Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:04:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524872.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_SRR10524872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524872.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:04:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,688,799
Mapped reads	1,563,251 / 92.57%
Unmapped reads	125,548 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,870 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	48,376 / 2.86%
Duplication rate	2.09%
Clipped reads	1,567,435 / 92.81%

2.2. ACGT Content

Number/percentage of A's	23,617,636 / 25.74%
Number/percentage of C's	17,472,684 / 19.04%
Number/percentage of T's	29,081,720 / 31.69%
Number/percentage of G's	21,573,810 / 23.51%
Number/percentage of N's	11,821 / 0.01%
GC Percentage	42.55%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.3001

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

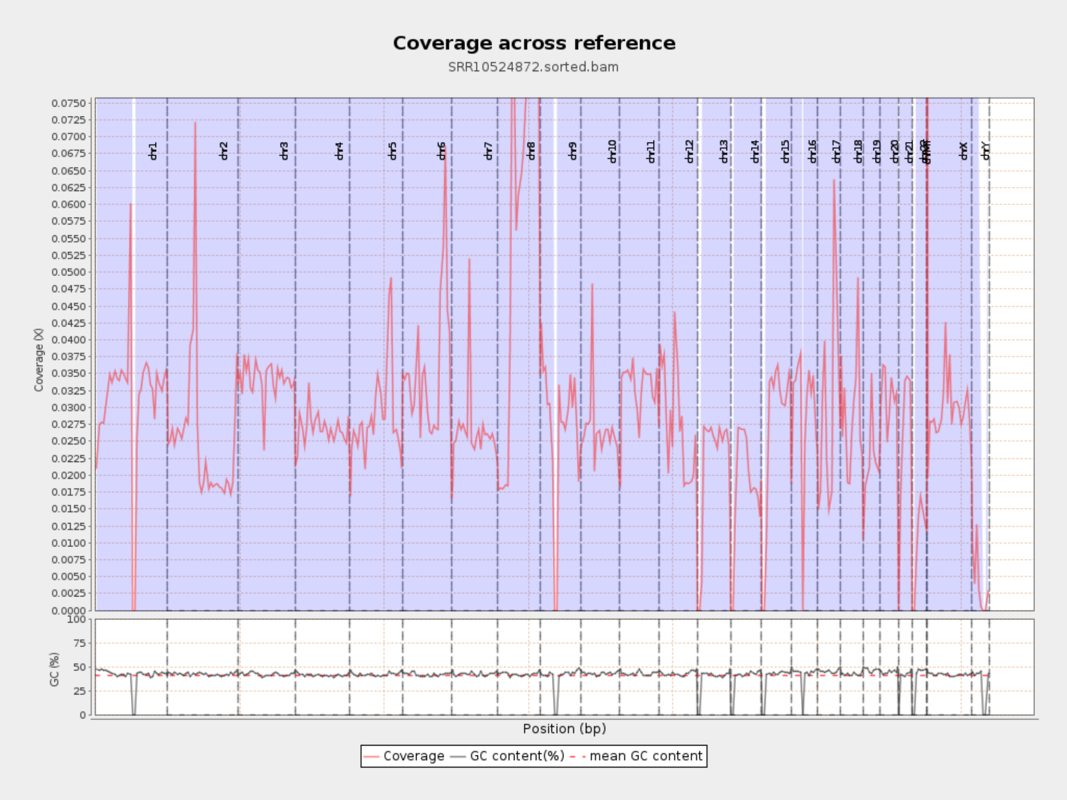
General error rate	0.49%
Mismatches	437,363
Insertions	6,117
Mapped reads with at least one insertion	0.39%
Deletions	17,143
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.88%

2.6. Chromosome stats

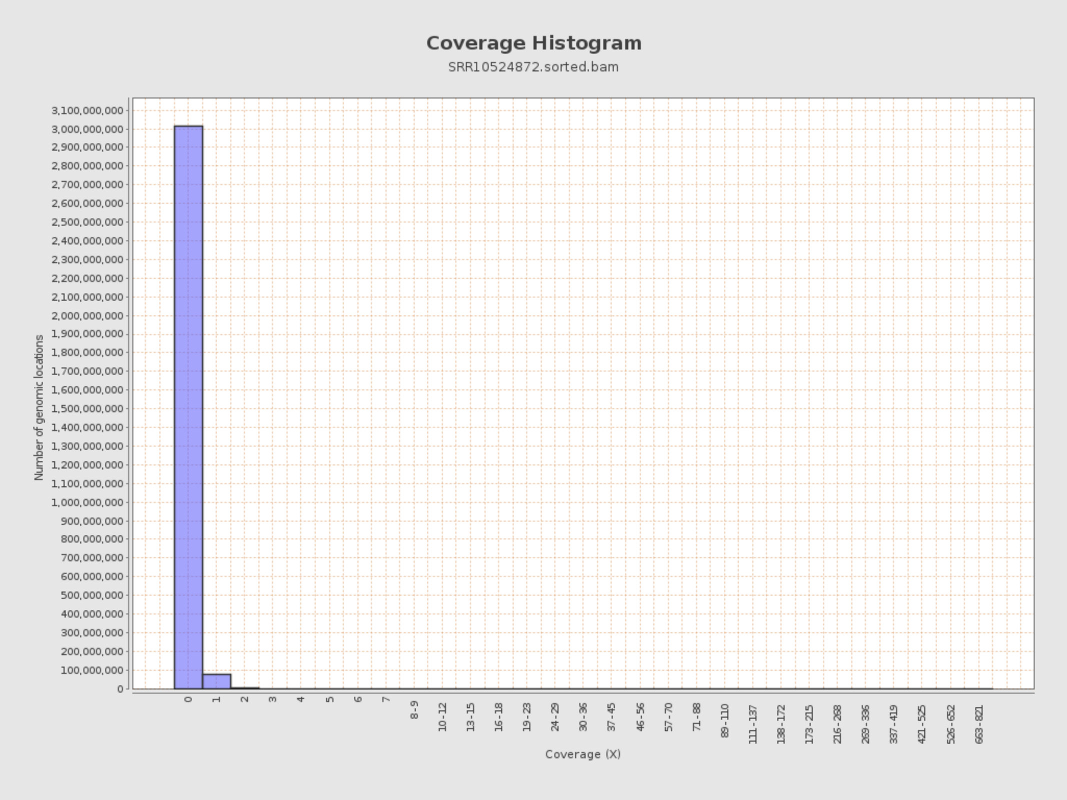
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7805038	0.0313	0.6085
chr2	243199373	6092289	0.0251	0.2801
chr3	198022430	6764767	0.0342	0.1968
chr4	191154276	5121381	0.0268	0.1865
chr5	180915260	5292562	0.0293	0.1842
chr6	171115067	6092732	0.0356	0.2216
chr7	159138663	4262966	0.0268	0.4049

chr8	146364022	10154628	0.0694	0.4191
chr9	141213431	3840133	0.0272	0.2522
chr10	135534747	3625772	0.0268	0.2567
chr11	135006516	4483818	0.0332	0.2668
chr12	133851895	3686847	0.0275	0.1831
chr13	115169878	2479116	0.0215	0.1567
chr14	107349540	1964585	0.0183	0.156
chr15	102531392	2757892	0.0269	0.1756
chr16	90354753	2624074	0.029	0.1959
chr17	81195210	2534912	0.0312	0.2137
chr18	78077248	2275527	0.0291	0.4753
chr19	59128983	1321186	0.0223	0.3889
chr20	63025520	1960404	0.0311	0.1905
chr21	48129895	1253997	0.0261	0.185
chr22	51304566	533257	0.0104	0.1069
chrMT	16571	9821	0.5927	0.8825
chrX	155270560	4618144	0.0297	0.2111
chrY	59373566	228745	0.0039	0.1038

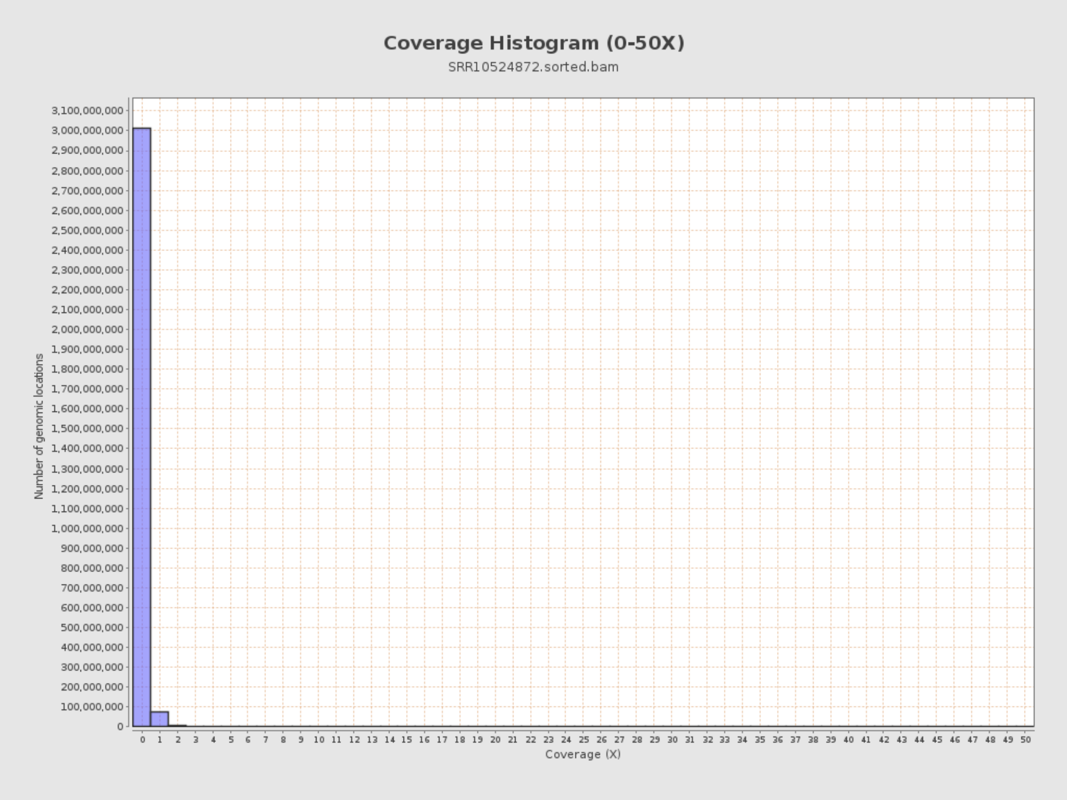
3. Results : Coverage across reference



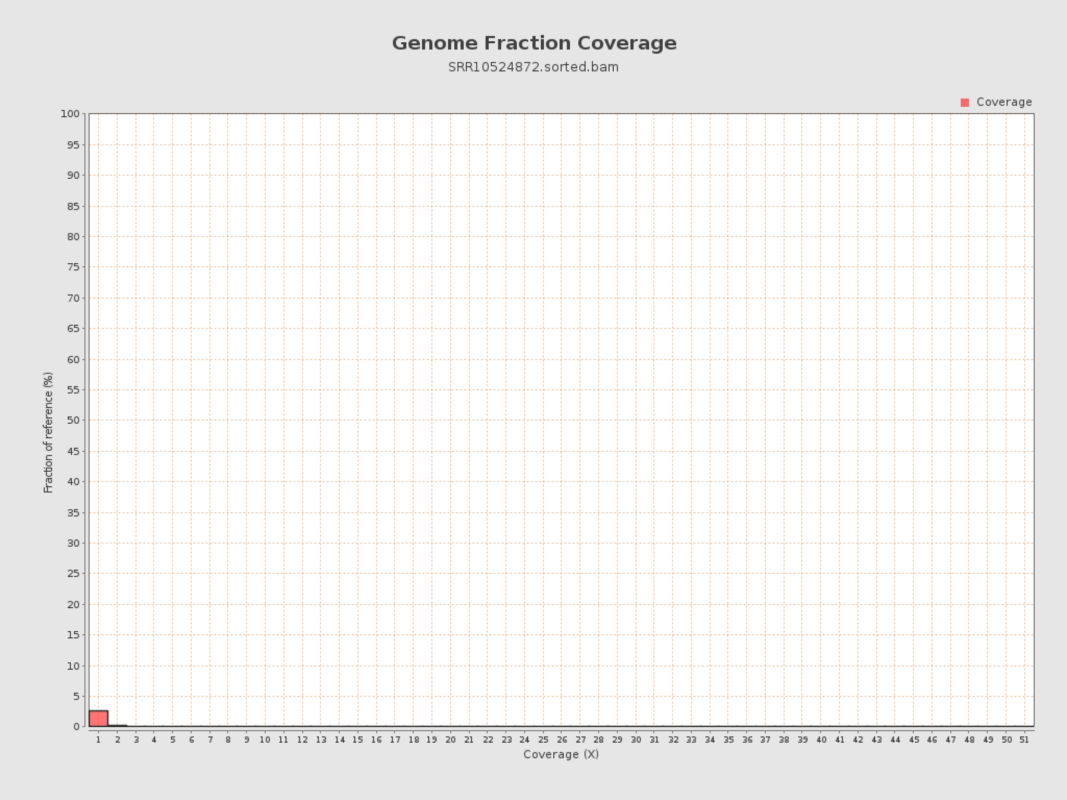
4. Results : Coverage Histogram



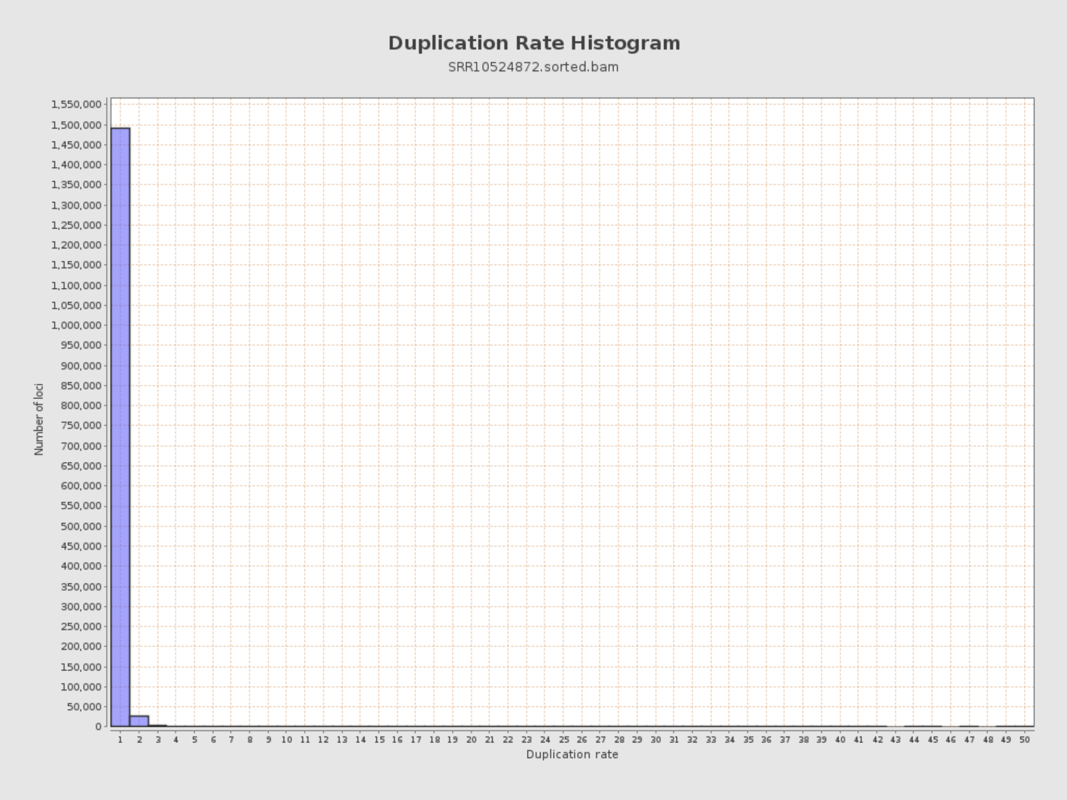
5. Results : Coverage Histogram (0-50X)



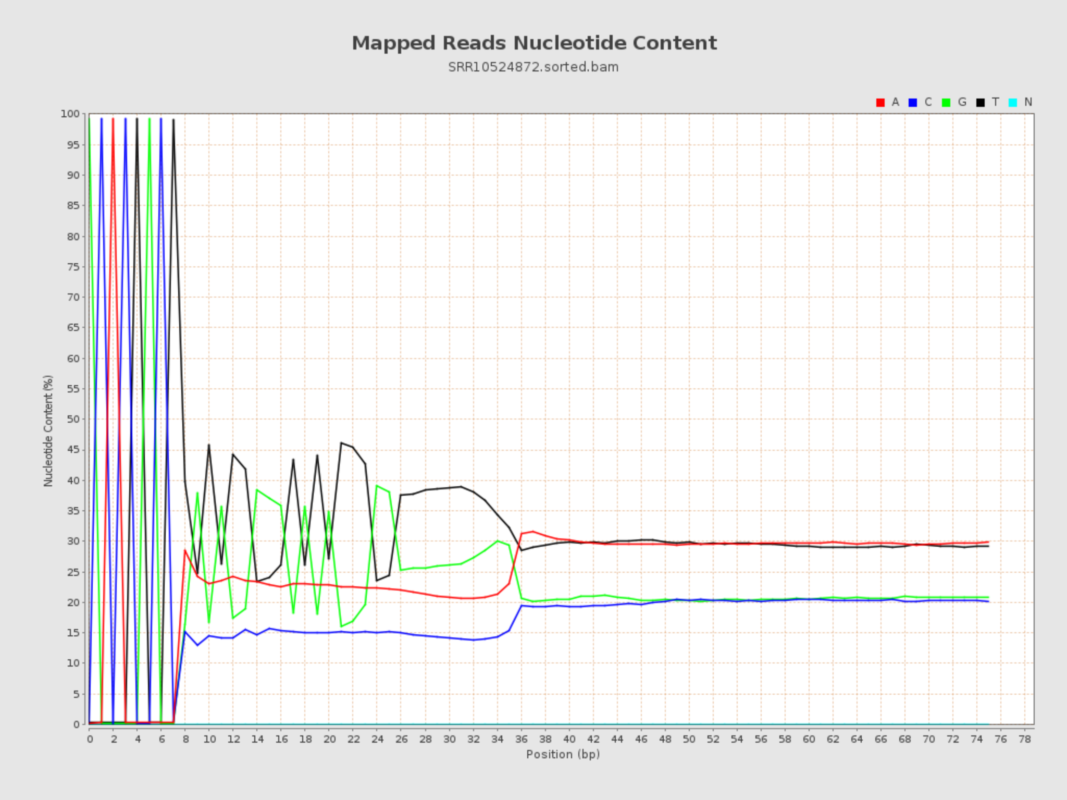
6. Results : Genome Fraction Coverage



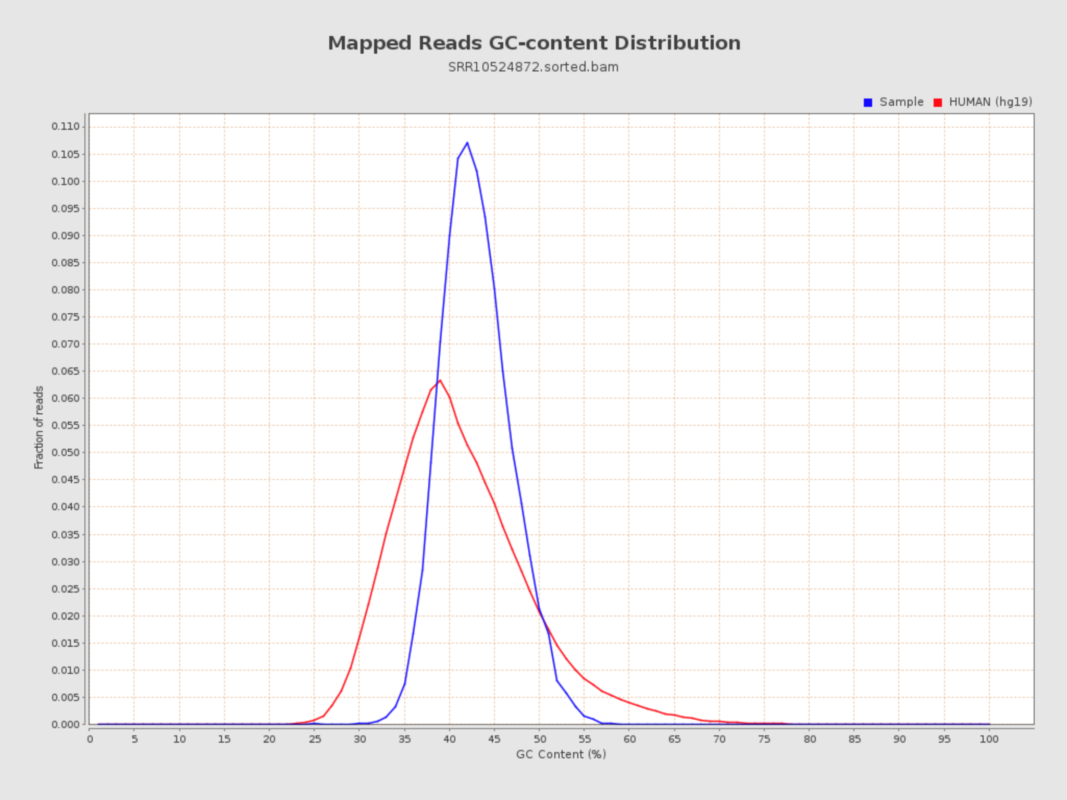
7. Results : Duplication Rate Histogram



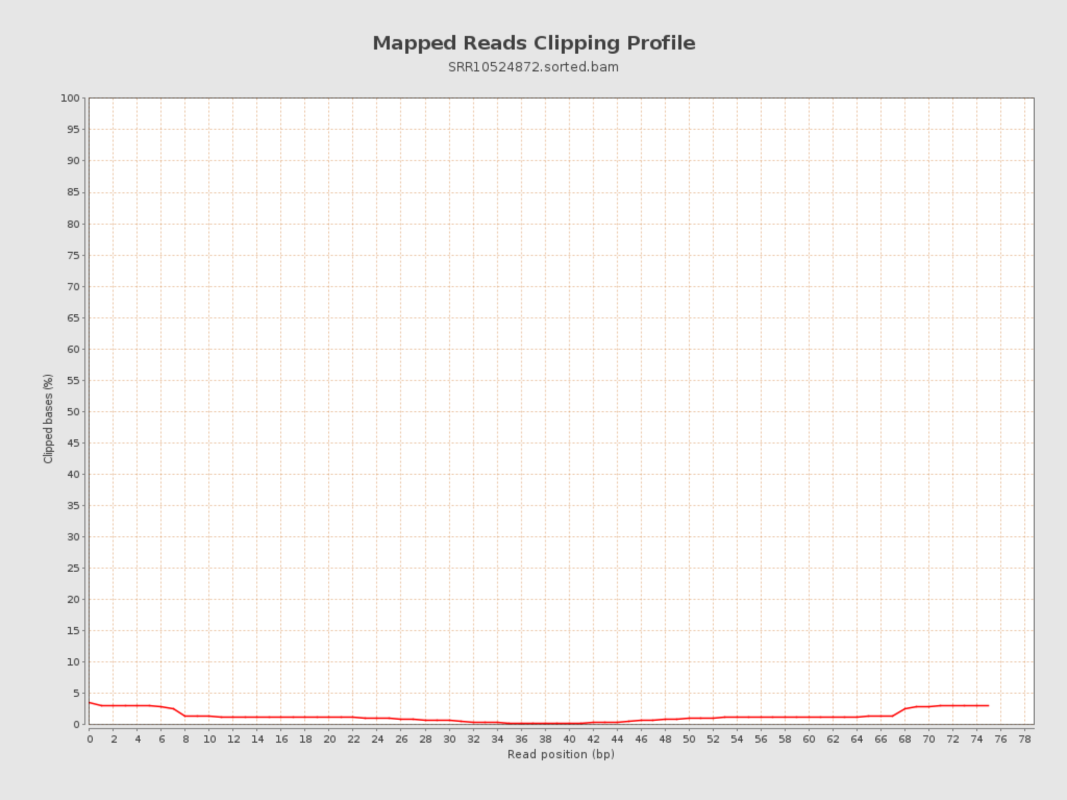
8. Results : Mapped Reads Nucleotide Content



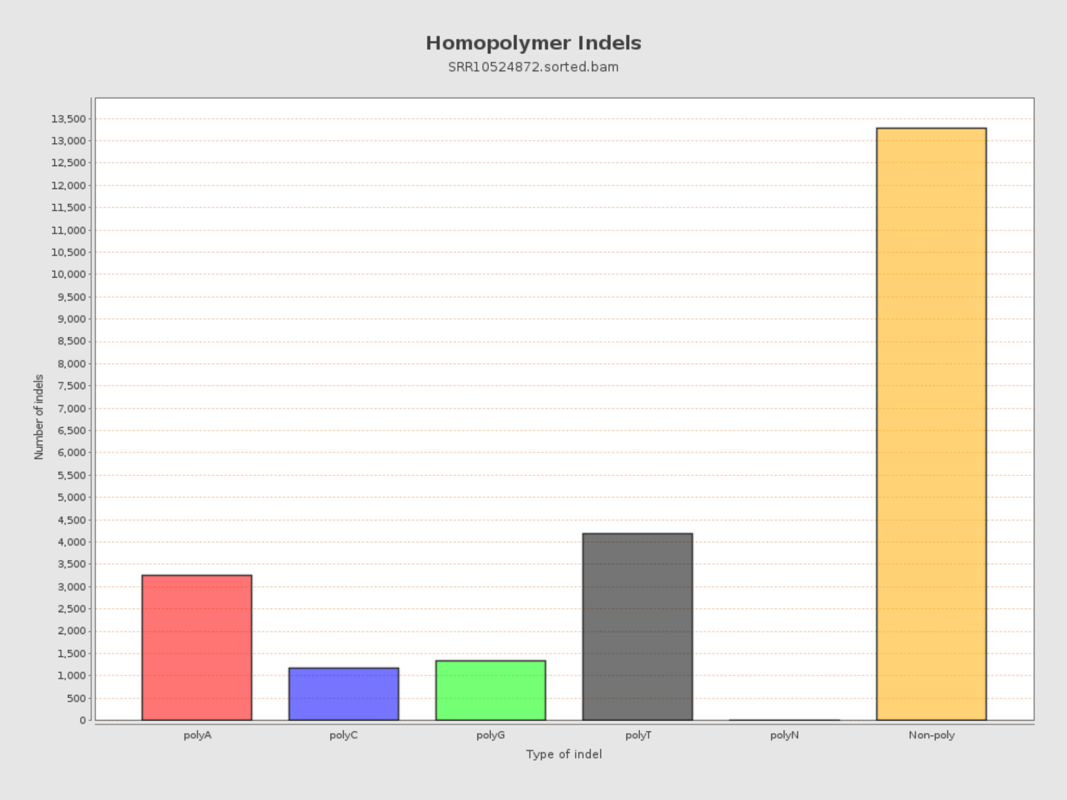
9. Results : Mapped Reads GC-content Distribution



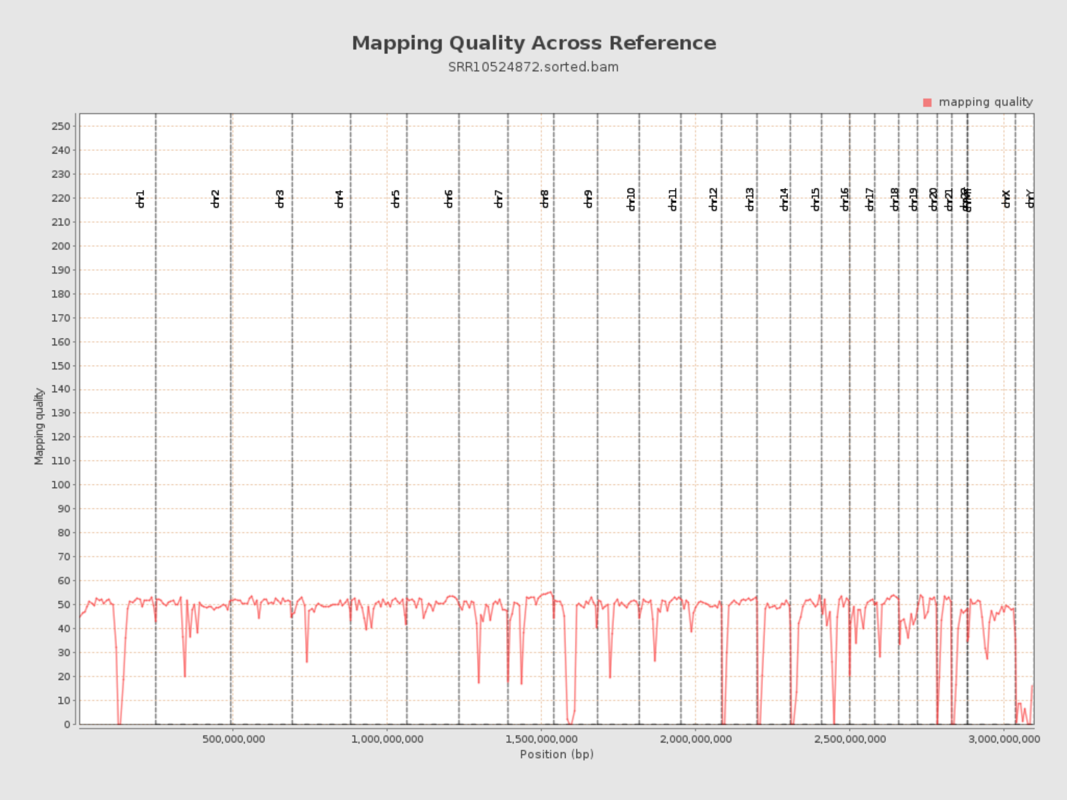
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram