Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:55:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524562.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_SRR10524562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524562.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:55:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,058,383
Mapped reads	958,657 / 90.58%
Unmapped reads	99,726 / 9.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,972 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,333 / 2.2%
Duplication rate	1.74%
Clipped reads	959,099 / 90.62%

2.2. ACGT Content

Number/percentage of A's	13,093,028 / 23.7%
Number/percentage of C's	10,758,153 / 19.47%
Number/percentage of T's	18,137,573 / 32.83%
Number/percentage of G's	13,254,282 / 23.99%
Number/percentage of N's	789 / 0%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0179

Standard Deviation	0.1841

2.4. Mapping Quality

Mean Mapping Quality	44

2.5. Mismatches and indels

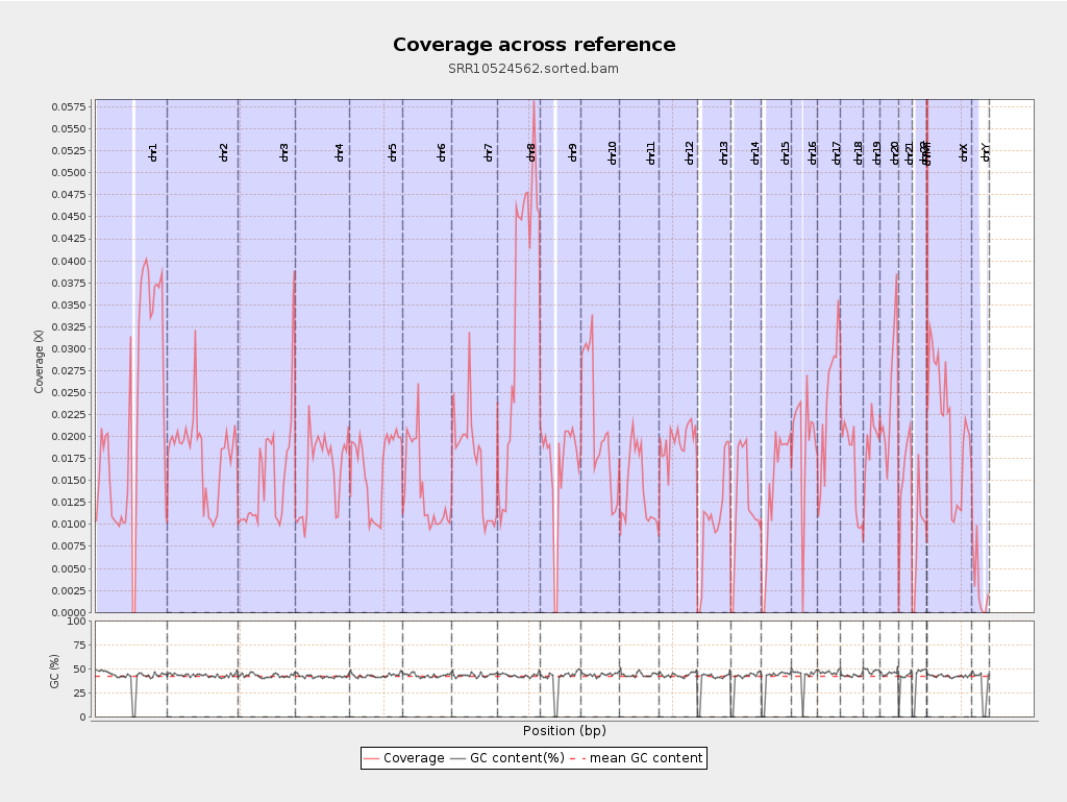
General error rate	0.52%
Mismatches	282,844
Insertions	3,815
Mapped reads with at least one insertion	0.4%
Deletions	10,469
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.71%

2.6. Chromosome stats

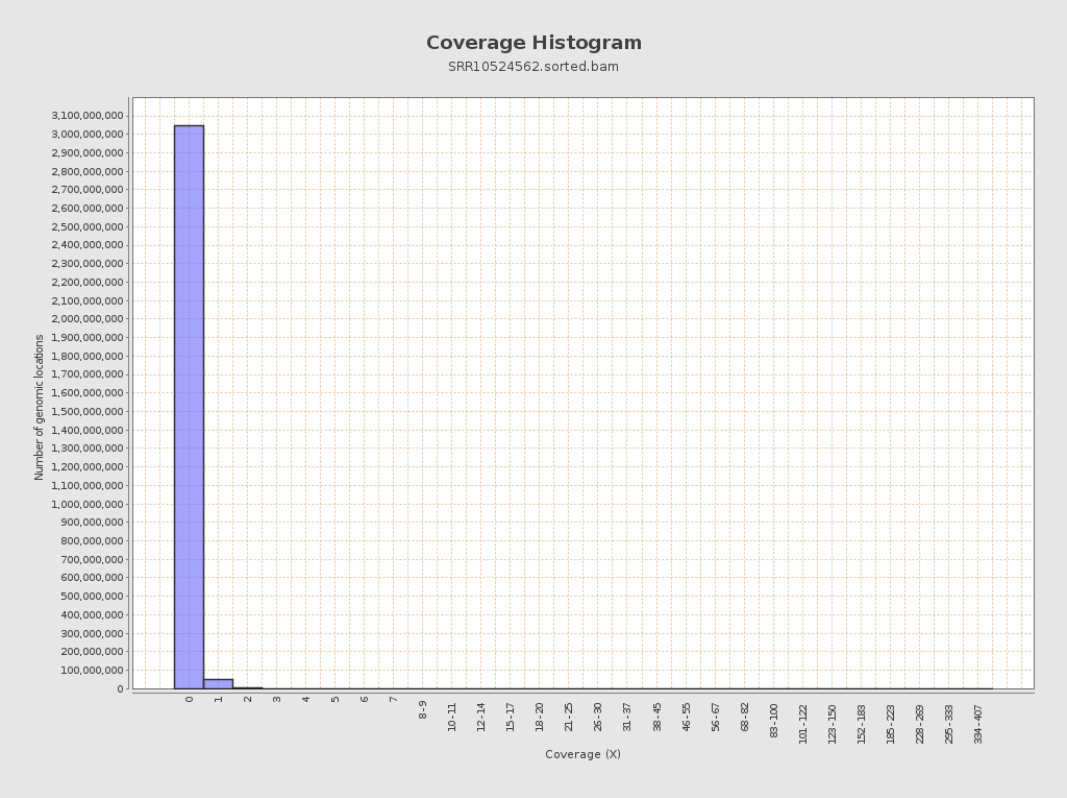
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5411712	0.0217	0.3152
chr2	243199373	4359595	0.0179	0.2015
chr3	198022430	3009636	0.0152	0.1302
chr4	191154276	3109117	0.0163	0.1433
chr5	180915260	3001932	0.0166	0.1365
chr6	171115067	2372599	0.0139	0.1463
chr7	159138663	2749466	0.0173	0.2221

chr8	146364022	5021078	0.0343	0.2149
chr9	141213431	2350677	0.0166	0.1631
chr10	135534747	2898796	0.0214	0.1944
chr11	135006516	1899300	0.0141	0.1708
chr12	133851895	2615387	0.0195	0.1476
chr13	115169878	1233417	0.0107	0.1094
chr14	107349540	1314869	0.0122	0.1189
chr15	102531392	1450663	0.0141	0.1281
chr16	90354753	1753343	0.0194	0.1541
chr17	81195210	1934960	0.0238	0.1671
chr18	78077248	1307619	0.0167	0.2644
chr19	59128983	1145694	0.0194	0.2173
chr20	63025520	1560693	0.0248	0.1669
chr21	48129895	755256	0.0157	0.1386
chr22	51304566	448757	0.0087	0.0986
chrMT	16571	51021	3.0789	2.3953
chrX	155270560	3330593	0.0215	0.1687
chrY	59373566	174962	0.0029	0.0834

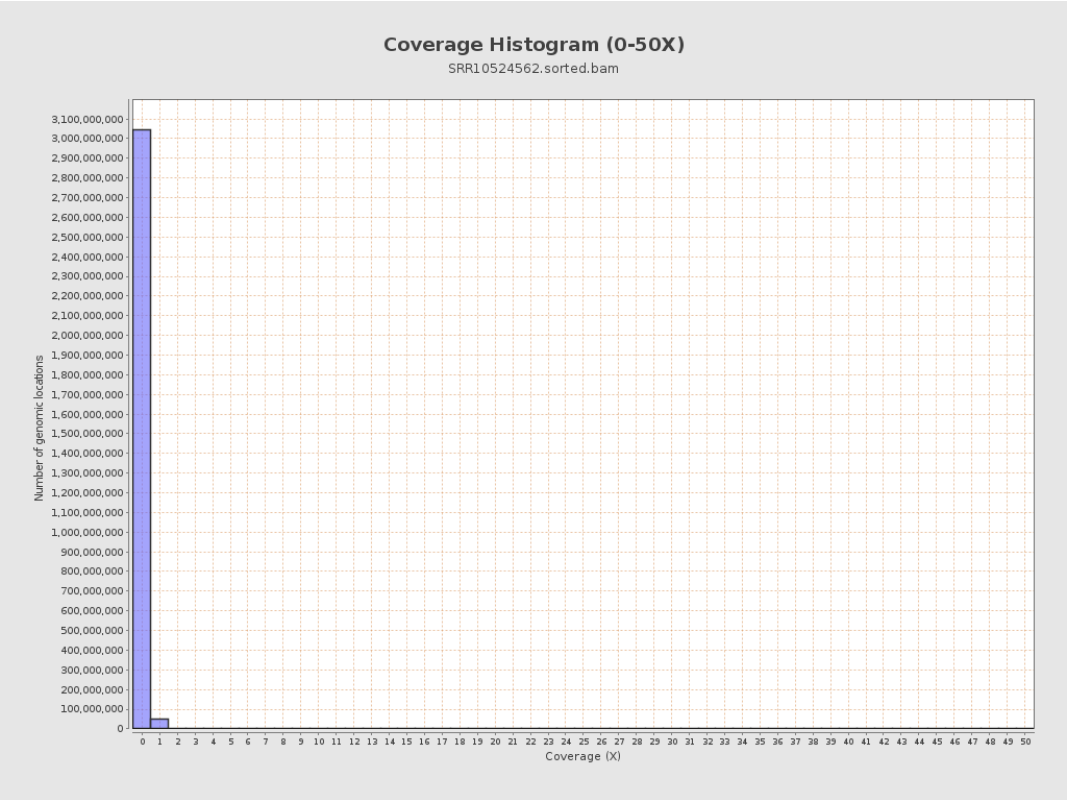
3. Results : Coverage across reference



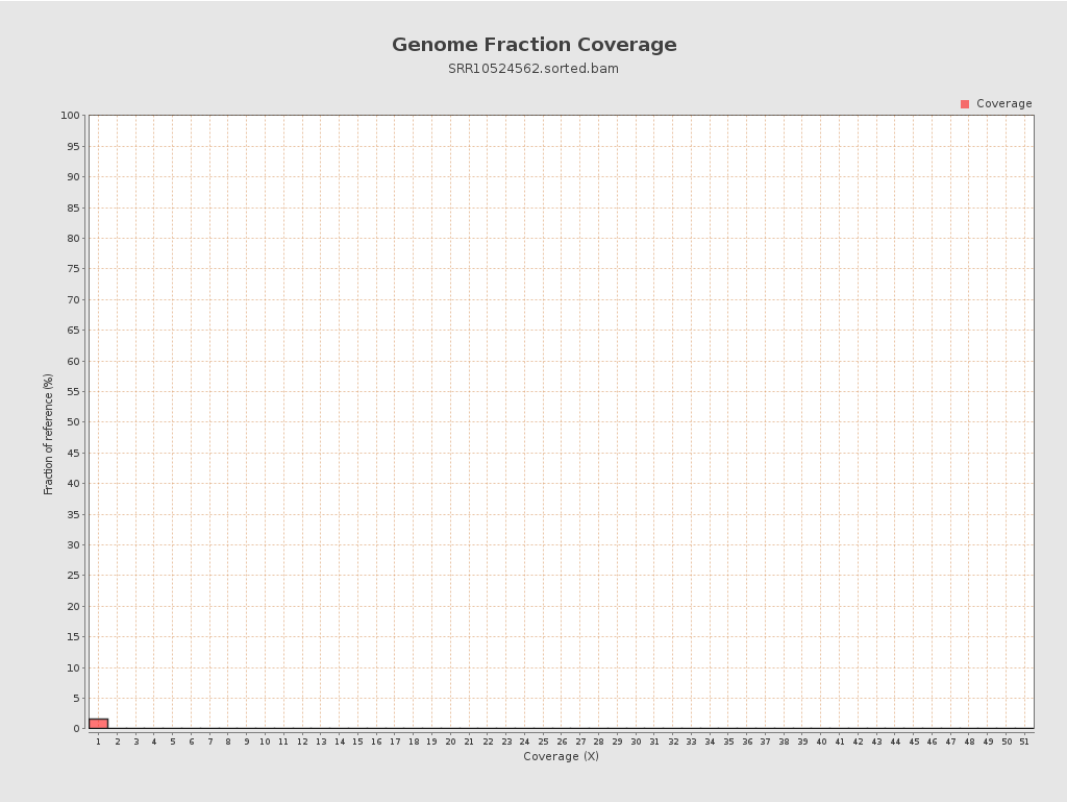
4. Results : Coverage Histogram



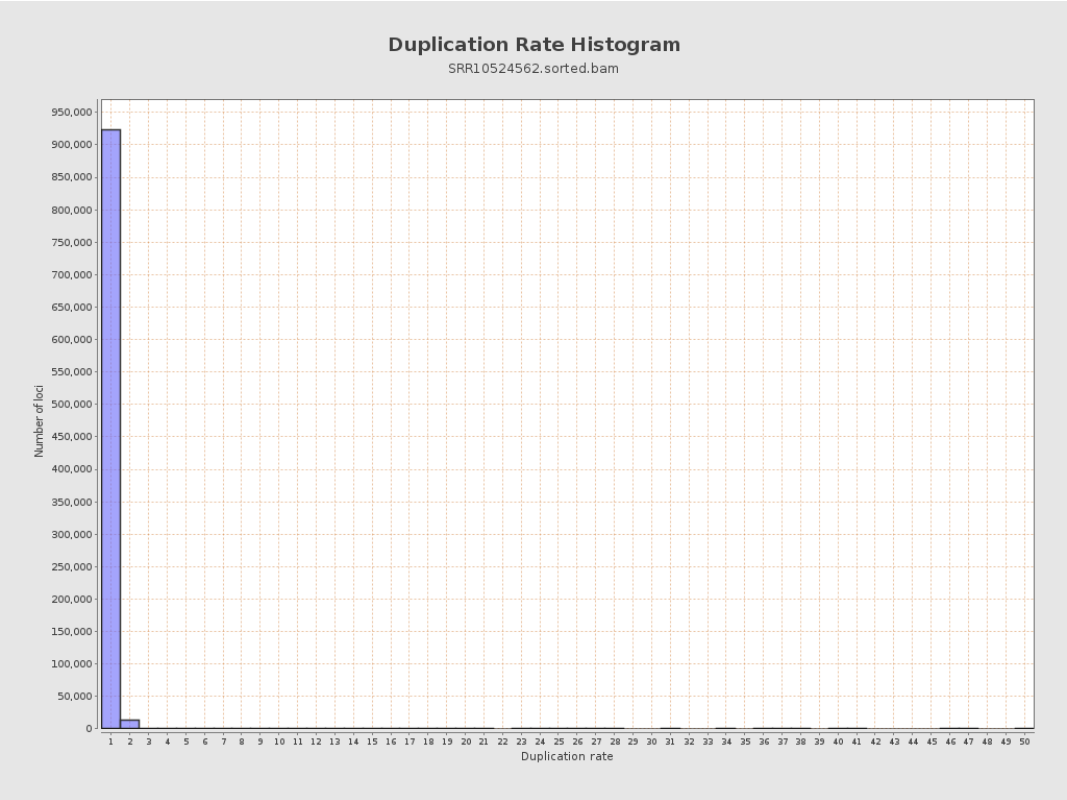
5. Results : Coverage Histogram (0-50X)



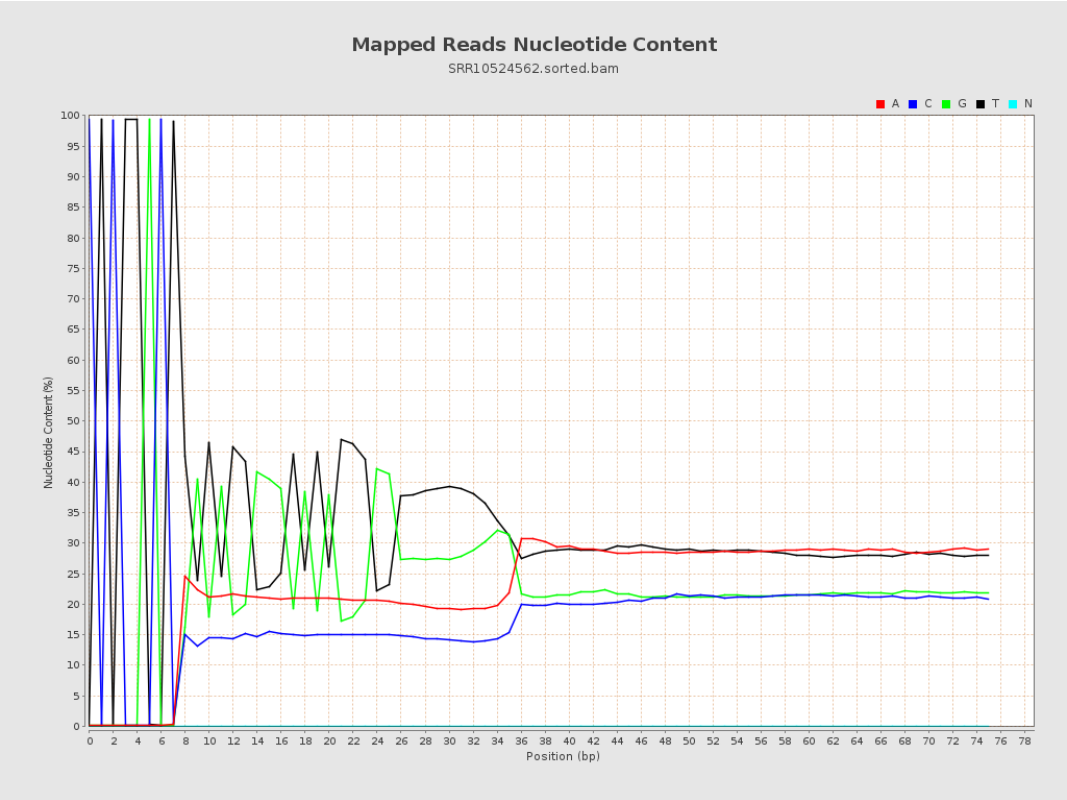
6. Results : Genome Fraction Coverage



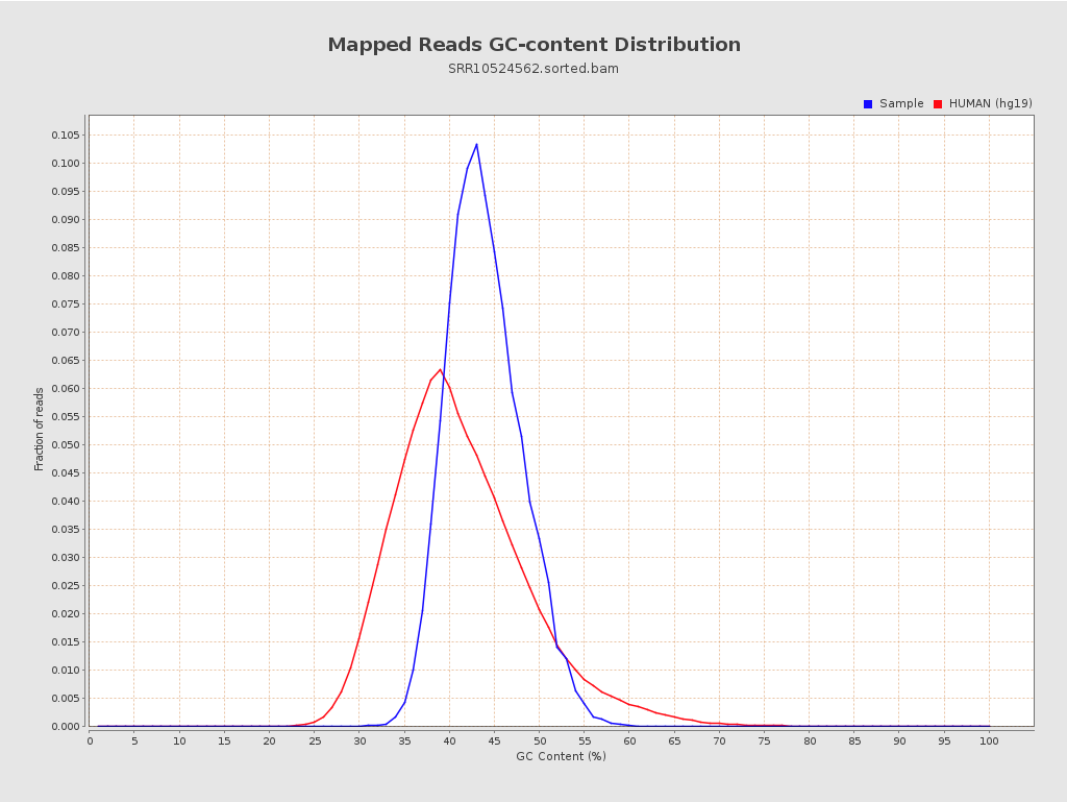
7. Results : Duplication Rate Histogram



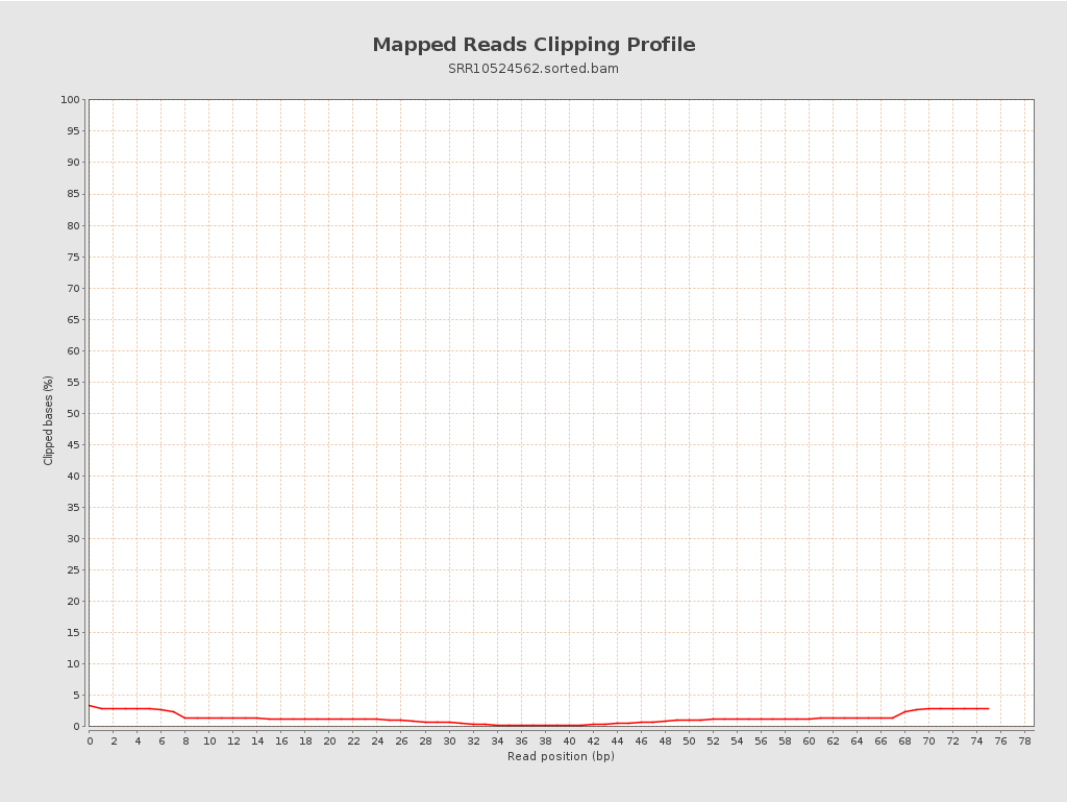
8. Results : Mapped Reads Nucleotide Content



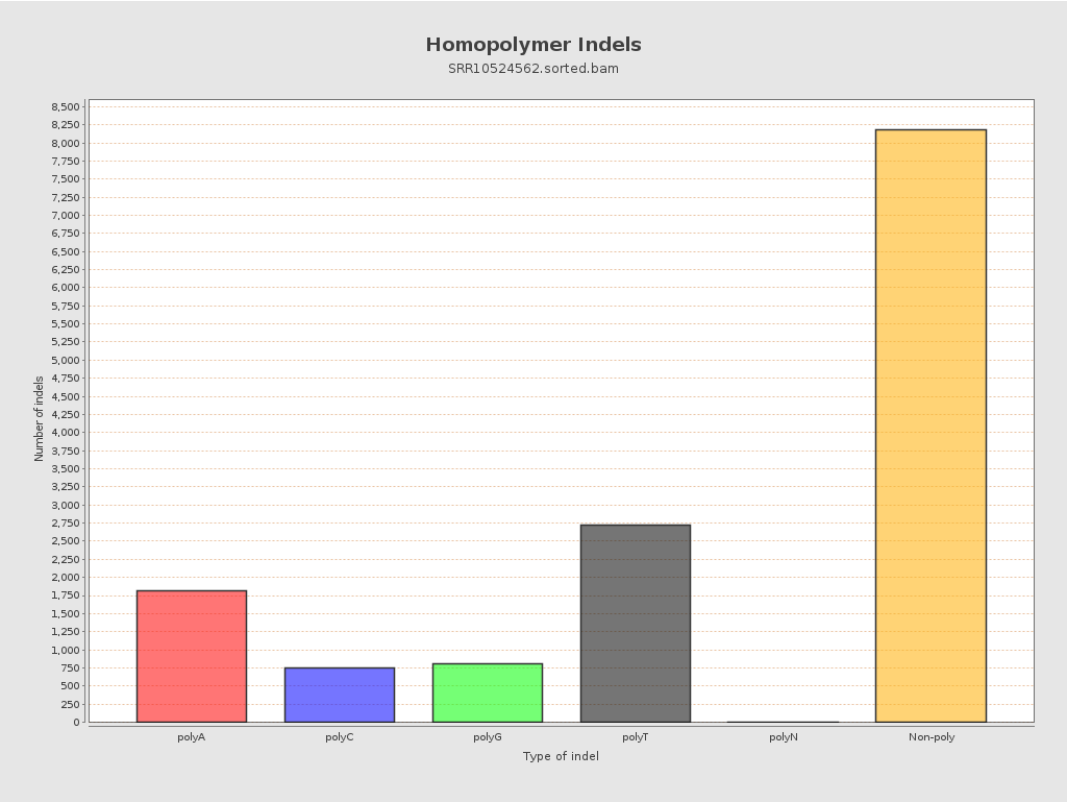
9. Results : Mapped Reads GC-content Distribution



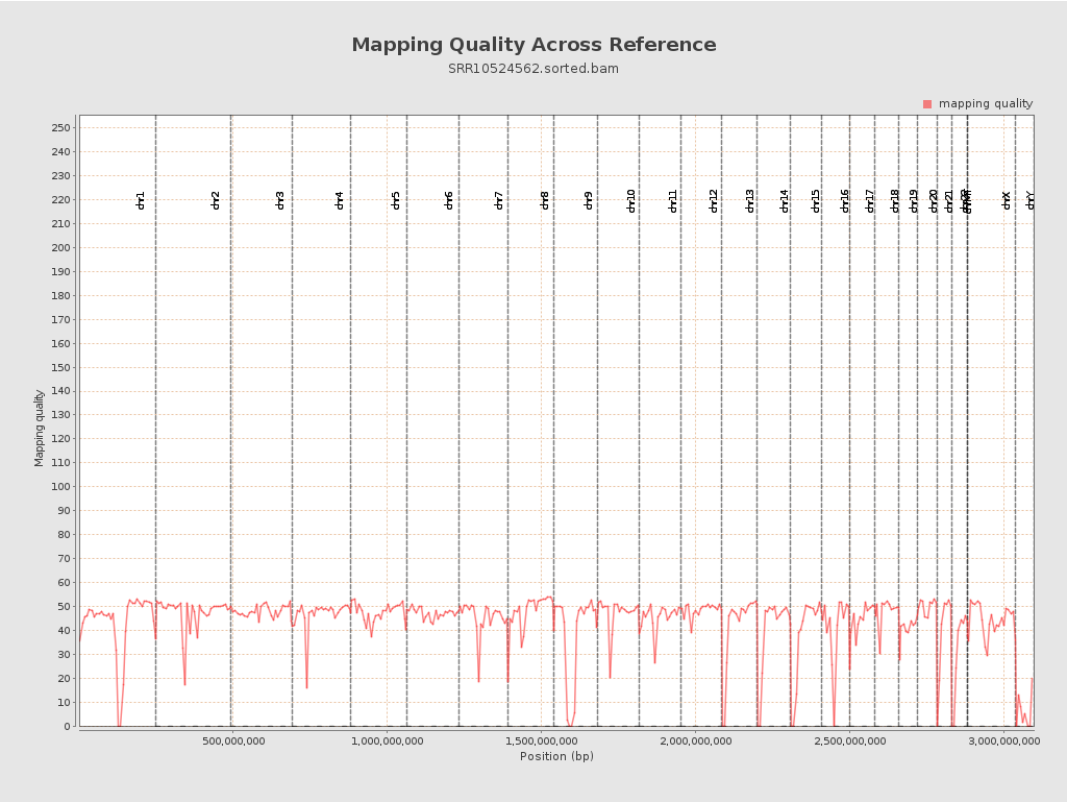
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram