Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:00:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867863.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_SRR9867863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867863.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:00:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,054,736
Mapped reads	973,298 / 92.28%
Unmapped reads	81,438 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,244 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	26,673 / 2.53%
Duplication rate	1.96%
Clipped reads	974,074 / 92.35%

2.2. ACGT Content

Number/percentage of A's	14,959,457 / 26.03%
Number/percentage of C's	10,733,632 / 18.68%
Number/percentage of T's	18,451,510 / 32.11%
Number/percentage of G's	13,317,875 / 23.17%
Number/percentage of N's	8,225 / 0.01%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1962

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

General error rate	0.52%
Mismatches	288,514
Insertions	4,284
Mapped reads with at least one insertion	0.44%
Deletions	10,711
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.89%

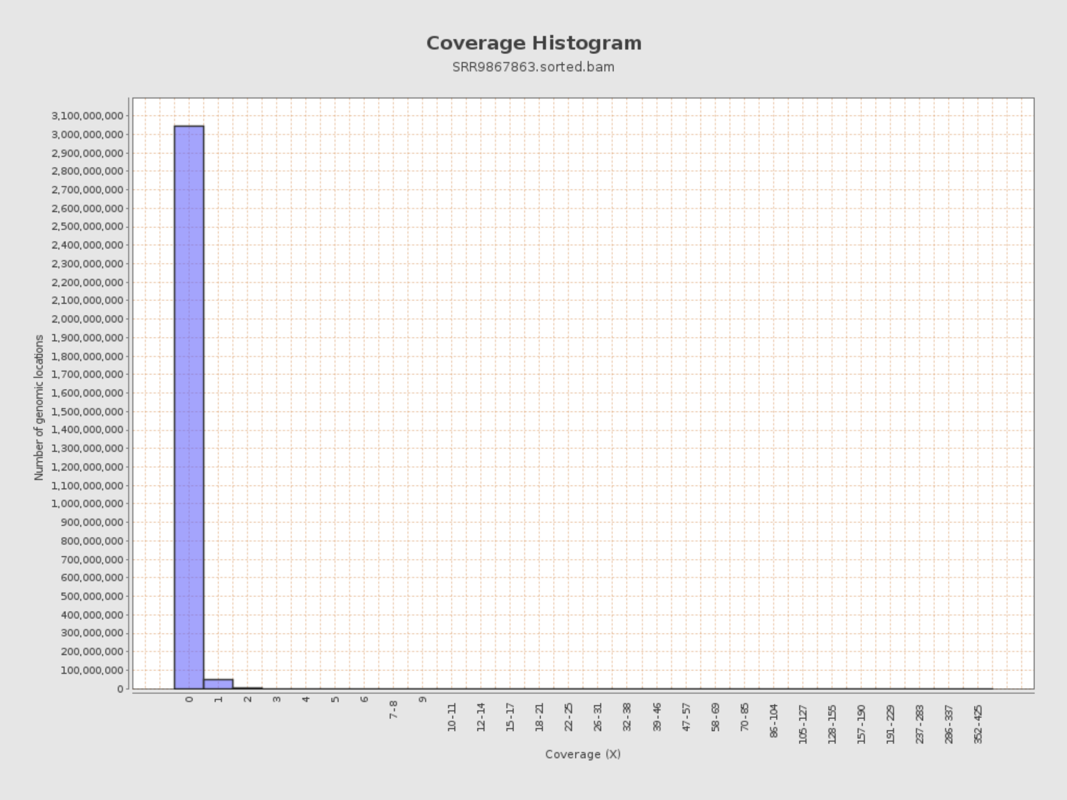
2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4613633	0.0185	0.3261
chr2	243199373	4847873	0.0199	0.2476
chr3	198022430	3803229	0.0192	0.1456
chr4	191154276	3763573	0.0197	0.1627
chr5	180915260	3451228	0.0191	0.1456
chr6	171115067	3312384	0.0194	0.1611
chr7	159138663	3220944	0.0202	0.2355

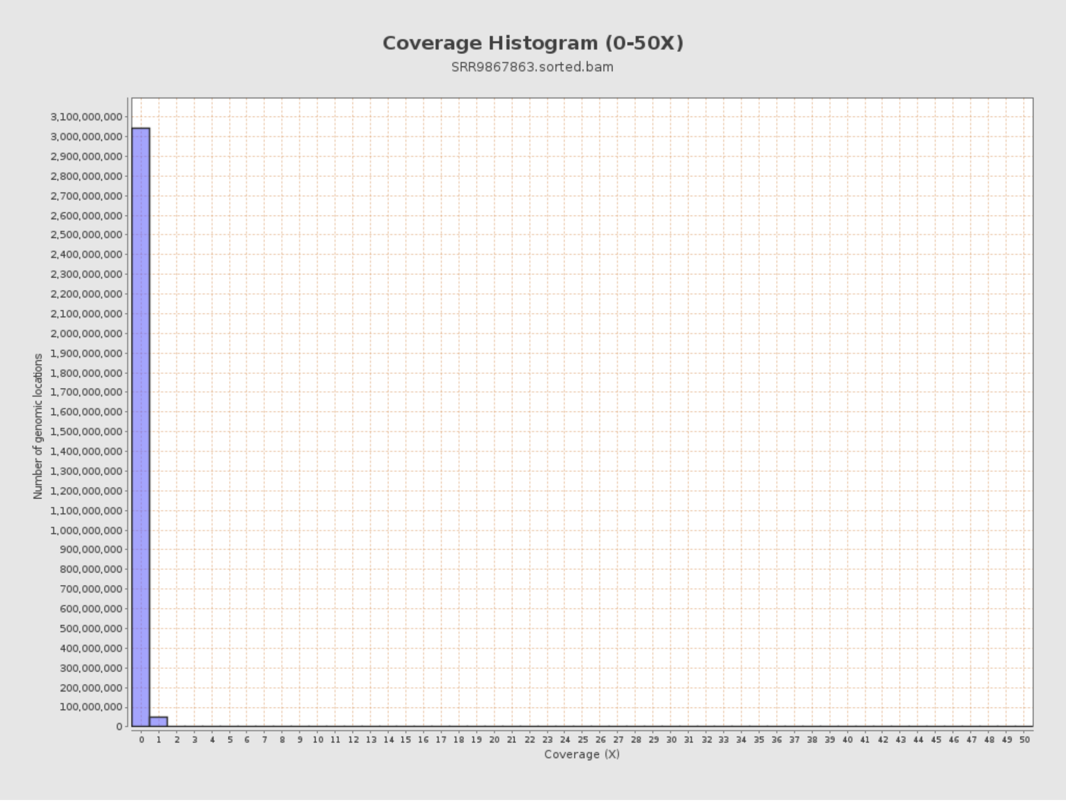
chr8	146364022	2928457	0.02	0.2001
chr9	141213431	2431721	0.0172	0.1708
chr10	135534747	2811367	0.0207	0.211
chr11	135006516	2609837	0.0193	0.1693
chr12	133851895	2601717	0.0194	0.1475
chr13	115169878	1824193	0.0158	0.1338
chr14	107349540	1732591	0.0161	0.1379
chr15	102531392	1637368	0.016	0.1342
chr16	90354753	1652266	0.0183	0.1502
chr17	81195210	1514165	0.0186	0.1484
chr18	78077248	1552556	0.0199	0.2931
chr19	59128983	1163205	0.0197	0.2615
chr20	63025520	1226696	0.0195	0.1487
chr21	48129895	740956	0.0154	0.1437
chr22	51304566	671528	0.0131	0.1201
chrMT	16571	18876	1.1391	1.2697
chrX	155270560	3163849	0.0204	0.1608
chrY	59373566	193745	0.0033	0.1234

3. Results : Coverage across reference

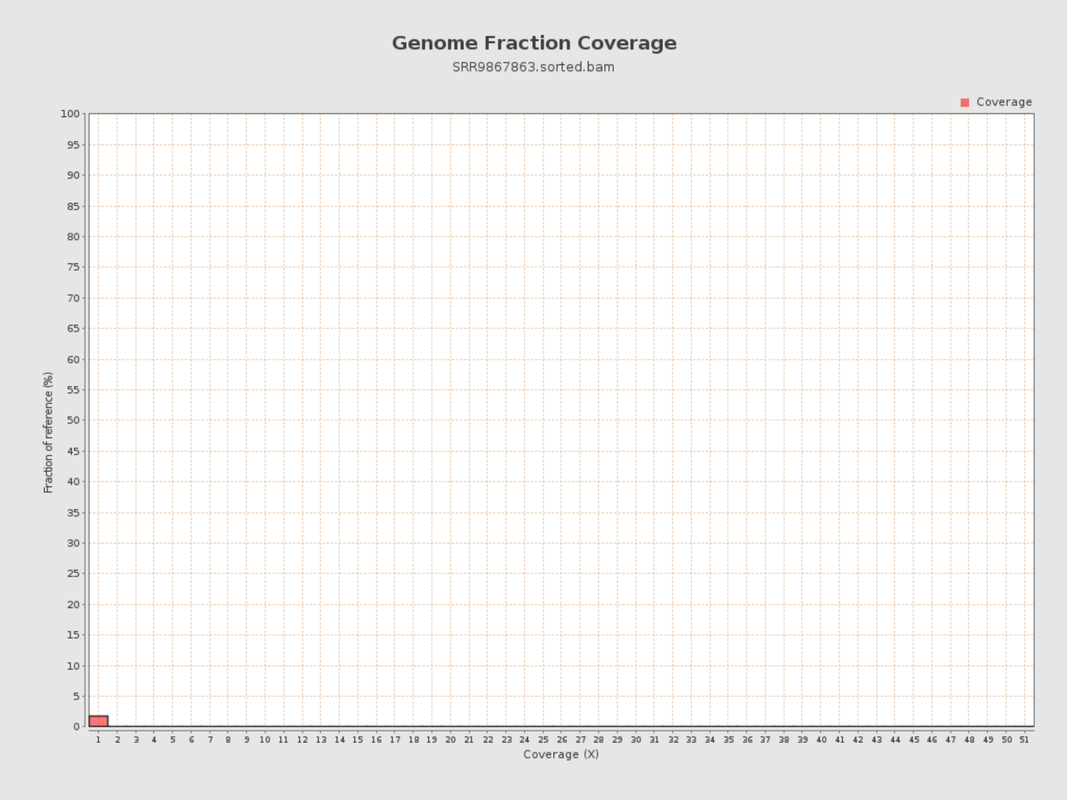
4. Results : Coverage Histogram



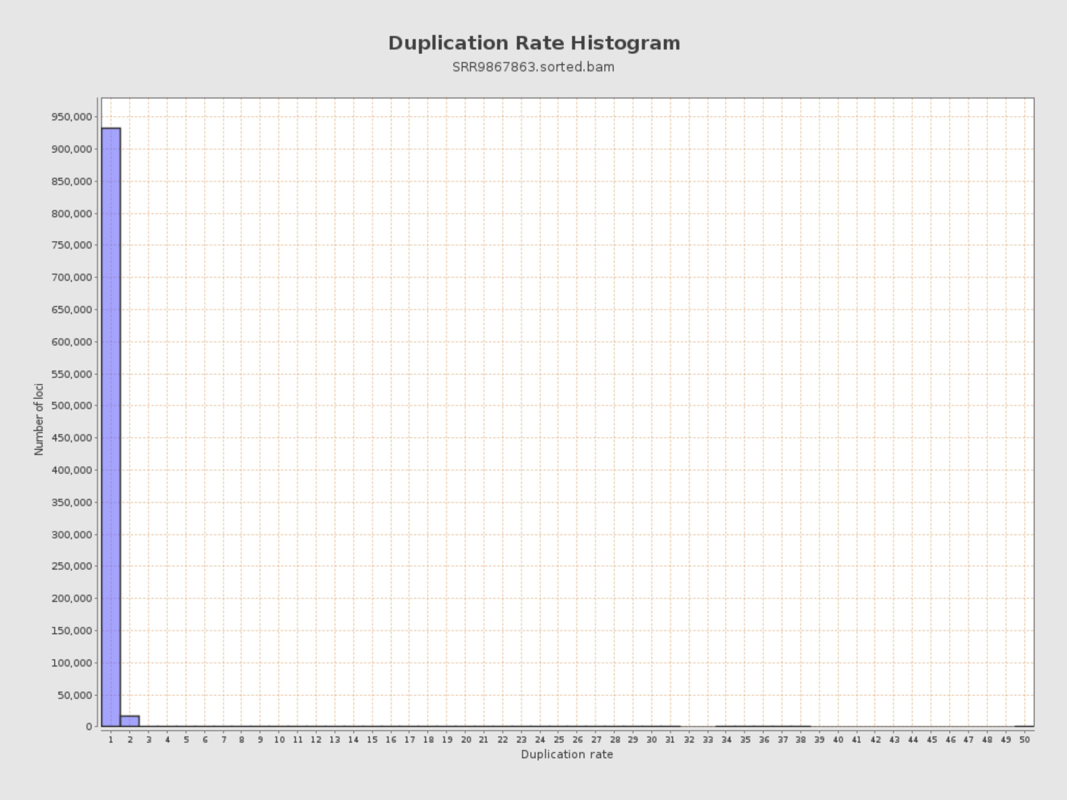
5. Results : Coverage Histogram (0-50X)



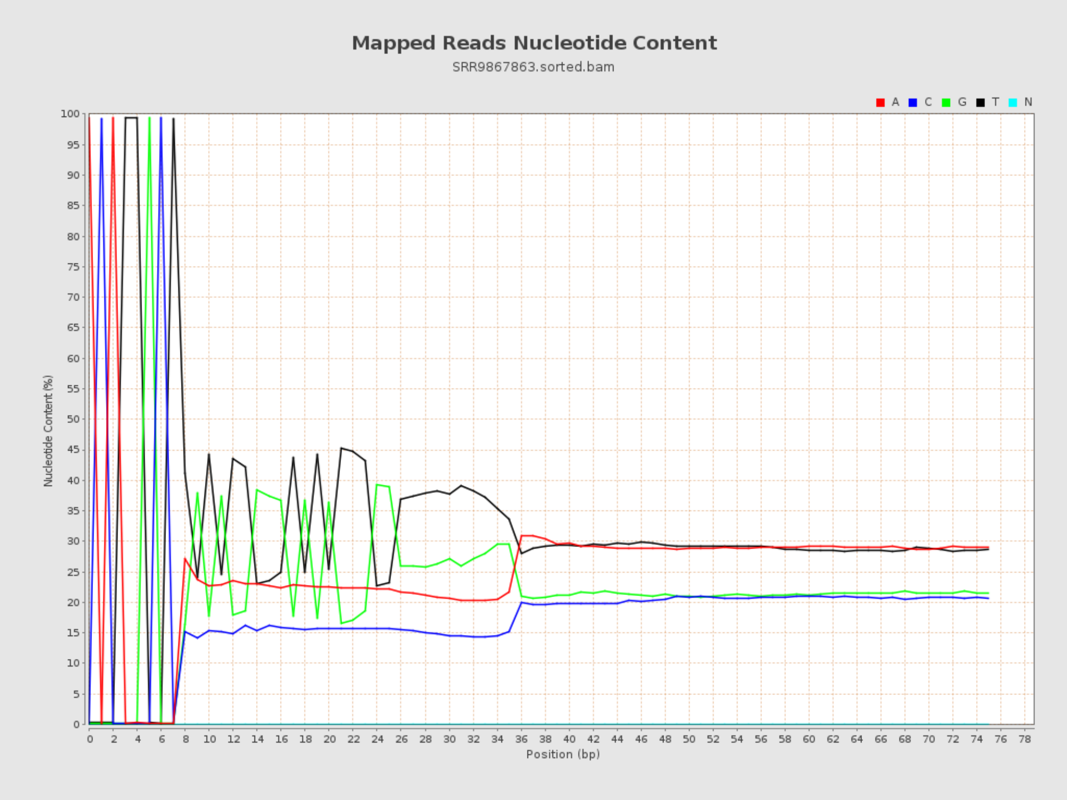
6. Results : Genome Fraction Coverage



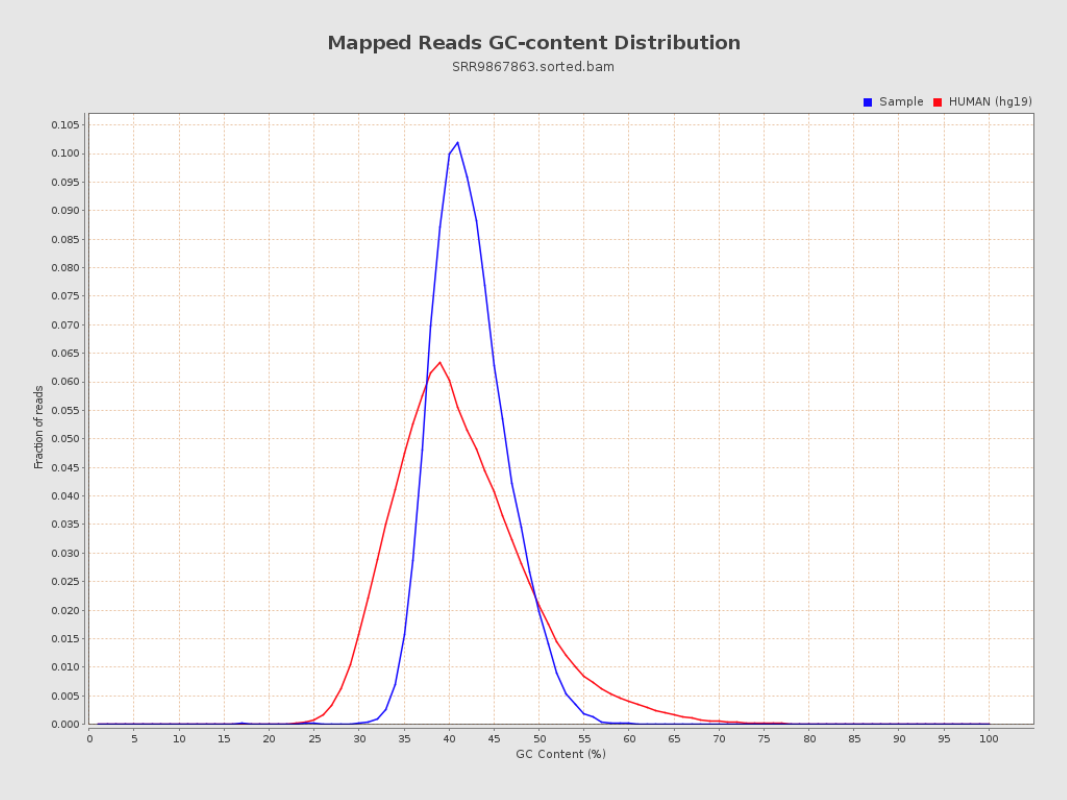
7. Results : Duplication Rate Histogram



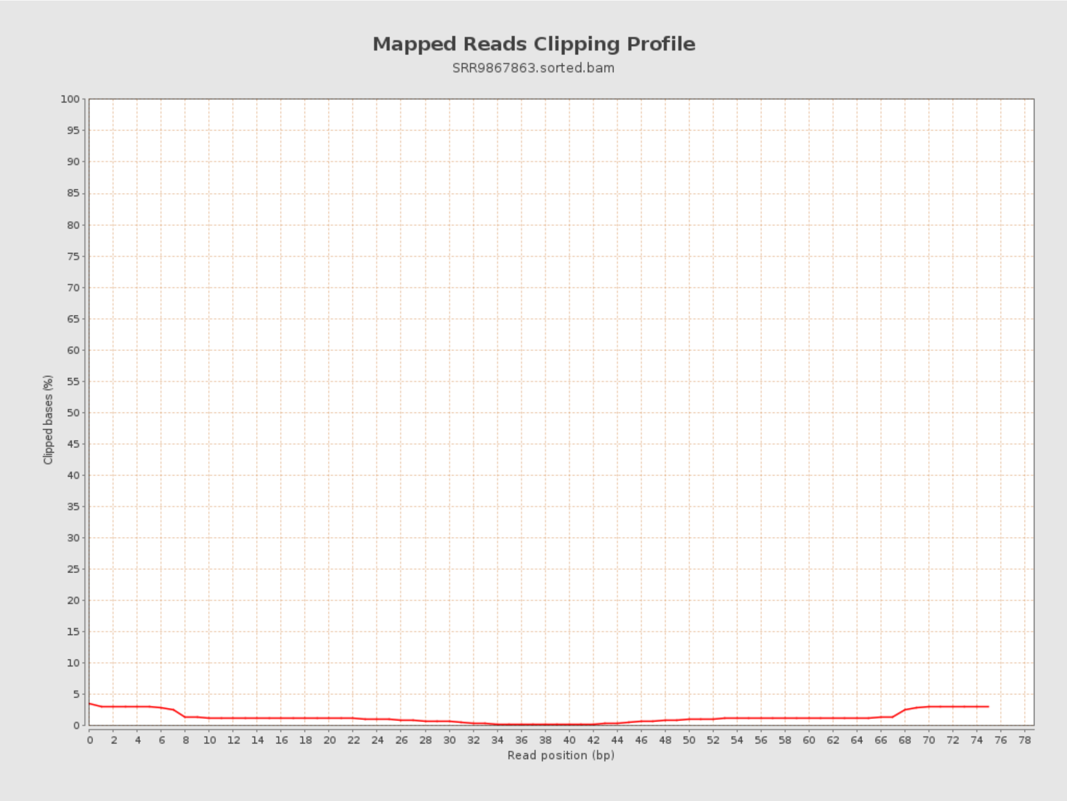
8. Results : Mapped Reads Nucleotide Content



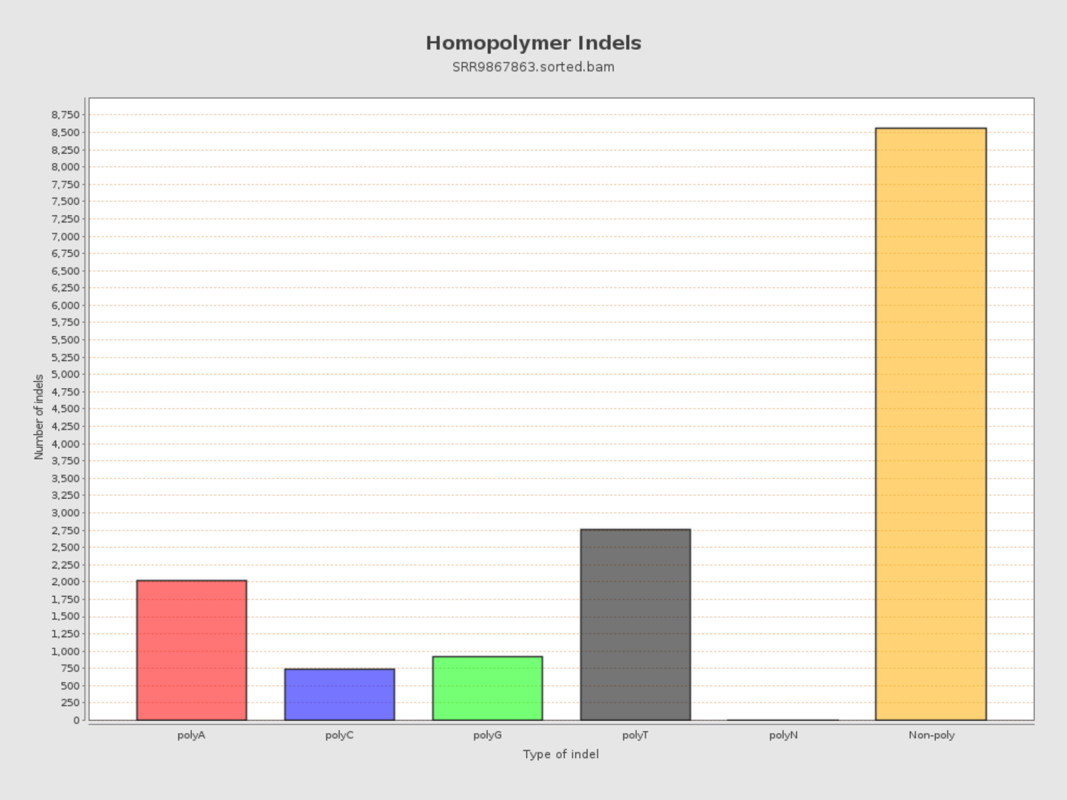
9. Results : Mapped Reads GC-content Distribution



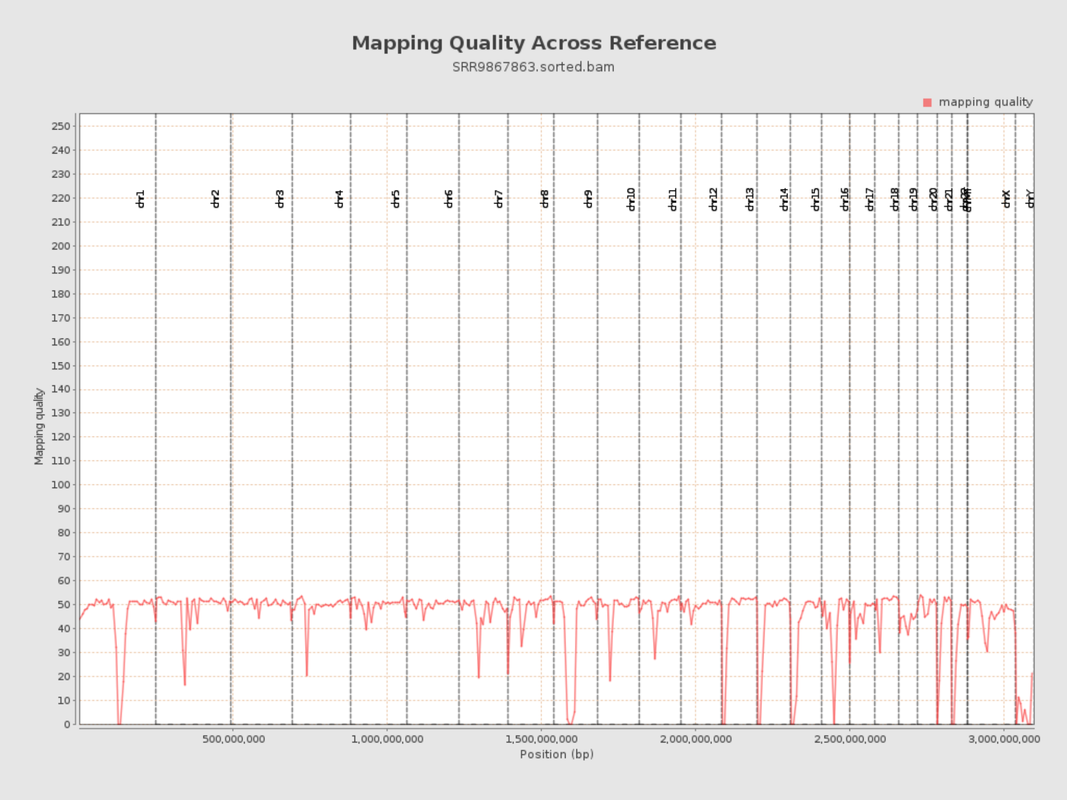
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram