Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:35:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524533.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_SRR10524533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:35:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,578,229
Mapped reads	5,130,303 / 91.97%
Unmapped reads	447,926 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,987 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	364,688 / 6.54%
Duplication rate	5.32%
Clipped reads	5,140,516 / 92.15%

2.2. ACGT Content

Number/percentage of A's	75,921,020 / 25.7%
Number/percentage of C's	57,895,639 / 19.6%
Number/percentage of T's	91,936,460 / 31.12%
Number/percentage of G's	69,659,601 / 23.58%
Number/percentage of N's	8,726 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0955

Standard Deviation	0.6938

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

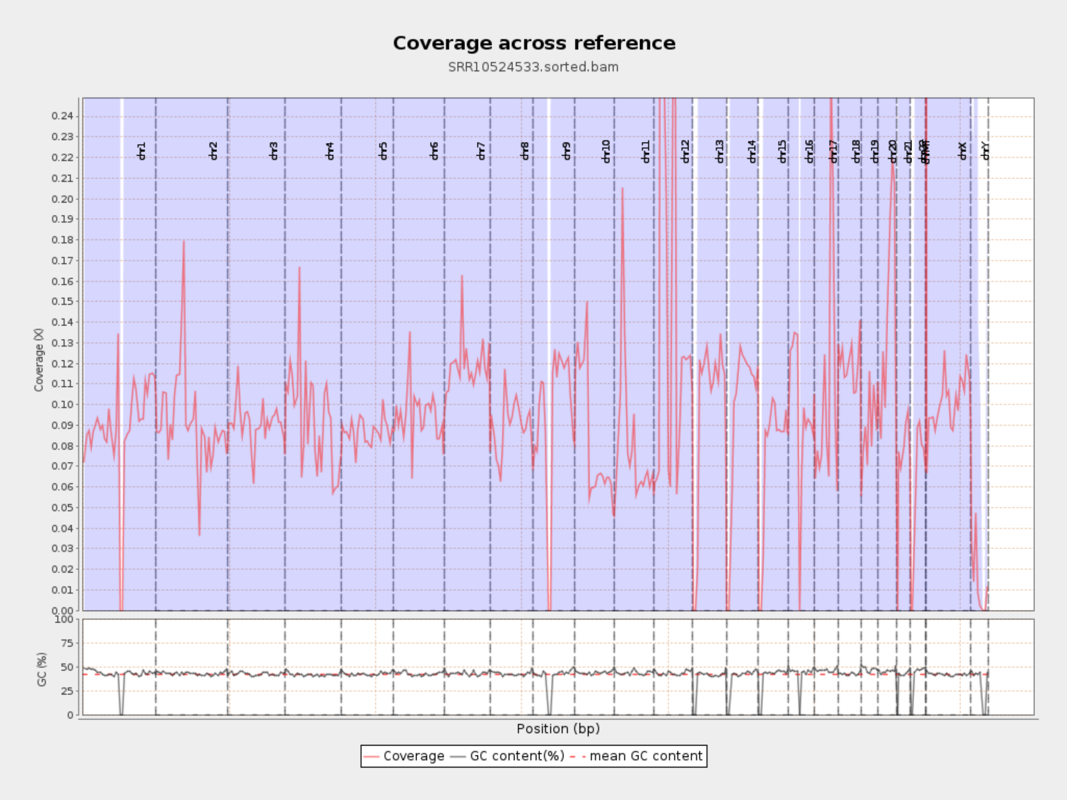
General error rate	0.48%
Mismatches	1,391,856
Insertions	18,232
Mapped reads with at least one insertion	0.35%
Deletions	46,617
Mapped reads with at least one deletion	0.9%
Homopolymer indels	43.73%

2.6. Chromosome stats

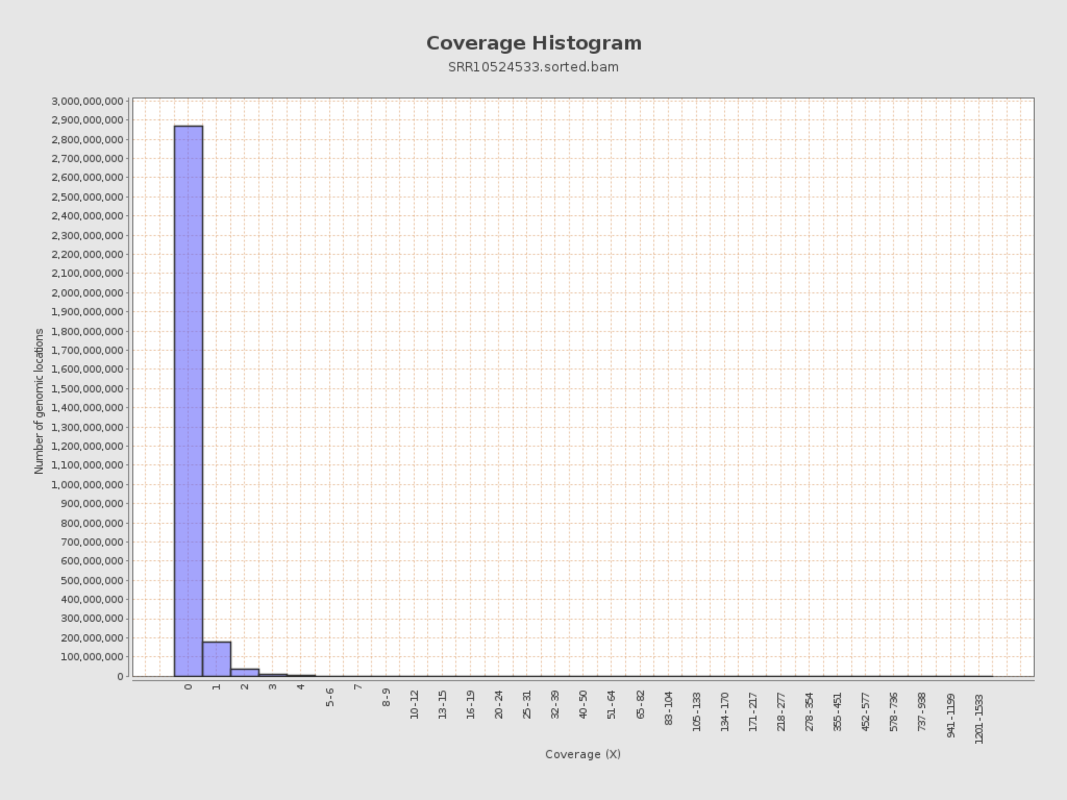
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22116148	0.0887	1.2643
chr2	243199373	22277680	0.0916	0.7811
chr3	198022430	18021984	0.091	0.3717
chr4	191154276	17848627	0.0934	0.4831
chr5	180915260	15716753	0.0869	0.3745
chr6	171115067	16335496	0.0955	0.455
chr7	159138663	18935329	0.119	0.9892

chr8	146364022	13140463	0.0898	0.6186
chr9	141213431	13424353	0.0951	0.7219
chr10	135534747	11292377	0.0833	0.6942
chr11	135006516	11110916	0.0823	0.5739
chr12	133851895	21653369	0.1618	0.6382
chr13	115169878	11298175	0.0981	0.3887
chr14	107349540	10378925	0.0967	0.4483
chr15	102531392	7518878	0.0733	0.3359
chr16	90354753	8565256	0.0948	0.4411
chr17	81195210	8923081	0.1099	0.4514
chr18	78077248	9319095	0.1194	1.3516
chr19	59128983	5280083	0.0893	0.9635
chr20	63025520	9224972	0.1464	0.5134
chr21	48129895	3558080	0.0739	0.4334
chr22	51304566	3022814	0.0589	0.298
chrMT	16571	17987	1.0855	1.4187
chrX	155270560	15704610	0.1011	0.5181
chrY	59373566	813646	0.0137	0.3041

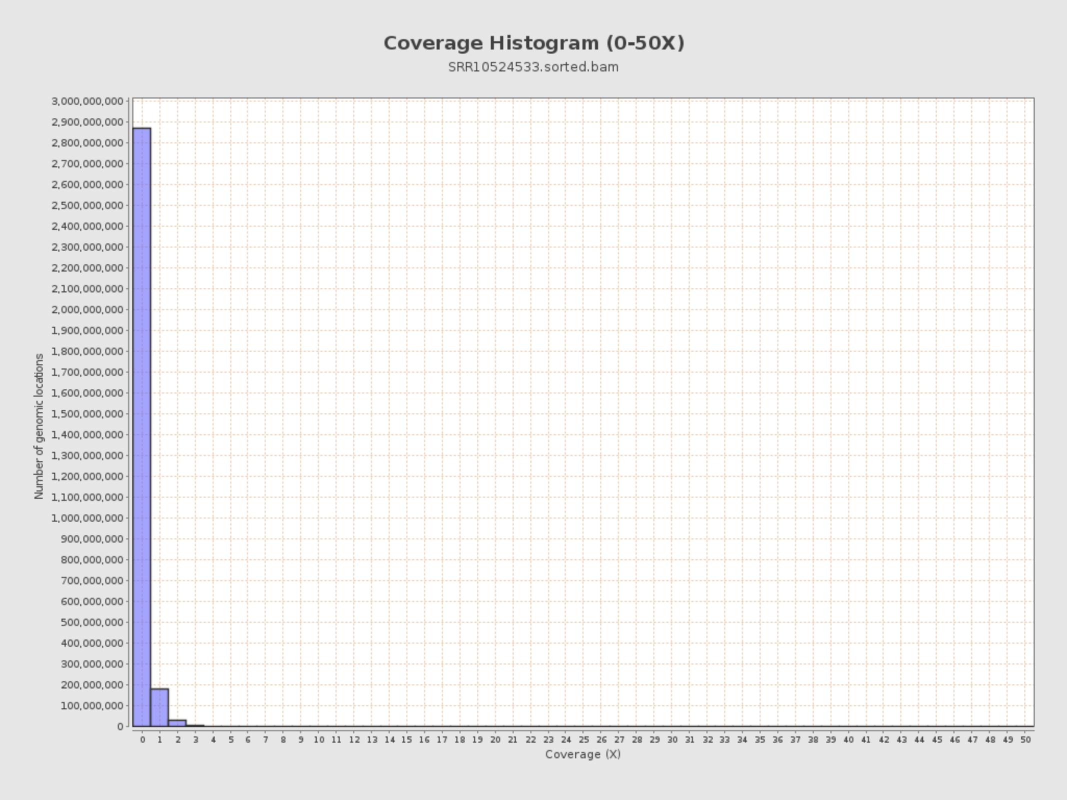
3. Results : Coverage across reference



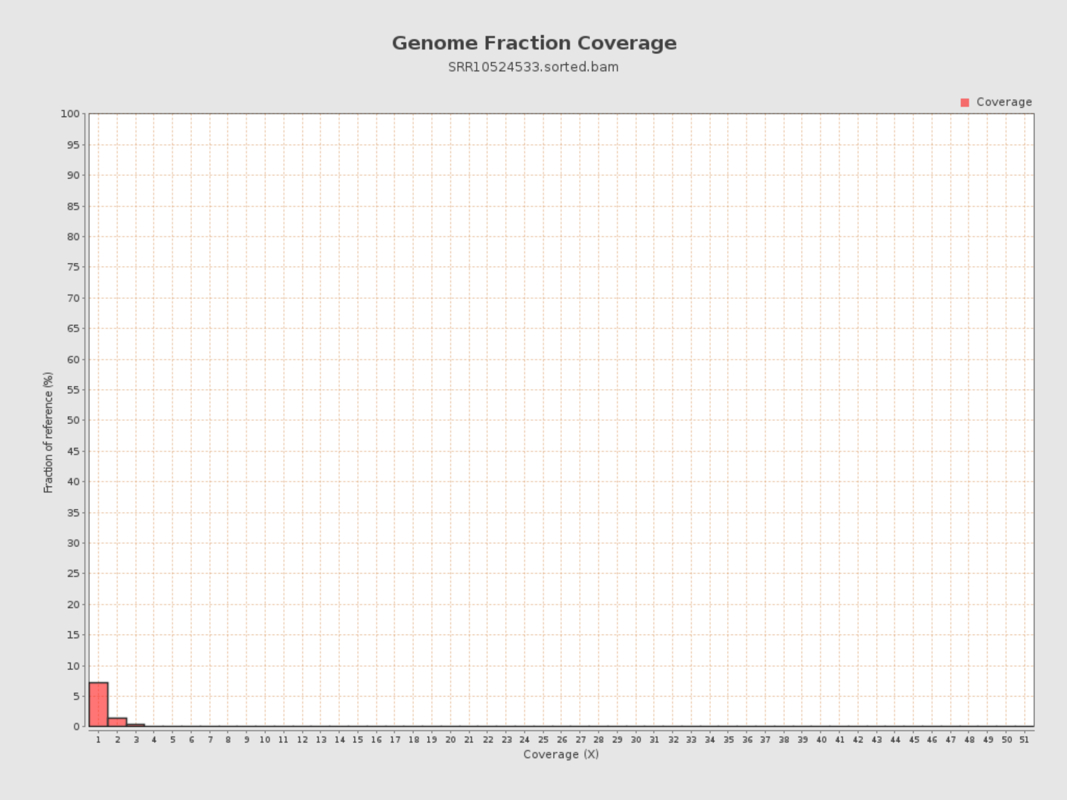
4. Results : Coverage Histogram



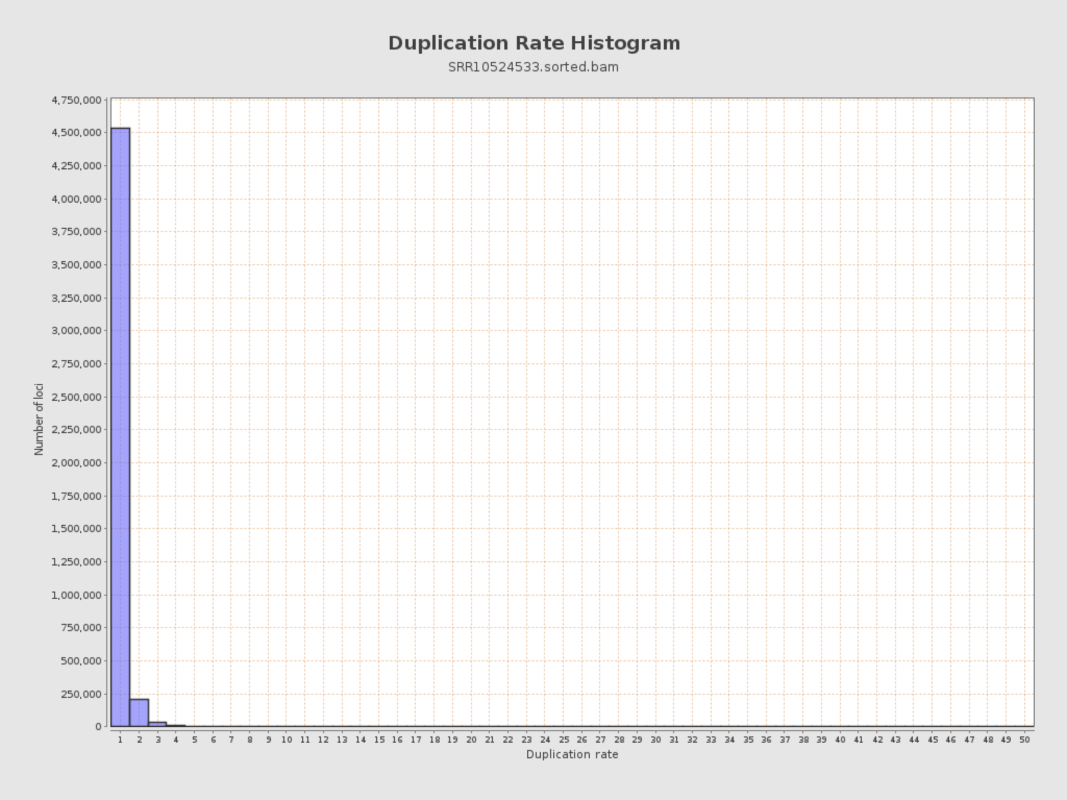
5. Results : Coverage Histogram (0-50X)



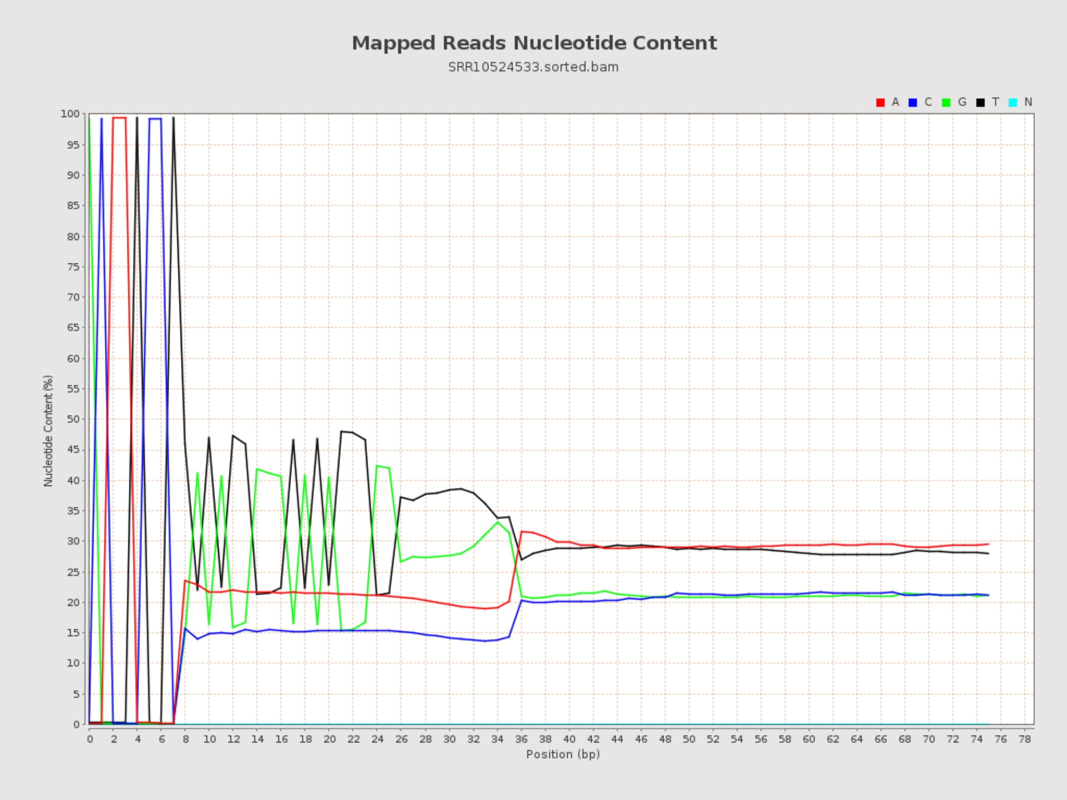
6. Results : Genome Fraction Coverage



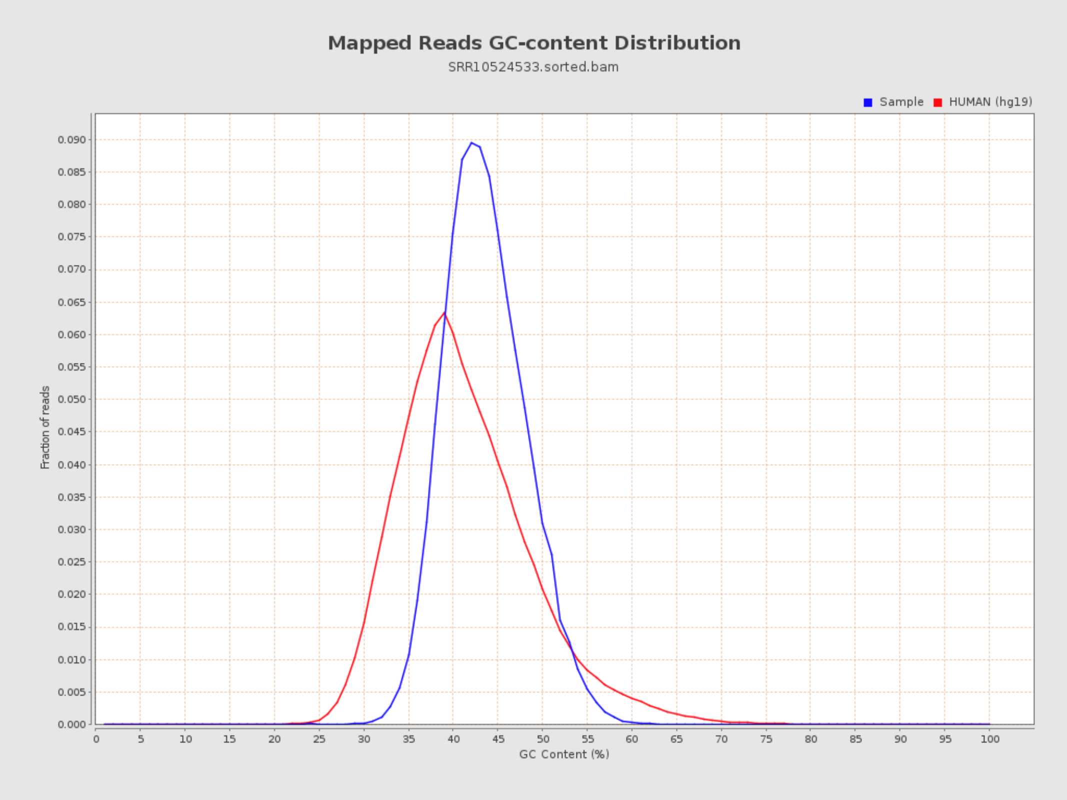
7. Results : Duplication Rate Histogram



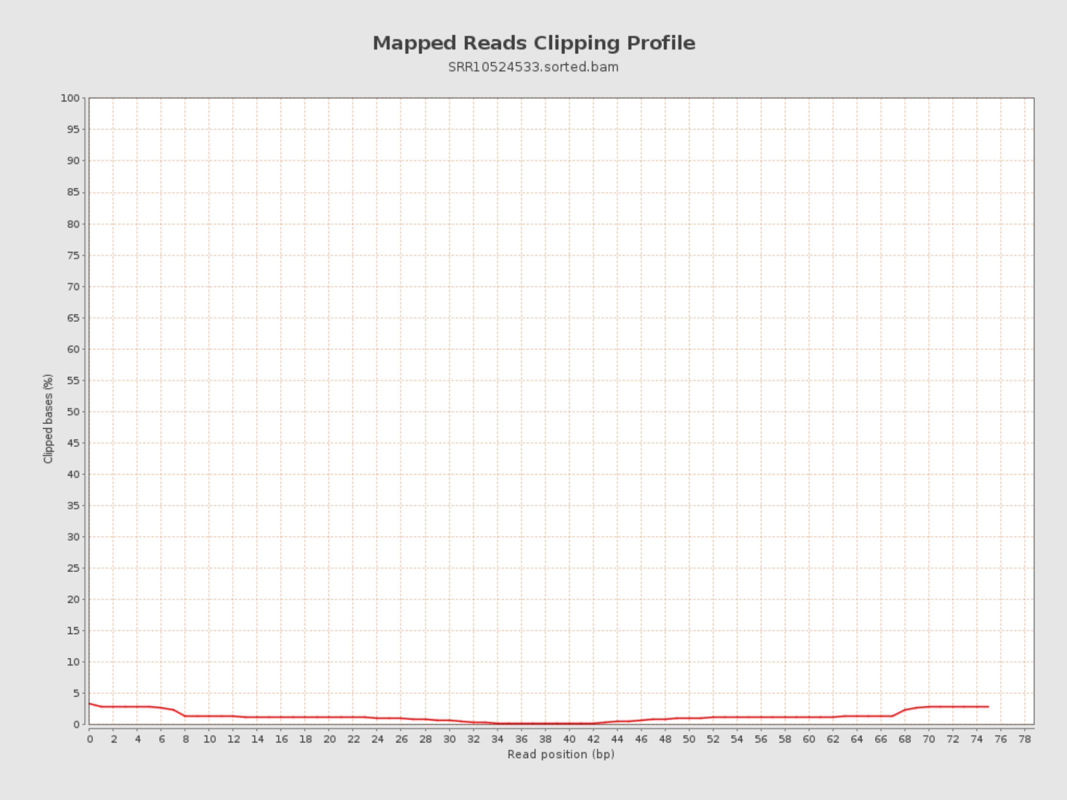
8. Results : Mapped Reads Nucleotide Content



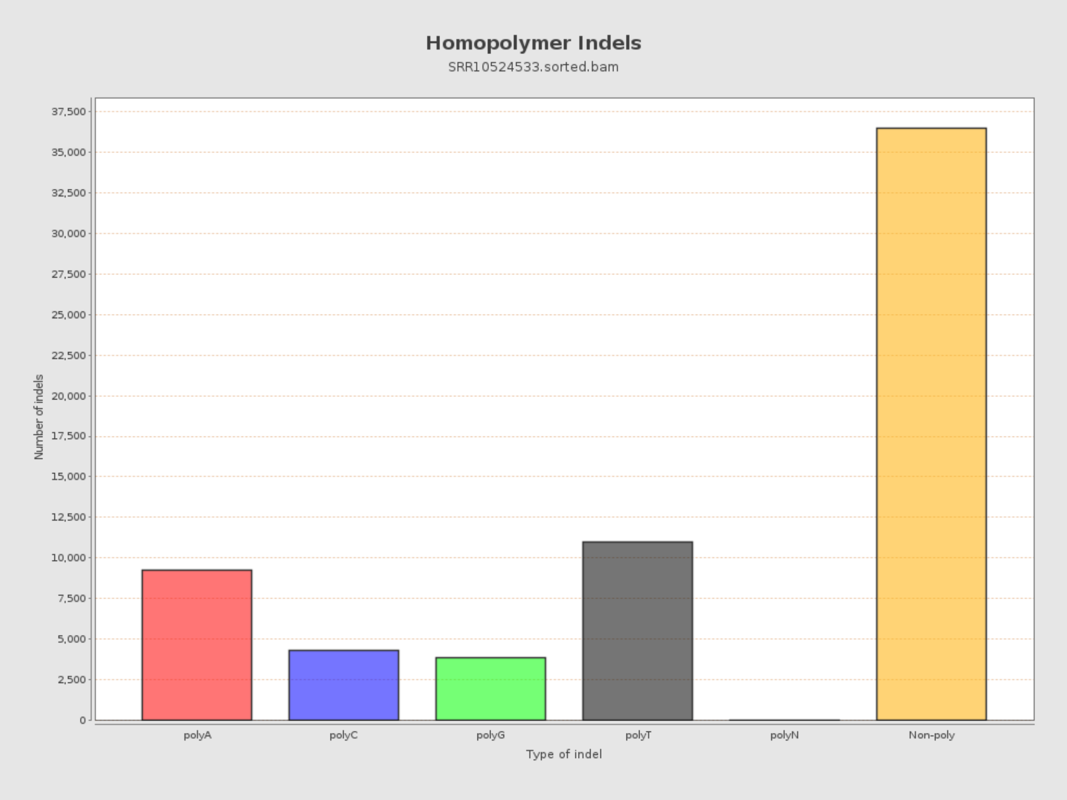
9. Results : Mapped Reads GC-content Distribution



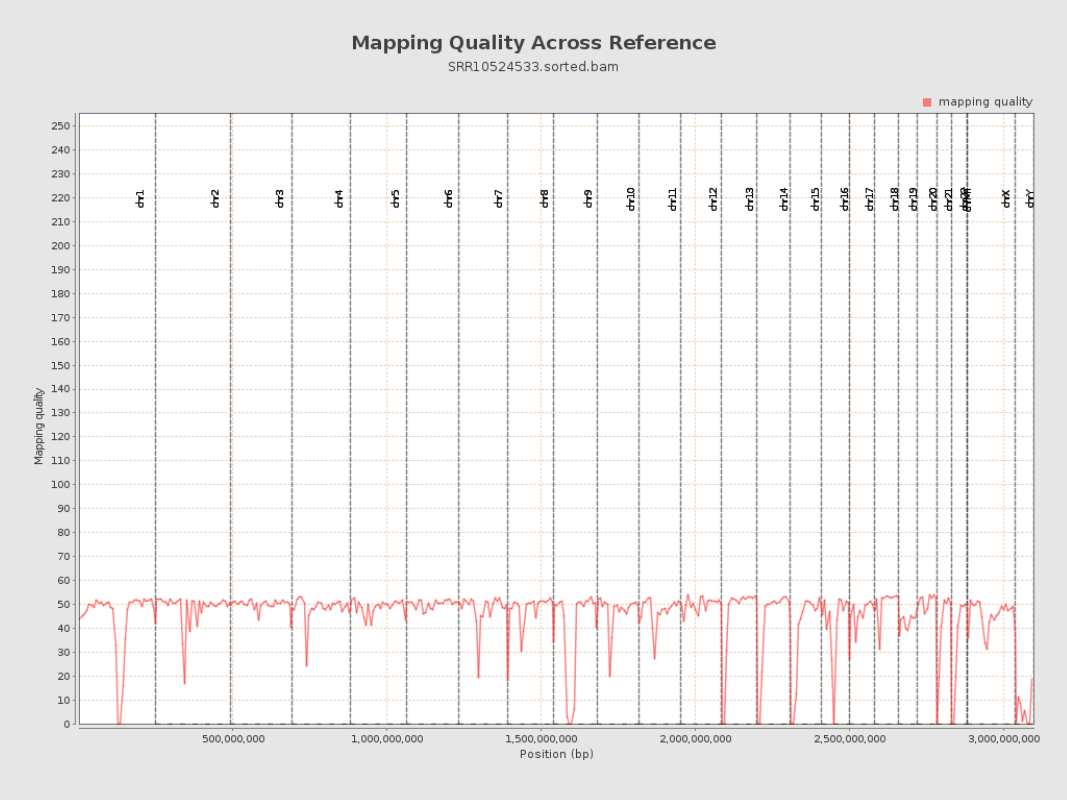
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram