Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 08:36:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867841.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_SRR9867841 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867841.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 08:36:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867841.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	627,308
Mapped reads	577,168 / 92.01%
Unmapped reads	50,140 / 7.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,706 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	12,176 / 1.94%
Duplication rate	1.55%
Clipped reads	579,159 / 92.32%

2.2. ACGT Content

Number/percentage of A's	8,669,555 / 25.27%
Number/percentage of C's	6,504,881 / 18.96%
Number/percentage of T's	10,937,904 / 31.88%
Number/percentage of G's	8,193,555 / 23.88%
Number/percentage of N's	4,380 / 0.01%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0111

Standard Deviation	0.1359

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

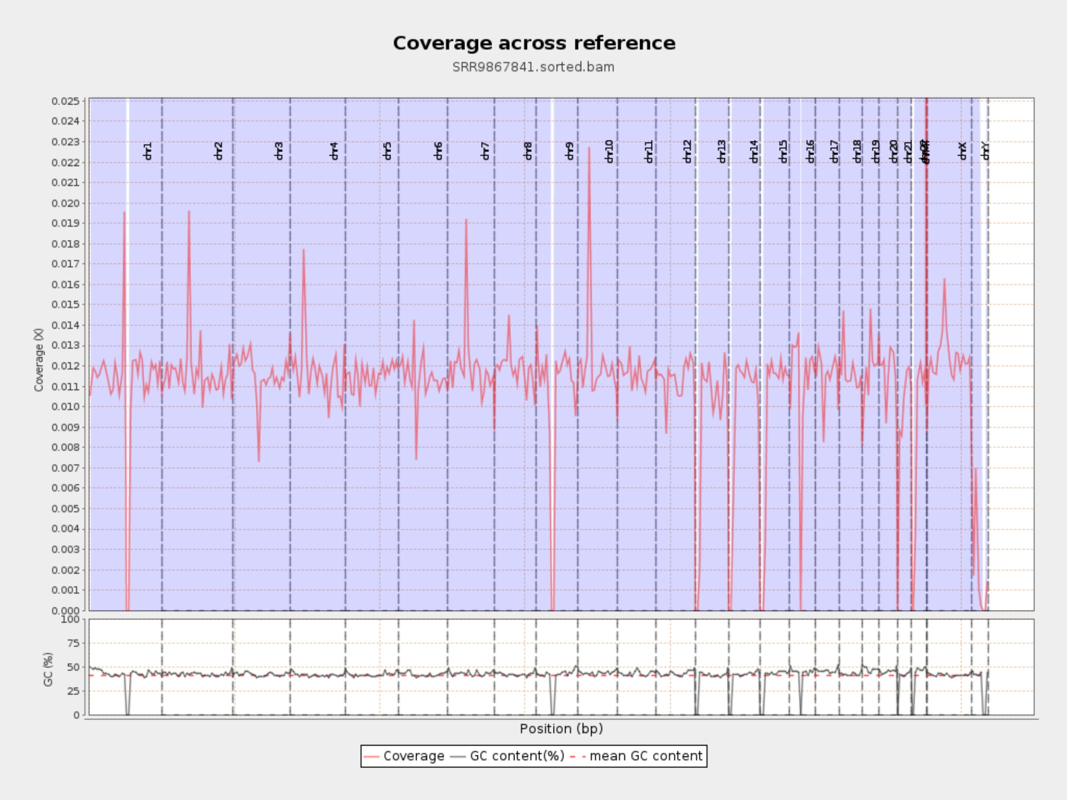
General error rate	0.51%
Mismatches	171,721
Insertions	2,025
Mapped reads with at least one insertion	0.35%
Deletions	6,291
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.84%

2.6. Chromosome stats

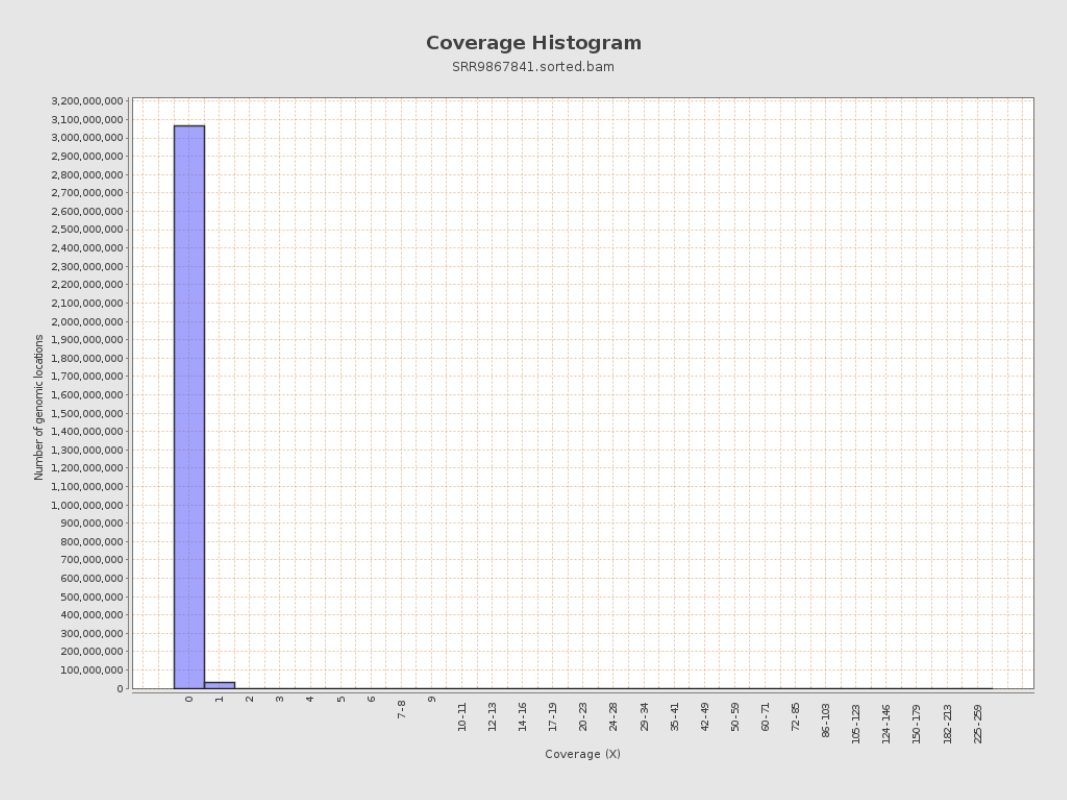
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2759470	0.0111	0.2145
chr2	243199373	2861787	0.0118	0.1624
chr3	198022430	2292330	0.0116	0.1114
chr4	191154276	2238634	0.0117	0.1177
chr5	180915260	2086241	0.0115	0.1111
chr6	171115067	1956122	0.0114	0.1159
chr7	159138663	1918284	0.0121	0.1549

chr8	146364022	1737893	0.0119	0.1409
chr9	141213431	1456430	0.0103	0.1195
chr10	135534747	1664044	0.0123	0.1416
chr11	135006516	1579018	0.0117	0.1271
chr12	133851895	1524850	0.0114	0.1106
chr13	115169878	1064788	0.0092	0.0989
chr14	107349540	1027842	0.0096	0.1037
chr15	102531392	970093	0.0095	0.1007
chr16	90354753	996158	0.011	0.1125
chr17	81195210	931268	0.0115	0.1136
chr18	78077248	918638	0.0118	0.1903
chr19	59128983	703551	0.0119	0.17
chr20	63025520	733369	0.0116	0.1119
chr21	48129895	453209	0.0094	0.1065
chr22	51304566	407208	0.0079	0.0924
chrMT	16571	5945	0.3588	0.6686
chrX	155270560	1920904	0.0124	0.1197
chrY	59373566	112265	0.0019	0.0772

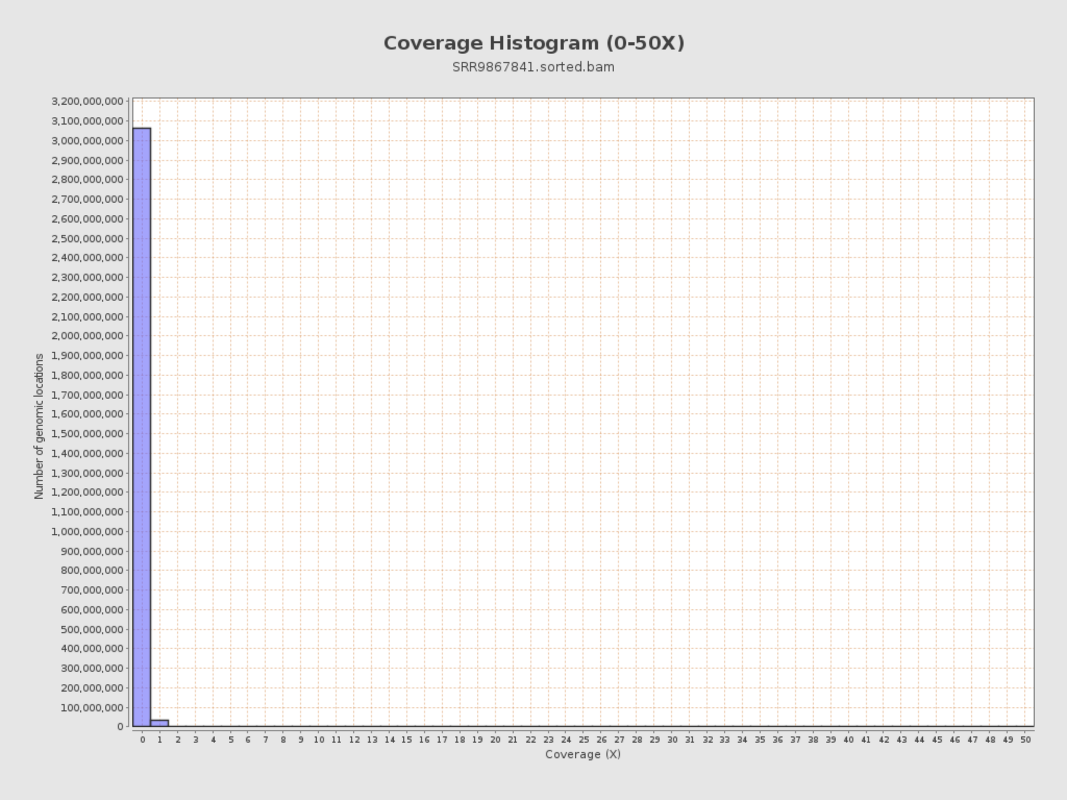
3. Results : Coverage across reference



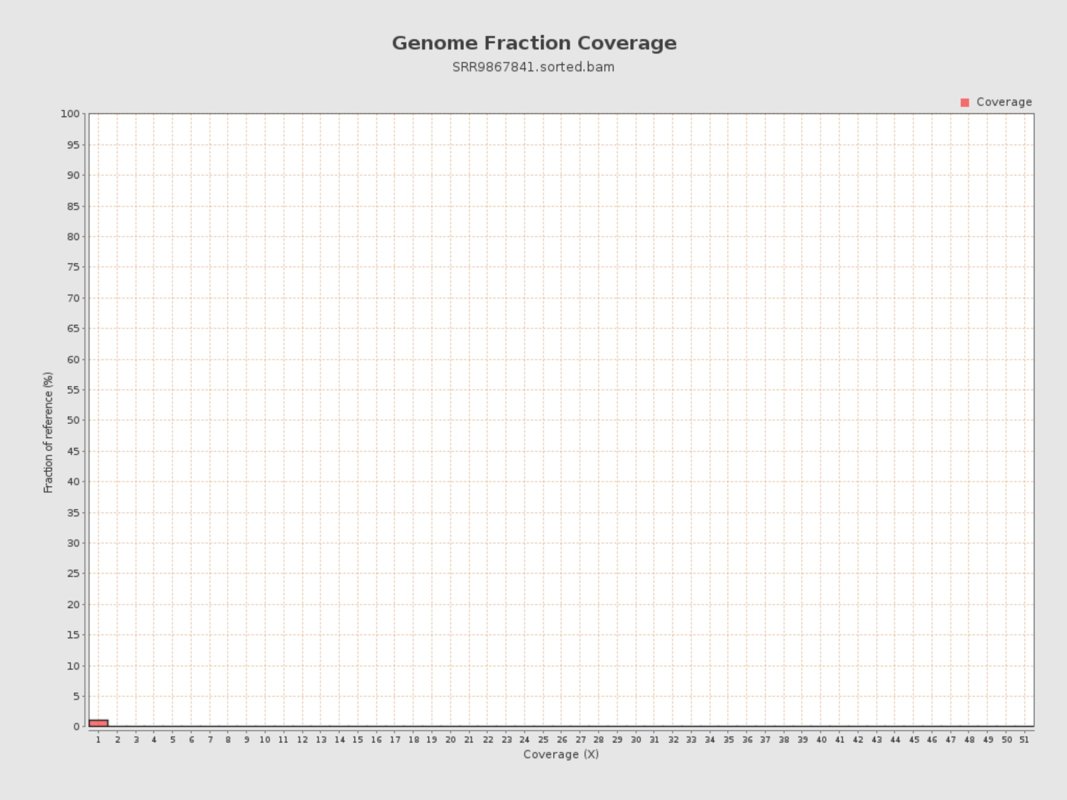
4. Results : Coverage Histogram



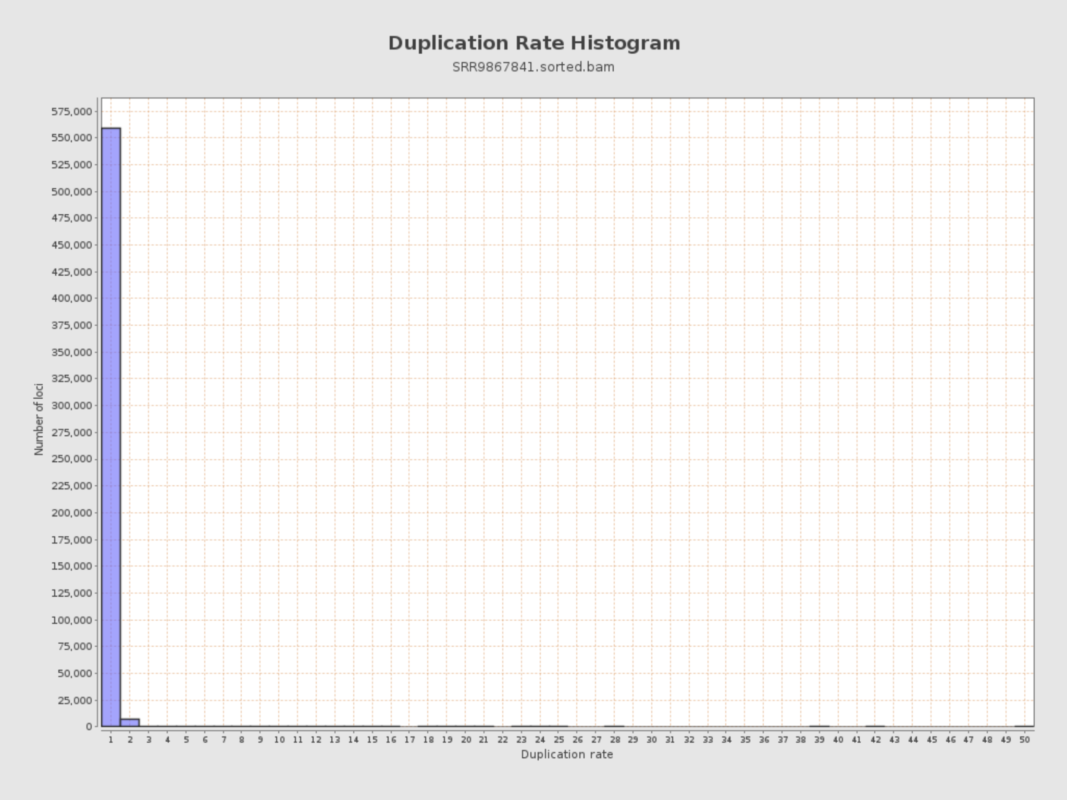
5. Results : Coverage Histogram (0-50X)



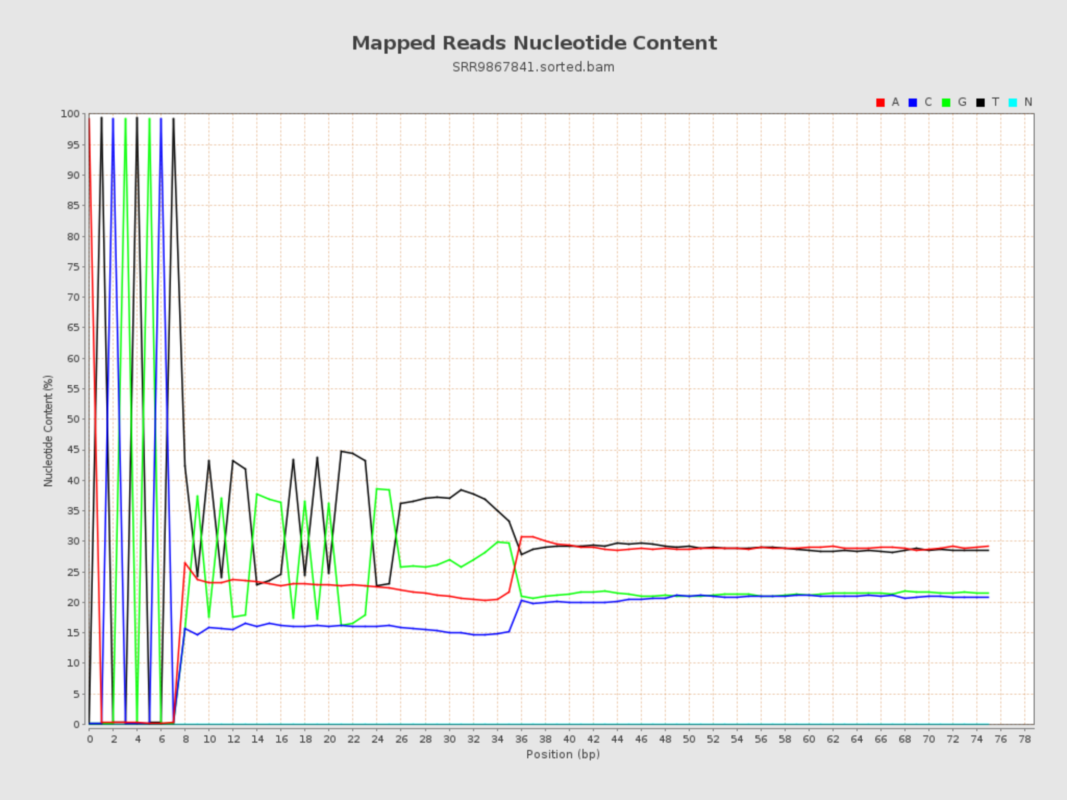
6. Results : Genome Fraction Coverage



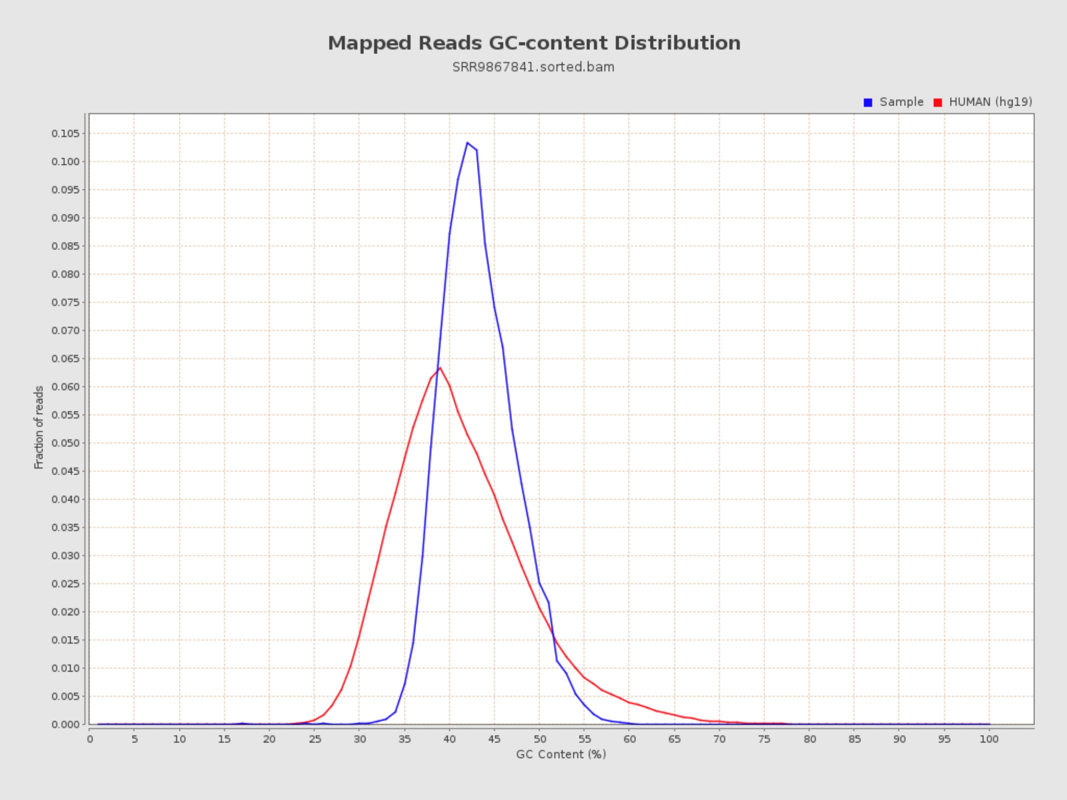
7. Results : Duplication Rate Histogram



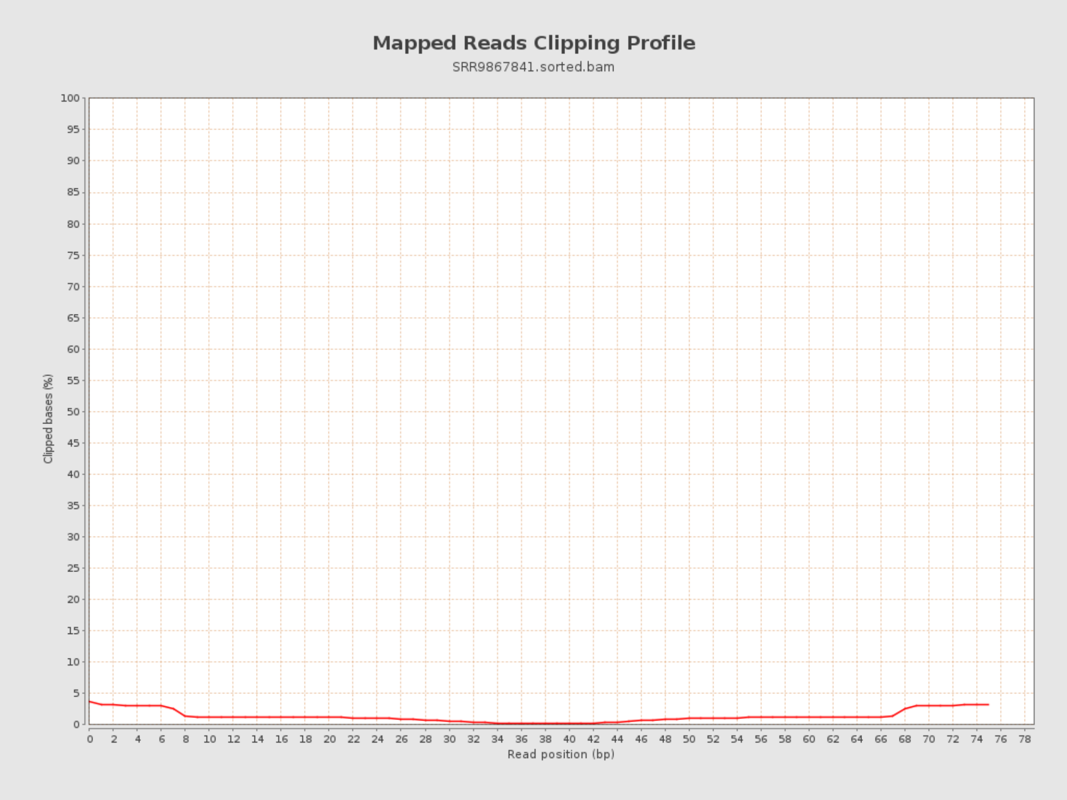
8. Results : Mapped Reads Nucleotide Content



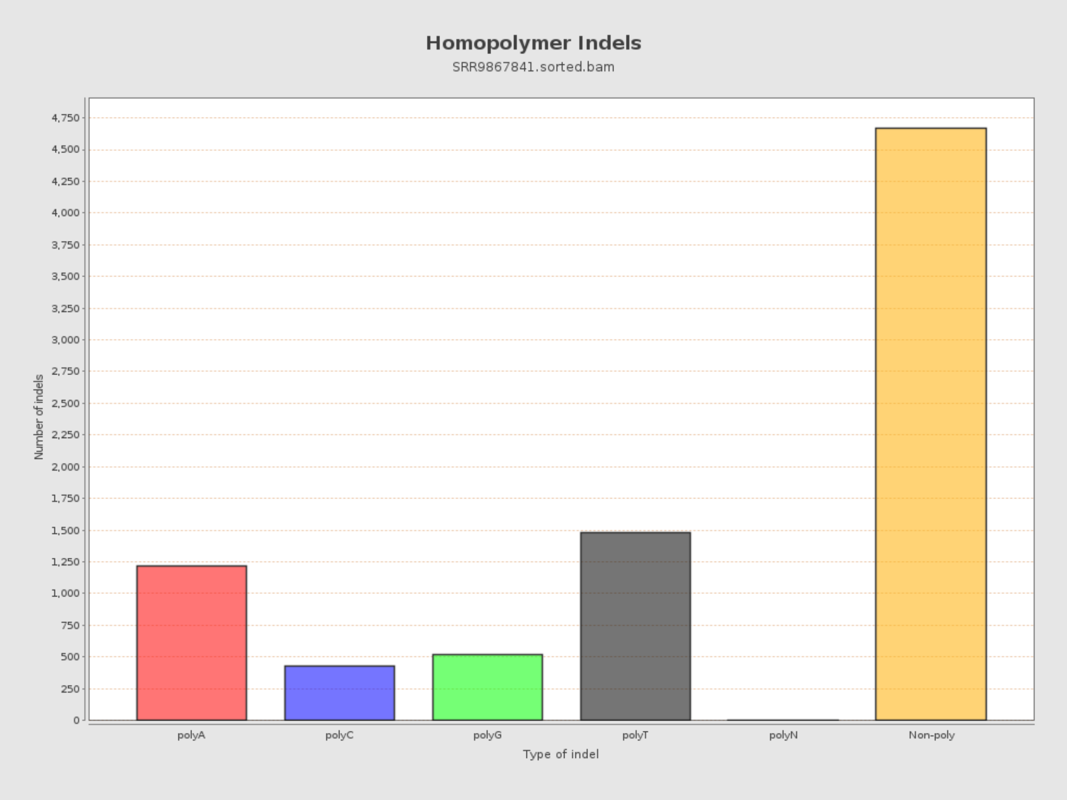
9. Results : Mapped Reads GC-content Distribution



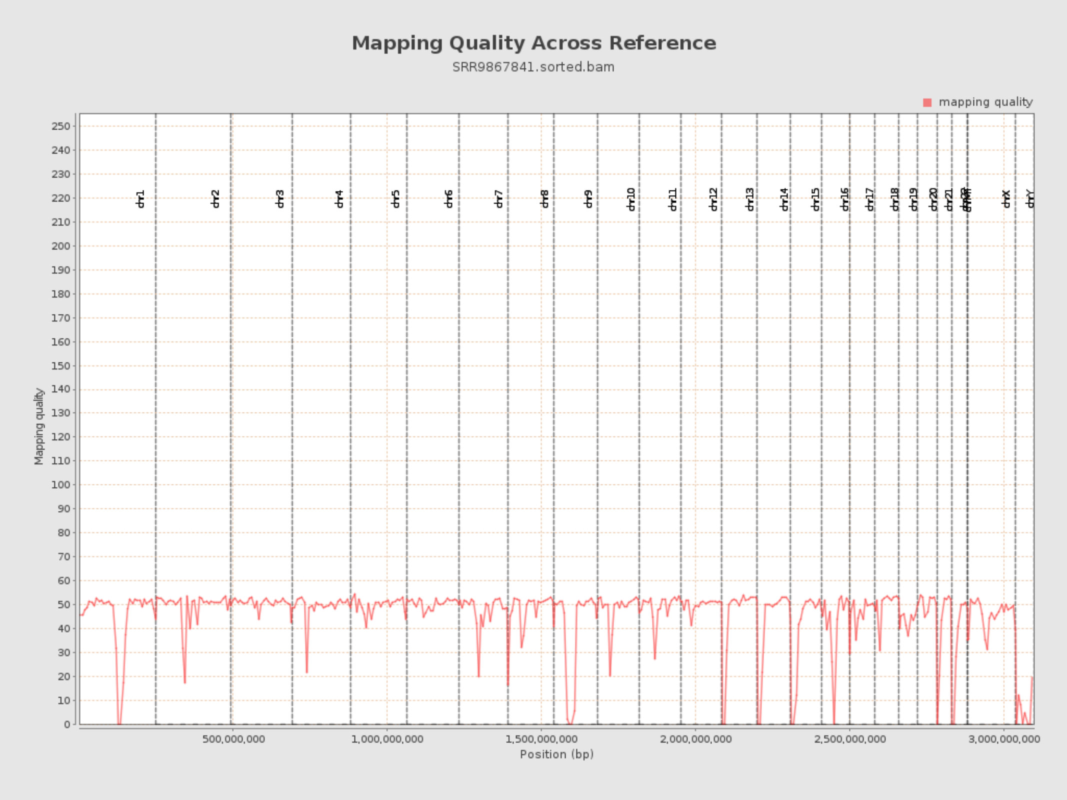
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram