Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:06:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524878.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_SRR10524878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524878.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:06:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,031,696
Mapped reads	2,746,649 / 90.6%
Unmapped reads	285,047 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,107 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	167,232 / 5.52%
Duplication rate	4.55%
Clipped reads	2,749,606 / 90.7%

2.2. ACGT Content

Number/percentage of A's	39,294,868 / 25%
Number/percentage of C's	26,019,949 / 16.55%
Number/percentage of T's	51,339,939 / 32.66%
Number/percentage of G's	40,516,830 / 25.78%
Number/percentage of N's	3,011 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.4396

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

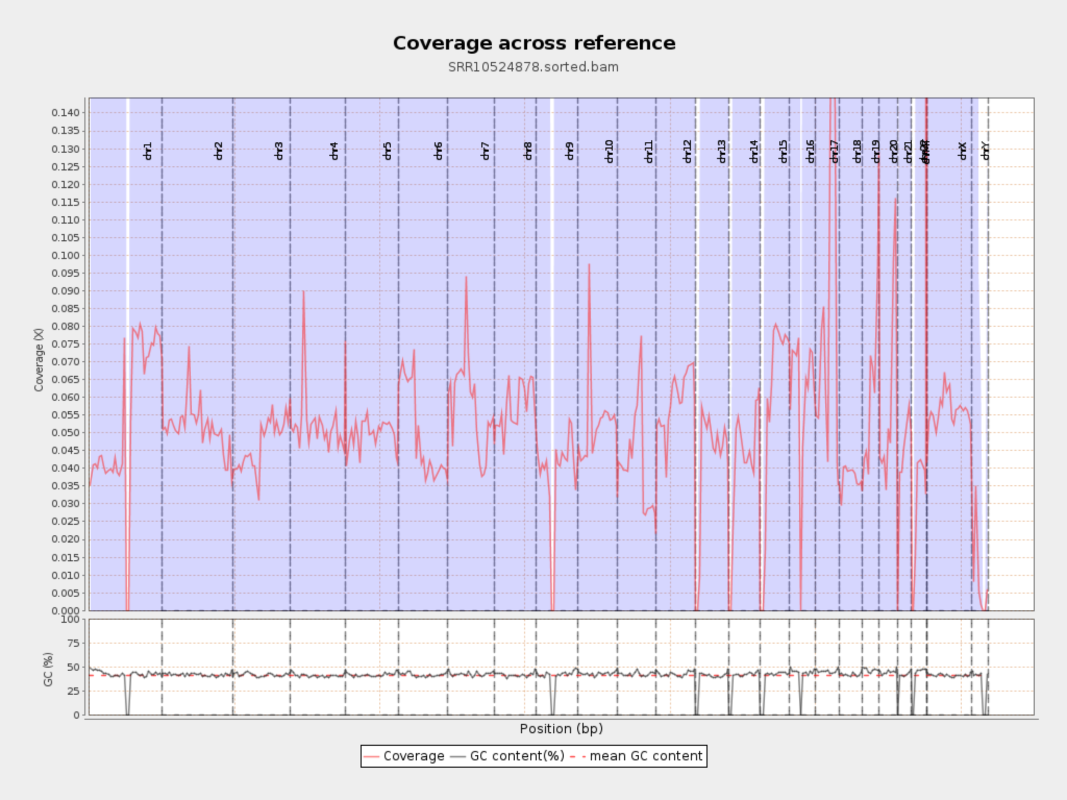
General error rate	0.53%
Mismatches	809,053
Insertions	11,449
Mapped reads with at least one insertion	0.42%
Deletions	30,801
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.47%

2.6. Chromosome stats

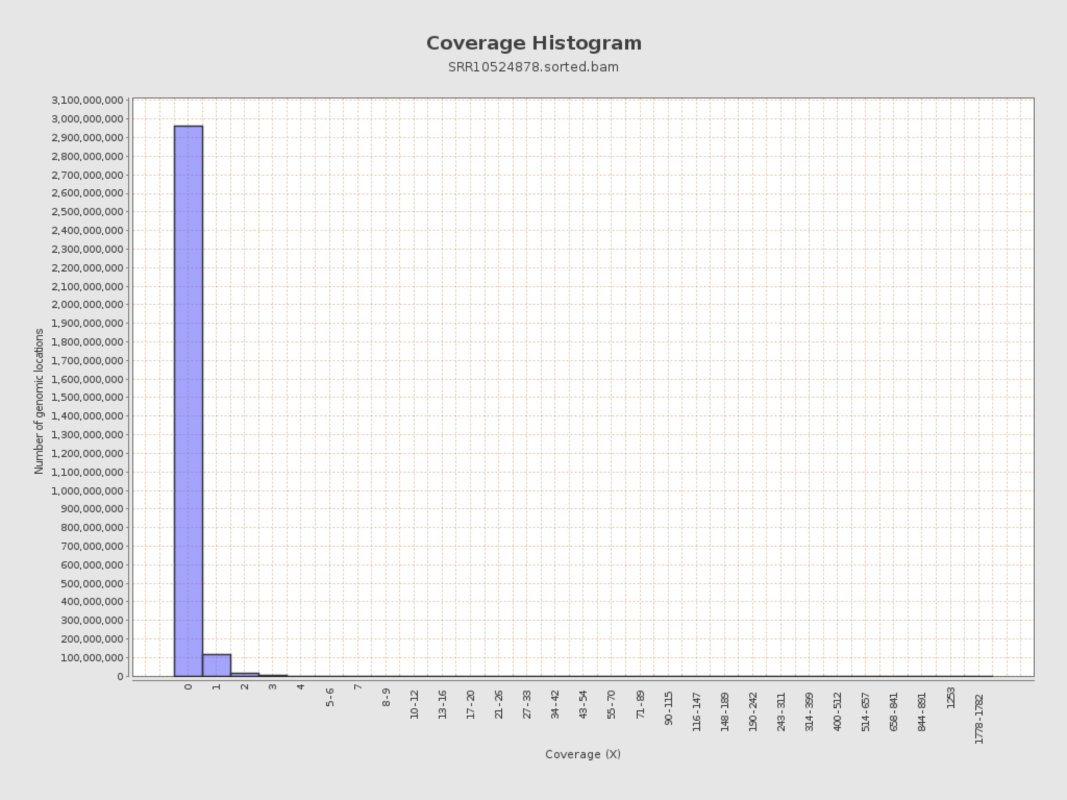
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13433222	0.0539	0.6791
chr2	243199373	12590929	0.0518	0.7476
chr3	198022430	9224871	0.0466	0.2588
chr4	191154276	9947099	0.052	0.3347
chr5	180915260	9019226	0.0499	0.2593
chr6	171115067	8553213	0.05	0.3237
chr7	159138663	9264699	0.0582	0.5883

chr8	146364022	8411823	0.0575	0.5947
chr9	141213431	5321103	0.0377	0.3021
chr10	135534747	7123614	0.0526	0.4516
chr11	135006516	5673692	0.042	0.3326
chr12	133851895	7931204	0.0593	0.2863
chr13	115169878	4785293	0.0415	0.2401
chr14	107349540	4332426	0.0404	0.2434
chr15	102531392	5920847	0.0577	0.2895
chr16	90354753	5533763	0.0612	0.3115
chr17	81195210	6923842	0.0853	0.3672
chr18	78077248	2924270	0.0375	0.4923
chr19	59128983	3663048	0.062	0.5121
chr20	63025520	3817239	0.0606	0.3025
chr21	48129895	2061234	0.0428	0.3015
chr22	51304566	1458734	0.0284	0.1984
chrMT	16571	46596	2.8119	2.4462
chrX	155270560	8715681	0.0561	0.3102
chrY	59373566	545552	0.0092	0.3124

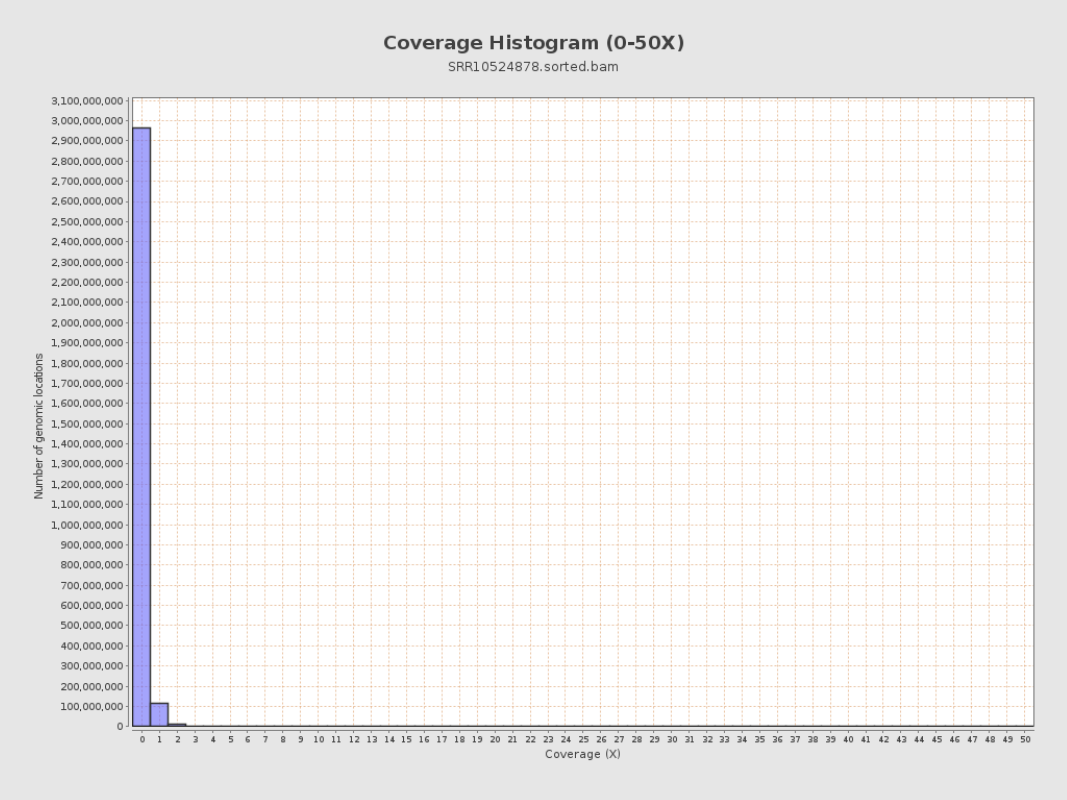
3. Results : Coverage across reference



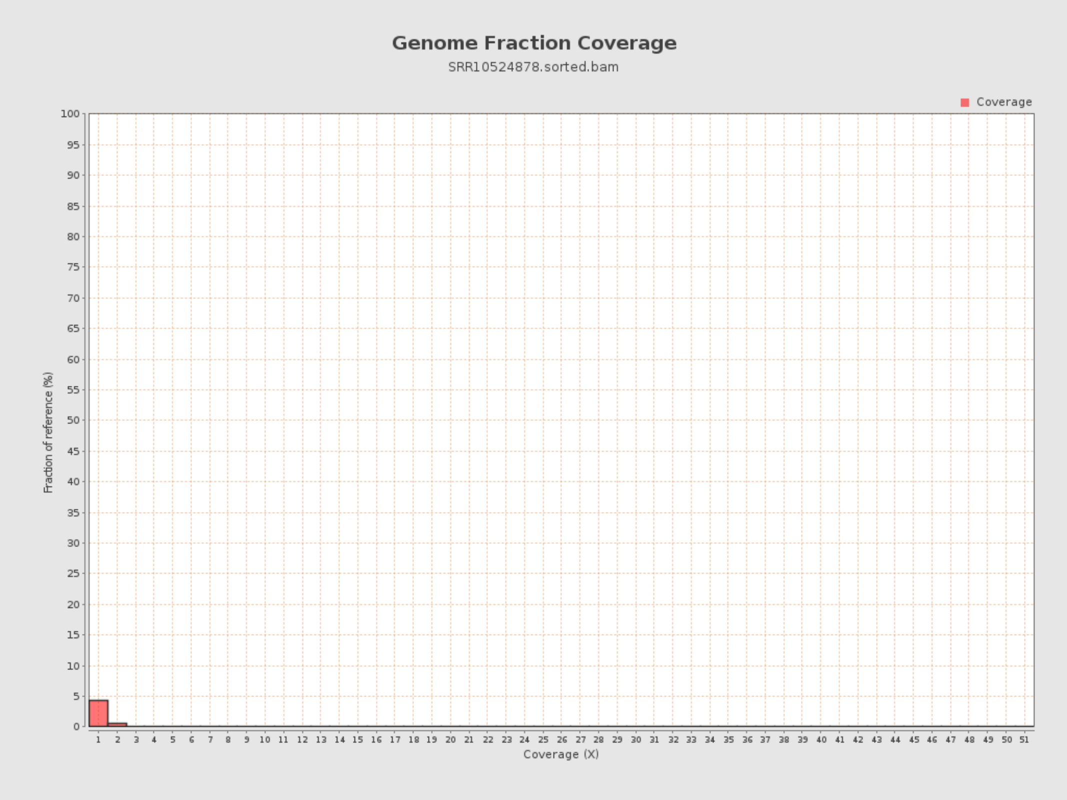
4. Results : Coverage Histogram



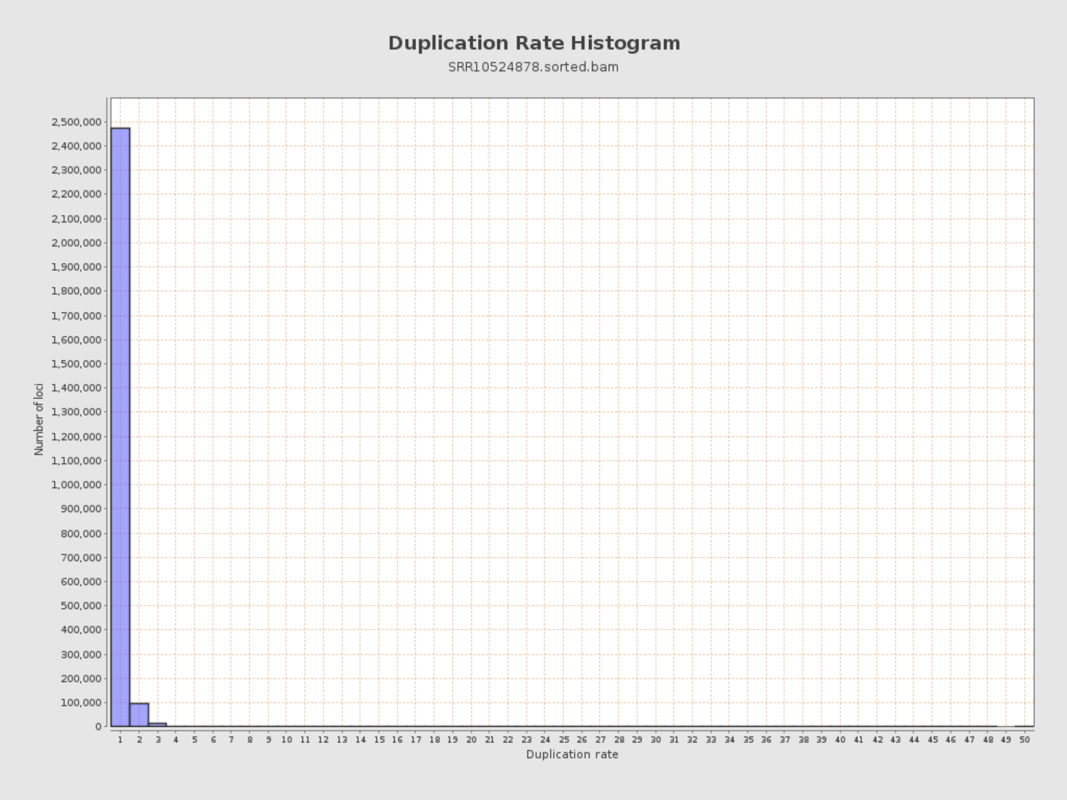
5. Results : Coverage Histogram (0-50X)



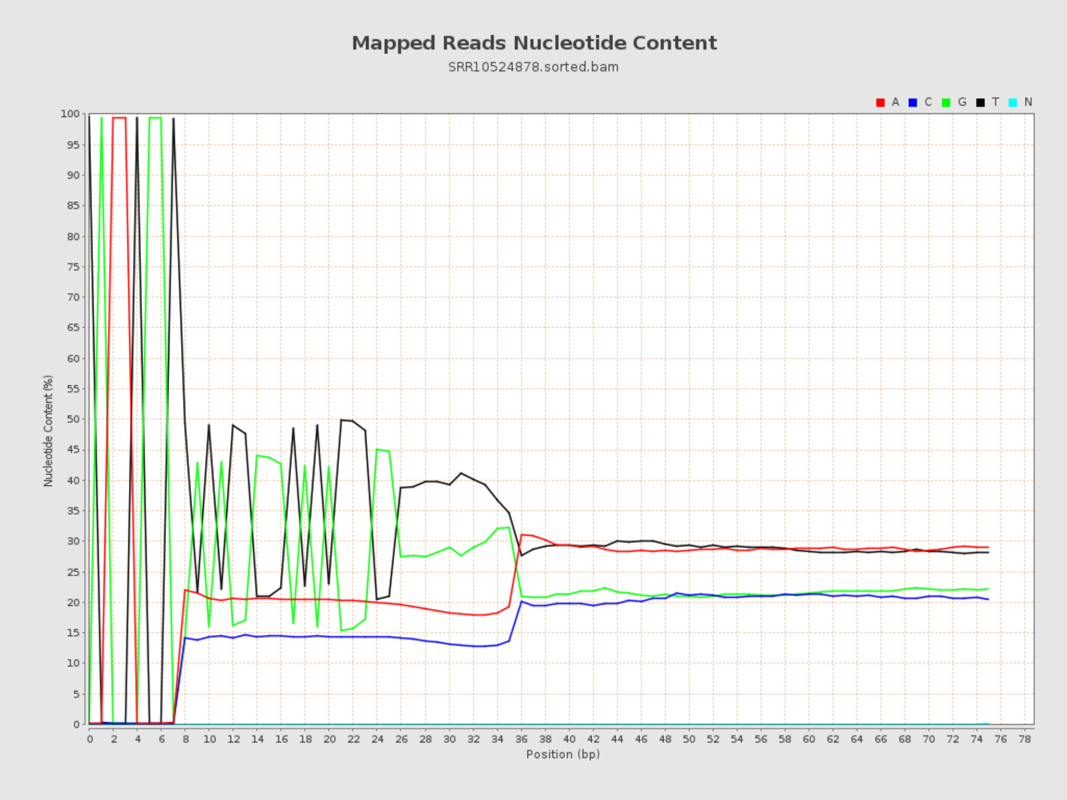
6. Results : Genome Fraction Coverage



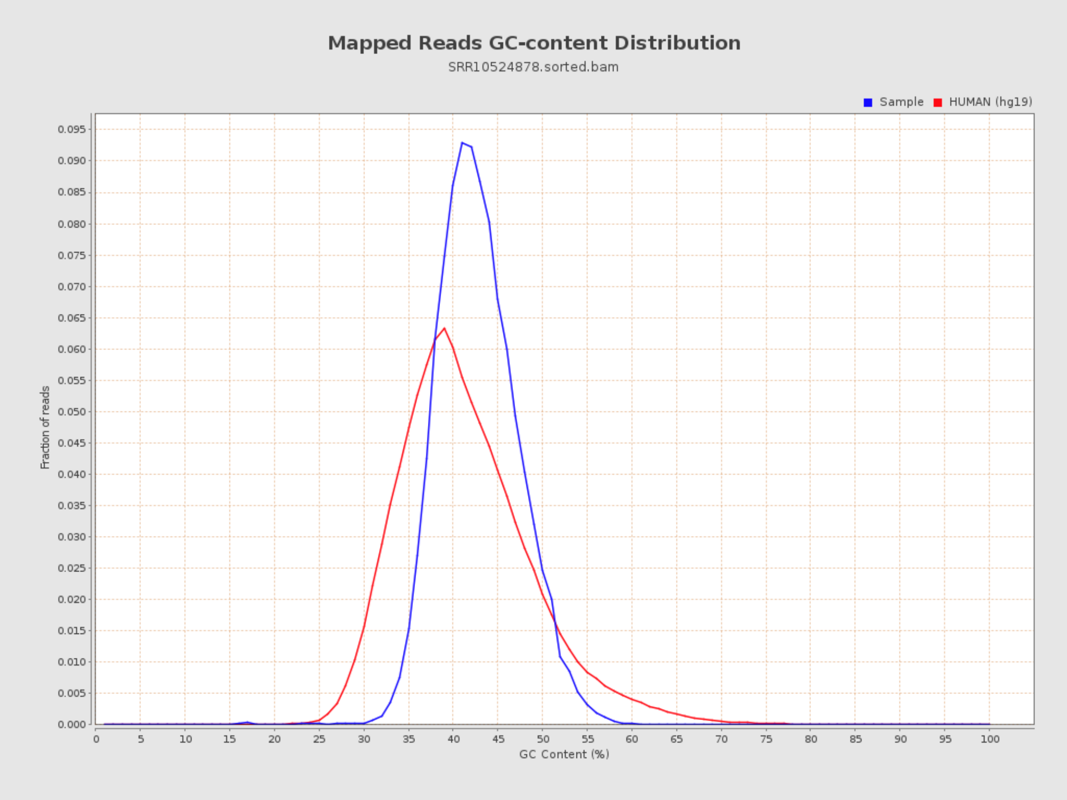
7. Results : Duplication Rate Histogram



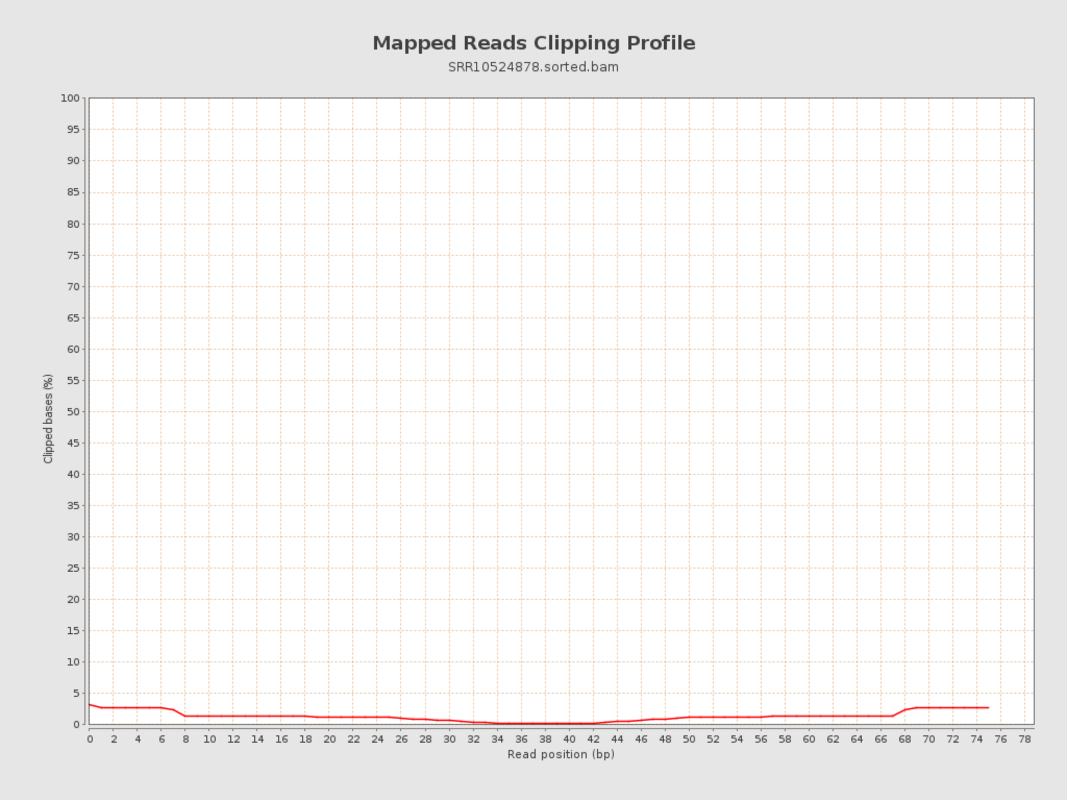
8. Results : Mapped Reads Nucleotide Content



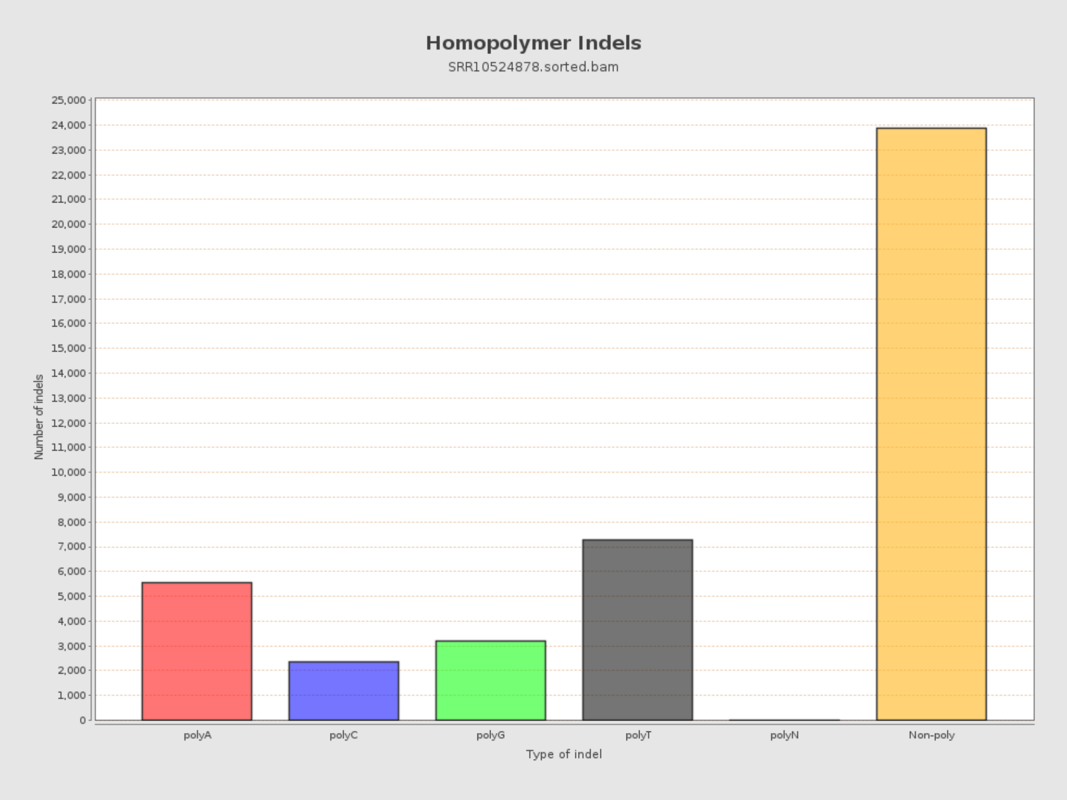
9. Results : Mapped Reads GC-content Distribution



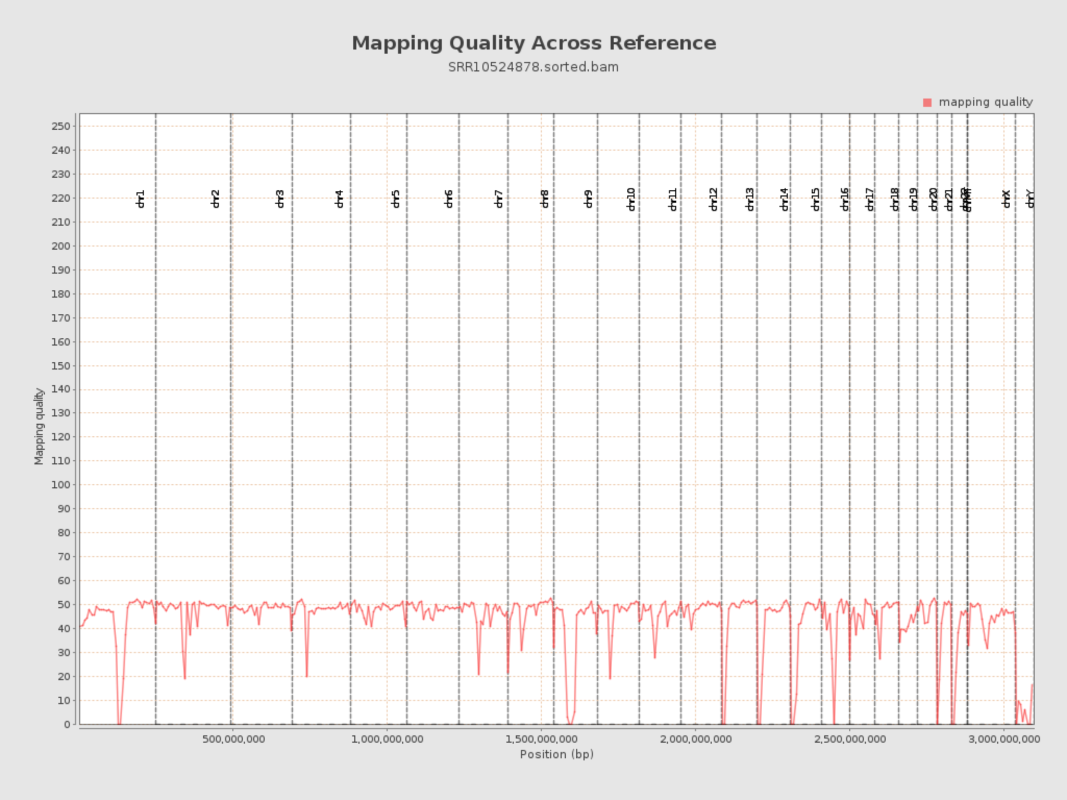
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram