Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524532.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_SRR10524532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524532.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:31:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,099,031
Mapped reads	1,003,119 / 91.27%
Unmapped reads	95,912 / 8.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,379 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,581 / 3.42%
Duplication rate	2.88%
Clipped reads	1,003,970 / 91.35%

2.2. ACGT Content

Number/percentage of A's	14,879,699 / 25.51%
Number/percentage of C's	10,944,774 / 18.76%
Number/percentage of T's	18,796,453 / 32.22%
Number/percentage of G's	13,714,956 / 23.51%
Number/percentage of N's	956 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0189

Standard Deviation	0.2039

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

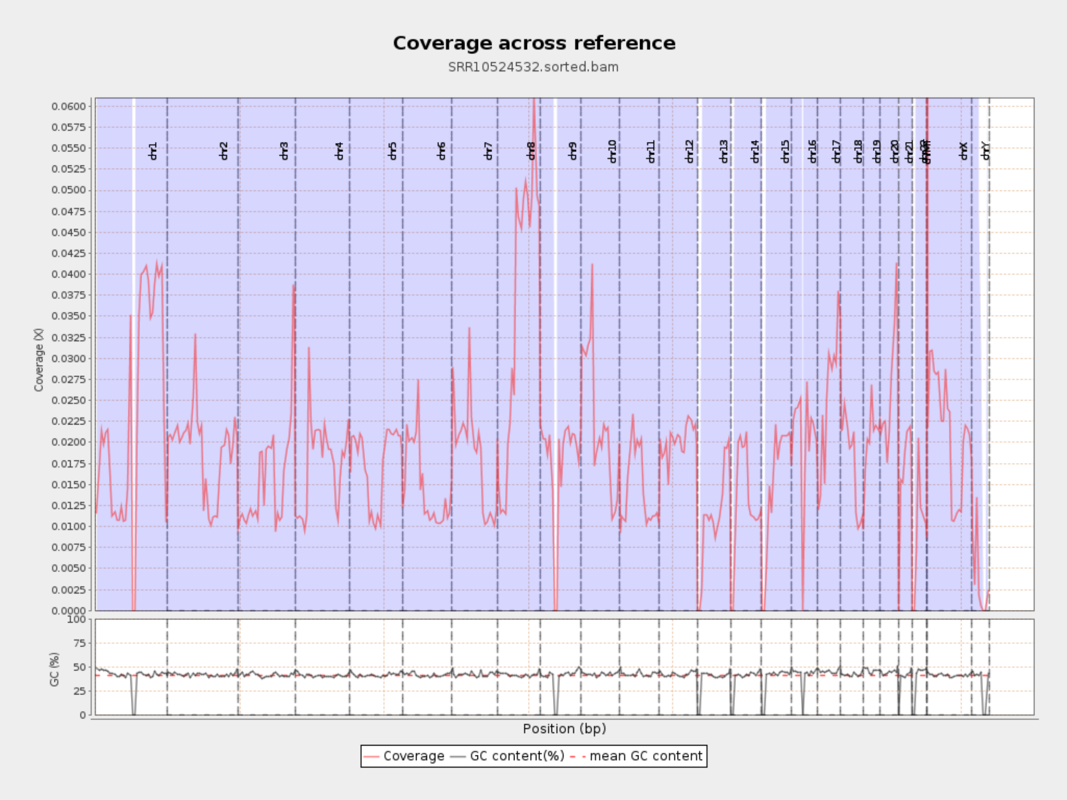
General error rate	0.53%
Mismatches	299,740
Insertions	4,111
Mapped reads with at least one insertion	0.41%
Deletions	11,195
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.34%

2.6. Chromosome stats

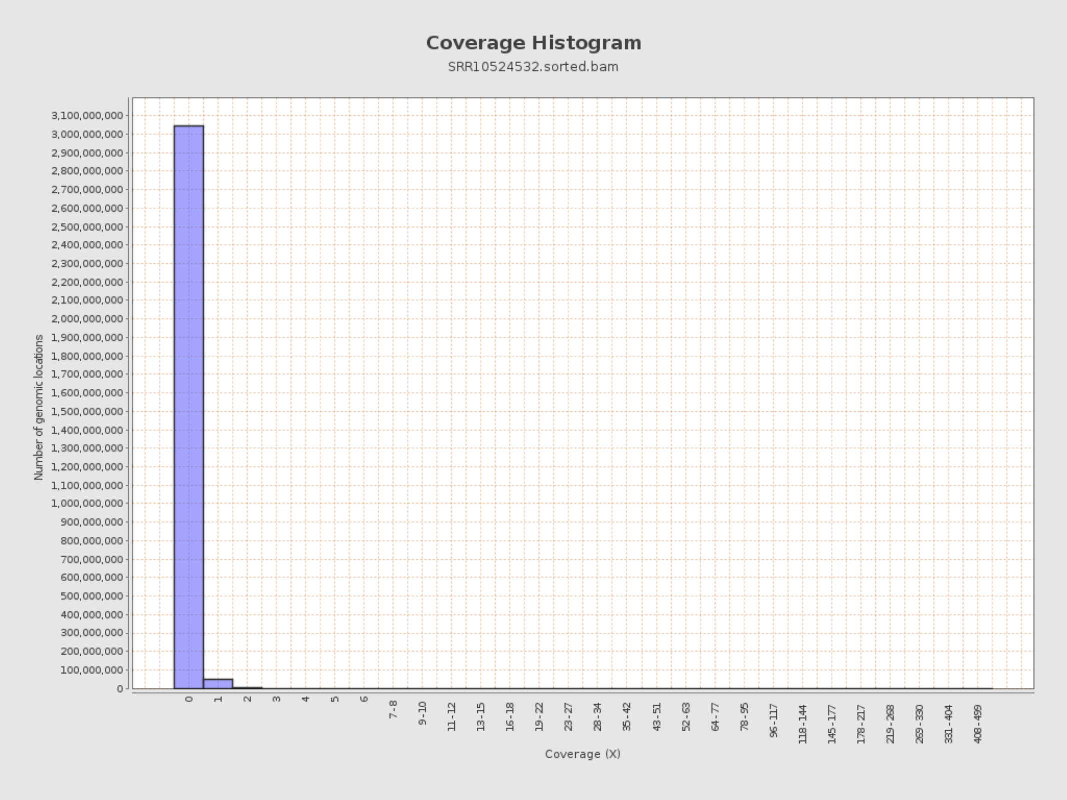
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5738729	0.023	0.3764
chr2	243199373	4660888	0.0192	0.2284
chr3	198022430	3125294	0.0158	0.1356
chr4	191154276	3356163	0.0176	0.1621
chr5	180915260	3182455	0.0176	0.1428
chr6	171115067	2523609	0.0147	0.1533
chr7	159138663	2964436	0.0186	0.239

chr8	146364022	5320858	0.0364	0.234
chr9	141213431	2469580	0.0175	0.1671
chr10	135534747	3095706	0.0228	0.2247
chr11	135006516	1975655	0.0146	0.1688
chr12	133851895	2713581	0.0203	0.1546
chr13	115169878	1270222	0.011	0.1139
chr14	107349540	1386806	0.0129	0.1238
chr15	102531392	1544495	0.0151	0.1331
chr16	90354753	1825659	0.0202	0.1616
chr17	81195210	2049176	0.0252	0.1766
chr18	78077248	1368782	0.0175	0.2866
chr19	59128983	1228811	0.0208	0.2644
chr20	63025520	1673597	0.0266	0.1766
chr21	48129895	815479	0.0169	0.1515
chr22	51304566	493171	0.0096	0.106
chrMT	16571	17861	1.0778	1.2598
chrX	155270560	3342558	0.0215	0.1669
chrY	59373566	211947	0.0036	0.1212

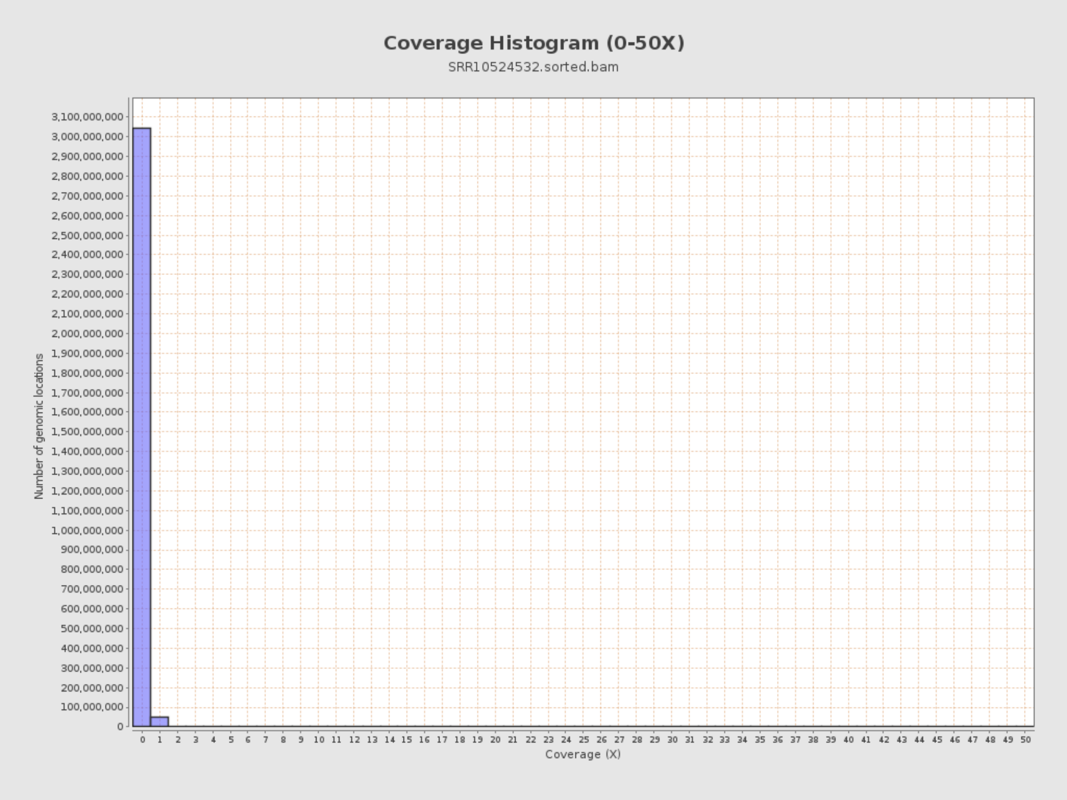
3. Results : Coverage across reference



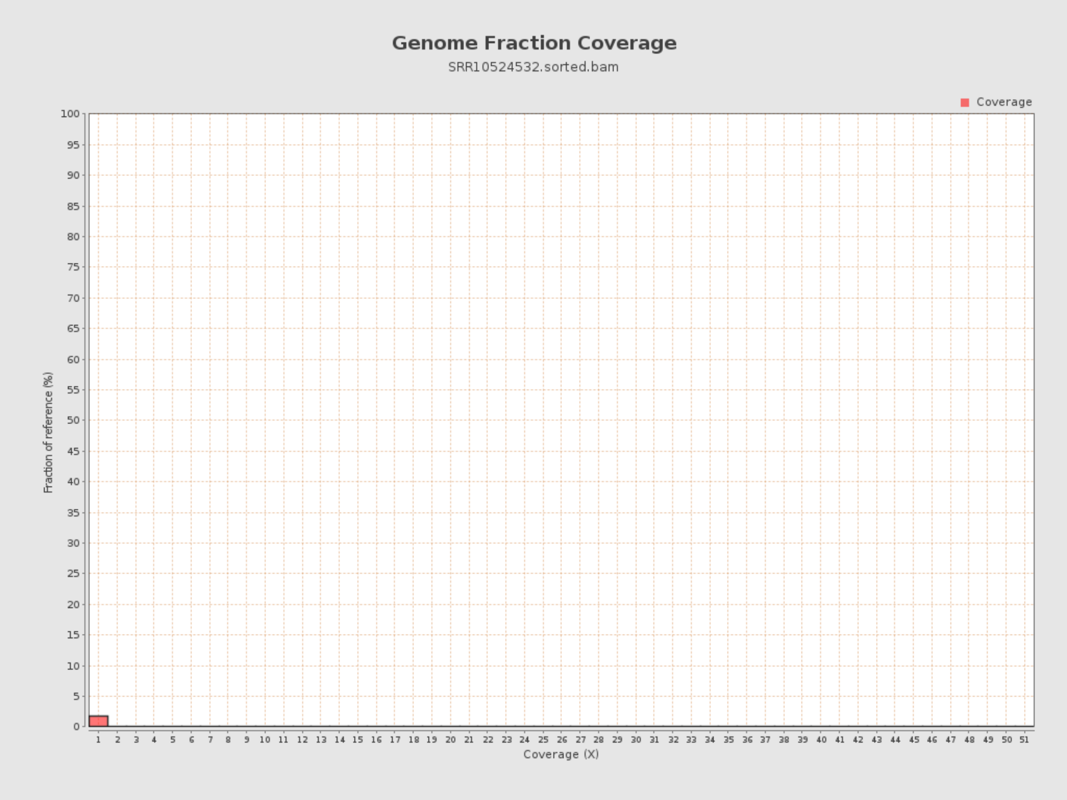
4. Results : Coverage Histogram



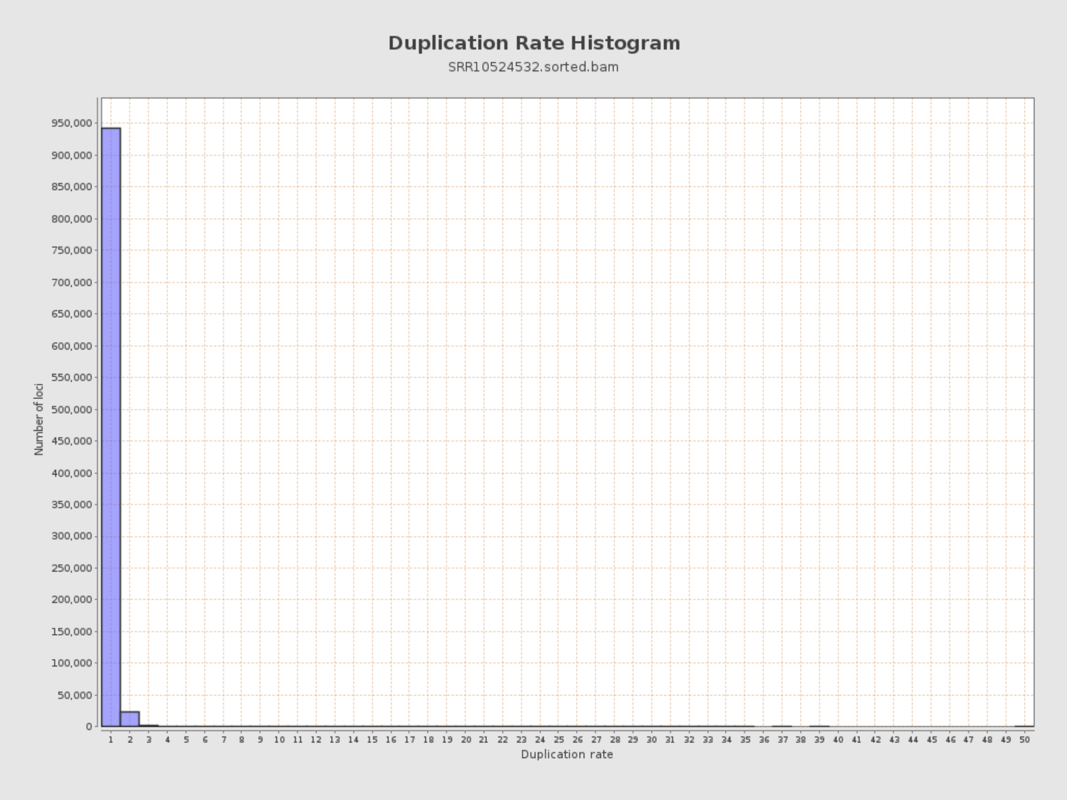
5. Results : Coverage Histogram (0-50X)



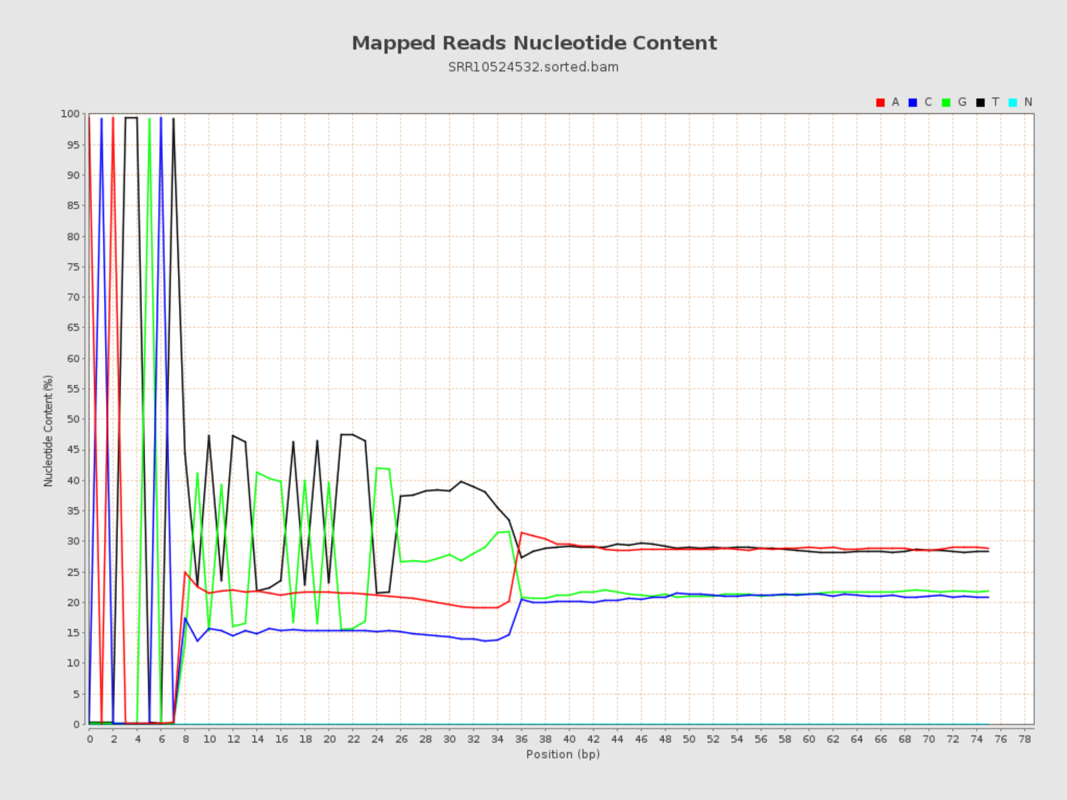
6. Results : Genome Fraction Coverage



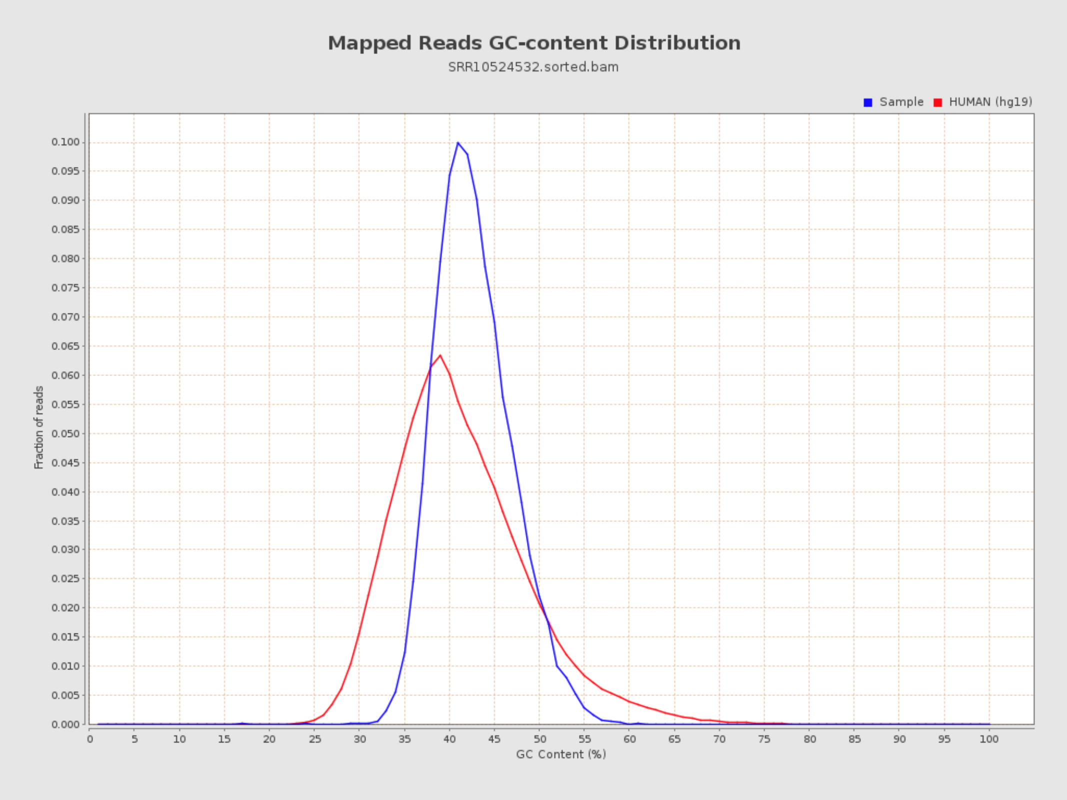
7. Results : Duplication Rate Histogram



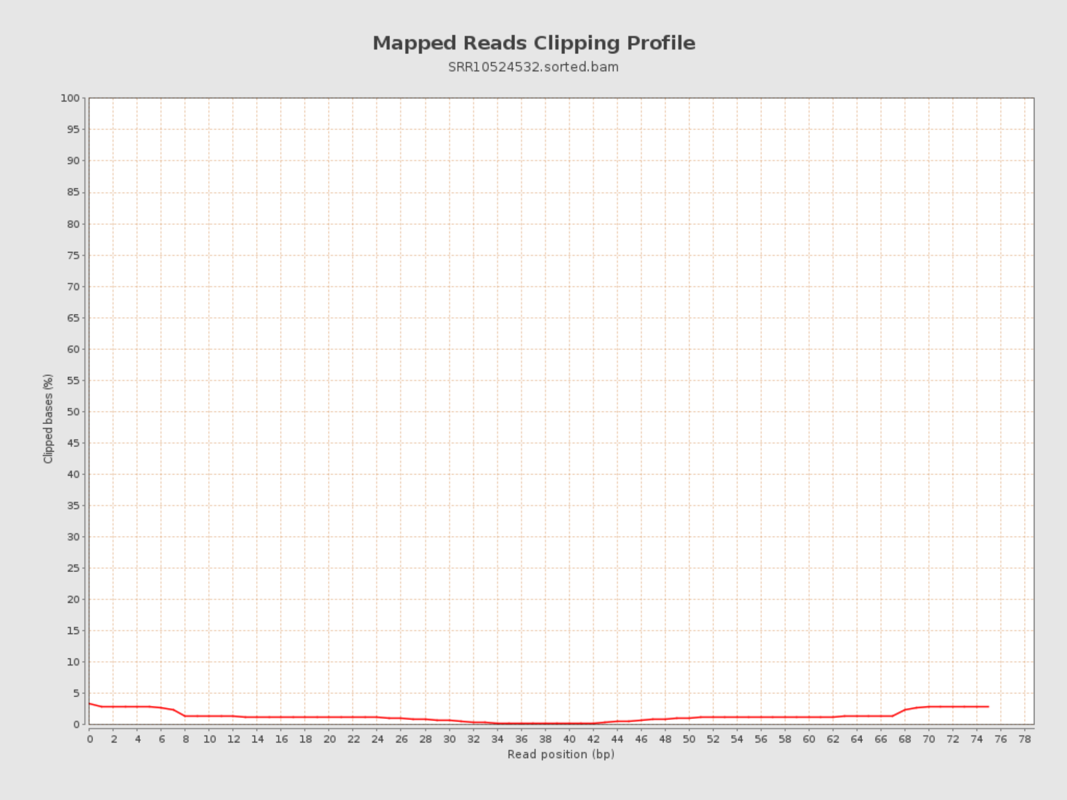
8. Results : Mapped Reads Nucleotide Content



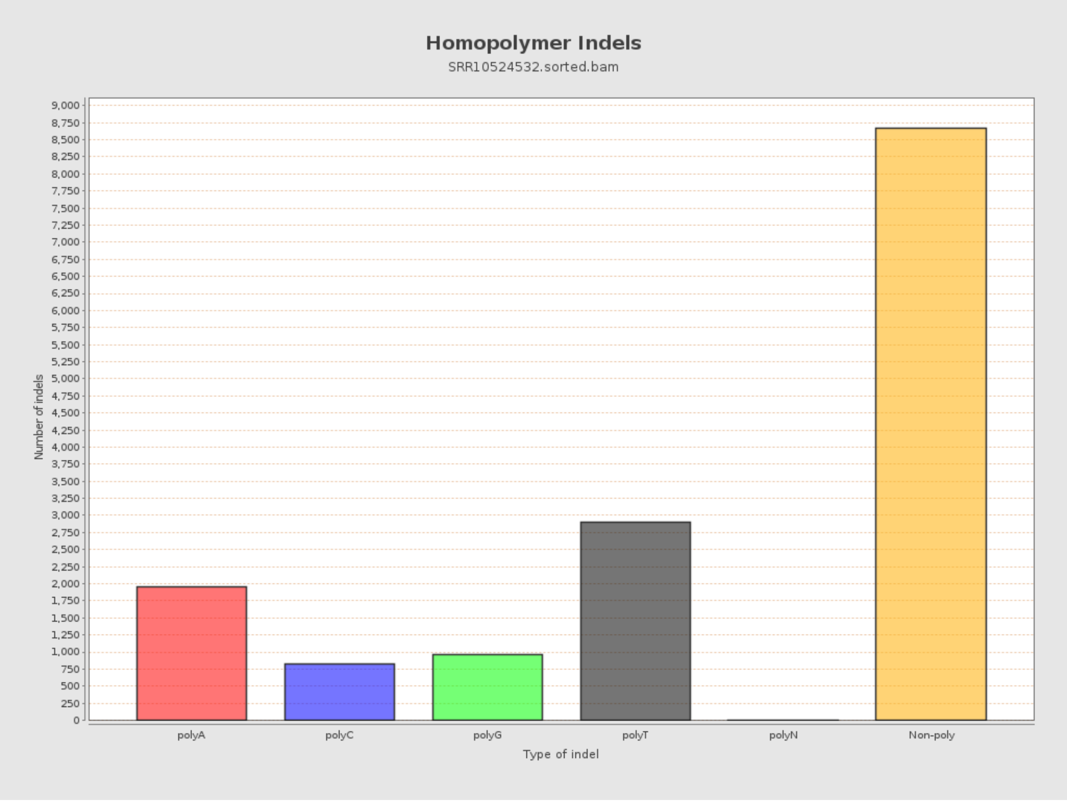
9. Results : Mapped Reads GC-content Distribution



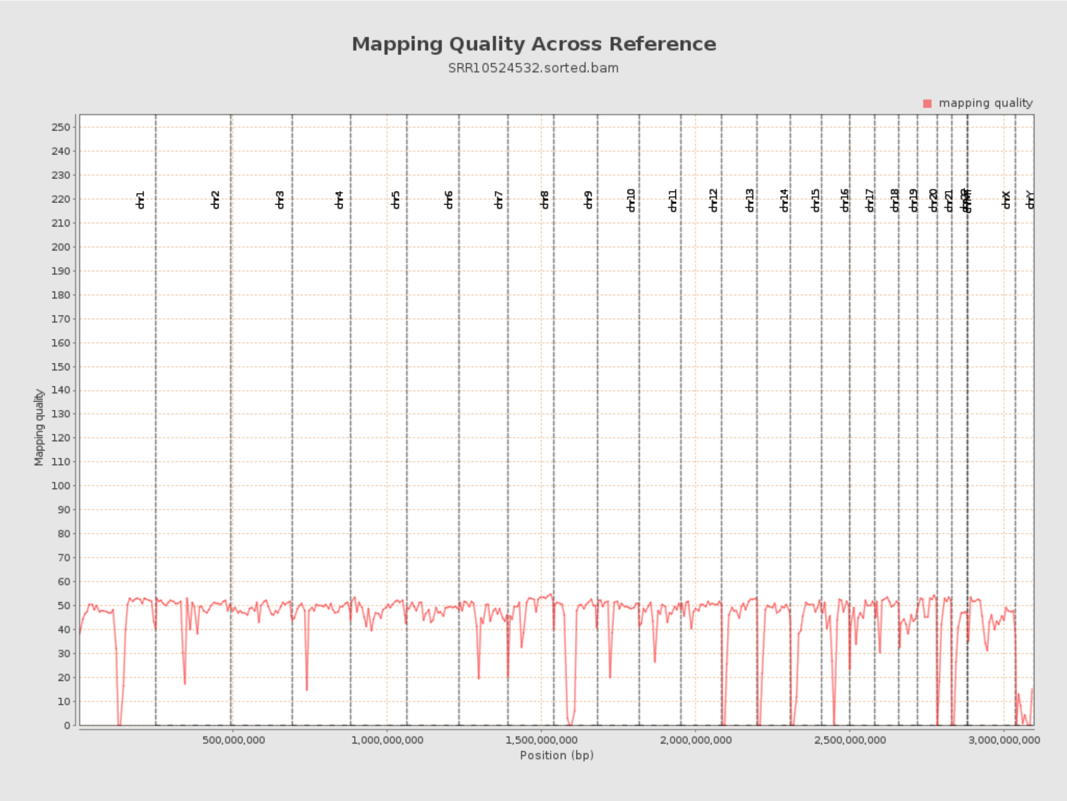
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram