Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:55:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524507.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_SRR10524507 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524507.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:55:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524507.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,259,202
Mapped reads	1,151,887 / 91.48%
Unmapped reads	107,315 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,365 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	45,383 / 3.6%
Duplication rate	3.06%
Clipped reads	1,151,423 / 91.44%

2.2. ACGT Content

Number/percentage of A's	16,357,027 / 24.59%
Number/percentage of C's	11,637,329 / 17.5%
Number/percentage of T's	22,043,964 / 33.14%
Number/percentage of G's	16,476,238 / 24.77%
Number/percentage of N's	1,206 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2138

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

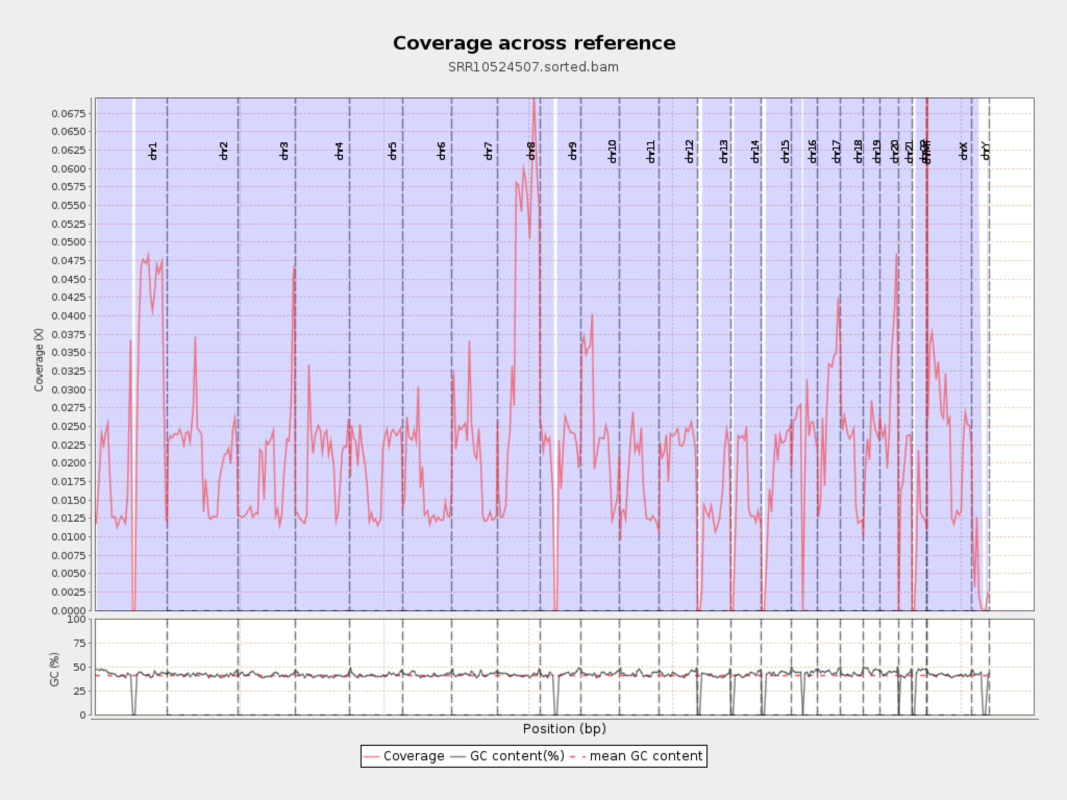
General error rate	0.48%
Mismatches	313,165
Insertions	4,125
Mapped reads with at least one insertion	0.36%
Deletions	11,955
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.31%

2.6. Chromosome stats

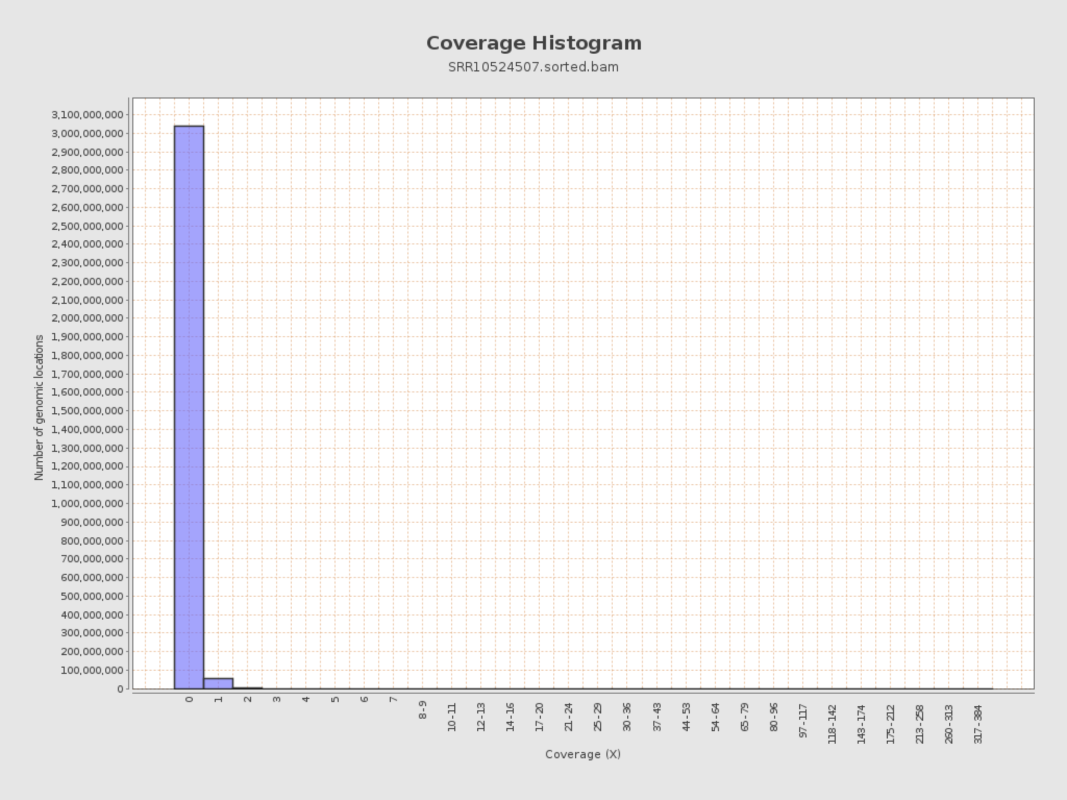
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6543057	0.0263	0.3543
chr2	243199373	5211879	0.0214	0.2488
chr3	198022430	3678897	0.0186	0.1492
chr4	191154276	3808062	0.0199	0.1739
chr5	180915260	3652324	0.0202	0.1554
chr6	171115067	2878988	0.0168	0.1711
chr7	159138663	3344162	0.021	0.2637

chr8	146364022	6151906	0.042	0.2519
chr9	141213431	2836463	0.0201	0.1928
chr10	135534747	3473960	0.0256	0.223
chr11	135006516	2274070	0.0168	0.205
chr12	133851895	3057331	0.0228	0.1659
chr13	115169878	1501409	0.013	0.1262
chr14	107349540	1602368	0.0149	0.137
chr15	102531392	1759436	0.0172	0.1497
chr16	90354753	2068921	0.0229	0.1734
chr17	81195210	2284371	0.0281	0.1904
chr18	78077248	1586591	0.0203	0.31
chr19	59128983	1364020	0.0231	0.2634
chr20	63025520	1920741	0.0305	0.1926
chr21	48129895	896317	0.0186	0.1584
chr22	51304566	539995	0.0105	0.1112
chrMT	16571	3941	0.2378	0.5582
chrX	155270560	3880330	0.025	0.189
chrY	59373566	216765	0.0037	0.0997

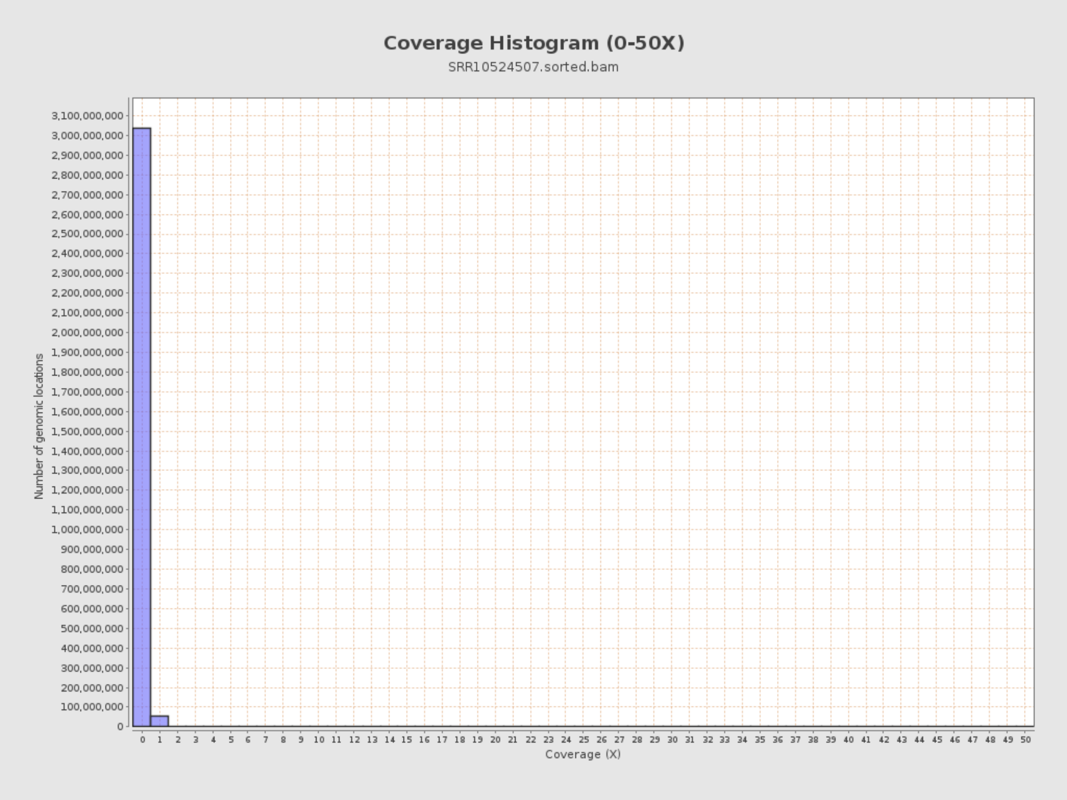
3. Results : Coverage across reference



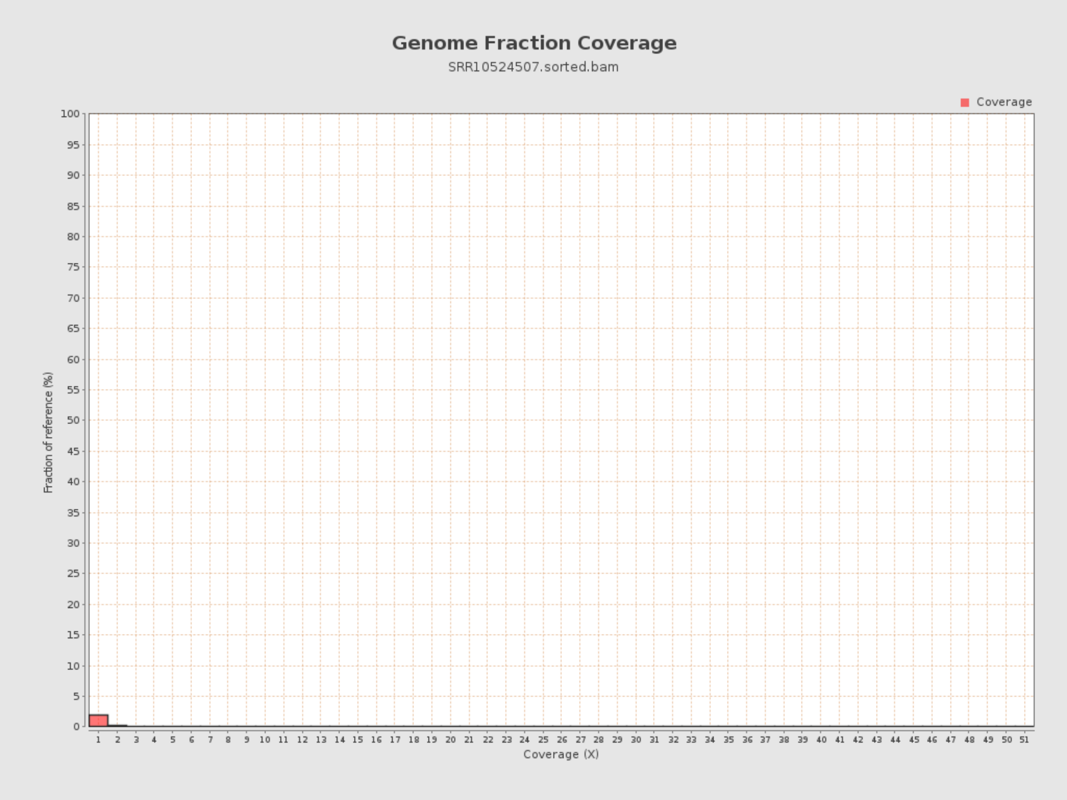
4. Results : Coverage Histogram



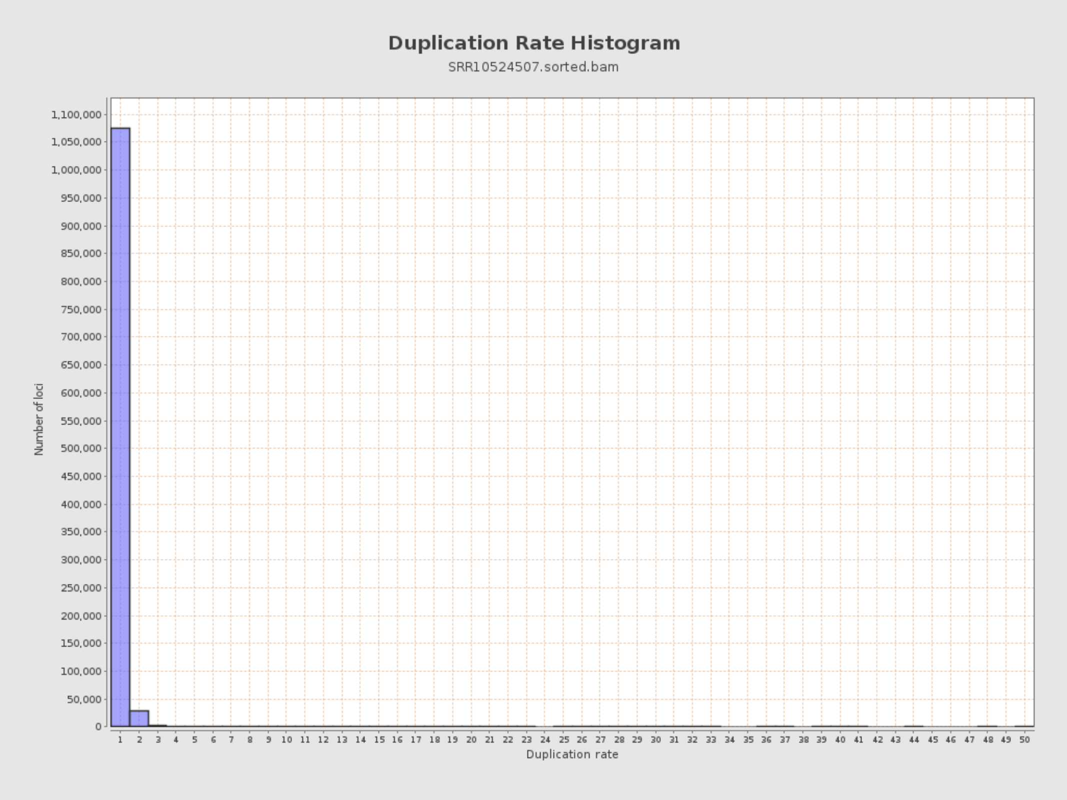
5. Results : Coverage Histogram (0-50X)



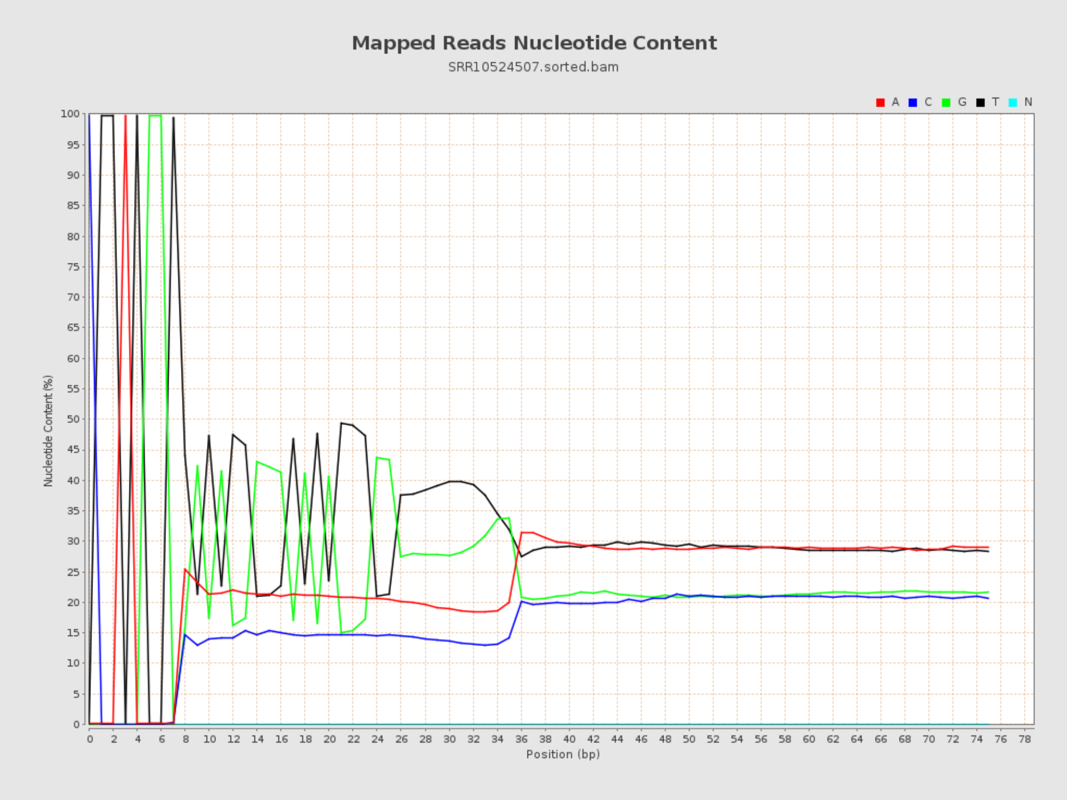
6. Results : Genome Fraction Coverage



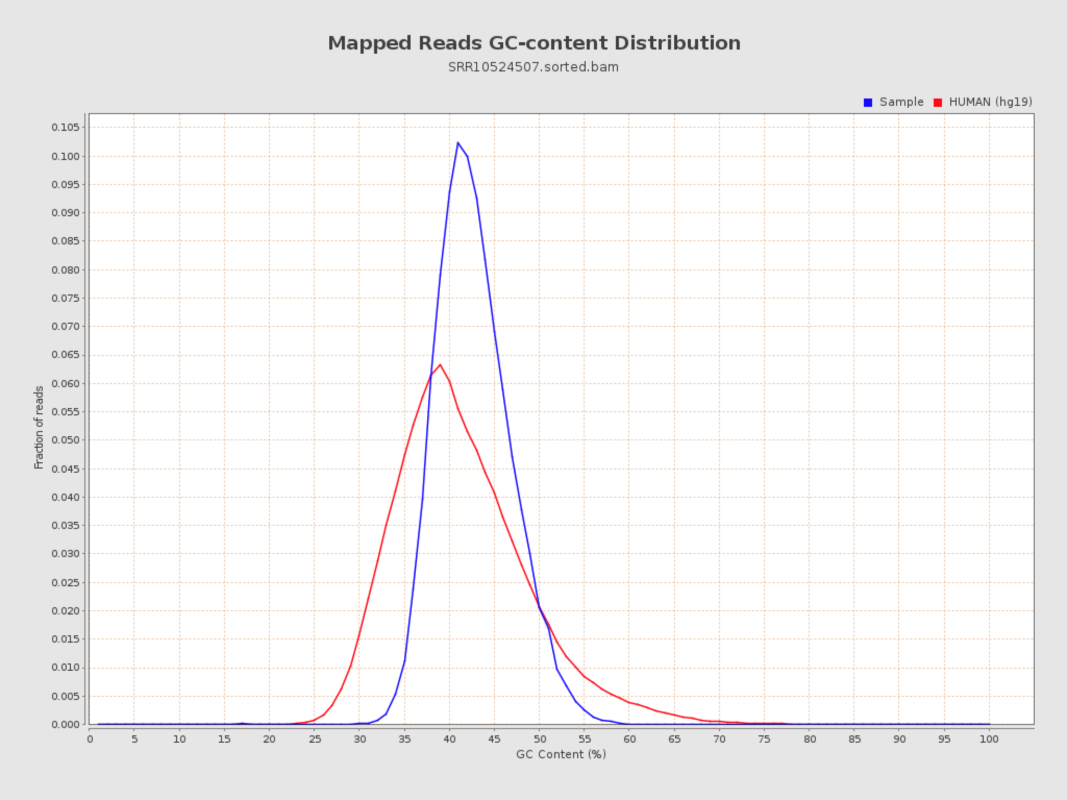
7. Results : Duplication Rate Histogram



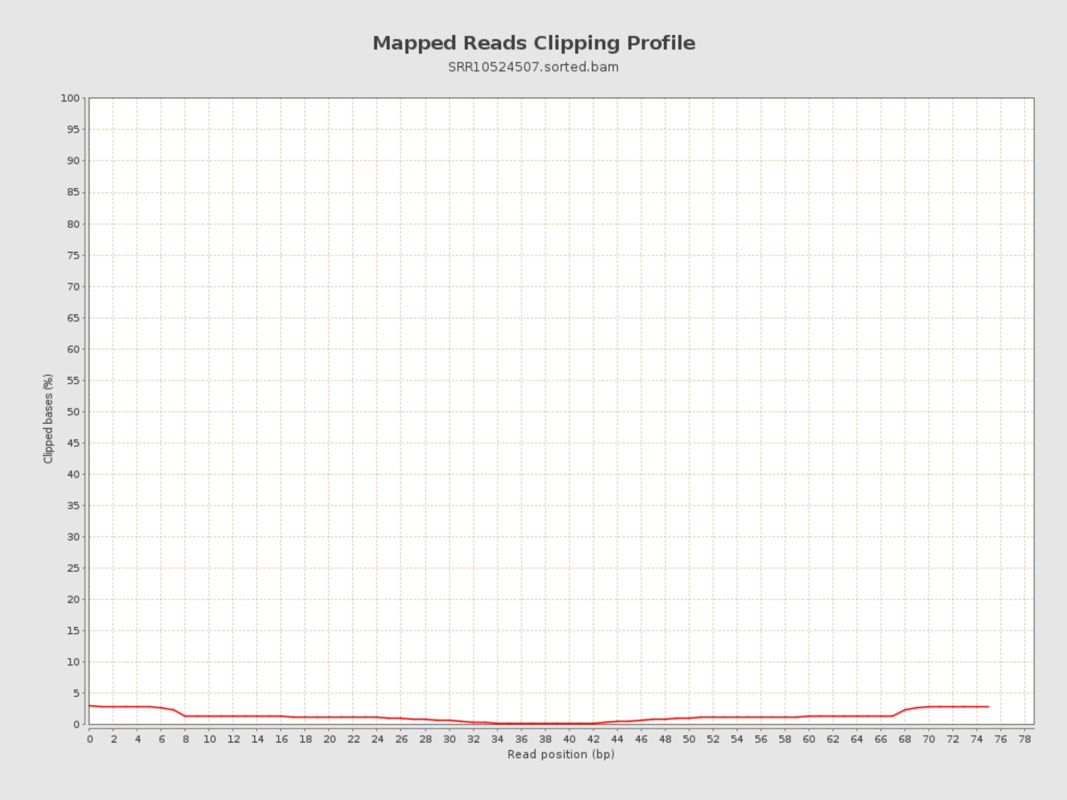
8. Results : Mapped Reads Nucleotide Content



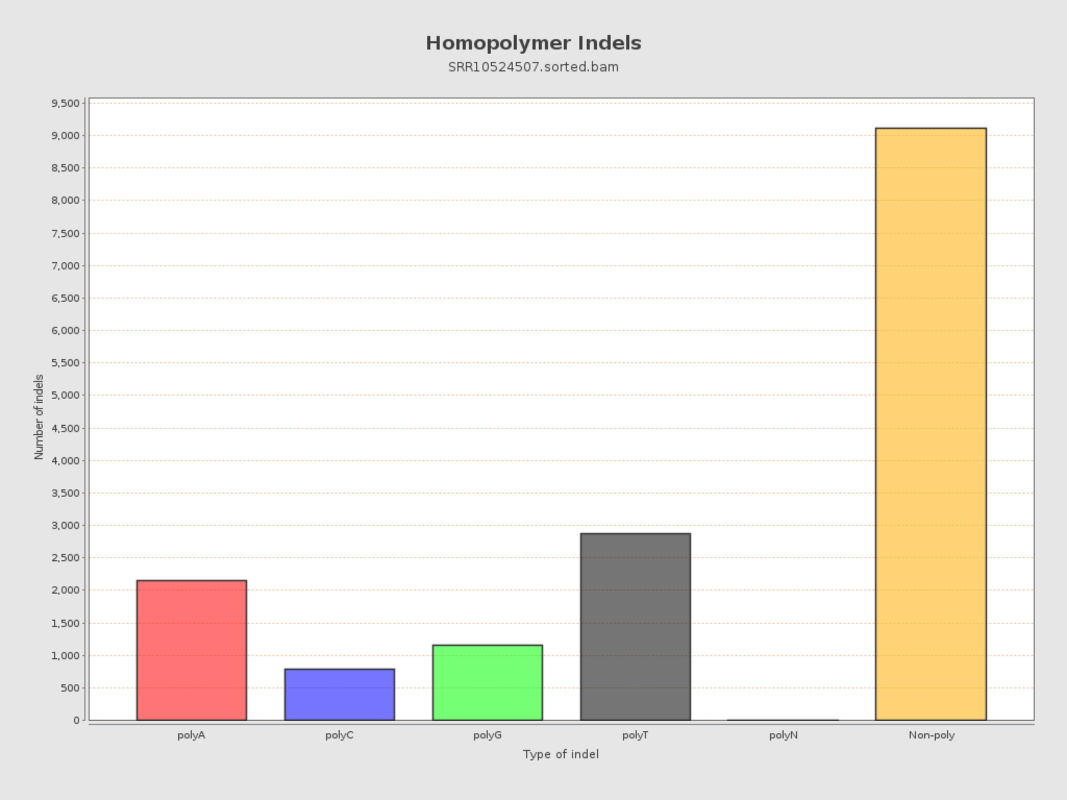
9. Results : Mapped Reads GC-content Distribution



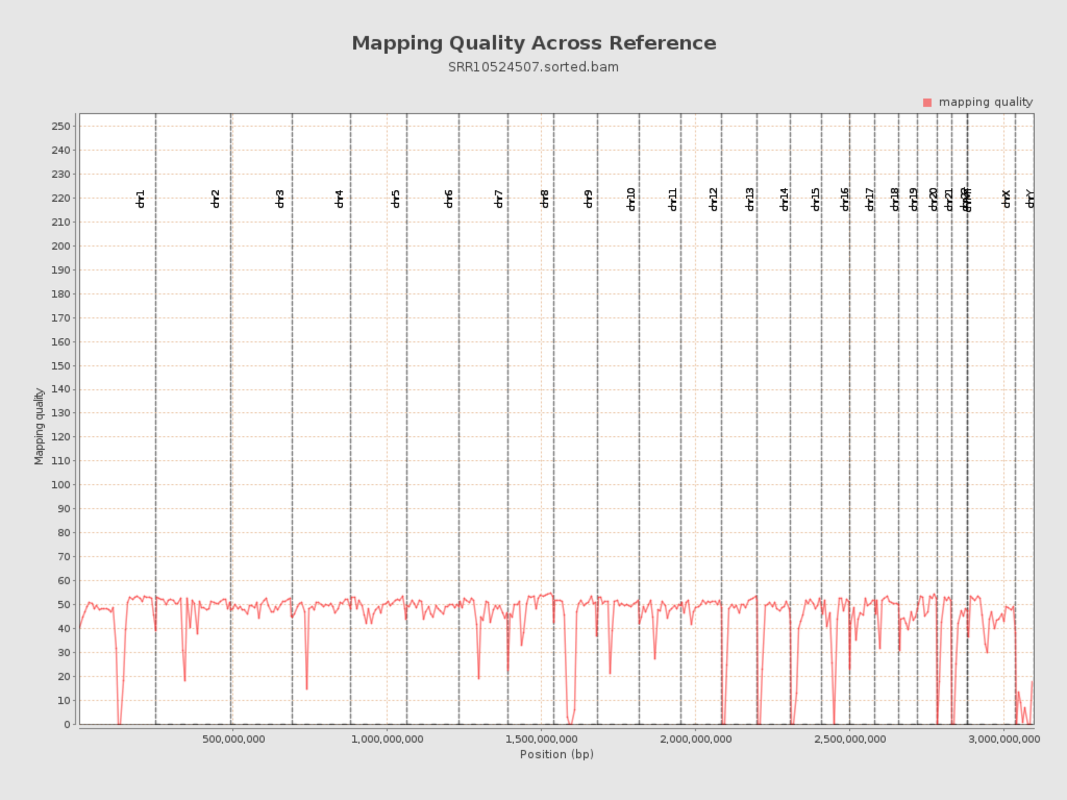
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram