Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:33:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524688.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_SRR10524688 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524688.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:33:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524688.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	831,965
Mapped reads	770,767 / 92.64%
Unmapped reads	61,198 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,227 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	20,493 / 2.46%
Duplication rate	1.99%
Clipped reads	771,897 / 92.78%

2.2. ACGT Content

Number/percentage of A's	11,992,363 / 26.17%
Number/percentage of C's	9,023,795 / 19.69%
Number/percentage of T's	14,206,436 / 31%
Number/percentage of G's	10,591,739 / 23.12%
Number/percentage of N's	6,209 / 0.01%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0148

Standard Deviation	0.1646

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

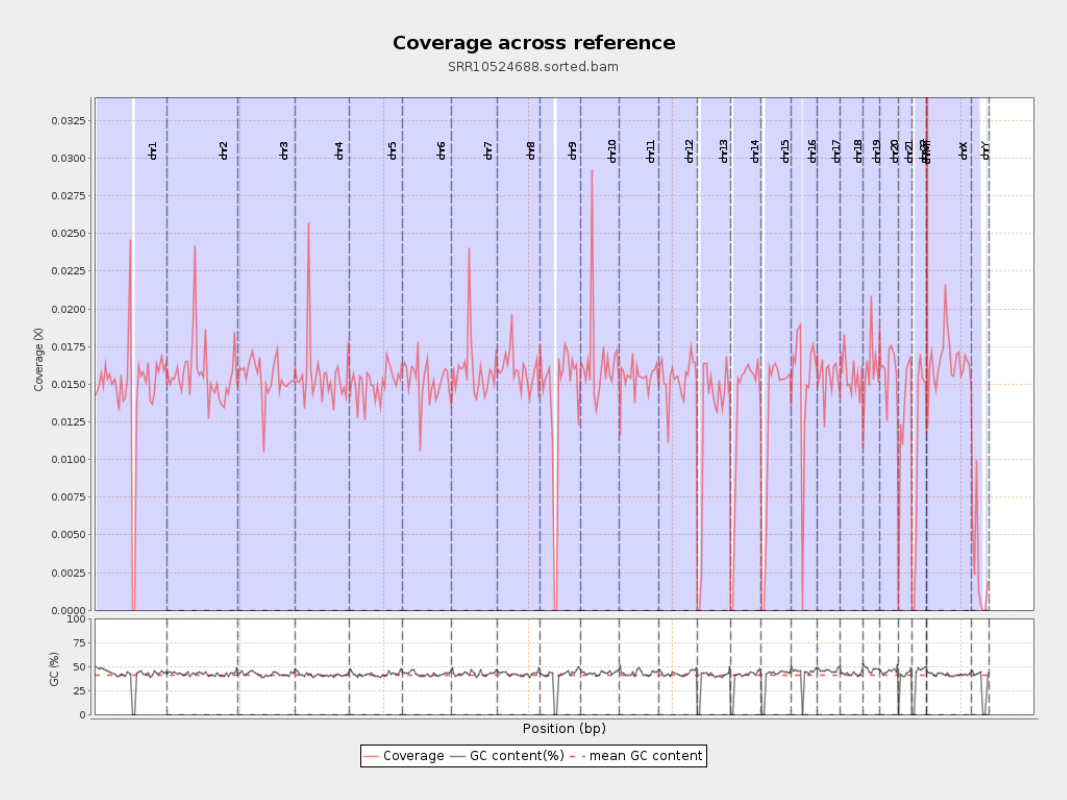
General error rate	0.51%
Mismatches	225,402
Insertions	3,524
Mapped reads with at least one insertion	0.45%
Deletions	8,618
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.45%

2.6. Chromosome stats

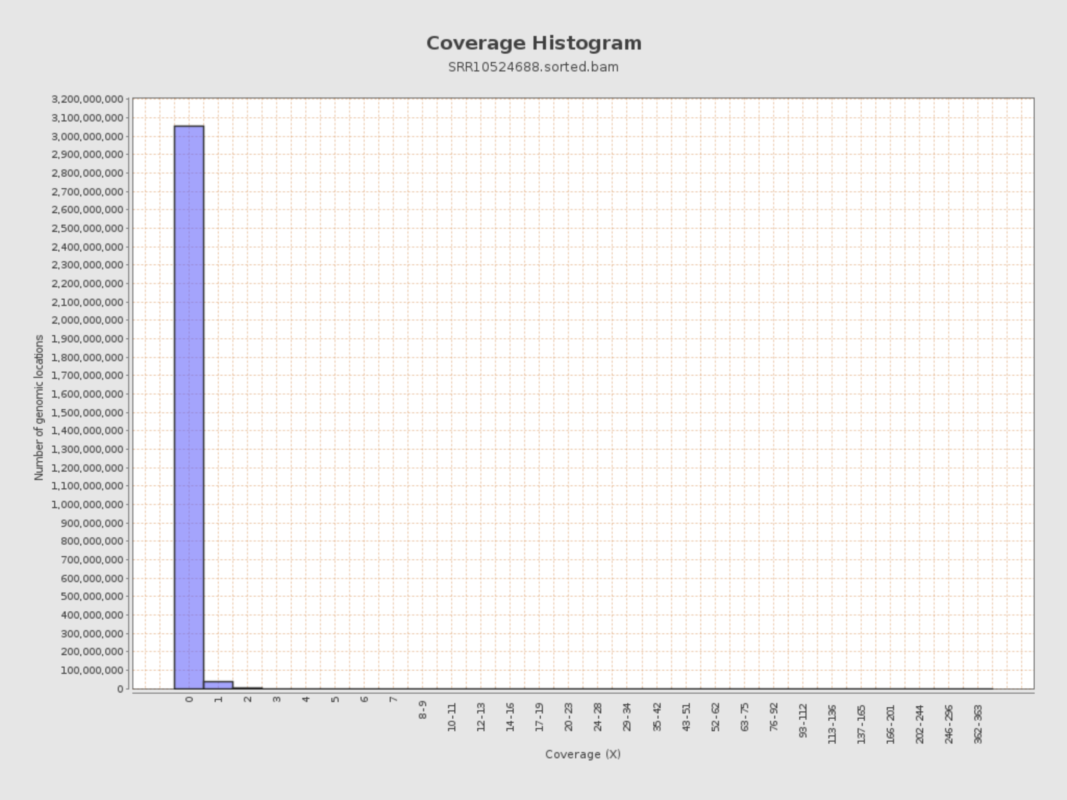
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3621922	0.0145	0.2544
chr2	243199373	3817308	0.0157	0.2083
chr3	198022430	3062583	0.0155	0.1304
chr4	191154276	2983068	0.0156	0.1419
chr5	180915260	2728747	0.0151	0.1292
chr6	171115067	2596215	0.0152	0.1369
chr7	159138663	2542726	0.016	0.1849

chr8	146364022	2331715	0.0159	0.1803
chr9	141213431	1957770	0.0139	0.1481
chr10	135534747	2237253	0.0165	0.1733
chr11	135006516	2092537	0.0155	0.1549
chr12	133851895	2058880	0.0154	0.1307
chr13	115169878	1428766	0.0124	0.1169
chr14	107349540	1395480	0.013	0.1236
chr15	102531392	1298612	0.0127	0.1186
chr16	90354753	1340781	0.0148	0.1334
chr17	81195210	1249139	0.0154	0.1333
chr18	78077248	1216735	0.0156	0.2351
chr19	59128983	959664	0.0162	0.2082
chr20	63025520	1003383	0.0159	0.1336
chr21	48129895	622790	0.0129	0.1306
chr22	51304566	548474	0.0107	0.1086
chrMT	16571	16113	0.9724	1.1373
chrX	155270560	2569590	0.0165	0.1411
chrY	59373566	153812	0.0026	0.0985

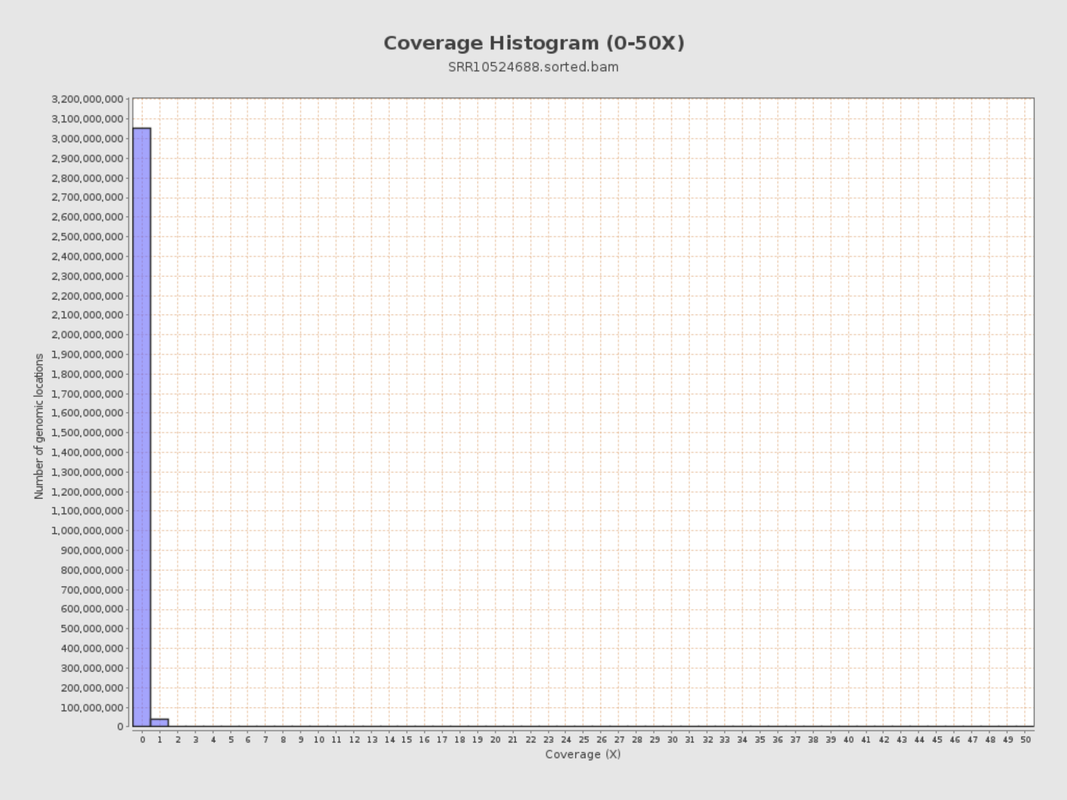
3. Results : Coverage across reference



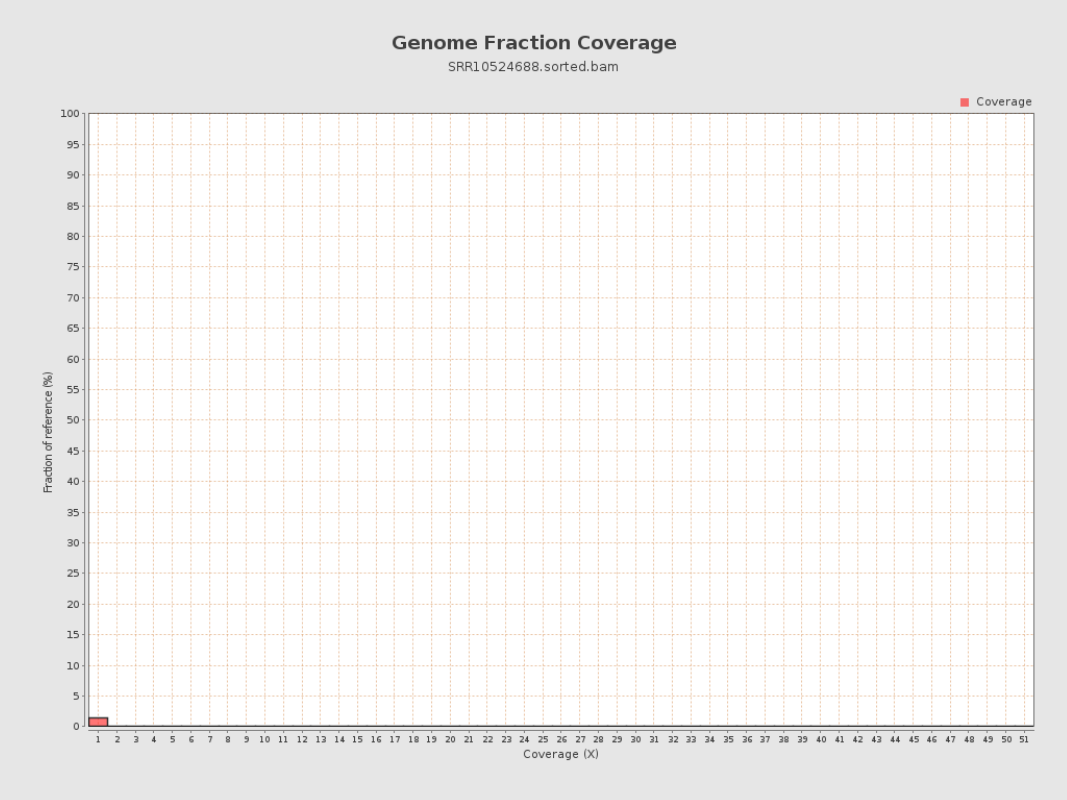
4. Results : Coverage Histogram



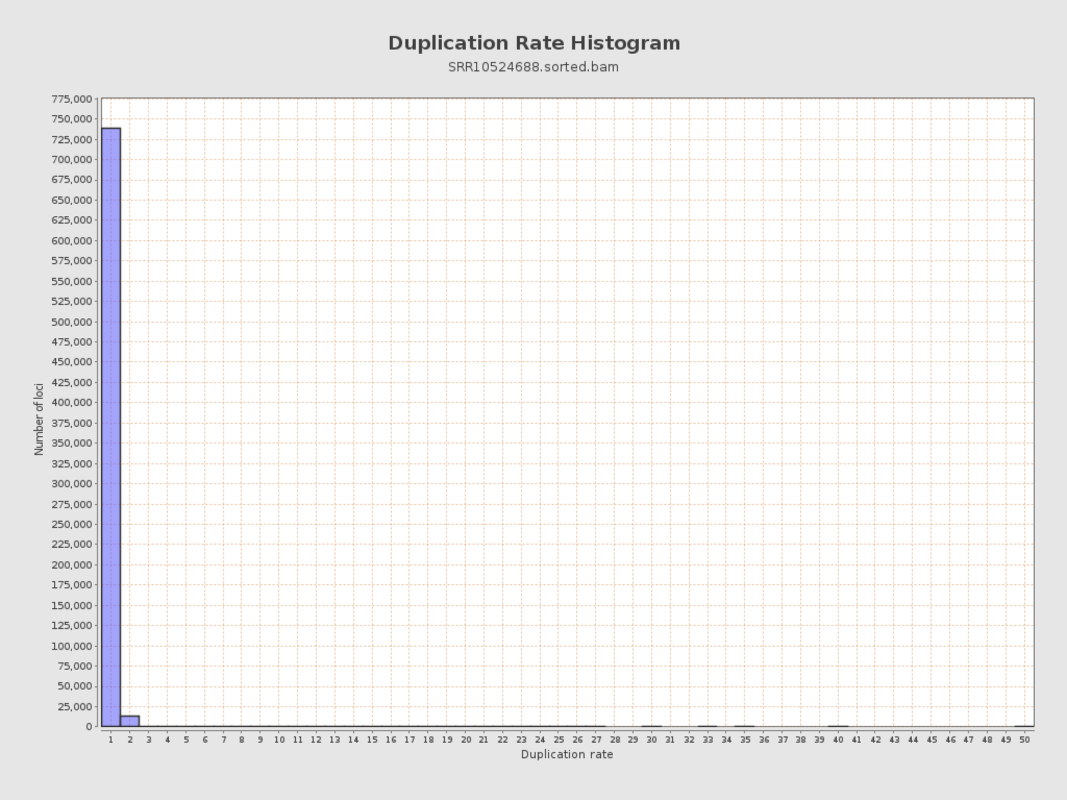
5. Results : Coverage Histogram (0-50X)



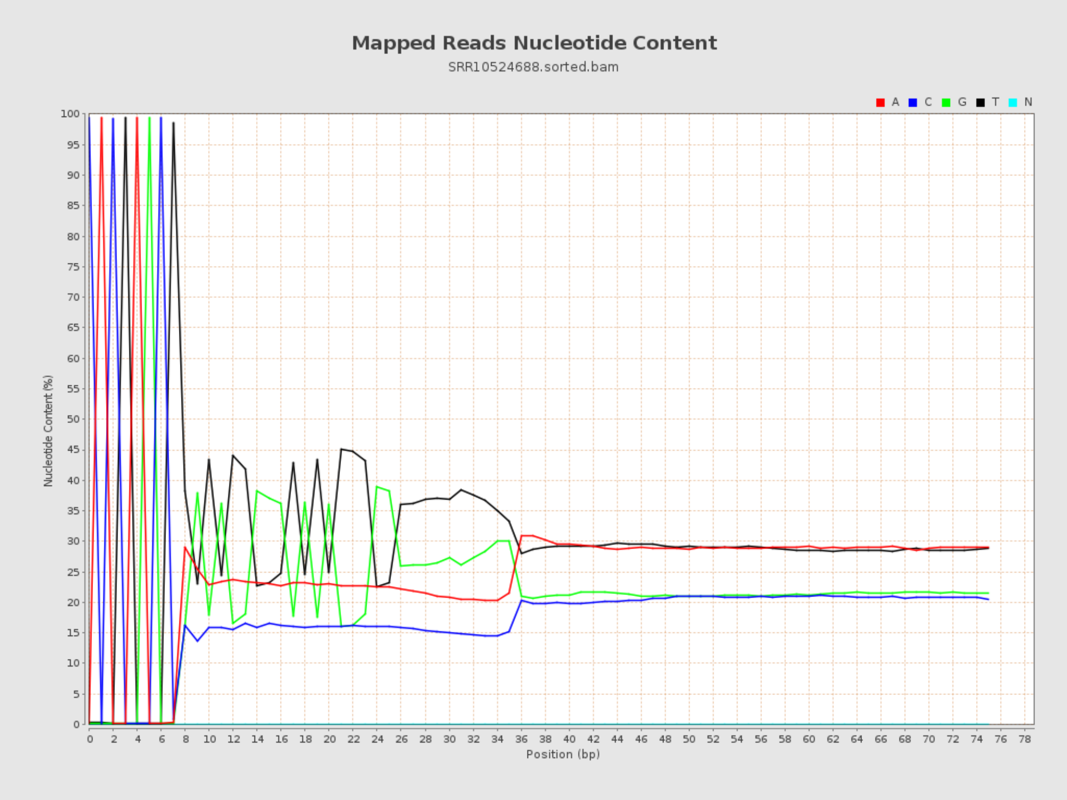
6. Results : Genome Fraction Coverage



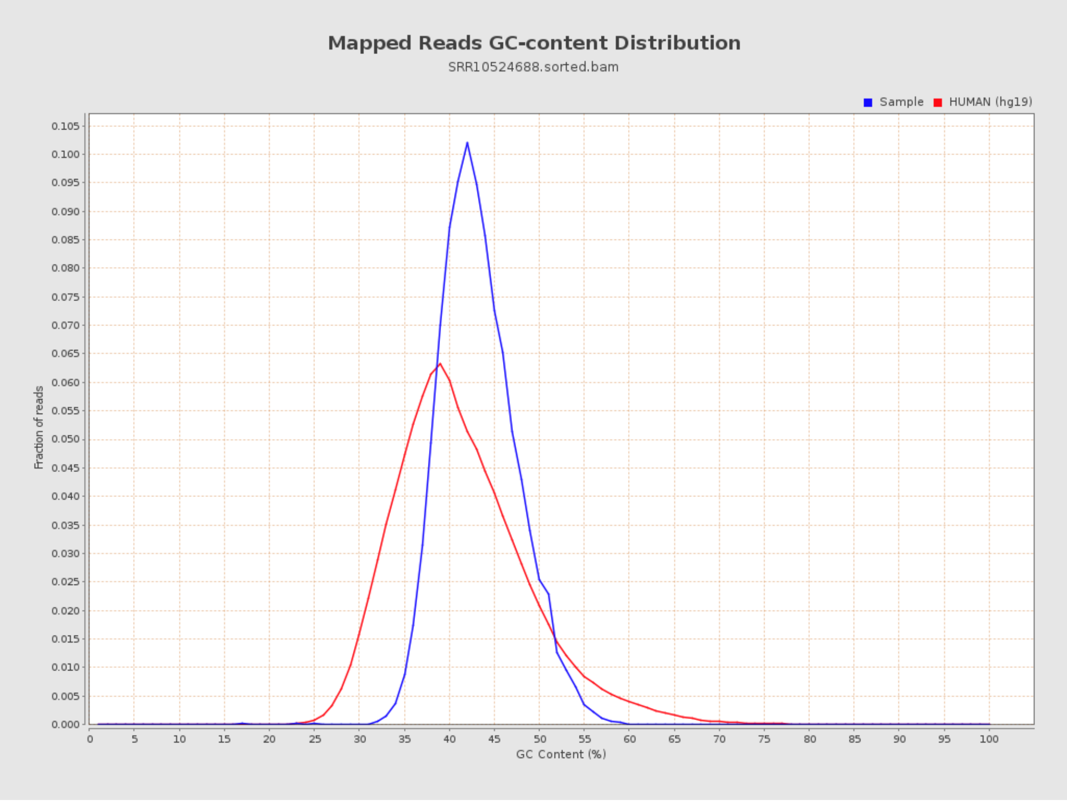
7. Results : Duplication Rate Histogram



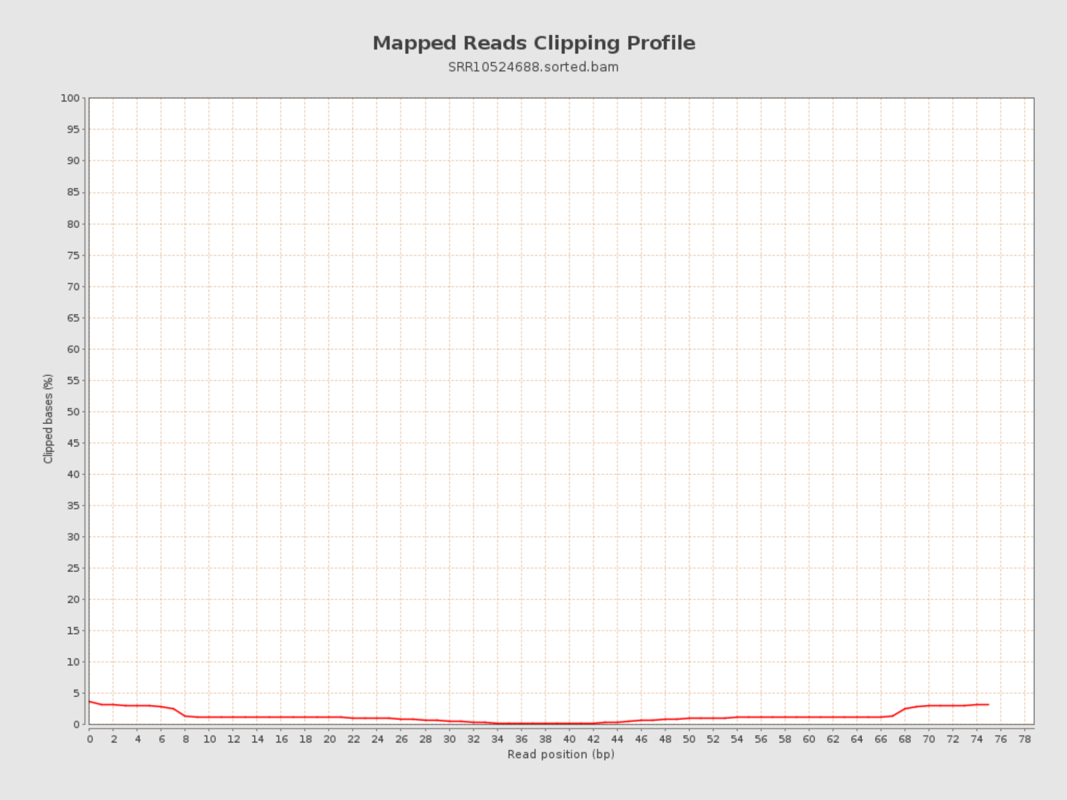
8. Results : Mapped Reads Nucleotide Content



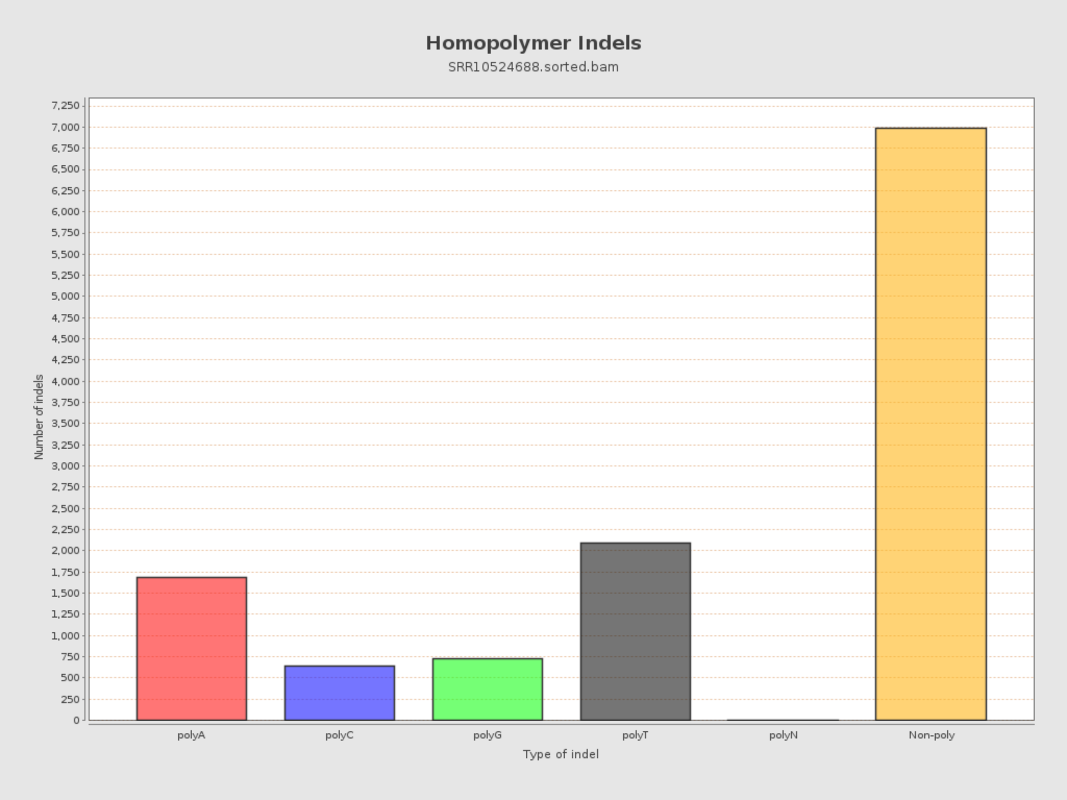
9. Results : Mapped Reads GC-content Distribution



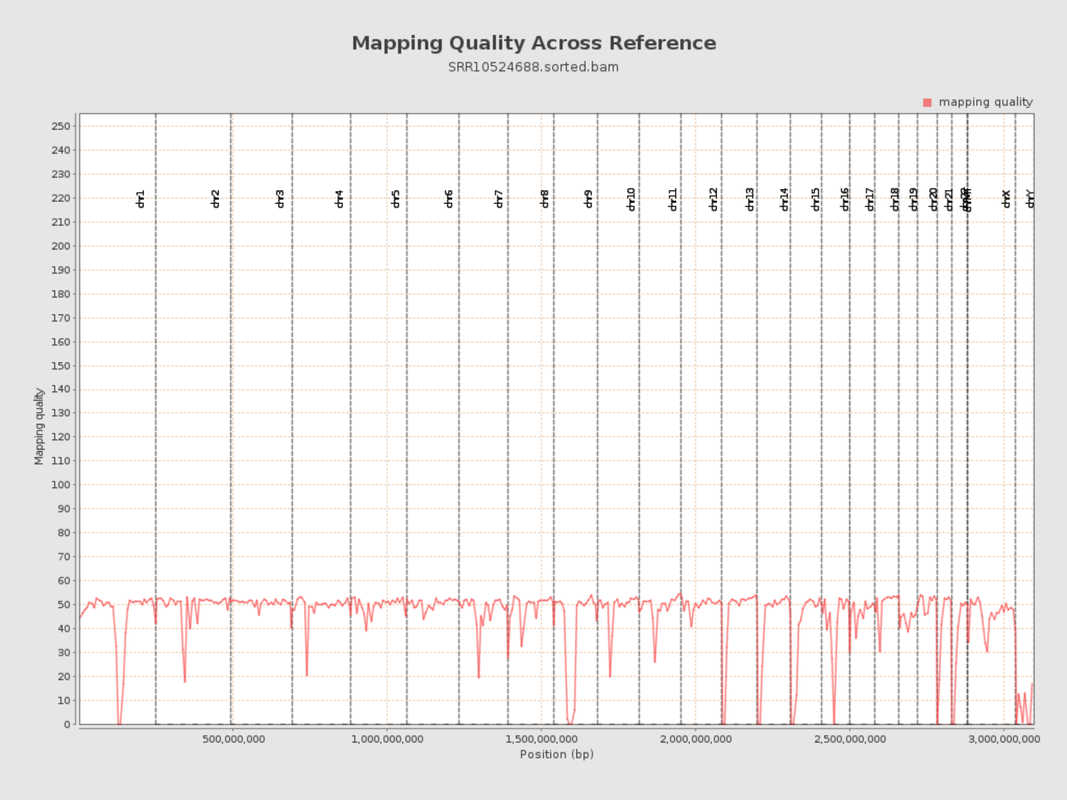
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram