Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:36:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867869.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_SRR9867869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867869.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:36:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,044,452
Mapped reads	1,886,575 / 92.28%
Unmapped reads	157,877 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,487 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	85,393 / 4.18%
Duplication rate	3.31%
Clipped reads	1,889,678 / 92.43%

2.2. ACGT Content

Number/percentage of A's	28,061,512 / 25.21%
Number/percentage of C's	20,817,570 / 18.7%
Number/percentage of T's	35,655,239 / 32.03%
Number/percentage of G's	26,768,130 / 24.05%
Number/percentage of N's	15,766 / 0.01%
GC Percentage	42.75%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3399

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

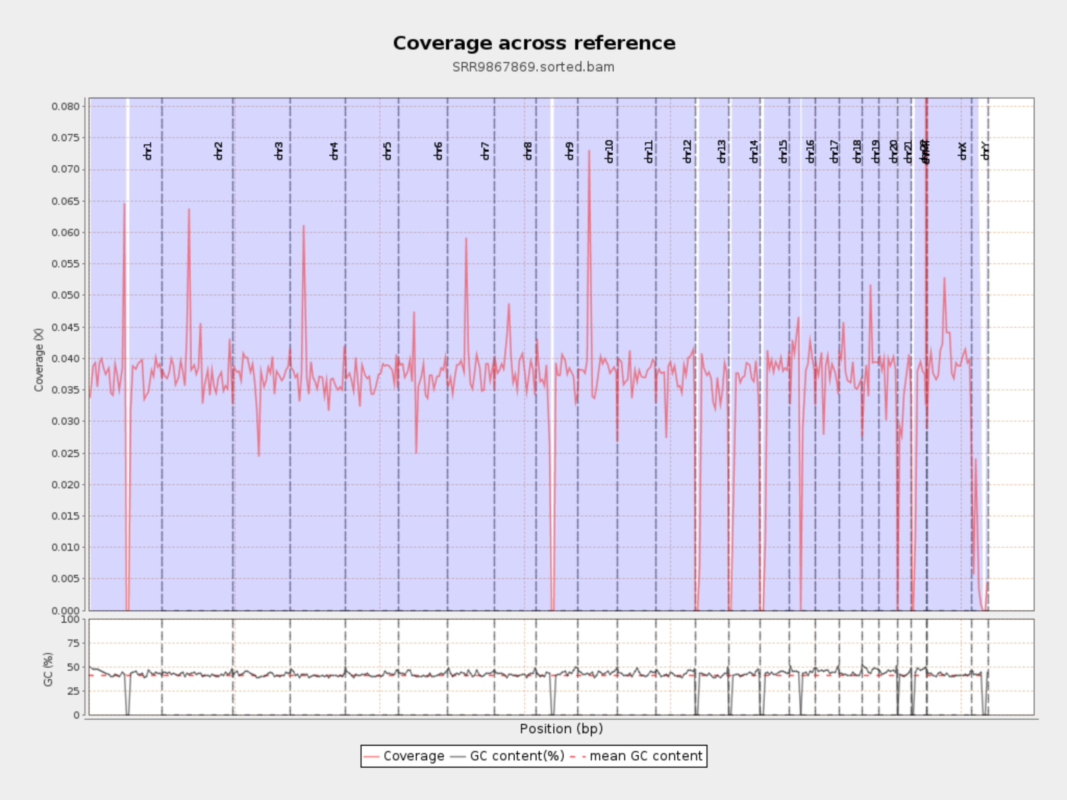
General error rate	0.52%
Mismatches	558,789
Insertions	7,880
Mapped reads with at least one insertion	0.42%
Deletions	20,887
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.63%

2.6. Chromosome stats

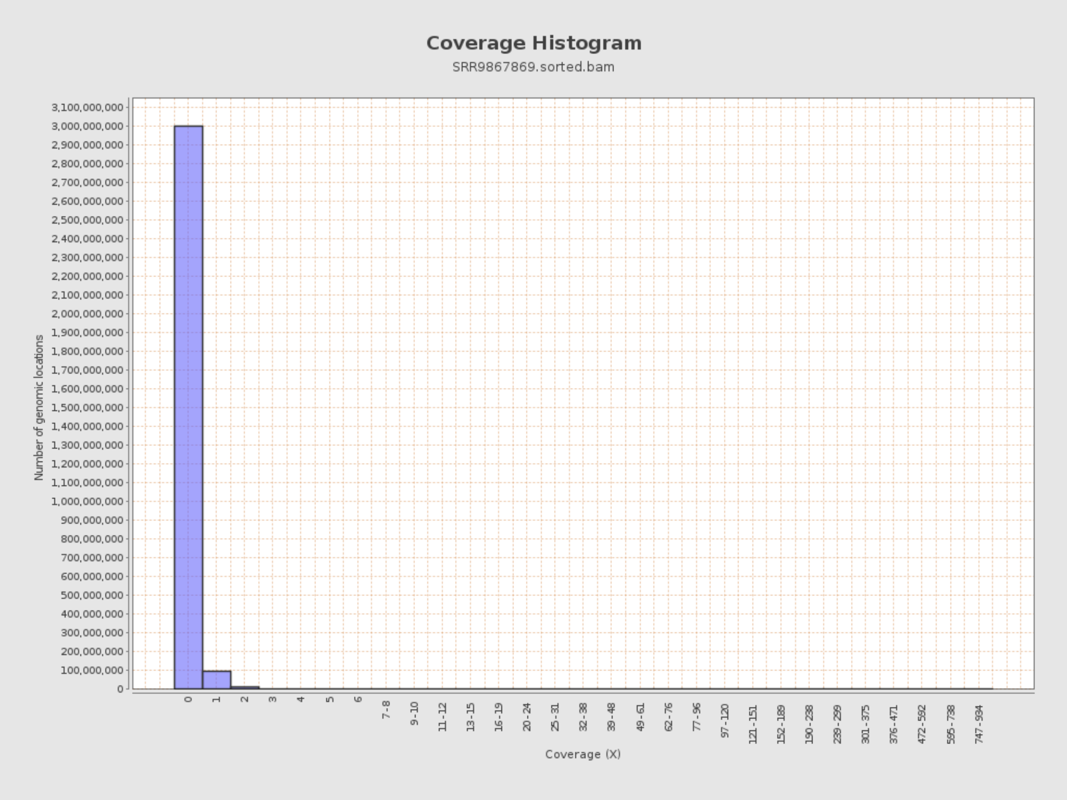
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8945675	0.0359	0.6473
chr2	243199373	9362274	0.0385	0.4661
chr3	198022430	7350200	0.0371	0.2121
chr4	191154276	7144032	0.0374	0.2468
chr5	180915260	6721897	0.0372	0.214
chr6	171115067	6382688	0.0373	0.2501
chr7	159138663	6160955	0.0387	0.3858

chr8	146364022	5677627	0.0388	0.3504
chr9	141213431	4658144	0.033	0.2767
chr10	135534747	5403233	0.0399	0.3515
chr11	135006516	5073403	0.0376	0.2828
chr12	133851895	5007832	0.0374	0.2159
chr13	115169878	3508480	0.0305	0.1928
chr14	107349540	3334509	0.0311	0.2022
chr15	102531392	3220749	0.0314	0.1947
chr16	90354753	3278523	0.0363	0.2282
chr17	81195210	3023889	0.0372	0.2269
chr18	78077248	2970777	0.038	0.5155
chr19	59128983	2319799	0.0392	0.4594
chr20	63025520	2381058	0.0378	0.2173
chr21	48129895	1484476	0.0308	0.2319
chr22	51304566	1338106	0.0261	0.1768
chrMT	16571	33249	2.0065	1.8181
chrX	155270560	6195830	0.0399	0.2436
chrY	59373566	374341	0.0063	0.2356

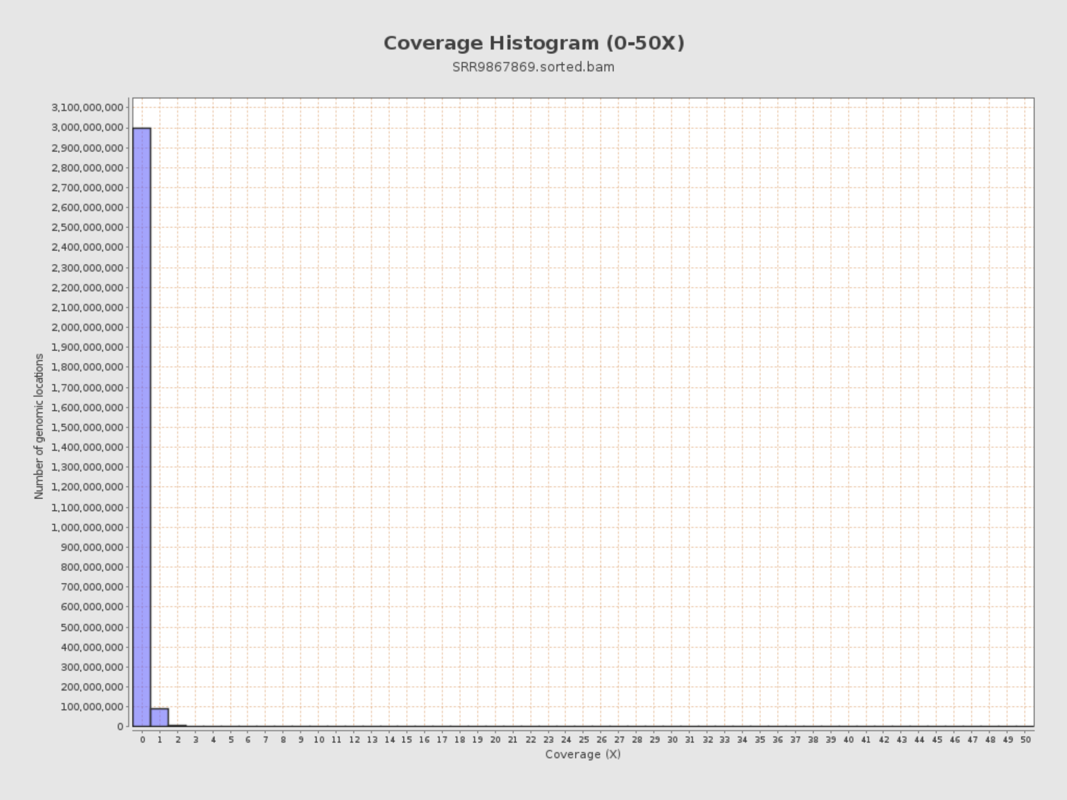
3. Results : Coverage across reference



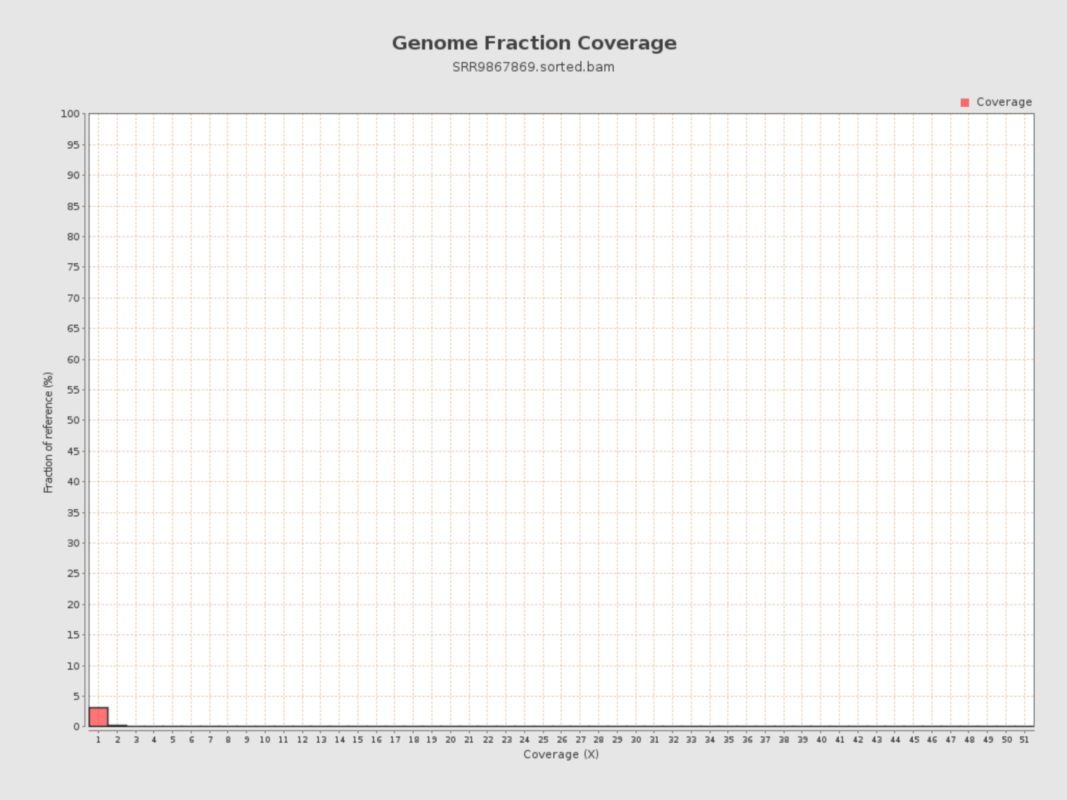
4. Results : Coverage Histogram



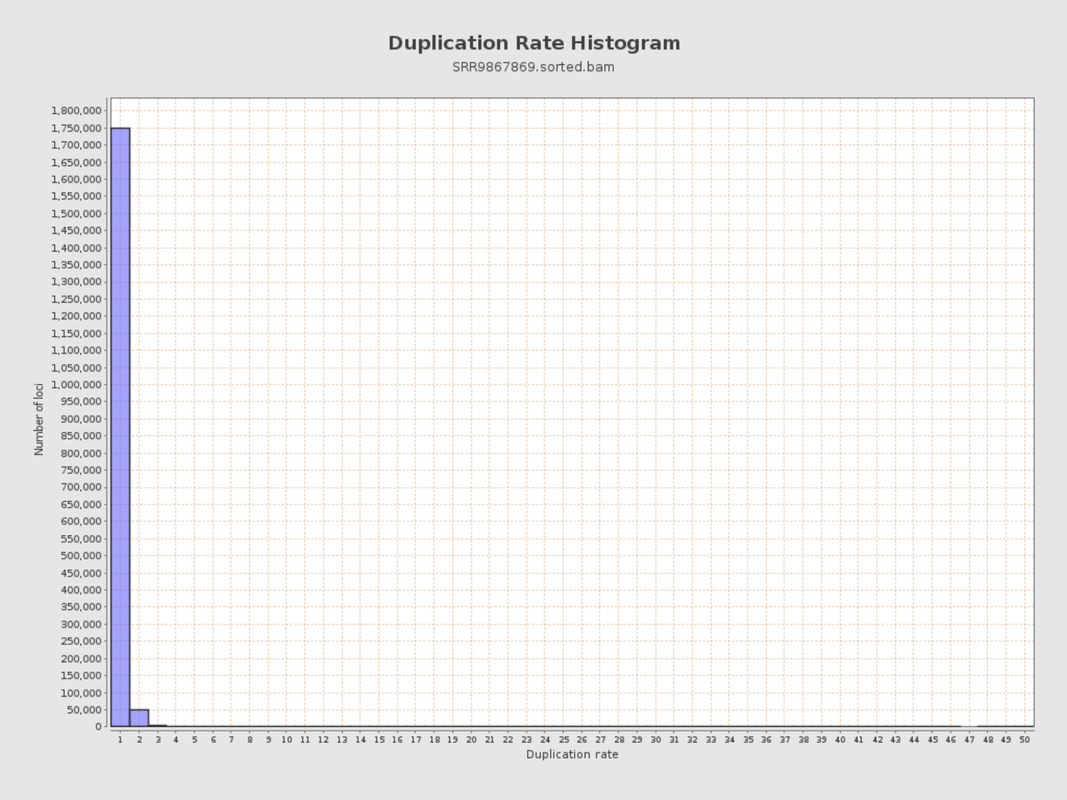
5. Results : Coverage Histogram (0-50X)



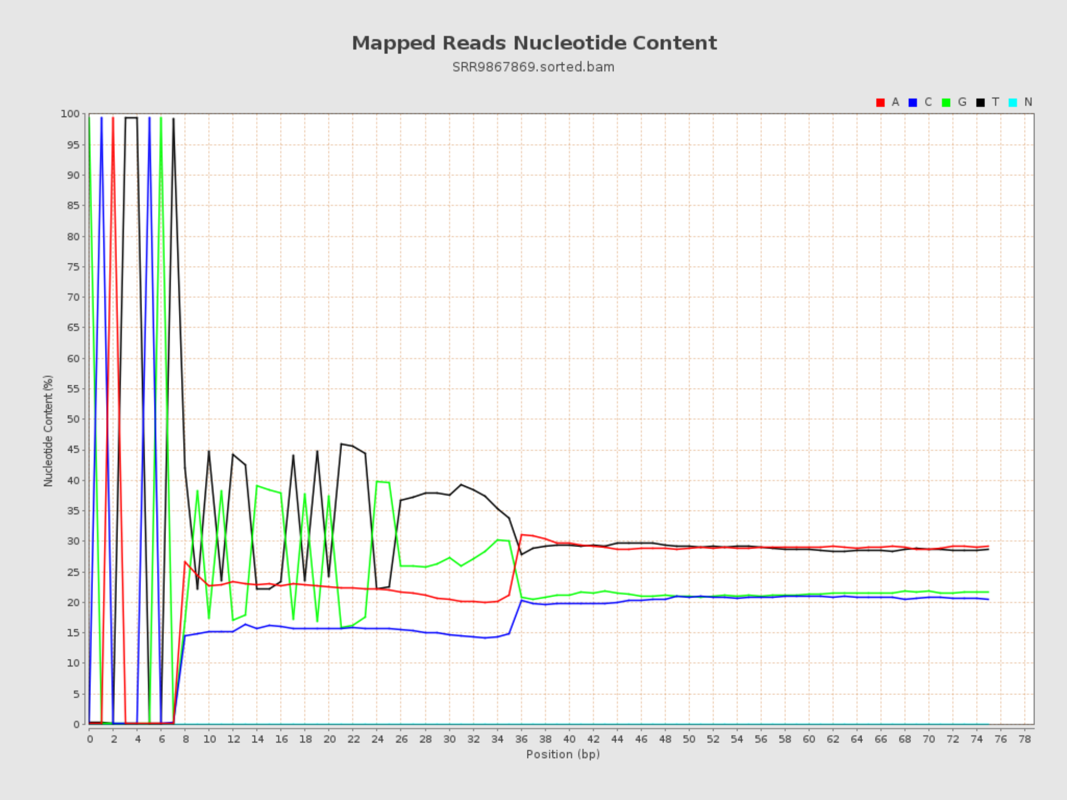
6. Results : Genome Fraction Coverage



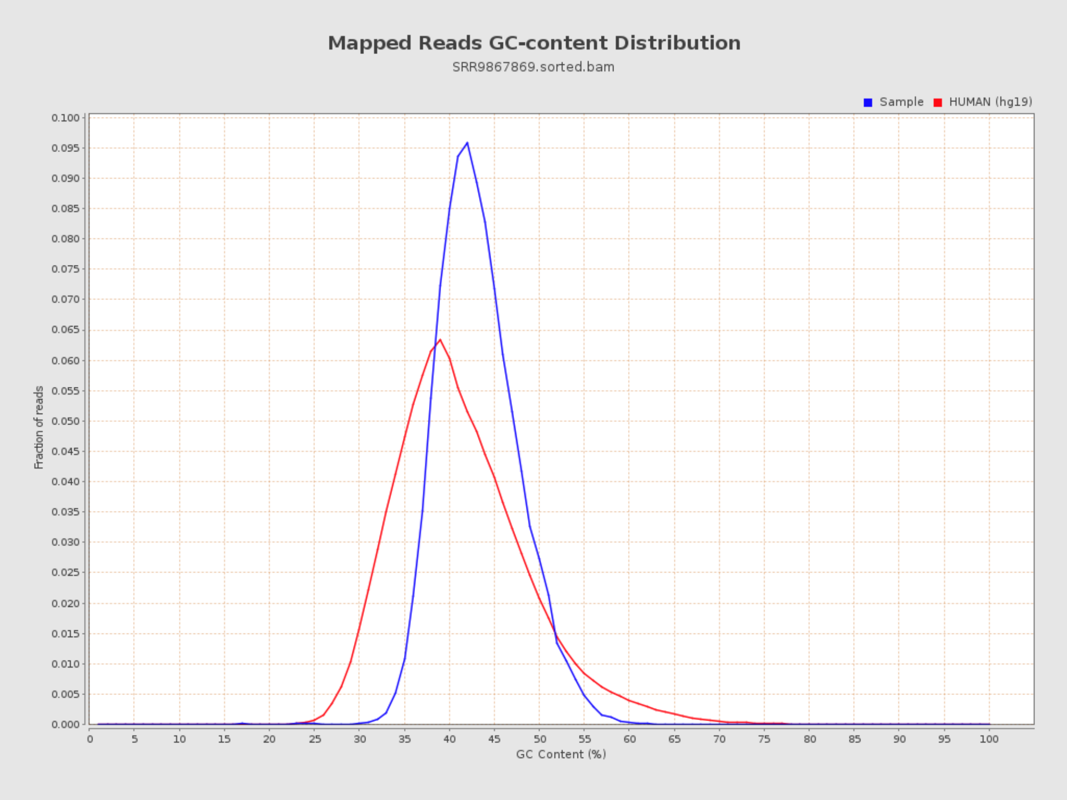
7. Results : Duplication Rate Histogram



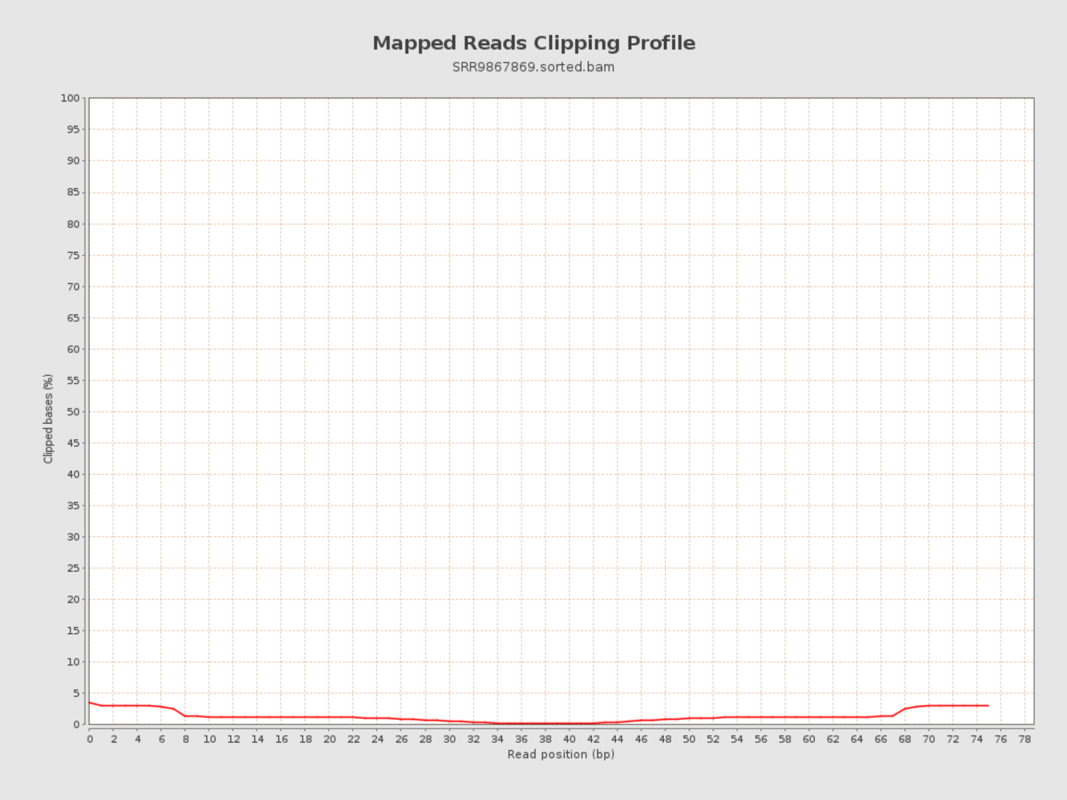
8. Results : Mapped Reads Nucleotide Content



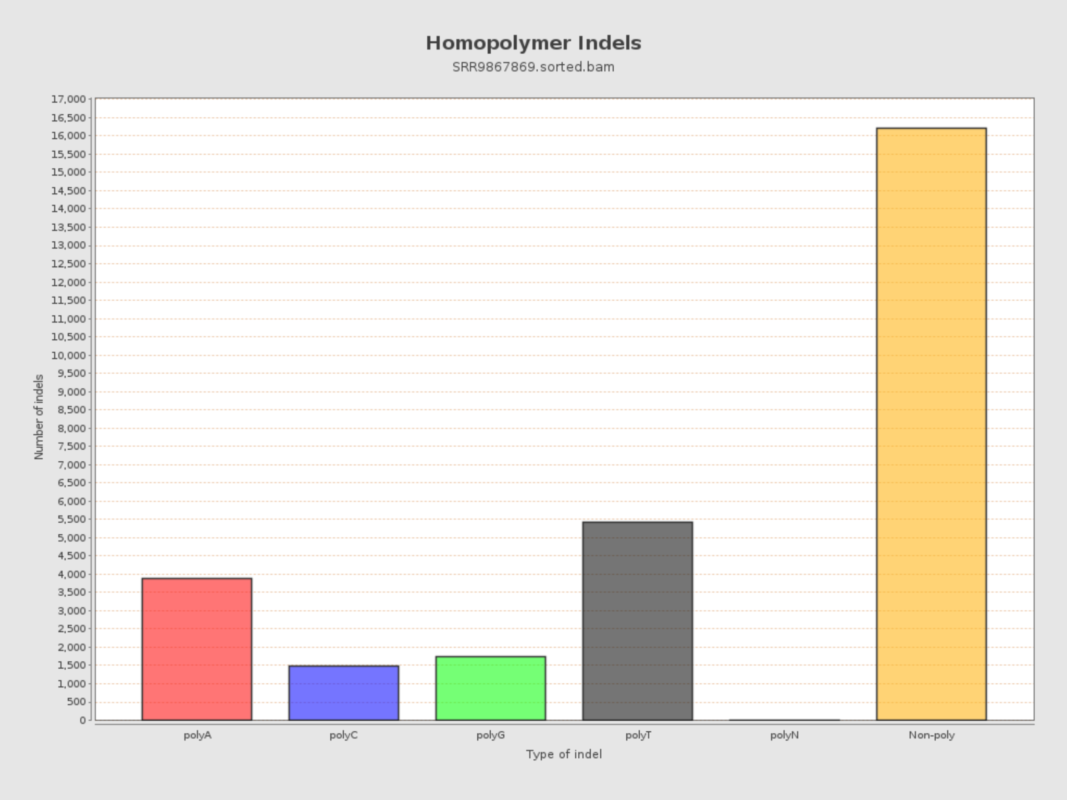
9. Results : Mapped Reads GC-content Distribution



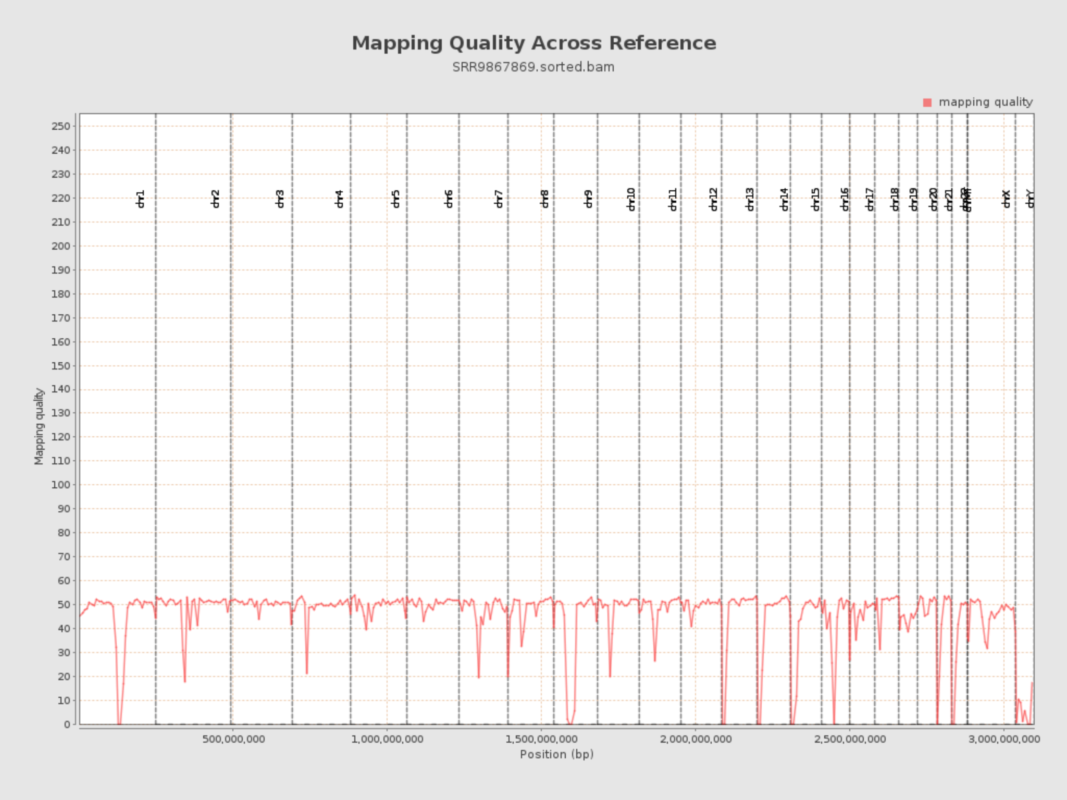
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram