Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:06:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524748.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_SRR10524748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:06:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,858,627
Mapped reads	1,692,660 / 91.07%
Unmapped reads	165,967 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,553 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	67,053 / 3.61%
Duplication rate	2.99%
Clipped reads	1,697,453 / 91.33%

2.2. ACGT Content

Number/percentage of A's	23,482,480 / 24.11%
Number/percentage of C's	18,175,086 / 18.66%
Number/percentage of T's	31,365,083 / 32.2%
Number/percentage of G's	24,374,940 / 25.02%
Number/percentage of N's	11,927 / 0.01%
GC Percentage	43.68%

2.3. Coverage

Mean	0.0315

Standard Deviation	0.2675

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

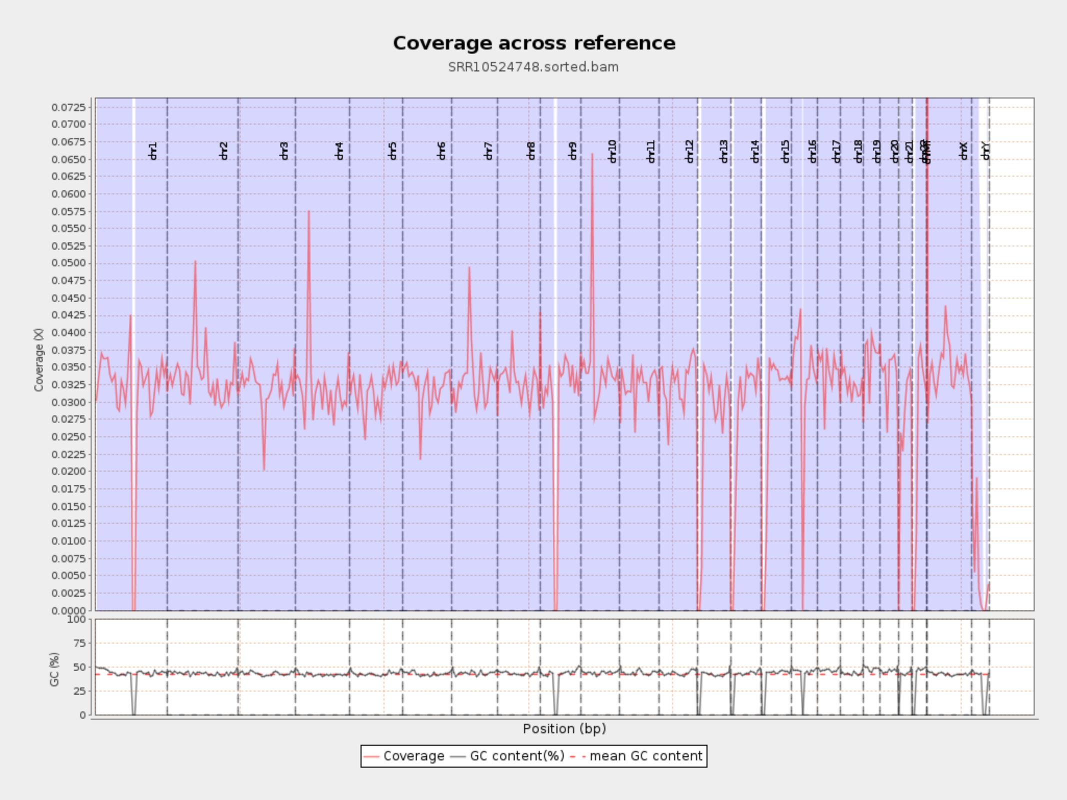
General error rate	0.52%
Mismatches	496,548
Insertions	5,702
Mapped reads with at least one insertion	0.34%
Deletions	19,285
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.45%

2.6. Chromosome stats

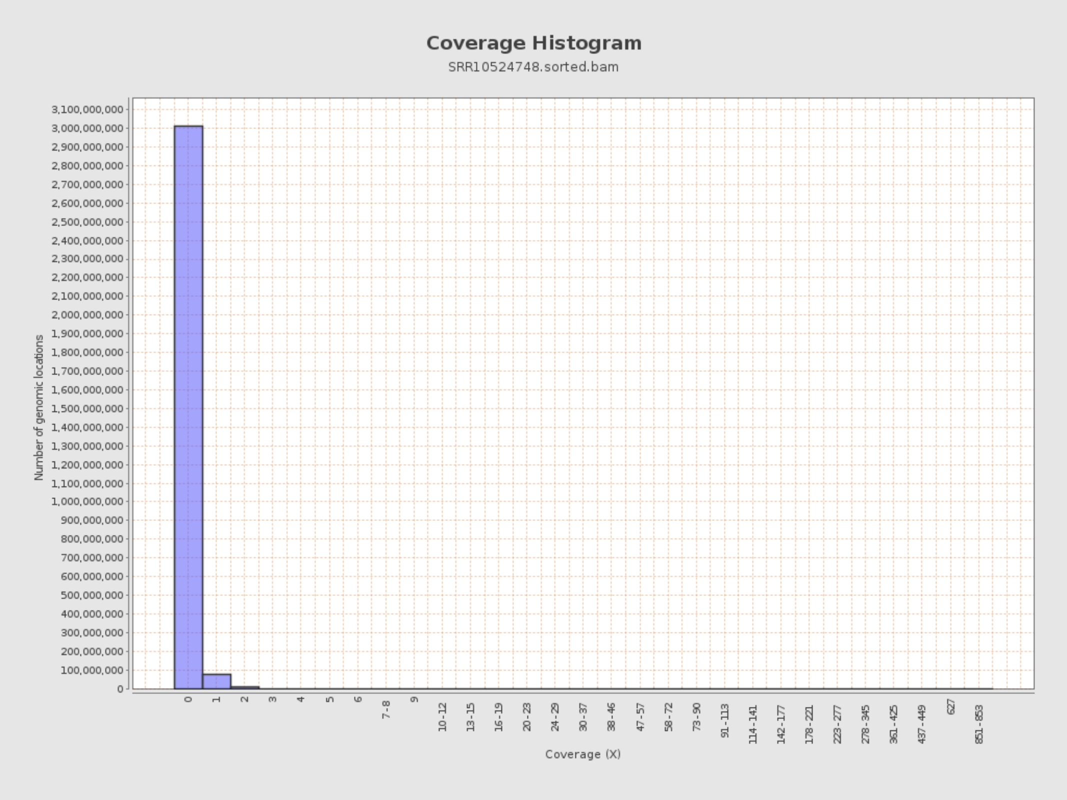
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7802661	0.0313	0.3686
chr2	243199373	8196945	0.0337	0.4199
chr3	198022430	6360414	0.0321	0.2028
chr4	191154276	6190883	0.0324	0.2283
chr5	180915260	5785128	0.032	0.1979
chr6	171115067	5518408	0.0322	0.2186
chr7	159138663	5337025	0.0335	0.3199

chr8	146364022	4819495	0.0329	0.243
chr9	141213431	4169613	0.0295	0.2395
chr10	135534747	4786968	0.0353	0.3267
chr11	135006516	4415486	0.0327	0.2362
chr12	133851895	4392519	0.0328	0.2025
chr13	115169878	3002906	0.0261	0.1786
chr14	107349540	2923570	0.0272	0.1888
chr15	102531392	2830281	0.0276	0.1855
chr16	90354753	2963989	0.0328	0.2256
chr17	81195210	2801182	0.0345	0.2146
chr18	78077248	2544880	0.0326	0.3566
chr19	59128983	2163871	0.0366	0.3123
chr20	63025520	2135278	0.0339	0.2131
chr21	48129895	1280407	0.0266	0.2086
chr22	51304566	1239529	0.0242	0.1742
chrMT	16571	35067	2.1162	1.9497
chrX	155270560	5418324	0.0349	0.2229
chrY	59373566	325931	0.0055	0.1551

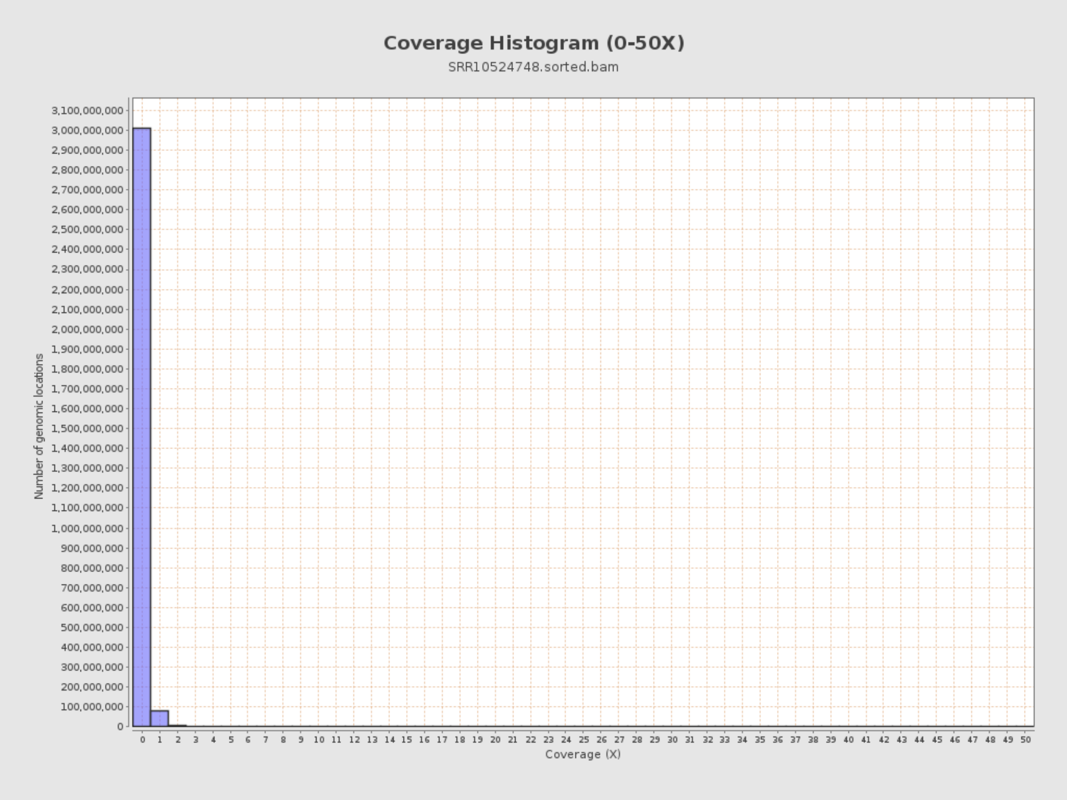
3. Results : Coverage across reference



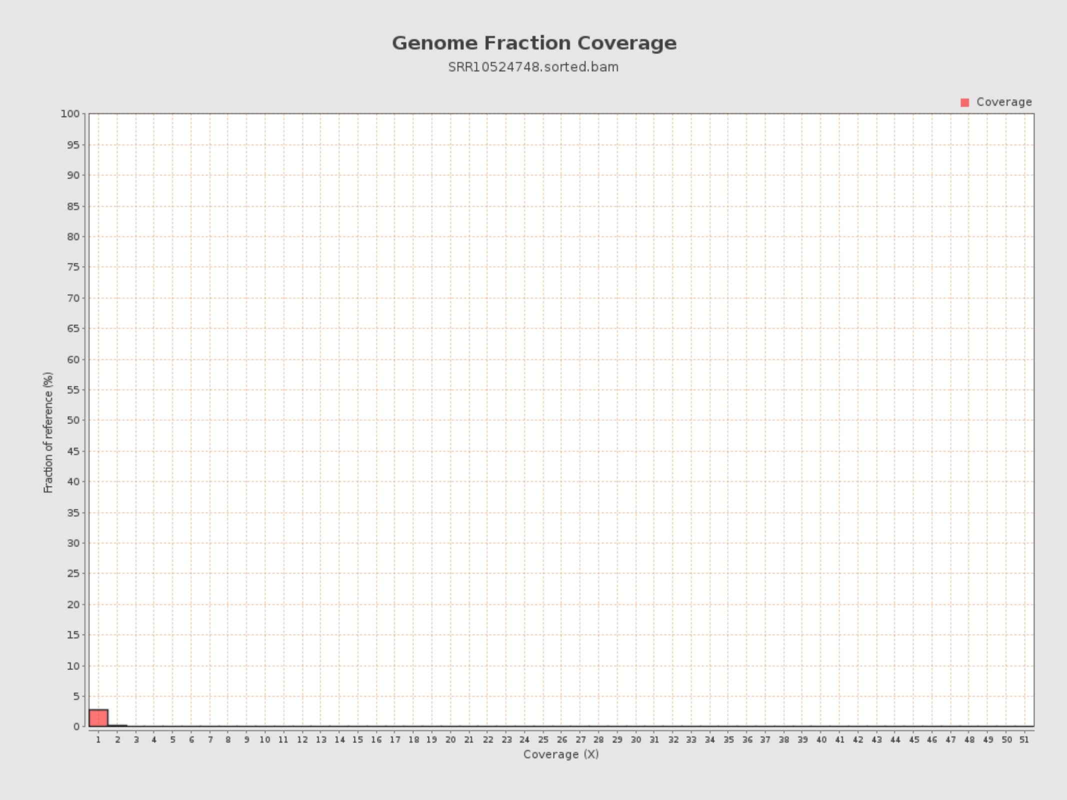
4. Results : Coverage Histogram



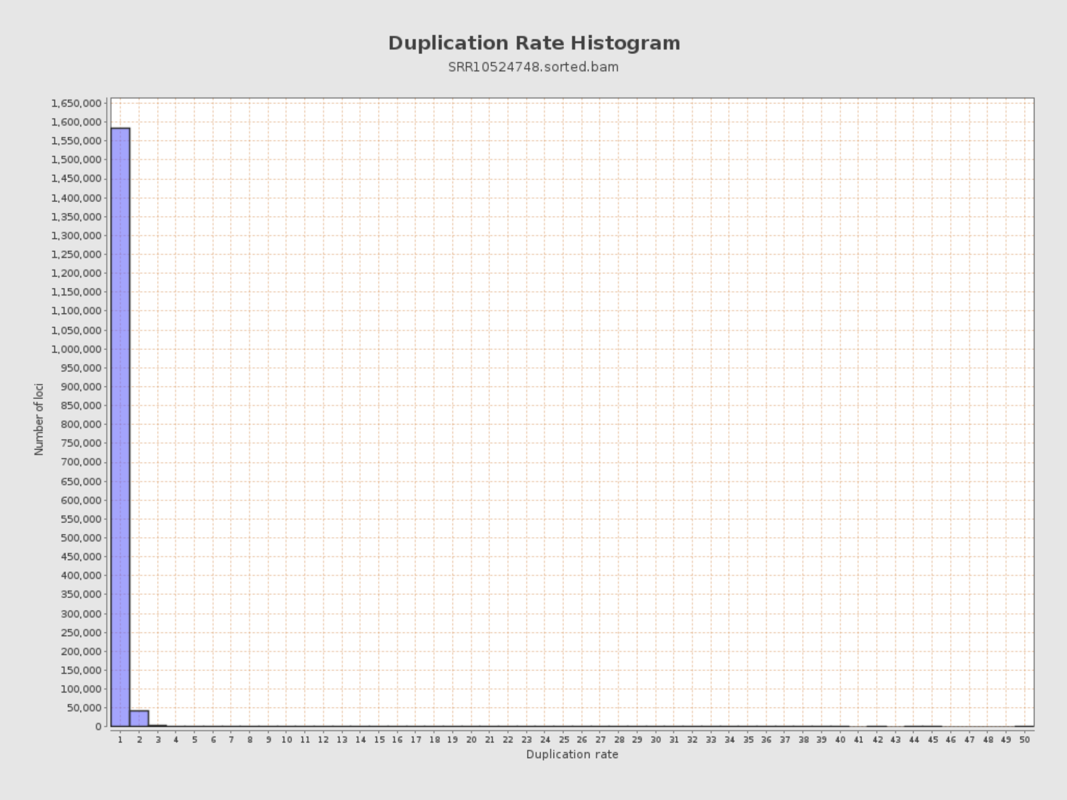
5. Results : Coverage Histogram (0-50X)



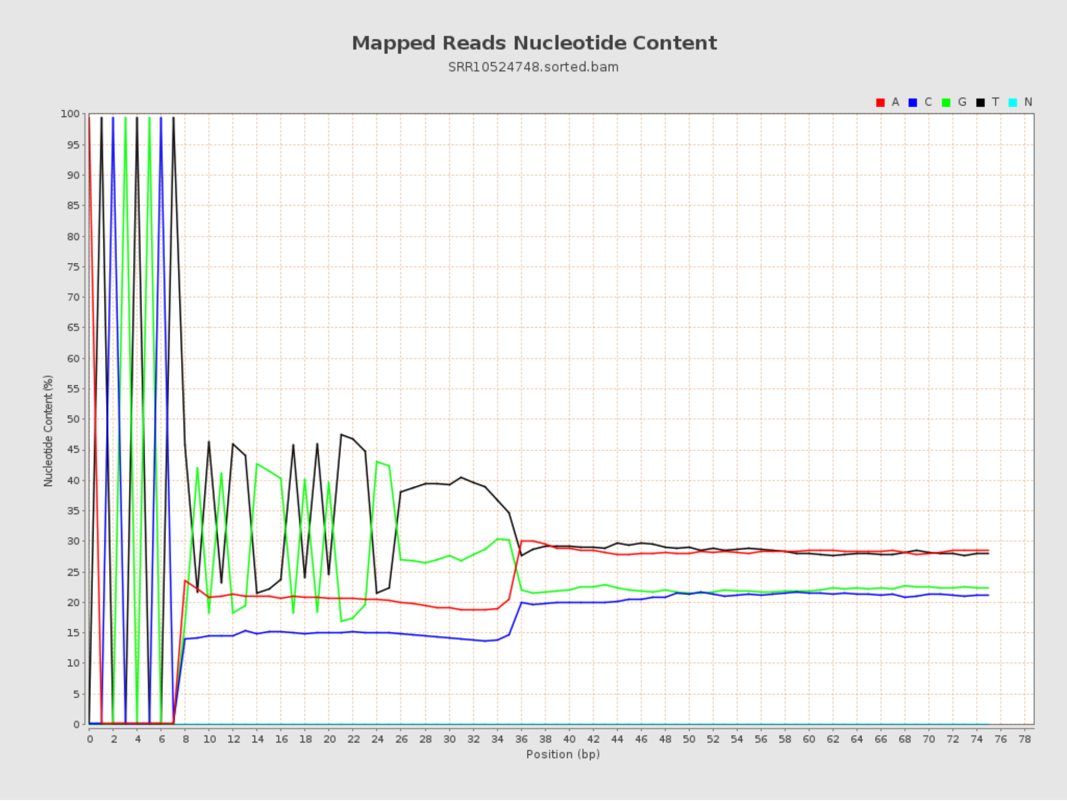
6. Results : Genome Fraction Coverage



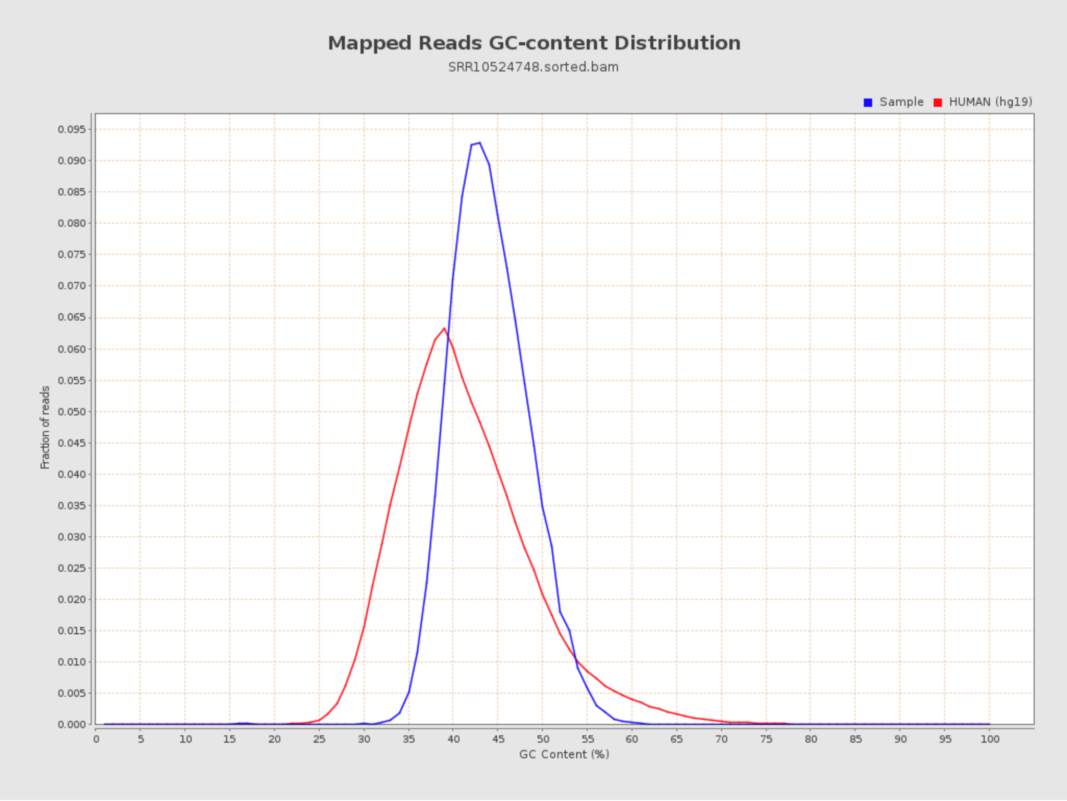
7. Results : Duplication Rate Histogram



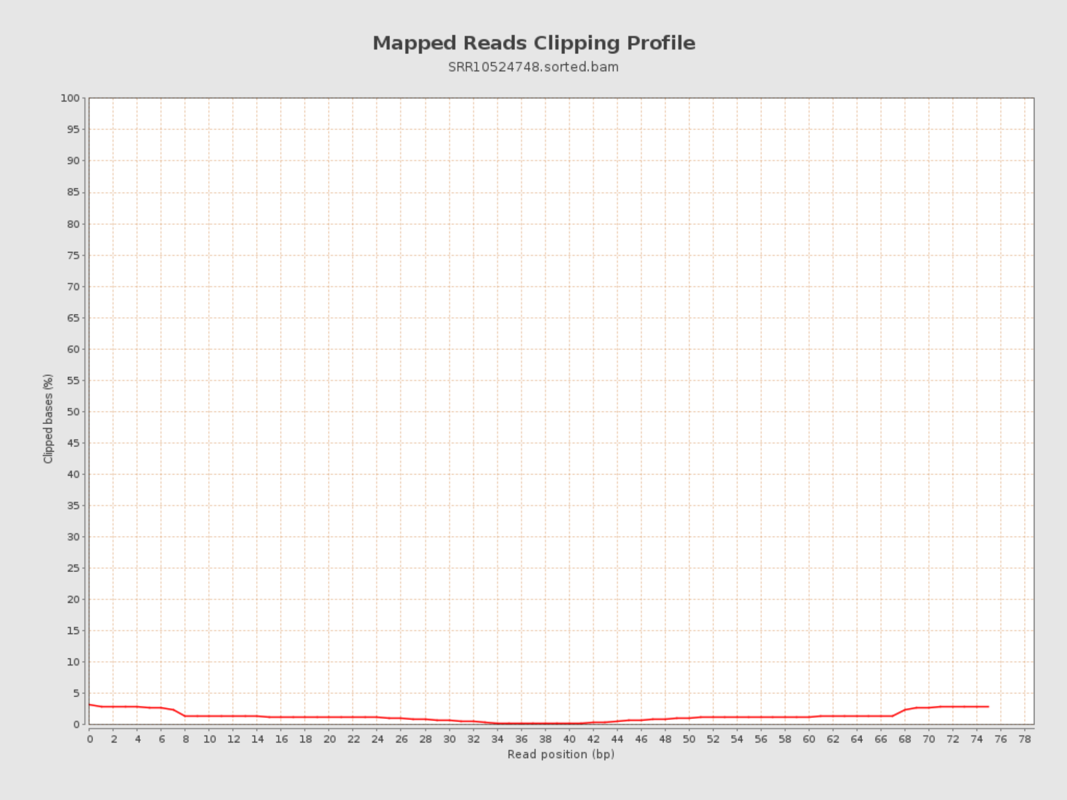
8. Results : Mapped Reads Nucleotide Content



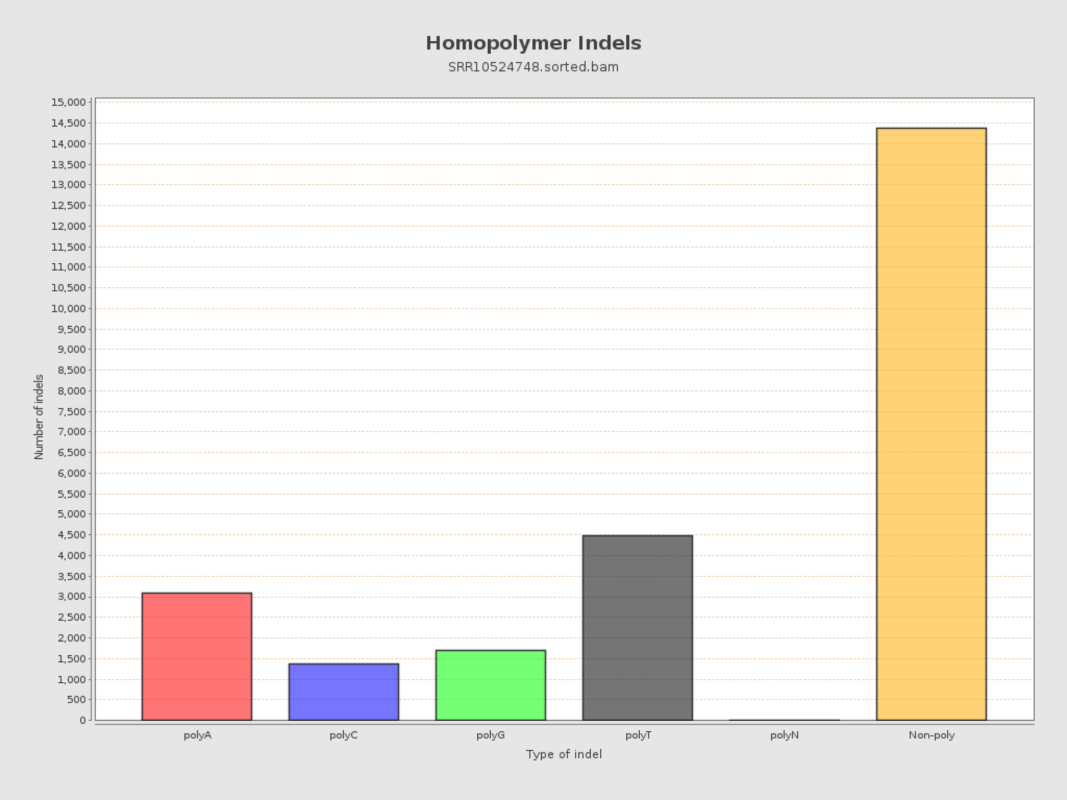
9. Results : Mapped Reads GC-content Distribution



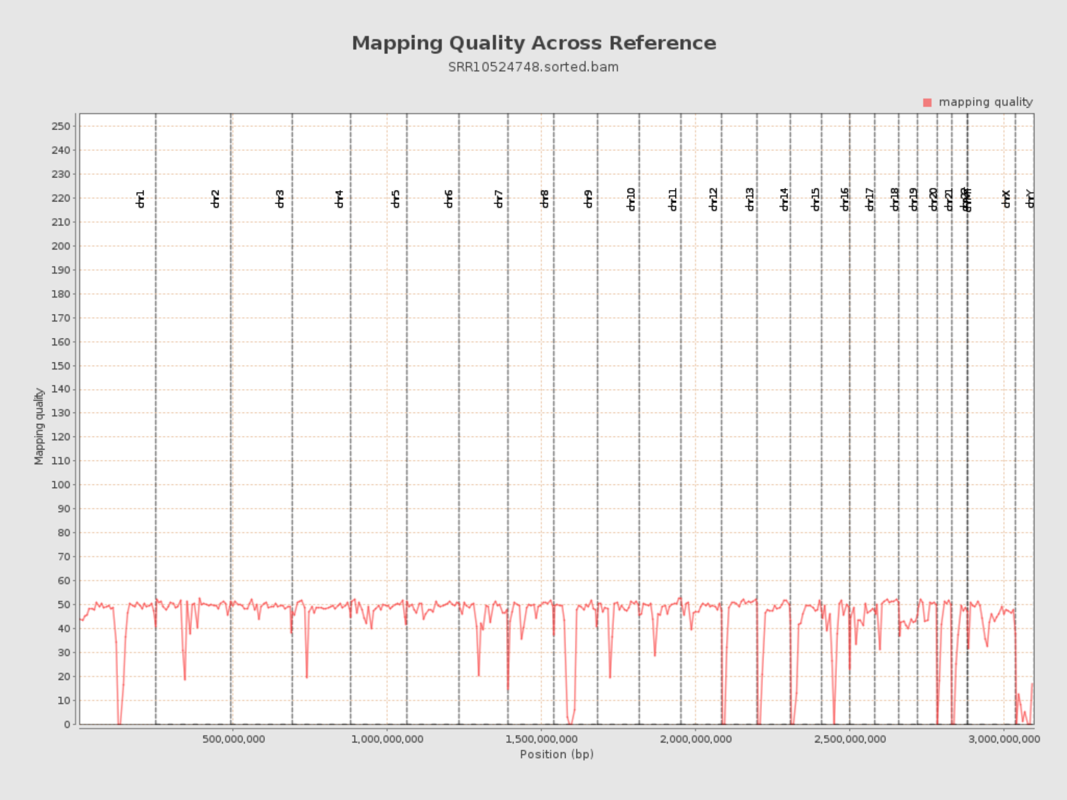
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram