Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 12:52:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867851.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_SRR9867851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867851.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 12:52:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,052,657
Mapped reads	1,894,631 / 92.3%
Unmapped reads	158,026 / 7.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,373 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	97,073 / 4.73%
Duplication rate	3.81%
Clipped reads	1,900,448 / 92.58%

2.2. ACGT Content

Number/percentage of A's	27,195,522 / 24.28%
Number/percentage of C's	22,901,848 / 20.45%
Number/percentage of T's	35,800,396 / 31.96%
Number/percentage of G's	26,090,348 / 23.29%
Number/percentage of N's	14,346 / 0.01%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0362

Standard Deviation	0.3485

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

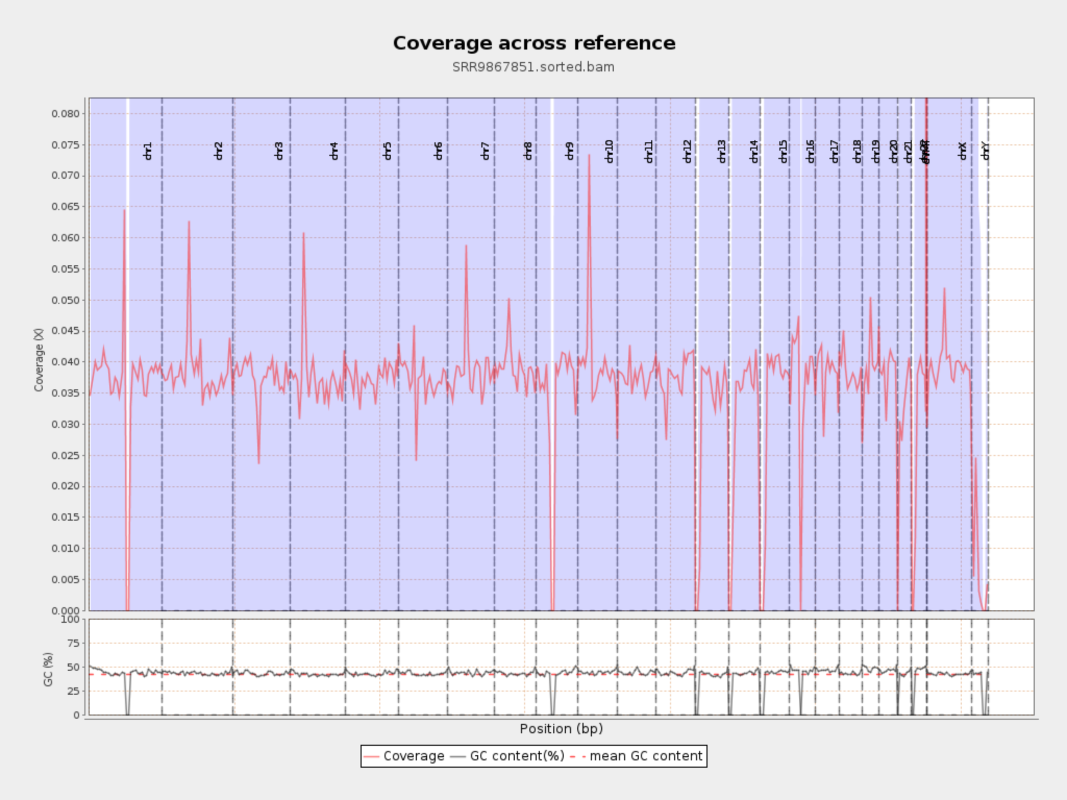
General error rate	0.52%
Mismatches	564,394
Insertions	7,038
Mapped reads with at least one insertion	0.37%
Deletions	20,898
Mapped reads with at least one deletion	1.09%
Homopolymer indels	45.07%

2.6. Chromosome stats

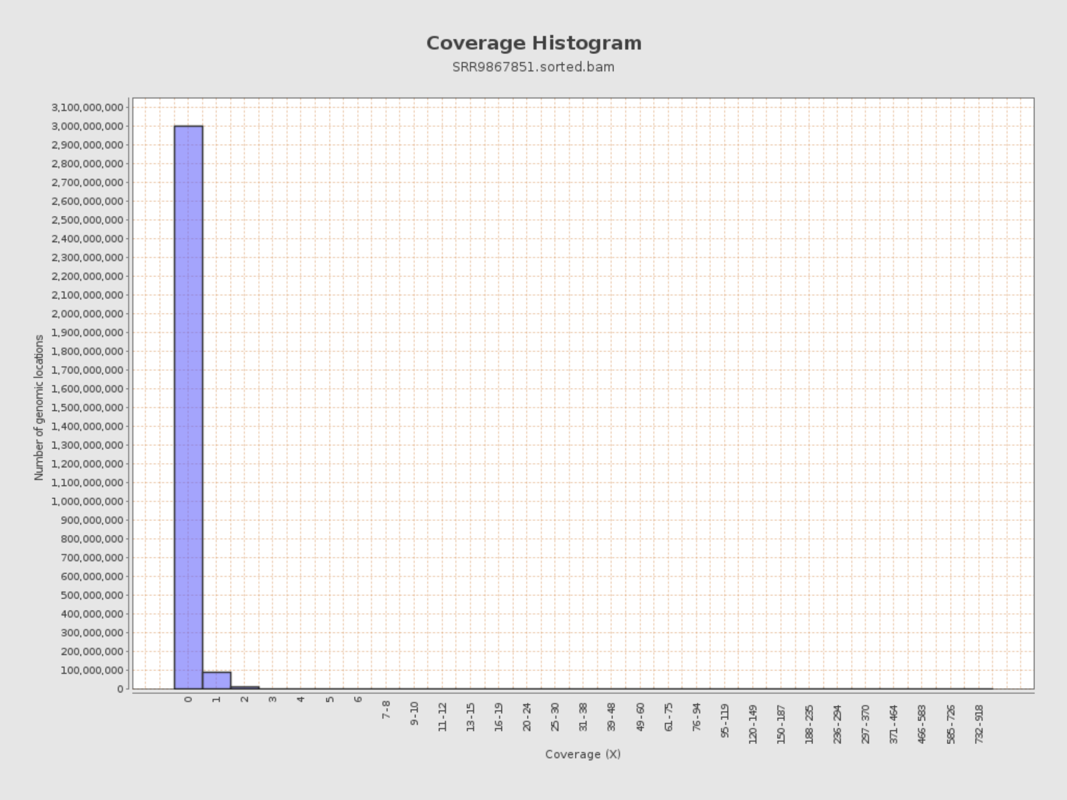
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9053481	0.0363	0.6668
chr2	243199373	9401322	0.0387	0.4697
chr3	198022430	7399435	0.0374	0.214
chr4	191154276	7165962	0.0375	0.2492
chr5	180915260	6788907	0.0375	0.2175
chr6	171115067	6389321	0.0373	0.2472
chr7	159138663	6173424	0.0388	0.4042

chr8	146364022	5734720	0.0392	0.3845
chr9	141213431	4737790	0.0336	0.2778
chr10	135534747	5453904	0.0402	0.355
chr11	135006516	5074291	0.0376	0.2972
chr12	133851895	5051884	0.0377	0.2189
chr13	115169878	3527525	0.0306	0.194
chr14	107349540	3321676	0.0309	0.2027
chr15	102531392	3247710	0.0317	0.1963
chr16	90354753	3298519	0.0365	0.2327
chr17	81195210	3098406	0.0382	0.2323
chr18	78077248	3008056	0.0385	0.5179
chr19	59128983	2332535	0.0394	0.489
chr20	63025520	2404663	0.0382	0.2236
chr21	48129895	1485049	0.0309	0.2367
chr22	51304566	1353181	0.0264	0.1804
chrMT	16571	37225	2.2464	2.007
chrX	155270560	6121626	0.0394	0.2437
chrY	59373566	375156	0.0063	0.2437

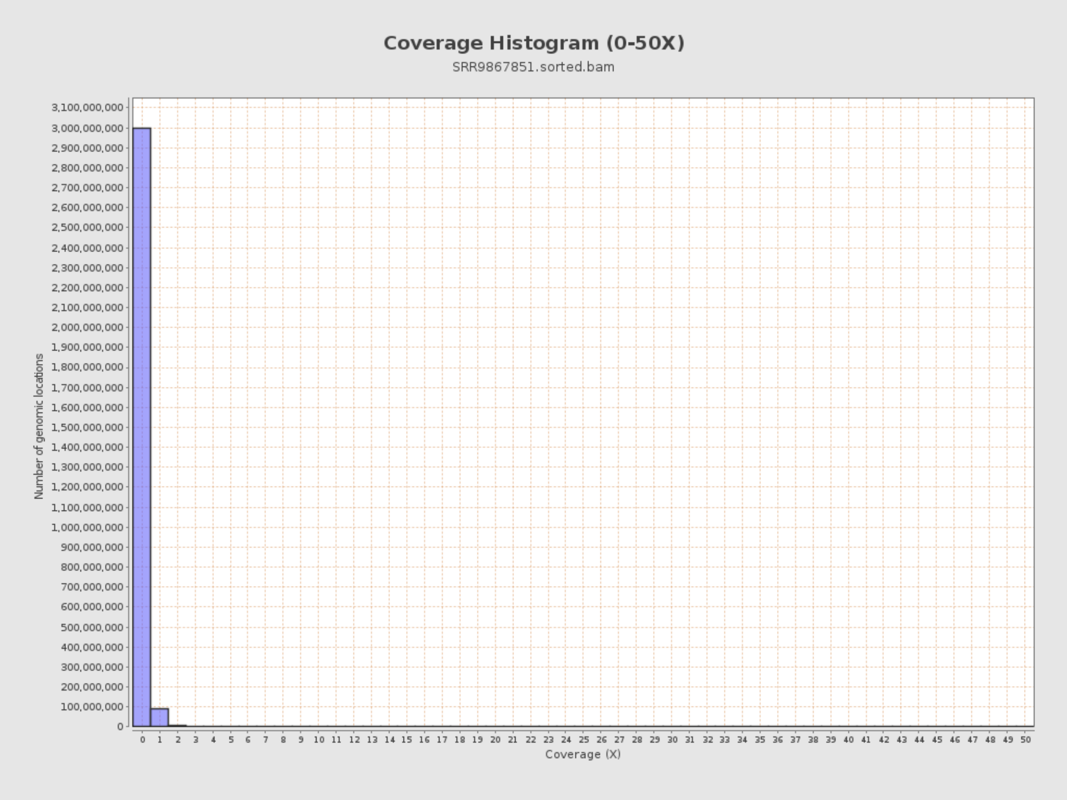
3. Results : Coverage across reference



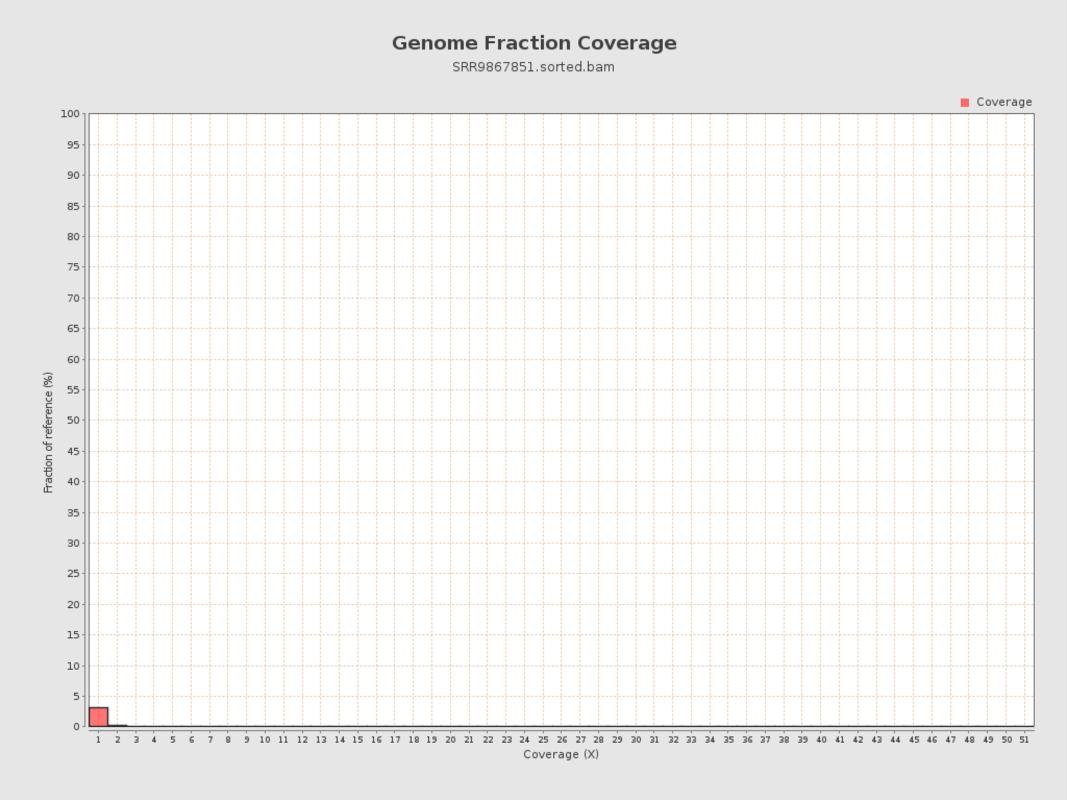
4. Results : Coverage Histogram



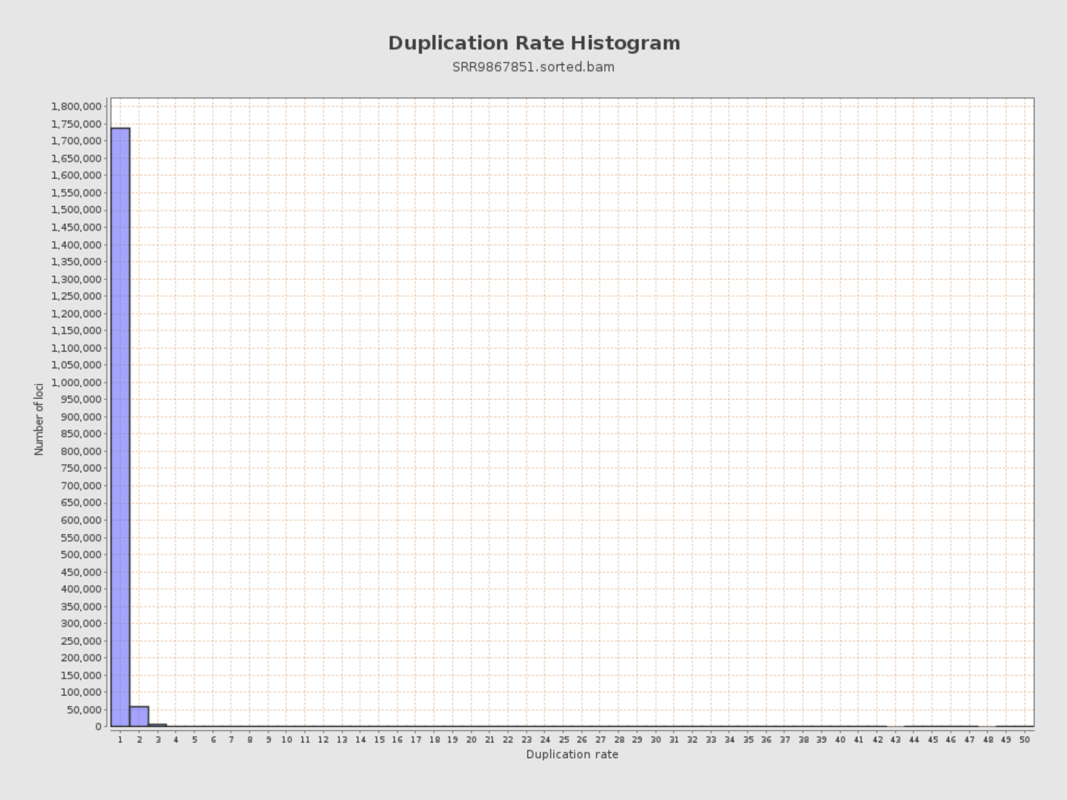
5. Results : Coverage Histogram (0-50X)



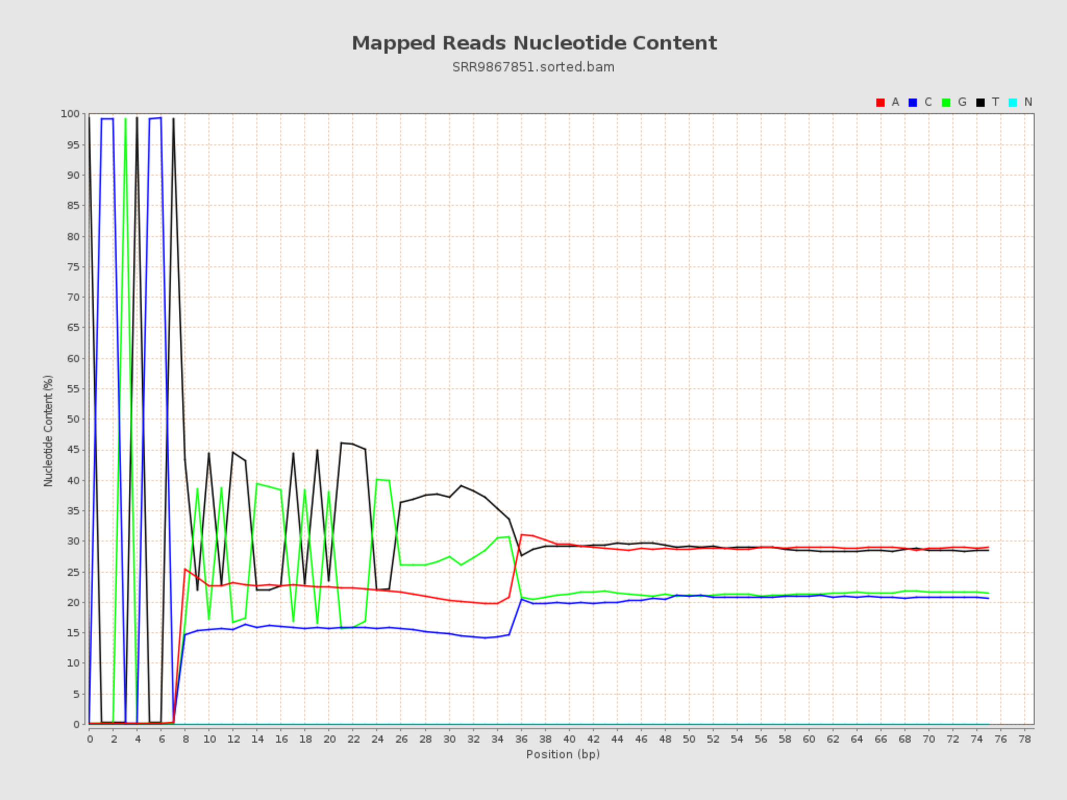
6. Results : Genome Fraction Coverage



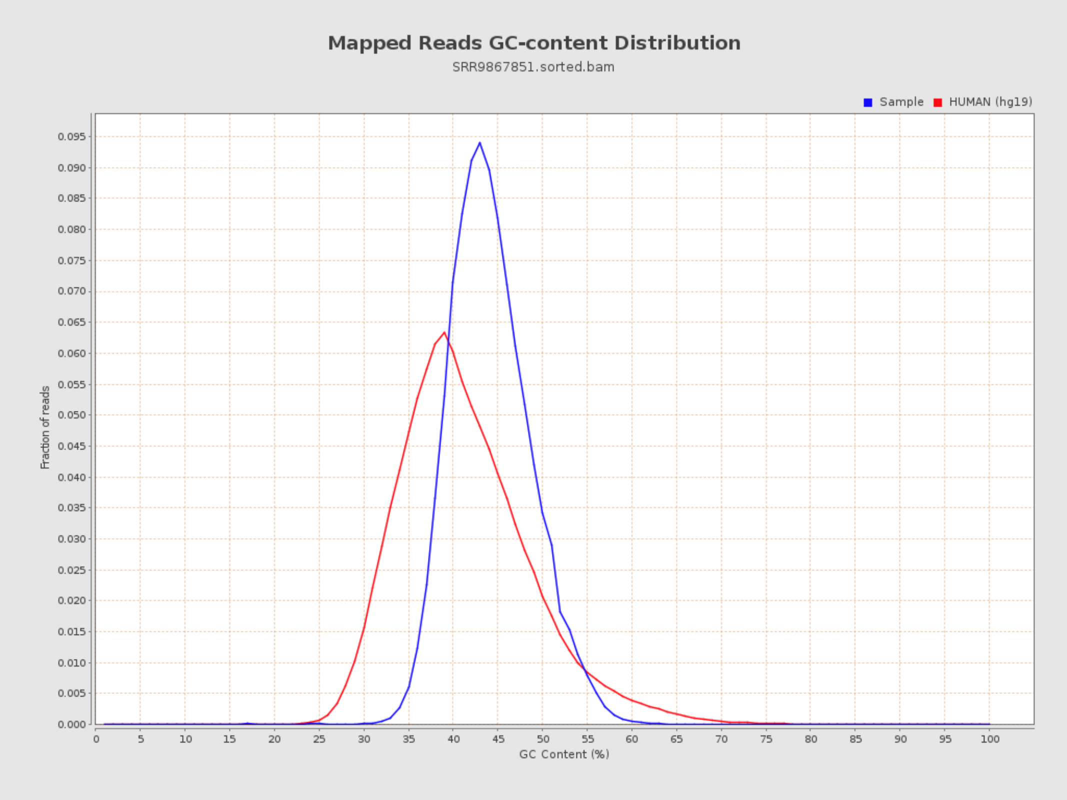
7. Results : Duplication Rate Histogram



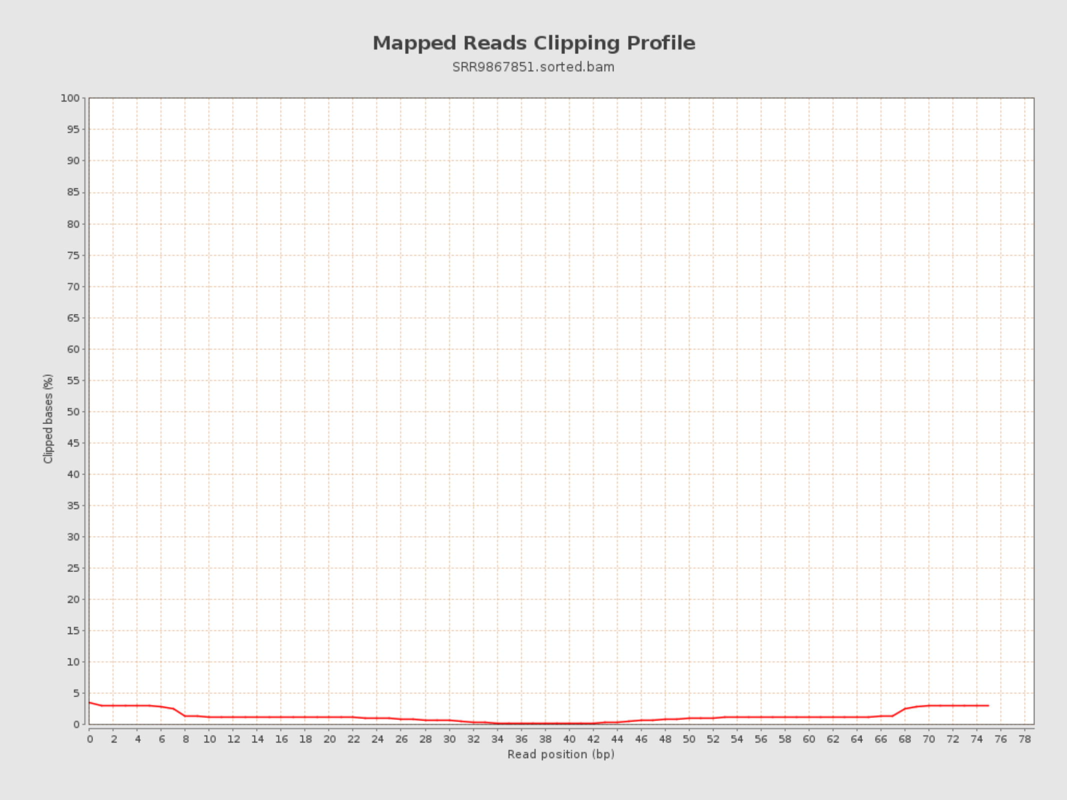
8. Results : Mapped Reads Nucleotide Content



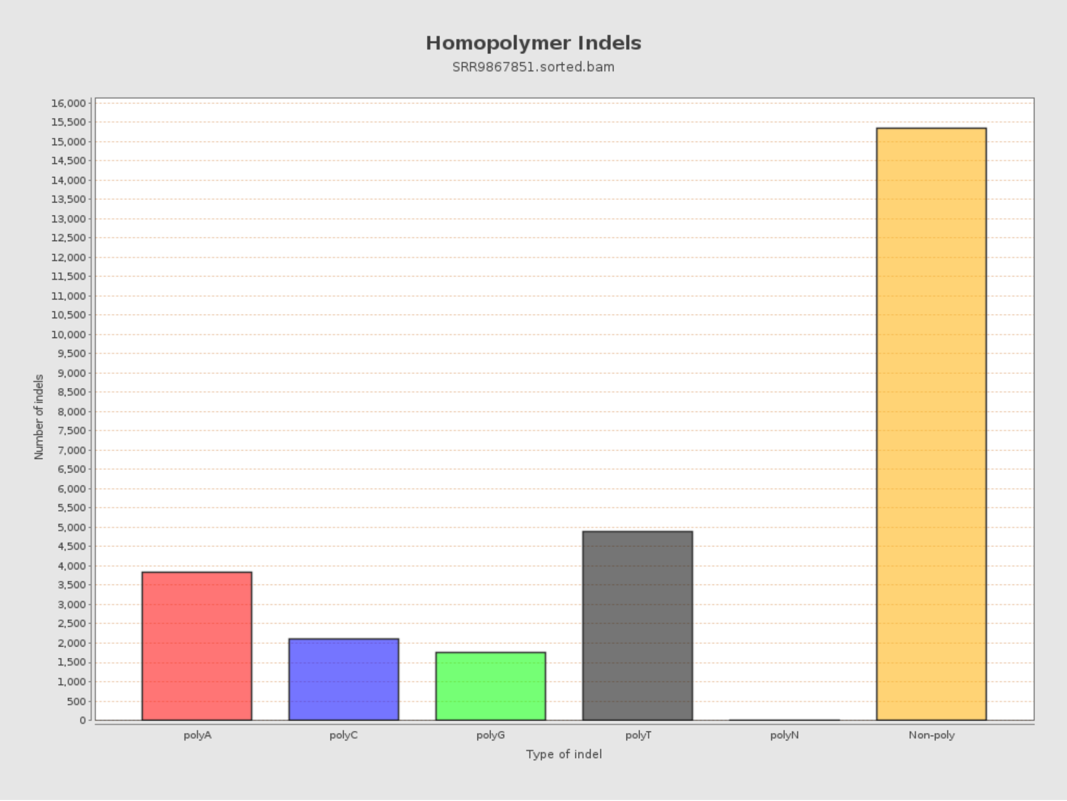
9. Results : Mapped Reads GC-content Distribution



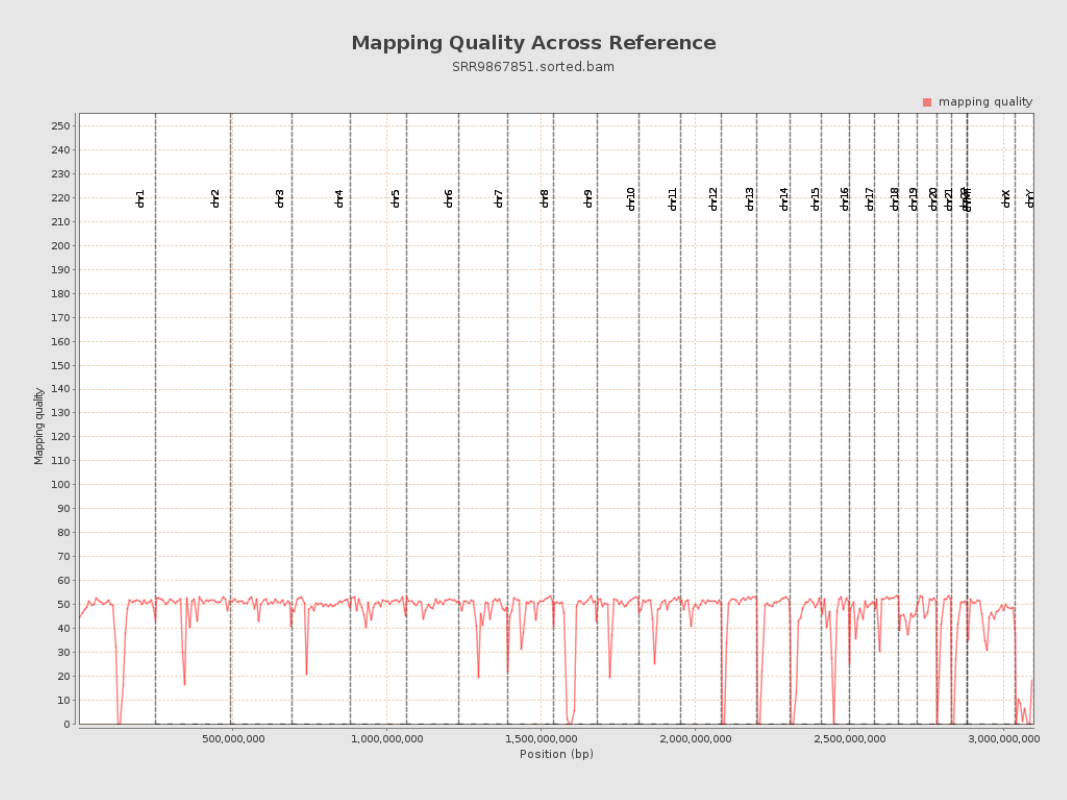
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram