Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 01:00:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524373.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_SRR10524373 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524373.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 01:00:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524373.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,681,413
Mapped reads	1,560,720 / 92.82%
Unmapped reads	120,693 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,971 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	64,061 / 3.81%
Duplication rate	3.07%
Clipped reads	1,561,433 / 92.86%

2.2. ACGT Content

Number/percentage of A's	22,179,997 / 24.15%
Number/percentage of C's	18,006,890 / 19.61%
Number/percentage of T's	29,992,282 / 32.65%
Number/percentage of G's	21,656,248 / 23.58%
Number/percentage of N's	11,703 / 0.01%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0297

Standard Deviation	0.3063

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

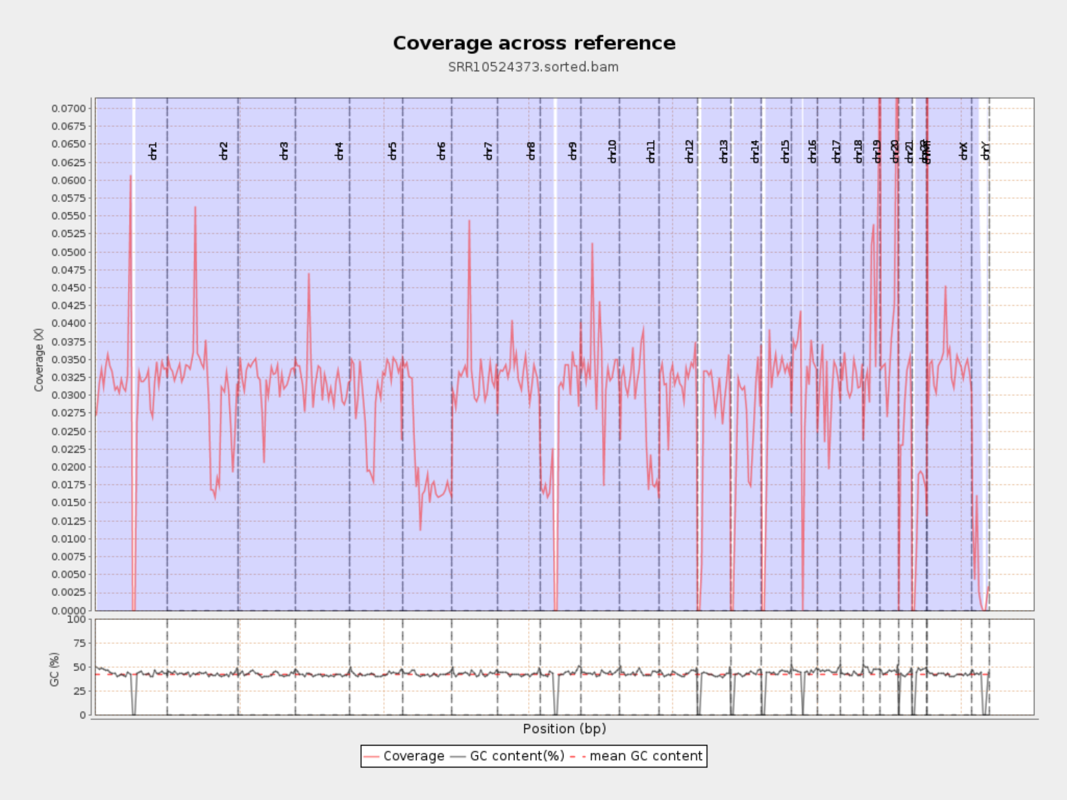
General error rate	0.5%
Mismatches	445,410
Insertions	6,587
Mapped reads with at least one insertion	0.42%
Deletions	16,631
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.02%

2.6. Chromosome stats

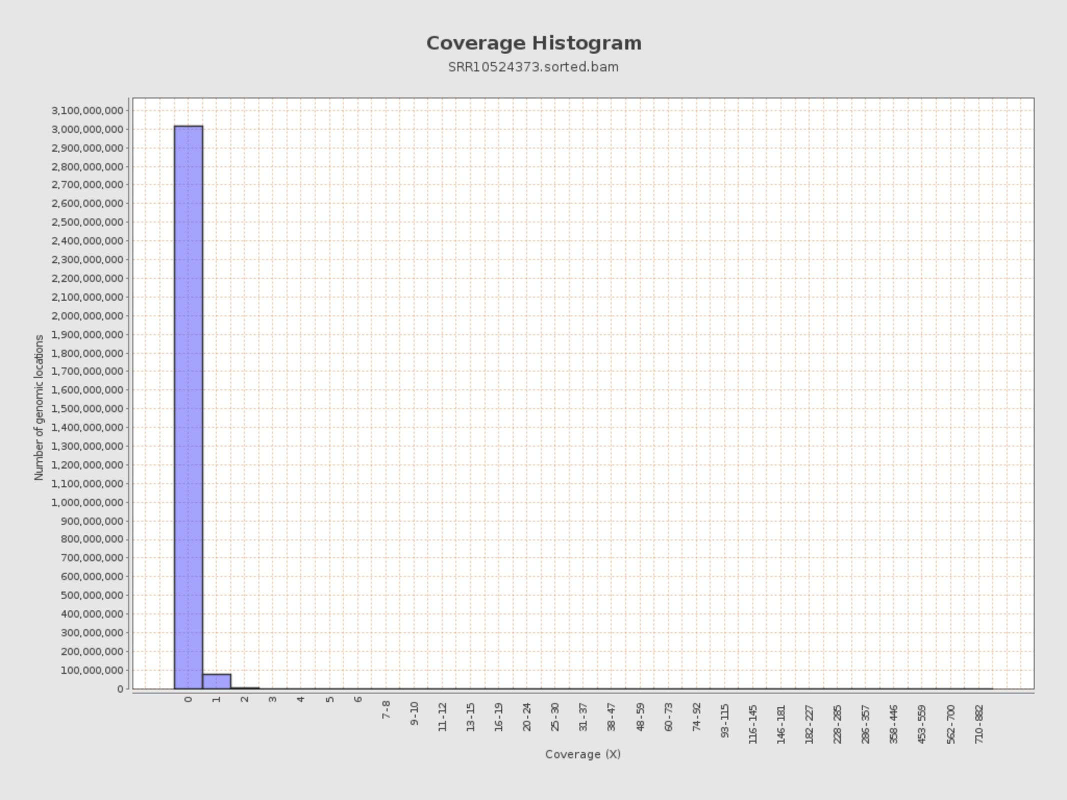
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7675348	0.0308	0.6727
chr2	243199373	7431549	0.0306	0.3286
chr3	198022430	6365789	0.0321	0.1946
chr4	191154276	6141933	0.0321	0.2179
chr5	180915260	5409262	0.0299	0.1888
chr6	171115067	3523796	0.0206	0.1681
chr7	159138663	5242946	0.0329	0.4036

chr8	146364022	4872384	0.0333	0.276
chr9	141213431	3398765	0.0241	0.2253
chr10	135534747	4591141	0.0339	0.2616
chr11	135006516	3817929	0.0283	0.2346
chr12	133851895	4314262	0.0322	0.2012
chr13	115169878	3025682	0.0263	0.1761
chr14	107349540	2540965	0.0237	0.1734
chr15	102531392	2869129	0.028	0.1818
chr16	90354753	2858011	0.0316	0.2026
chr17	81195210	2496190	0.0307	0.2132
chr18	78077248	2533828	0.0325	0.3845
chr19	59128983	2599792	0.044	0.4715
chr20	63025520	2643449	0.0419	0.2305
chr21	48129895	1261800	0.0262	0.1985
chr22	51304566	665466	0.013	0.1229
chrMT	16571	16710	1.0084	1.1667
chrX	155270560	5297740	0.0341	0.2235
chrY	59373566	279453	0.0047	0.1285

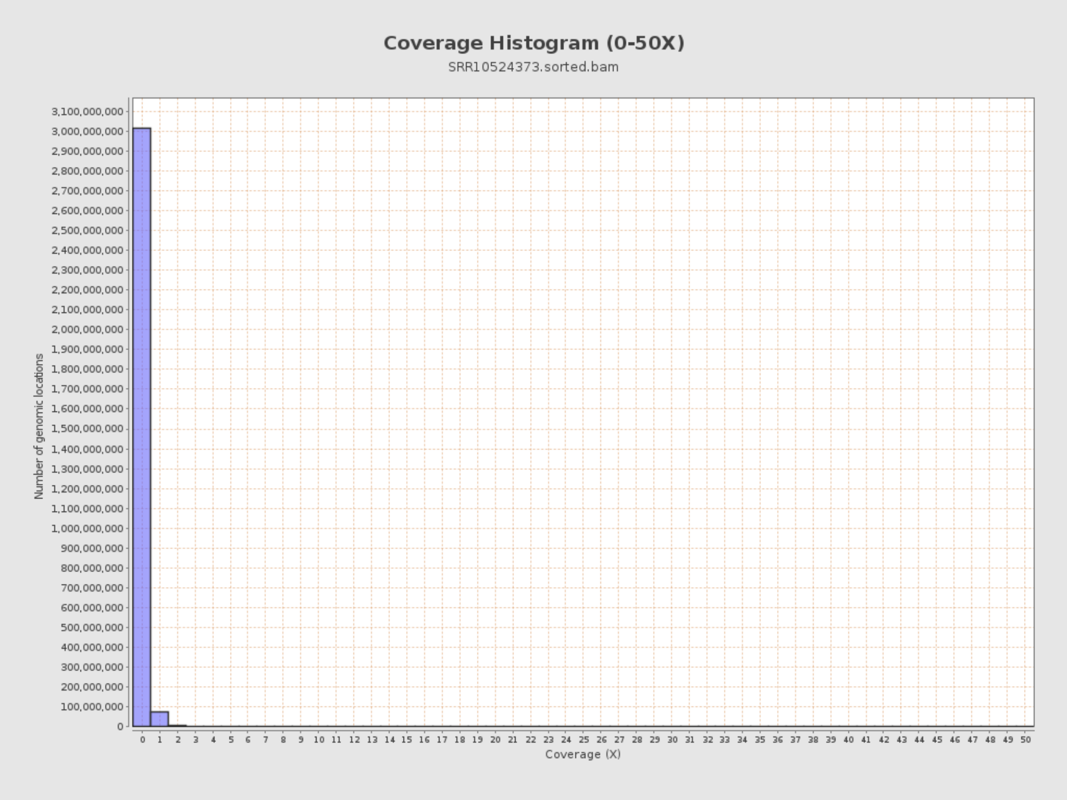
3. Results : Coverage across reference



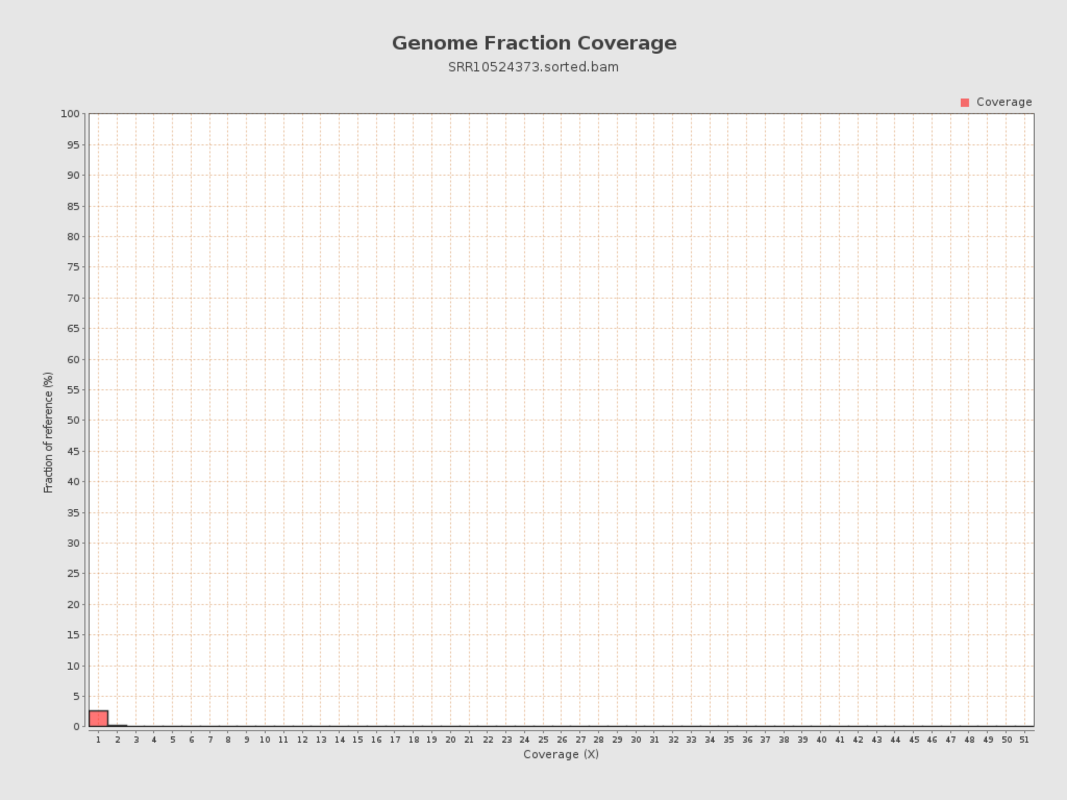
4. Results : Coverage Histogram



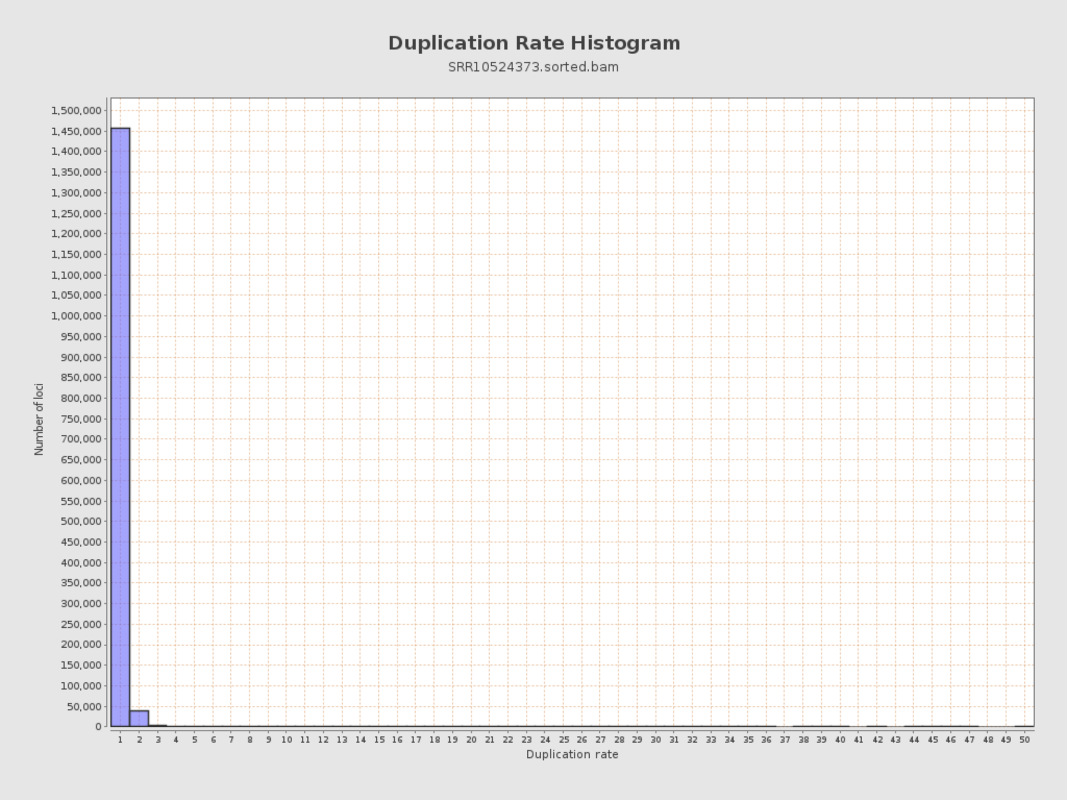
5. Results : Coverage Histogram (0-50X)



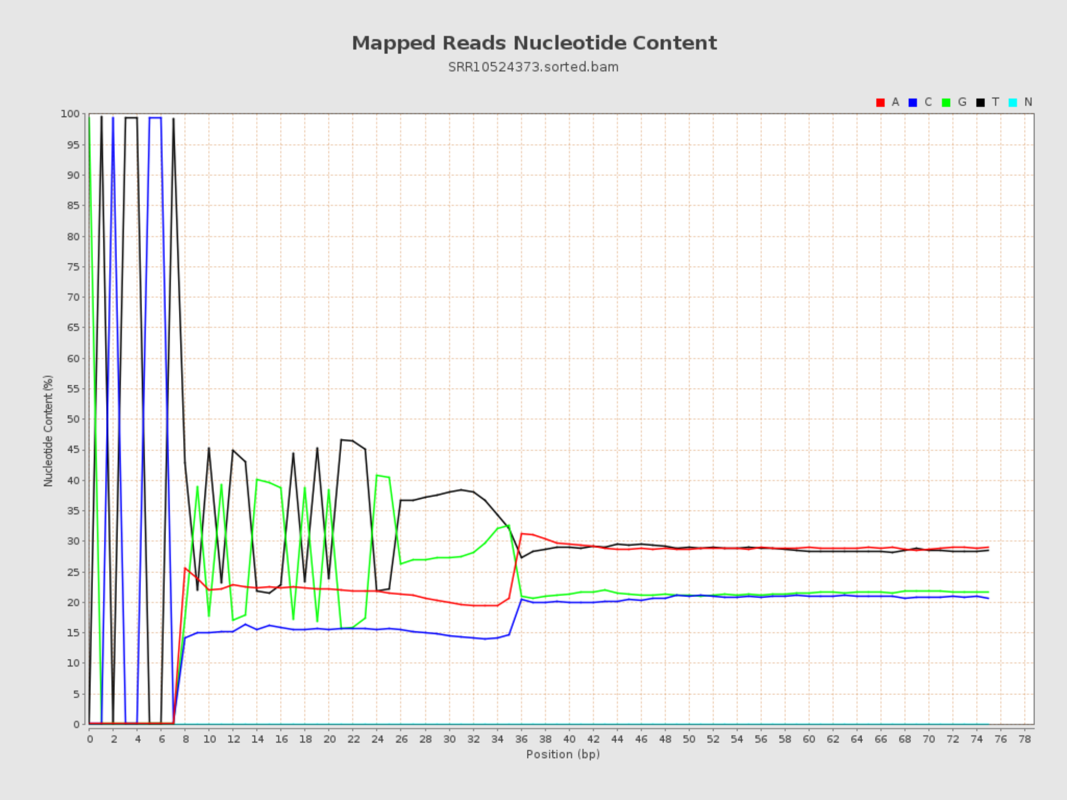
6. Results : Genome Fraction Coverage



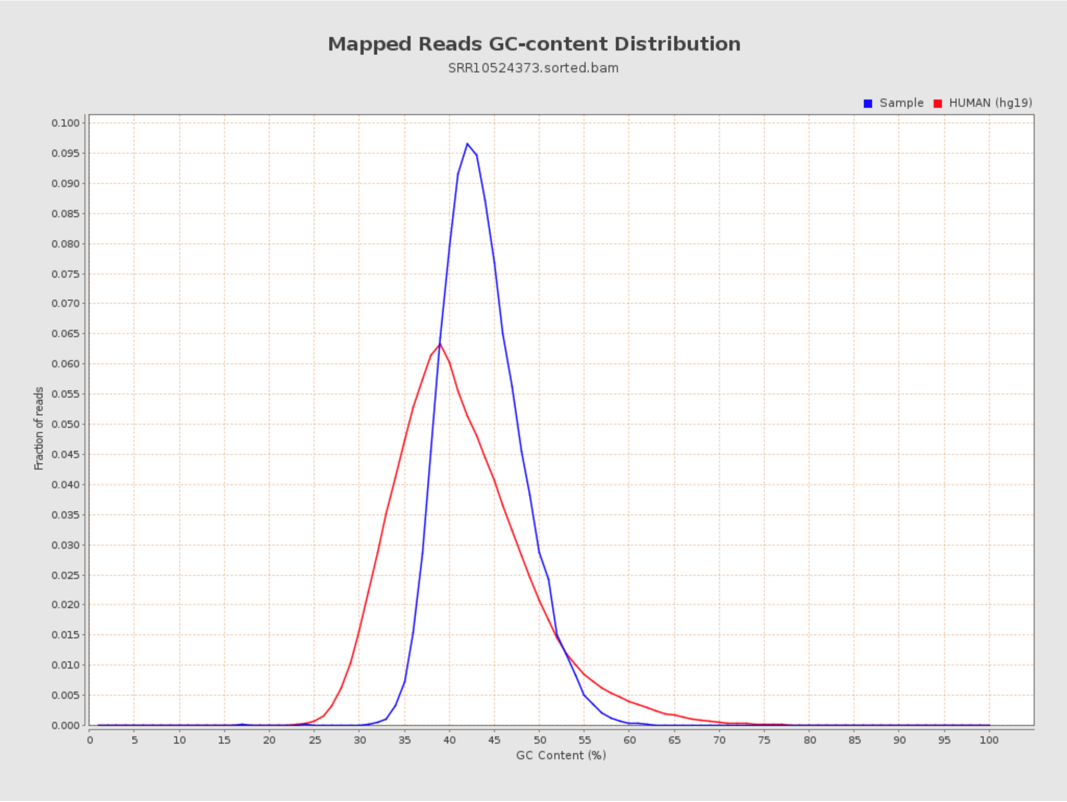
7. Results : Duplication Rate Histogram



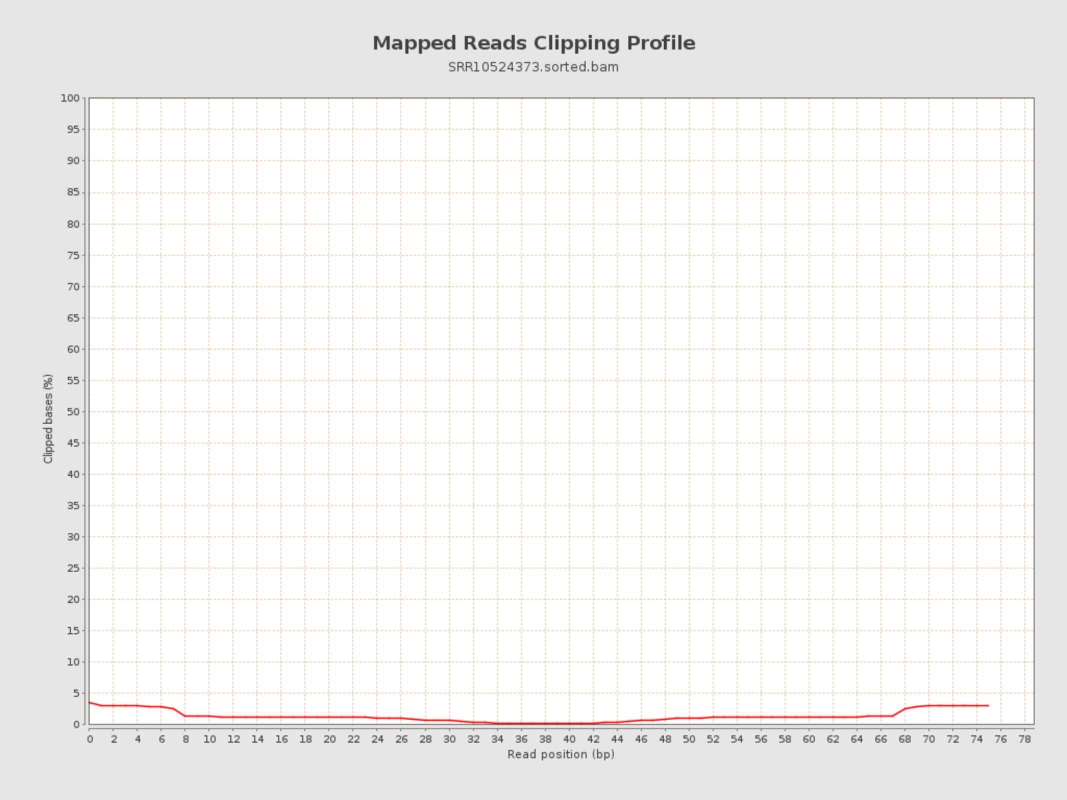
8. Results : Mapped Reads Nucleotide Content



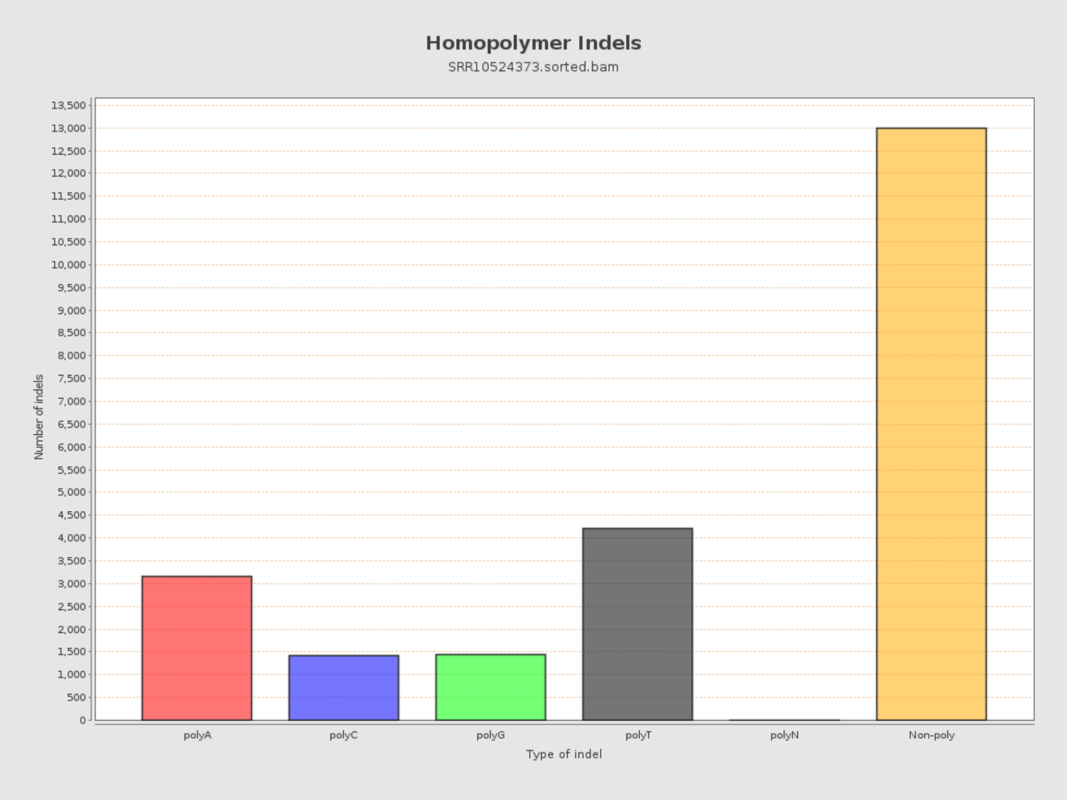
9. Results : Mapped Reads GC-content Distribution



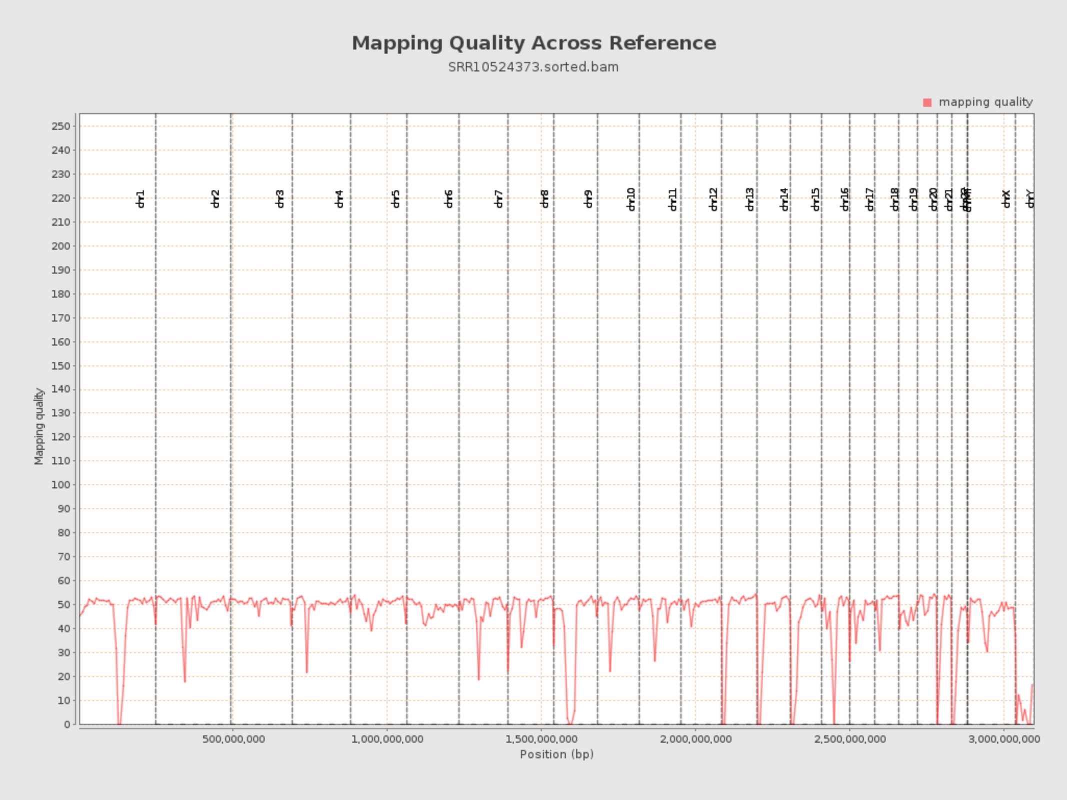
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram