Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:30:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867861.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_SRR9867861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867861.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:30:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,008,986
Mapped reads	1,861,544 / 92.66%
Unmapped reads	147,442 / 7.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,339 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	99,002 / 4.93%
Duplication rate	4%
Clipped reads	1,862,715 / 92.72%

2.2. ACGT Content

Number/percentage of A's	28,711,003 / 26.03%
Number/percentage of C's	19,841,916 / 17.99%
Number/percentage of T's	34,270,726 / 31.07%
Number/percentage of G's	27,452,384 / 24.89%
Number/percentage of N's	14,363 / 0.01%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.3356

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

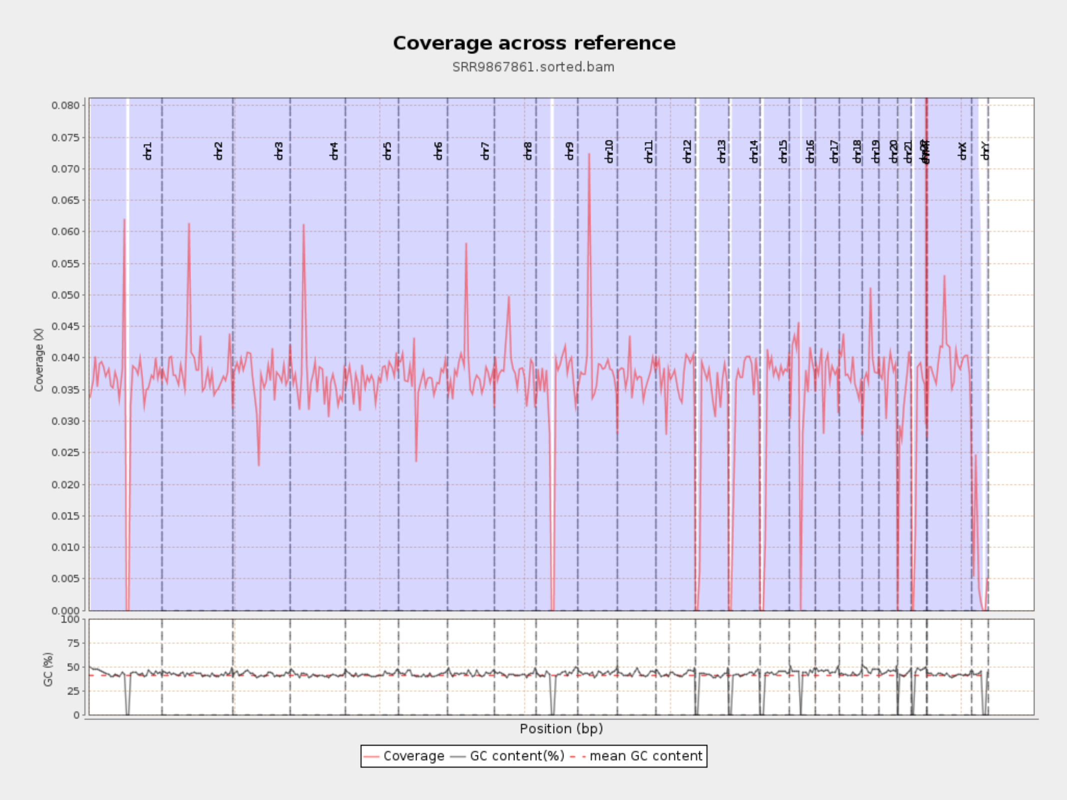
General error rate	0.52%
Mismatches	548,862
Insertions	9,443
Mapped reads with at least one insertion	0.5%
Deletions	21,491
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.5%

2.6. Chromosome stats

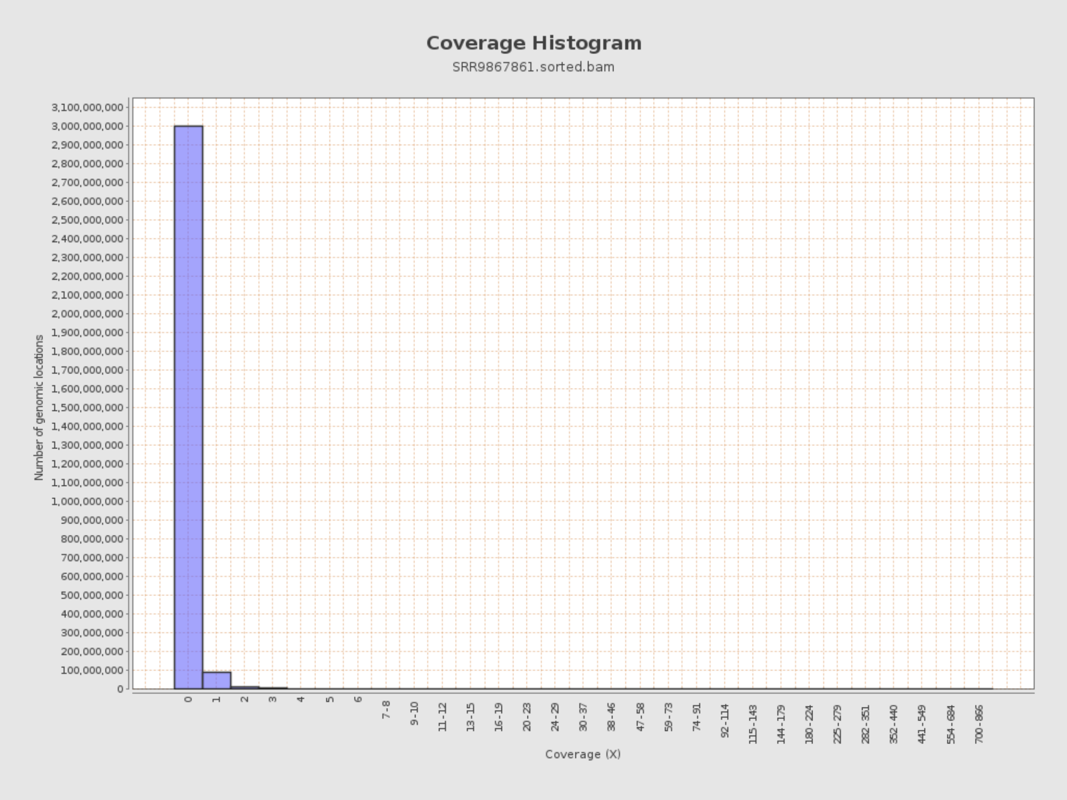
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8831549	0.0354	0.6074
chr2	243199373	9378709	0.0386	0.4521
chr3	198022430	7285005	0.0368	0.2139
chr4	191154276	7032529	0.0368	0.2517
chr5	180915260	6659813	0.0368	0.2158
chr6	171115067	6301457	0.0368	0.2436
chr7	159138663	6051762	0.038	0.3906

chr8	146364022	5615659	0.0384	0.396
chr9	141213431	4686927	0.0332	0.2757
chr10	135534747	5344087	0.0394	0.3497
chr11	135006516	5009484	0.0371	0.289
chr12	133851895	4943635	0.0369	0.217
chr13	115169878	3474742	0.0302	0.195
chr14	107349540	3375389	0.0314	0.2075
chr15	102531392	3184863	0.0311	0.1972
chr16	90354753	3199533	0.0354	0.2286
chr17	81195210	3033085	0.0374	0.2354
chr18	78077248	2954859	0.0378	0.5073
chr19	59128983	2307781	0.039	0.4488
chr20	63025520	2341677	0.0372	0.2212
chr21	48129895	1477144	0.0307	0.2444
chr22	51304566	1316091	0.0257	0.1795
chrMT	16571	35662	2.1521	1.9651
chrX	155270560	6105819	0.0393	0.2466
chrY	59373566	377526	0.0064	0.2445

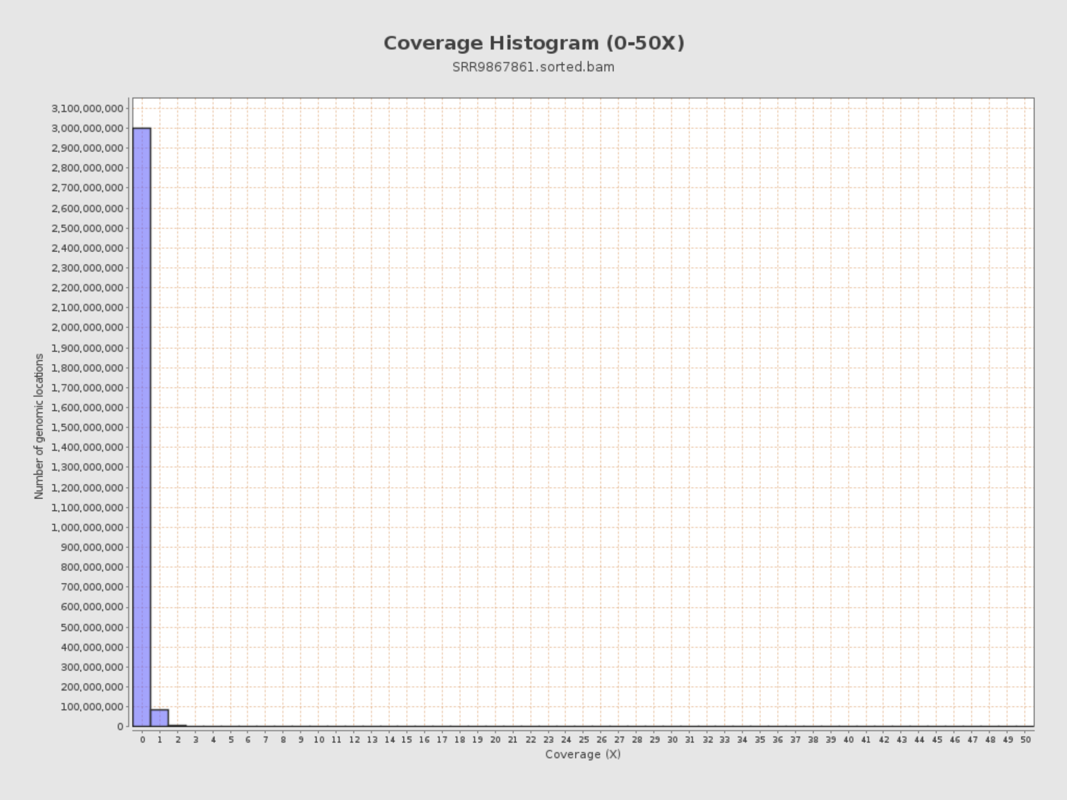
3. Results : Coverage across reference



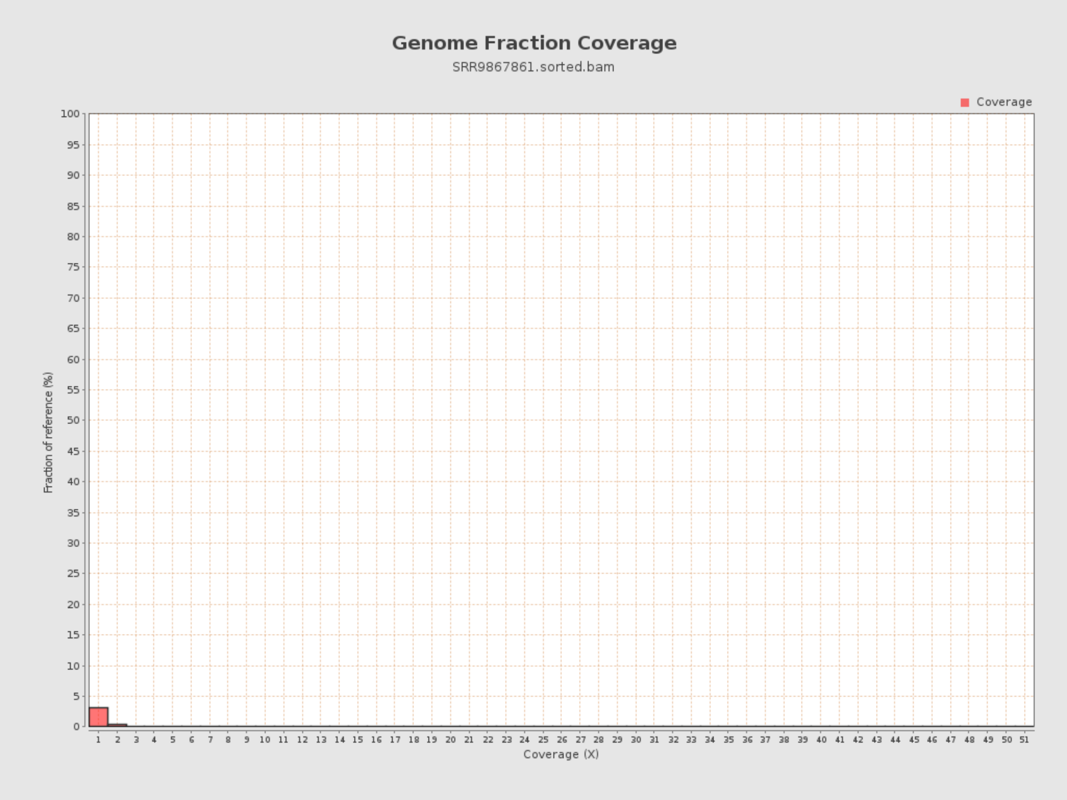
4. Results : Coverage Histogram



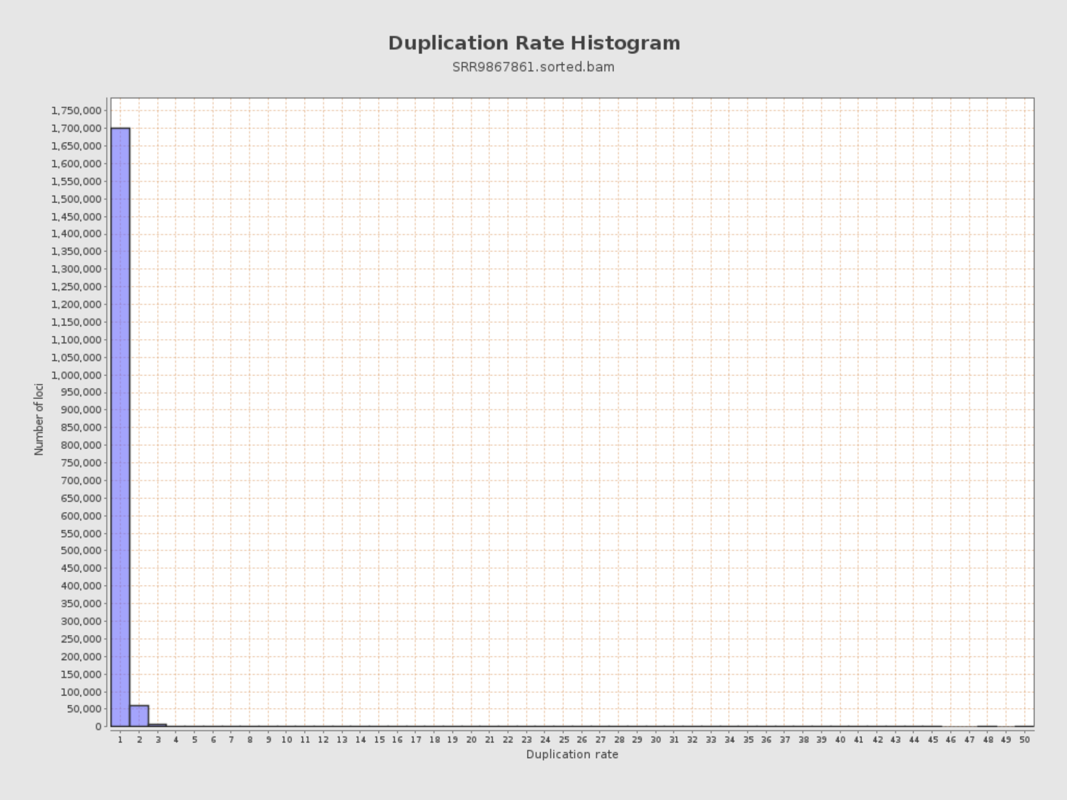
5. Results : Coverage Histogram (0-50X)



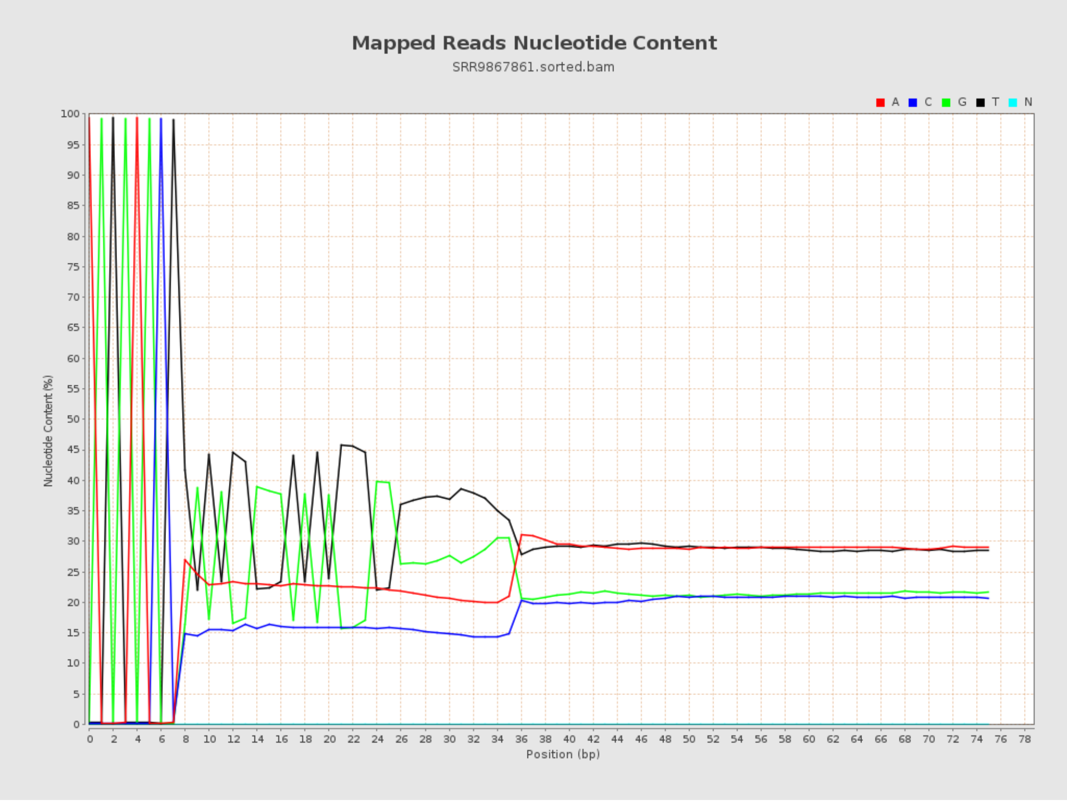
6. Results : Genome Fraction Coverage



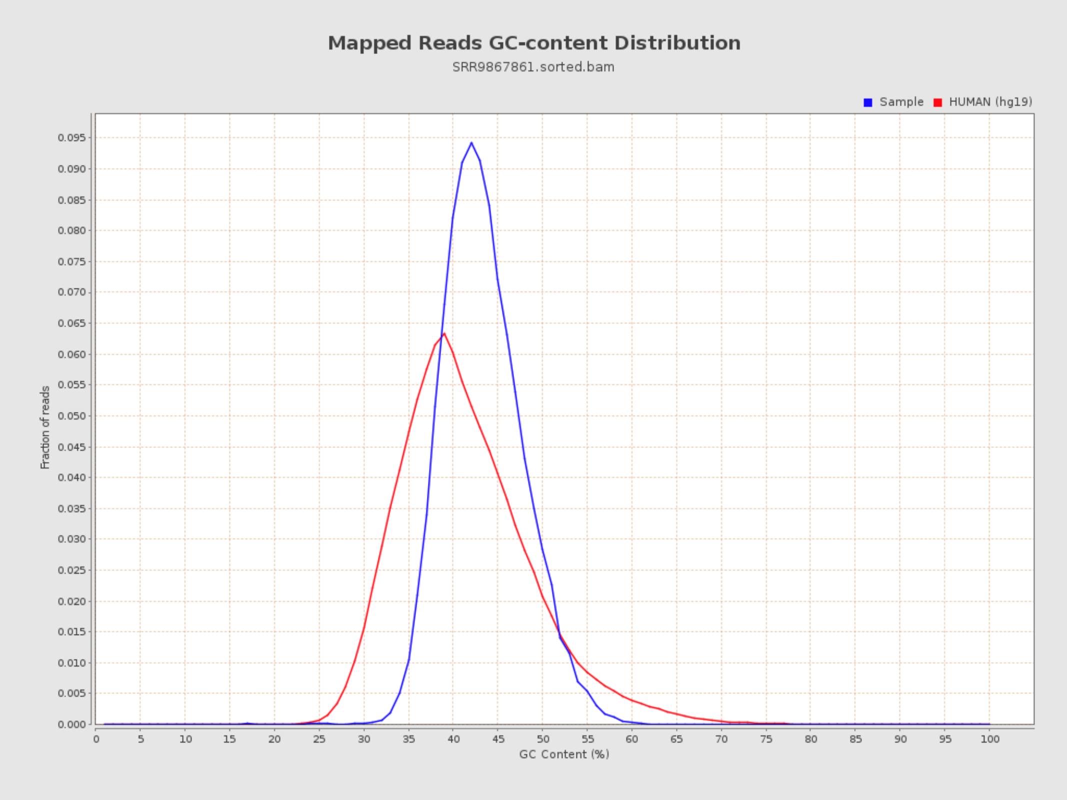
7. Results : Duplication Rate Histogram



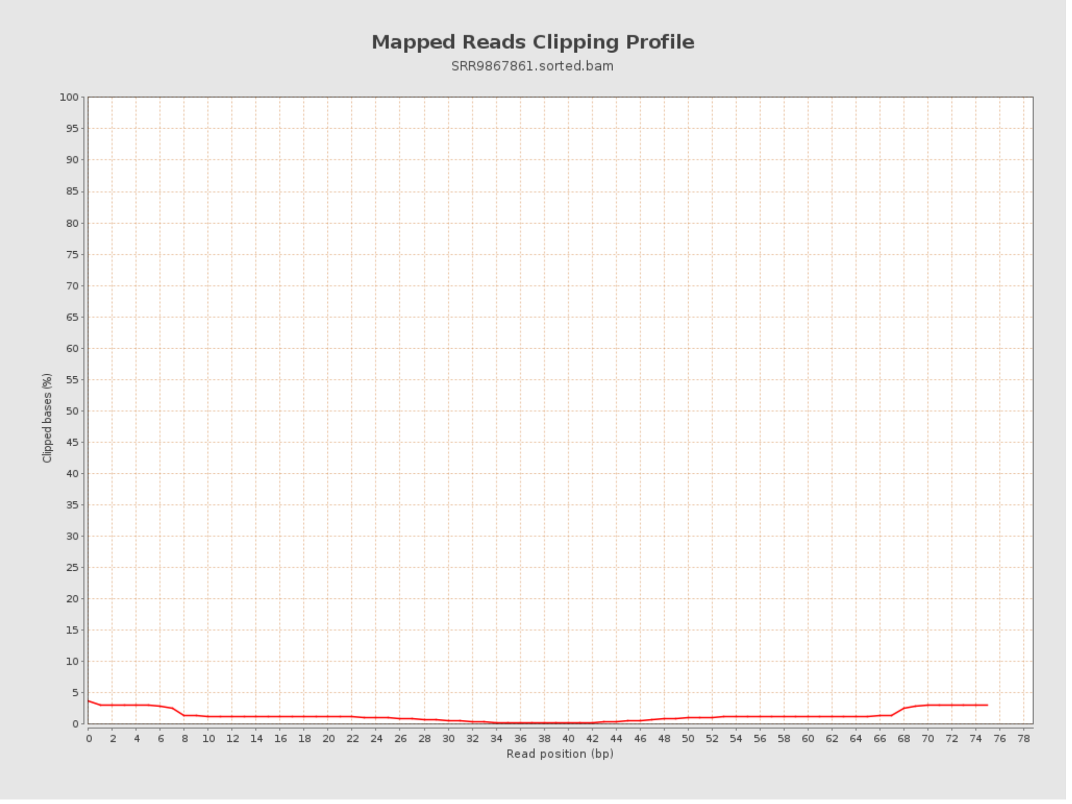
8. Results : Mapped Reads Nucleotide Content



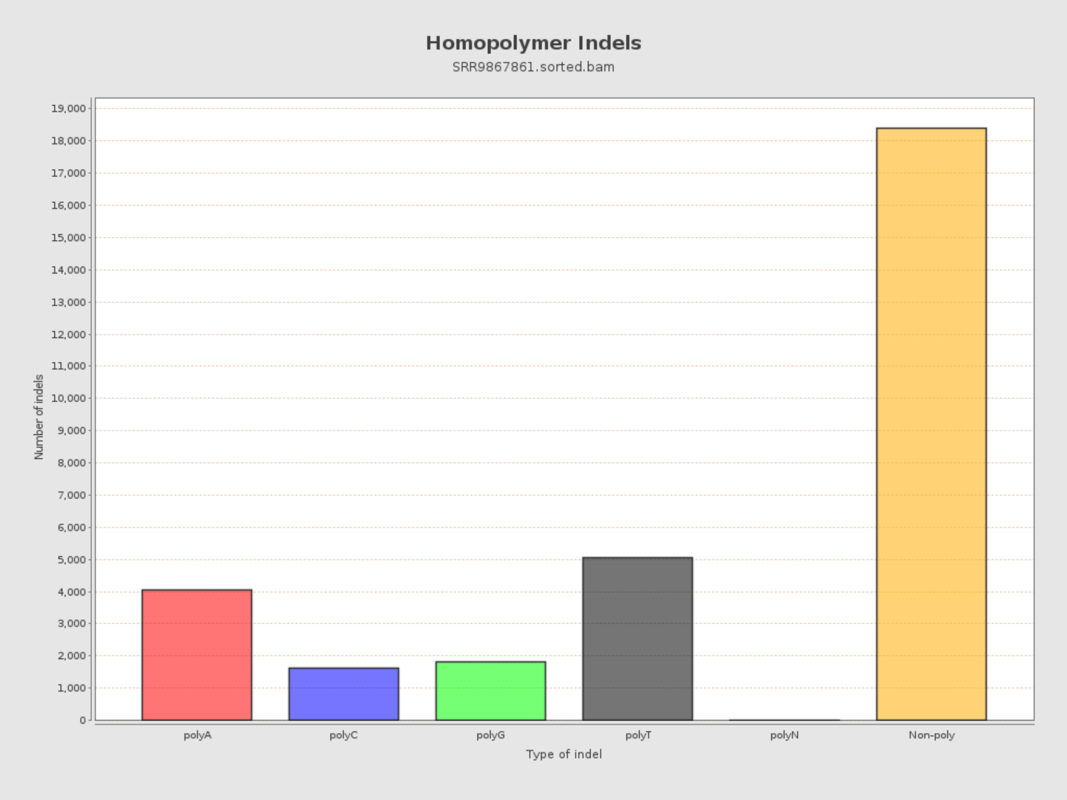
9. Results : Mapped Reads GC-content Distribution



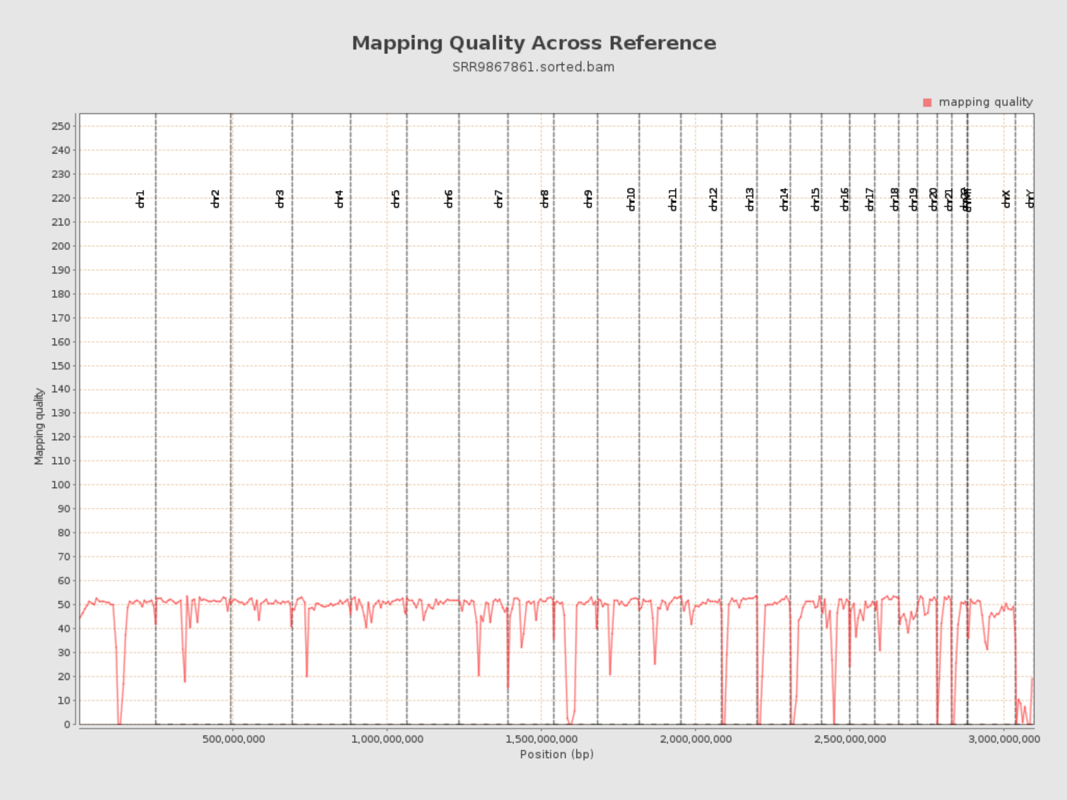
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram