Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 09:12:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867842.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_SRR9867842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 09:12:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,093,341
Mapped reads	1,939,793 / 92.66%
Unmapped reads	153,548 / 7.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,054 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	85,785 / 4.1%
Duplication rate	3.25%
Clipped reads	1,942,364 / 92.79%

2.2. ACGT Content

Number/percentage of A's	28,135,491 / 24.44%
Number/percentage of C's	21,695,646 / 18.84%
Number/percentage of T's	36,646,212 / 31.83%
Number/percentage of G's	28,639,416 / 24.88%
Number/percentage of N's	15,462 / 0.01%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3363

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

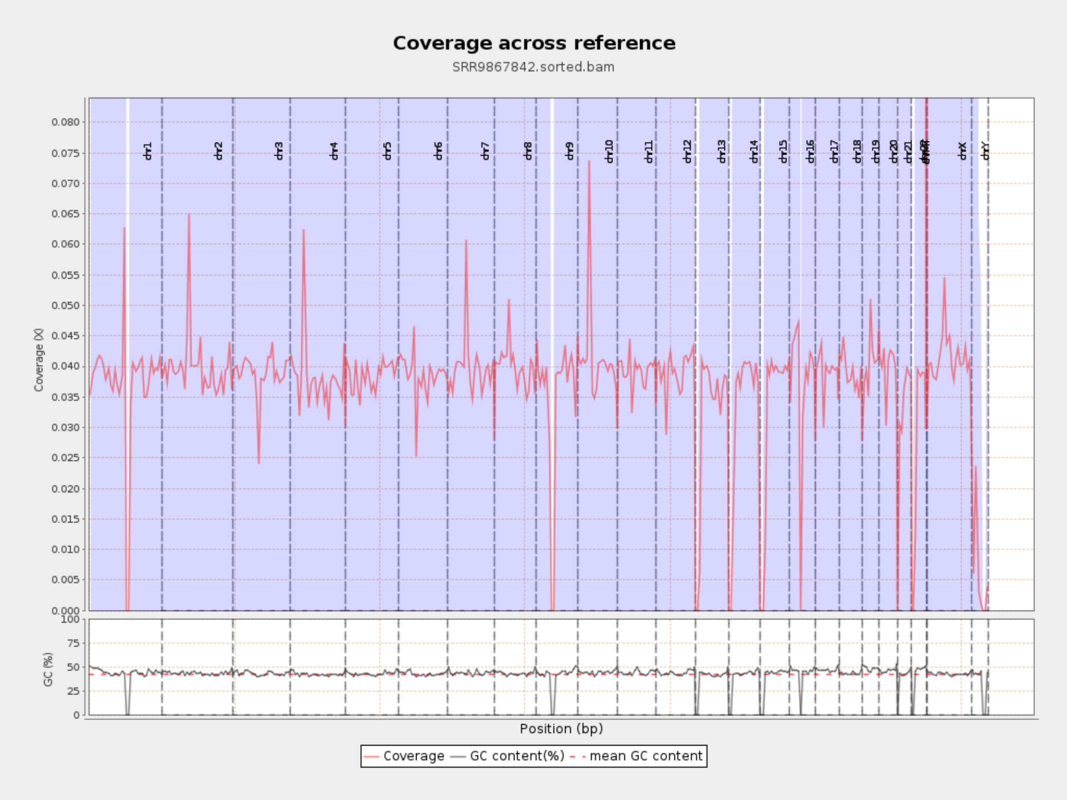
General error rate	0.52%
Mismatches	579,689
Insertions	8,315
Mapped reads with at least one insertion	0.43%
Deletions	22,397
Mapped reads with at least one deletion	1.14%
Homopolymer indels	43.82%

2.6. Chromosome stats

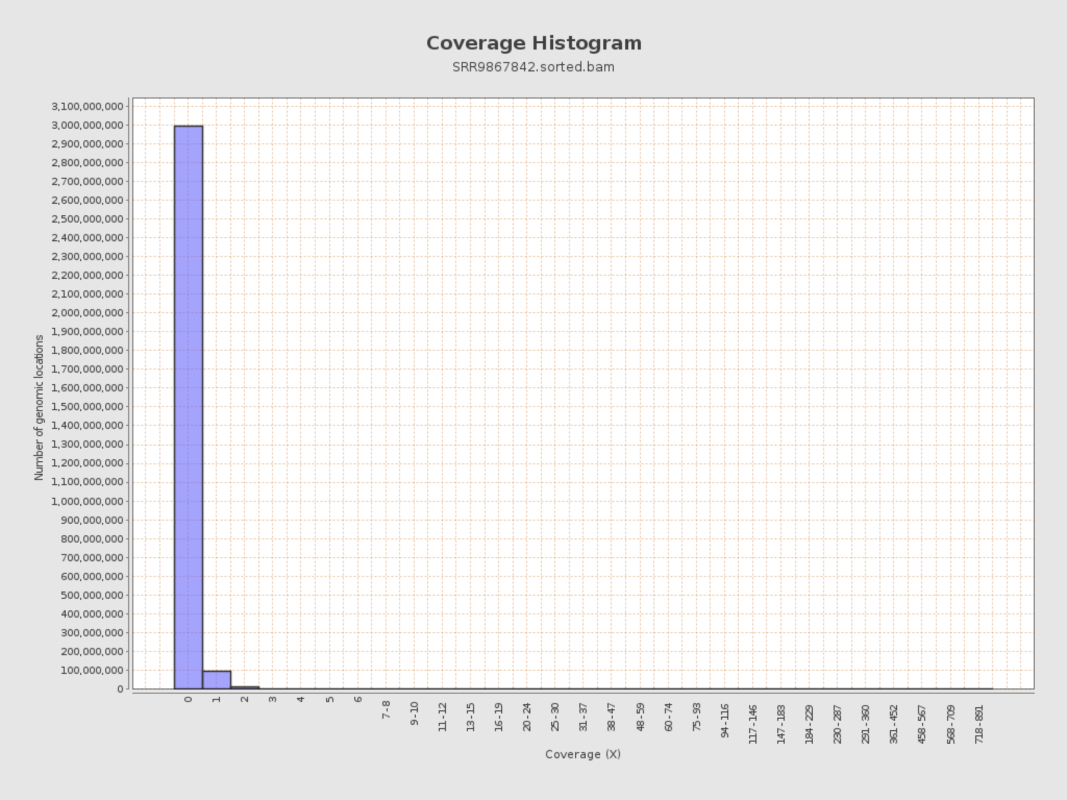
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9235567	0.0371	0.6094
chr2	243199373	9729395	0.04	0.4587
chr3	198022430	7684795	0.0388	0.2162
chr4	191154276	7294546	0.0382	0.2519
chr5	180915260	6970723	0.0385	0.2185
chr6	171115067	6603510	0.0386	0.2482
chr7	159138663	6350765	0.0399	0.3994

chr8	146364022	5853333	0.04	0.3593
chr9	141213431	4812211	0.0341	0.2725
chr10	135534747	5609891	0.0414	0.3512
chr11	135006516	5284632	0.0391	0.2894
chr12	133851895	5238818	0.0391	0.2202
chr13	115169878	3585843	0.0311	0.1951
chr14	107349540	3447695	0.0321	0.204
chr15	102531392	3266045	0.0319	0.1974
chr16	90354753	3382255	0.0374	0.2372
chr17	81195210	3164906	0.039	0.2327
chr18	78077248	3055237	0.0391	0.5169
chr19	59128983	2398634	0.0406	0.4731
chr20	63025520	2500552	0.0397	0.2247
chr21	48129895	1537711	0.0319	0.2378
chr22	51304566	1360689	0.0265	0.1792
chrMT	16571	15080	0.91	1.0944
chrX	155270560	6409485	0.0413	0.2504
chrY	59373566	375529	0.0063	0.2151

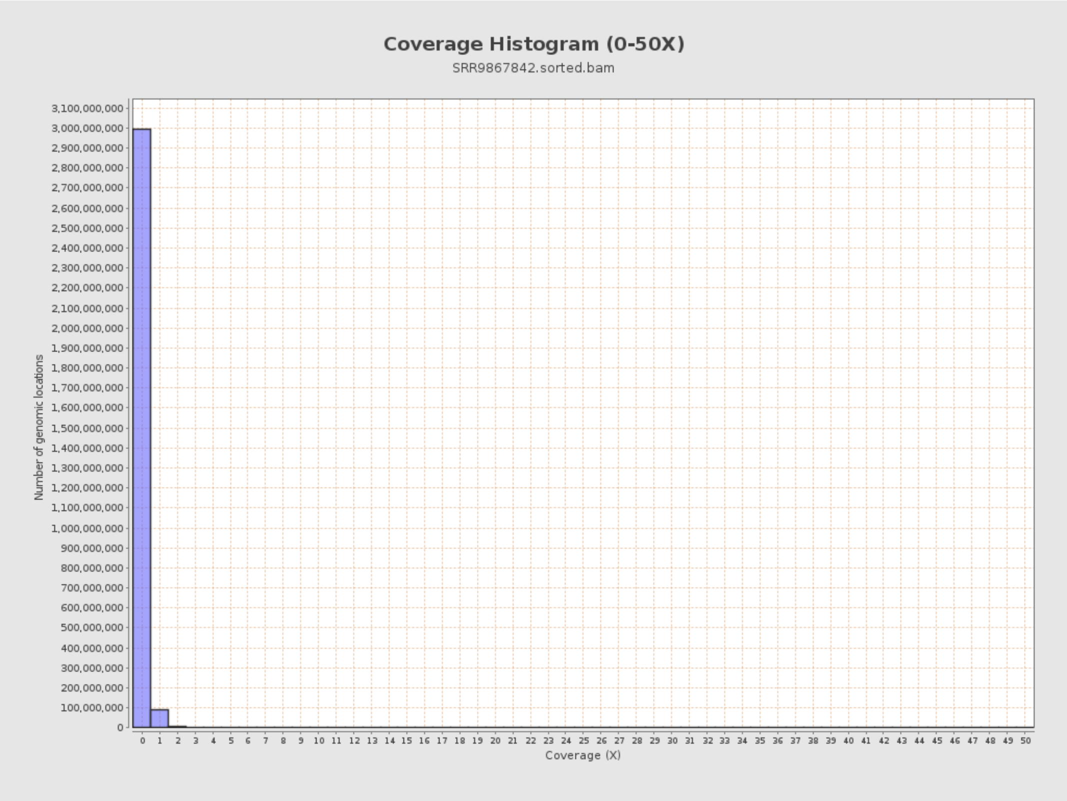
3. Results : Coverage across reference



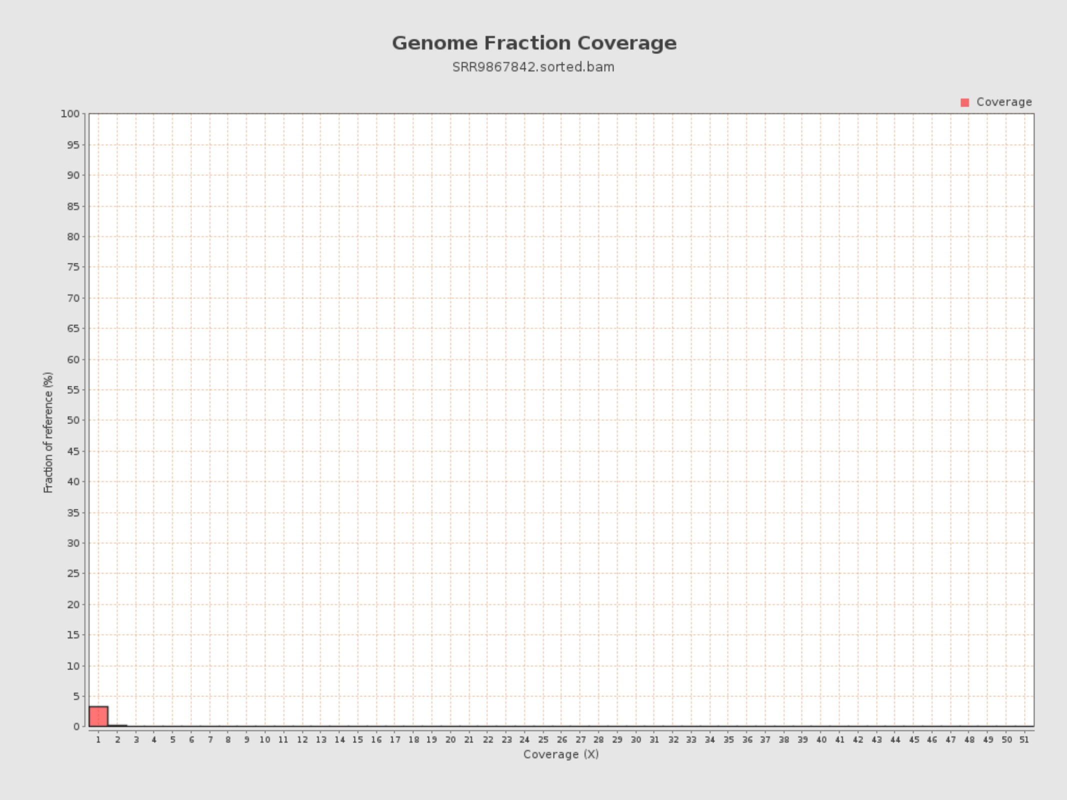
4. Results : Coverage Histogram



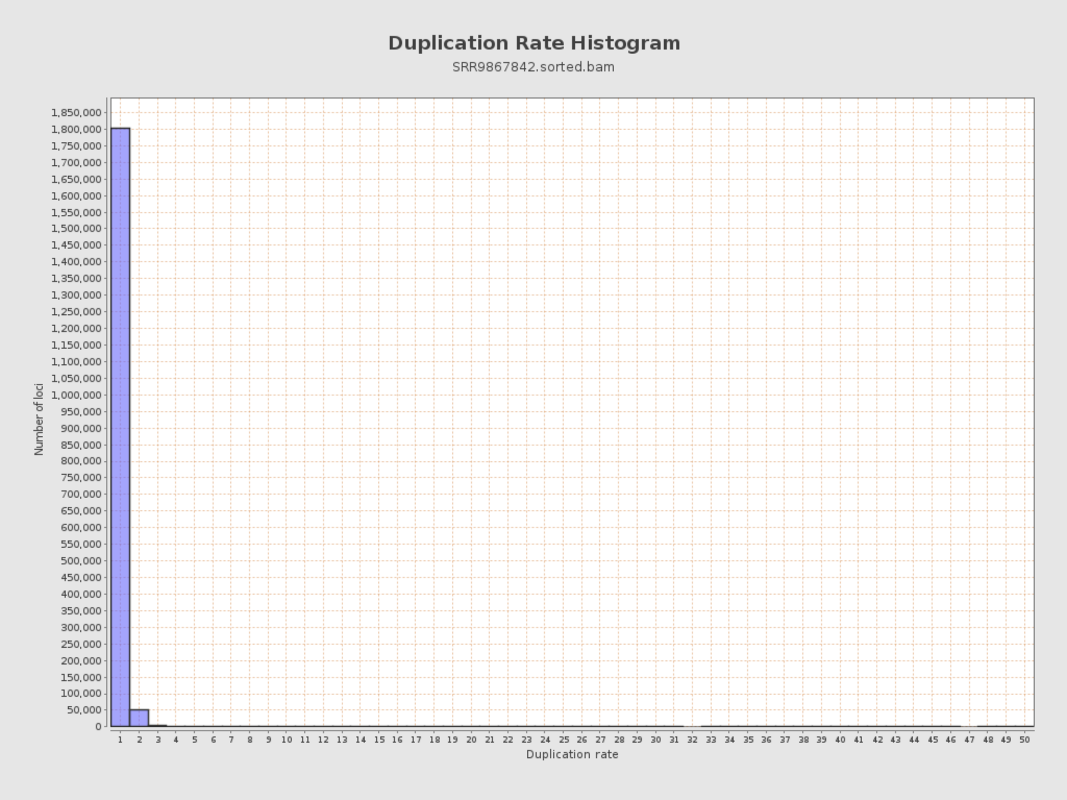
5. Results : Coverage Histogram (0-50X)



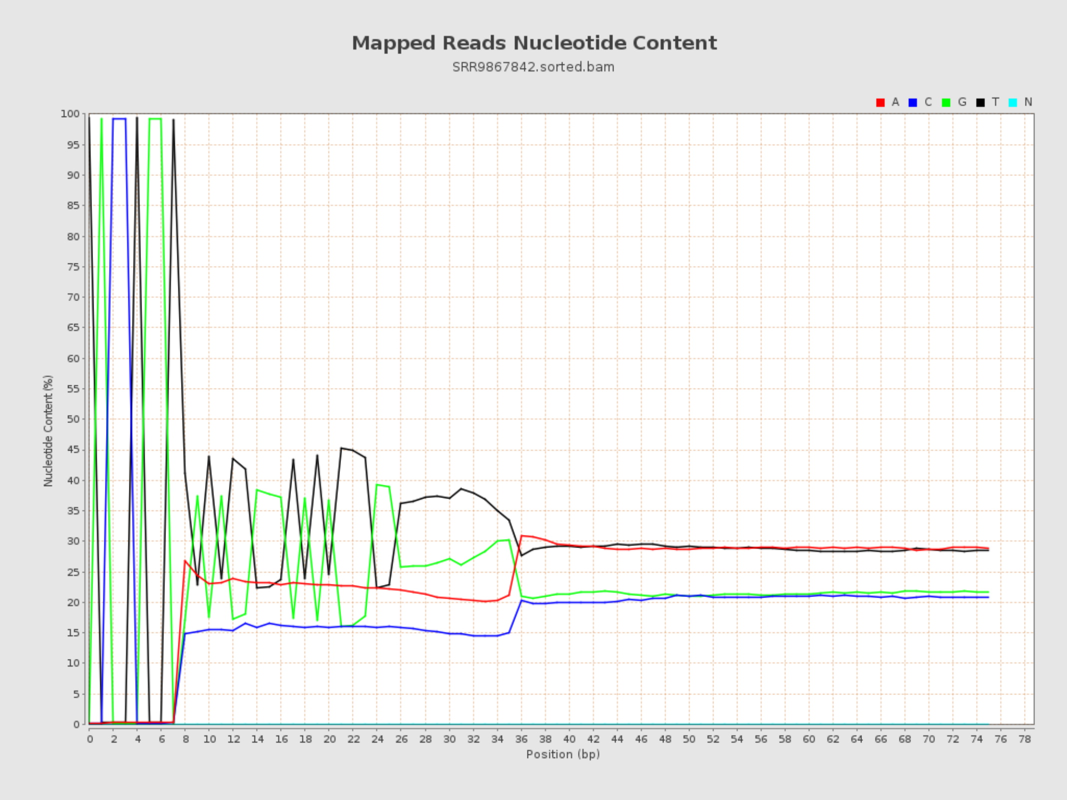
6. Results : Genome Fraction Coverage



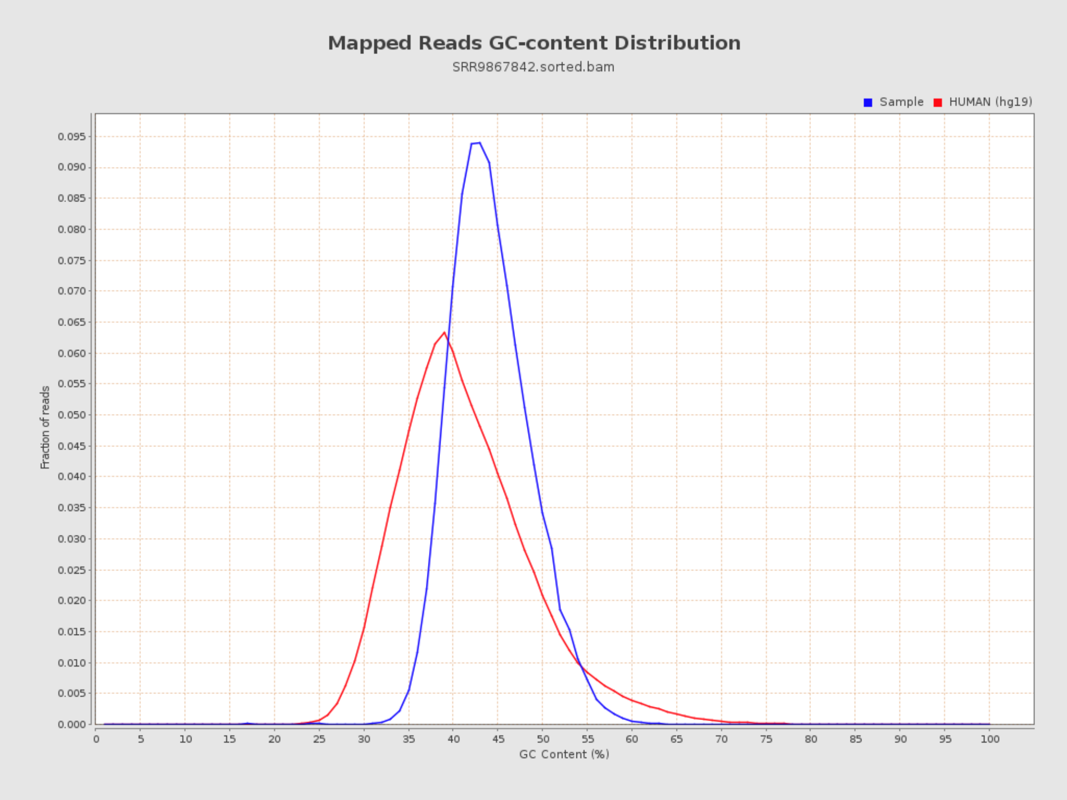
7. Results : Duplication Rate Histogram



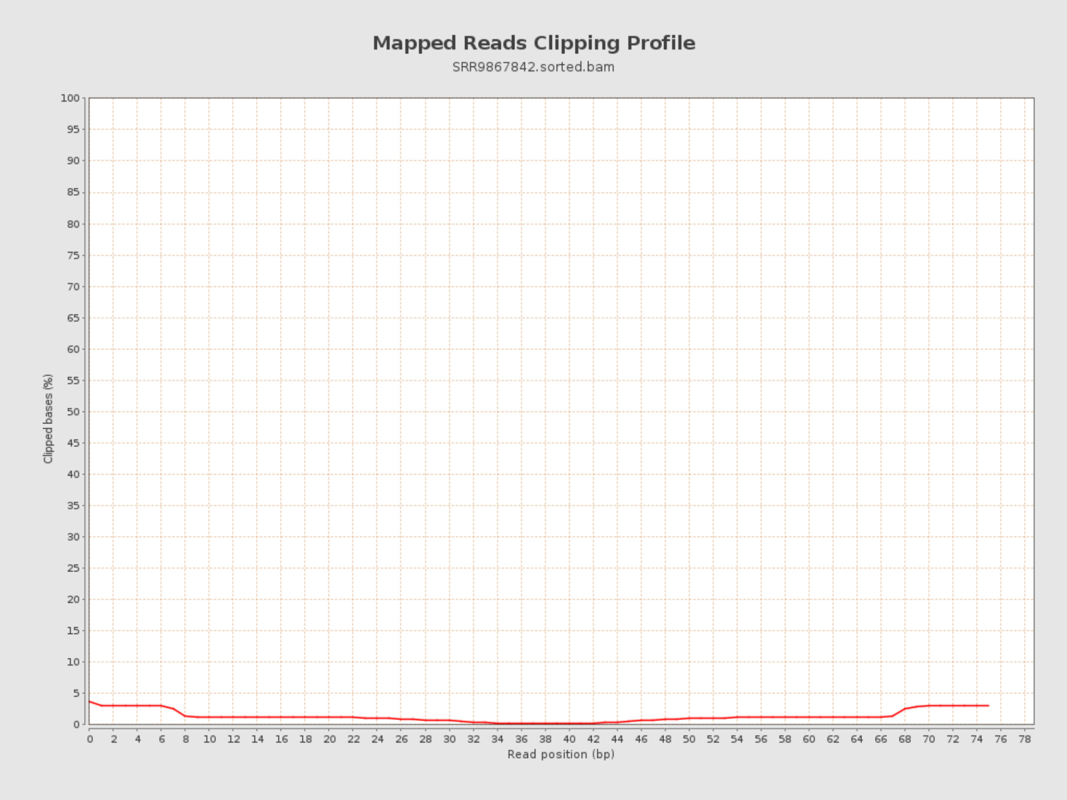
8. Results : Mapped Reads Nucleotide Content



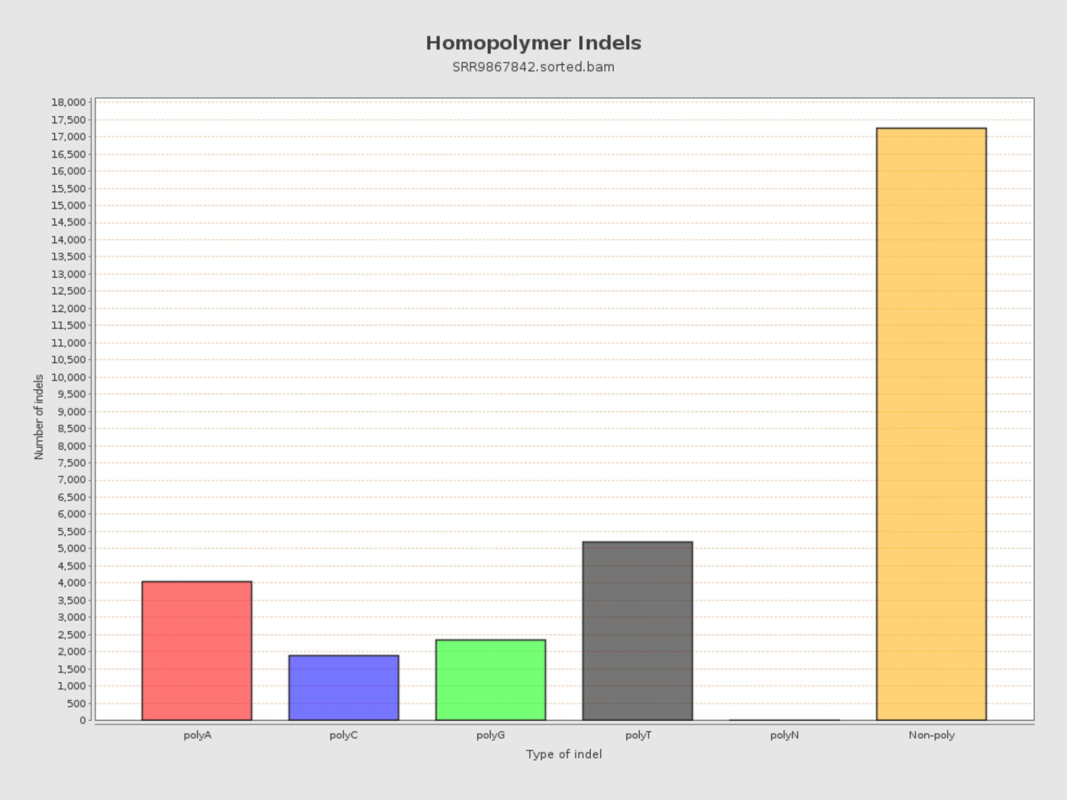
9. Results : Mapped Reads GC-content Distribution



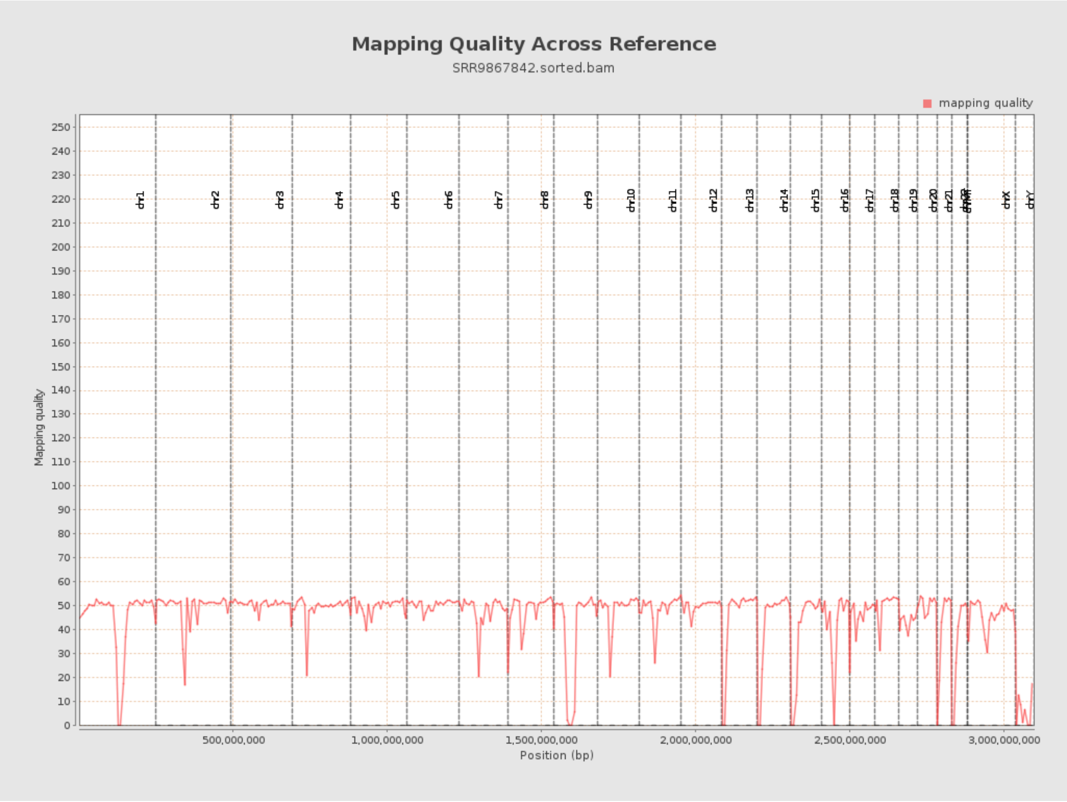
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram