Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524783.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_SRR10524783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:28:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	735,269
Mapped reads	674,361 / 91.72%
Unmapped reads	60,908 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,408 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	16,369 / 2.23%
Duplication rate	1.85%
Clipped reads	675,162 / 91.83%

2.2. ACGT Content

Number/percentage of A's	9,370,314 / 24.21%
Number/percentage of C's	7,496,639 / 19.37%
Number/percentage of T's	12,229,206 / 31.6%
Number/percentage of G's	9,603,943 / 24.81%
Number/percentage of N's	4,804 / 0.01%
GC Percentage	44.18%

2.3. Coverage

Mean	0.0125

Standard Deviation	0.1404

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

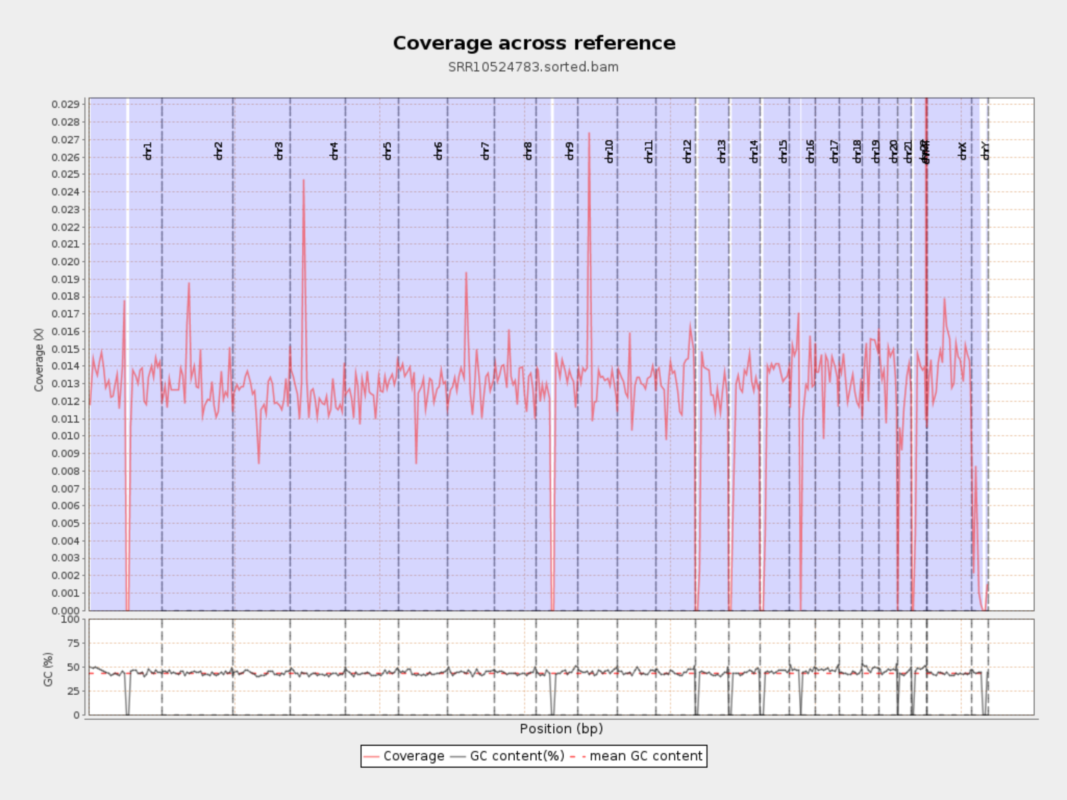
General error rate	0.52%
Mismatches	197,171
Insertions	2,688
Mapped reads with at least one insertion	0.4%
Deletions	7,961
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.08%

2.6. Chromosome stats

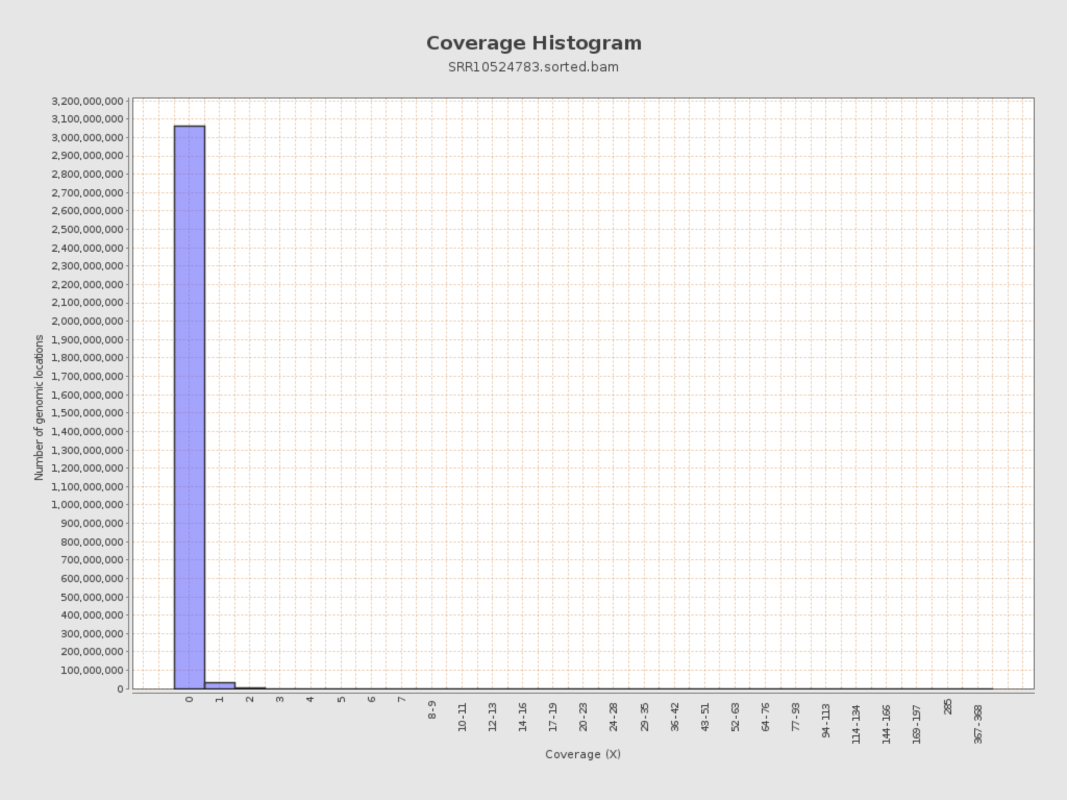
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3136254	0.0126	0.1786
chr2	243199373	3162734	0.013	0.195
chr3	198022430	2429061	0.0123	0.1171
chr4	191154276	2434445	0.0127	0.1291
chr5	180915260	2293254	0.0127	0.1183
chr6	171115067	2204890	0.0129	0.1247
chr7	159138663	2121771	0.0133	0.1603

chr8	146364022	1939945	0.0133	0.133
chr9	141213431	1661699	0.0118	0.1314
chr10	135534747	1883997	0.0139	0.1655
chr11	135006516	1772359	0.0131	0.1335
chr12	133851895	1786563	0.0133	0.1224
chr13	115169878	1245207	0.0108	0.1092
chr14	107349540	1183402	0.011	0.112
chr15	102531392	1139521	0.0111	0.1108
chr16	90354753	1146279	0.0127	0.1241
chr17	81195210	1094256	0.0135	0.1256
chr18	78077248	1014639	0.013	0.1716
chr19	59128983	860063	0.0145	0.1559
chr20	63025520	859730	0.0136	0.125
chr21	48129895	517548	0.0108	0.1149
chr22	51304566	492832	0.0096	0.1033
chrMT	16571	5485	0.331	0.6707
chrX	155270560	2201425	0.0142	0.1298
chrY	59373566	130634	0.0022	0.0726

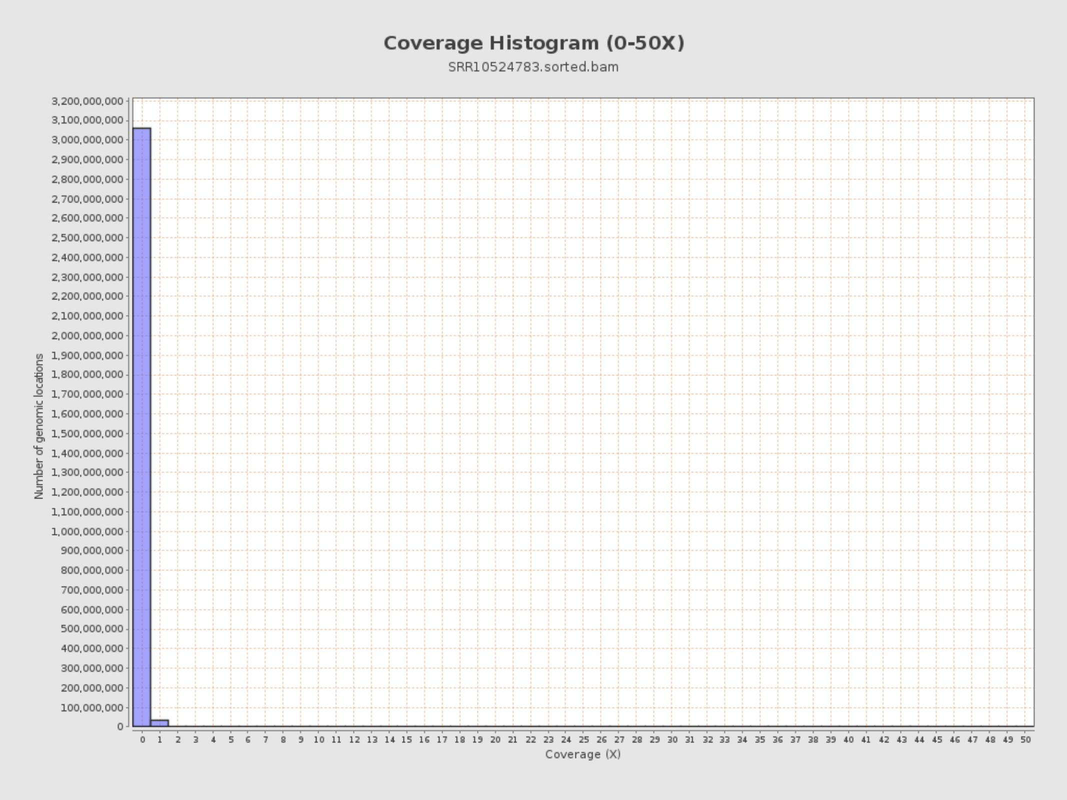
3. Results : Coverage across reference



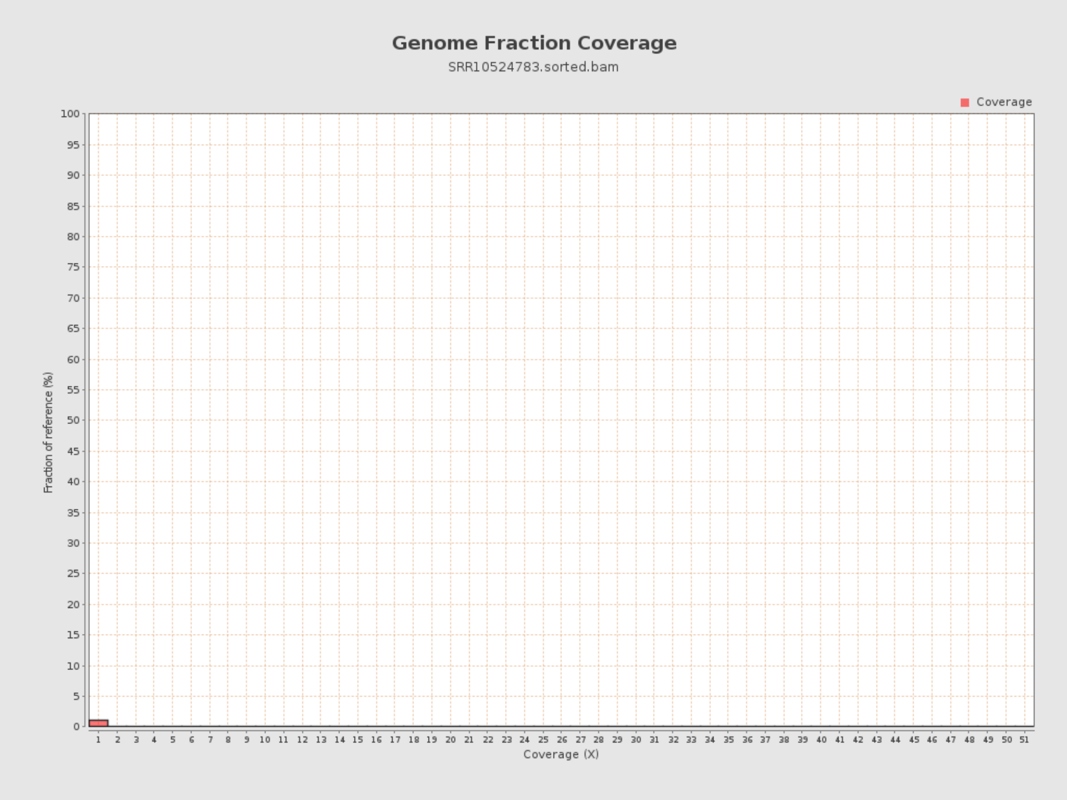
4. Results : Coverage Histogram



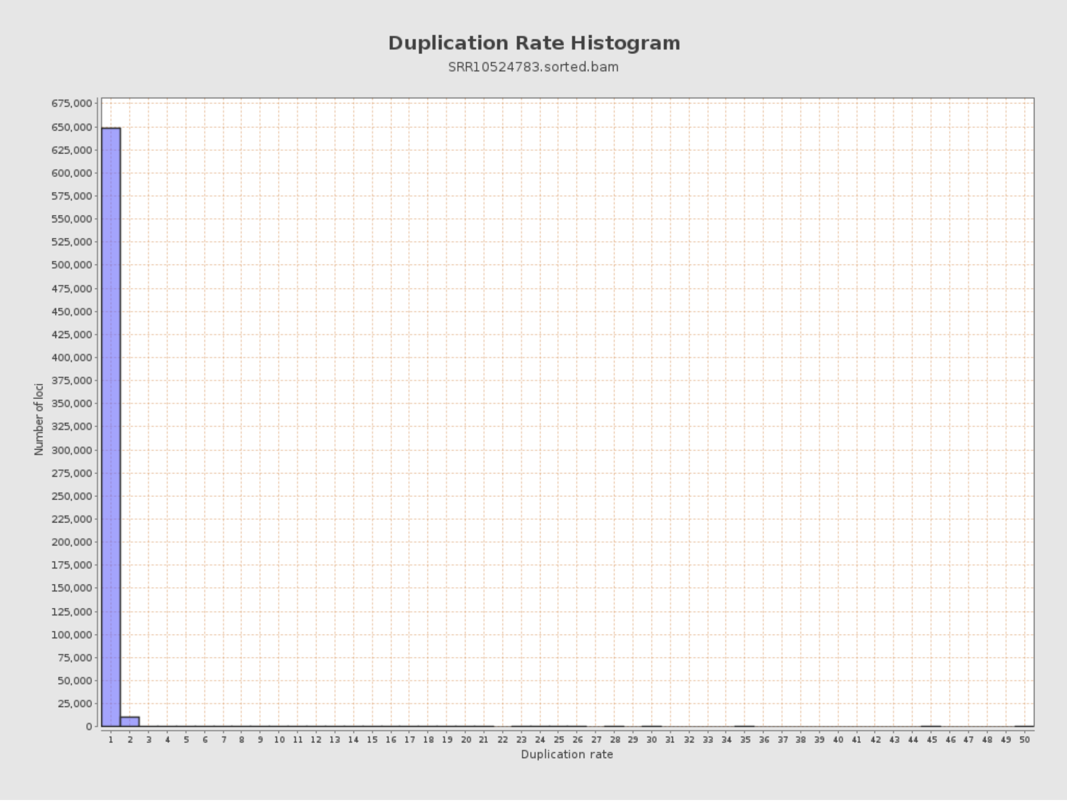
5. Results : Coverage Histogram (0-50X)



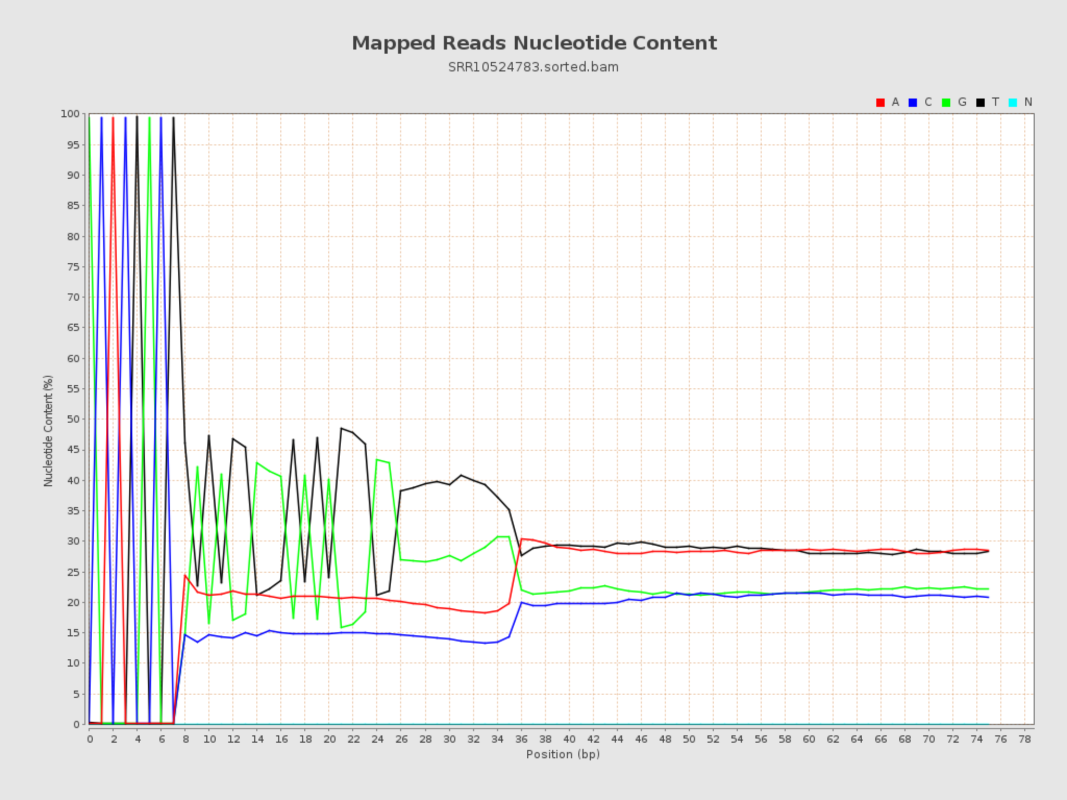
6. Results : Genome Fraction Coverage



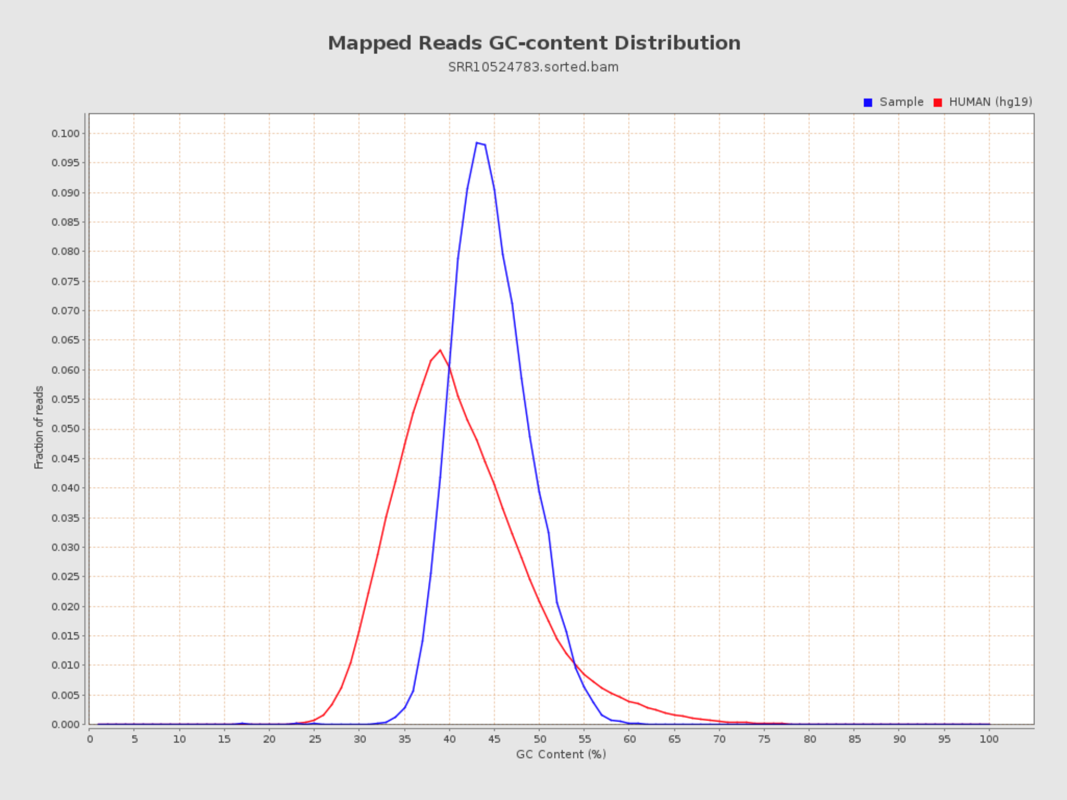
7. Results : Duplication Rate Histogram



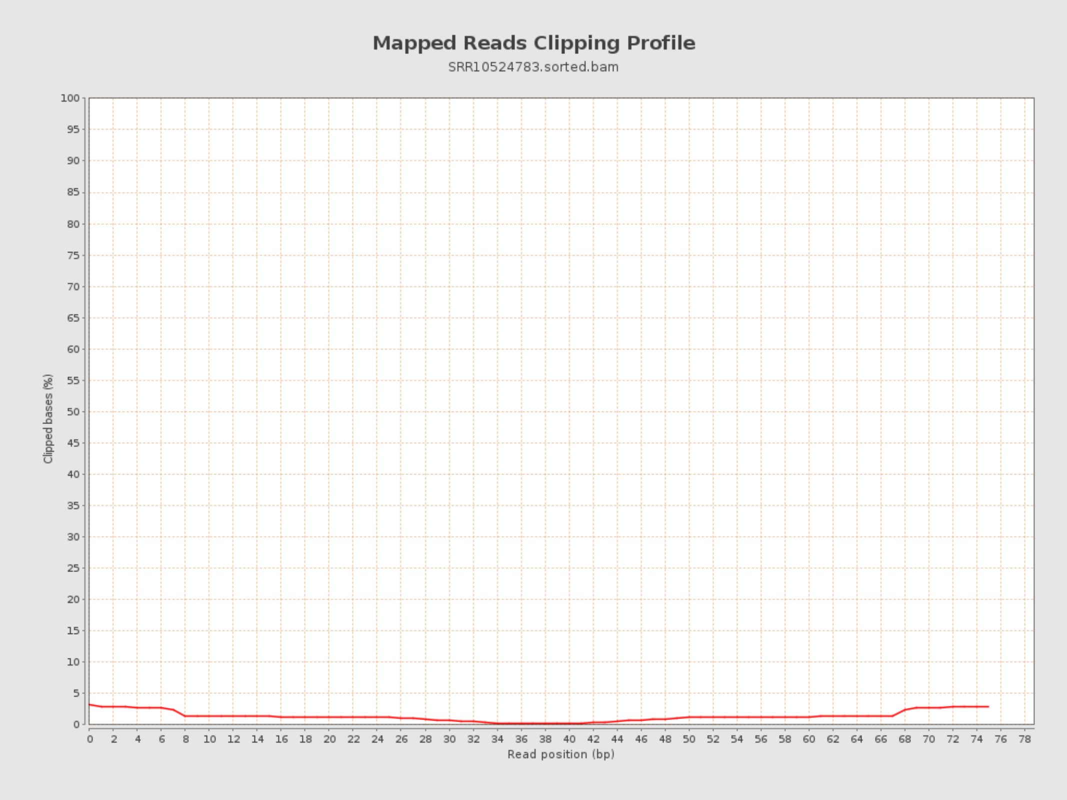
8. Results : Mapped Reads Nucleotide Content



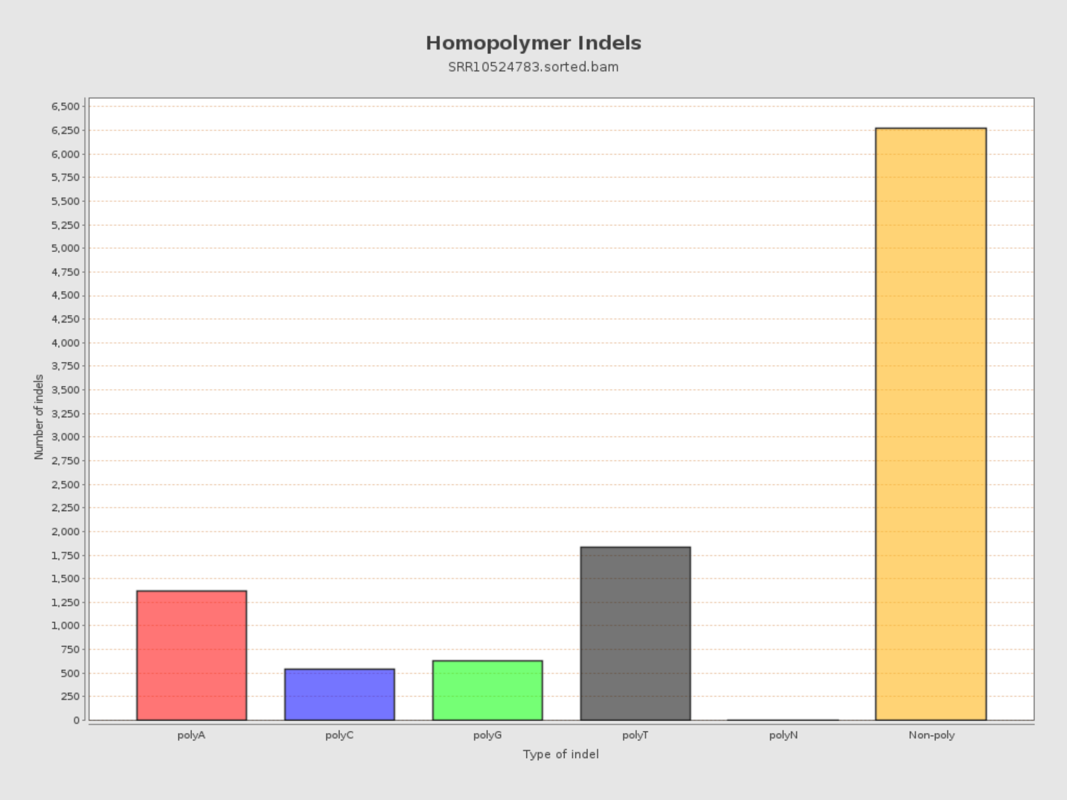
9. Results : Mapped Reads GC-content Distribution



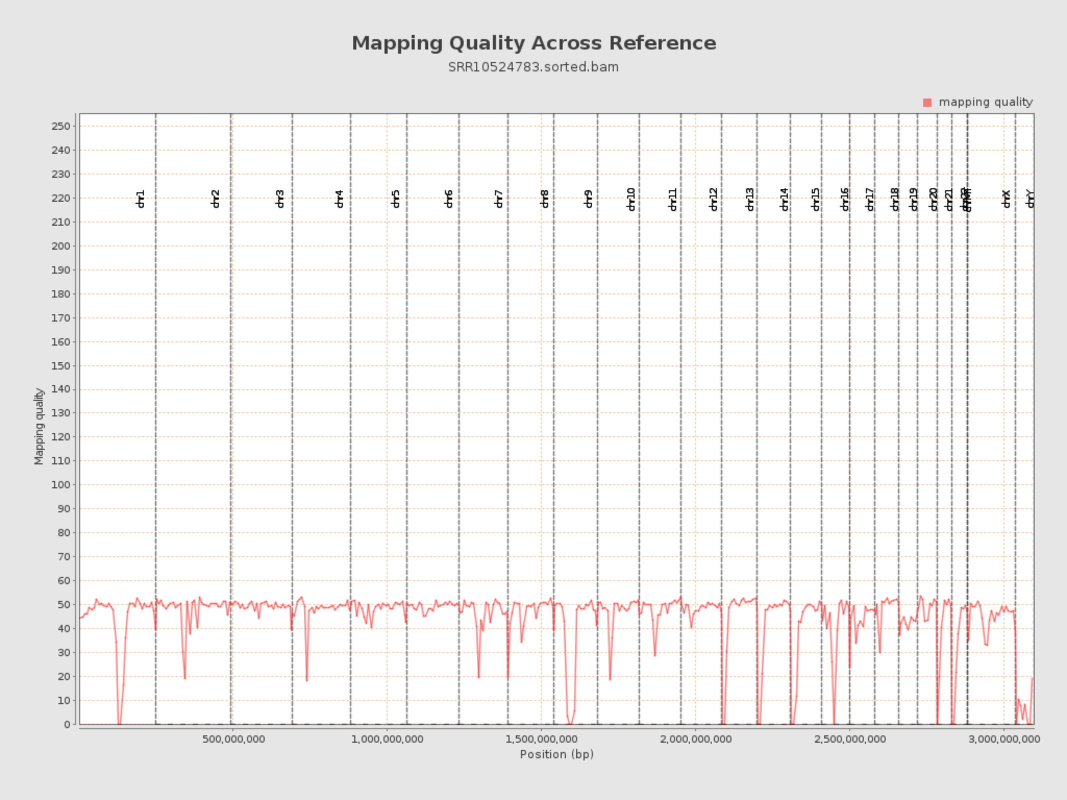
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram