Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:09:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524749.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_SRR10524749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,430,056
Mapped reads	1,299,613 / 90.88%
Unmapped reads	130,443 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,747 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	52,176 / 3.65%
Duplication rate	3.09%
Clipped reads	1,300,446 / 90.94%

2.2. ACGT Content

Number/percentage of A's	18,371,063 / 24.8%
Number/percentage of C's	13,550,336 / 18.3%
Number/percentage of T's	24,222,817 / 32.7%
Number/percentage of G's	17,911,613 / 24.18%
Number/percentage of N's	8,956 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.2244

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

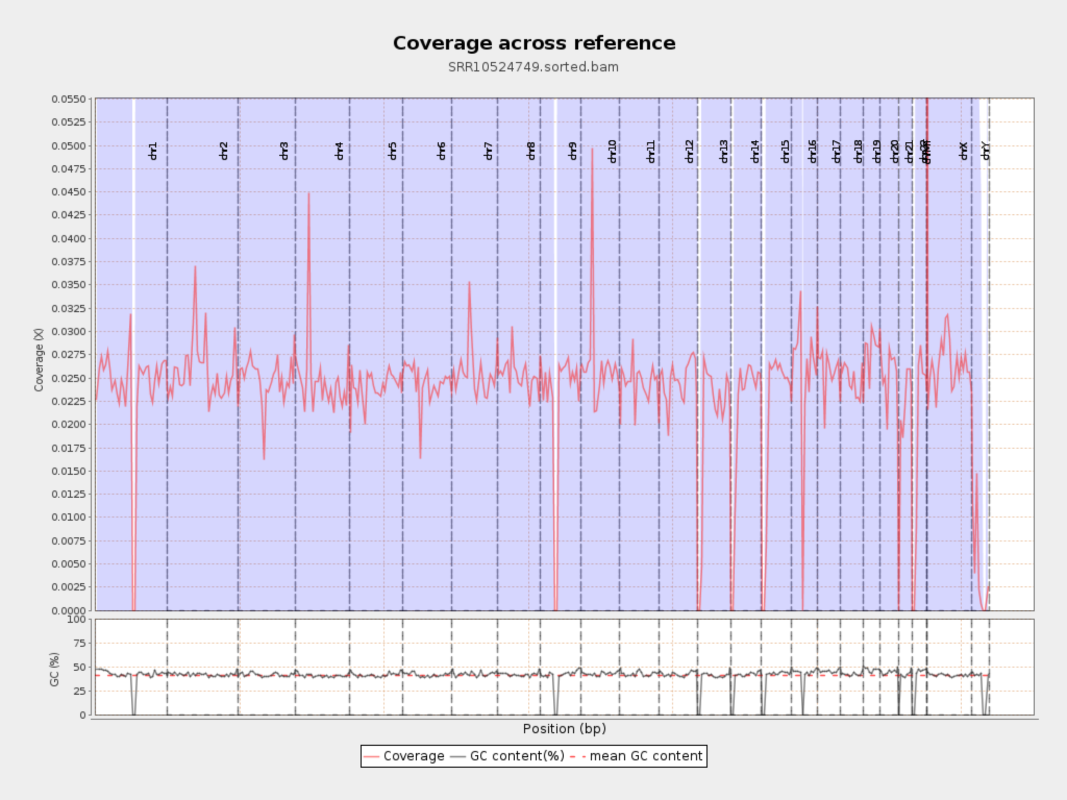
General error rate	0.53%
Mismatches	380,014
Insertions	5,399
Mapped reads with at least one insertion	0.41%
Deletions	14,803
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.43%

2.6. Chromosome stats

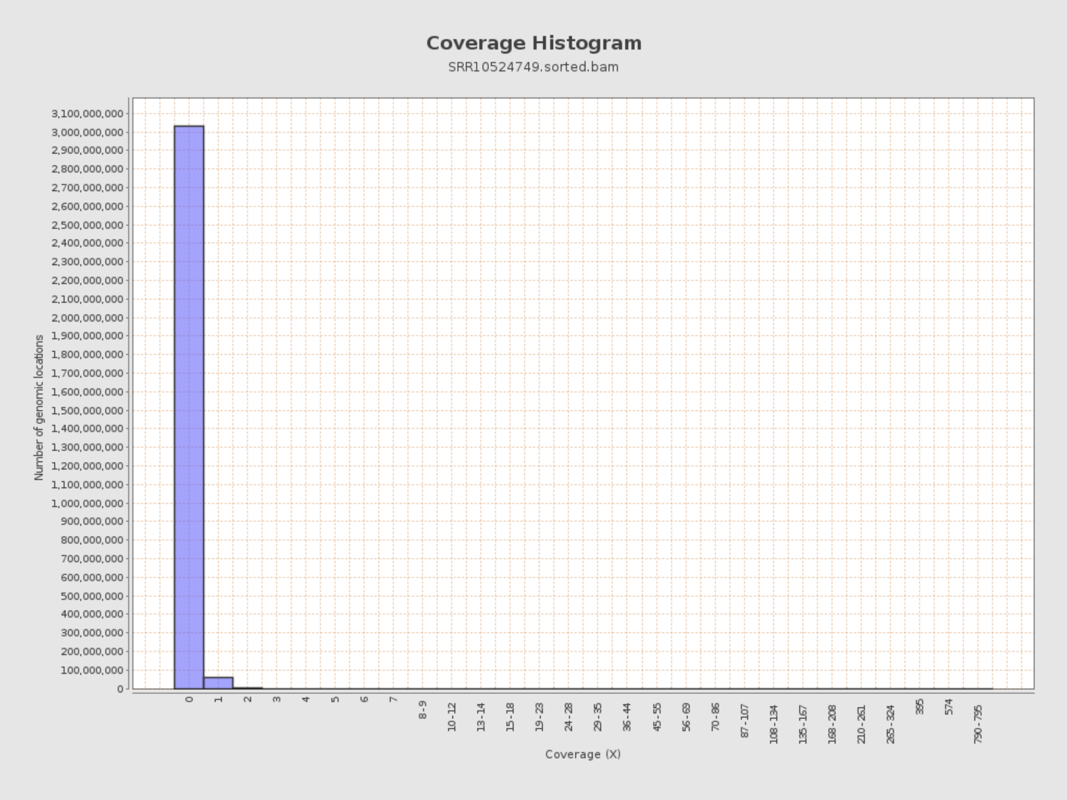
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5905218	0.0237	0.2882
chr2	243199373	6262863	0.0258	0.368
chr3	198022430	4915562	0.0248	0.1751
chr4	191154276	4769176	0.0249	0.1964
chr5	180915260	4404475	0.0243	0.171
chr6	171115067	4186205	0.0245	0.1861
chr7	159138663	4076151	0.0256	0.2593

chr8	146364022	3703082	0.0253	0.2148
chr9	141213431	3149623	0.0223	0.1958
chr10	135534747	3617260	0.0267	0.2573
chr11	135006516	3328556	0.0247	0.2056
chr12	133851895	3314509	0.0248	0.1746
chr13	115169878	2284740	0.0198	0.1537
chr14	107349540	2232839	0.0208	0.162
chr15	102531392	2124539	0.0207	0.1614
chr16	90354753	2244021	0.0248	0.1871
chr17	81195210	2090594	0.0257	0.1856
chr18	78077248	1928035	0.0247	0.2919
chr19	59128983	1662940	0.0281	0.254
chr20	63025520	1588670	0.0252	0.1831
chr21	48129895	990871	0.0206	0.1747
chr22	51304566	935114	0.0182	0.1497
chrMT	16571	24241	1.4629	1.541
chrX	155270560	4100131	0.0264	0.1908
chrY	59373566	249371	0.0042	0.1174

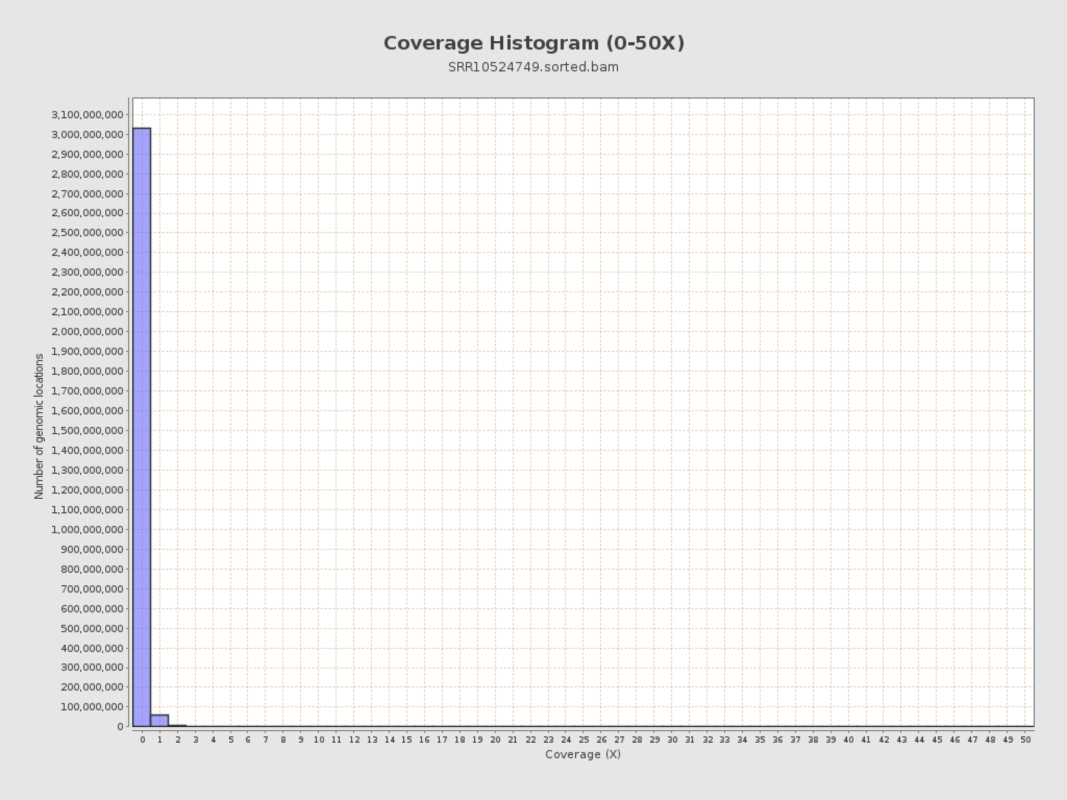
3. Results : Coverage across reference



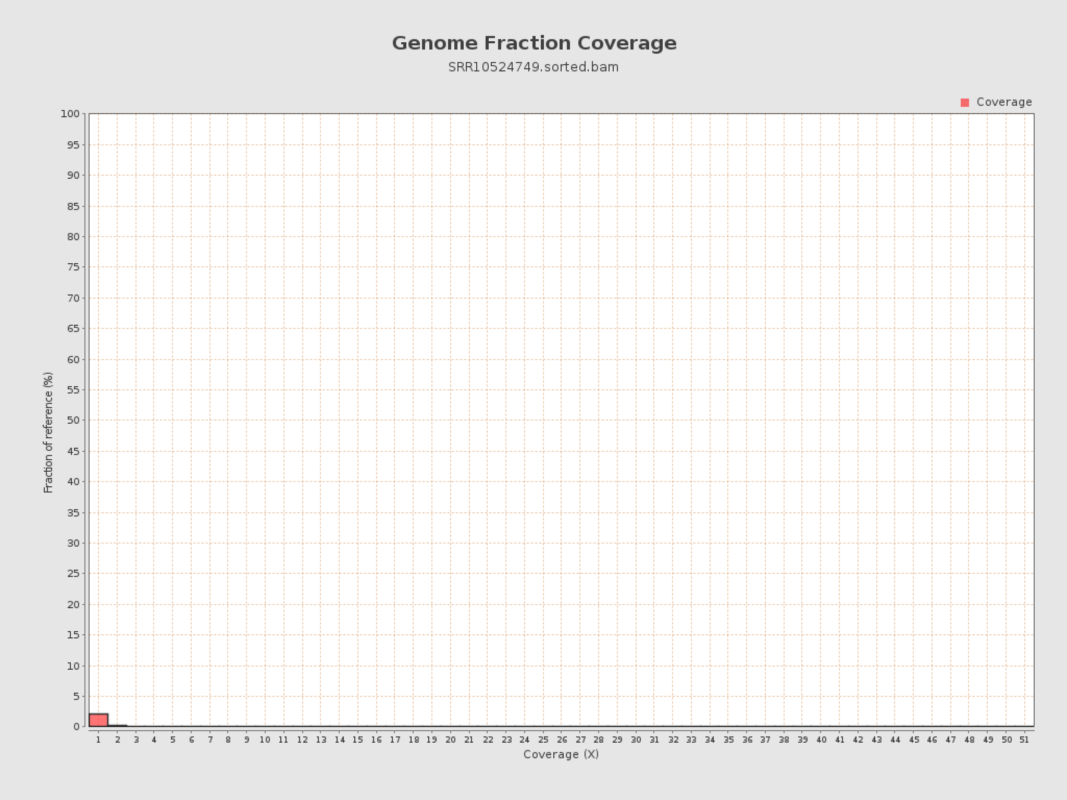
4. Results : Coverage Histogram



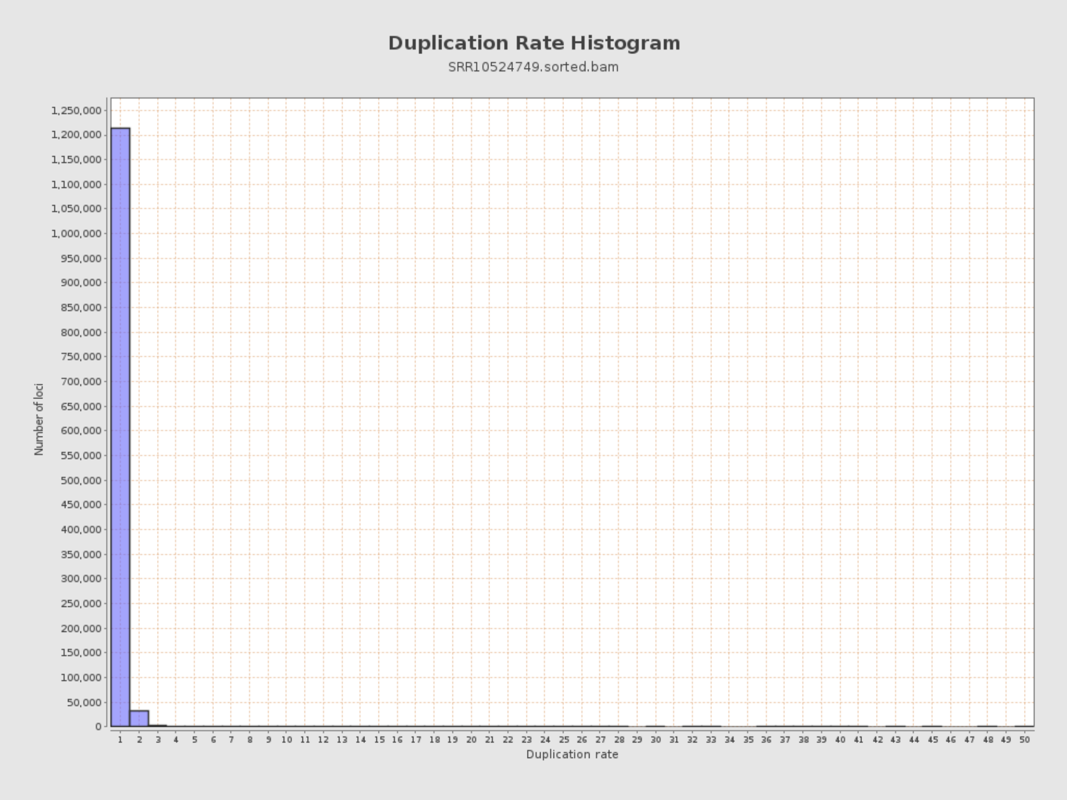
5. Results : Coverage Histogram (0-50X)



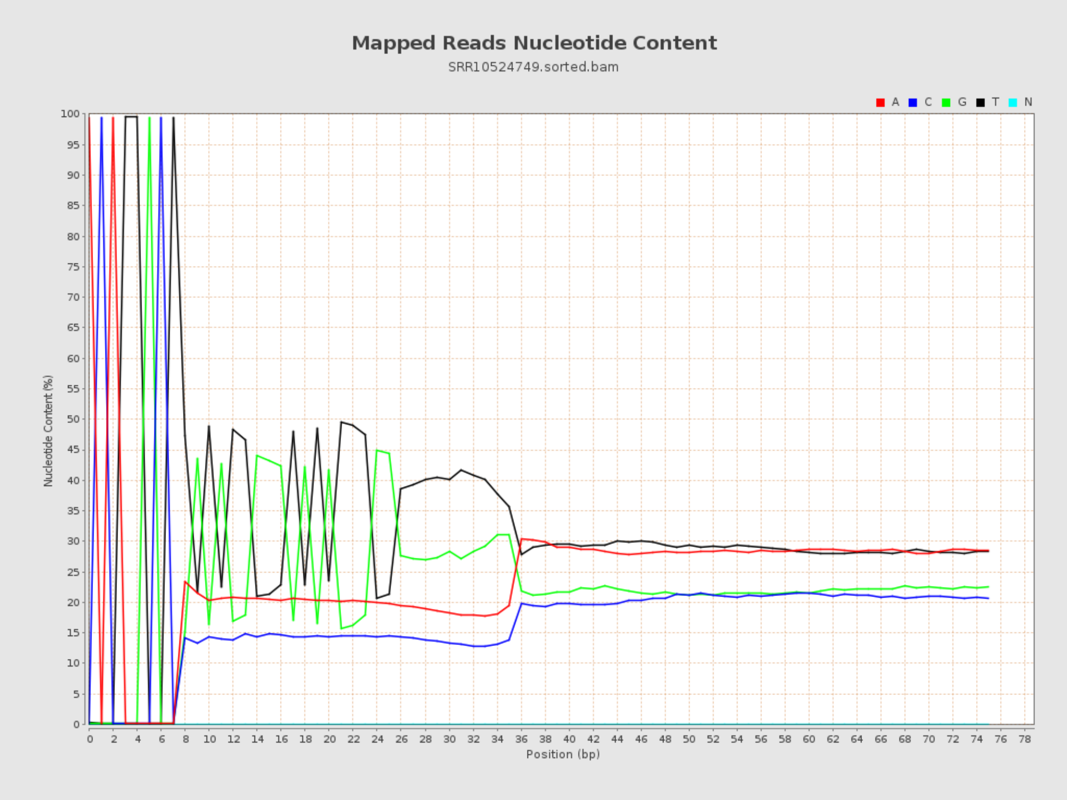
6. Results : Genome Fraction Coverage



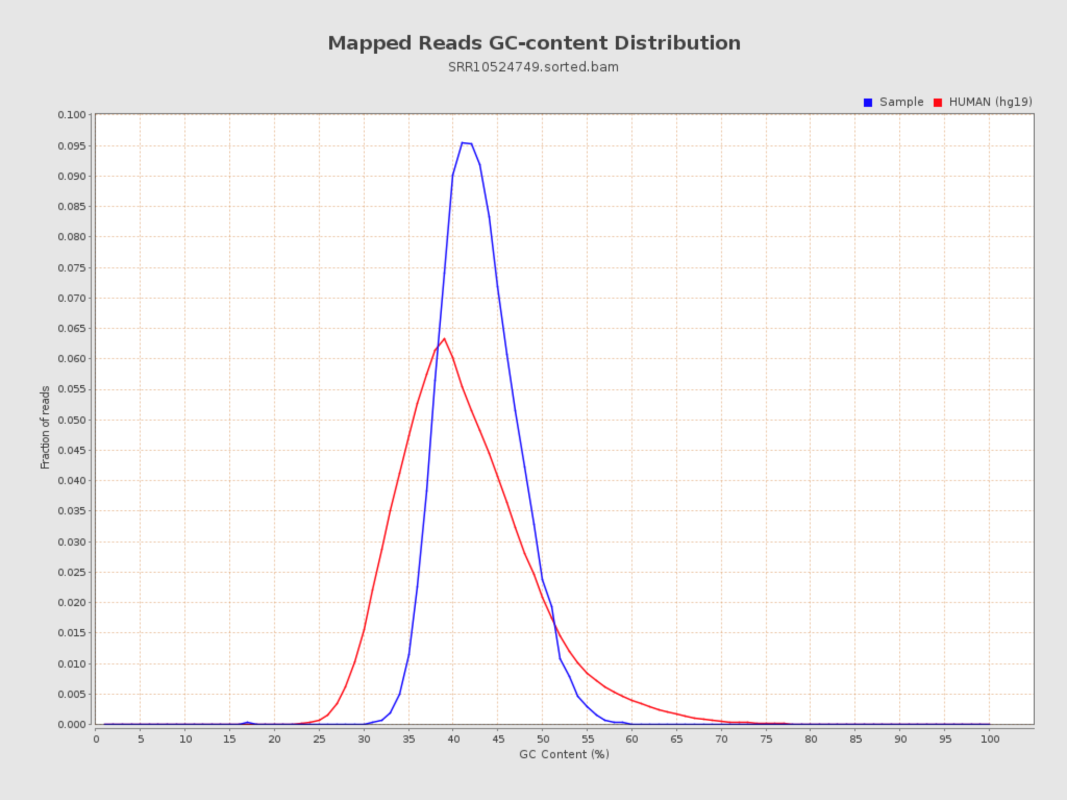
7. Results : Duplication Rate Histogram



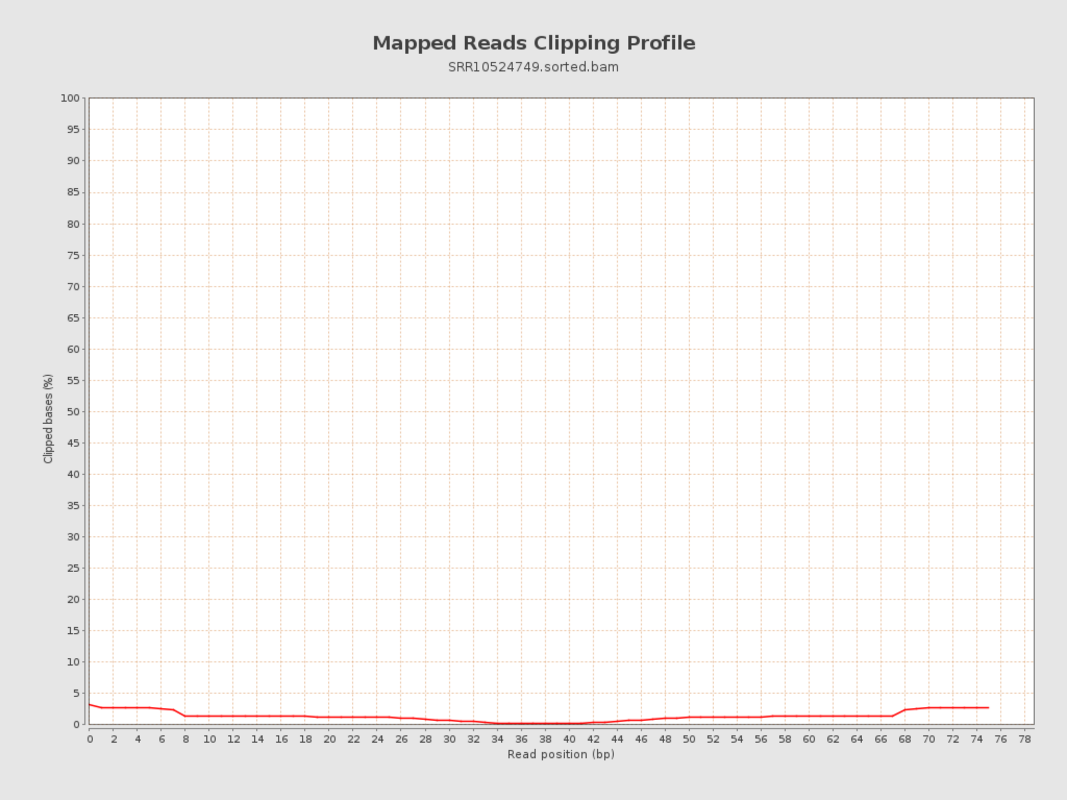
8. Results : Mapped Reads Nucleotide Content



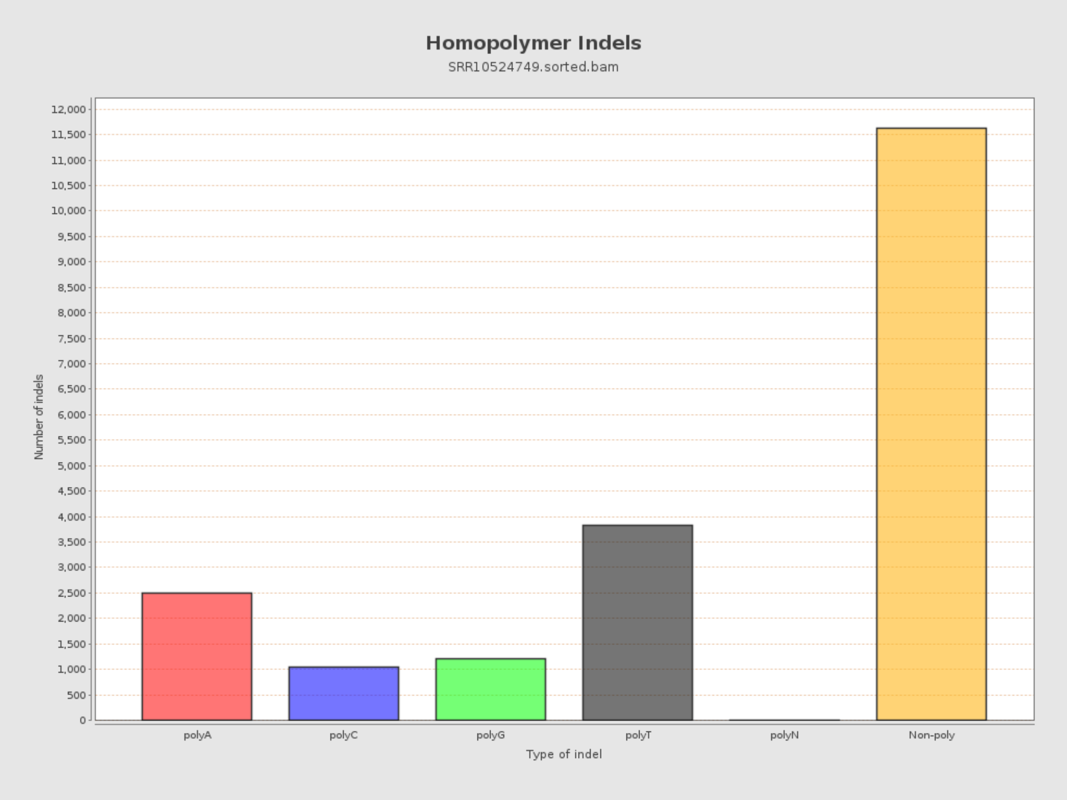
9. Results : Mapped Reads GC-content Distribution



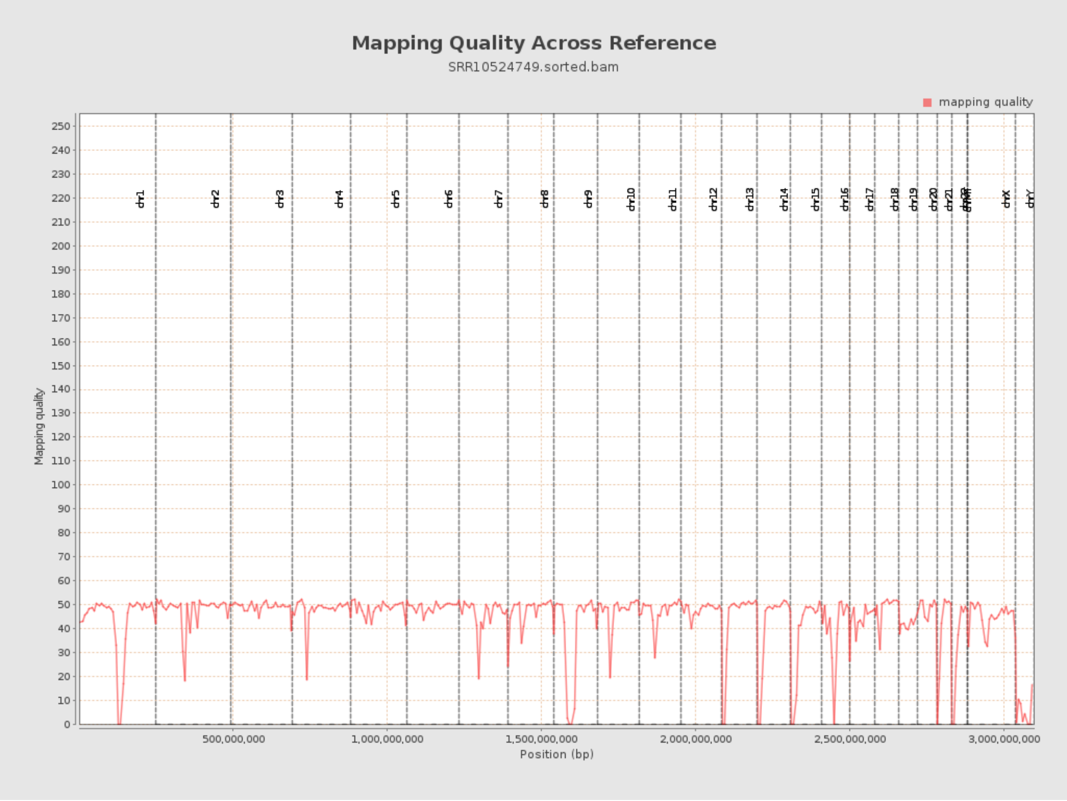
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram