Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:31:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524848.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_SRR10524848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524848.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:31:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524848.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,549,865
Mapped reads	1,422,605 / 91.79%
Unmapped reads	127,260 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,495 / 0.55%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	41,530 / 2.68%
Duplication rate	1.98%
Clipped reads	1,427,022 / 92.07%

2.2. ACGT Content

Number/percentage of A's	20,372,484 / 24.62%
Number/percentage of C's	14,359,218 / 17.35%
Number/percentage of T's	27,644,434 / 33.41%
Number/percentage of G's	20,355,308 / 24.6%
Number/percentage of N's	11,065 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.2712

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

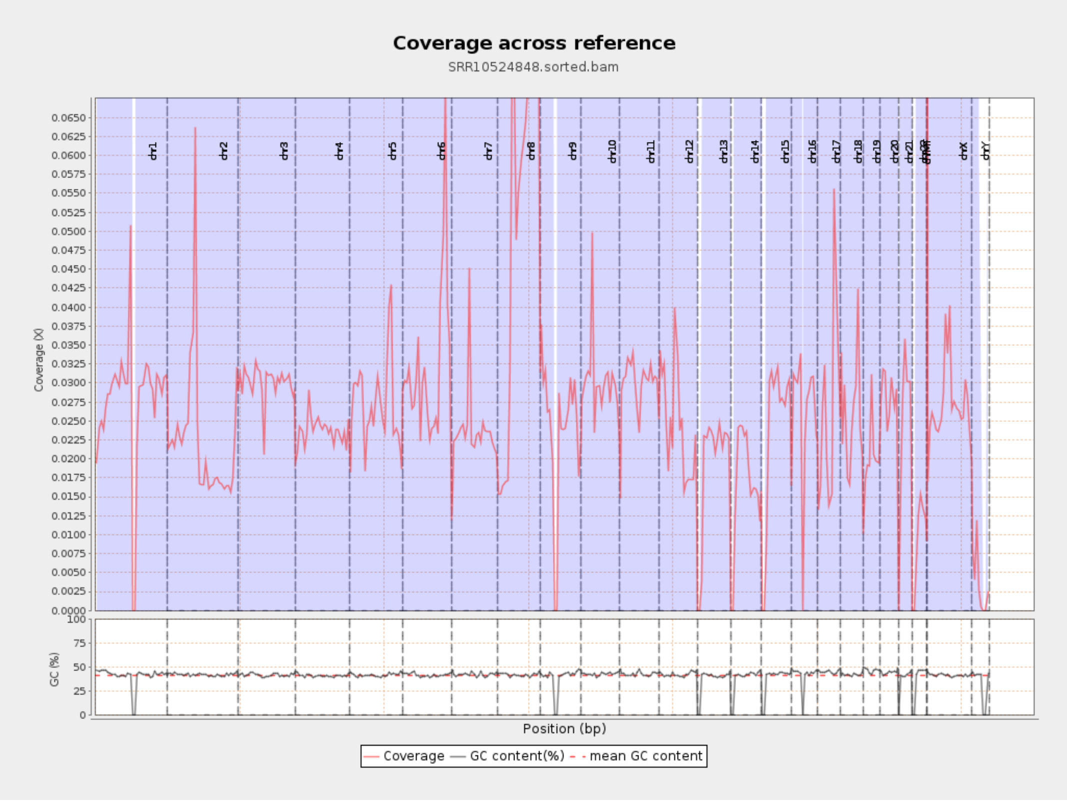
General error rate	0.5%
Mismatches	402,464
Insertions	5,930
Mapped reads with at least one insertion	0.41%
Deletions	15,308
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.2%

2.6. Chromosome stats

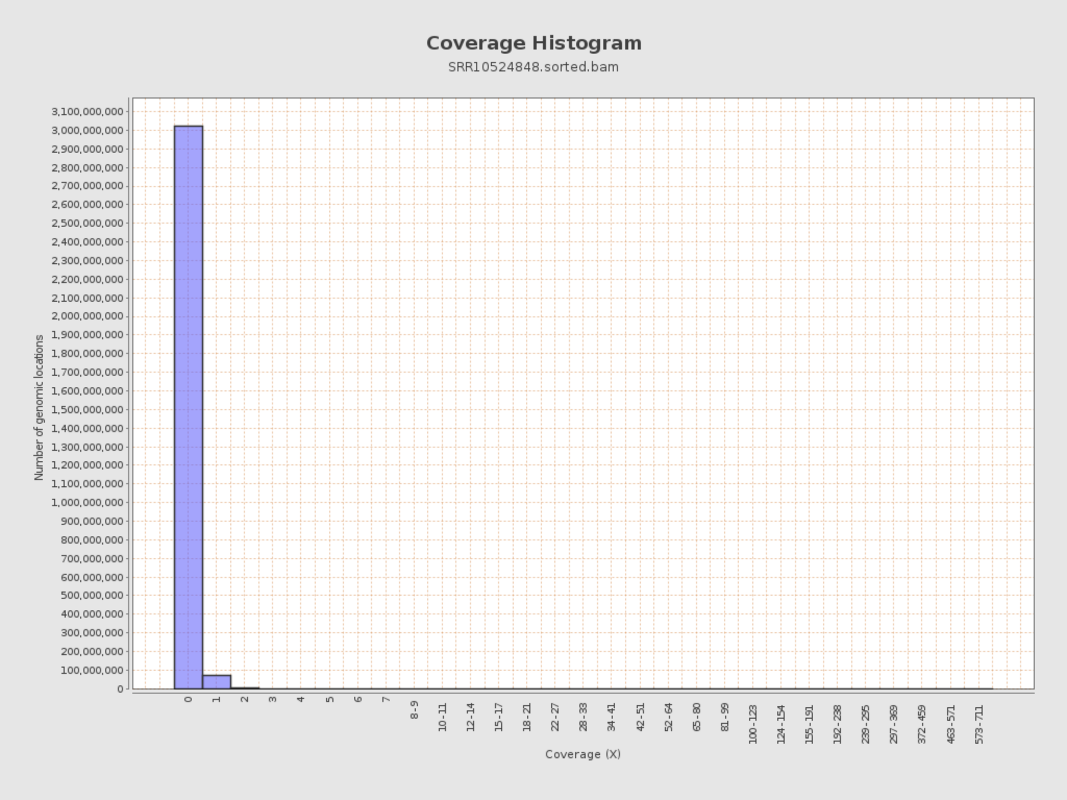
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6884748	0.0276	0.5319
chr2	243199373	5390360	0.0222	0.2662
chr3	198022430	5952548	0.0301	0.1851
chr4	191154276	4516157	0.0236	0.1723
chr5	180915260	4989164	0.0276	0.1772
chr6	171115067	5437878	0.0318	0.2072
chr7	159138663	3796388	0.0239	0.355

chr8	146364022	8946947	0.0611	0.365
chr9	141213431	3384696	0.024	0.2303
chr10	135534747	4093402	0.0302	0.2568
chr11	135006516	4058033	0.0301	0.2516
chr12	133851895	3255888	0.0243	0.1723
chr13	115169878	2188667	0.019	0.1478
chr14	107349540	1759447	0.0164	0.1496
chr15	102531392	2441995	0.0238	0.1648
chr16	90354753	2327539	0.0258	0.187
chr17	81195210	2205354	0.0272	0.1956
chr18	78077248	2026287	0.026	0.4211
chr19	59128983	1209825	0.0205	0.3403
chr20	63025520	1751256	0.0278	0.179
chr21	48129895	1201767	0.025	0.1775
chr22	51304566	484973	0.0095	0.1029
chrMT	16571	5772	0.3483	0.6578
chrX	155270560	4248860	0.0274	0.2024
chrY	59373566	207999	0.0035	0.0932

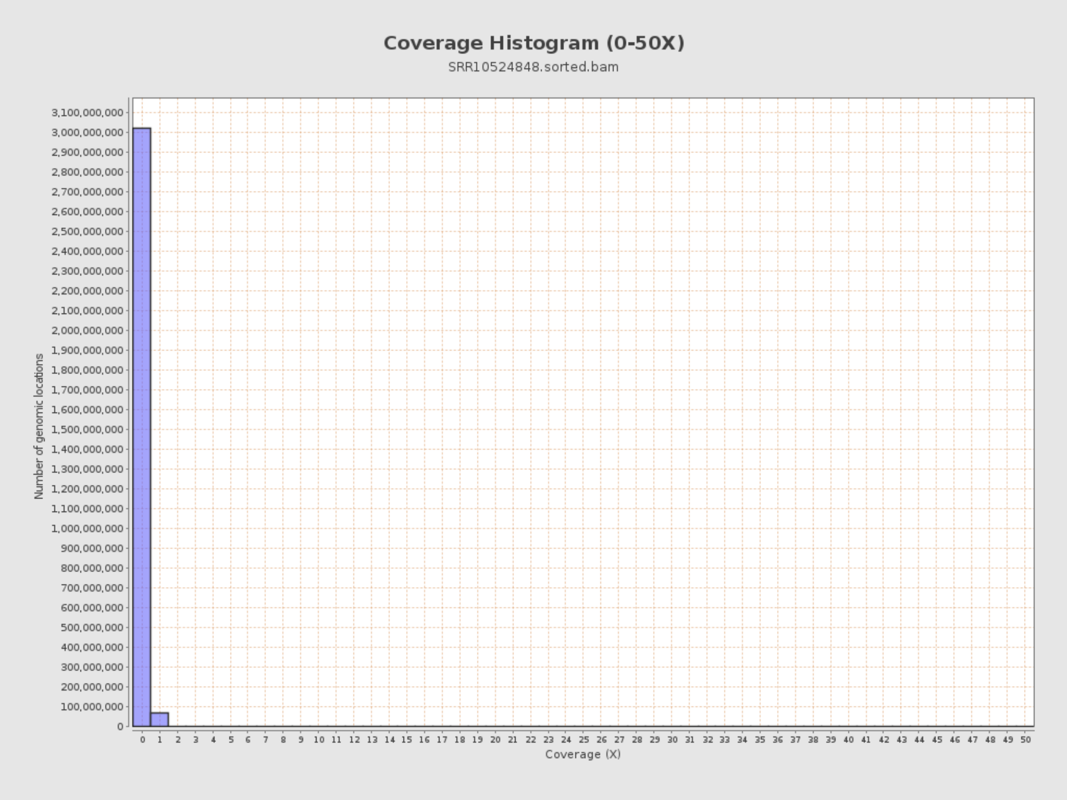
3. Results : Coverage across reference



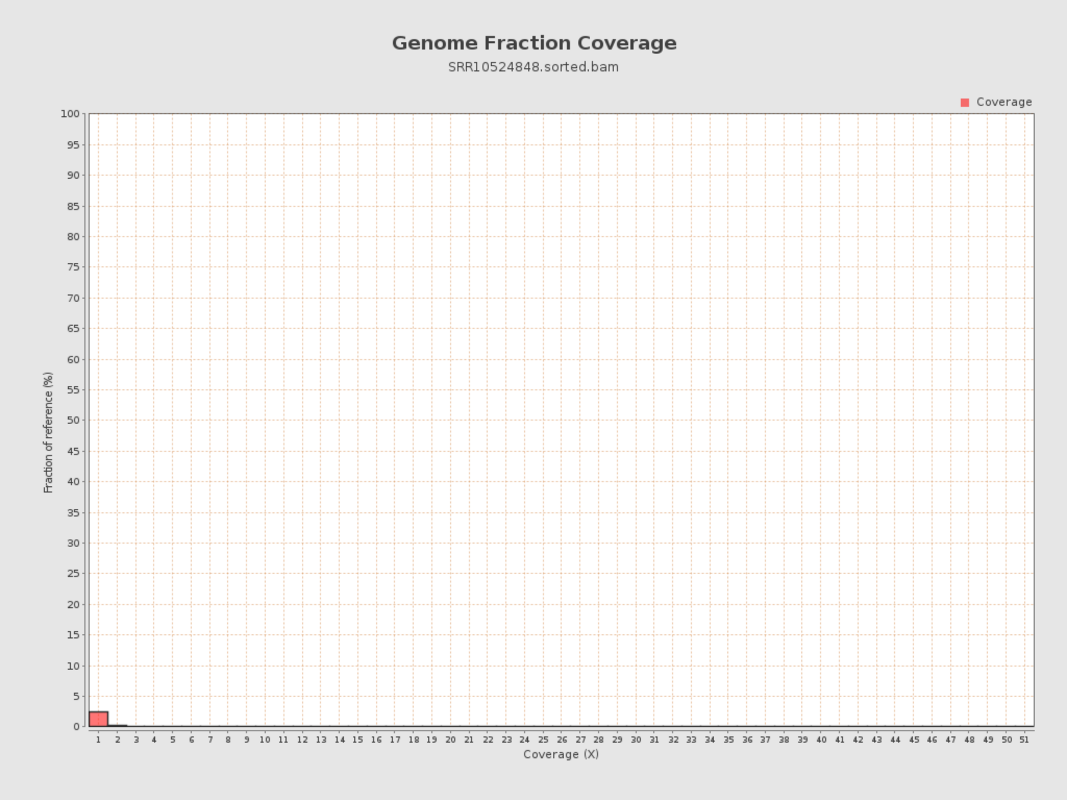
4. Results : Coverage Histogram



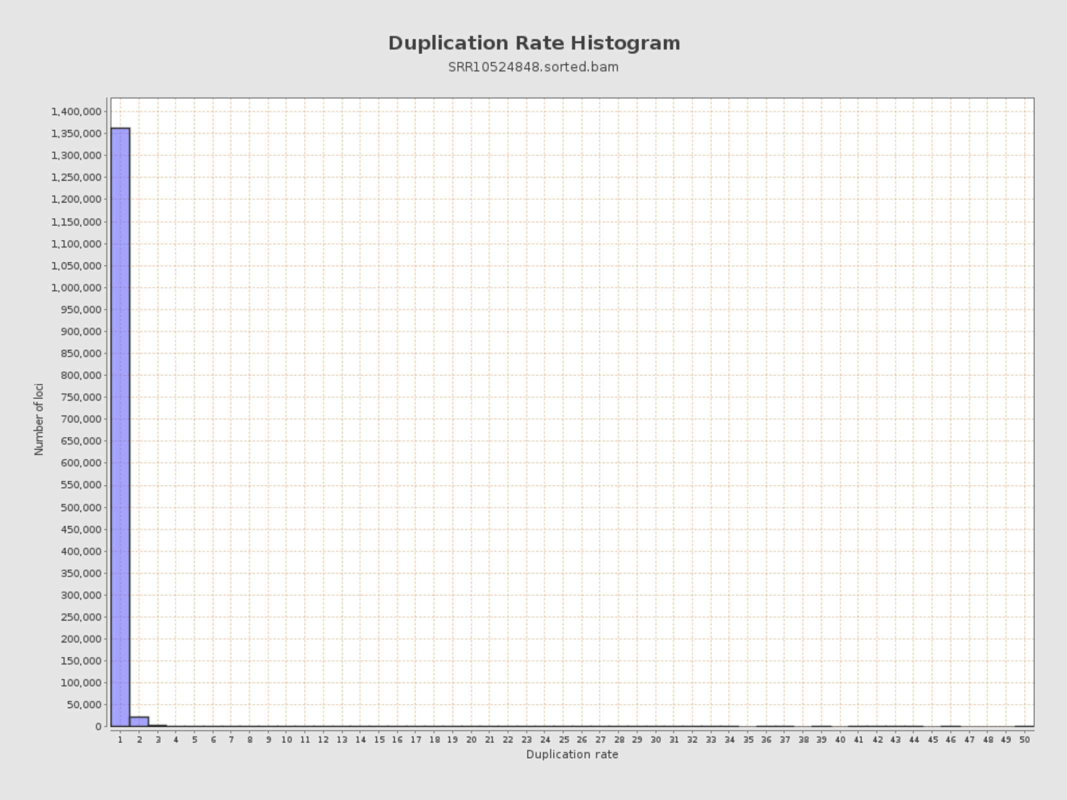
5. Results : Coverage Histogram (0-50X)



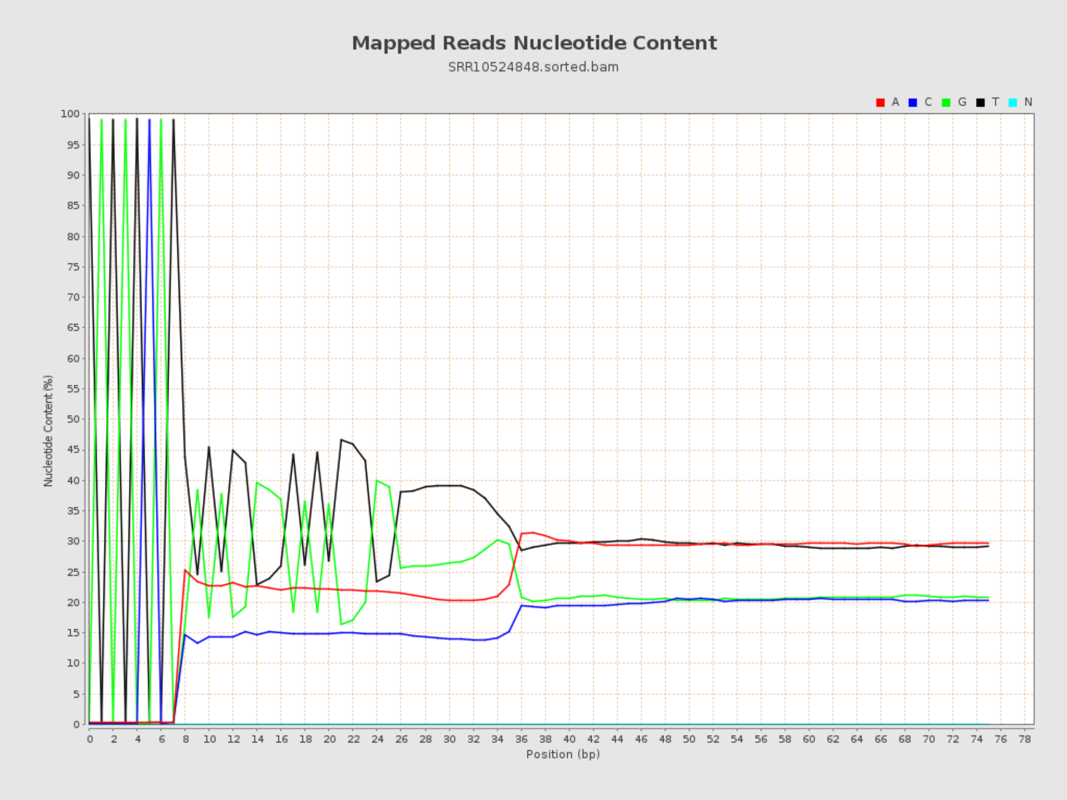
6. Results : Genome Fraction Coverage



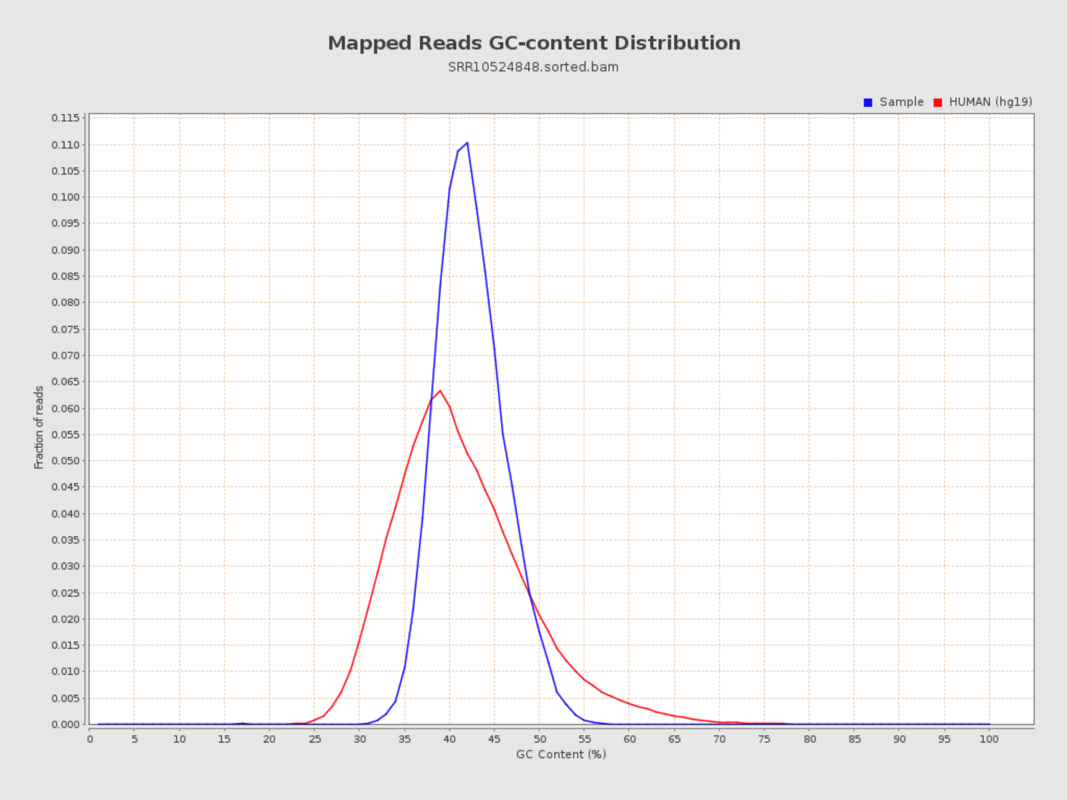
7. Results : Duplication Rate Histogram



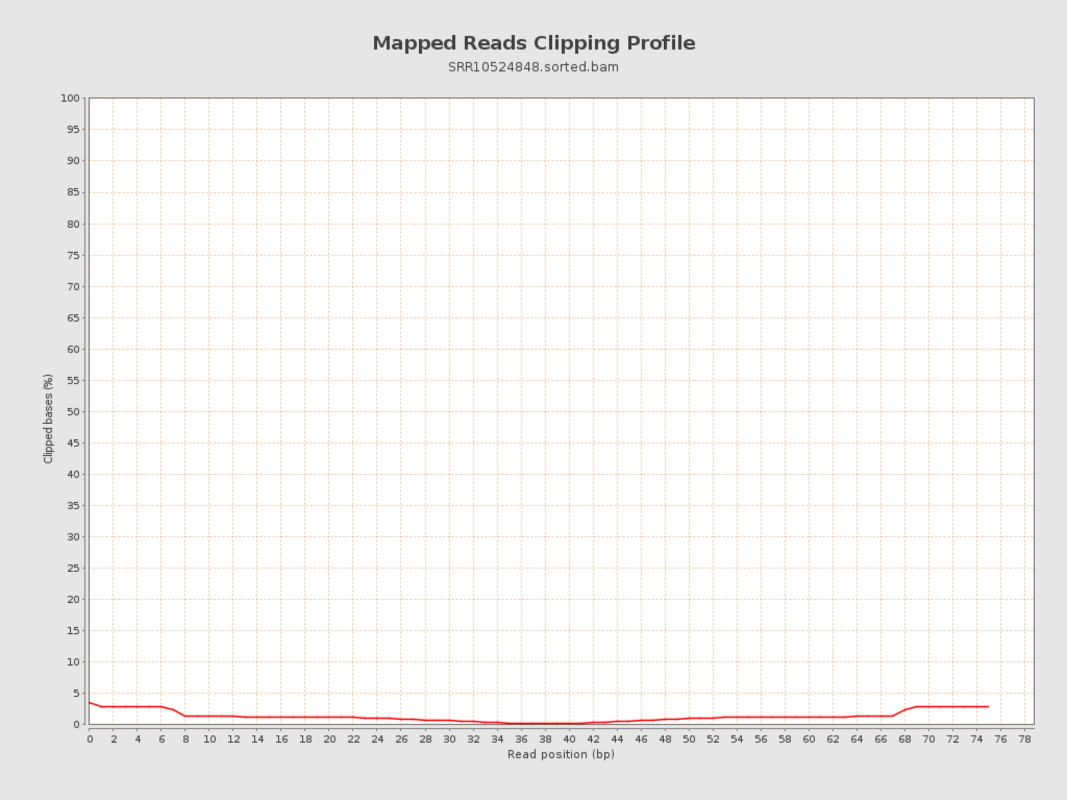
8. Results : Mapped Reads Nucleotide Content



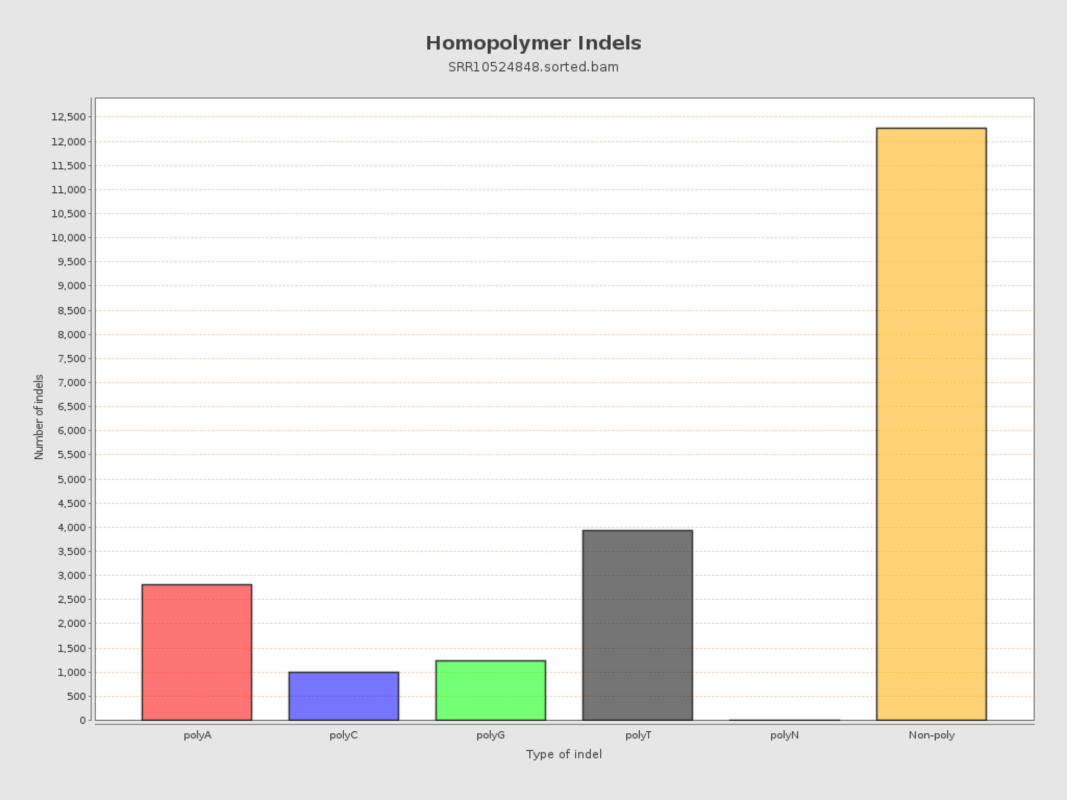
9. Results : Mapped Reads GC-content Distribution



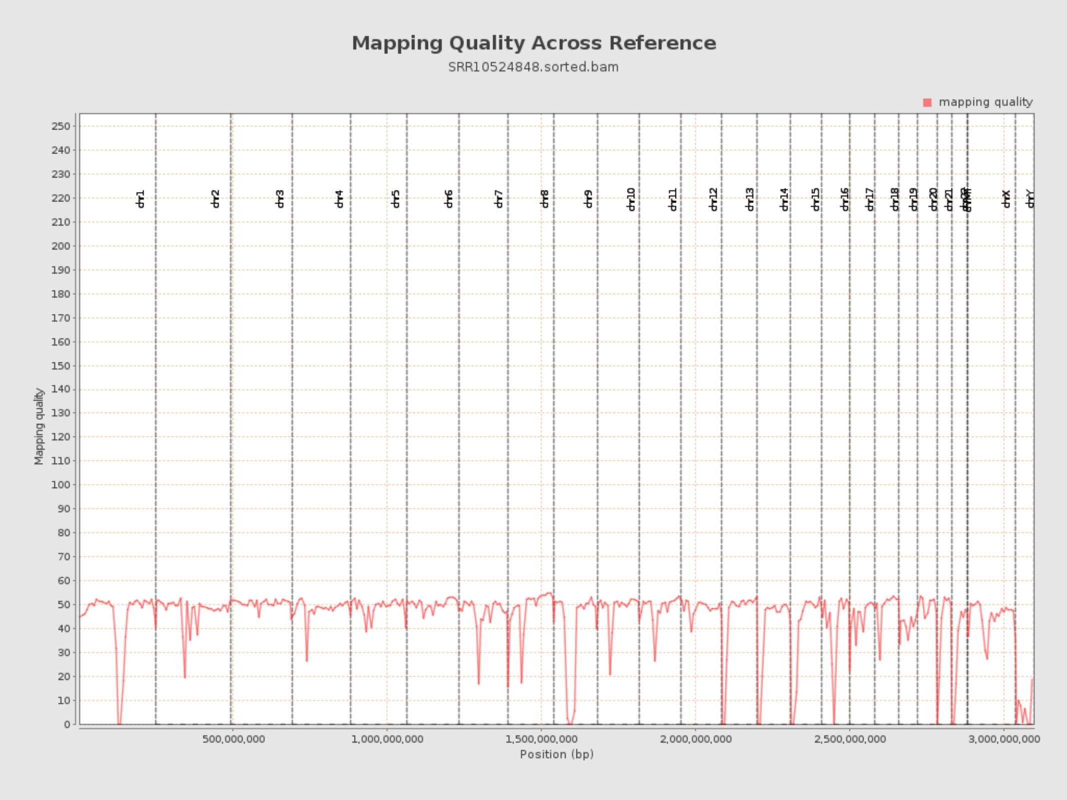
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram