Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 09:38:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867843.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_SRR9867843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 09:37:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,317,177
Mapped reads	1,217,081 / 92.4%
Unmapped reads	100,096 / 7.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,645 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	45,020 / 3.42%
Duplication rate	2.77%
Clipped reads	1,219,114 / 92.56%

2.2. ACGT Content

Number/percentage of A's	17,423,111 / 24.23%
Number/percentage of C's	12,965,842 / 18.03%
Number/percentage of T's	23,561,662 / 32.76%
Number/percentage of G's	17,951,748 / 24.96%
Number/percentage of N's	9,775 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2356

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

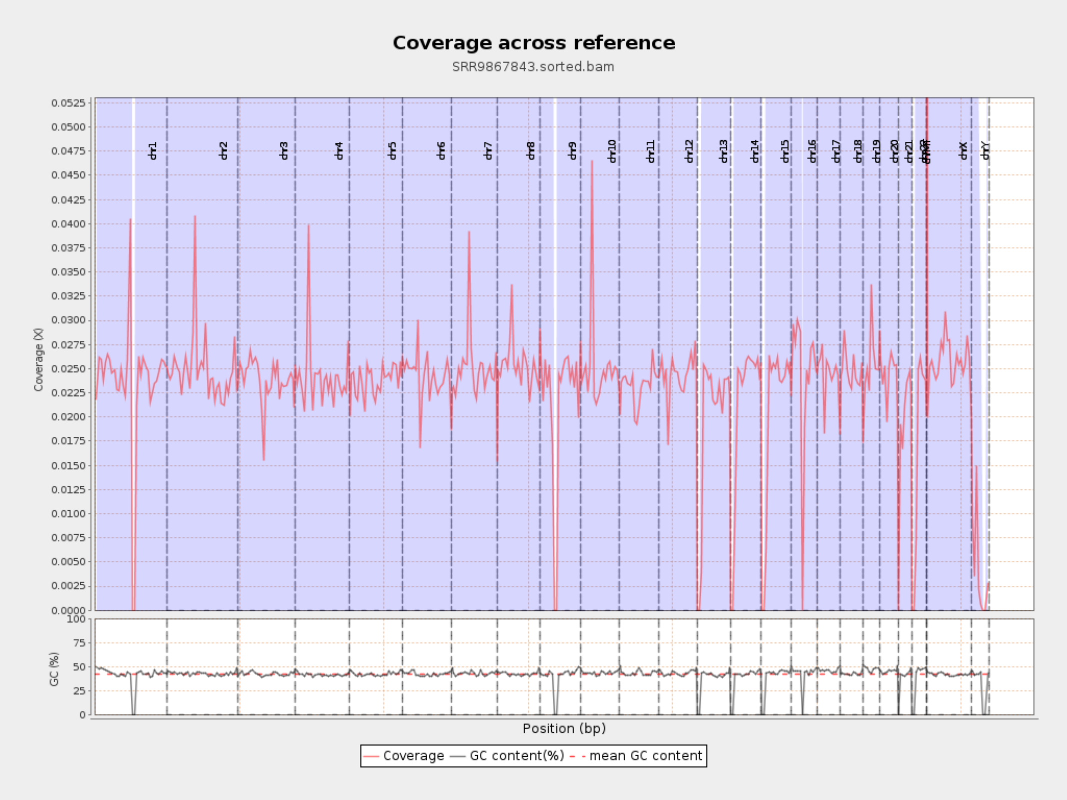
General error rate	0.52%
Mismatches	364,318
Insertions	5,198
Mapped reads with at least one insertion	0.43%
Deletions	13,446
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.28%

2.6. Chromosome stats

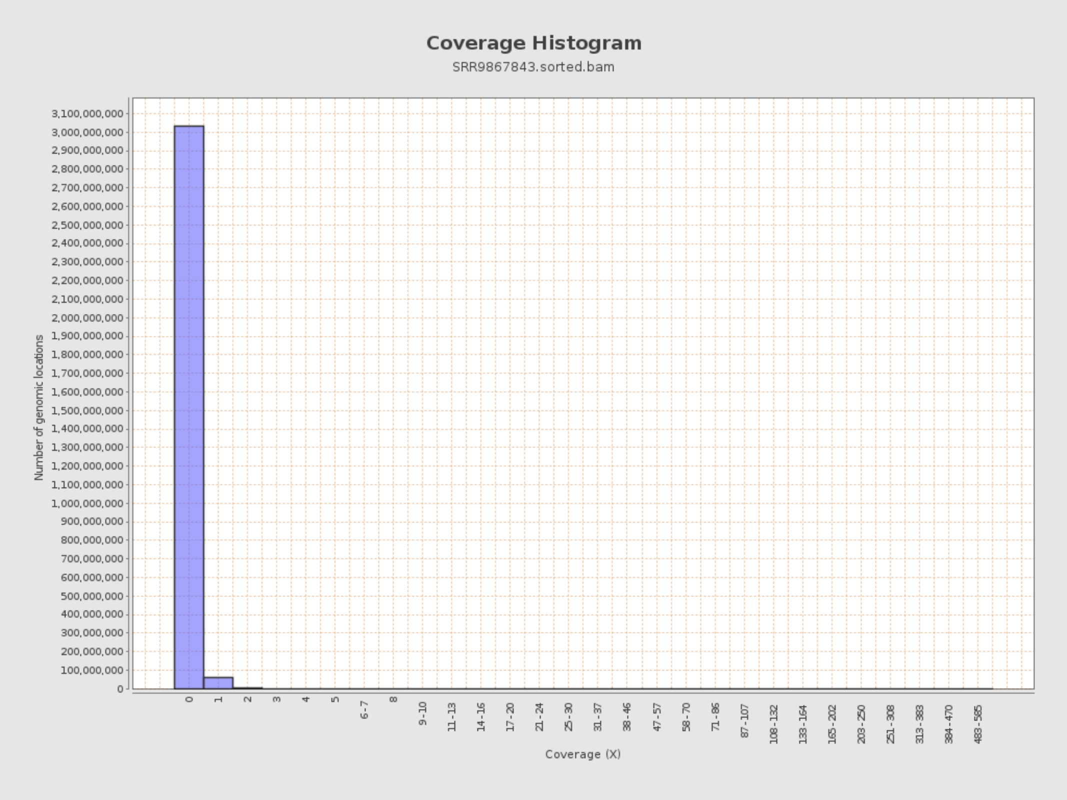
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5832228	0.0234	0.4123
chr2	243199373	6045326	0.0249	0.3131
chr3	198022430	4726622	0.0239	0.165
chr4	191154276	4633923	0.0242	0.1862
chr5	180915260	4322561	0.0239	0.1667
chr6	171115067	4138807	0.0242	0.1859
chr7	159138663	4007949	0.0252	0.2742

chr8	146364022	3722375	0.0254	0.248
chr9	141213431	3009481	0.0213	0.1941
chr10	135534747	3430730	0.0253	0.2414
chr11	135006516	3135846	0.0232	0.2015
chr12	133851895	3254198	0.0243	0.1693
chr13	115169878	2232956	0.0194	0.149
chr14	107349540	2231443	0.0208	0.1595
chr15	102531392	2058794	0.0201	0.1535
chr16	90354753	2154314	0.0238	0.176
chr17	81195210	1975985	0.0243	0.1751
chr18	78077248	1932081	0.0247	0.3356
chr19	59128983	1519530	0.0257	0.3315
chr20	63025520	1533561	0.0243	0.1698
chr21	48129895	928013	0.0193	0.1686
chr22	51304566	864676	0.0169	0.1392
chrMT	16571	14168	0.855	1.07
chrX	155270560	3990399	0.0257	0.1857
chrY	59373566	237797	0.004	0.1507

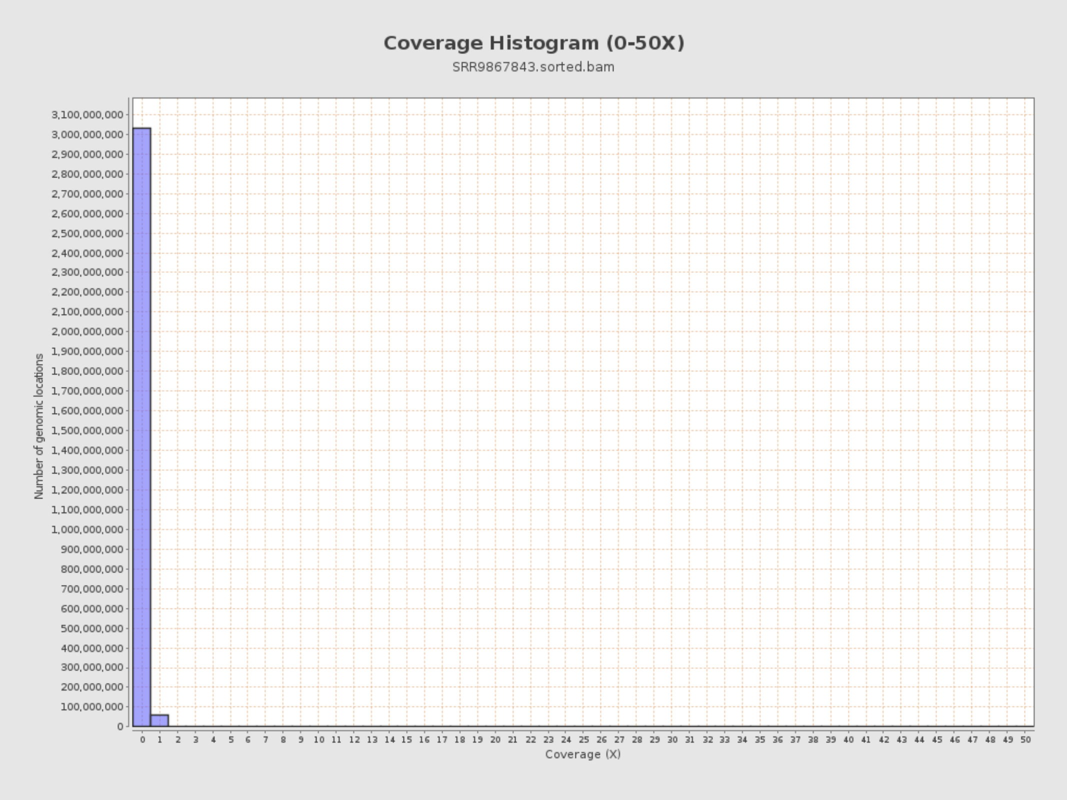
3. Results : Coverage across reference



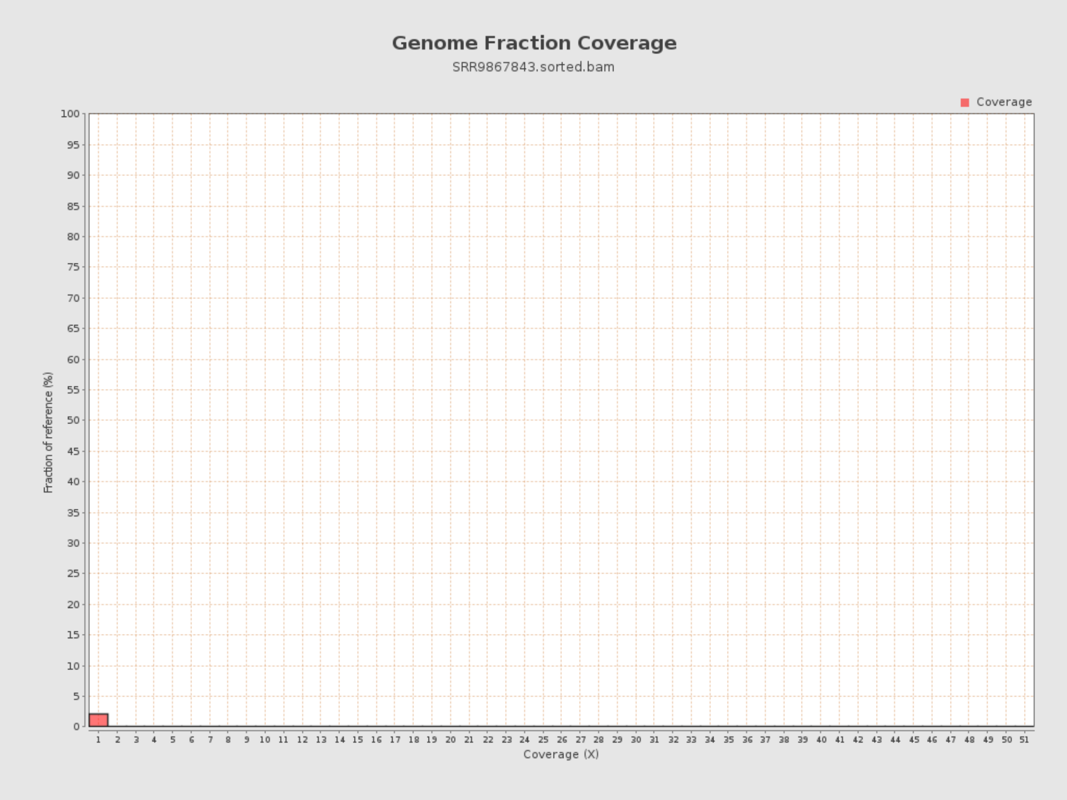
4. Results : Coverage Histogram



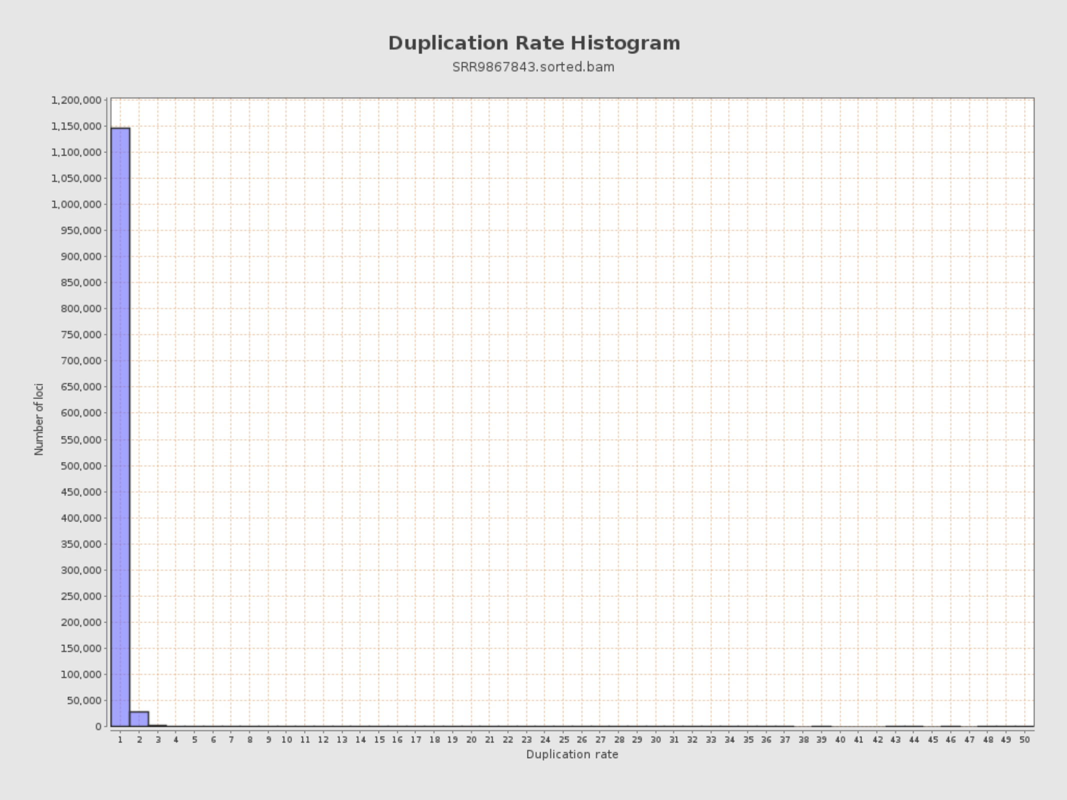
5. Results : Coverage Histogram (0-50X)



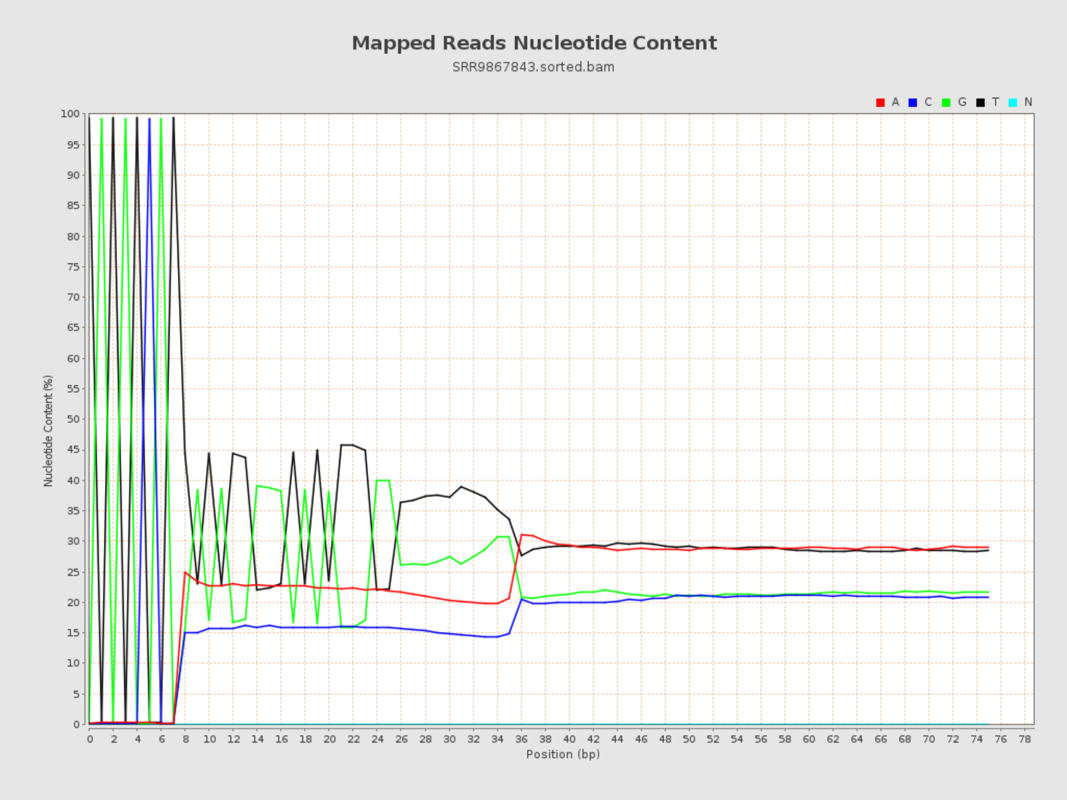
6. Results : Genome Fraction Coverage



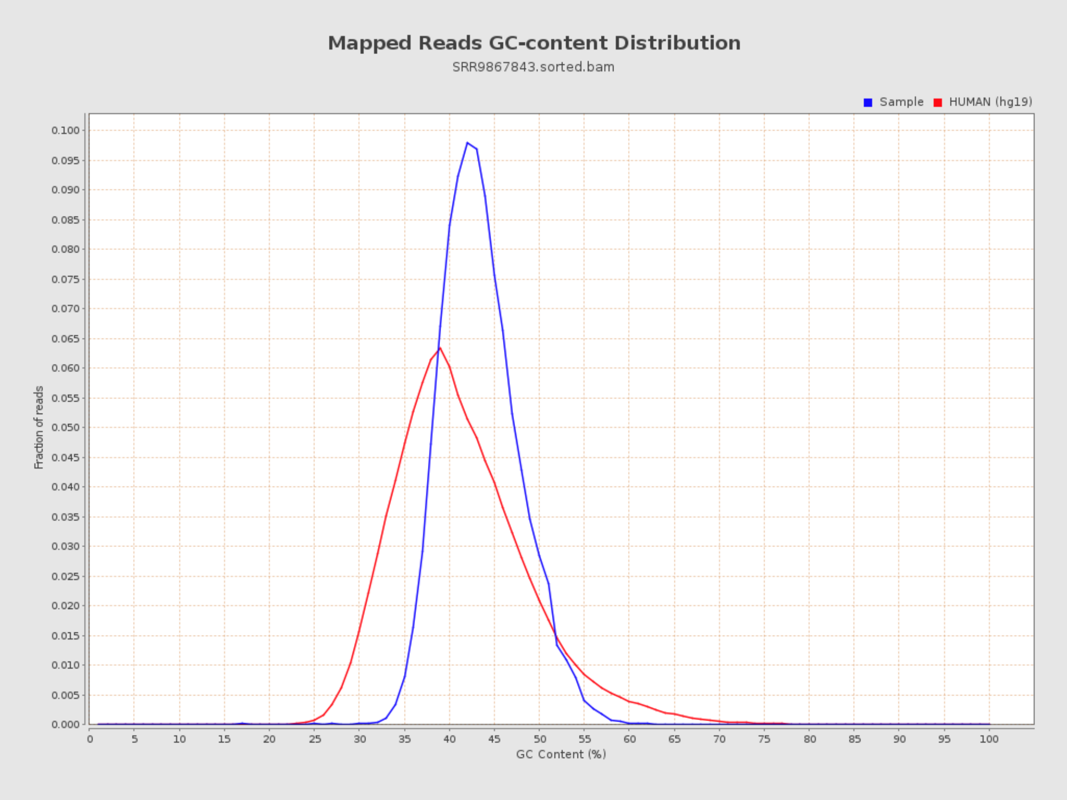
7. Results : Duplication Rate Histogram



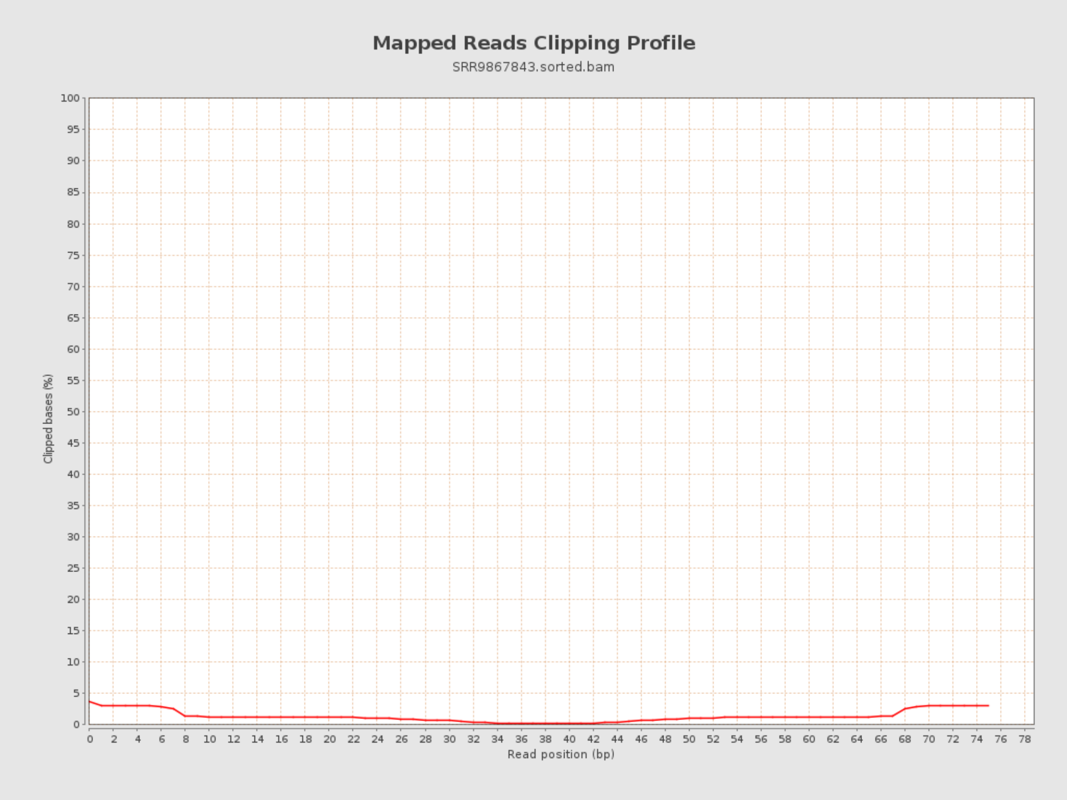
8. Results : Mapped Reads Nucleotide Content



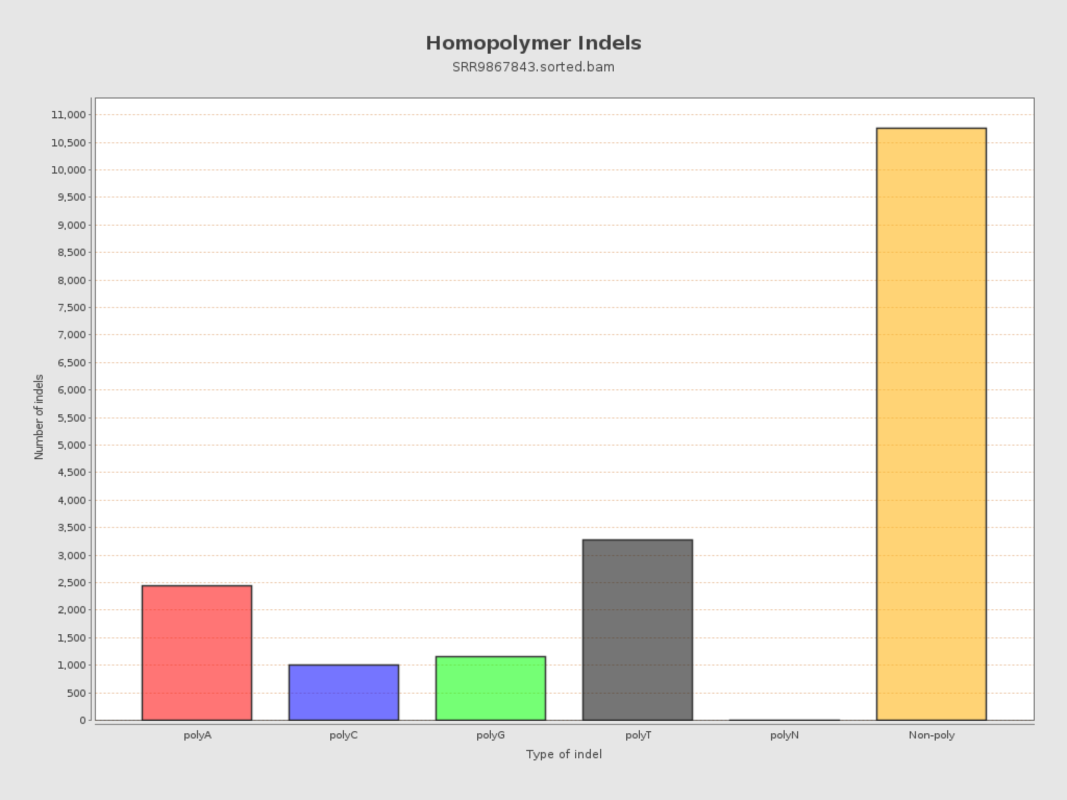
9. Results : Mapped Reads GC-content Distribution



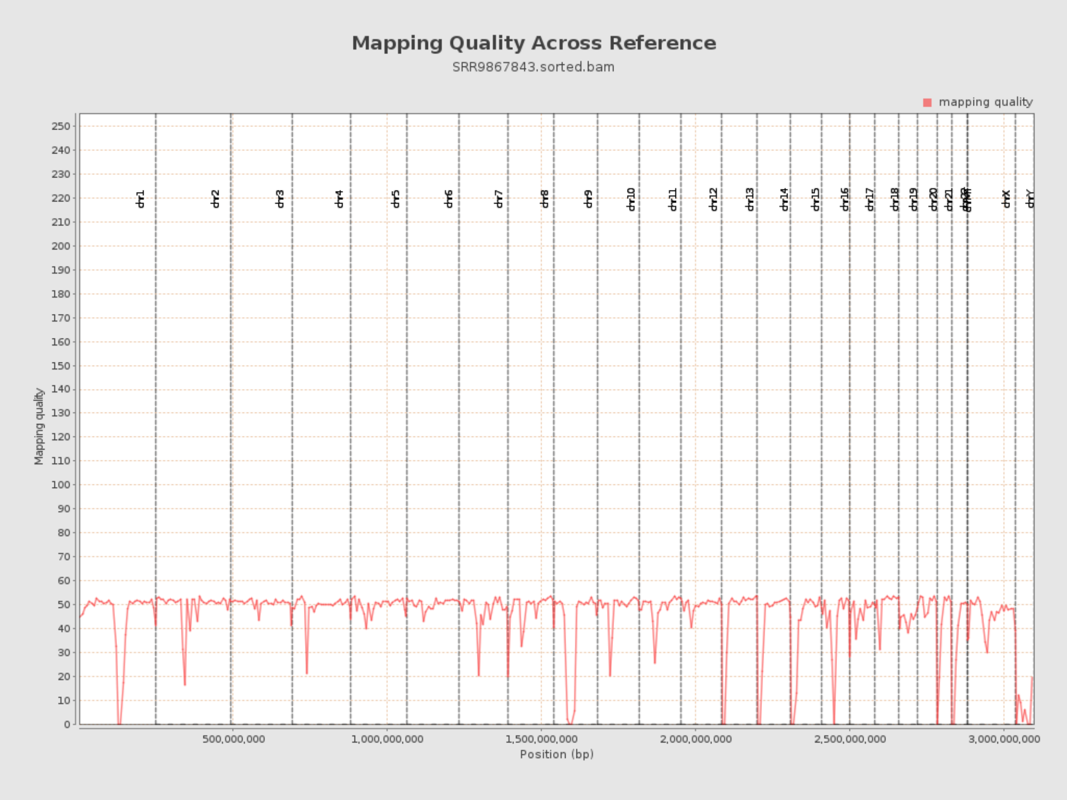
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram