Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:02:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524328.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_SRR10524328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:01:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,640
Mapped reads	703,310 / 91.5%
Unmapped reads	65,330 / 8.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,078 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	14,667 / 1.91%
Duplication rate	1.49%
Clipped reads	704,940 / 91.71%

2.2. ACGT Content

Number/percentage of A's	10,014,104 / 24.42%
Number/percentage of C's	7,487,385 / 18.26%
Number/percentage of T's	12,689,245 / 30.94%
Number/percentage of G's	10,811,555 / 26.36%
Number/percentage of N's	5,742 / 0.01%
GC Percentage	44.62%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1508

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

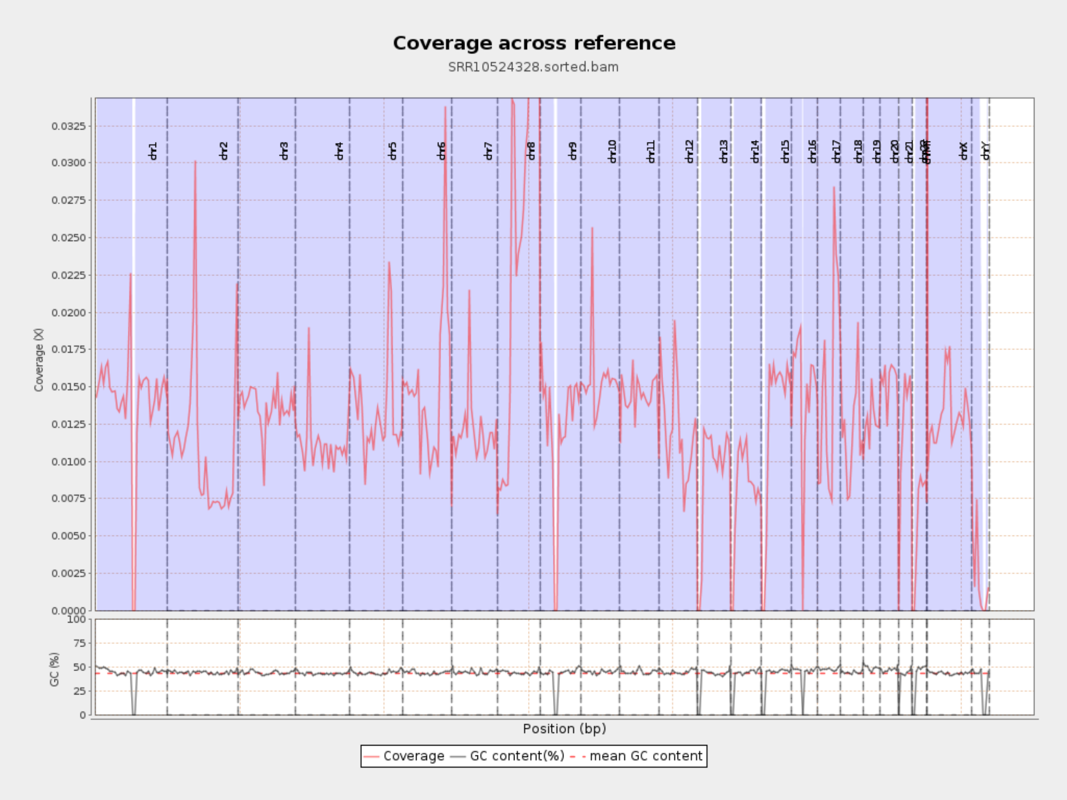
General error rate	0.53%
Mismatches	211,245
Insertions	2,786
Mapped reads with at least one insertion	0.39%
Deletions	7,000
Mapped reads with at least one deletion	0.99%
Homopolymer indels	41.24%

2.6. Chromosome stats

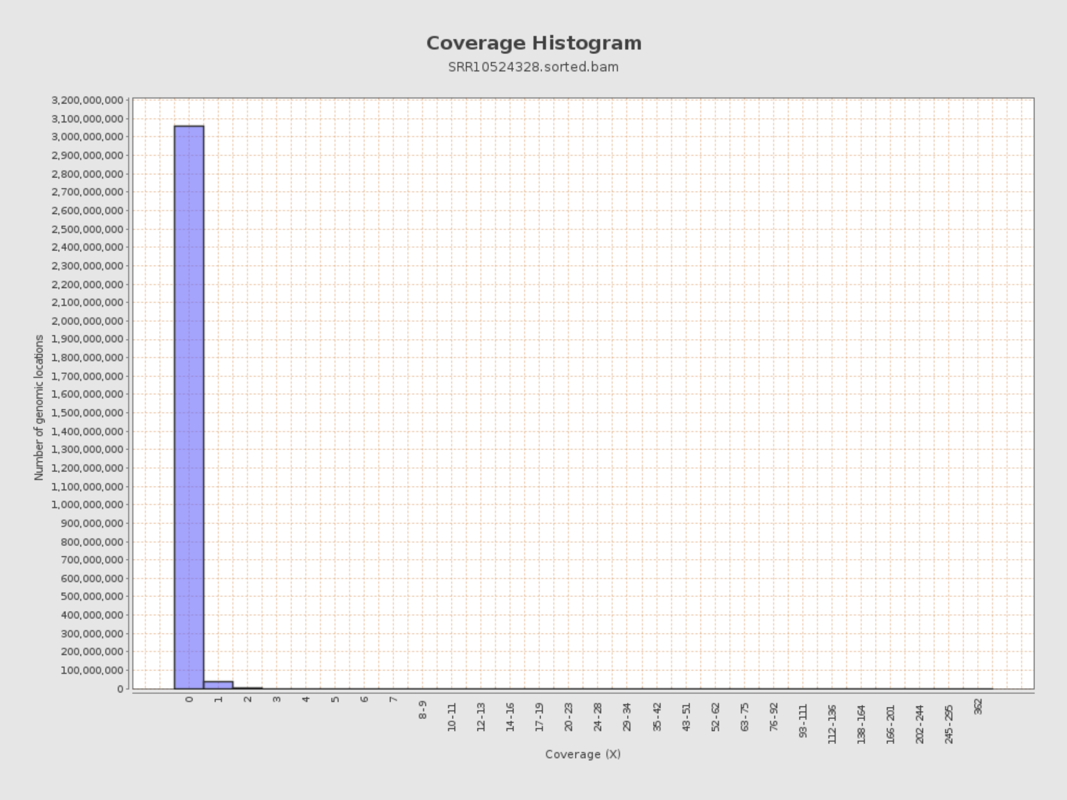
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3490258	0.014	0.2346
chr2	243199373	2607800	0.0107	0.183
chr3	198022430	2695479	0.0136	0.1223
chr4	191154276	2148859	0.0112	0.1177
chr5	180915260	2443089	0.0135	0.121
chr6	171115067	2551640	0.0149	0.1331
chr7	159138663	1935902	0.0122	0.1784

chr8	146364022	4247213	0.029	0.2031
chr9	141213431	1717836	0.0122	0.1281
chr10	135534747	2105573	0.0155	0.1571
chr11	135006516	1968230	0.0146	0.1404
chr12	133851895	1624654	0.0121	0.1156
chr13	115169878	1048490	0.0091	0.0998
chr14	107349540	851621	0.0079	0.0948
chr15	102531392	1298063	0.0127	0.1168
chr16	90354753	1300373	0.0144	0.1284
chr17	81195210	1245059	0.0153	0.1343
chr18	78077248	946847	0.0121	0.1821
chr19	59128983	753541	0.0127	0.1874
chr20	63025520	972775	0.0154	0.1307
chr21	48129895	593100	0.0123	0.1195
chr22	51304566	308365	0.006	0.0808
chrMT	16571	2660	0.1605	0.4019
chrX	155270560	2038909	0.0131	0.1263
chrY	59373566	122621	0.0021	0.0716

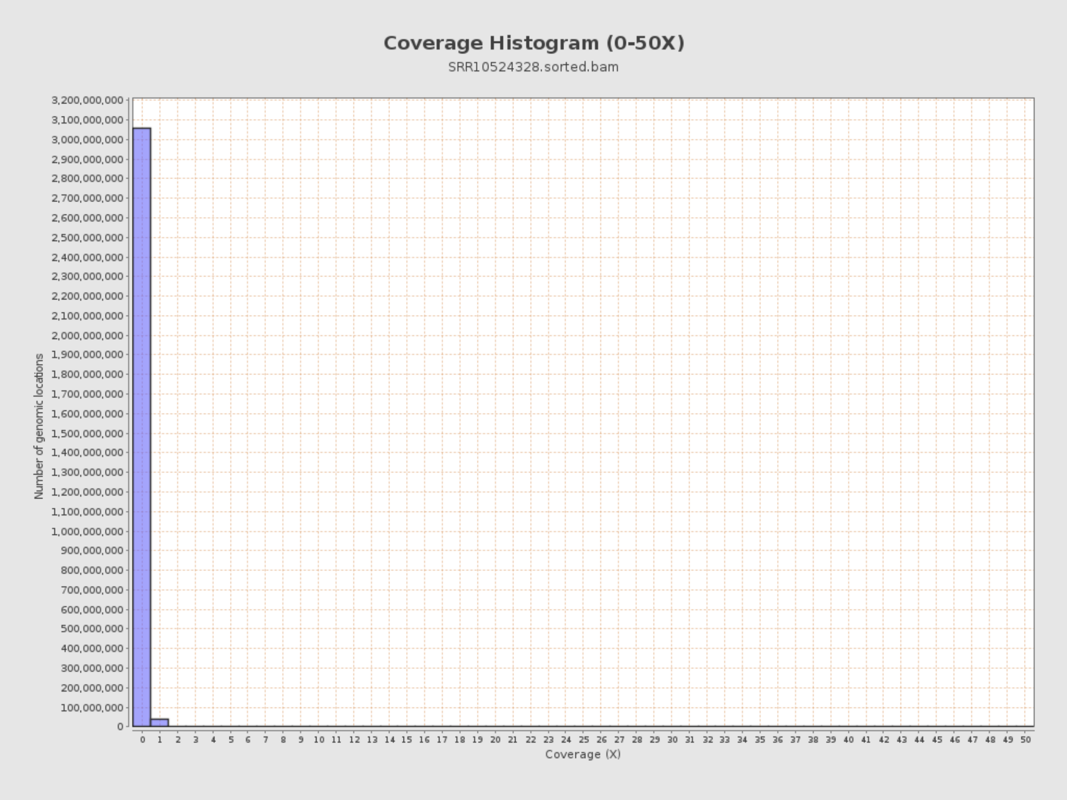
3. Results : Coverage across reference



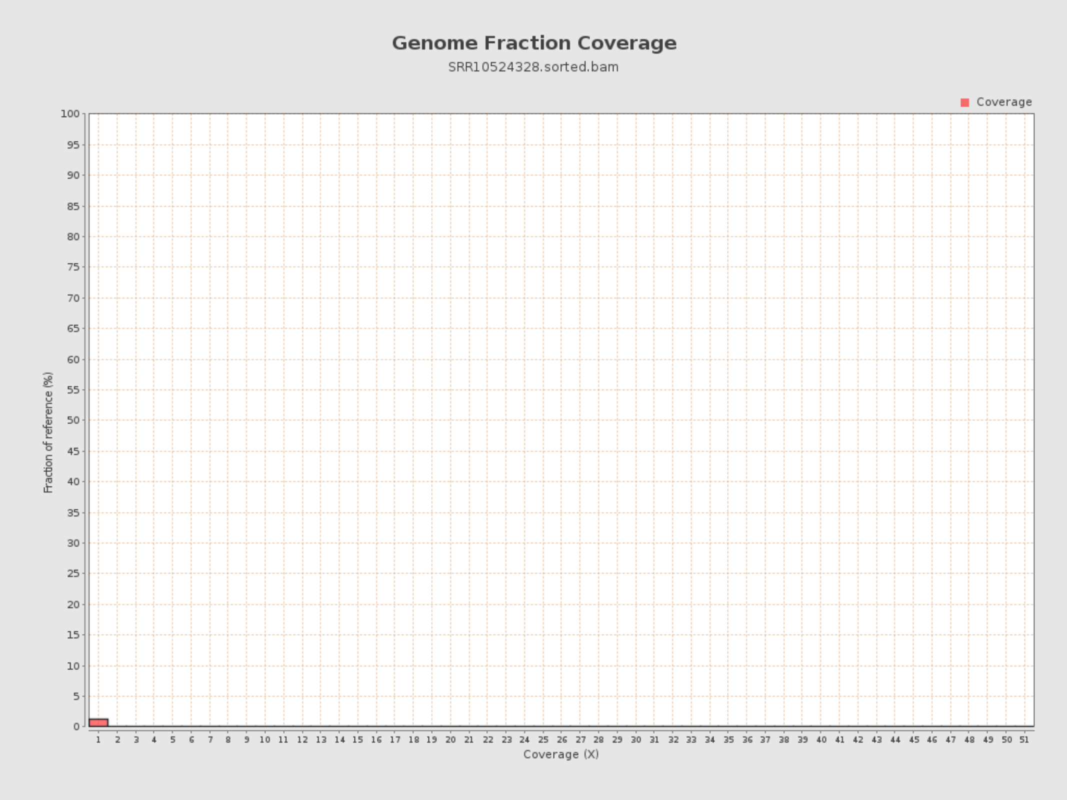
4. Results : Coverage Histogram



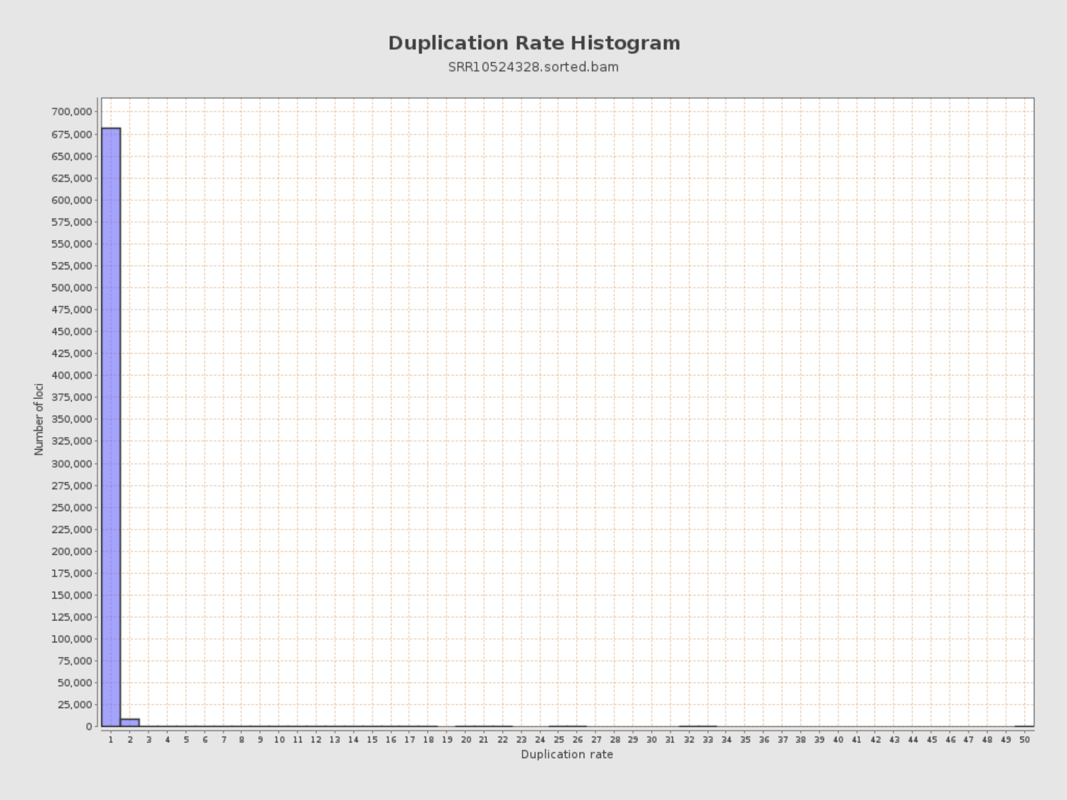
5. Results : Coverage Histogram (0-50X)



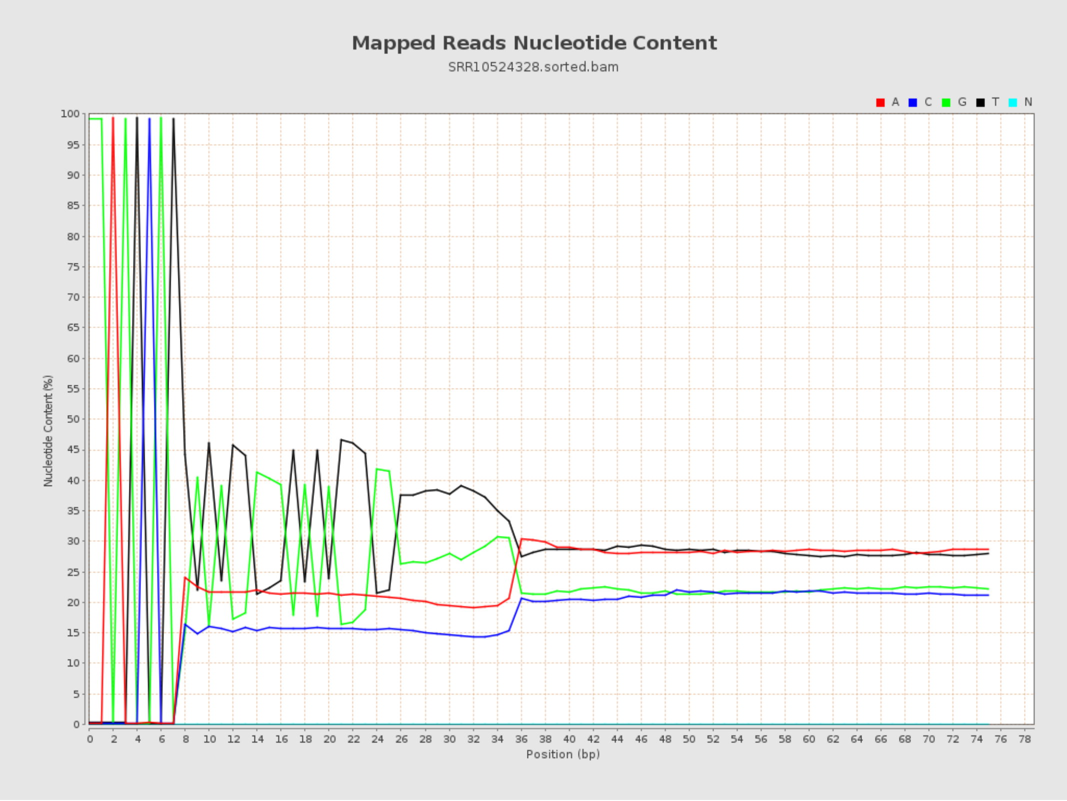
6. Results : Genome Fraction Coverage



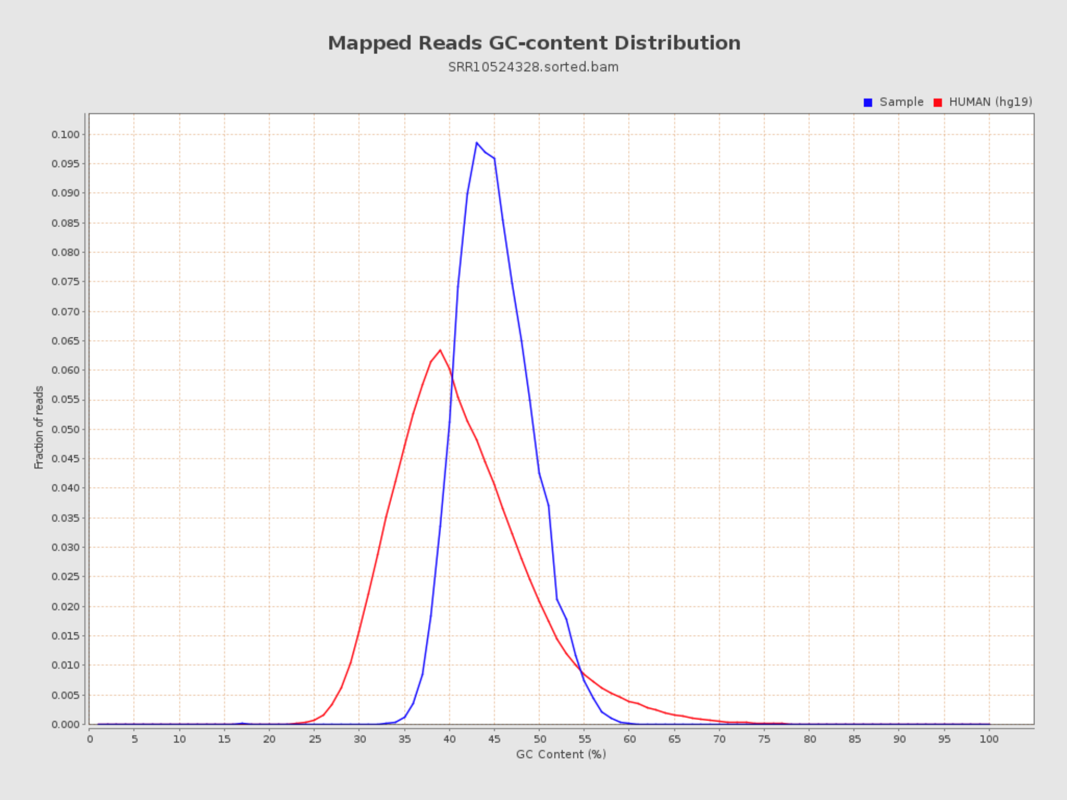
7. Results : Duplication Rate Histogram



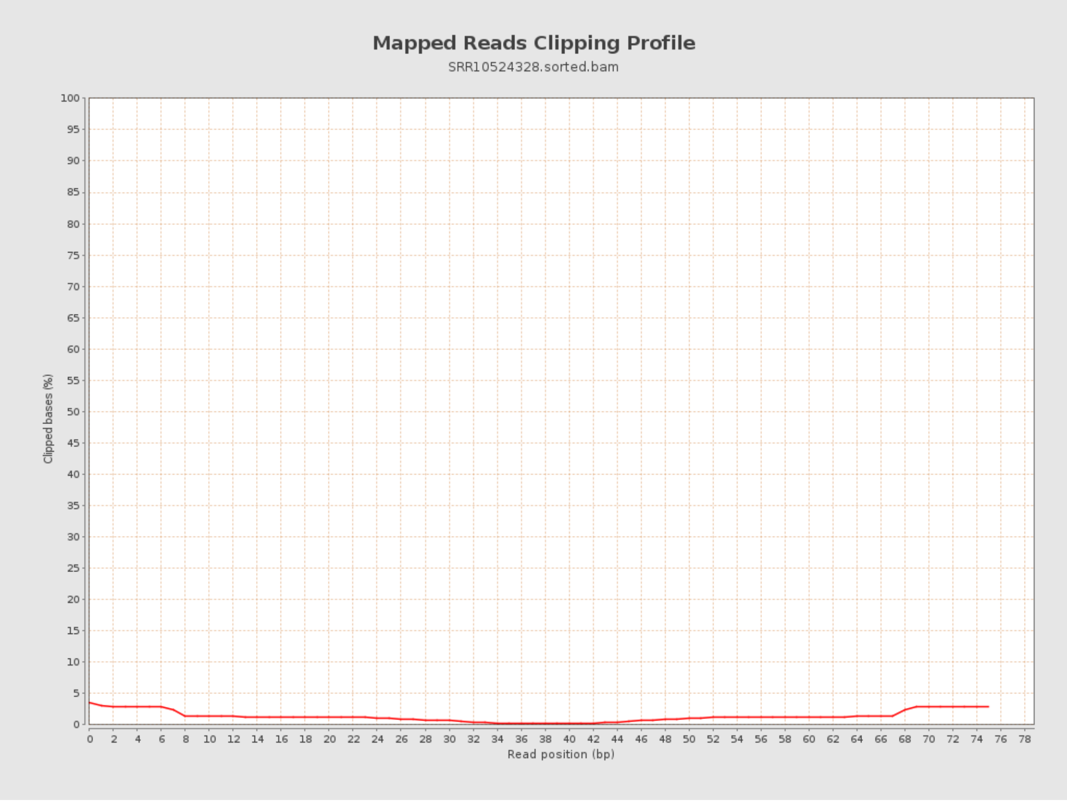
8. Results : Mapped Reads Nucleotide Content



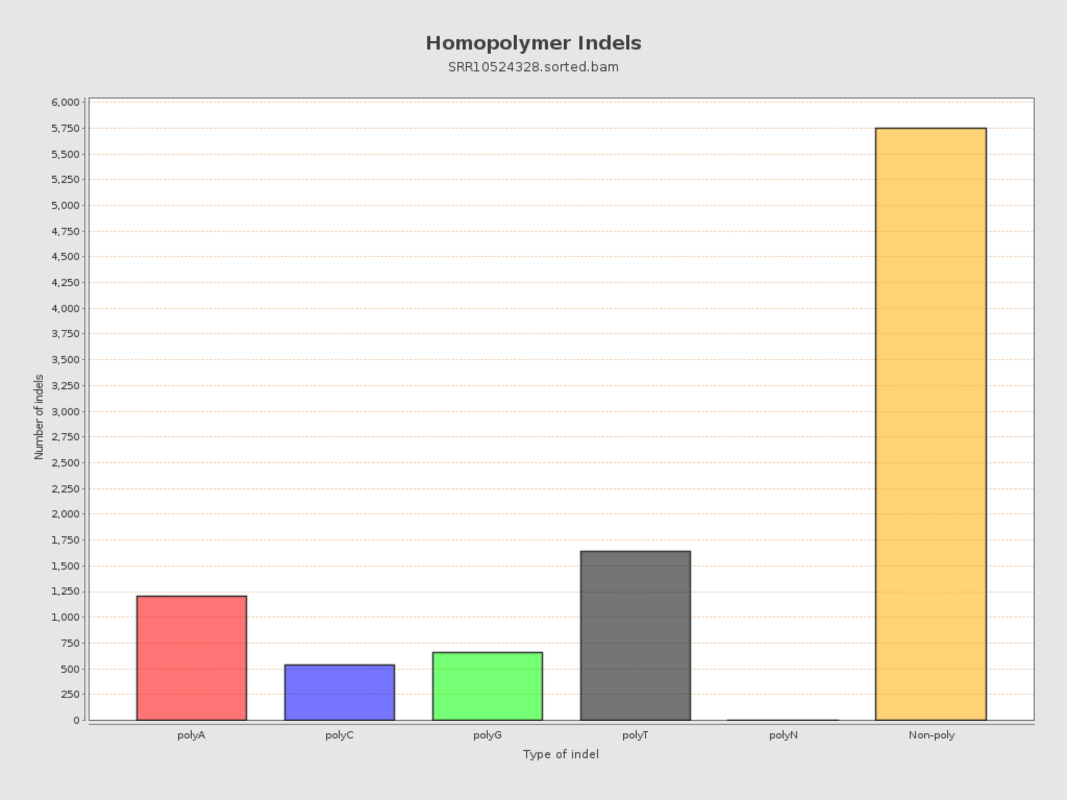
9. Results : Mapped Reads GC-content Distribution



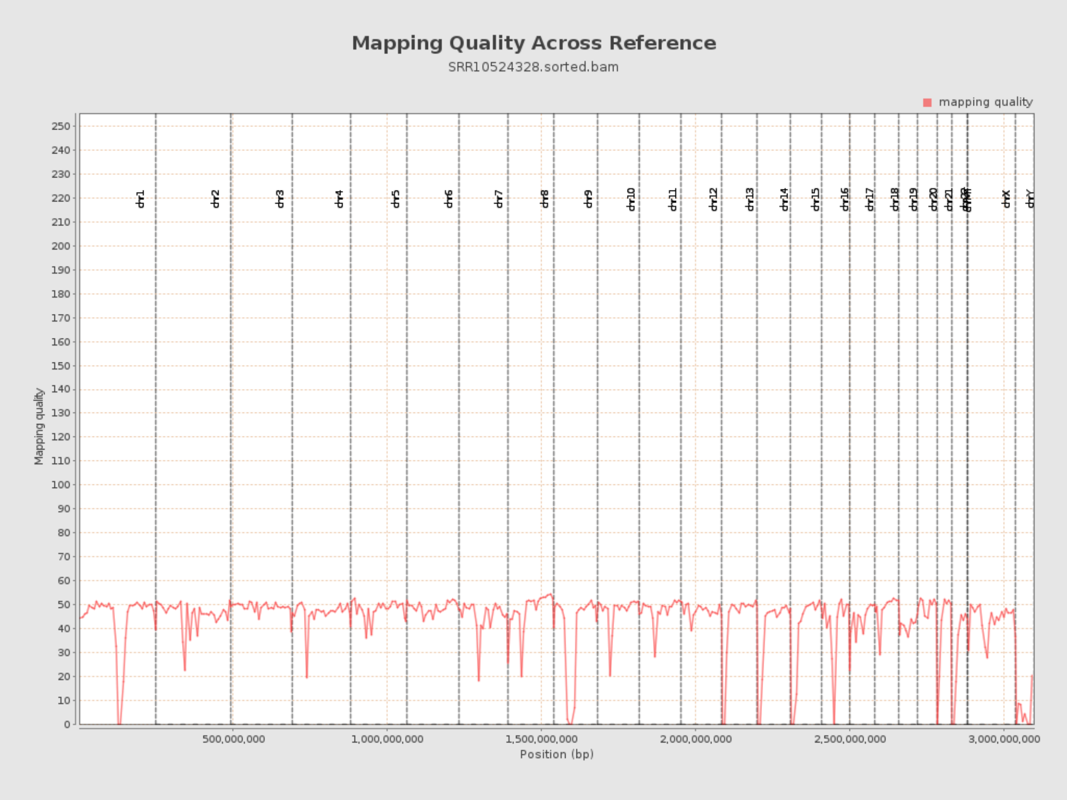
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram