Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867834.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_SRR9867834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:36:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,558,153
Mapped reads	1,437,576 / 92.26%
Unmapped reads	120,577 / 7.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,215 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	55,103 / 3.54%
Duplication rate	2.8%
Clipped reads	1,439,438 / 92.38%

2.2. ACGT Content

Number/percentage of A's	21,614,450 / 25.37%
Number/percentage of C's	14,600,530 / 17.14%
Number/percentage of T's	27,183,712 / 31.91%
Number/percentage of G's	21,791,520 / 25.58%
Number/percentage of N's	11,476 / 0.01%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2721

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

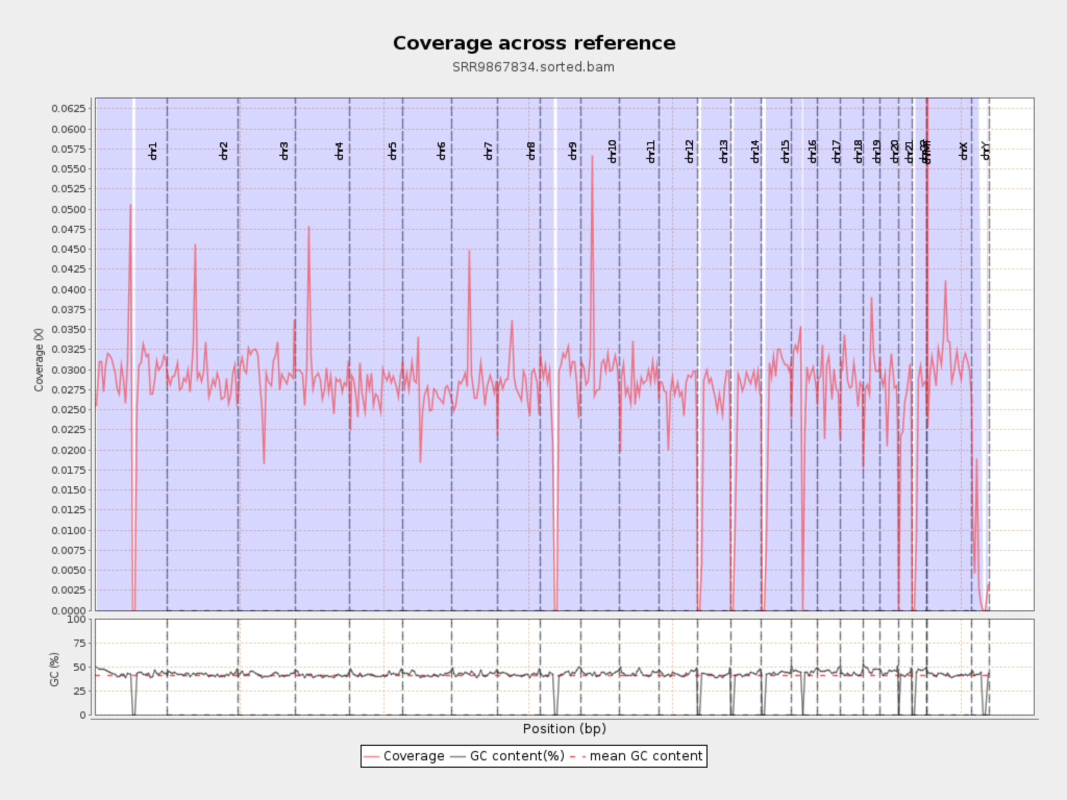
General error rate	0.51%
Mismatches	422,071
Insertions	6,125
Mapped reads with at least one insertion	0.42%
Deletions	16,179
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.01%

2.6. Chromosome stats

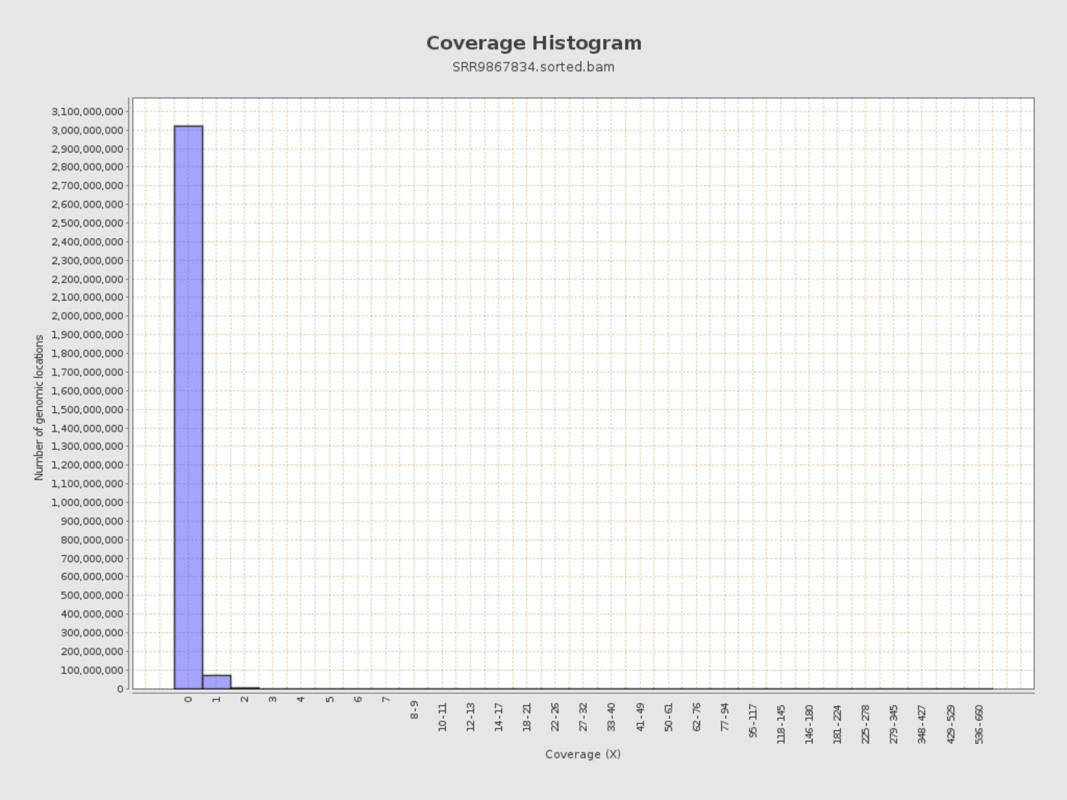
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7109915	0.0285	0.5104
chr2	243199373	7115944	0.0293	0.3412
chr3	198022430	5858566	0.0296	0.1862
chr4	191154276	5622878	0.0294	0.2095
chr5	180915260	5049927	0.0279	0.1817
chr6	171115067	4677412	0.0273	0.1995
chr7	159138663	4562130	0.0287	0.3014

chr8	146364022	4177615	0.0285	0.2915
chr9	141213431	3699819	0.0262	0.2293
chr10	135534747	4232049	0.0312	0.2868
chr11	135006516	3858645	0.0286	0.2305
chr12	133851895	3675843	0.0275	0.1814
chr13	115169878	2680545	0.0233	0.1653
chr14	107349540	2542713	0.0237	0.1703
chr15	102531392	2537412	0.0247	0.17
chr16	90354753	2464432	0.0273	0.1923
chr17	81195210	2291483	0.0282	0.1948
chr18	78077248	2272015	0.0291	0.404
chr19	59128983	1768231	0.0299	0.3729
chr20	63025520	1743842	0.0277	0.1853
chr21	48129895	1125171	0.0234	0.1879
chr22	51304566	1014914	0.0198	0.1516
chrMT	16571	26752	1.6144	1.613
chrX	155270560	4824906	0.0311	0.2077
chrY	59373566	294413	0.005	0.2024

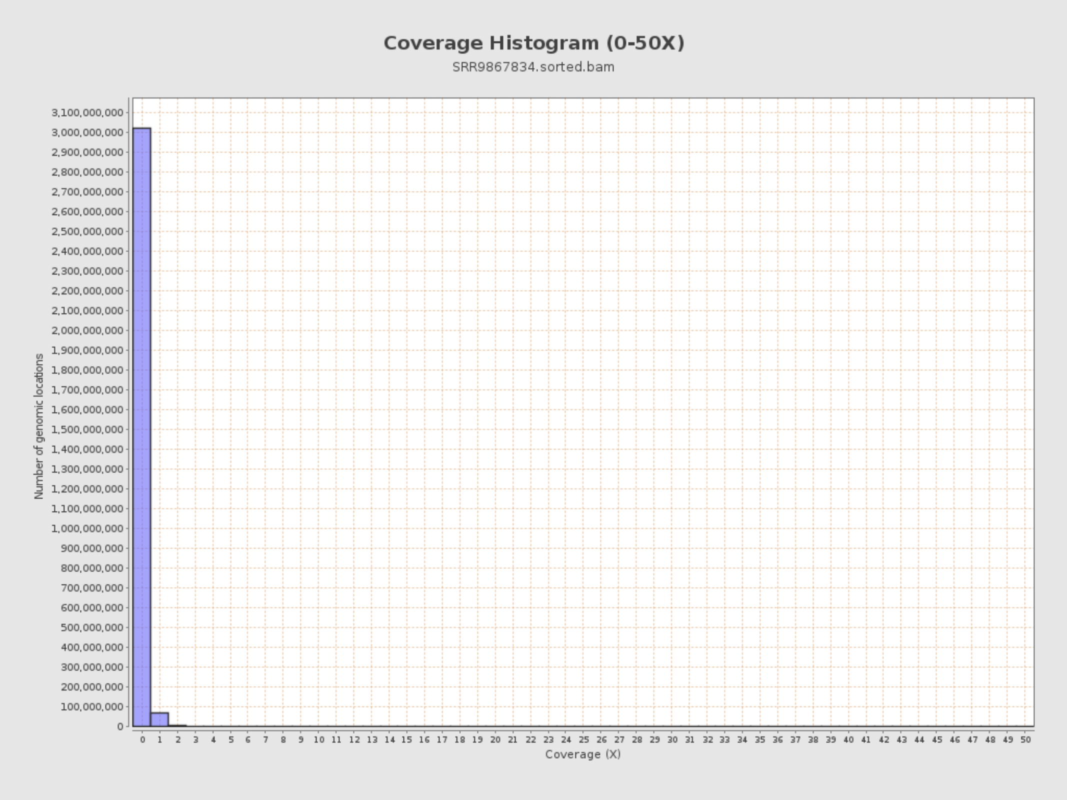
3. Results : Coverage across reference



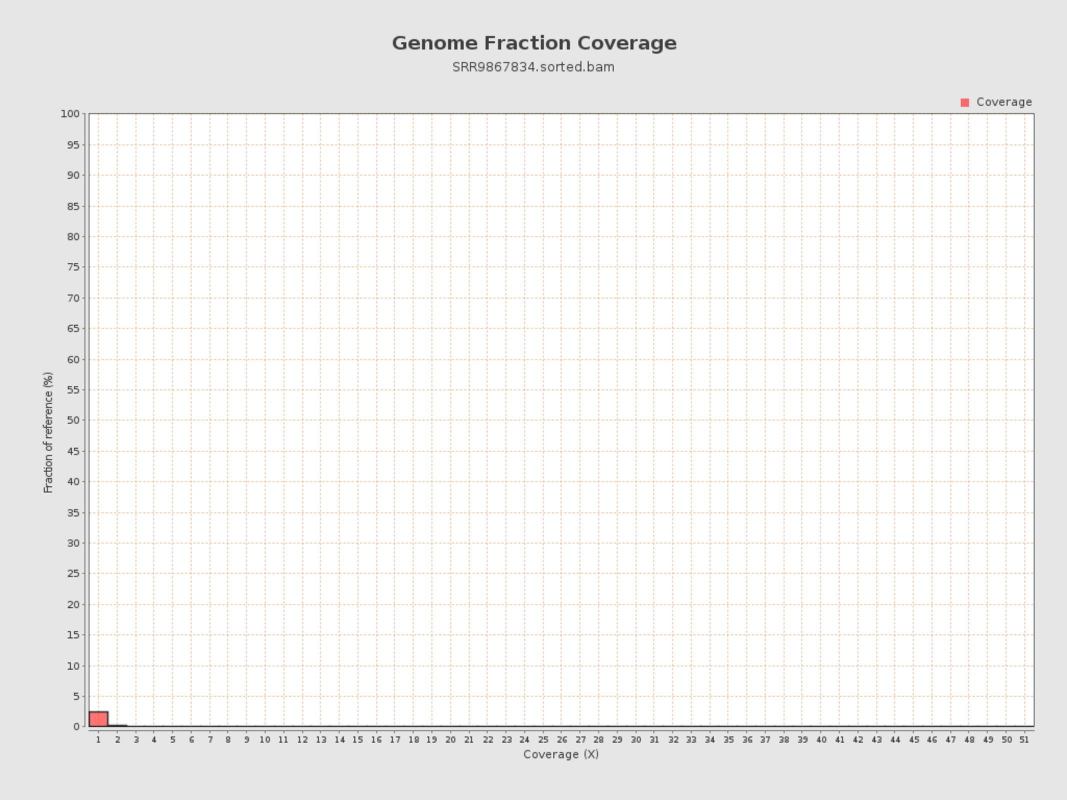
4. Results : Coverage Histogram



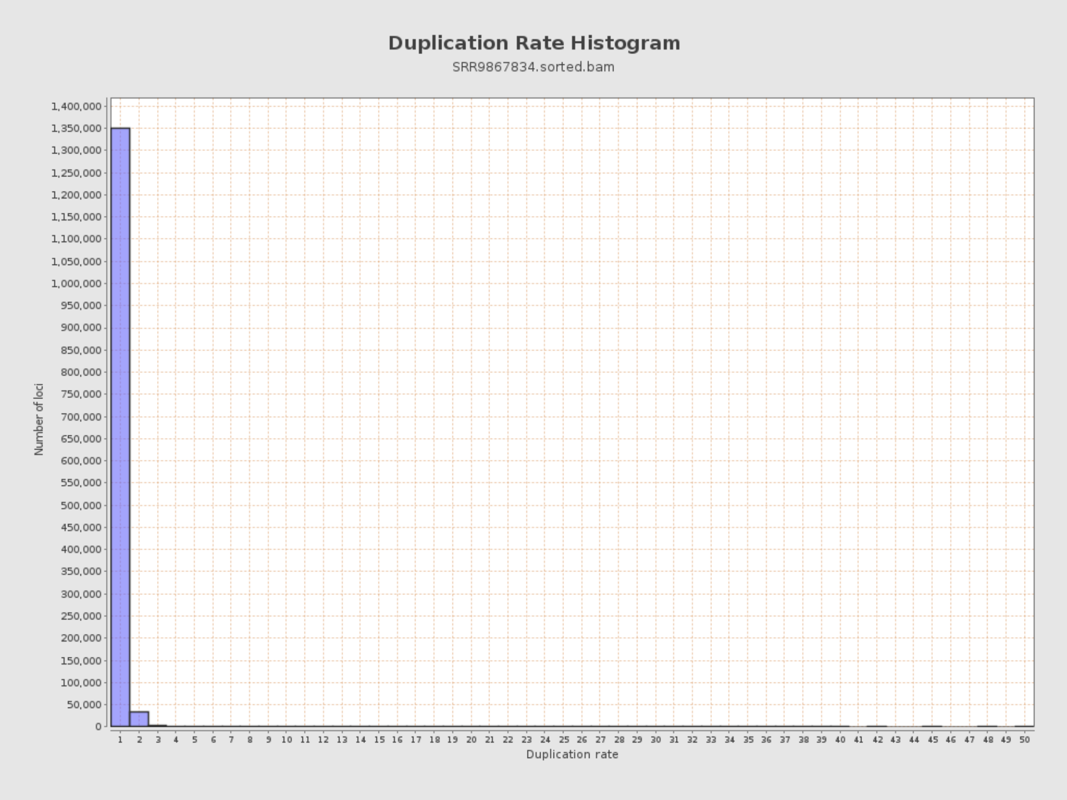
5. Results : Coverage Histogram (0-50X)



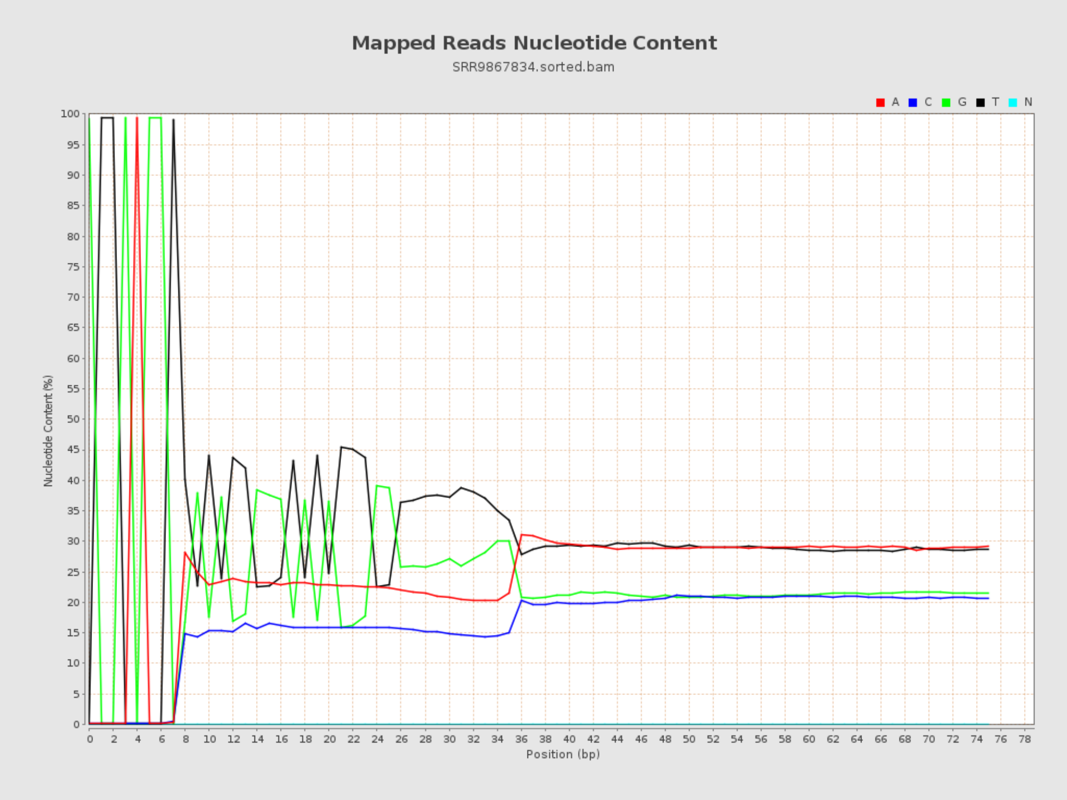
6. Results : Genome Fraction Coverage



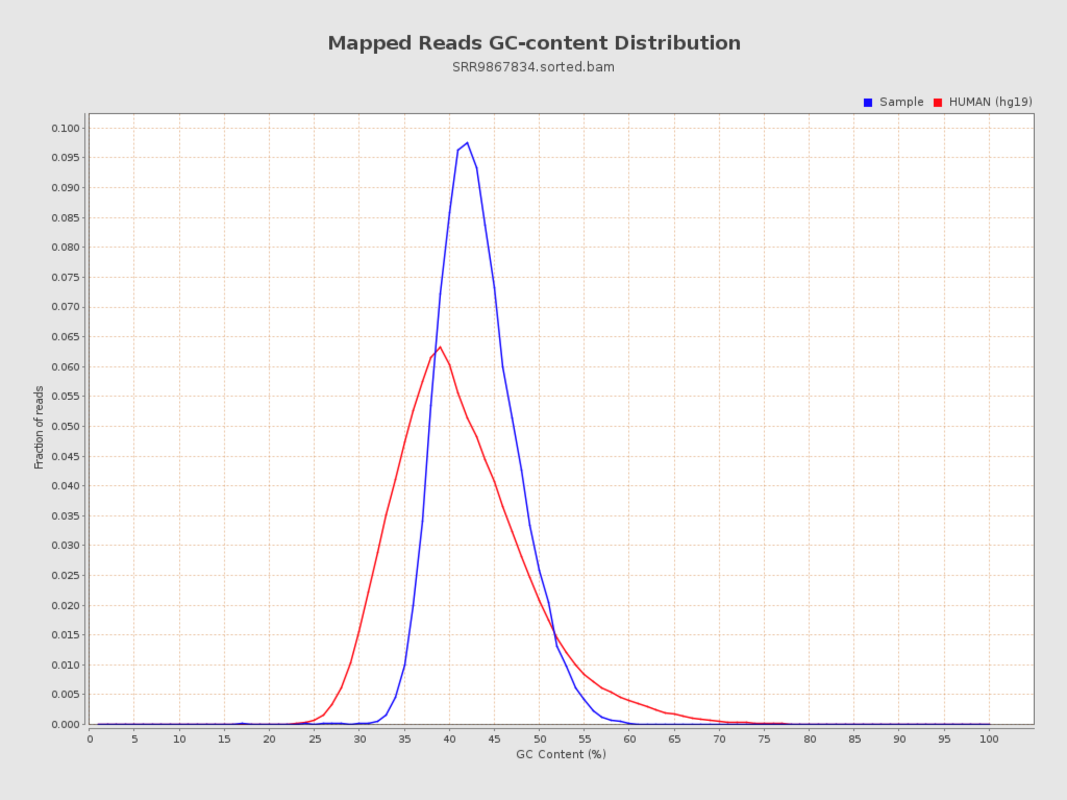
7. Results : Duplication Rate Histogram



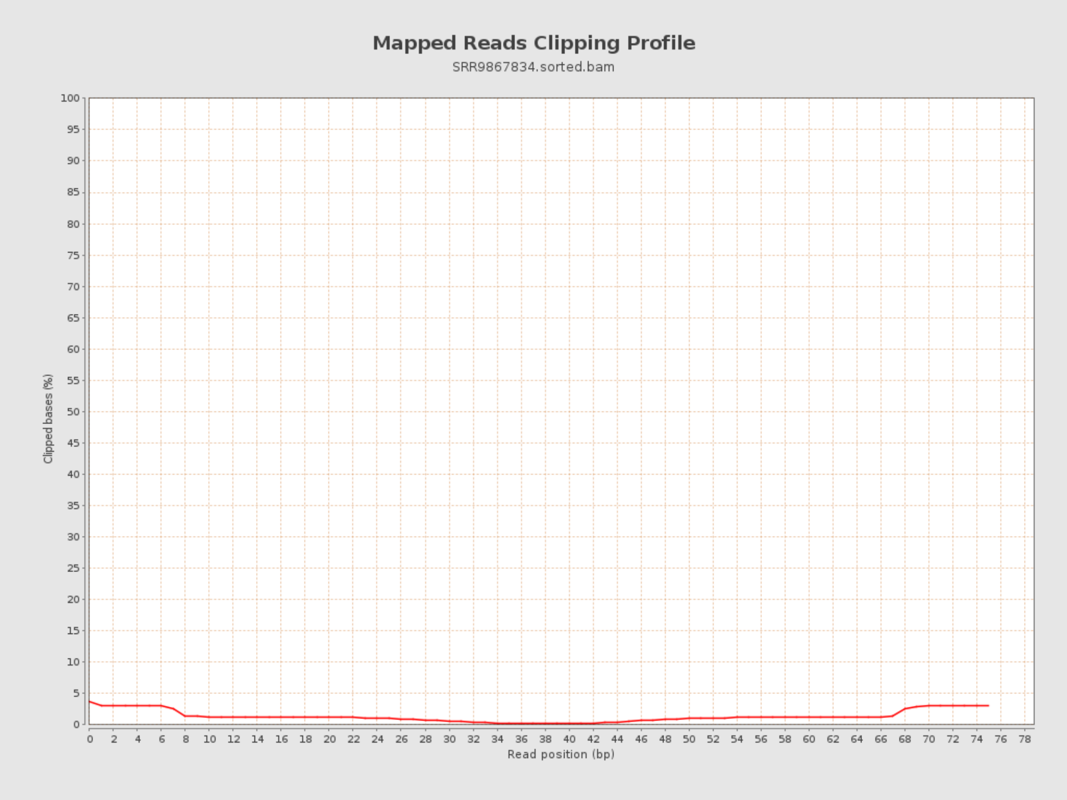
8. Results : Mapped Reads Nucleotide Content



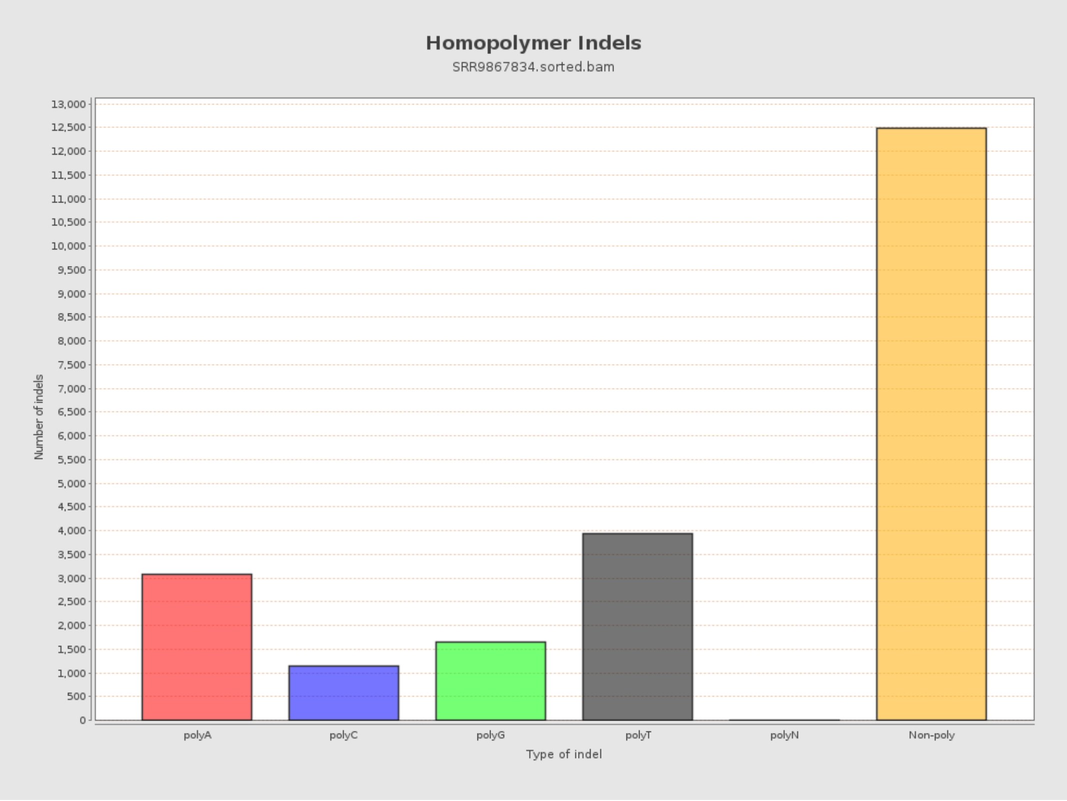
9. Results : Mapped Reads GC-content Distribution



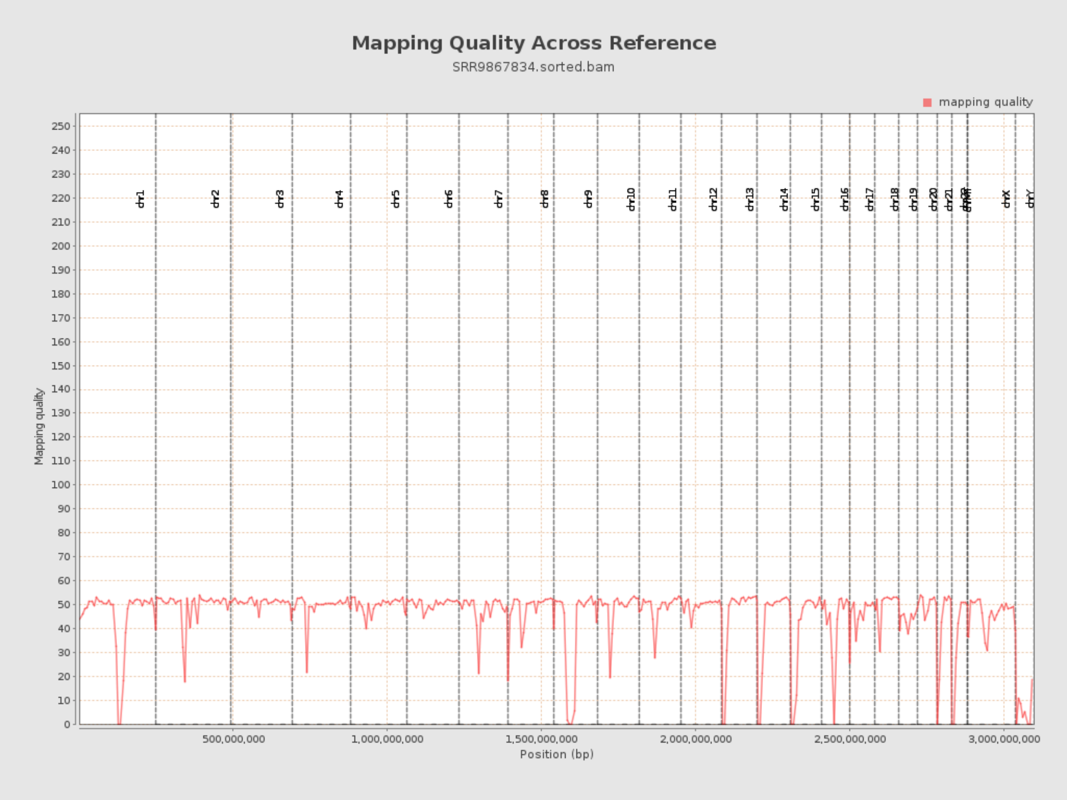
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram