Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:56:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524769.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_SRR10524769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:56:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,476,692
Mapped reads	1,347,216 / 91.23%
Unmapped reads	129,476 / 8.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,055 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	53,405 / 3.62%
Duplication rate	3.05%
Clipped reads	1,348,933 / 91.35%

2.2. ACGT Content

Number/percentage of A's	18,507,041 / 24.02%
Number/percentage of C's	13,550,404 / 17.59%
Number/percentage of T's	25,682,787 / 33.34%
Number/percentage of G's	19,289,188 / 25.04%
Number/percentage of N's	10,127 / 0.01%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2288

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

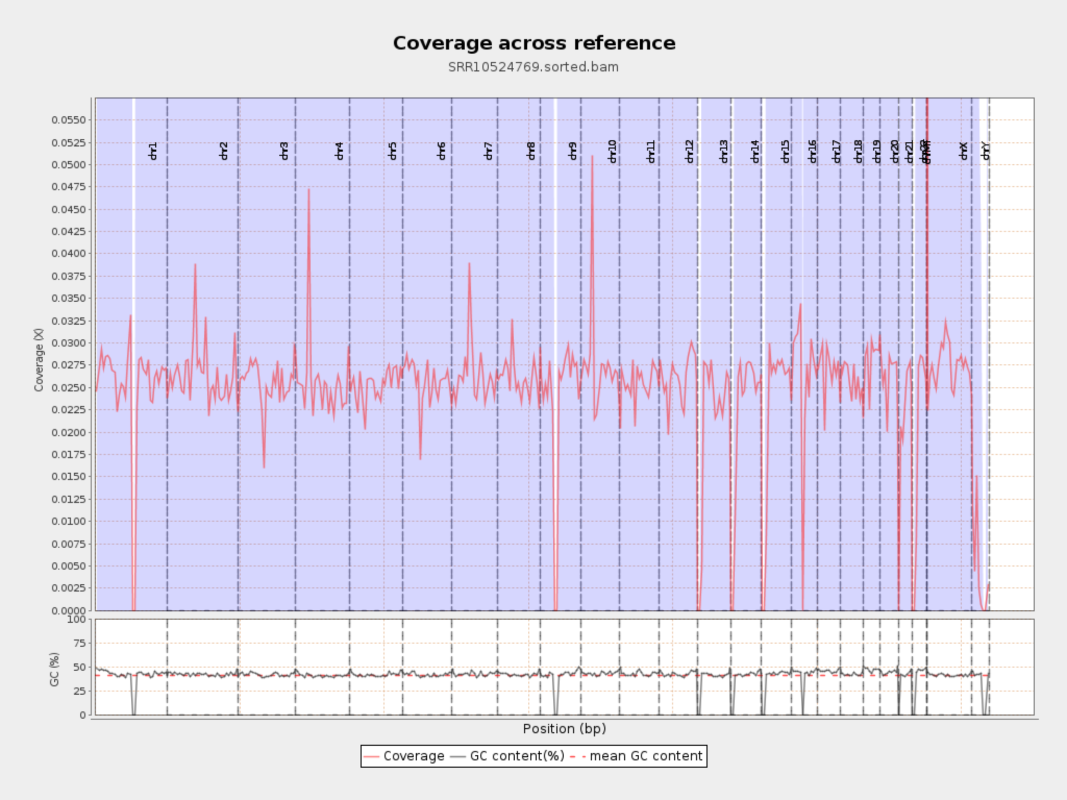
General error rate	0.53%
Mismatches	393,796
Insertions	5,524
Mapped reads with at least one insertion	0.41%
Deletions	15,658
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.88%

2.6. Chromosome stats

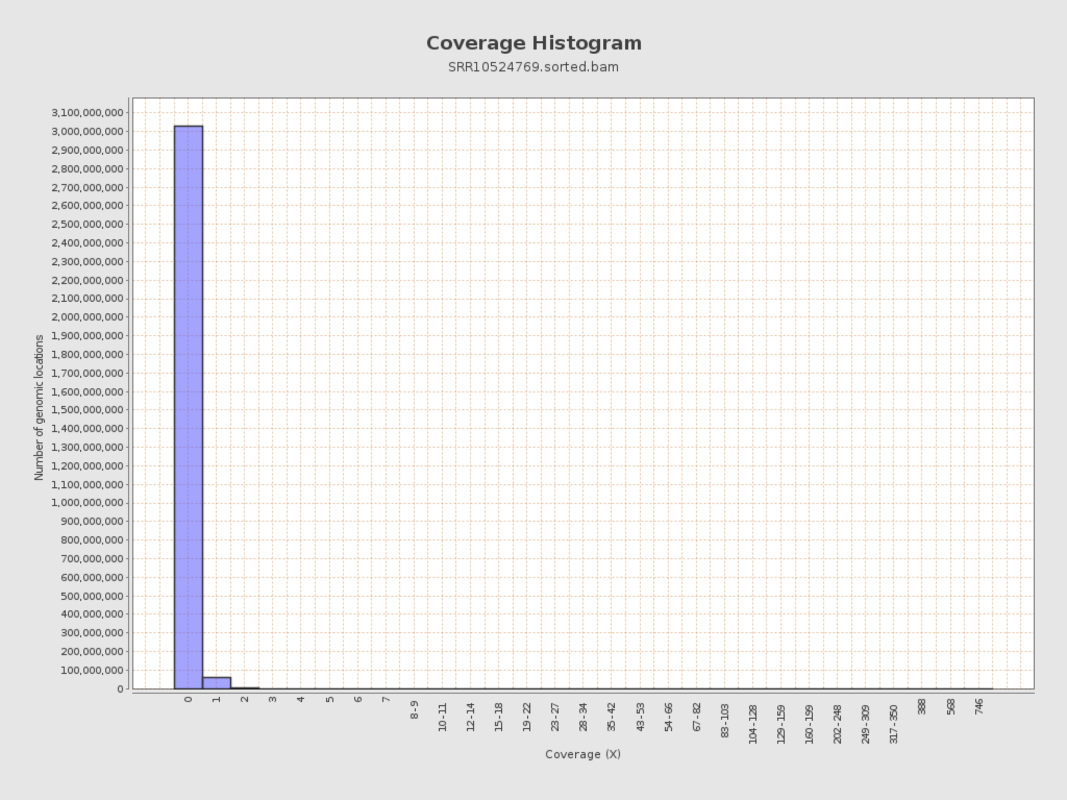
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6210818	0.0249	0.3017
chr2	243199373	6444655	0.0265	0.3638
chr3	198022430	5025765	0.0254	0.1788
chr4	191154276	4923594	0.0258	0.2
chr5	180915260	4581669	0.0253	0.1744
chr6	171115067	4387236	0.0256	0.1931
chr7	159138663	4222943	0.0265	0.2721

chr8	146364022	3817104	0.0261	0.216
chr9	141213431	3311034	0.0234	0.1978
chr10	135534747	3748244	0.0277	0.2672
chr11	135006516	3461769	0.0256	0.2081
chr12	133851895	3494701	0.0261	0.1814
chr13	115169878	2405459	0.0209	0.1584
chr14	107349540	2337159	0.0218	0.1645
chr15	102531392	2266804	0.0221	0.1635
chr16	90354753	2329582	0.0258	0.1892
chr17	81195210	2191966	0.027	0.1864
chr18	78077248	2016746	0.0258	0.3034
chr19	59128983	1663805	0.0281	0.2498
chr20	63025520	1658926	0.0263	0.1844
chr21	48129895	1034370	0.0215	0.1787
chr22	51304566	961894	0.0187	0.1528
chrMT	16571	39109	2.3601	2.2238
chrX	155270560	4272051	0.0275	0.1926
chrY	59373566	257767	0.0043	0.1228

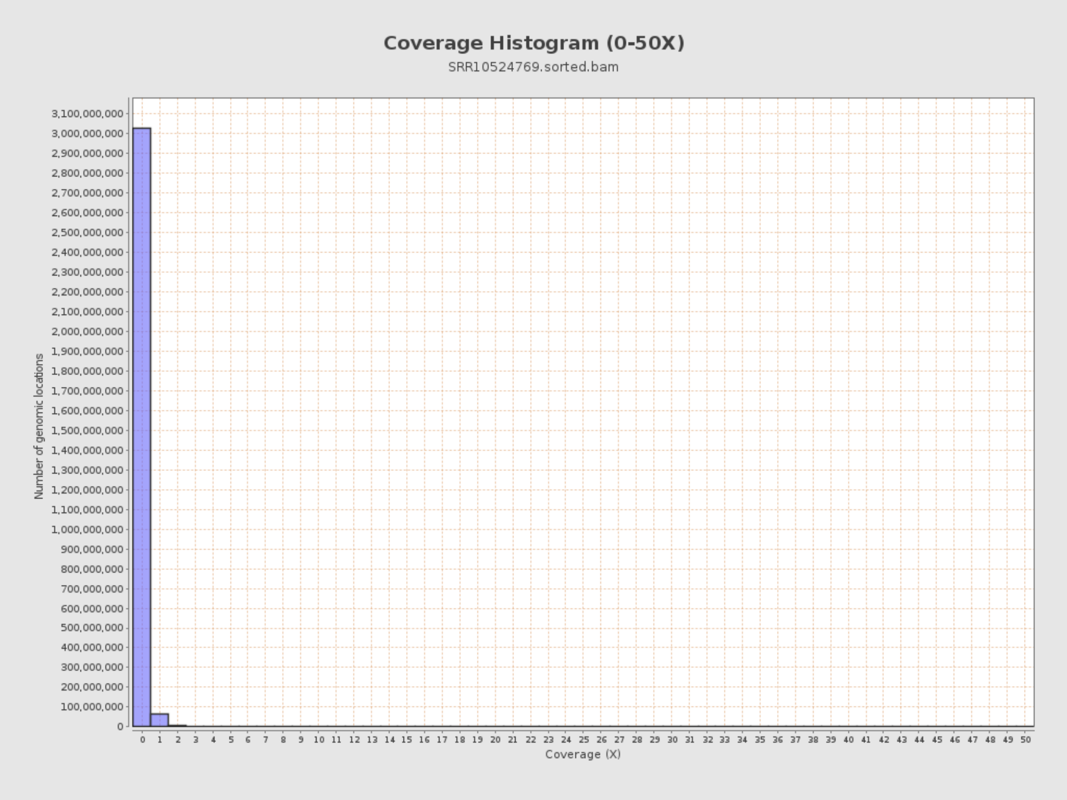
3. Results : Coverage across reference



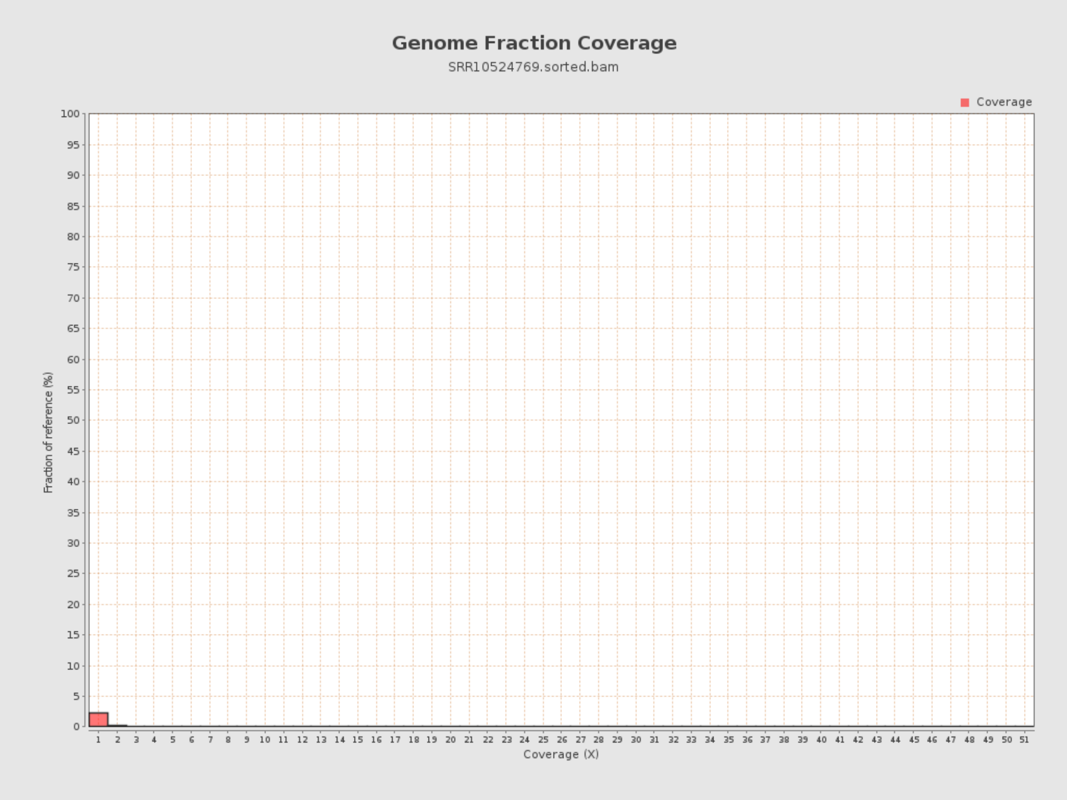
4. Results : Coverage Histogram



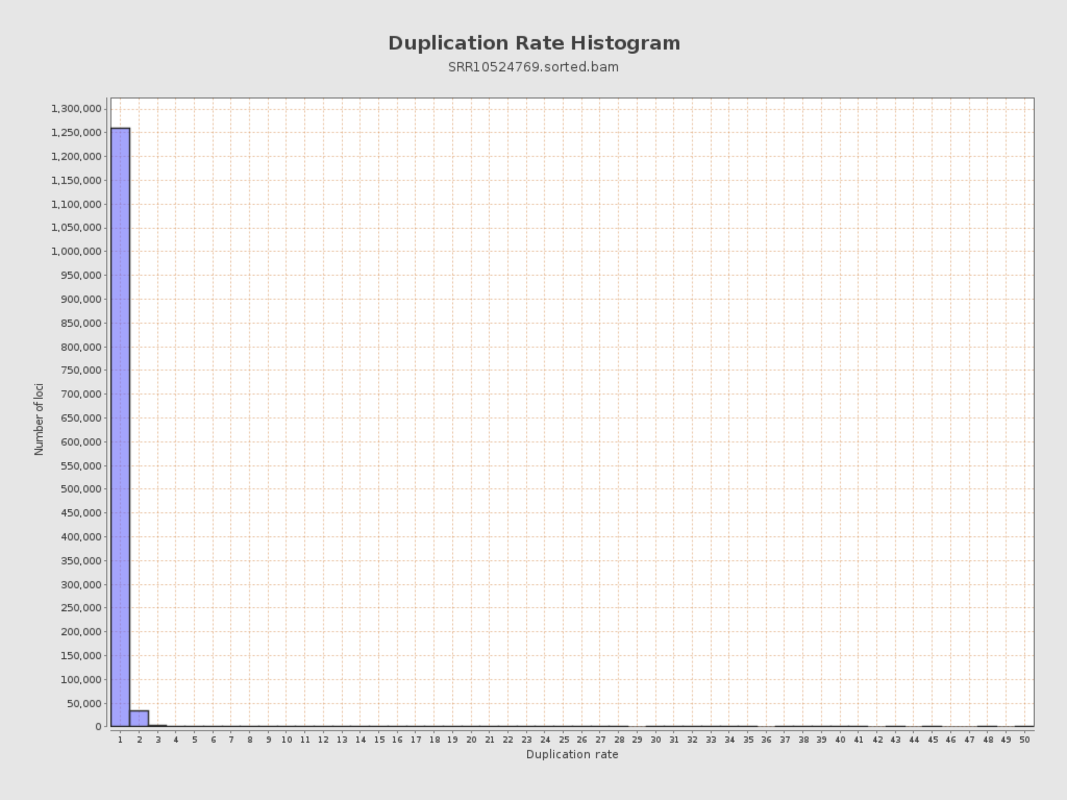
5. Results : Coverage Histogram (0-50X)



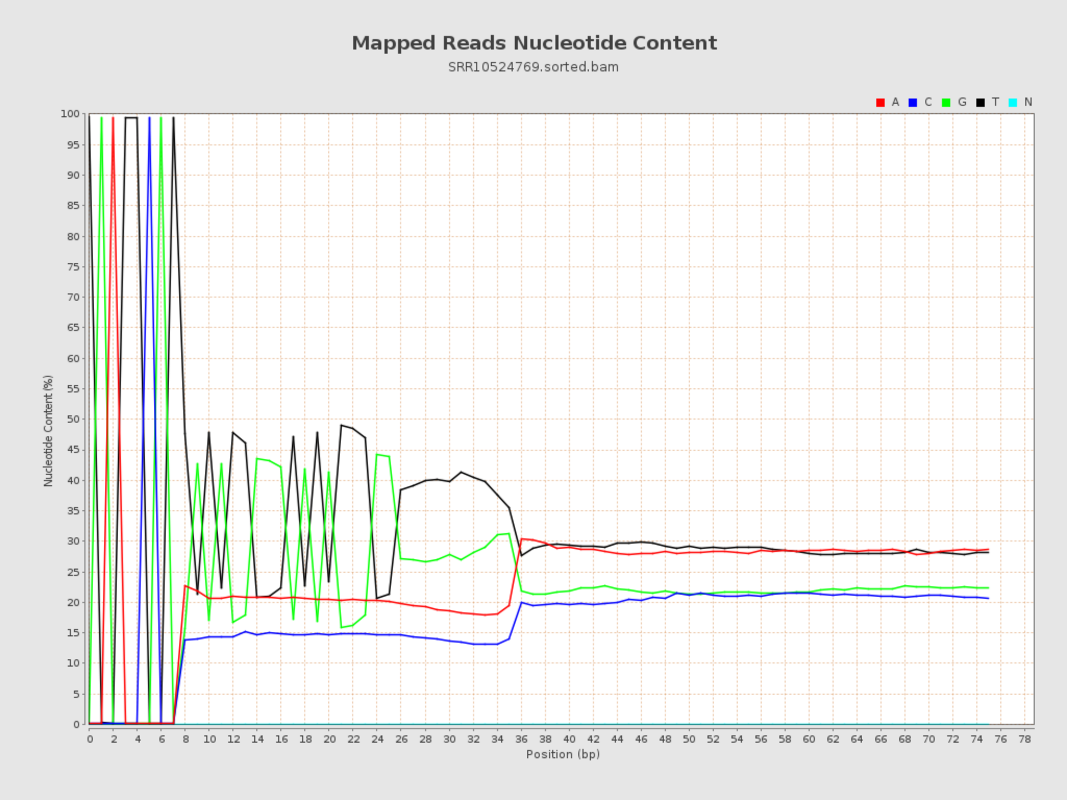
6. Results : Genome Fraction Coverage



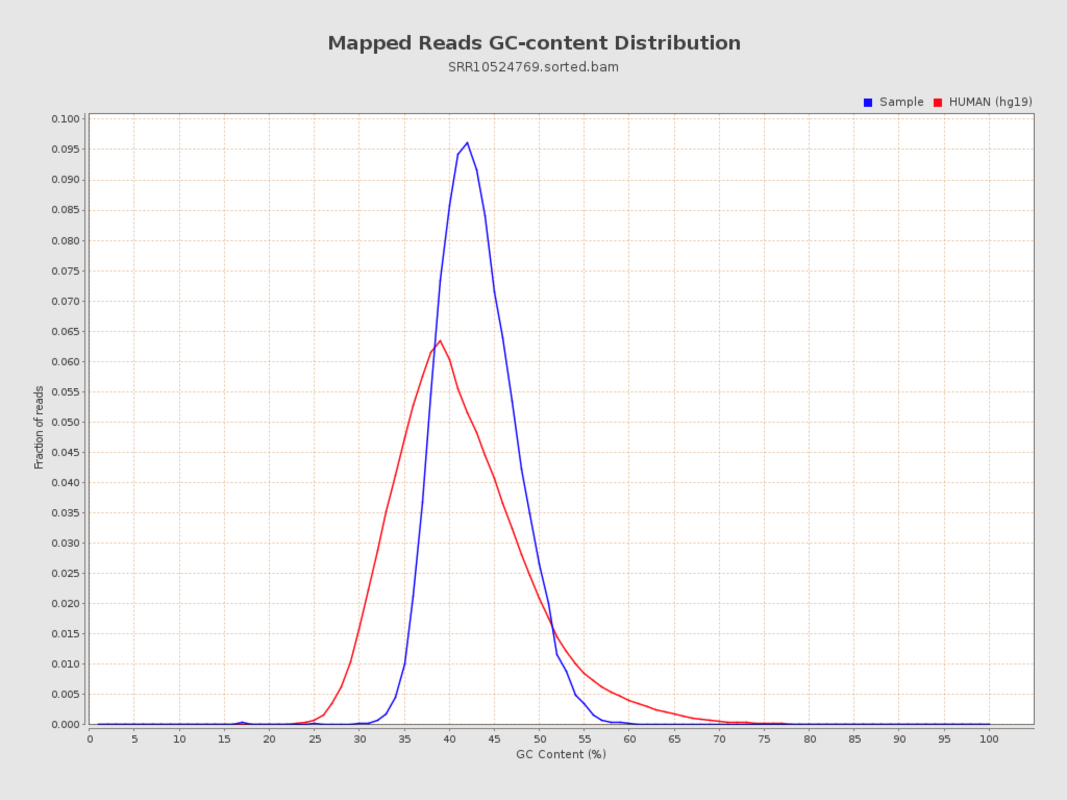
7. Results : Duplication Rate Histogram



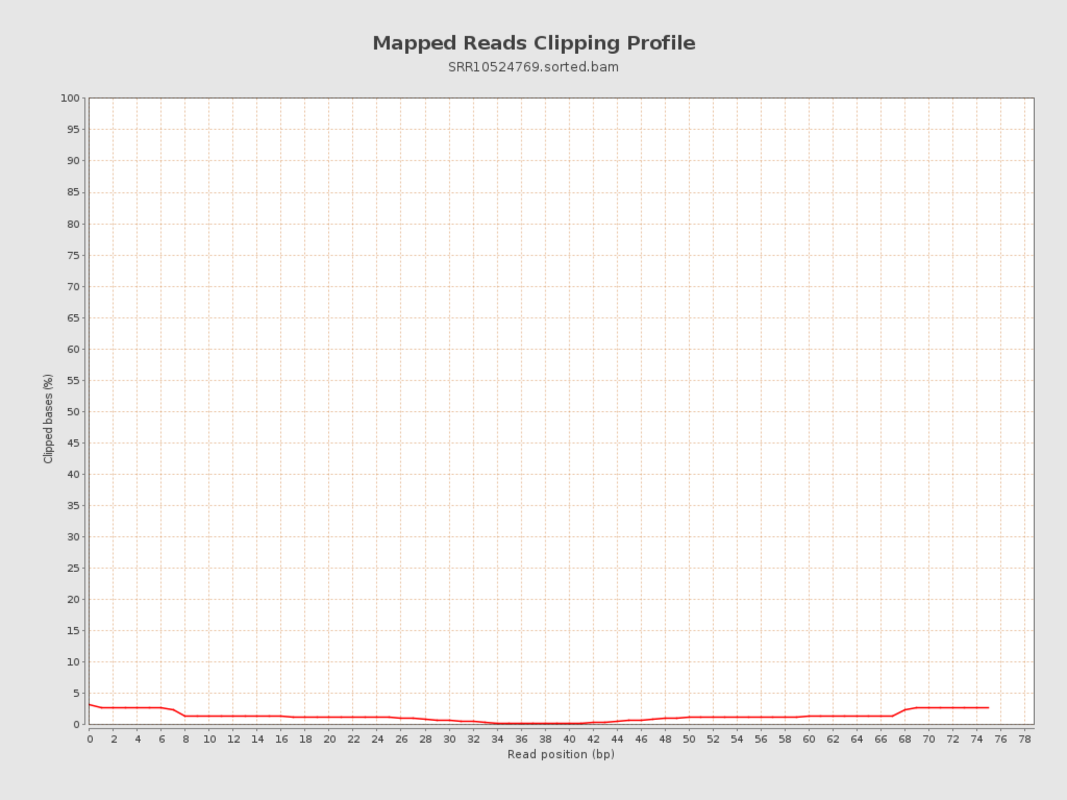
8. Results : Mapped Reads Nucleotide Content



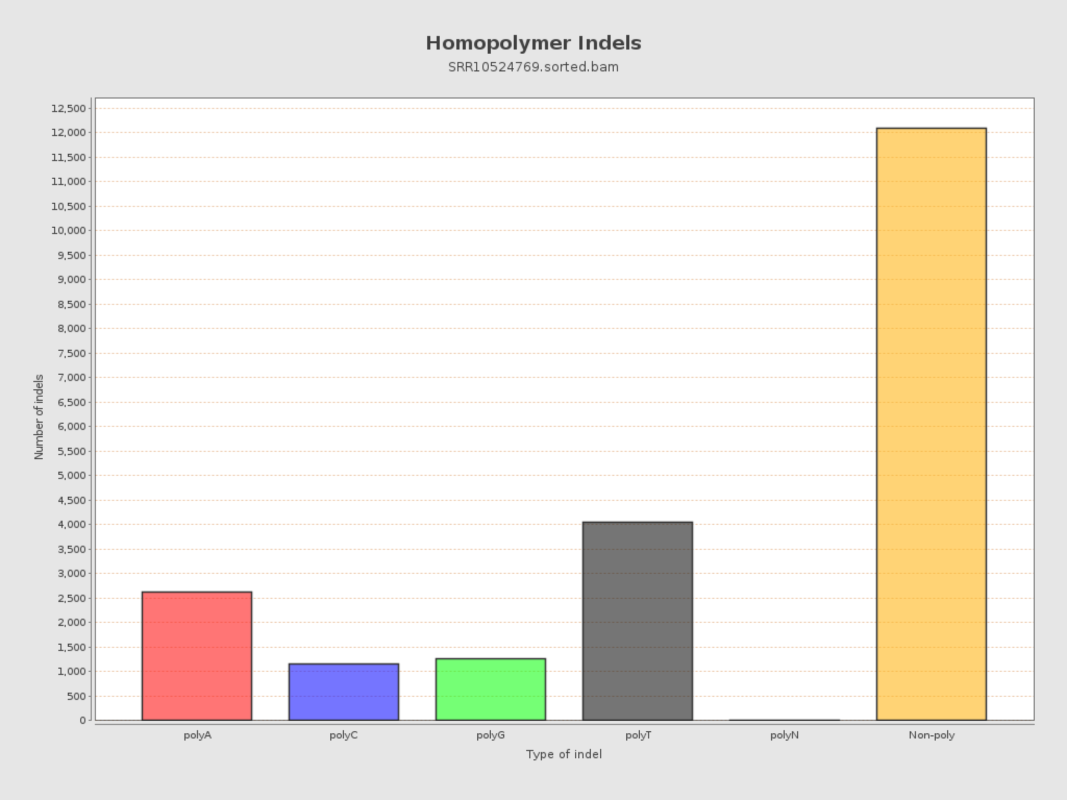
9. Results : Mapped Reads GC-content Distribution



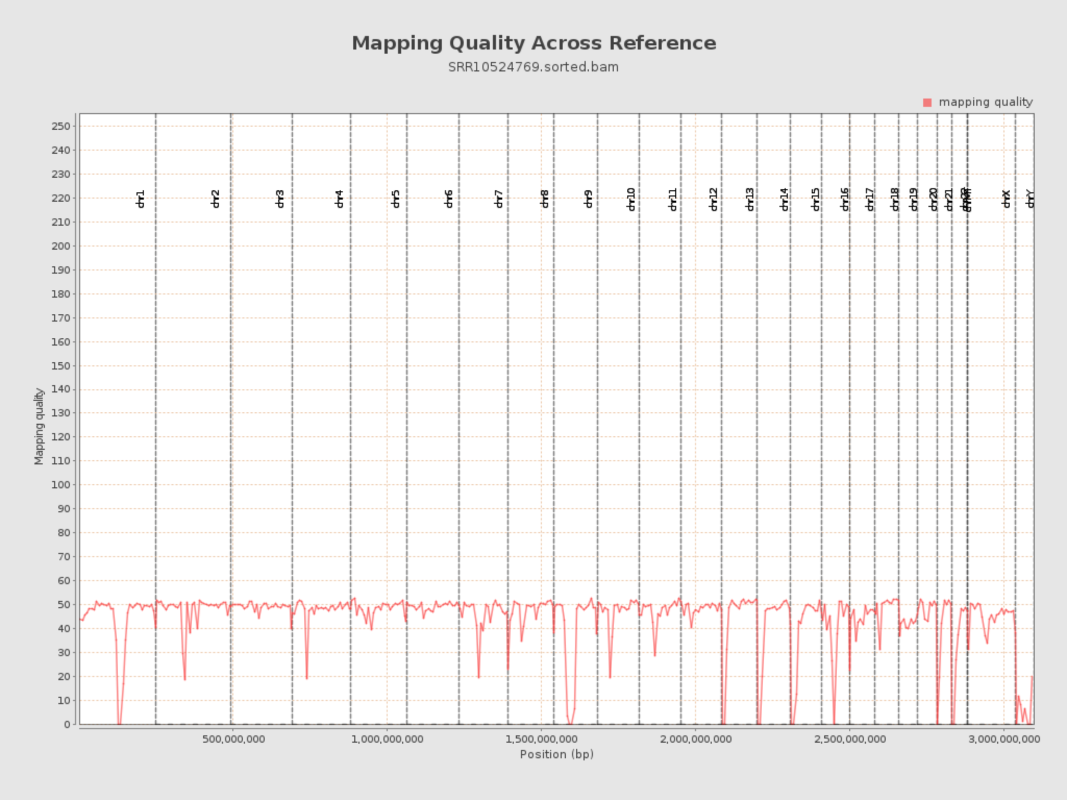
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram