Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 14:32:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867855.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_SRR9867855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 14:32:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,947,408
Mapped reads	2,728,380 / 92.57%
Unmapped reads	219,028 / 7.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,265 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	159,036 / 5.4%
Duplication rate	4.3%
Clipped reads	2,733,037 / 92.73%

2.2. ACGT Content

Number/percentage of A's	39,224,375 / 24.32%
Number/percentage of C's	28,983,049 / 17.97%
Number/percentage of T's	52,846,000 / 32.77%
Number/percentage of G's	40,197,294 / 24.93%
Number/percentage of N's	21,515 / 0.01%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0521

Standard Deviation	0.4552

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

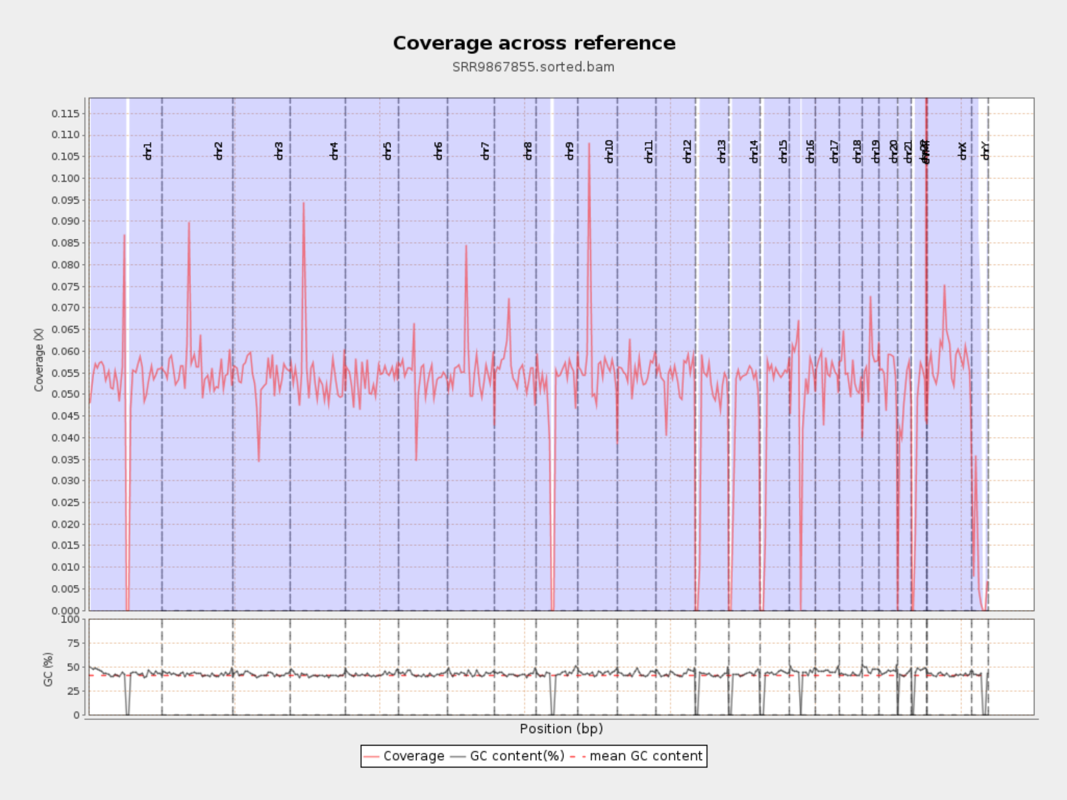
General error rate	0.51%
Mismatches	805,987
Insertions	11,441
Mapped reads with at least one insertion	0.42%
Deletions	30,155
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.87%

2.6. Chromosome stats

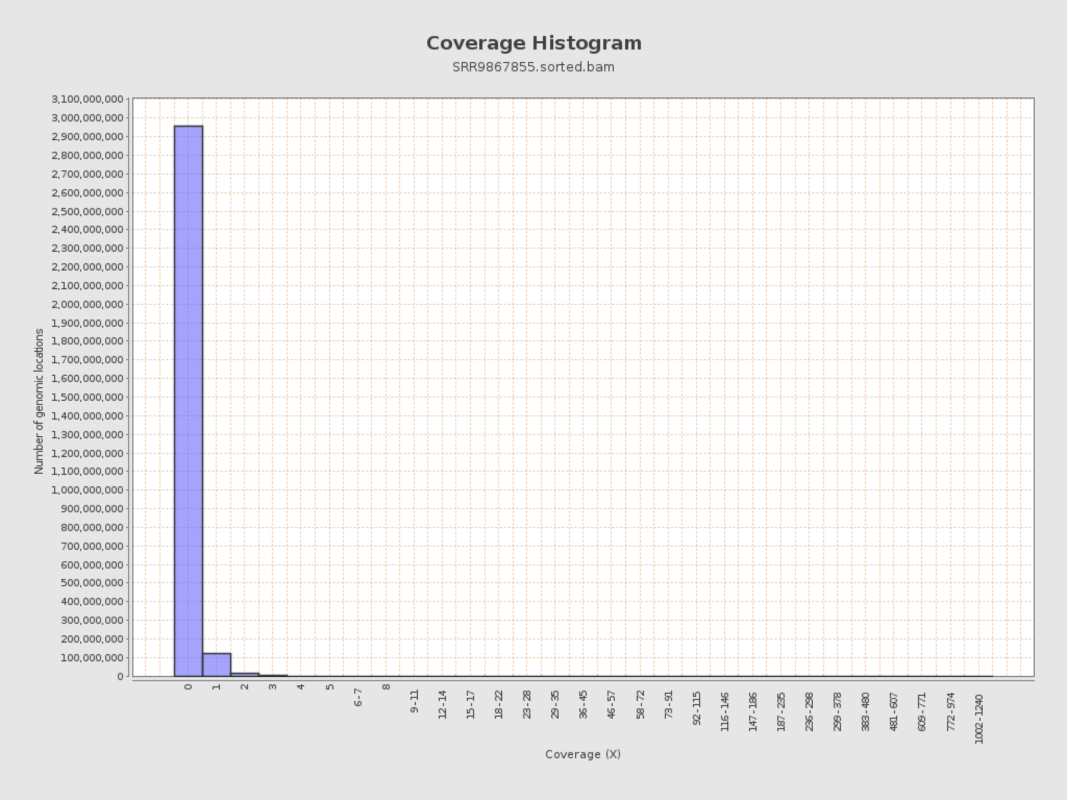
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12902849	0.0518	0.861
chr2	243199373	13702512	0.0563	0.6275
chr3	198022430	10665376	0.0539	0.2664
chr4	191154276	10416462	0.0545	0.3266
chr5	180915260	9710897	0.0537	0.2676
chr6	171115067	9263034	0.0541	0.3216
chr7	159138663	8902712	0.0559	0.5448

chr8	146364022	8189254	0.056	0.4772
chr9	141213431	6715146	0.0476	0.3631
chr10	135534747	7845059	0.0579	0.4834
chr11	135006516	7440832	0.0551	0.3879
chr12	133851895	7239018	0.0541	0.2701
chr13	115169878	5094967	0.0442	0.2415
chr14	107349540	4832815	0.045	0.2504
chr15	102531392	4583287	0.0447	0.2456
chr16	90354753	4618043	0.0511	0.2959
chr17	81195210	4451578	0.0548	0.2976
chr18	78077248	4285878	0.0549	0.7278
chr19	59128983	3395854	0.0574	0.646
chr20	63025520	3465384	0.055	0.2781
chr21	48129895	2118714	0.044	0.2985
chr22	51304566	1893578	0.0369	0.2201
chrMT	16571	7772	0.469	0.7428
chrX	155270560	9029367	0.0582	0.3163
chrY	59373566	550619	0.0093	0.3355

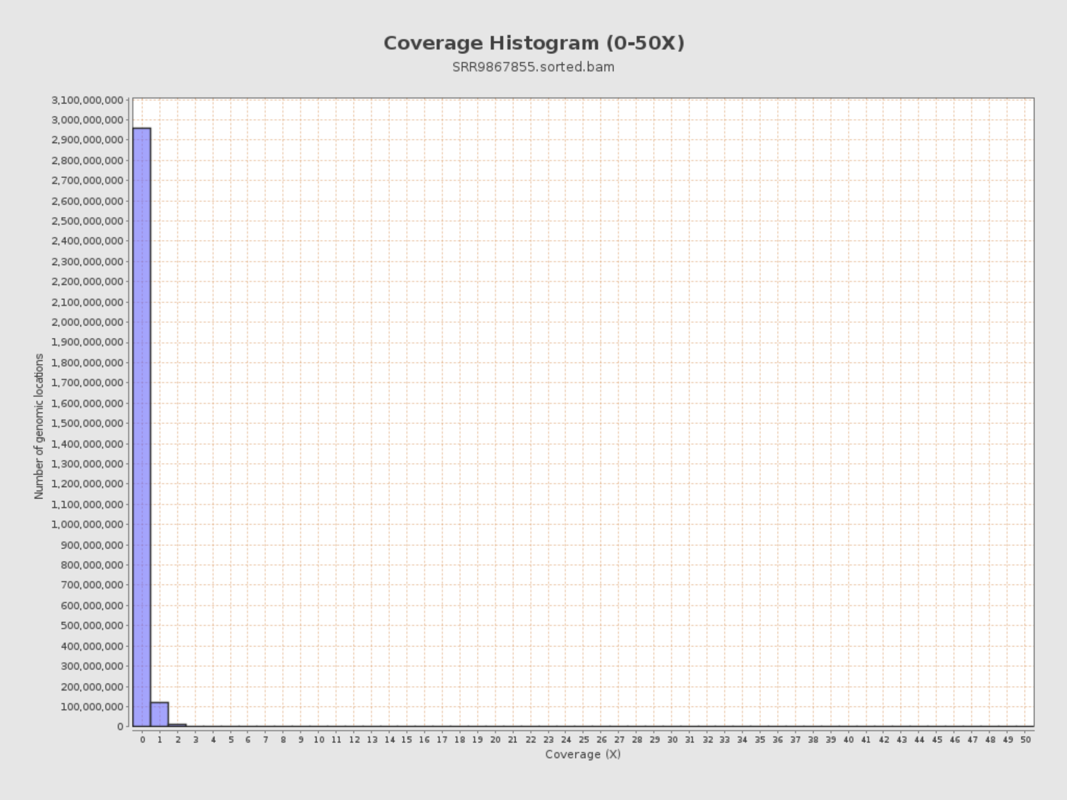
3. Results : Coverage across reference



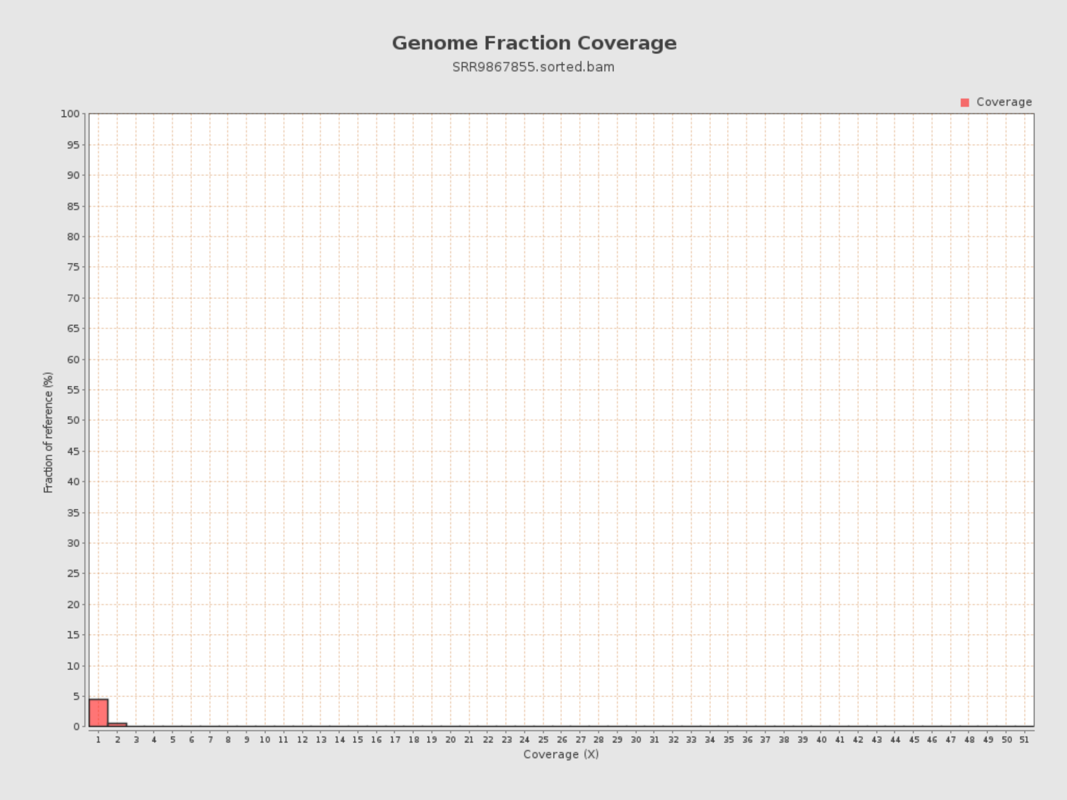
4. Results : Coverage Histogram



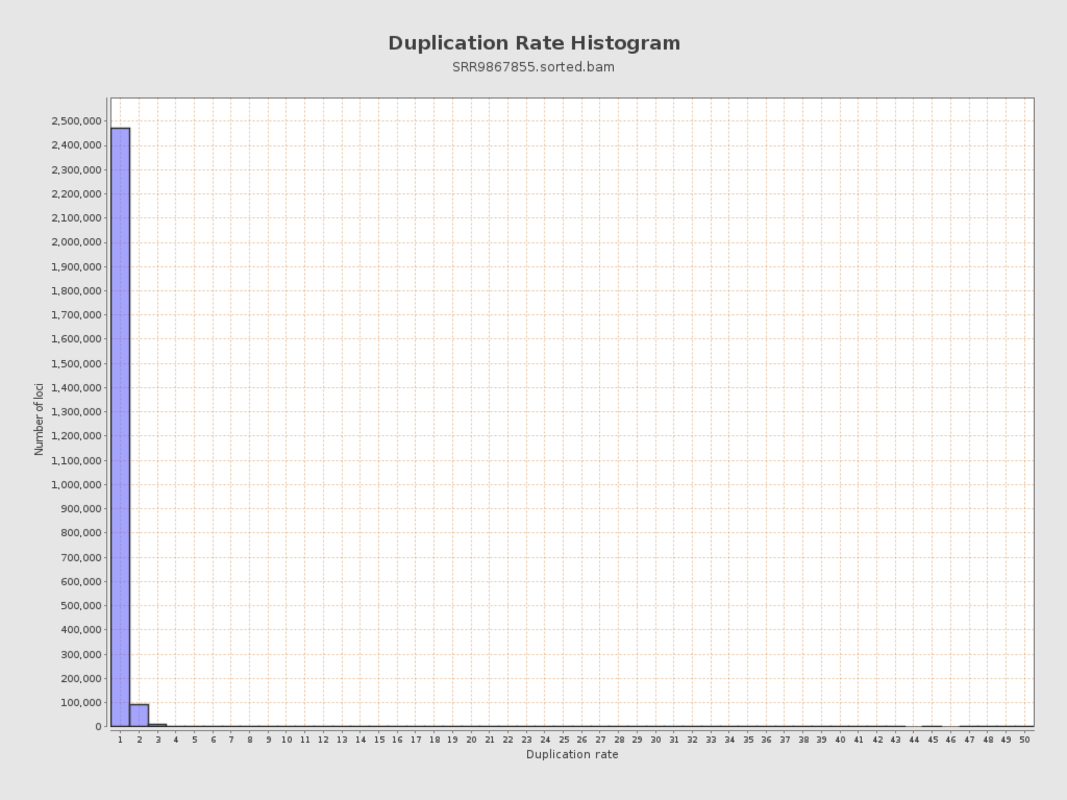
5. Results : Coverage Histogram (0-50X)



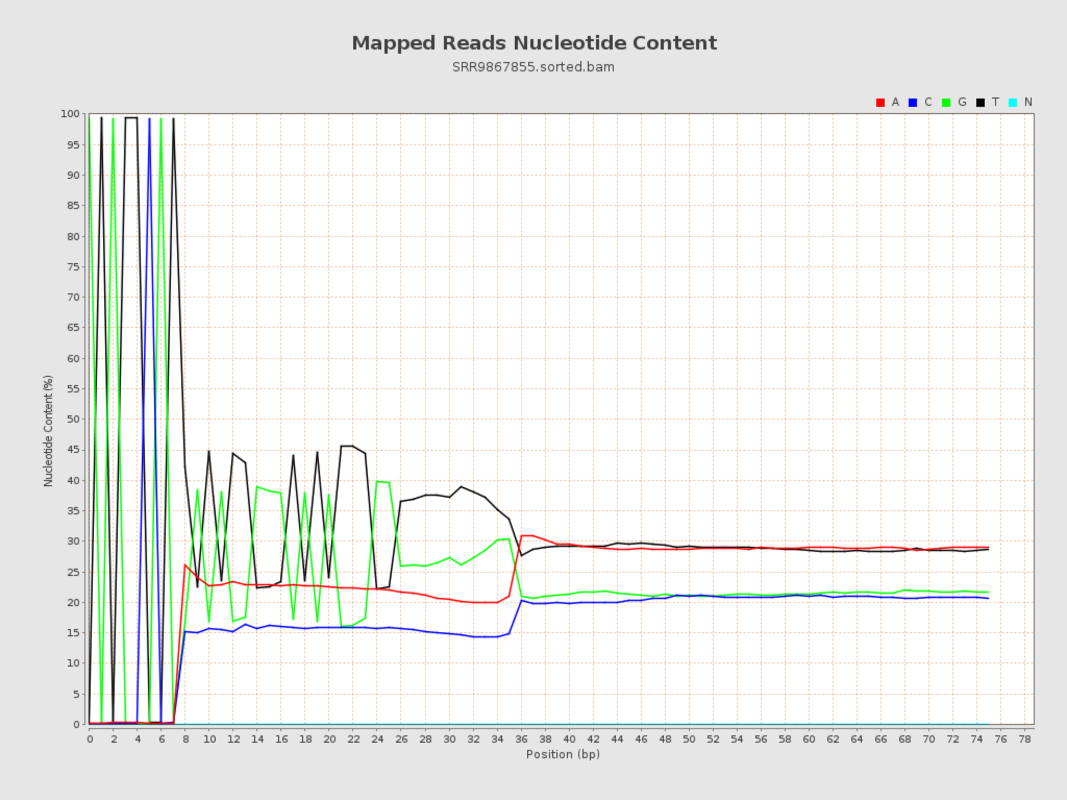
6. Results : Genome Fraction Coverage



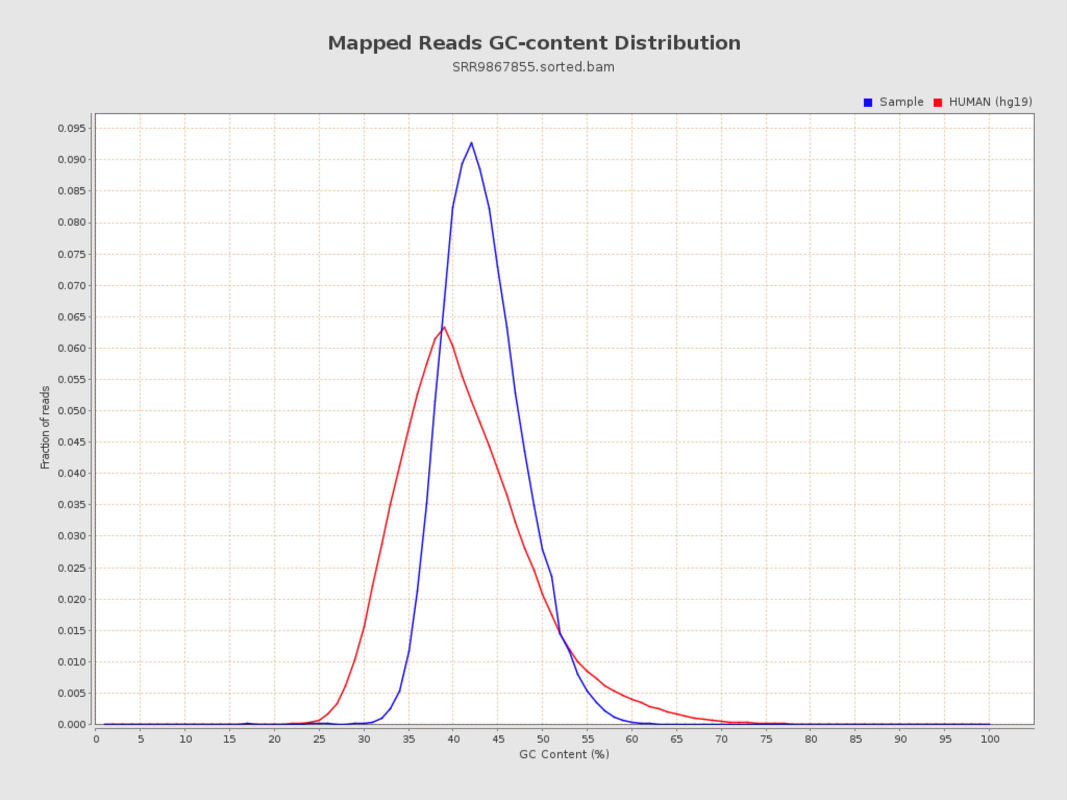
7. Results : Duplication Rate Histogram



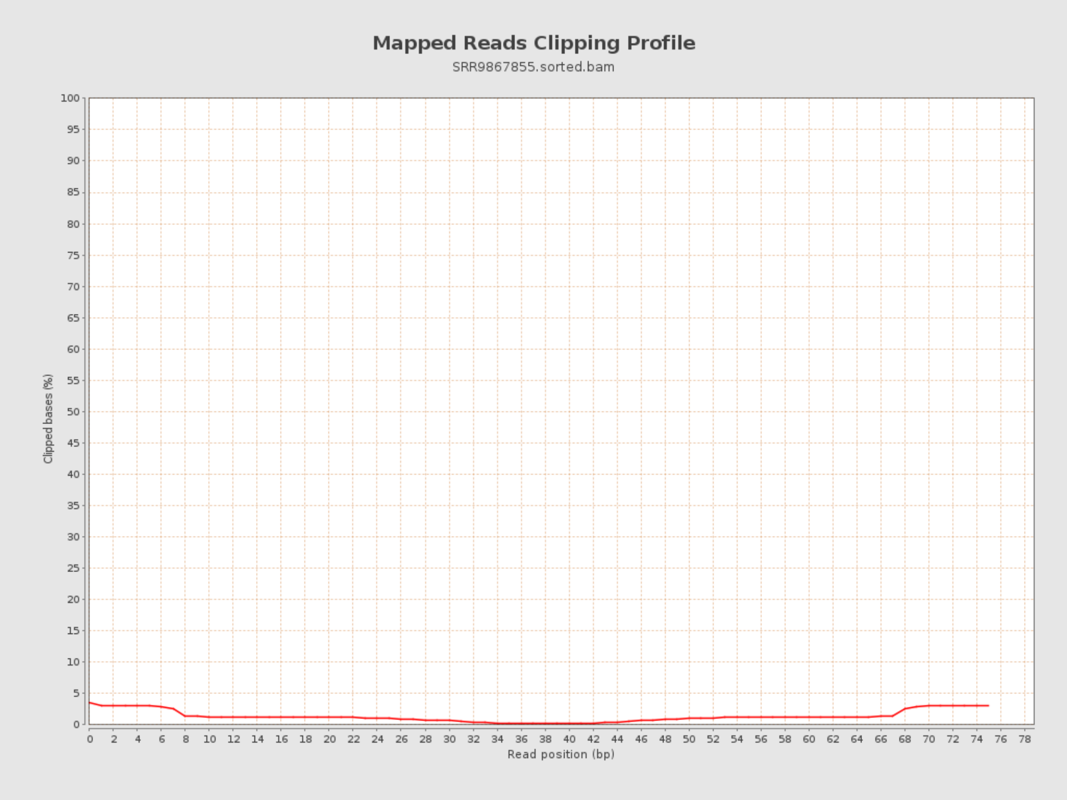
8. Results : Mapped Reads Nucleotide Content



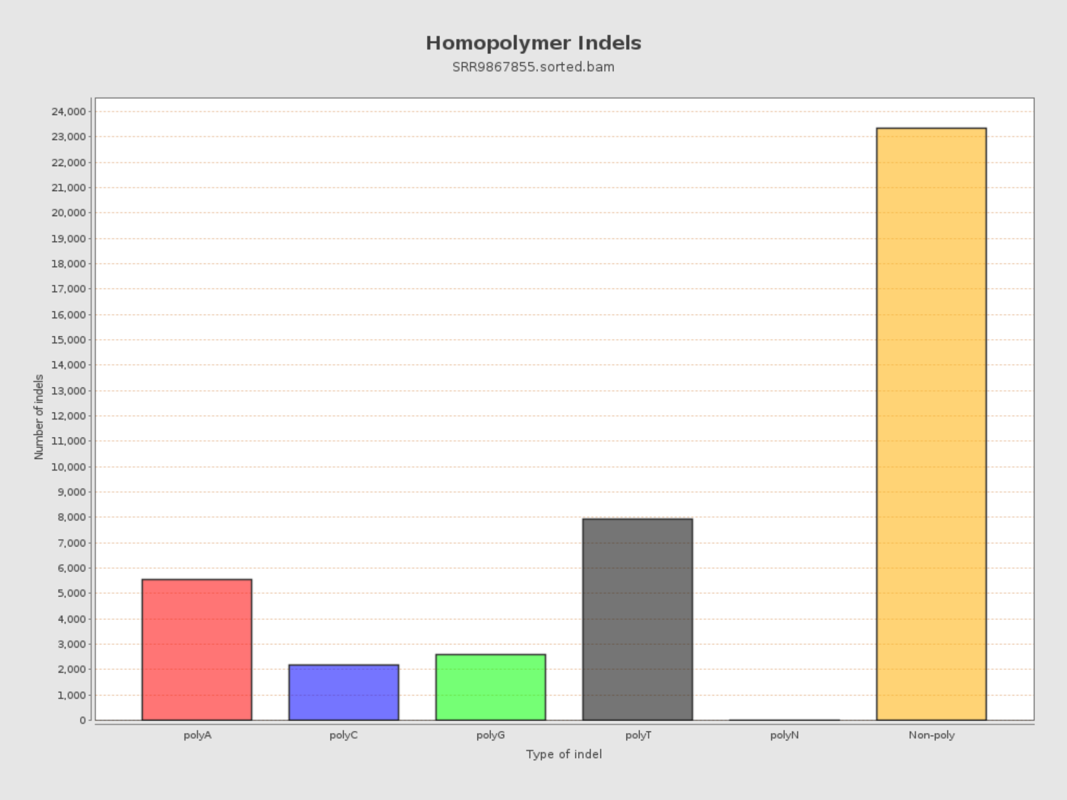
9. Results : Mapped Reads GC-content Distribution



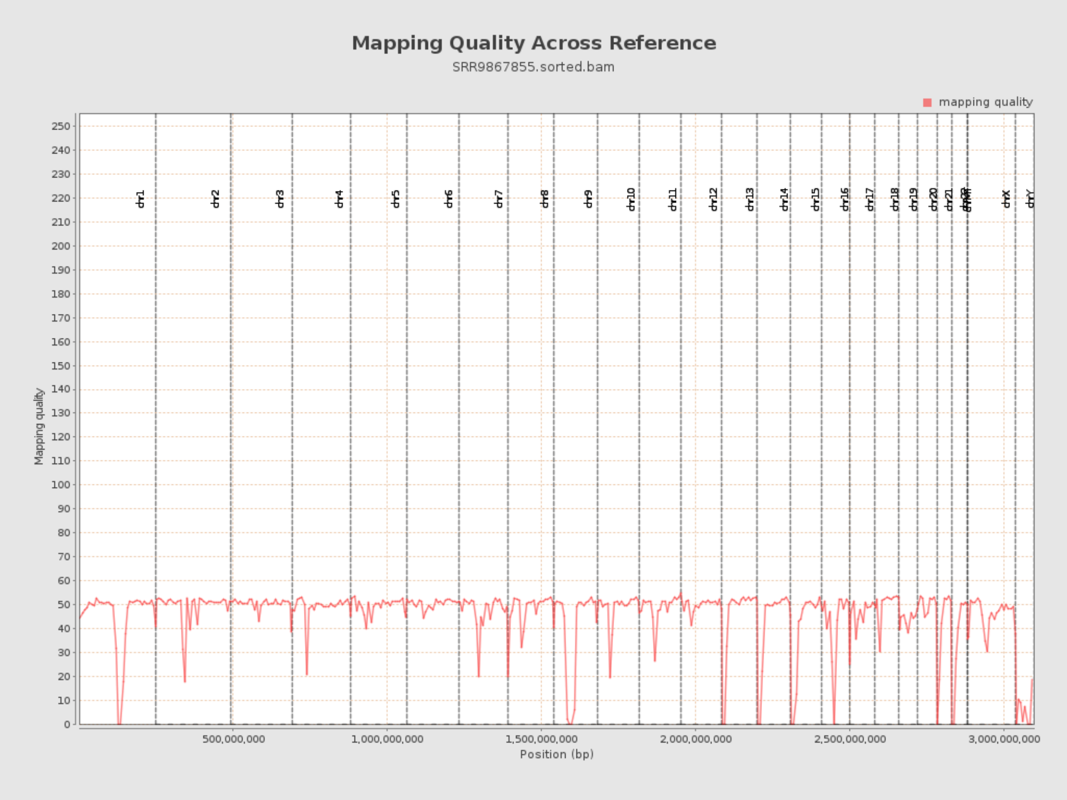
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram