Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 09:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867844.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_SRR9867844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867844.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 09:51:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,934,947
Mapped reads	1,789,115 / 92.46%
Unmapped reads	145,832 / 7.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,984 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	78,760 / 4.07%
Duplication rate	3.22%
Clipped reads	1,791,843 / 92.6%

2.2. ACGT Content

Number/percentage of A's	27,417,580 / 25.99%
Number/percentage of C's	18,840,875 / 17.86%
Number/percentage of T's	32,977,634 / 31.26%
Number/percentage of G's	26,246,394 / 24.88%
Number/percentage of N's	14,590 / 0.01%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0341

Standard Deviation	0.3203

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

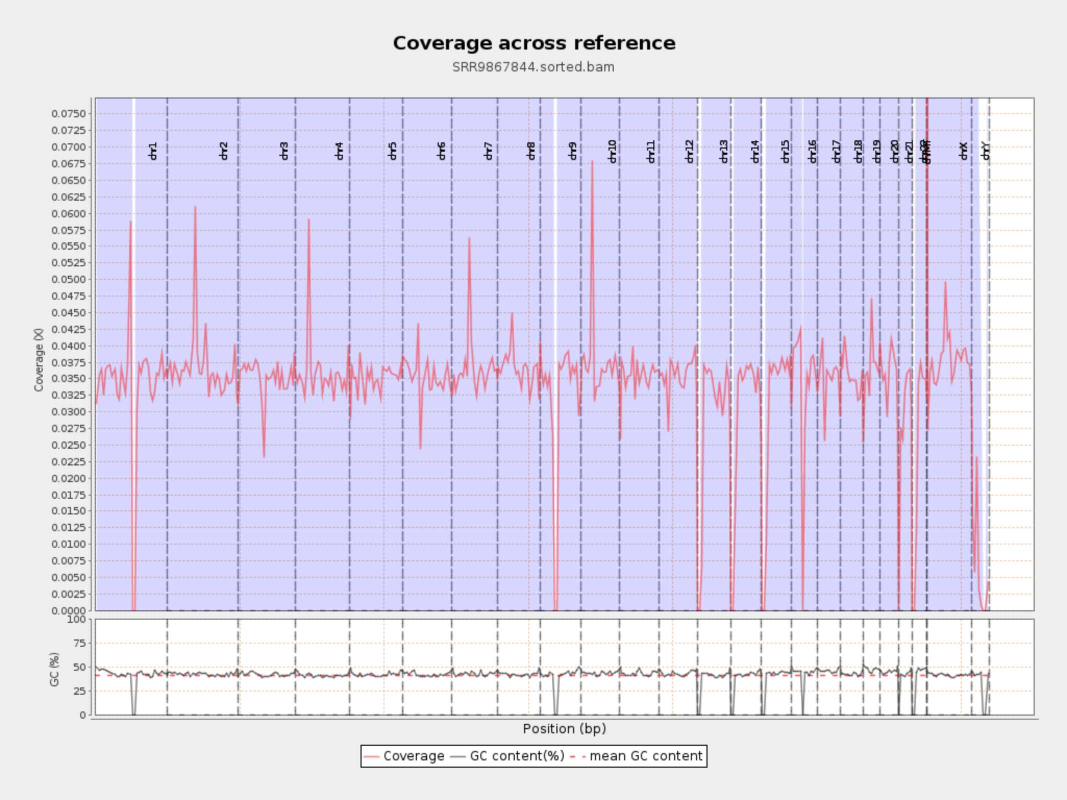
General error rate	0.52%
Mismatches	529,794
Insertions	7,576
Mapped reads with at least one insertion	0.42%
Deletions	20,286
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.7%

2.6. Chromosome stats

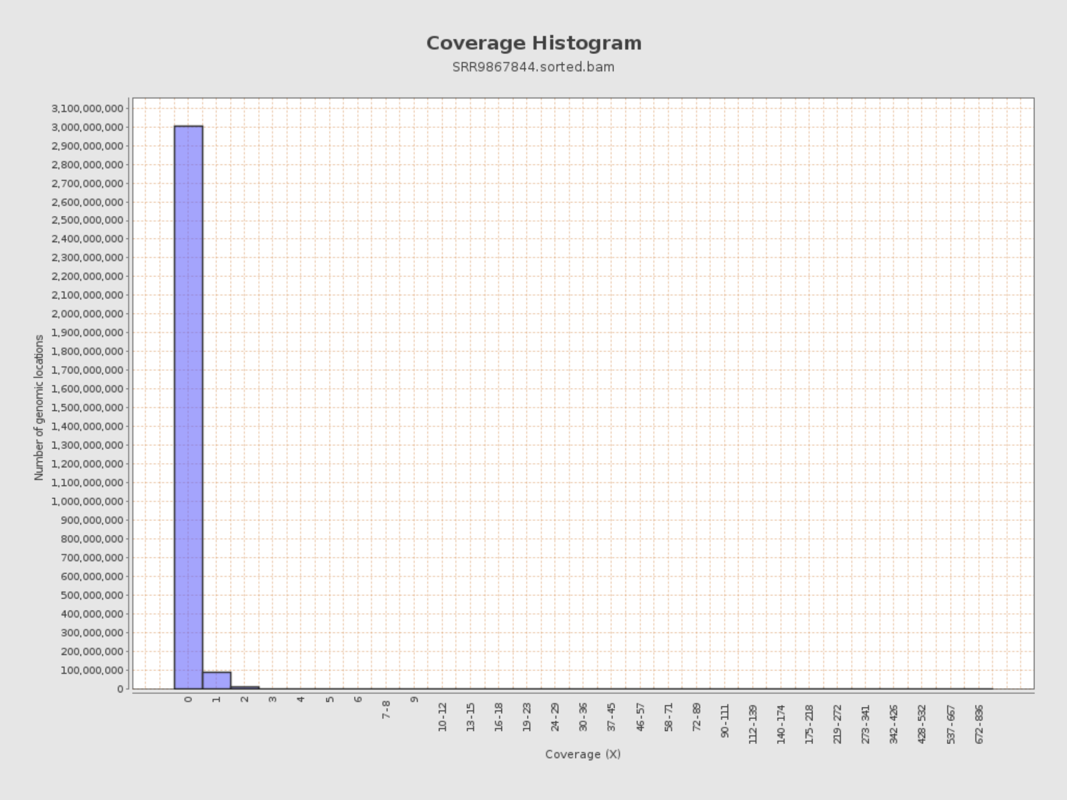
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8405791	0.0337	0.584
chr2	243199373	8964539	0.0369	0.4319
chr3	198022430	6941042	0.0351	0.2057
chr4	191154276	6871937	0.0359	0.2427
chr5	180915260	6394890	0.0353	0.2088
chr6	171115067	6047619	0.0353	0.236
chr7	159138663	5852647	0.0368	0.376

chr8	146364022	5360561	0.0366	0.3511
chr9	141213431	4449539	0.0315	0.2696
chr10	135534747	5154769	0.038	0.3365
chr11	135006516	4809637	0.0356	0.2682
chr12	133851895	4772988	0.0357	0.2105
chr13	115169878	3288967	0.0286	0.1859
chr14	107349540	3159388	0.0294	0.199
chr15	102531392	3038582	0.0296	0.1903
chr16	90354753	3031243	0.0335	0.2189
chr17	81195210	2855121	0.0352	0.2225
chr18	78077248	2769028	0.0355	0.4864
chr19	59128983	2184676	0.0369	0.4333
chr20	63025520	2258272	0.0358	0.2133
chr21	48129895	1387106	0.0288	0.2188
chr22	51304566	1253183	0.0244	0.1707
chrMT	16571	36815	2.2217	1.8029
chrX	155270560	5877265	0.0379	0.2359
chrY	59373566	363722	0.0061	0.2252

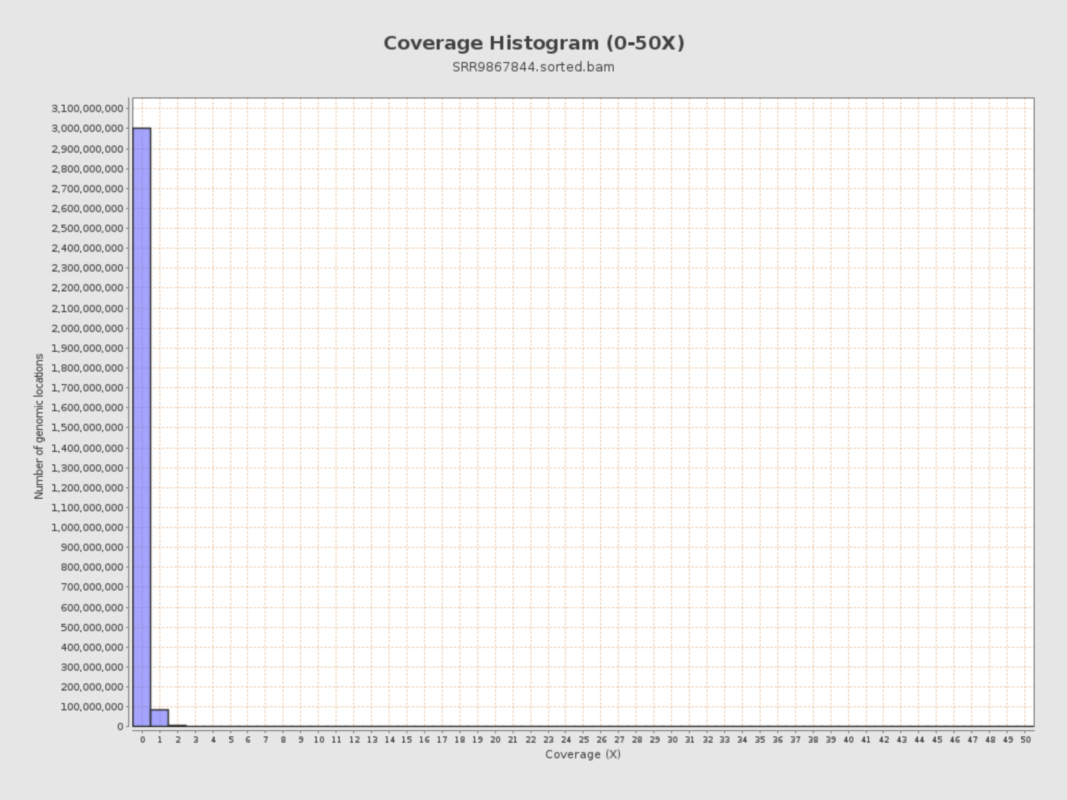
3. Results : Coverage across reference



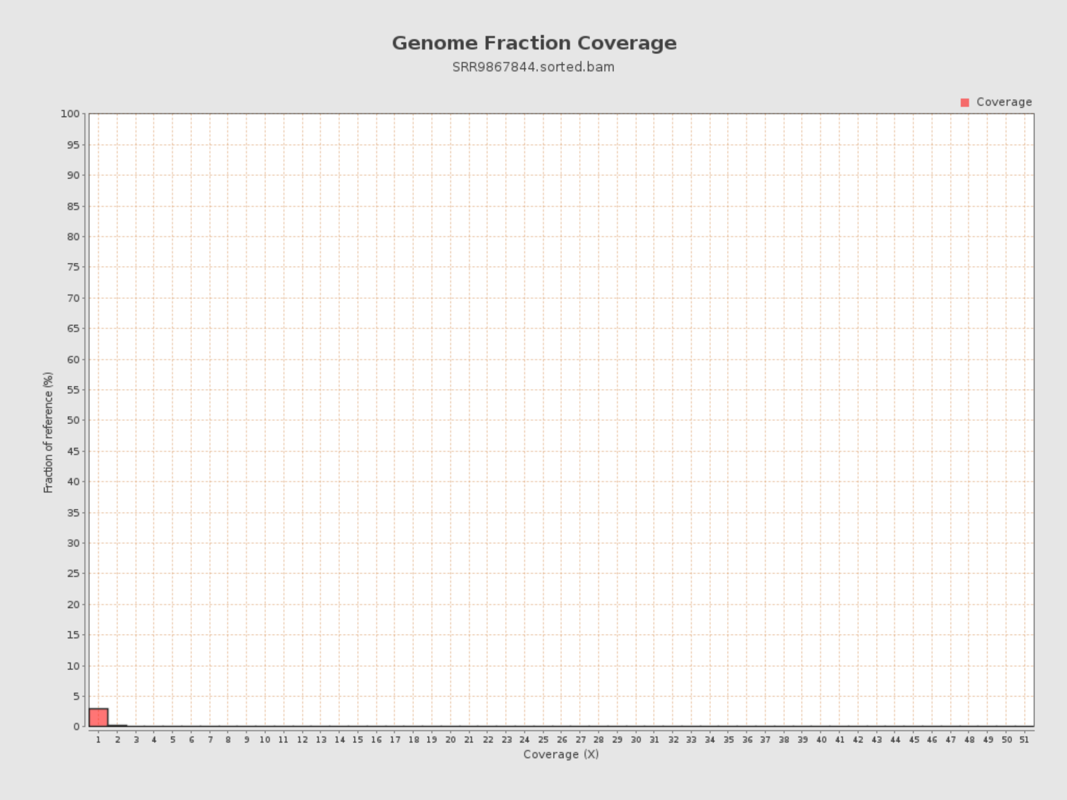
4. Results : Coverage Histogram



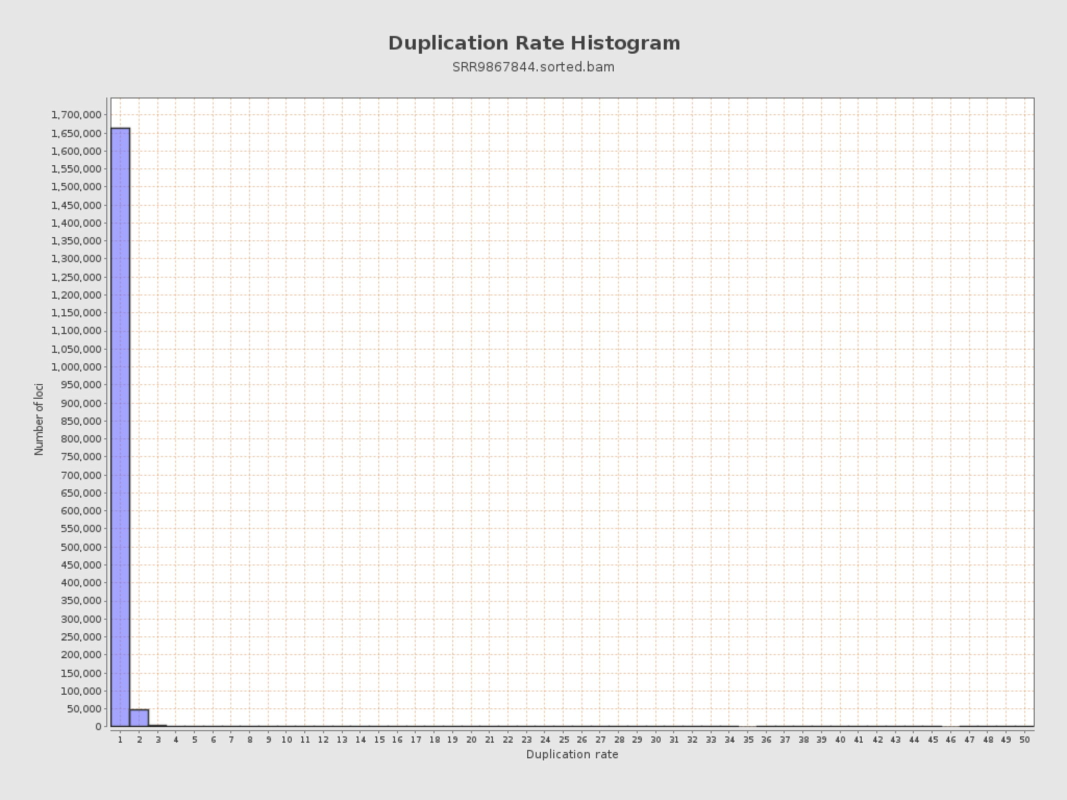
5. Results : Coverage Histogram (0-50X)



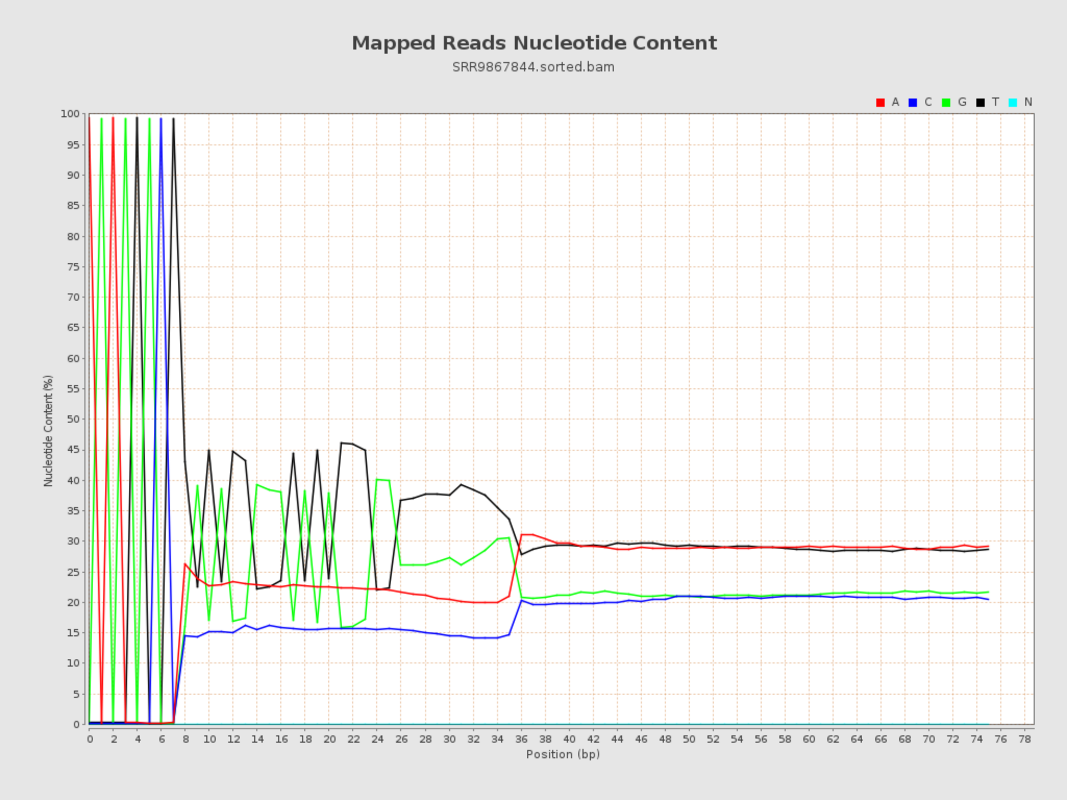
6. Results : Genome Fraction Coverage



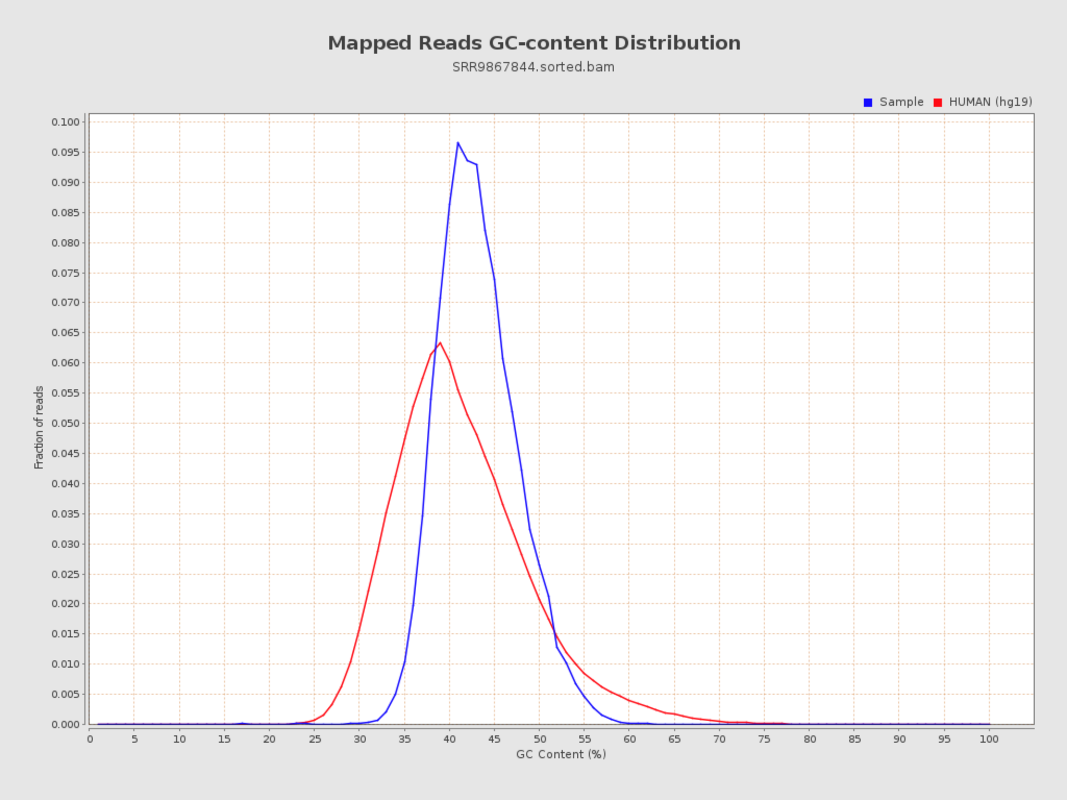
7. Results : Duplication Rate Histogram



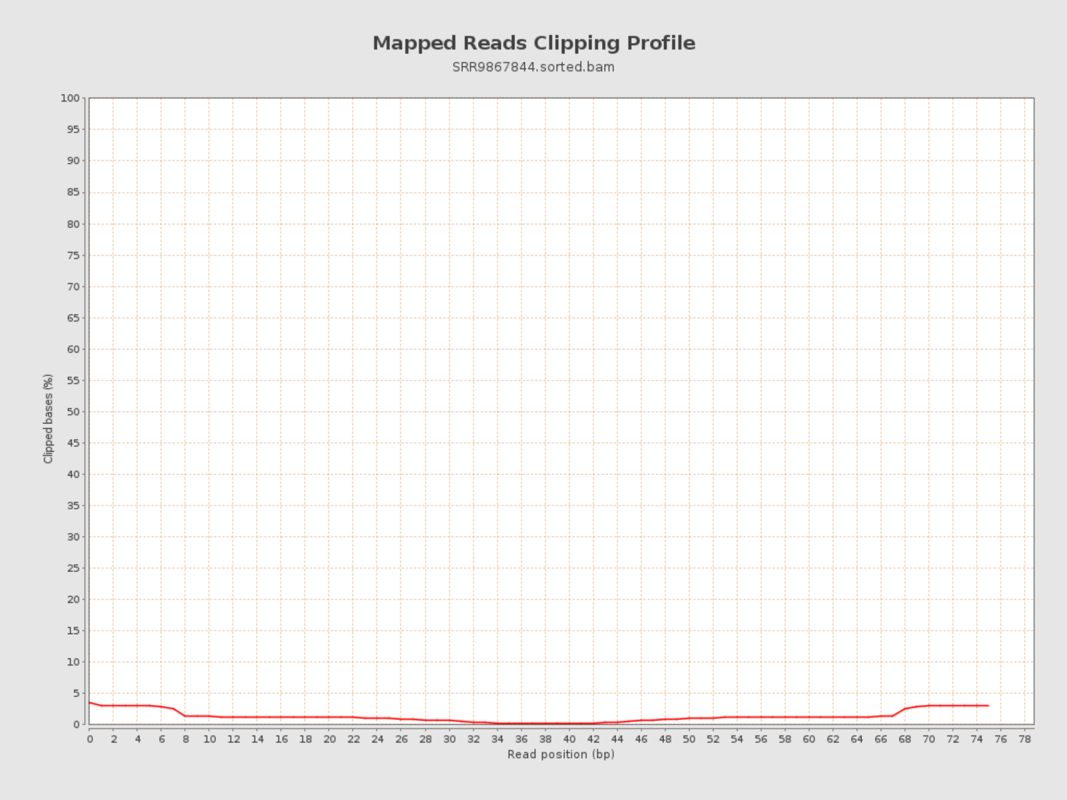
8. Results : Mapped Reads Nucleotide Content



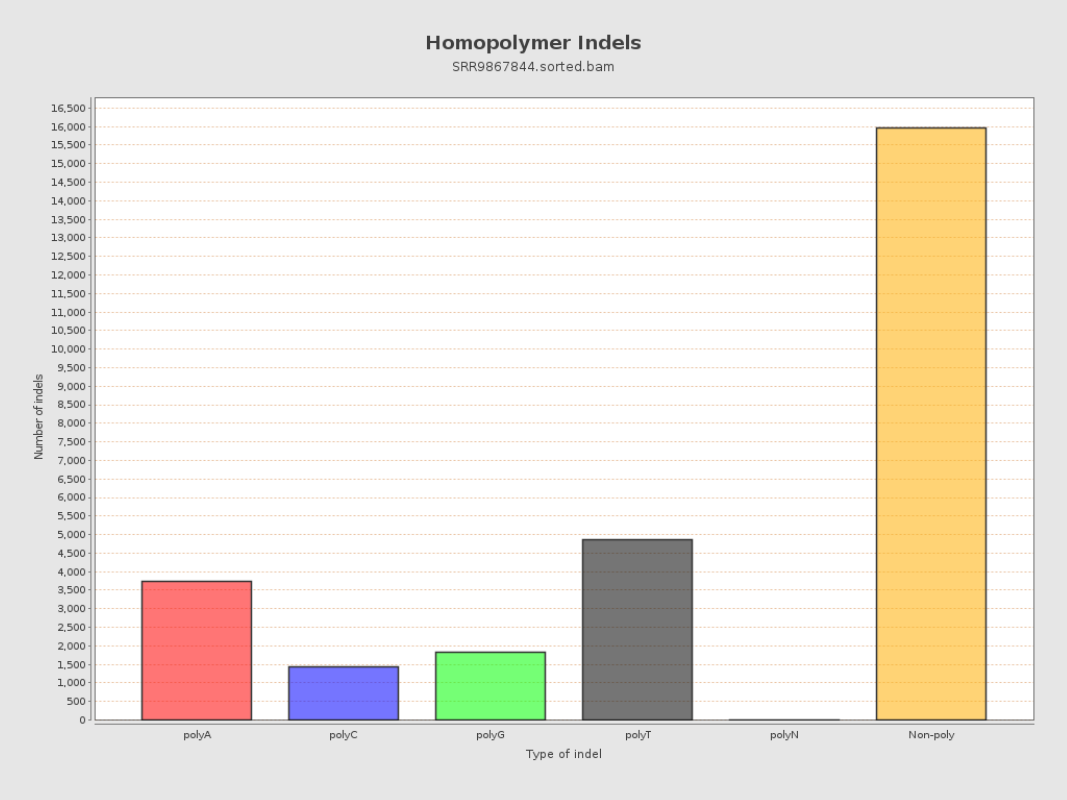
9. Results : Mapped Reads GC-content Distribution



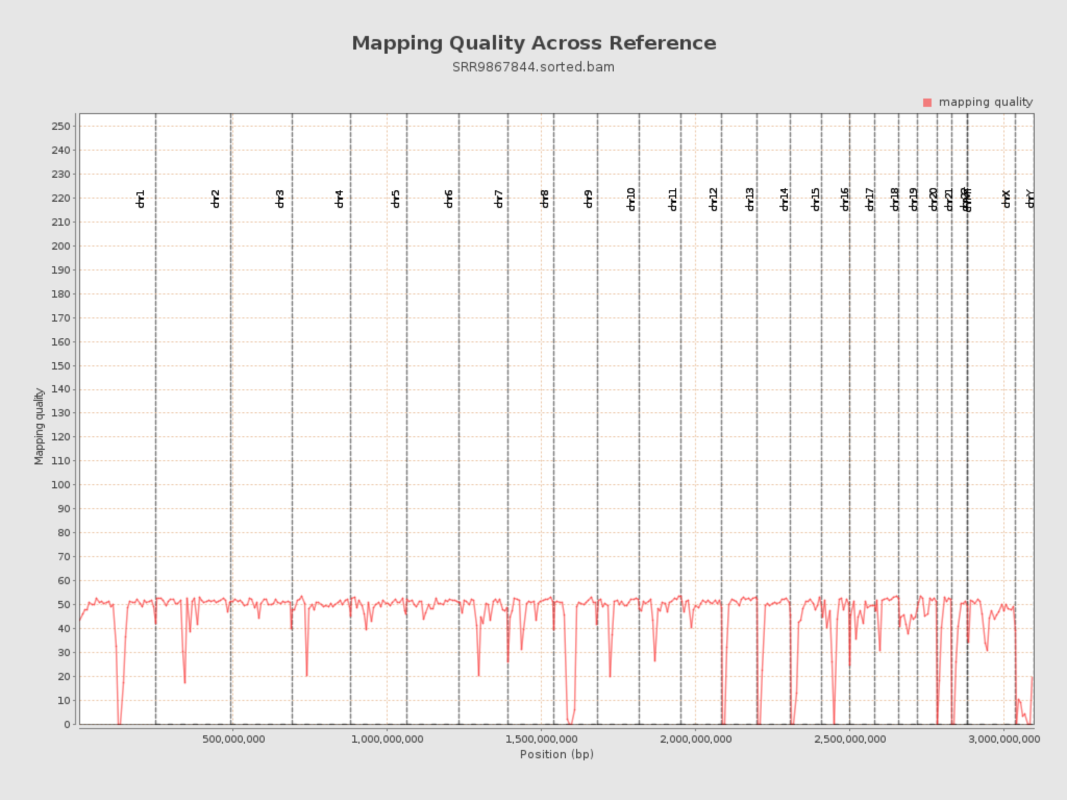
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram