Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:30:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524861.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_SRR10524861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:30:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,674,686
Mapped reads	1,533,000 / 91.54%
Unmapped reads	141,686 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,721 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	43,012 / 2.57%
Duplication rate	1.88%
Clipped reads	1,536,629 / 91.76%

2.2. ACGT Content

Number/percentage of A's	23,346,637 / 26.11%
Number/percentage of C's	17,234,857 / 19.27%
Number/percentage of T's	28,005,272 / 31.32%
Number/percentage of G's	20,827,886 / 23.29%
Number/percentage of N's	11,476 / 0.01%
GC Percentage	42.56%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2845

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

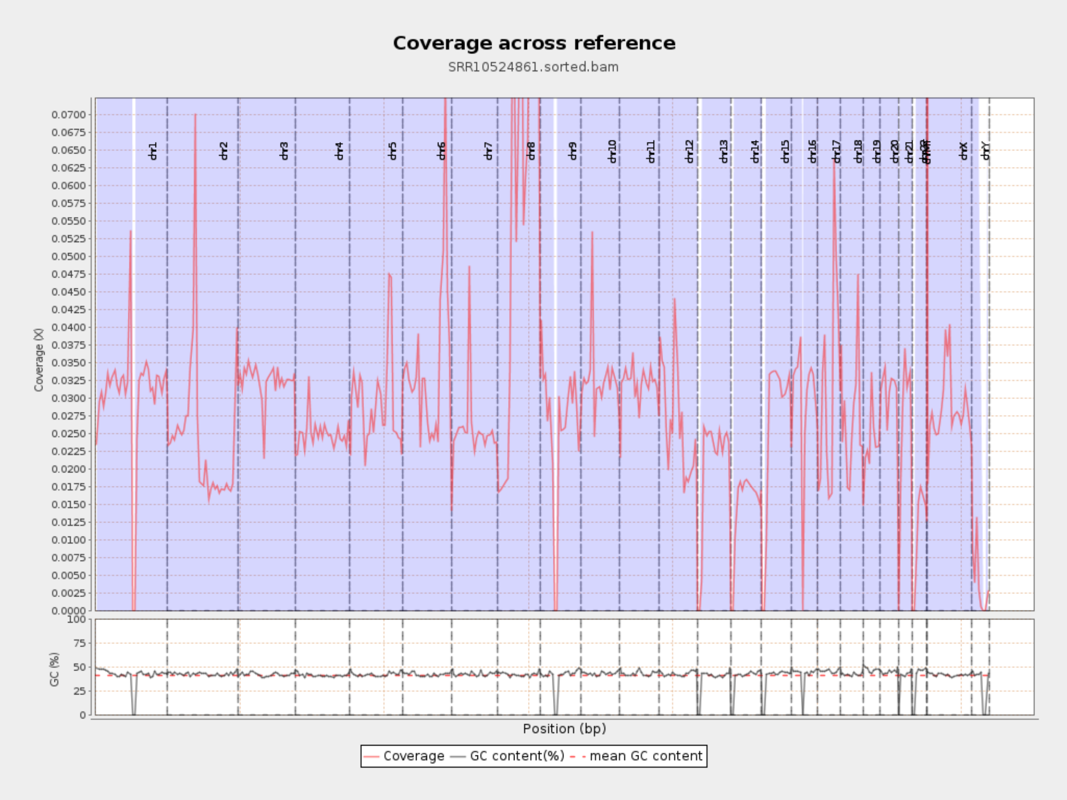
General error rate	0.49%
Mismatches	432,134
Insertions	5,858
Mapped reads with at least one insertion	0.38%
Deletions	16,658
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.82%

2.6. Chromosome stats

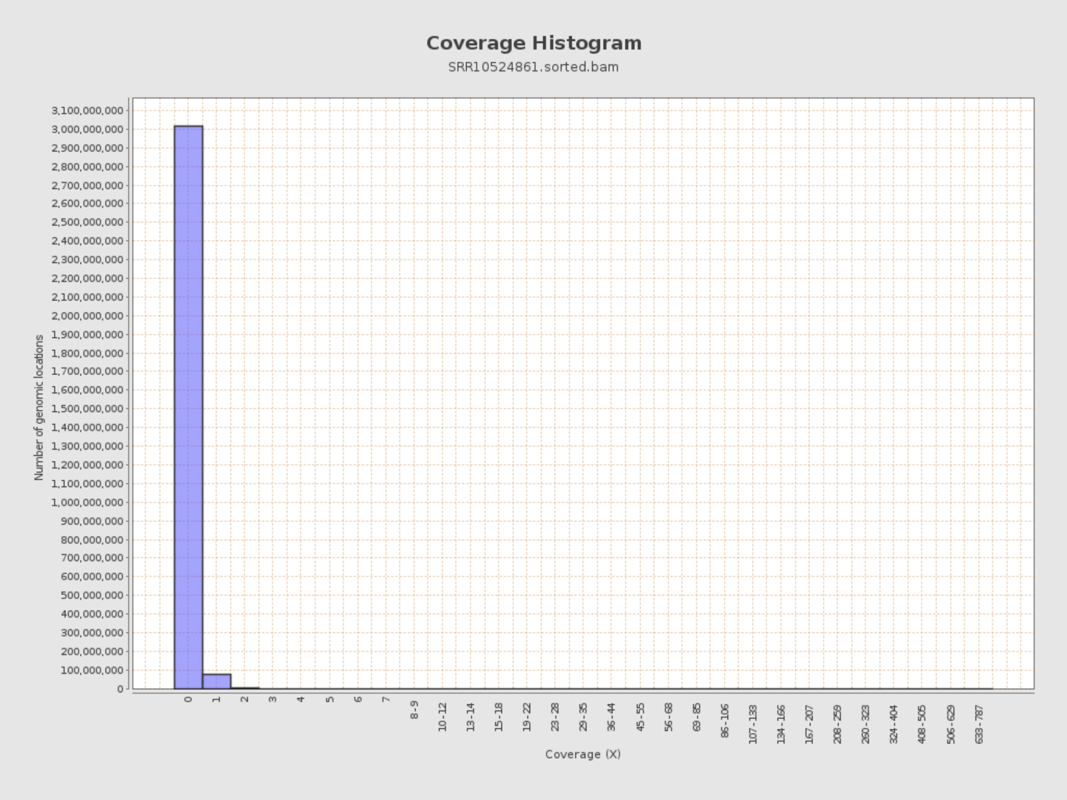
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7537253	0.0302	0.5653
chr2	243199373	5836389	0.024	0.2989
chr3	198022430	6406999	0.0324	0.1914
chr4	191154276	4761475	0.0249	0.1821
chr5	180915260	5361591	0.0296	0.1843
chr6	171115067	5843868	0.0342	0.2178
chr7	159138663	4101139	0.0258	0.376

chr8	146364022	9757604	0.0667	0.3722
chr9	141213431	3689097	0.0261	0.2339
chr10	135534747	4448937	0.0328	0.2685
chr11	135006516	4333892	0.0321	0.247
chr12	133851895	3546317	0.0265	0.1796
chr13	115169878	2311844	0.0201	0.1507
chr14	107349540	1566122	0.0146	0.1393
chr15	102531392	2684606	0.0262	0.1737
chr16	90354753	2640497	0.0292	0.194
chr17	81195210	2585824	0.0318	0.2145
chr18	78077248	2133763	0.0273	0.393
chr19	59128983	1417447	0.024	0.3974
chr20	63025520	1941118	0.0308	0.1891
chr21	48129895	1279656	0.0266	0.1863
chr22	51304566	575518	0.0112	0.1114
chrMT	16571	16517	0.9967	1.1687
chrX	155270560	4447975	0.0286	0.2063
chrY	59373566	226763	0.0038	0.1044

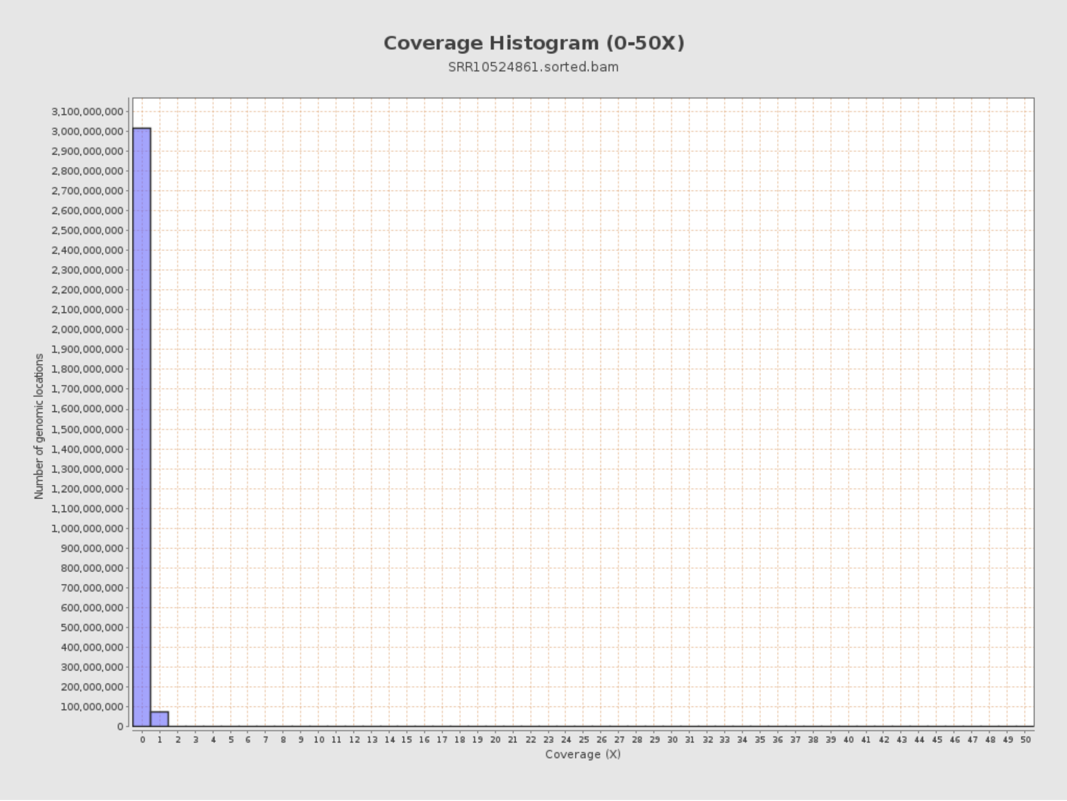
3. Results : Coverage across reference



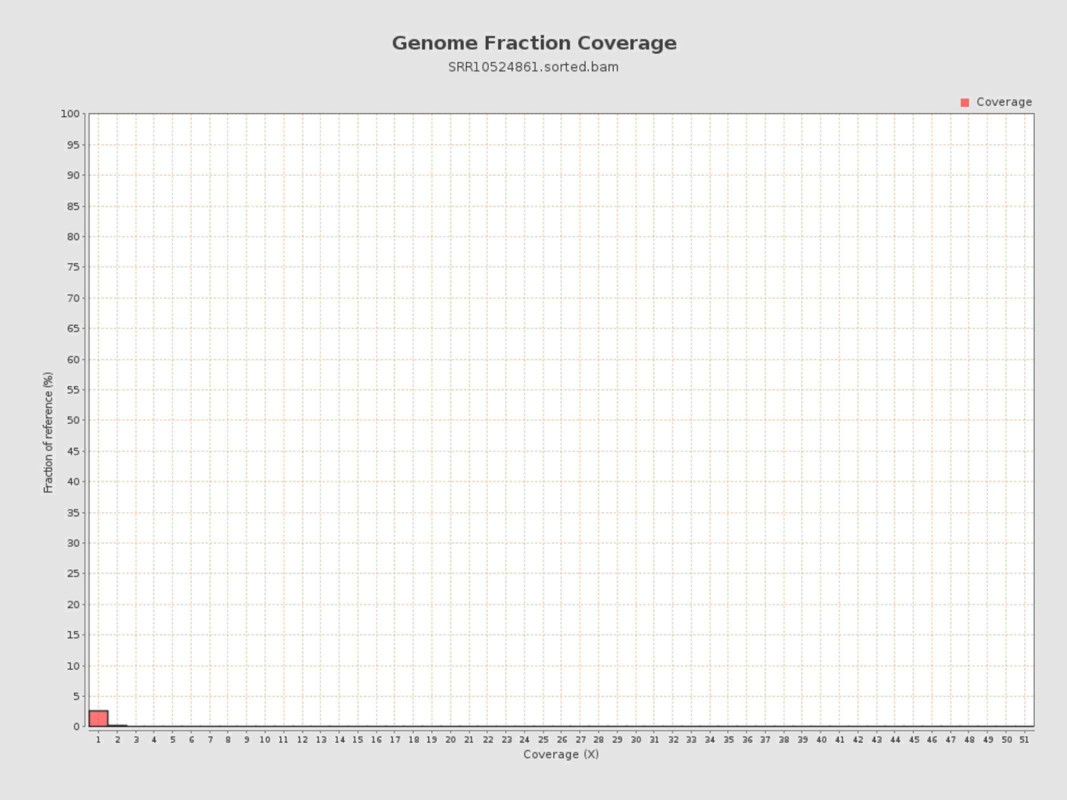
4. Results : Coverage Histogram



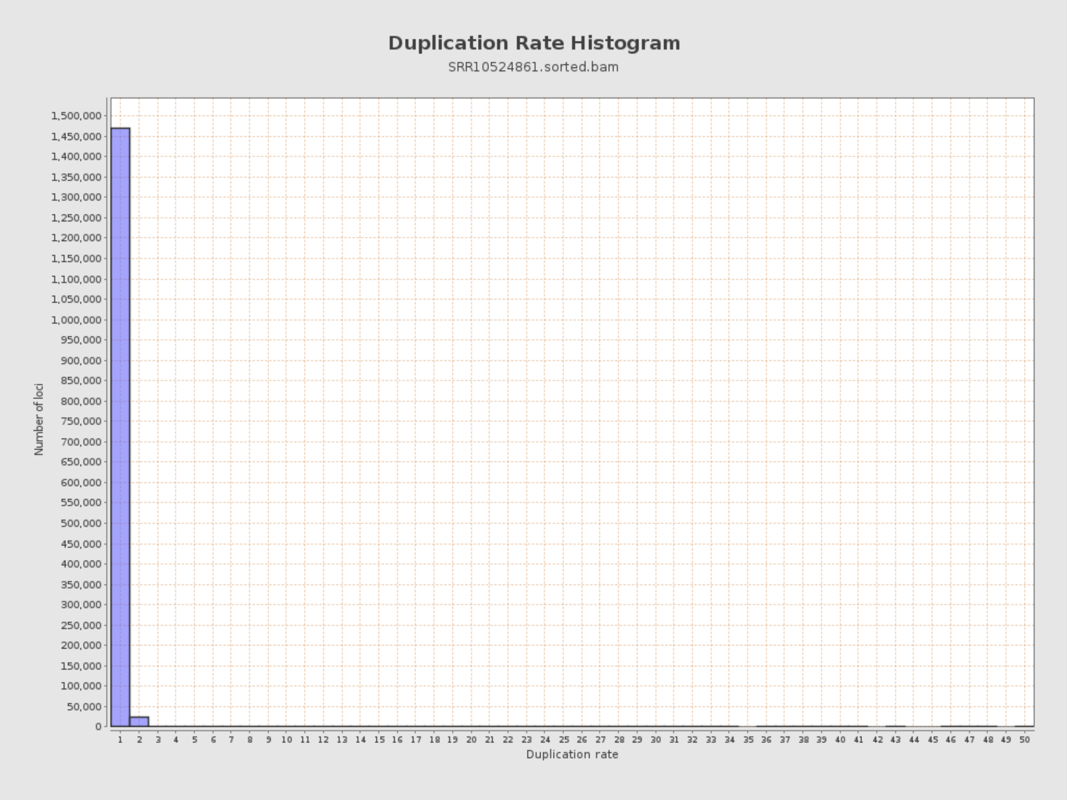
5. Results : Coverage Histogram (0-50X)



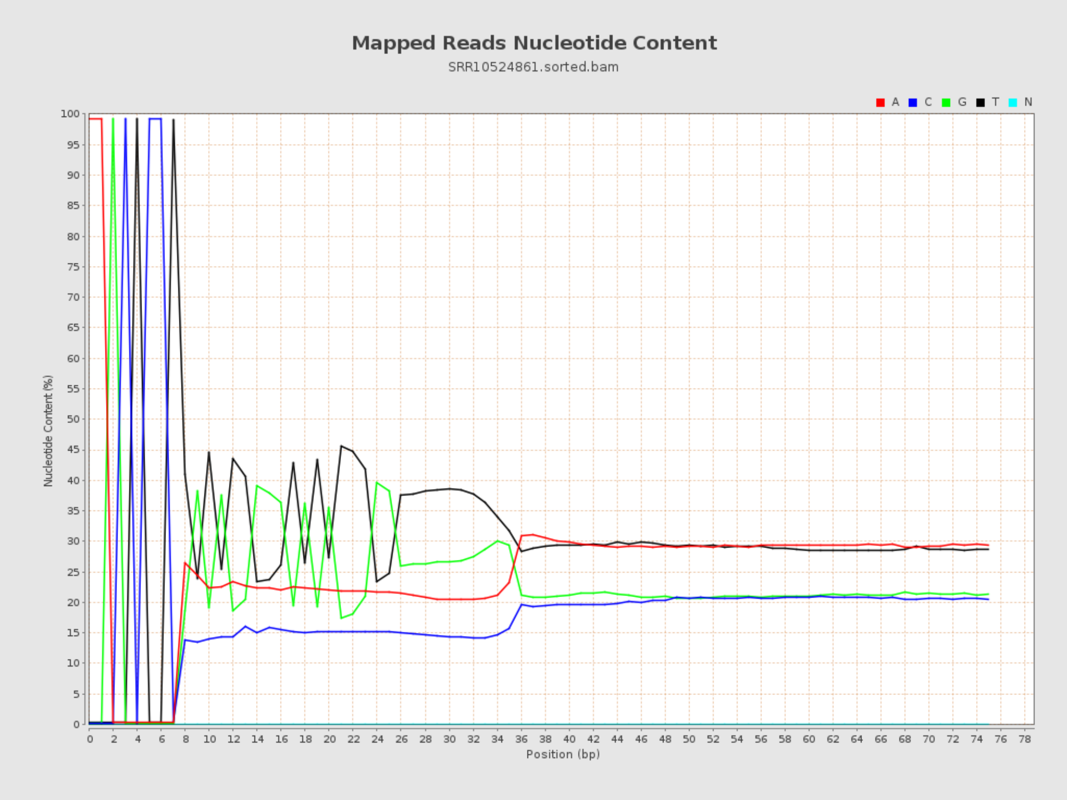
6. Results : Genome Fraction Coverage



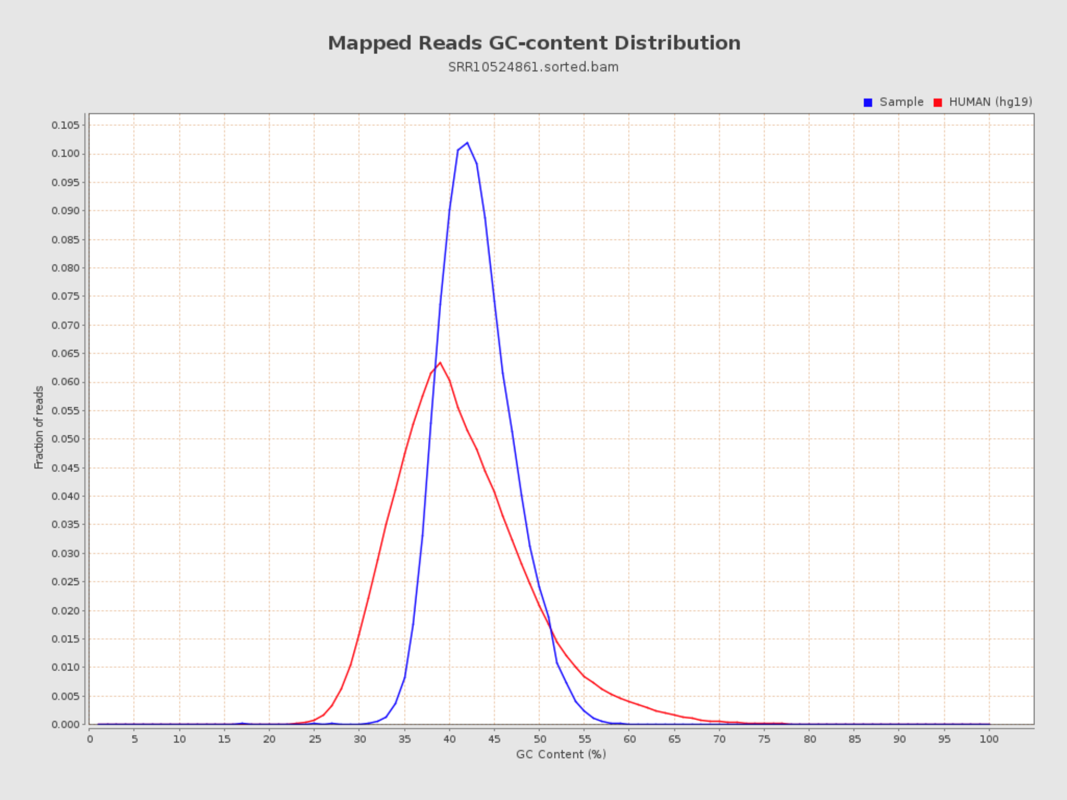
7. Results : Duplication Rate Histogram



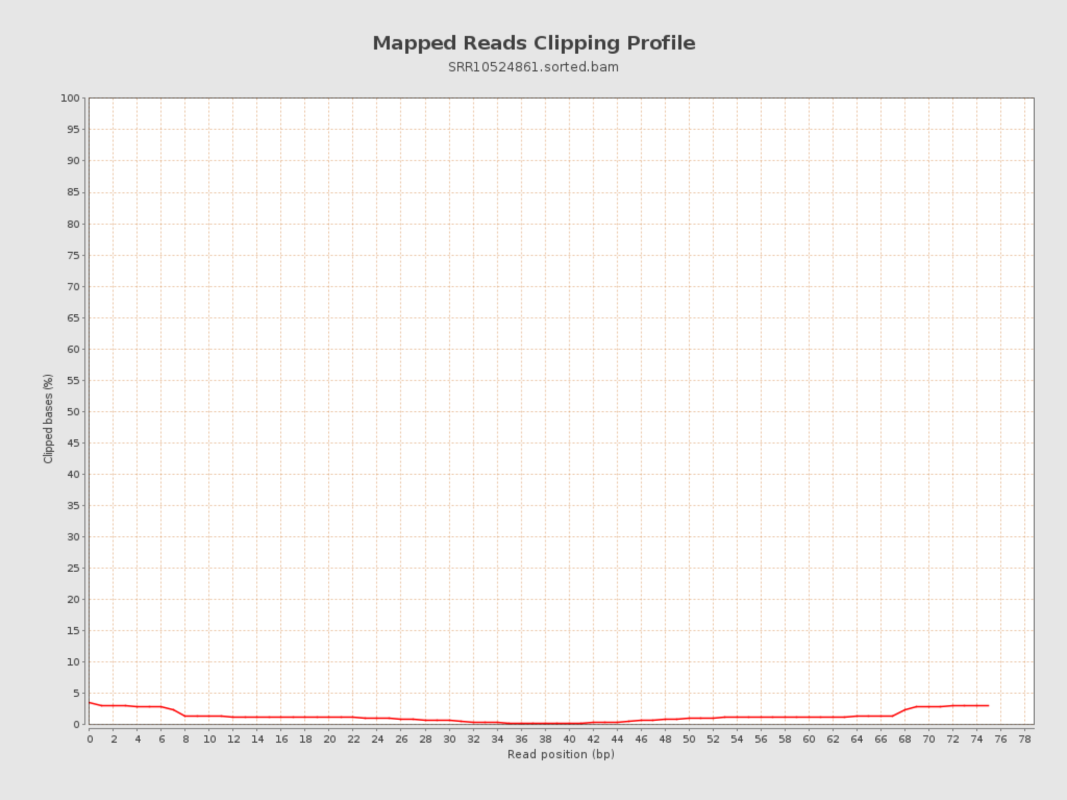
8. Results : Mapped Reads Nucleotide Content



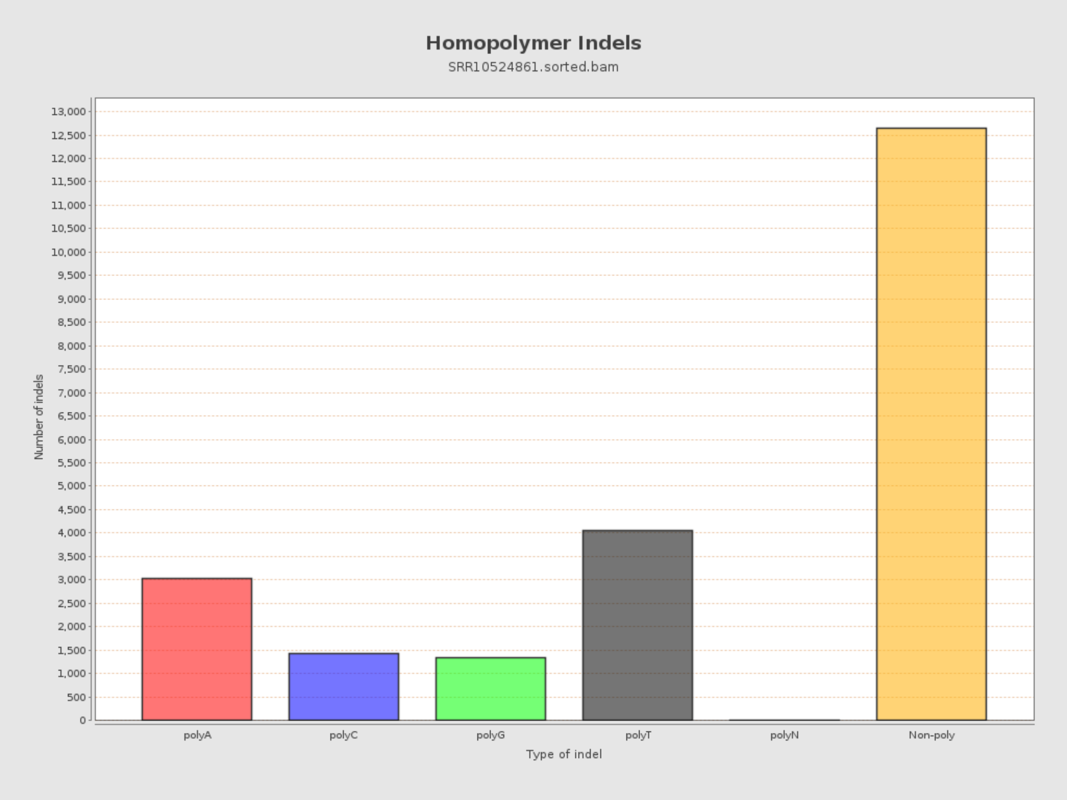
9. Results : Mapped Reads GC-content Distribution



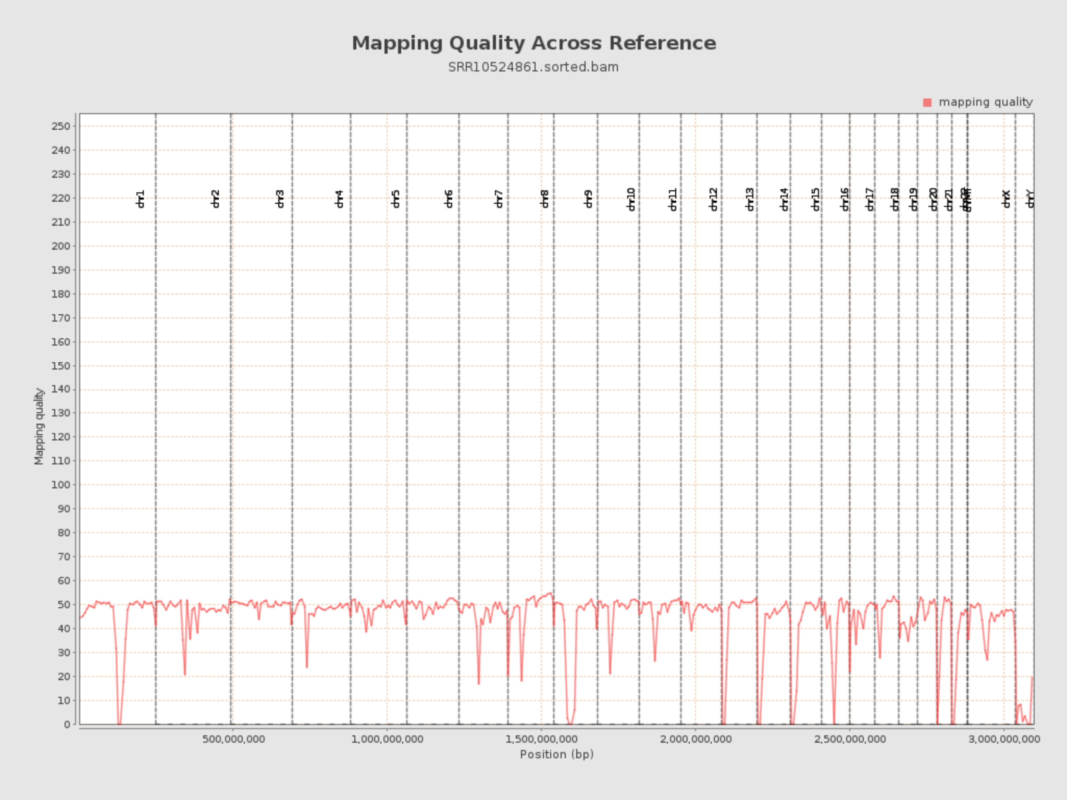
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram