Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:55:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716850.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_SRR9716850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:55:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,010
Mapped reads	697,115 / 90.77%
Unmapped reads	70,895 / 9.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,658 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	17,404 / 2.27%
Duplication rate	1.85%
Clipped reads	699,838 / 91.12%

2.2. ACGT Content

Number/percentage of A's	10,370,460 / 25.36%
Number/percentage of C's	7,887,359 / 19.29%
Number/percentage of T's	12,217,958 / 29.87%
Number/percentage of G's	10,420,909 / 25.48%
Number/percentage of N's	255 / 0%
GC Percentage	44.77%

2.3. Coverage

Mean	0.0132

Standard Deviation	0.1521

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

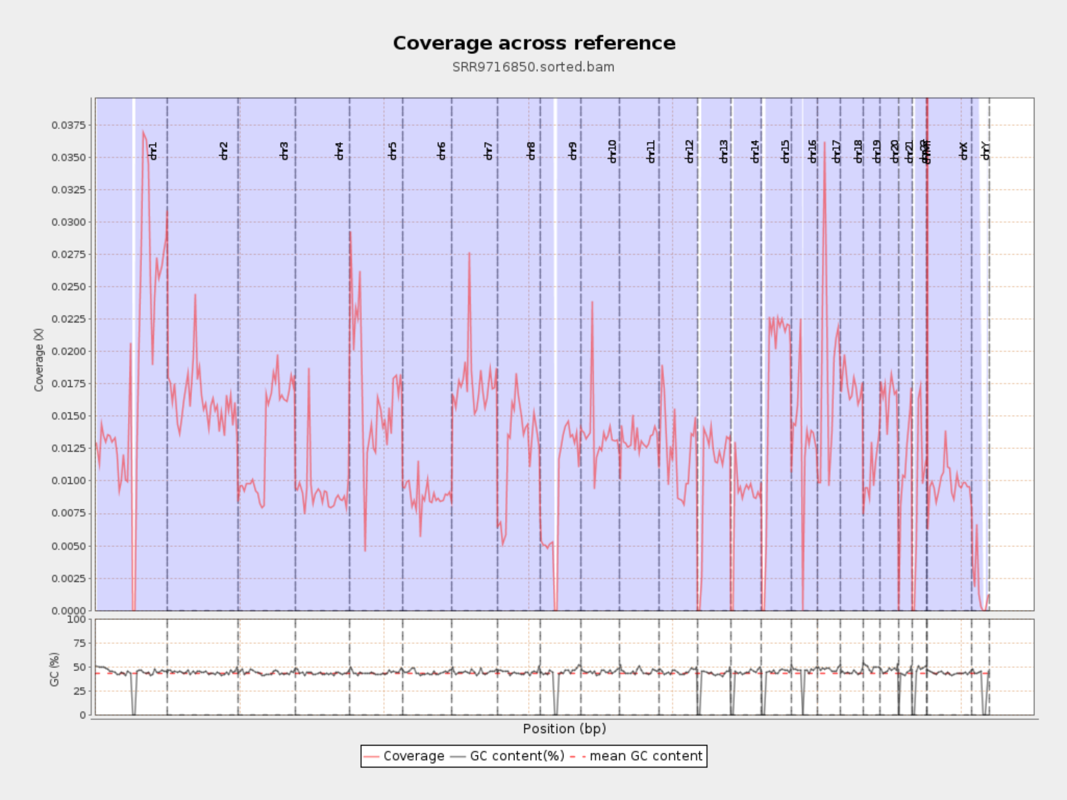
General error rate	0.53%
Mismatches	213,438
Insertions	2,490
Mapped reads with at least one insertion	0.36%
Deletions	7,362
Mapped reads with at least one deletion	1.05%
Homopolymer indels	46.02%

2.6. Chromosome stats

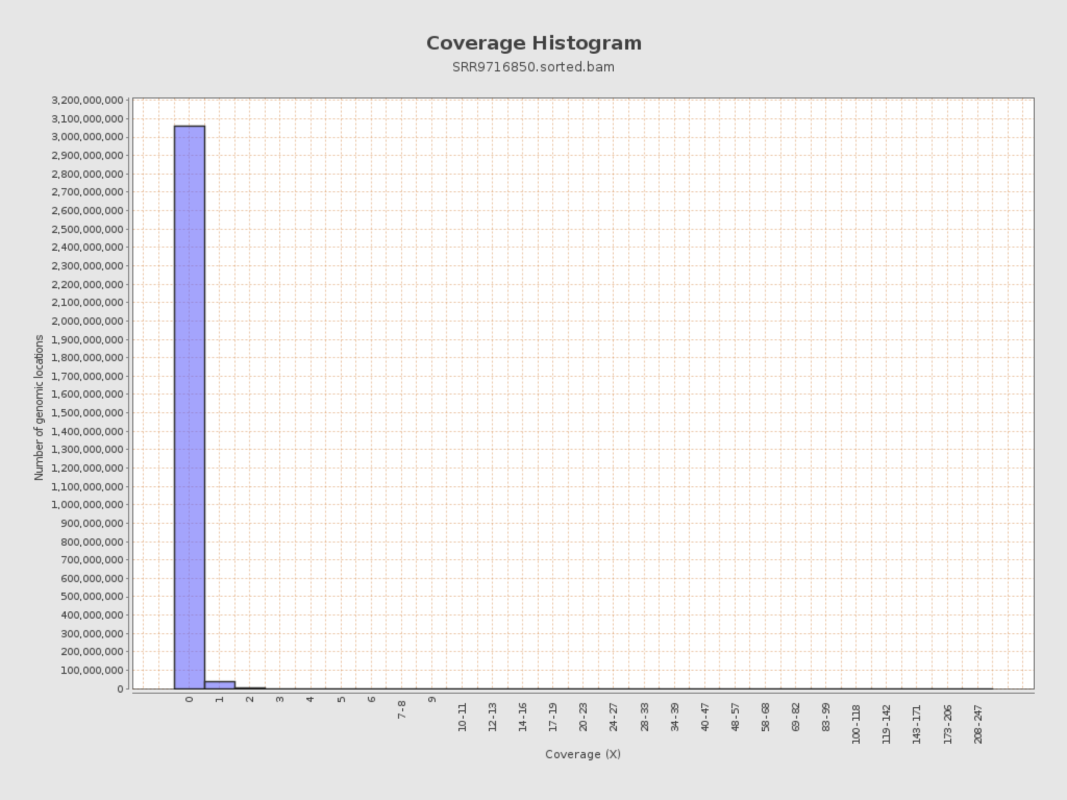
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4504406	0.0181	0.2282
chr2	243199373	3965728	0.0163	0.1861
chr3	198022430	2639364	0.0133	0.1205
chr4	191154276	1766918	0.0092	0.1173
chr5	180915260	2992569	0.0165	0.1347
chr6	171115067	1514238	0.0088	0.1051
chr7	159138663	2810645	0.0177	0.2229

chr8	146364022	1853630	0.0127	0.1425
chr9	141213431	1274267	0.009	0.1213
chr10	135534747	1841675	0.0136	0.1589
chr11	135006516	1783248	0.0132	0.1503
chr12	133851895	1635878	0.0122	0.1164
chr13	115169878	1225776	0.0106	0.1082
chr14	107349540	890743	0.0083	0.0989
chr15	102531392	1801228	0.0176	0.1386
chr16	90354753	1184880	0.0131	0.1238
chr17	81195210	1544856	0.019	0.1504
chr18	78077248	1348200	0.0173	0.2401
chr19	59128983	634243	0.0107	0.1641
chr20	63025520	1041736	0.0165	0.1363
chr21	48129895	528159	0.011	0.1176
chr22	51304566	489395	0.0095	0.1022
chrMT	16571	9689	0.5847	0.8299
chrX	155270560	1521360	0.0098	0.1107
chrY	59373566	105719	0.0018	0.0673

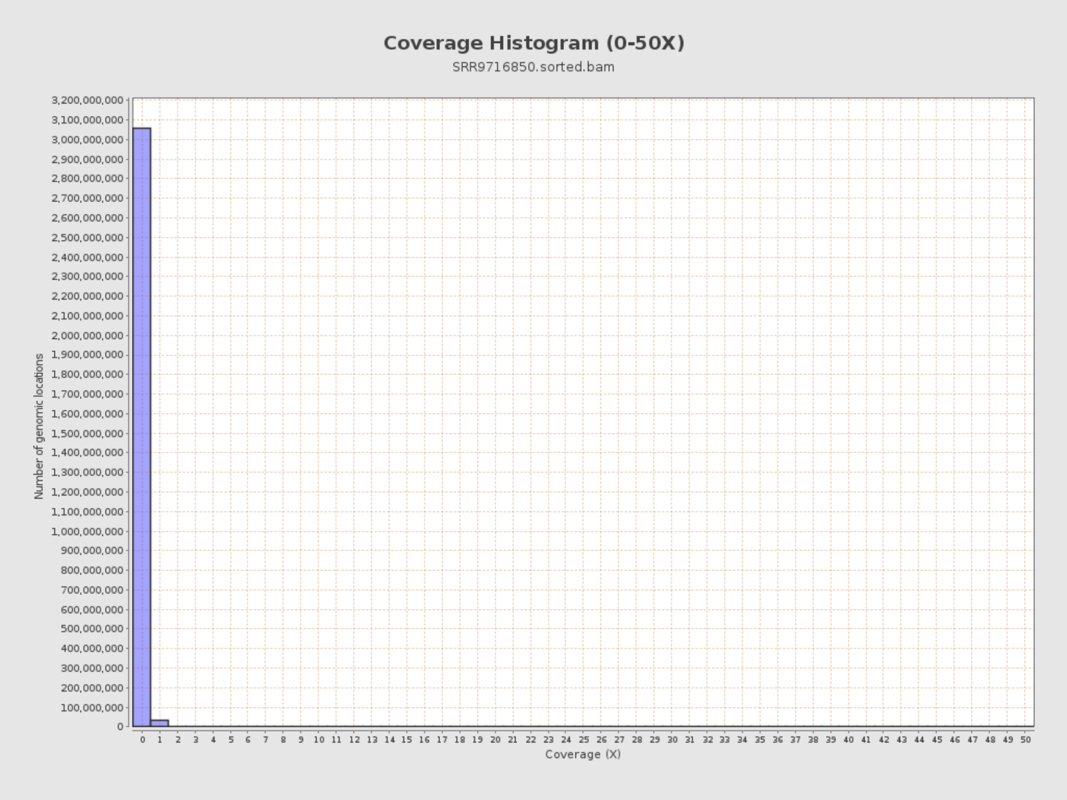
3. Results : Coverage across reference



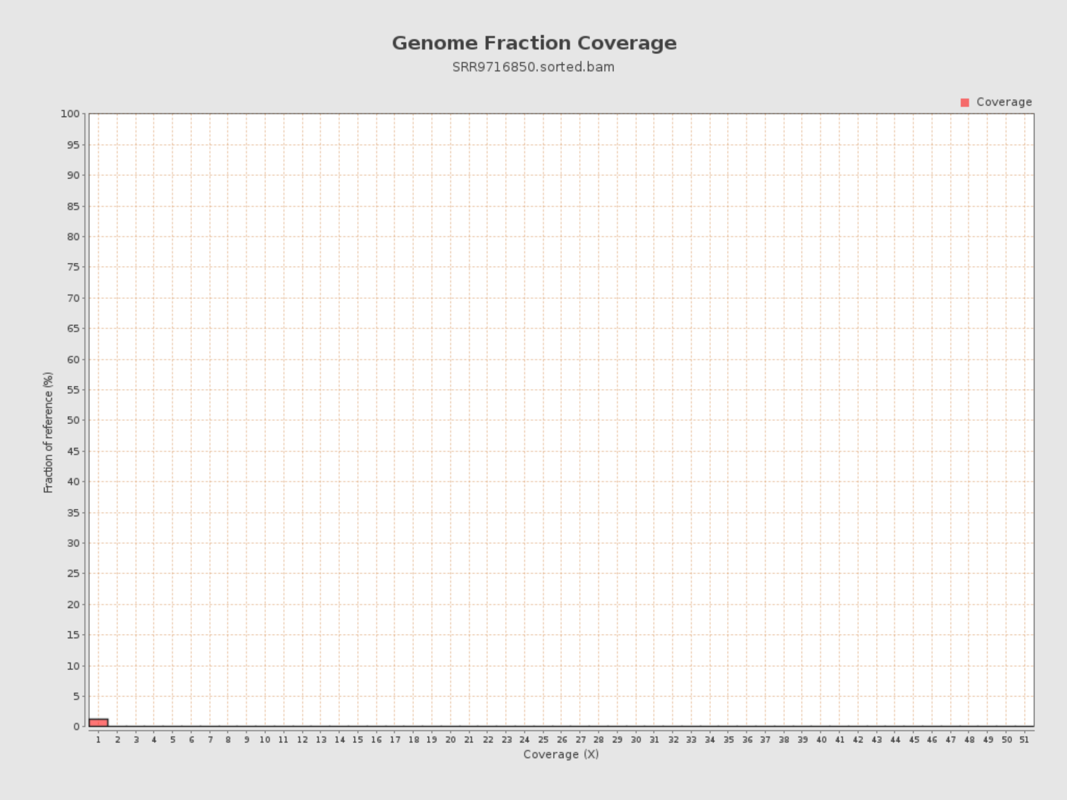
4. Results : Coverage Histogram



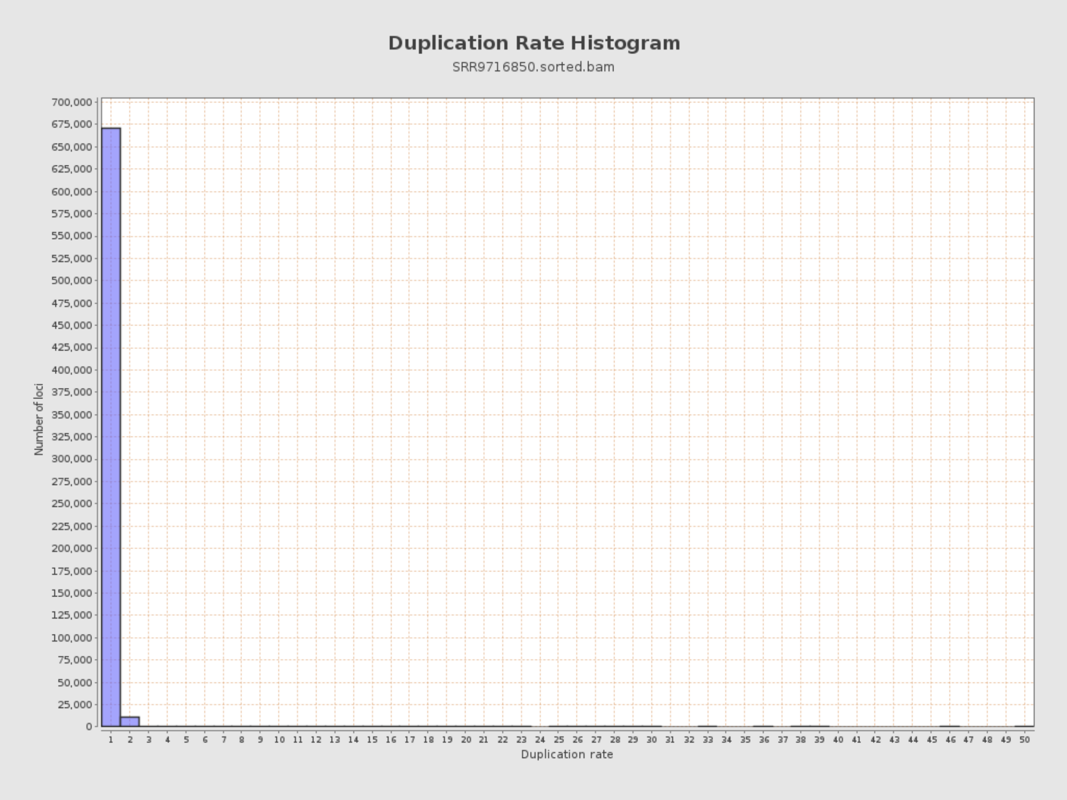
5. Results : Coverage Histogram (0-50X)



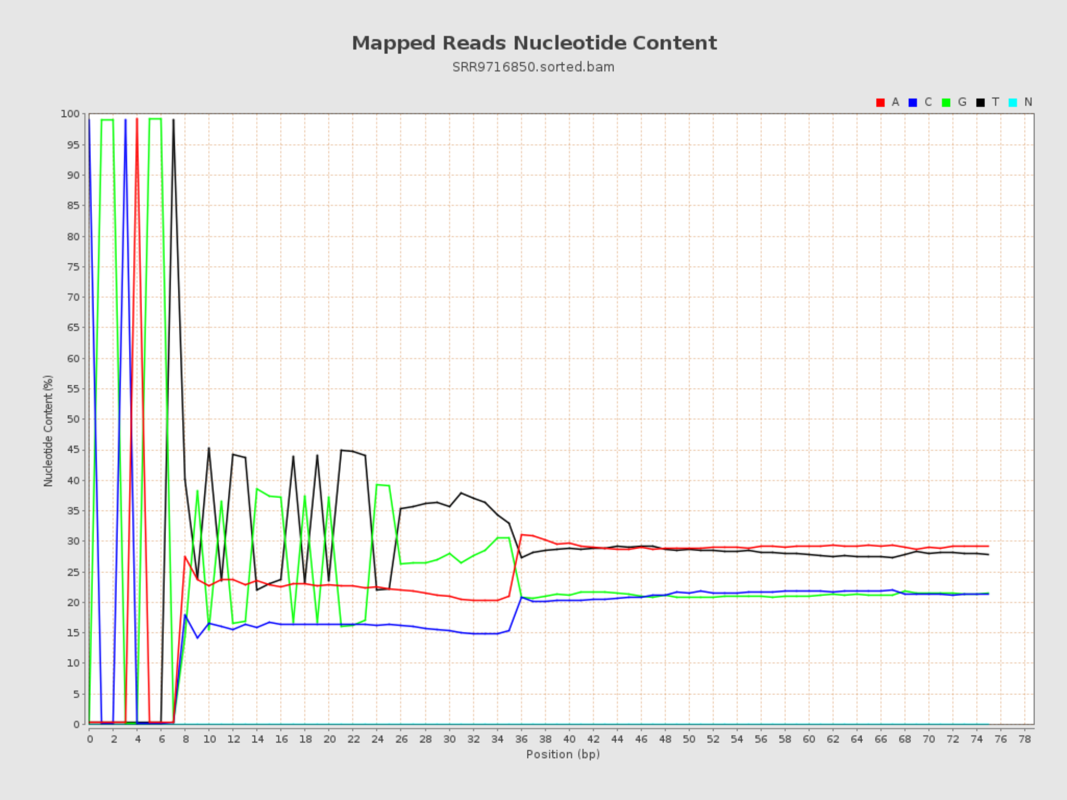
6. Results : Genome Fraction Coverage



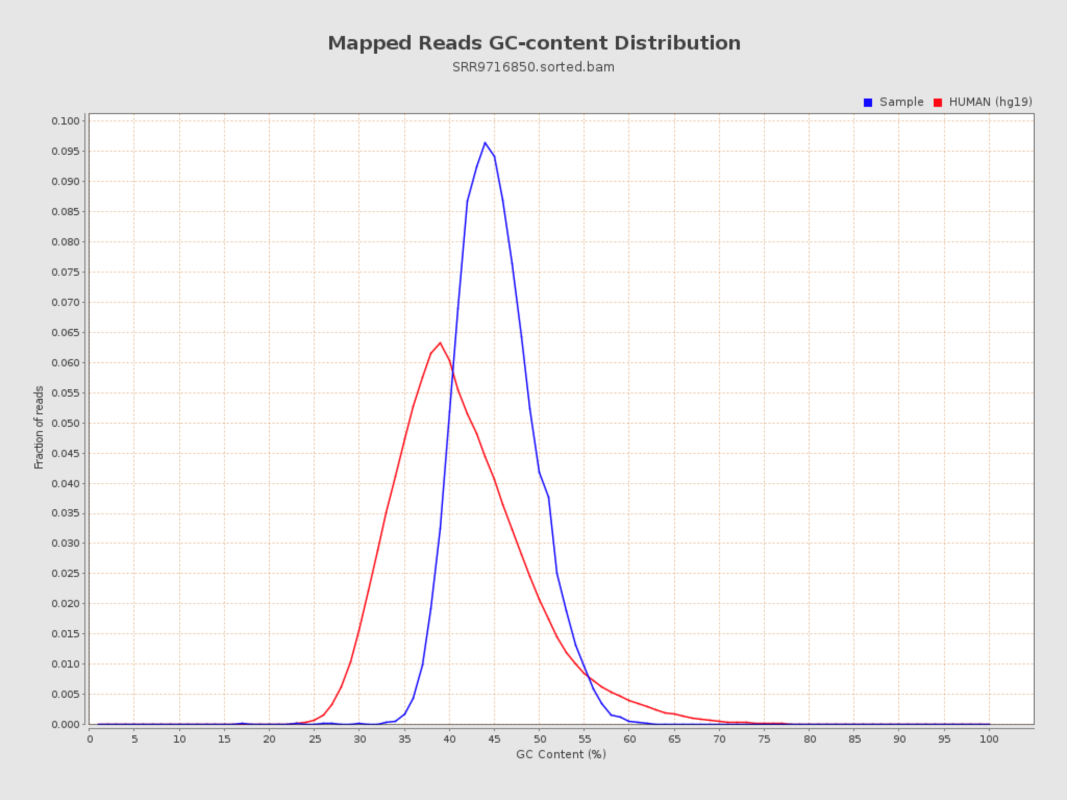
7. Results : Duplication Rate Histogram



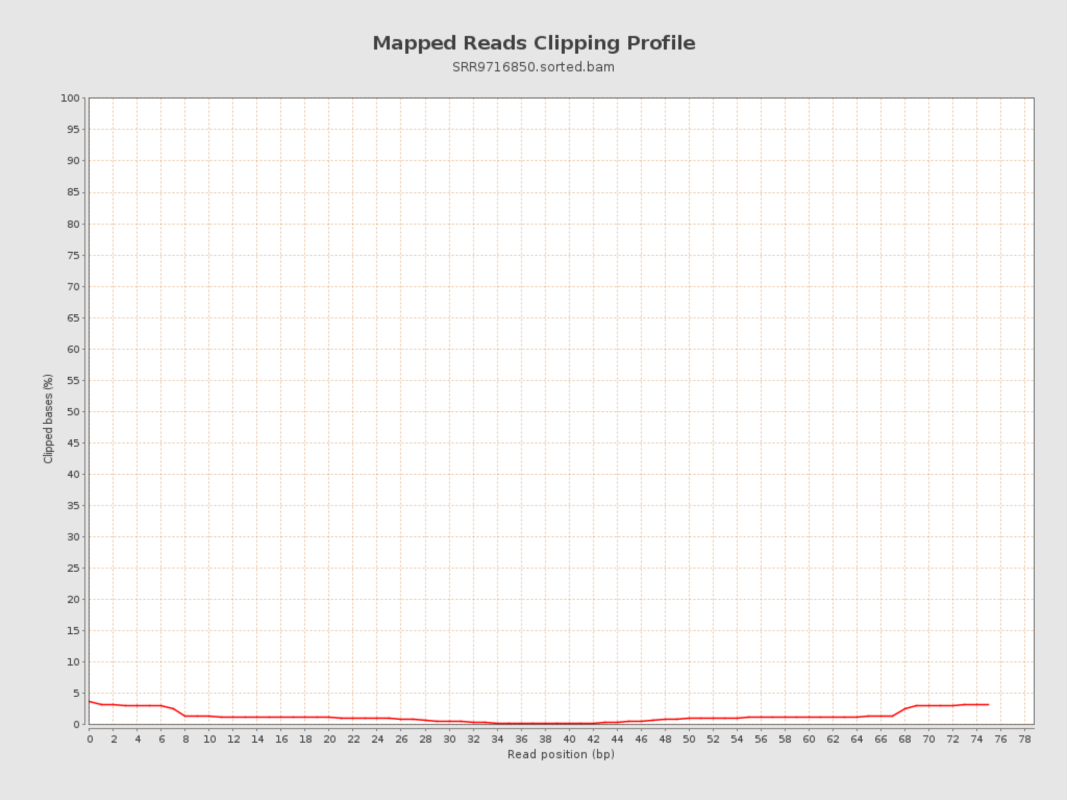
8. Results : Mapped Reads Nucleotide Content



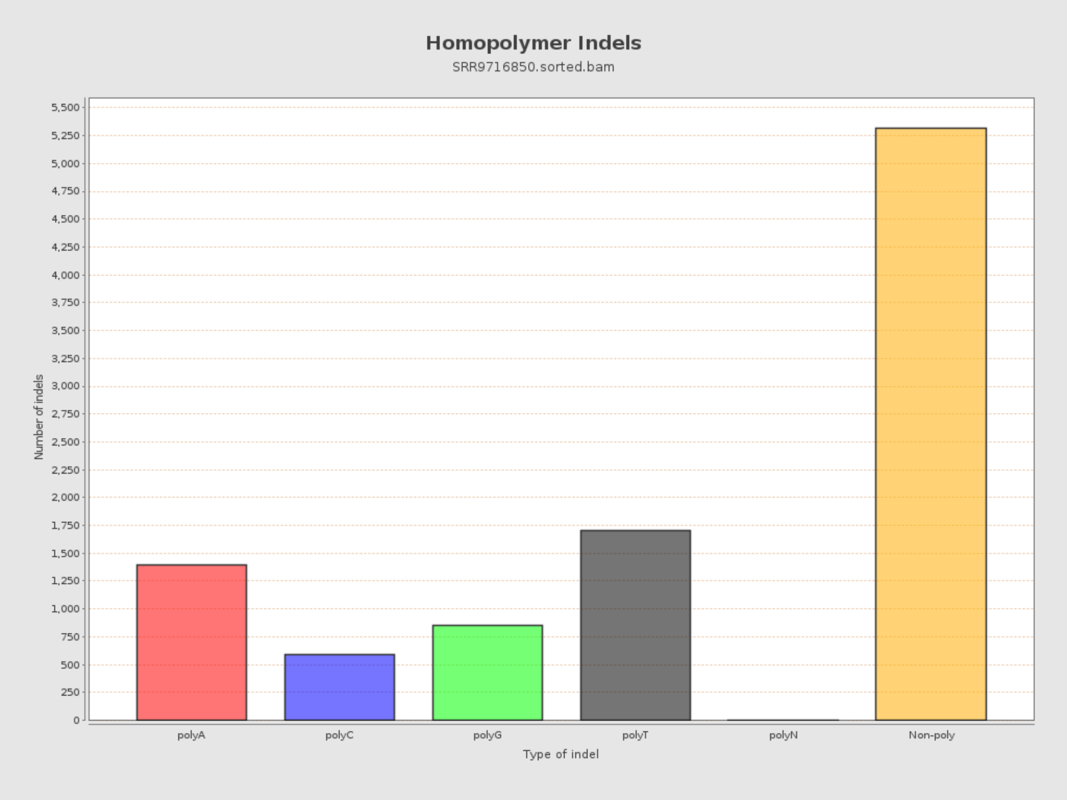
9. Results : Mapped Reads GC-content Distribution



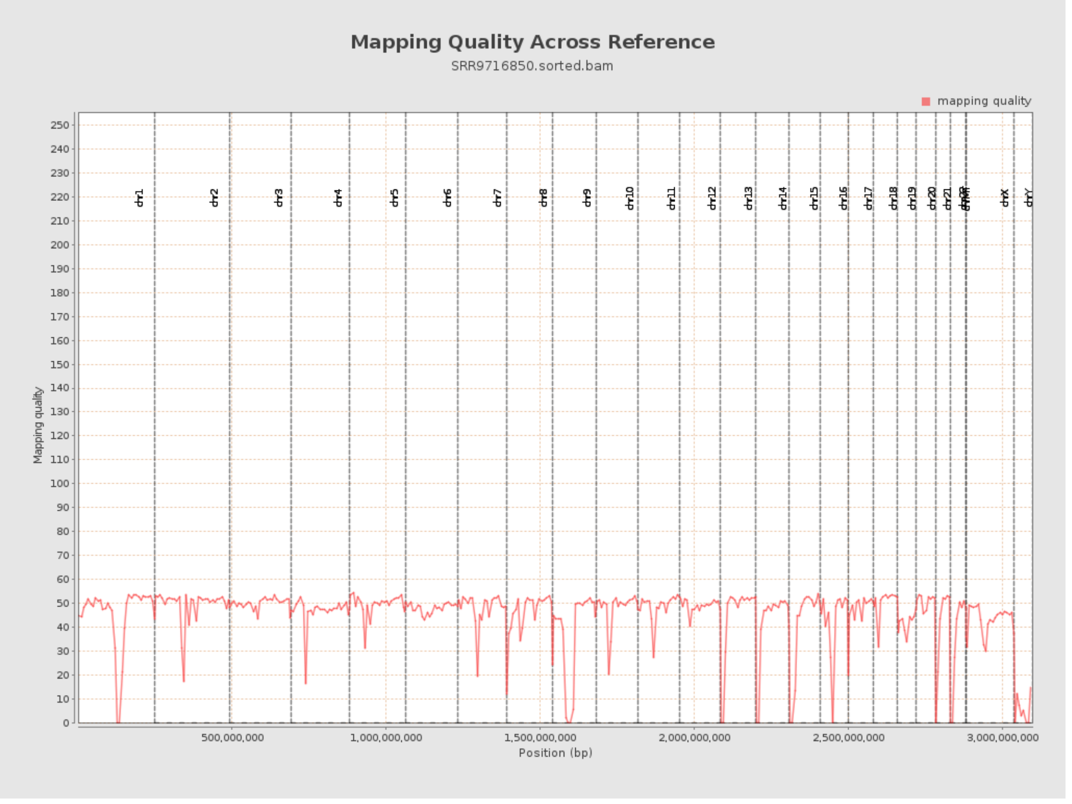
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram