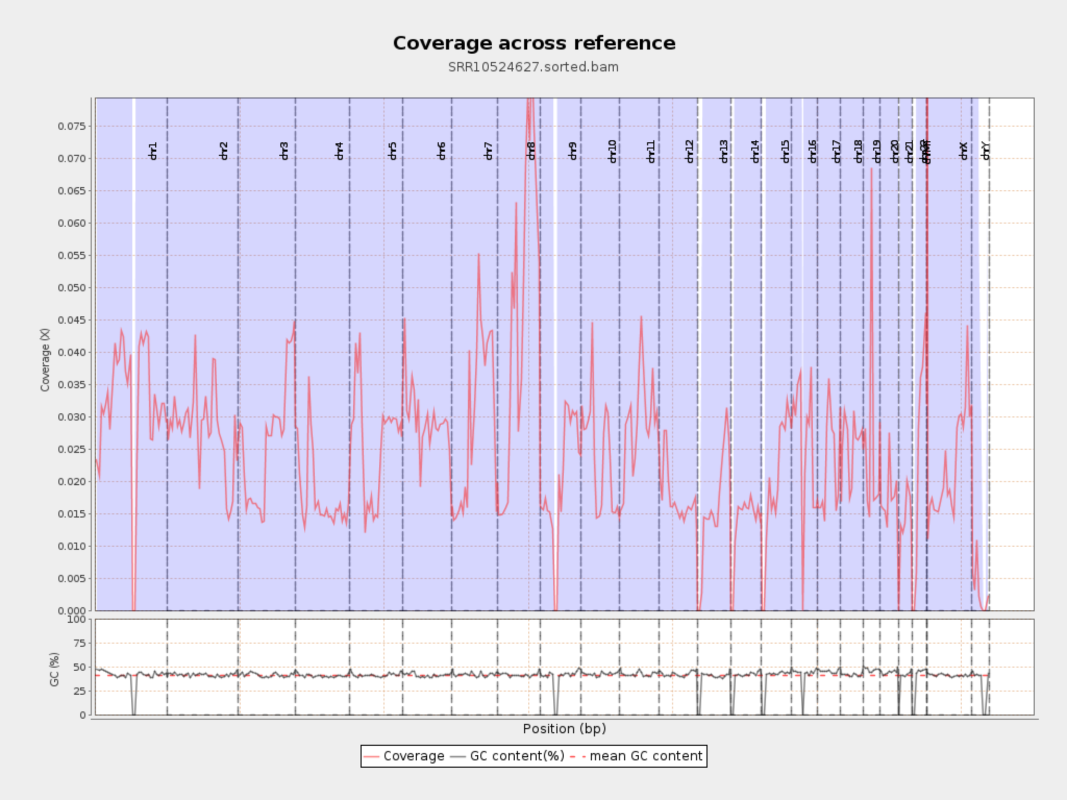
General error rate	0.48%
Mismatches	355,899
Insertions	5,268
Mapped reads with at least one insertion	0.4%
Deletions	14,505
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.7%

2.6. Chromosome stats

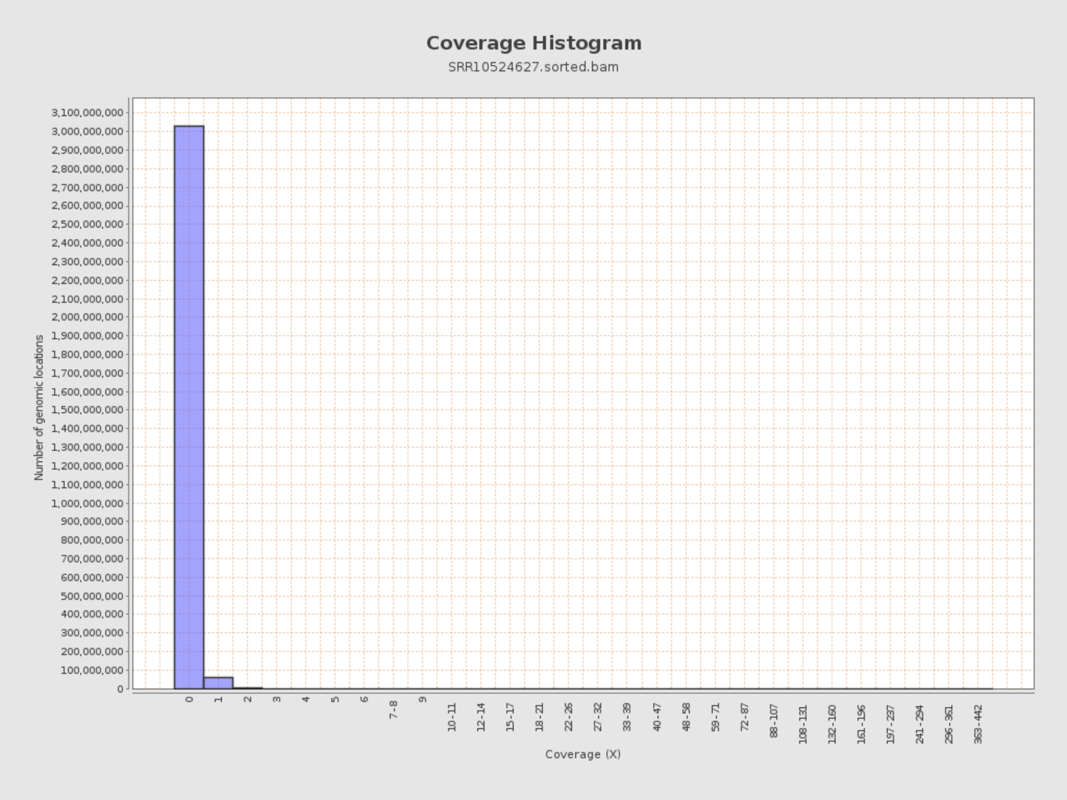
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7963854	0.032	0.3617
chr2	243199373	6793902	0.0279	0.2639
chr3	198022430	5155482	0.026	0.1785
chr4	191154276	3450825	0.0181	0.1676
chr5	180915260	4737117	0.0262	0.1772
chr6	171115067	5053683	0.0295	0.2009
chr7	159138663	4700260	0.0295	0.2956

chr8	146364022	6793147	0.0464	0.3056
chr9	141213431	2825395	0.02	0.1968
chr10	135534747	3308918	0.0244	0.2294
chr11	135006516	3929612	0.0291	0.2126
chr12	133851895	2361528	0.0176	0.1488
chr13	115169878	1821797	0.0158	0.1386
chr14	107349540	1439821	0.0134	0.1304
chr15	102531392	1995493	0.0195	0.1626
chr16	90354753	2344843	0.026	0.1839
chr17	81195210	1797317	0.0221	0.1669
chr18	78077248	1988562	0.0255	0.2717
chr19	59128983	1531222	0.0259	0.2738
chr20	63025520	1105760	0.0175	0.1497
chr21	48129895	659214	0.0137	0.1411
chr22	51304566	1254871	0.0245	0.1726
chrMT	16571	5564	0.3358	0.6421
chrX	155270560	3481143	0.0224	0.1814
chrY	59373566	178330	0.003	0.0958

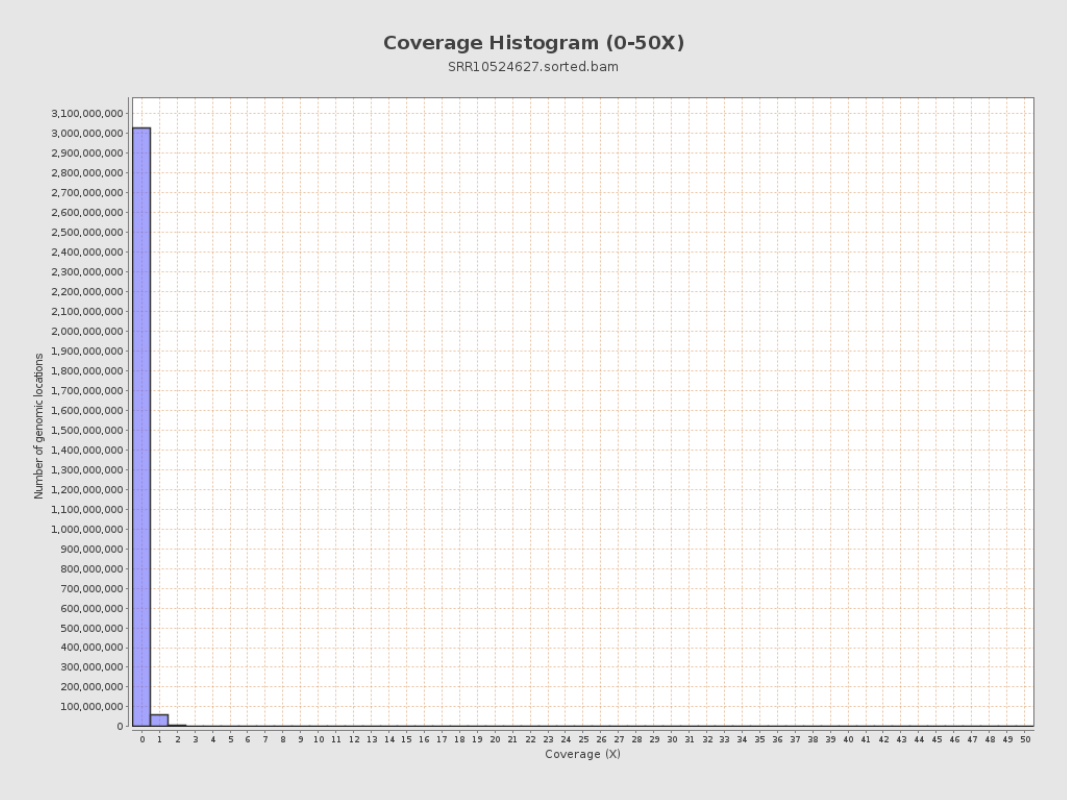
3. Results : Coverage across reference



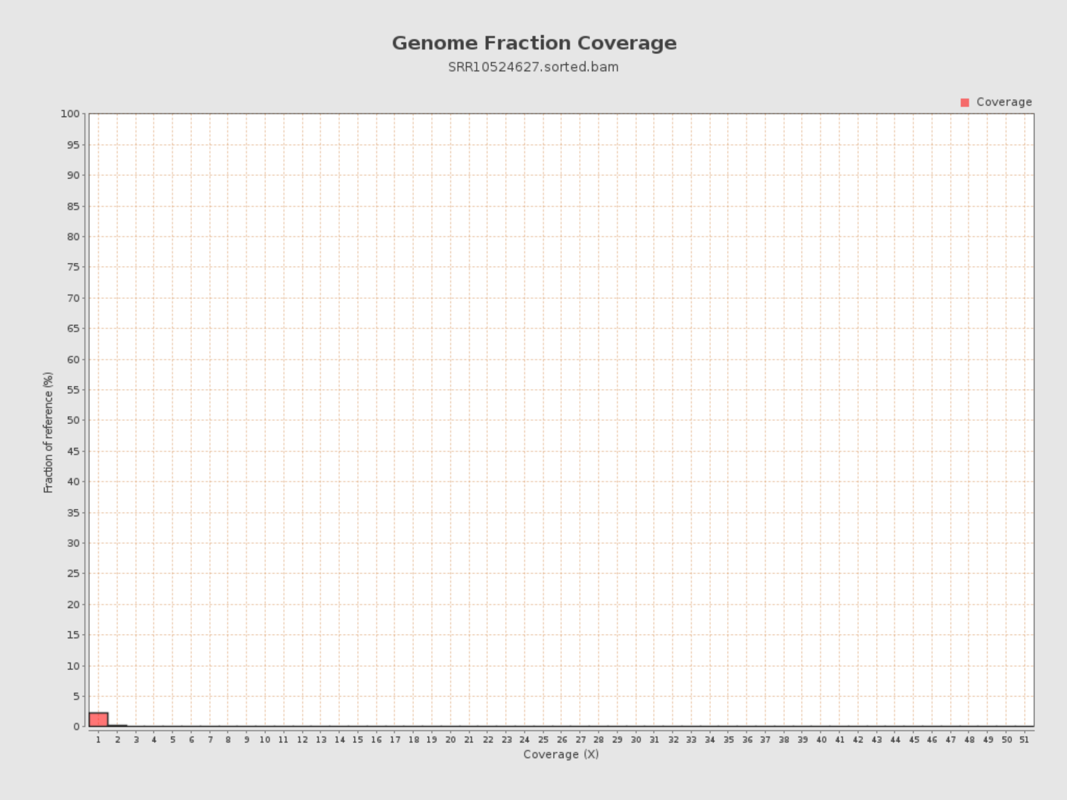
4. Results : Coverage Histogram



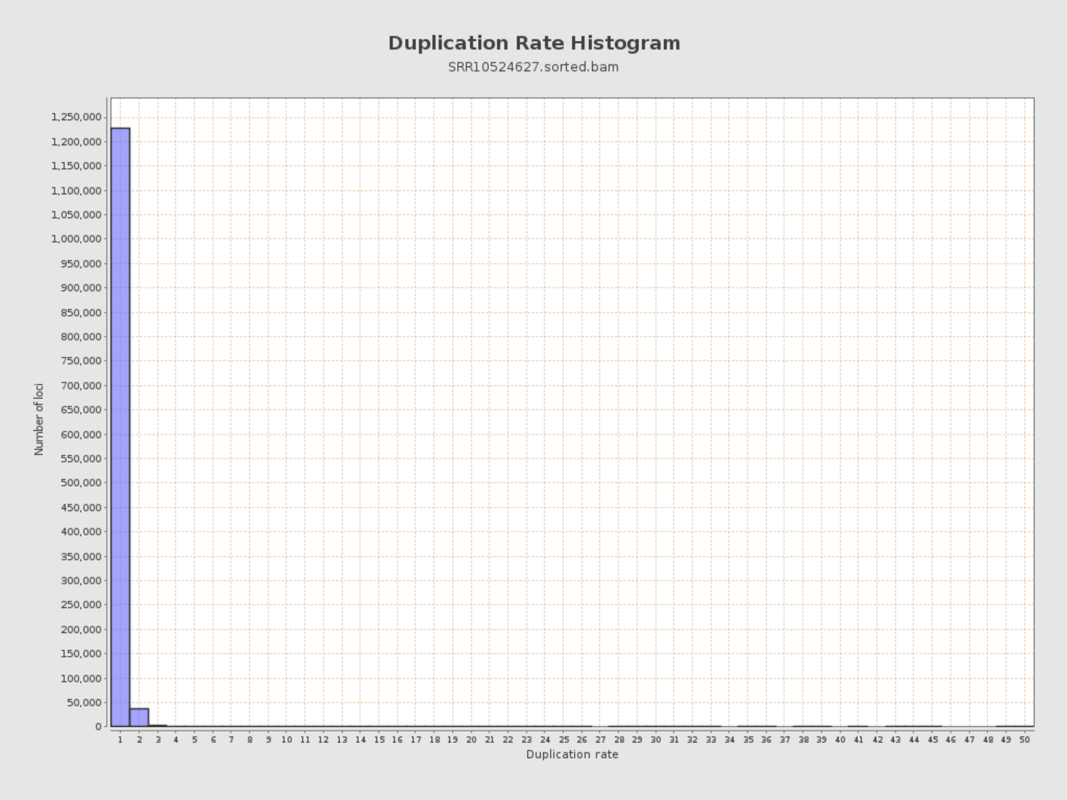
5. Results : Coverage Histogram (0-50X)



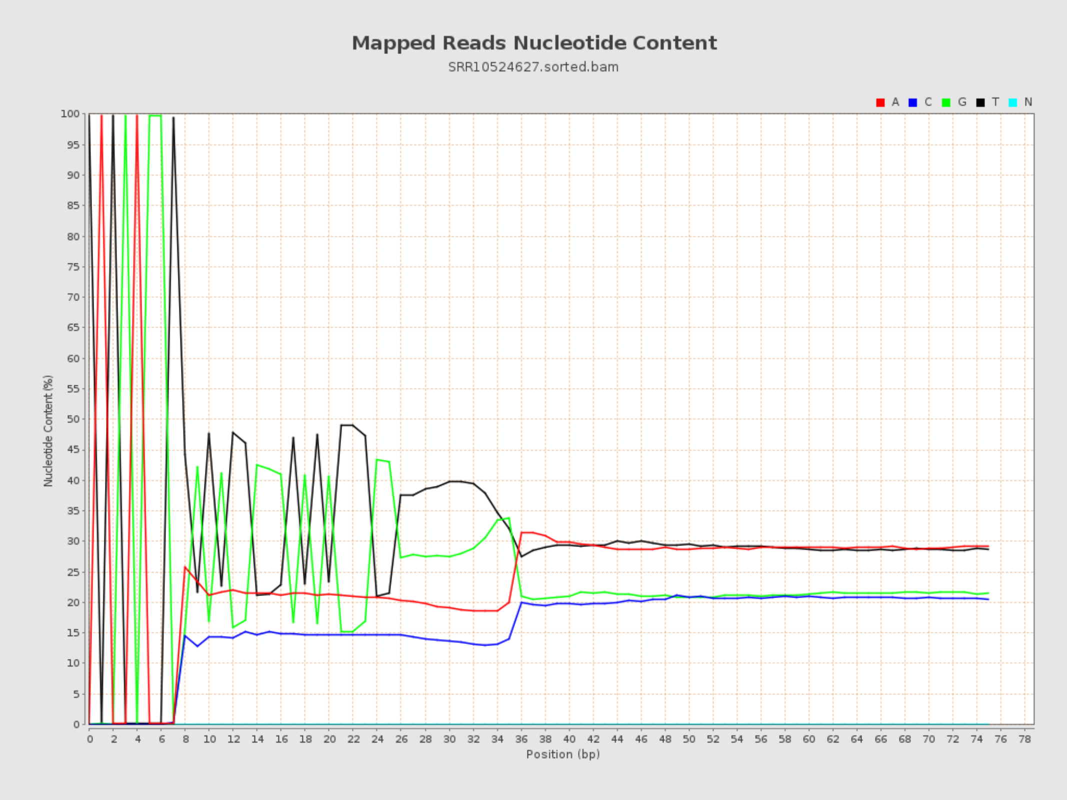
6. Results : Genome Fraction Coverage



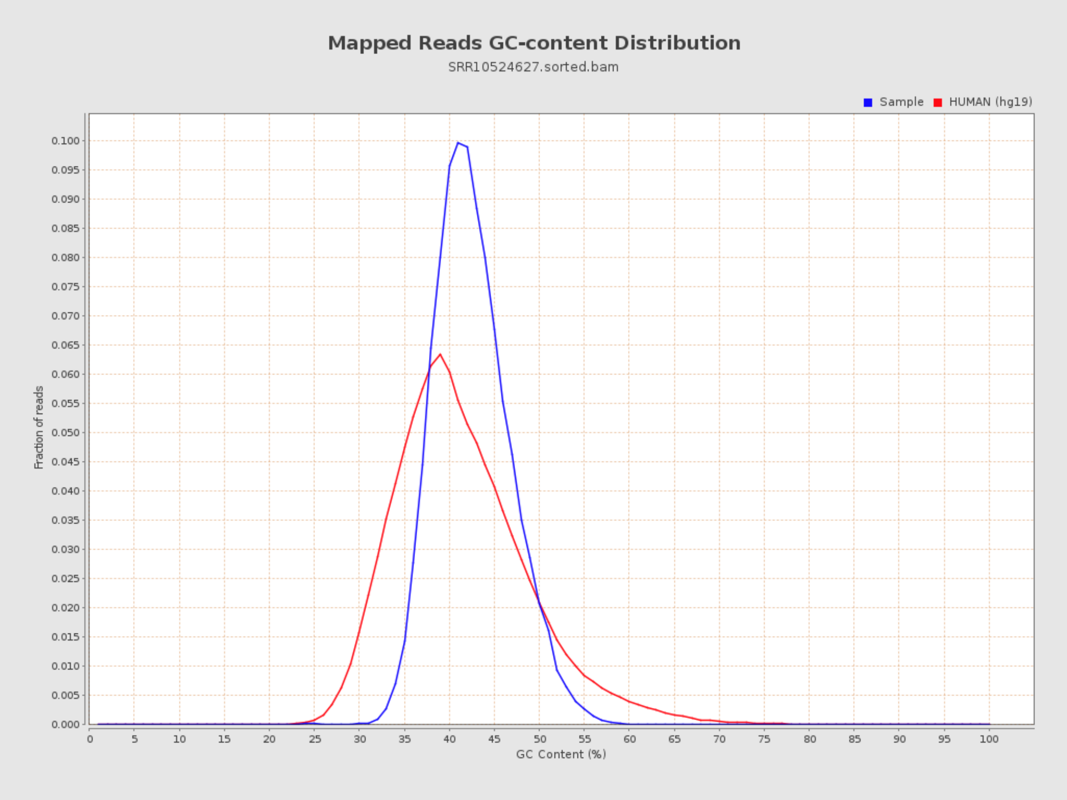
7. Results : Duplication Rate Histogram



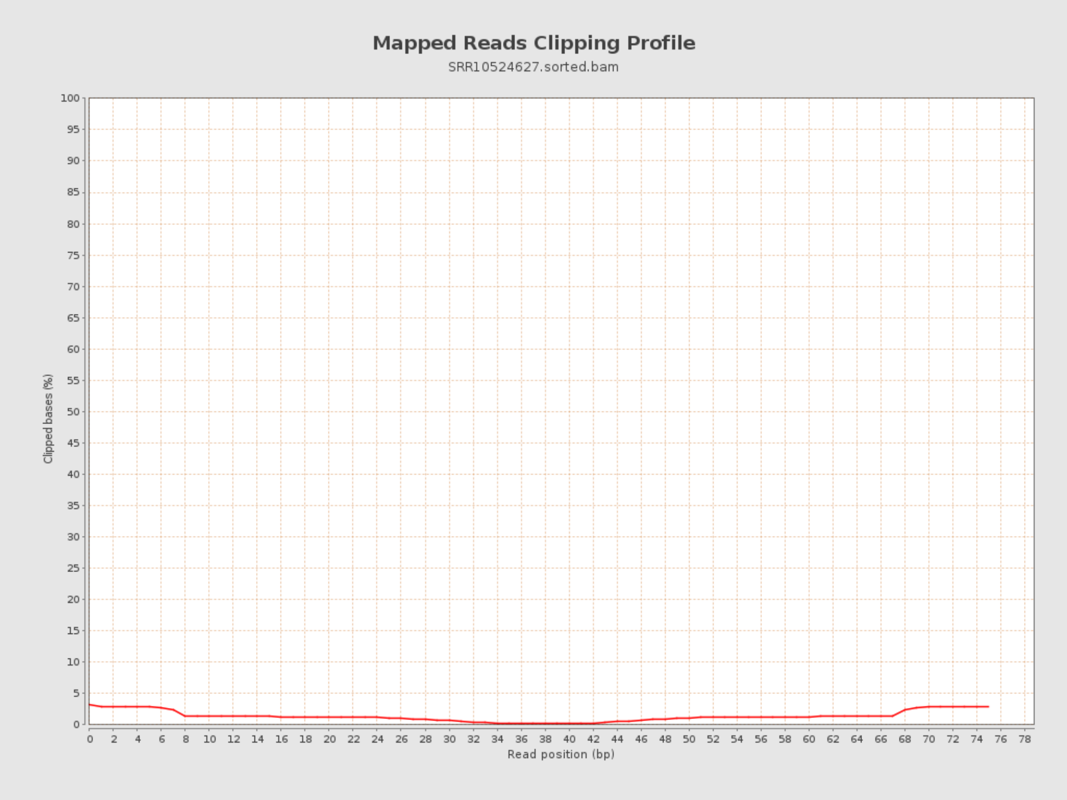
8. Results : Mapped Reads Nucleotide Content



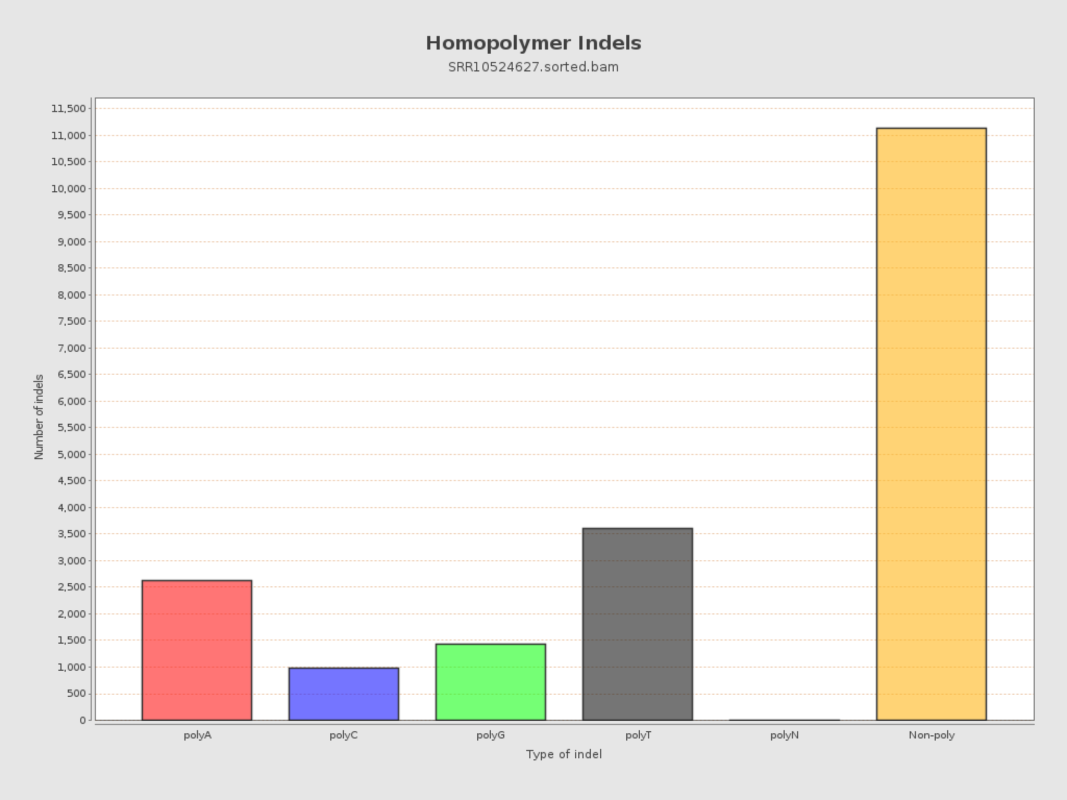
9. Results : Mapped Reads GC-content Distribution



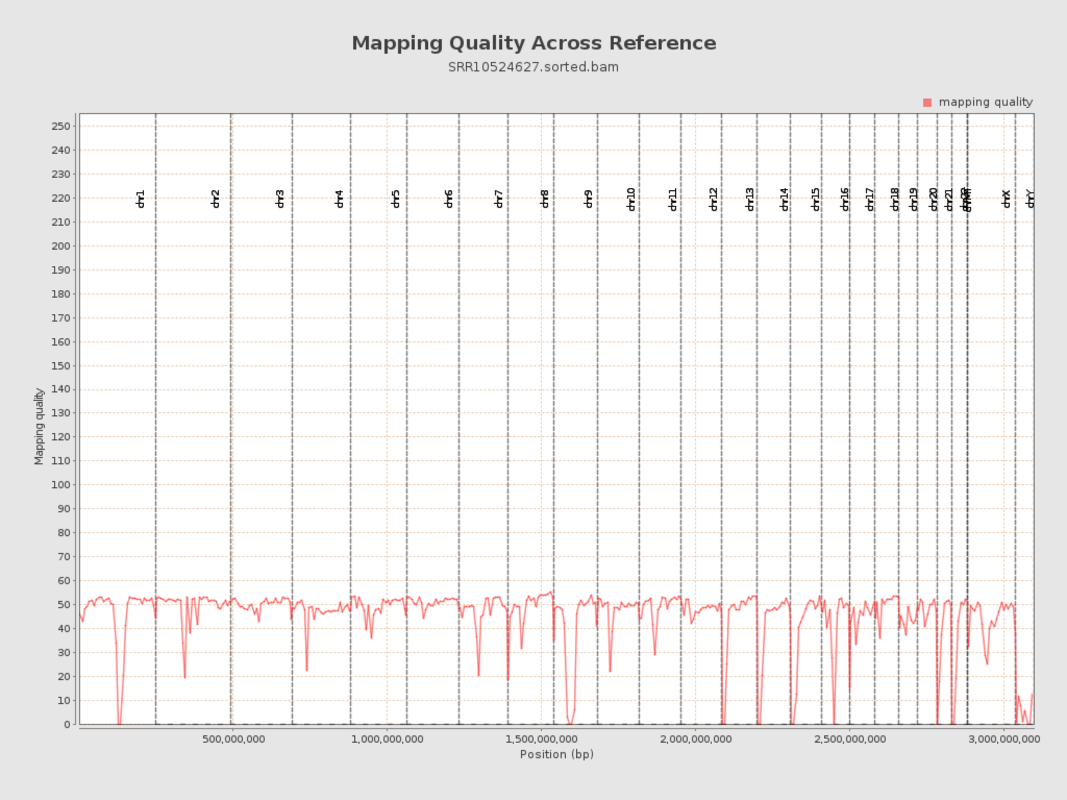
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram