Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:38:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524932.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_SRR10524932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:38:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,521,288
Mapped reads	1,409,072 / 92.62%
Unmapped reads	112,216 / 7.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,372 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	68,403 / 4.5%
Duplication rate	3.81%
Clipped reads	1,409,287 / 92.64%

2.2. ACGT Content

Number/percentage of A's	21,755,414 / 26.41%
Number/percentage of C's	15,548,010 / 18.88%
Number/percentage of T's	25,024,619 / 30.38%
Number/percentage of G's	20,034,165 / 24.32%
Number/percentage of N's	649 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0266

Standard Deviation	0.2524

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

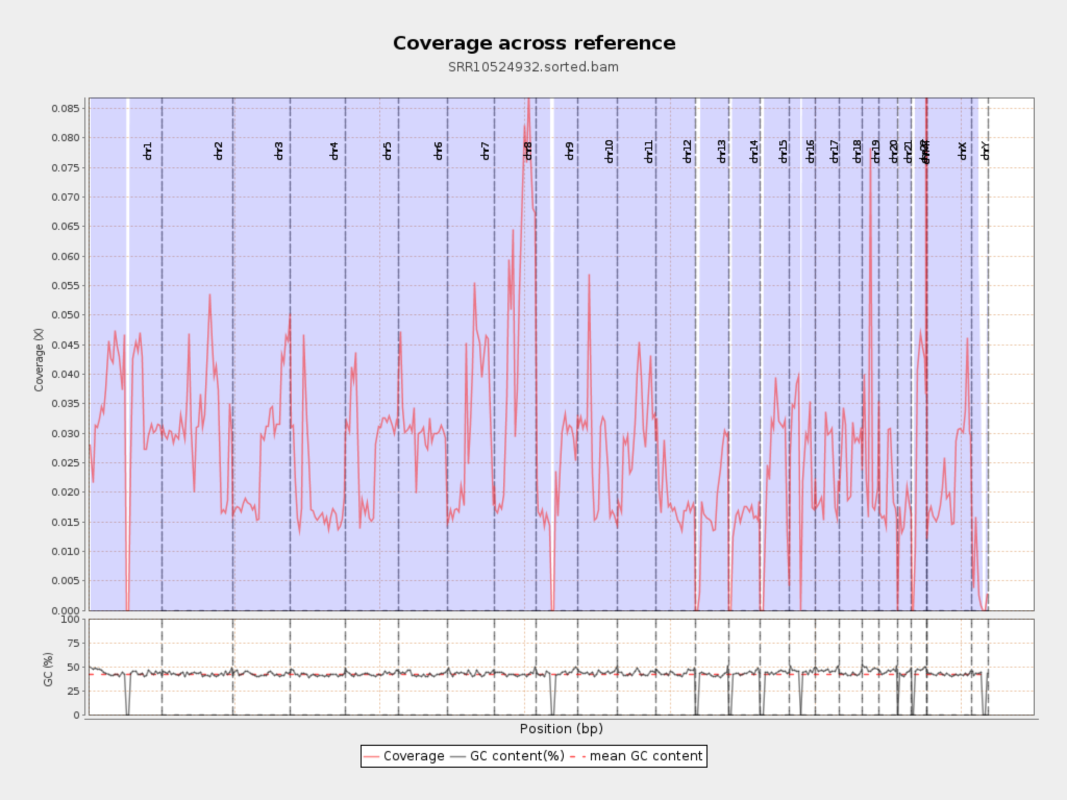
General error rate	0.52%
Mismatches	413,573
Insertions	6,602
Mapped reads with at least one insertion	0.47%
Deletions	15,931
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.14%

2.6. Chromosome stats

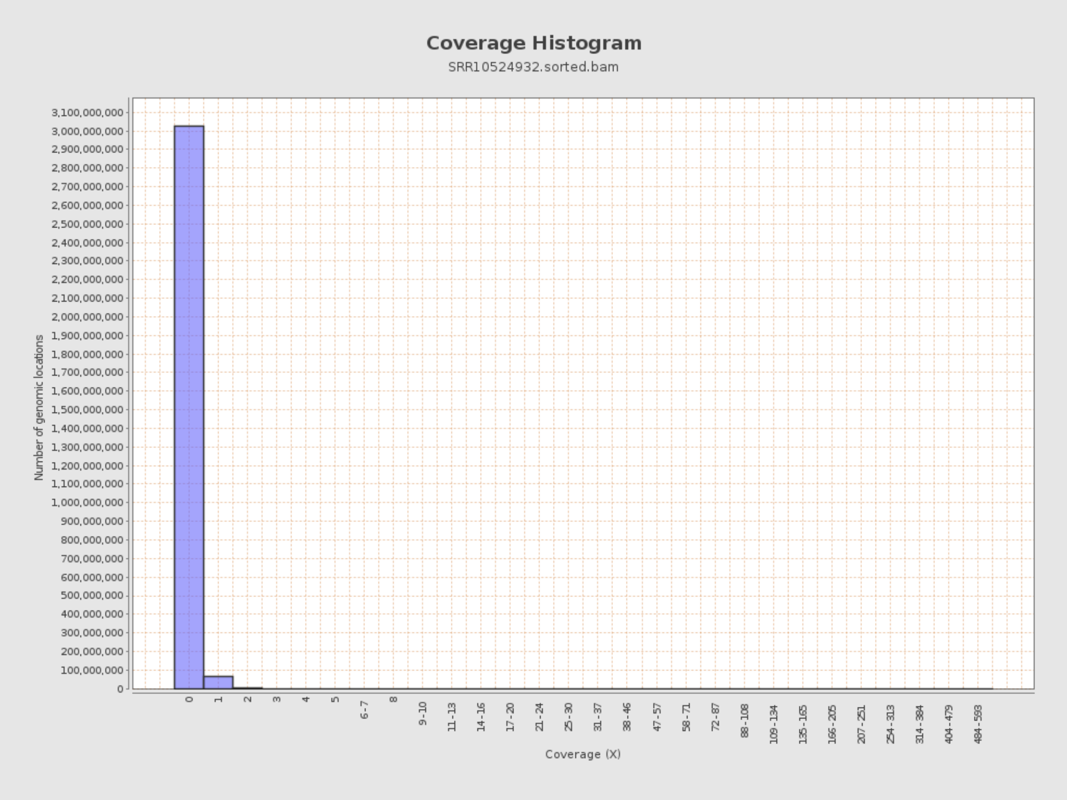
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8455588	0.0339	0.4507
chr2	243199373	7791108	0.032	0.3019
chr3	198022430	5298624	0.0268	0.183
chr4	191154276	3724364	0.0195	0.1859
chr5	180915260	5065069	0.028	0.185
chr6	171115067	5274987	0.0308	0.2032
chr7	159138663	5021590	0.0316	0.3184

chr8	146364022	7278970	0.0497	0.328
chr9	141213431	2910250	0.0206	0.1995
chr10	135534747	3569629	0.0263	0.2785
chr11	135006516	4141847	0.0307	0.2248
chr12	133851895	2518414	0.0188	0.158
chr13	115169878	1938704	0.0168	0.144
chr14	107349540	1515252	0.0141	0.1403
chr15	102531392	2355764	0.023	0.1692
chr16	90354753	2443039	0.027	0.1944
chr17	81195210	1844532	0.0227	0.172
chr18	78077248	2145870	0.0275	0.3328
chr19	59128983	1779126	0.0301	0.3269
chr20	63025520	1251541	0.0199	0.1628
chr21	48129895	730064	0.0152	0.1632
chr22	51304566	1506441	0.0294	0.1925
chrMT	16571	6039	0.3644	0.7106
chrX	155270560	3586336	0.0231	0.1821
chrY	59373566	236533	0.004	0.1463

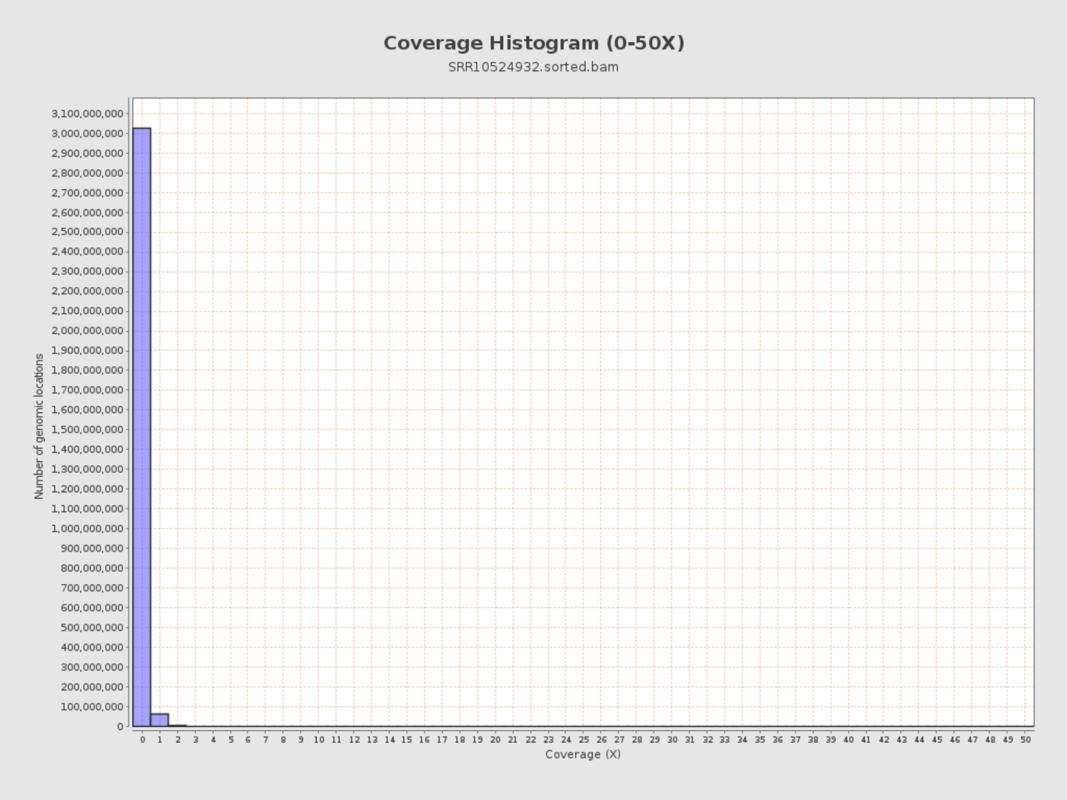
3. Results : Coverage across reference



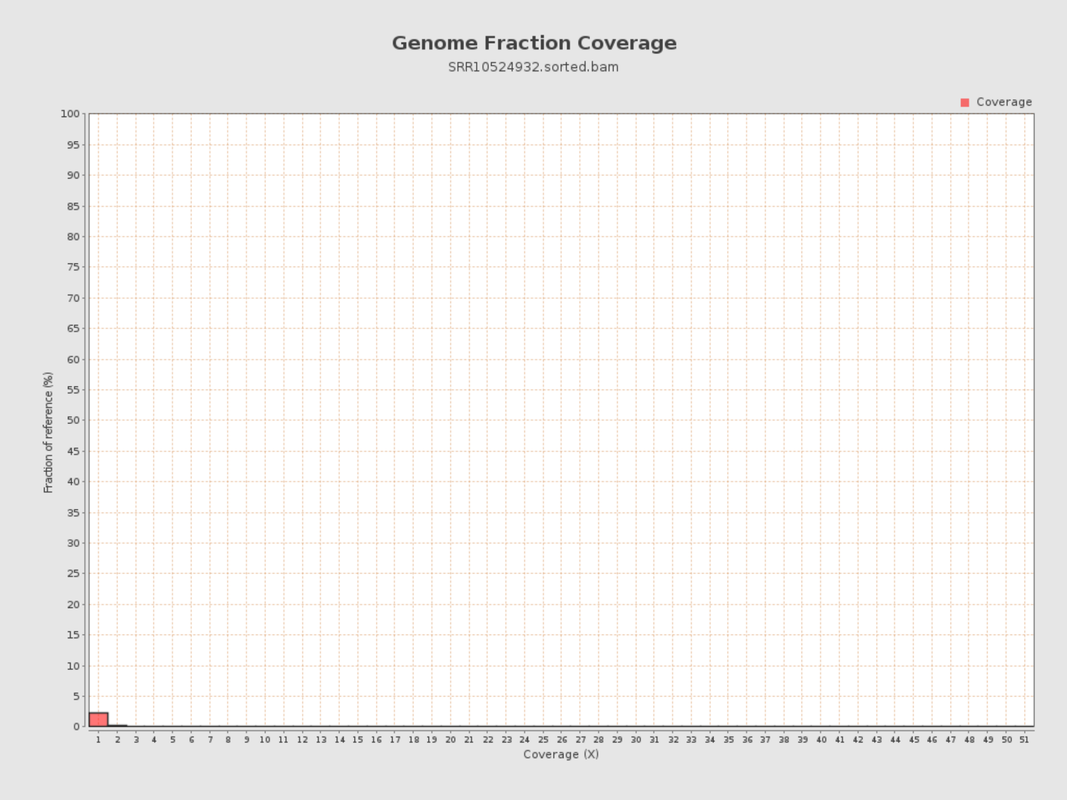
4. Results : Coverage Histogram



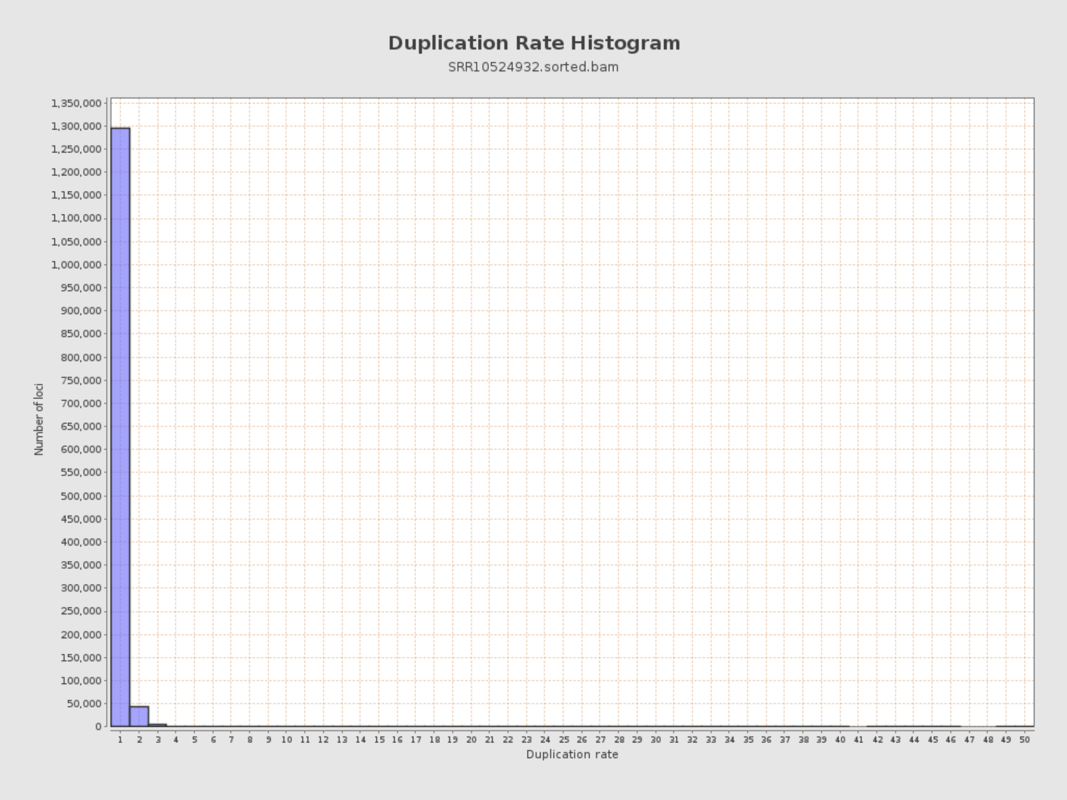
5. Results : Coverage Histogram (0-50X)



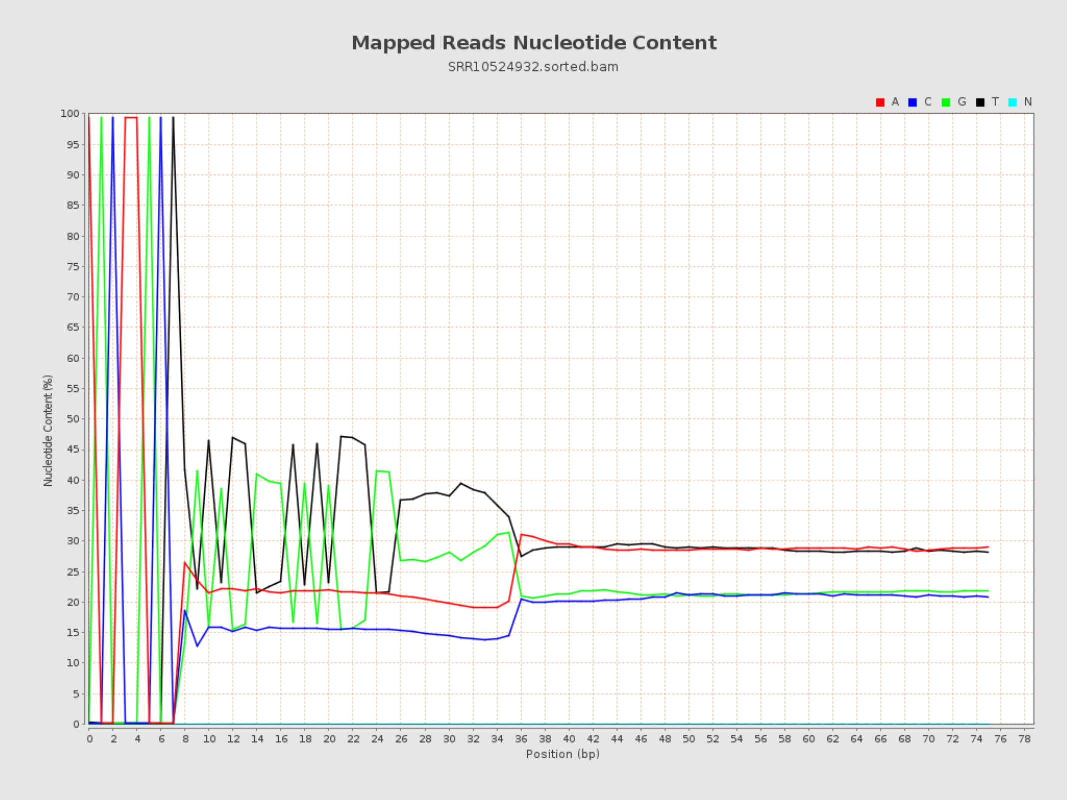
6. Results : Genome Fraction Coverage



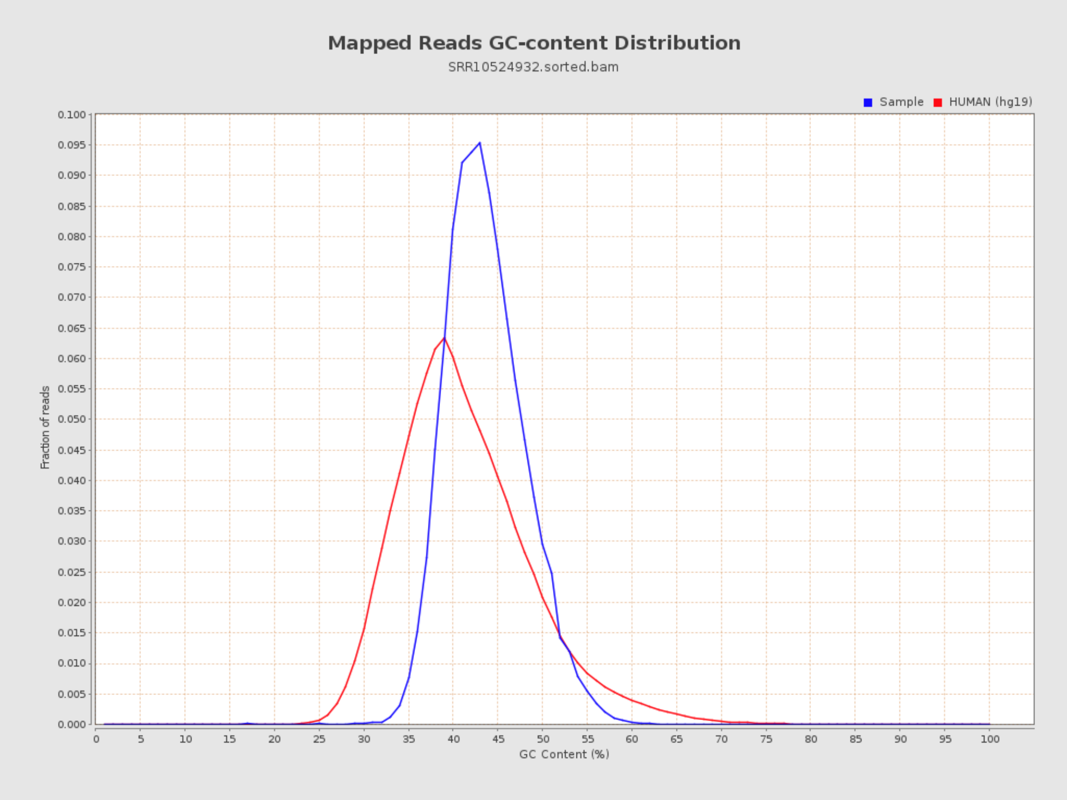
7. Results : Duplication Rate Histogram



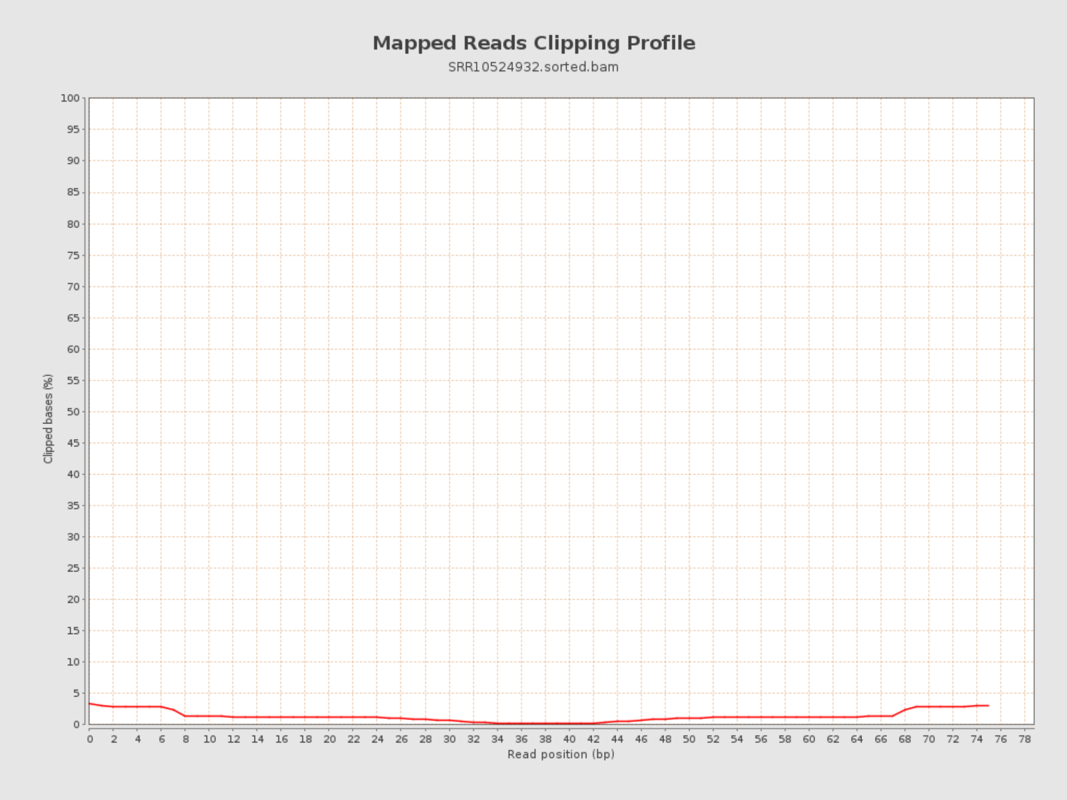
8. Results : Mapped Reads Nucleotide Content



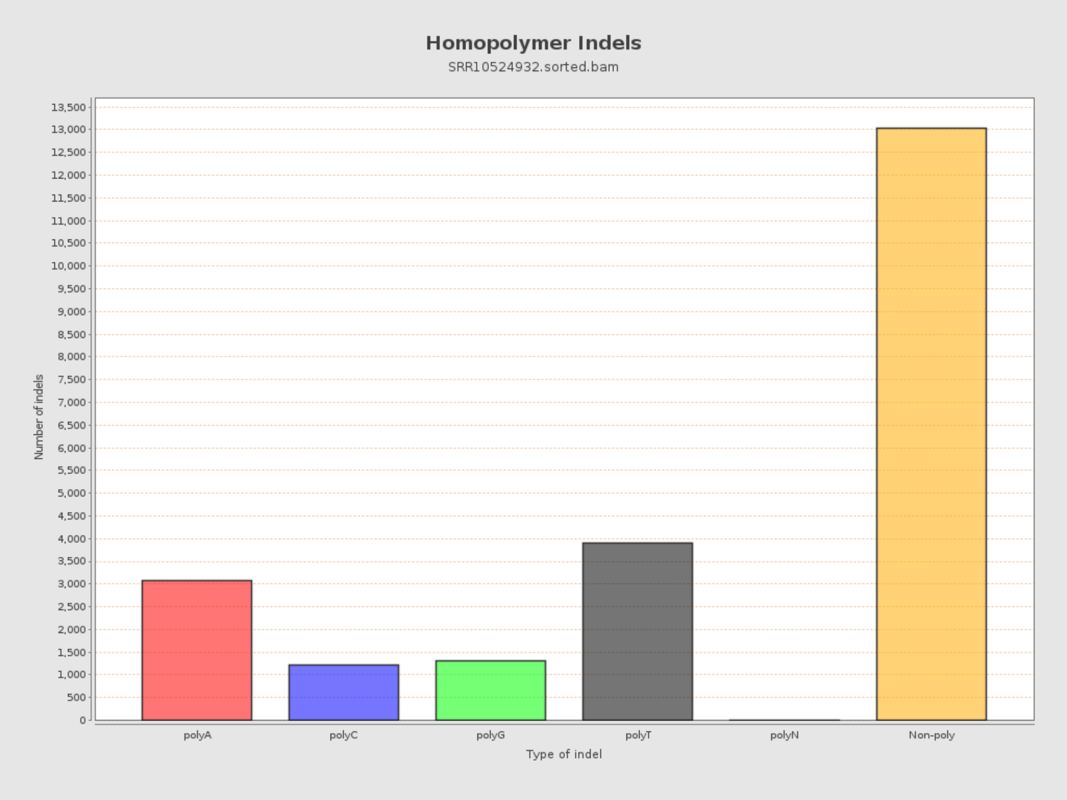
9. Results : Mapped Reads GC-content Distribution



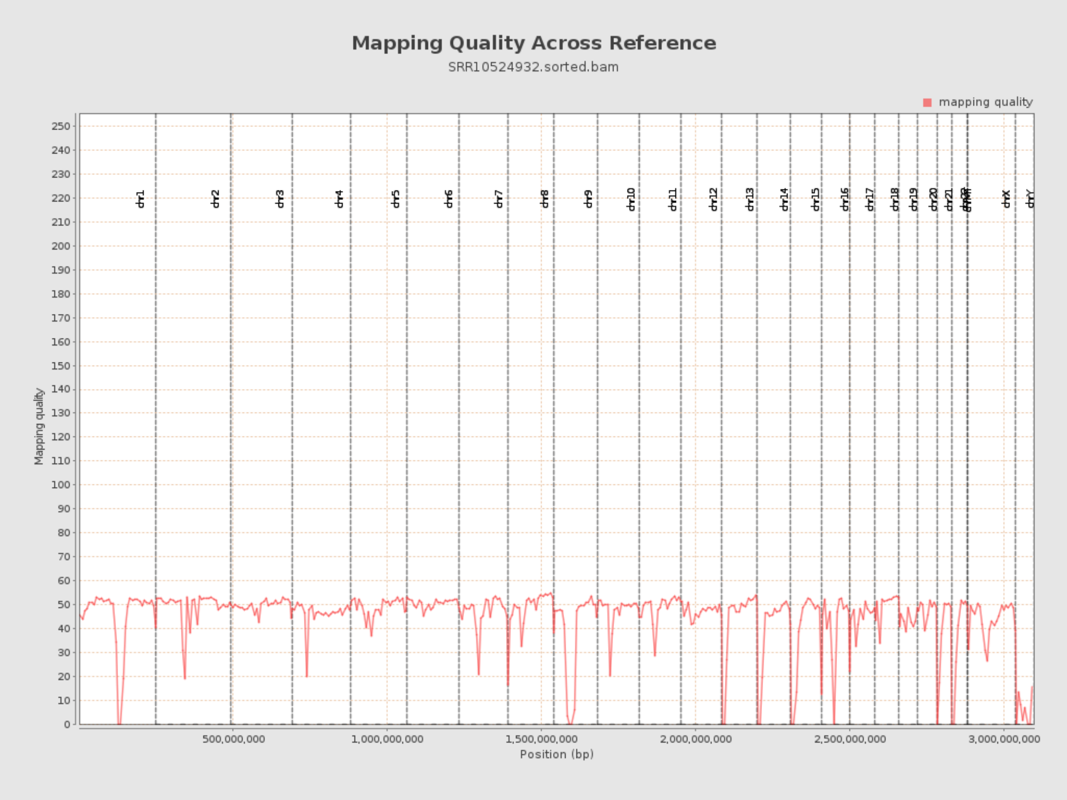
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram