Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 14:52:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867856.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_SRR9867856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 14:52:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	690,530
Mapped reads	612,122 / 88.65%
Unmapped reads	78,408 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,281 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	25,064 / 3.63%
Duplication rate	2%
Clipped reads	613,583 / 88.86%

2.2. ACGT Content

Number/percentage of A's	9,353,941 / 26.01%
Number/percentage of C's	6,649,717 / 18.49%
Number/percentage of T's	10,872,886 / 30.23%
Number/percentage of G's	9,083,041 / 25.26%
Number/percentage of N's	5,195 / 0.01%
GC Percentage	43.74%

2.3. Coverage

Mean	0.0116

Standard Deviation	0.2451

2.4. Mapping Quality

Mean Mapping Quality	36.95

2.5. Mismatches and indels

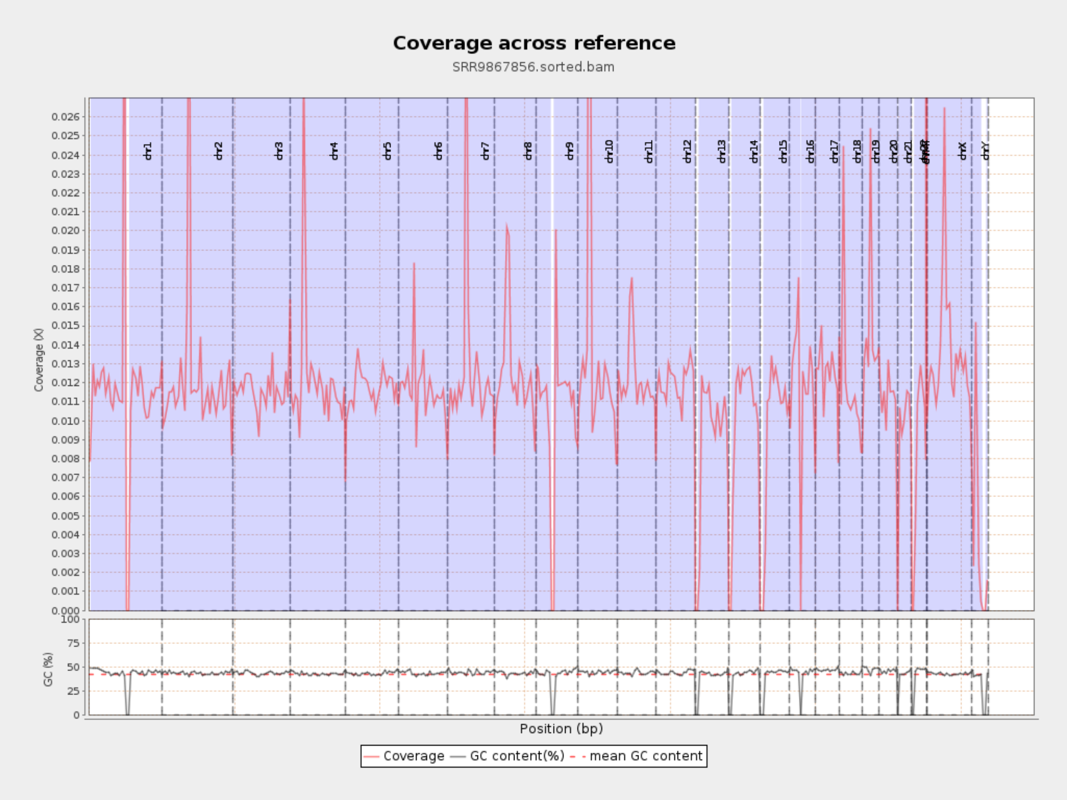
General error rate	0.6%
Mismatches	208,011
Insertions	3,103
Mapped reads with at least one insertion	0.5%
Deletions	6,153
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.7%

2.6. Chromosome stats

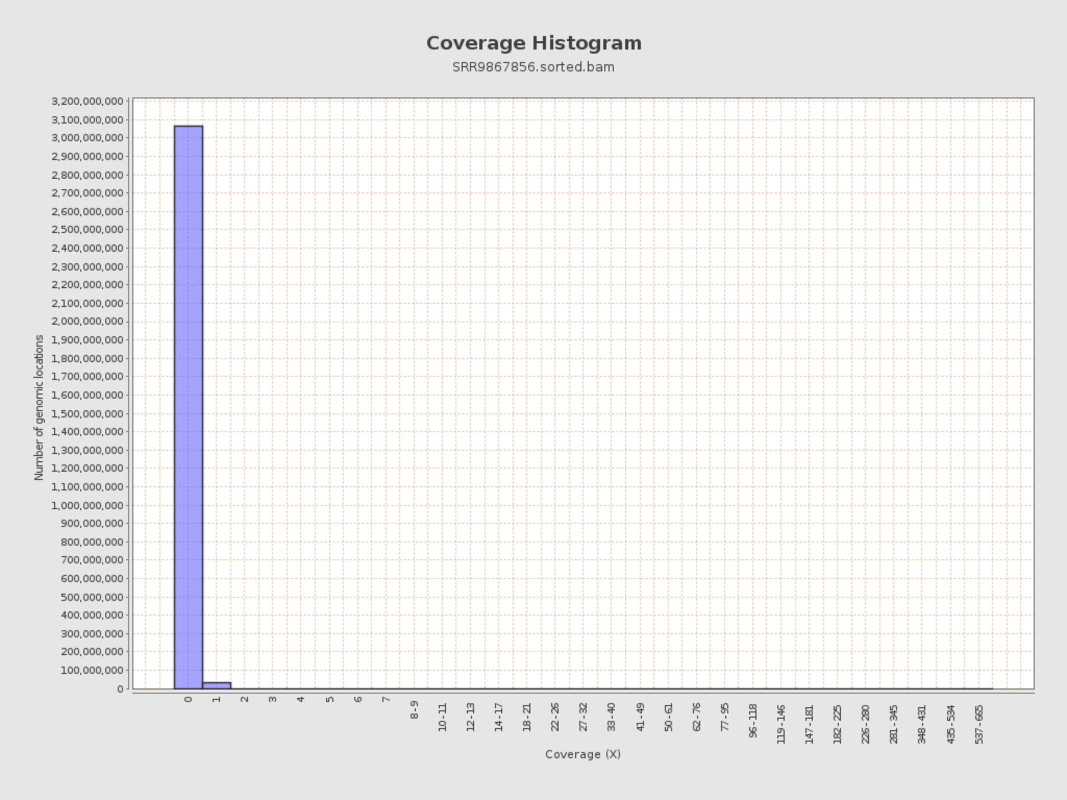
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2907151	0.0117	0.549
chr2	243199373	3006790	0.0124	0.2538
chr3	198022430	2291222	0.0116	0.1189
chr4	191154276	2323214	0.0122	0.1408
chr5	180915260	2131242	0.0118	0.118
chr6	171115067	2002547	0.0117	0.1358
chr7	159138663	2062473	0.013	0.3112

chr8	146364022	1823392	0.0125	0.2389
chr9	141213431	1497419	0.0106	0.1955
chr10	135534747	1857603	0.0137	0.2746
chr11	135006516	1643443	0.0122	0.1822
chr12	133851895	1607423	0.012	0.1198
chr13	115169878	1020587	0.0089	0.0985
chr14	107349540	1061945	0.0099	0.1286
chr15	102531392	955859	0.0093	0.1107
chr16	90354753	1063564	0.0118	0.1443
chr17	81195210	1005335	0.0124	0.1306
chr18	78077248	954993	0.0122	0.4016
chr19	59128983	874549	0.0148	0.404
chr20	63025520	700441	0.0111	0.1146
chr21	48129895	452729	0.0094	0.1291
chr22	51304566	407535	0.0079	0.0925
chrMT	16571	7189	0.4338	0.6978
chrX	155270560	2116555	0.0136	0.1505
chrY	59373566	199696	0.0034	0.1748

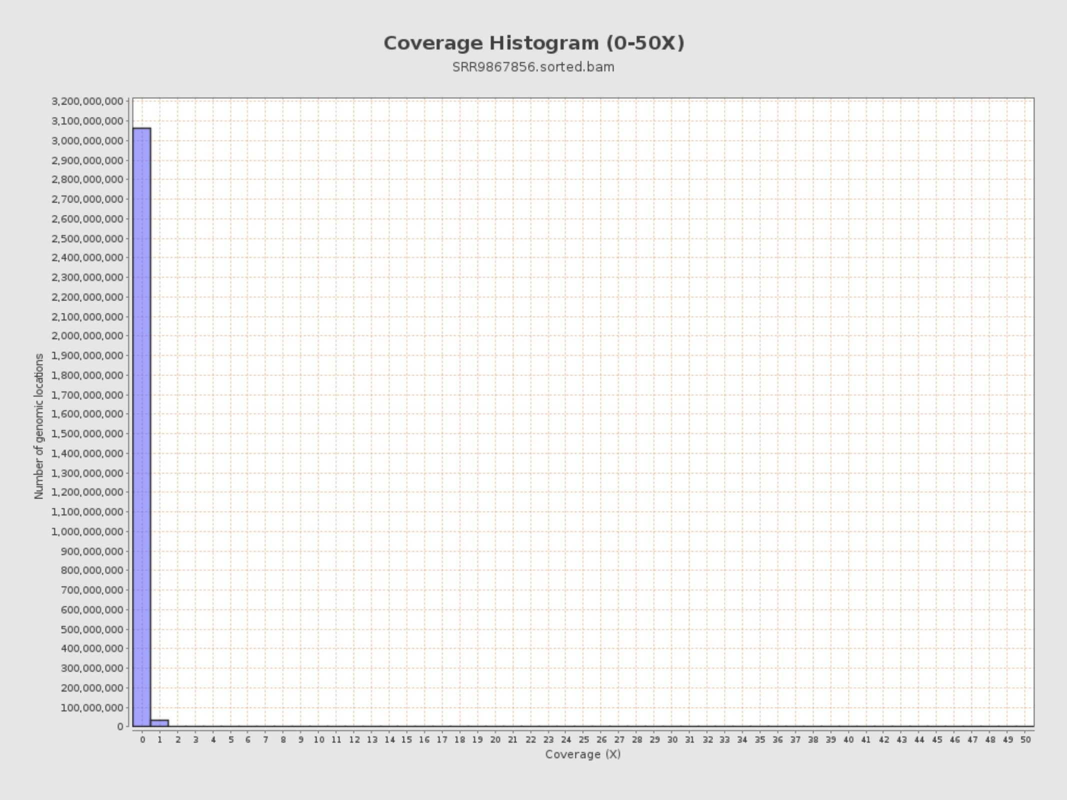
3. Results : Coverage across reference



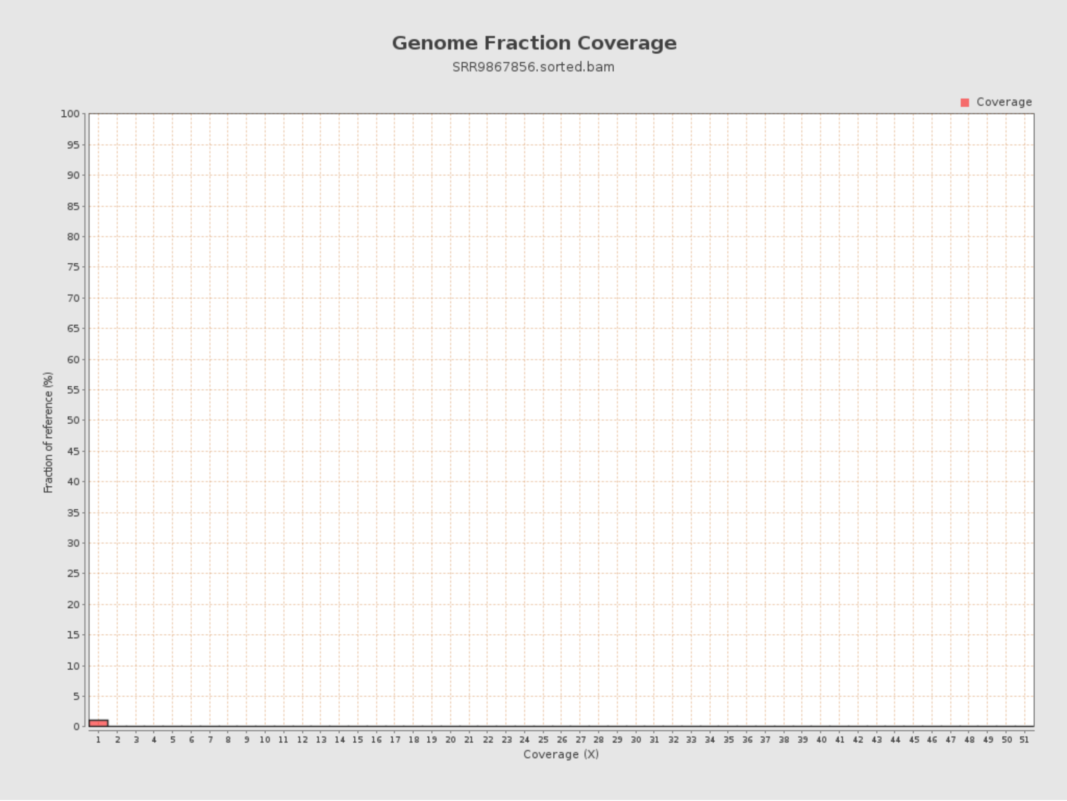
4. Results : Coverage Histogram



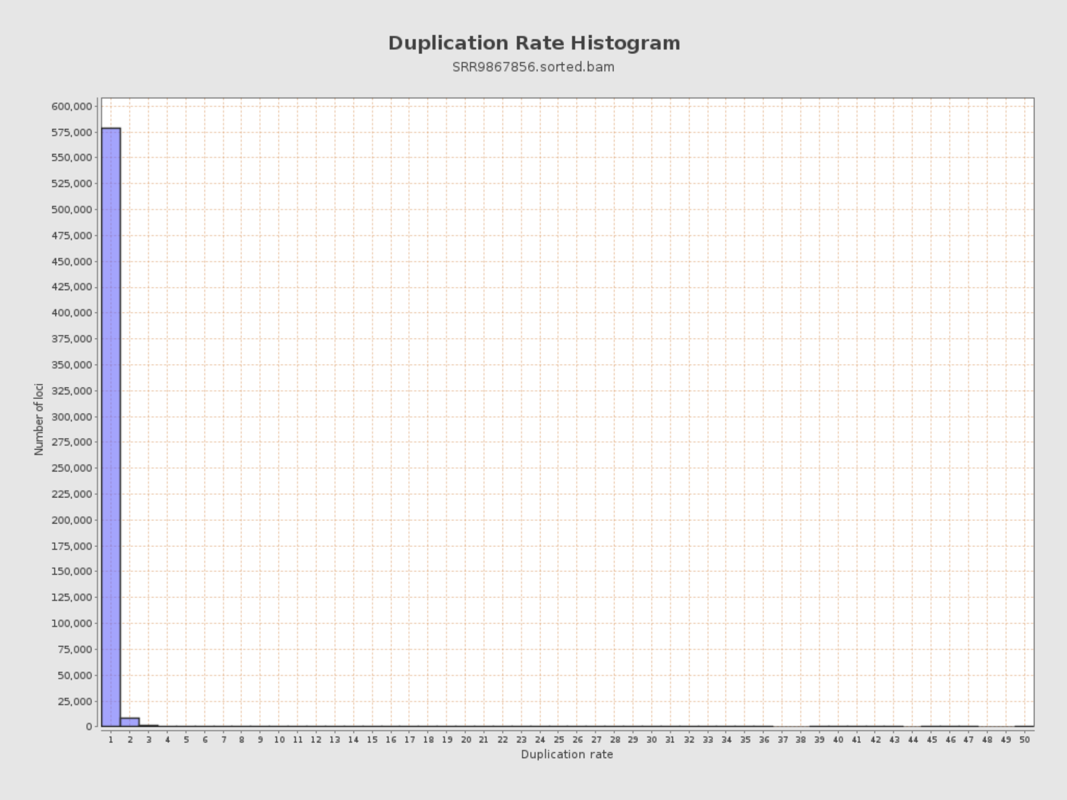
5. Results : Coverage Histogram (0-50X)



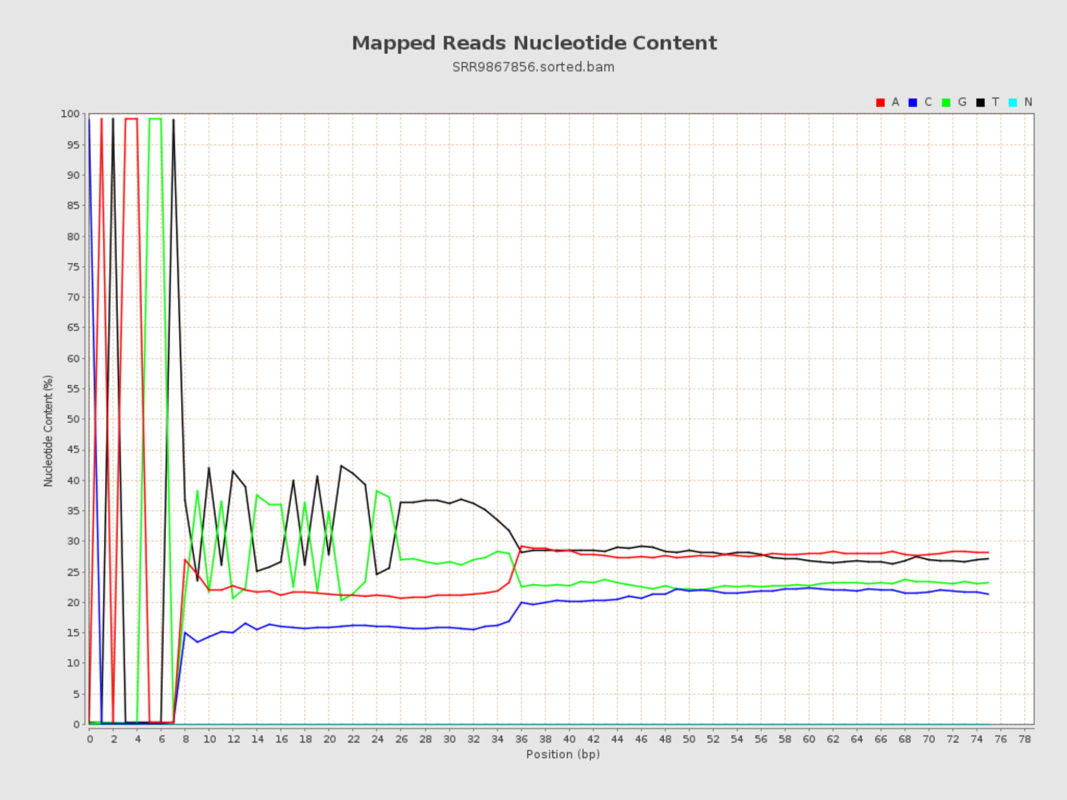
6. Results : Genome Fraction Coverage



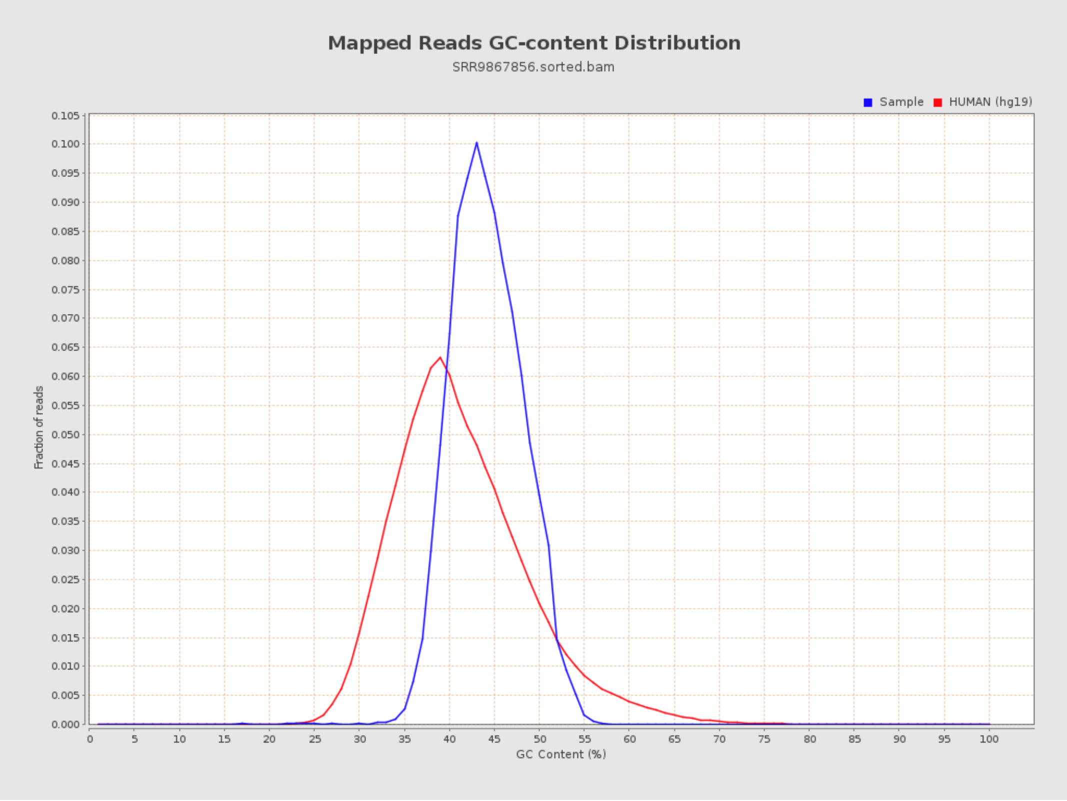
7. Results : Duplication Rate Histogram



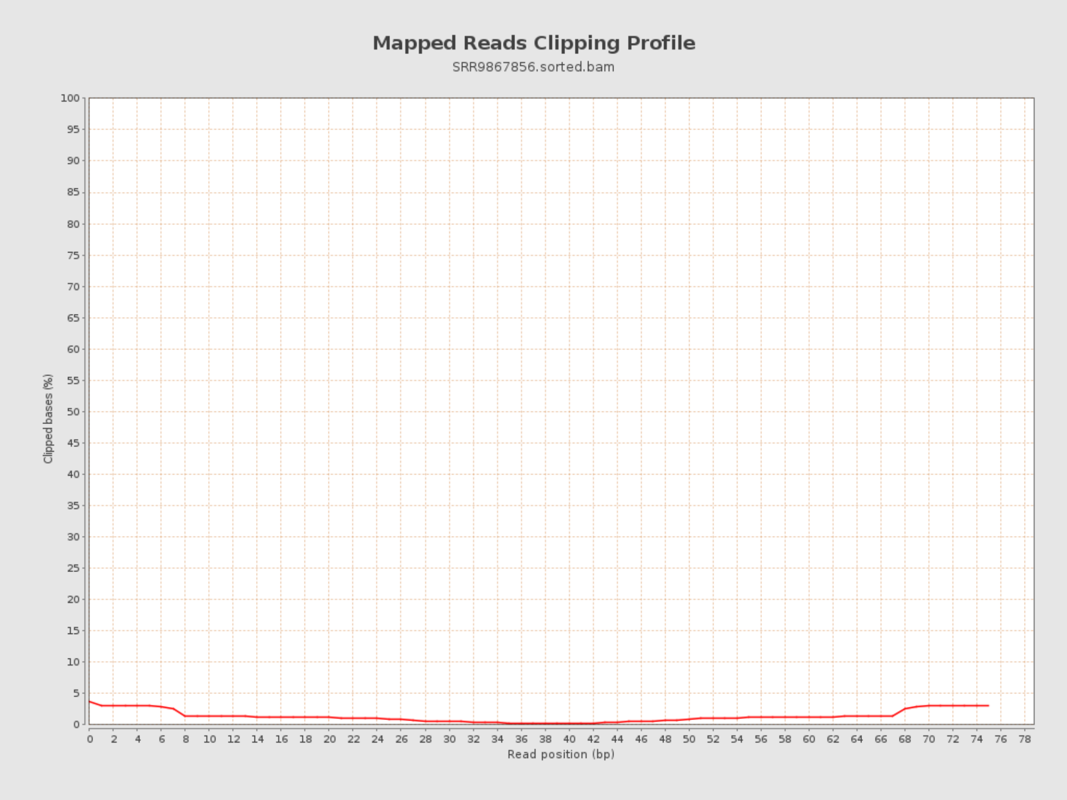
8. Results : Mapped Reads Nucleotide Content



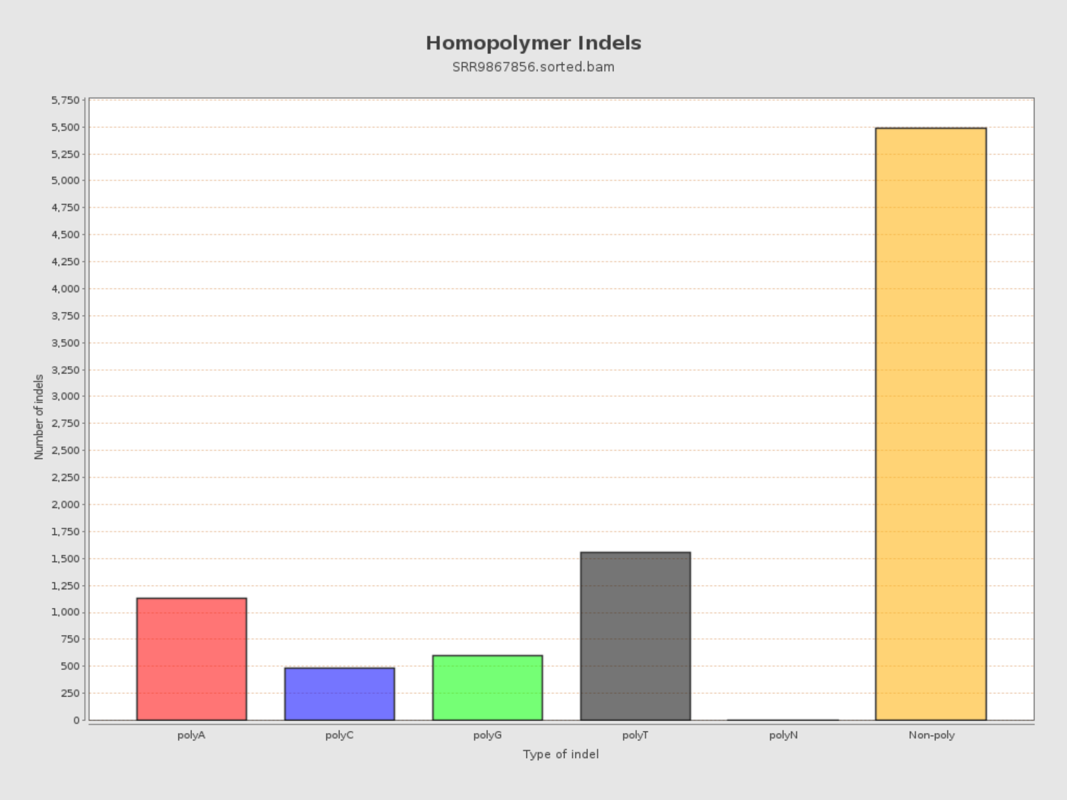
9. Results : Mapped Reads GC-content Distribution



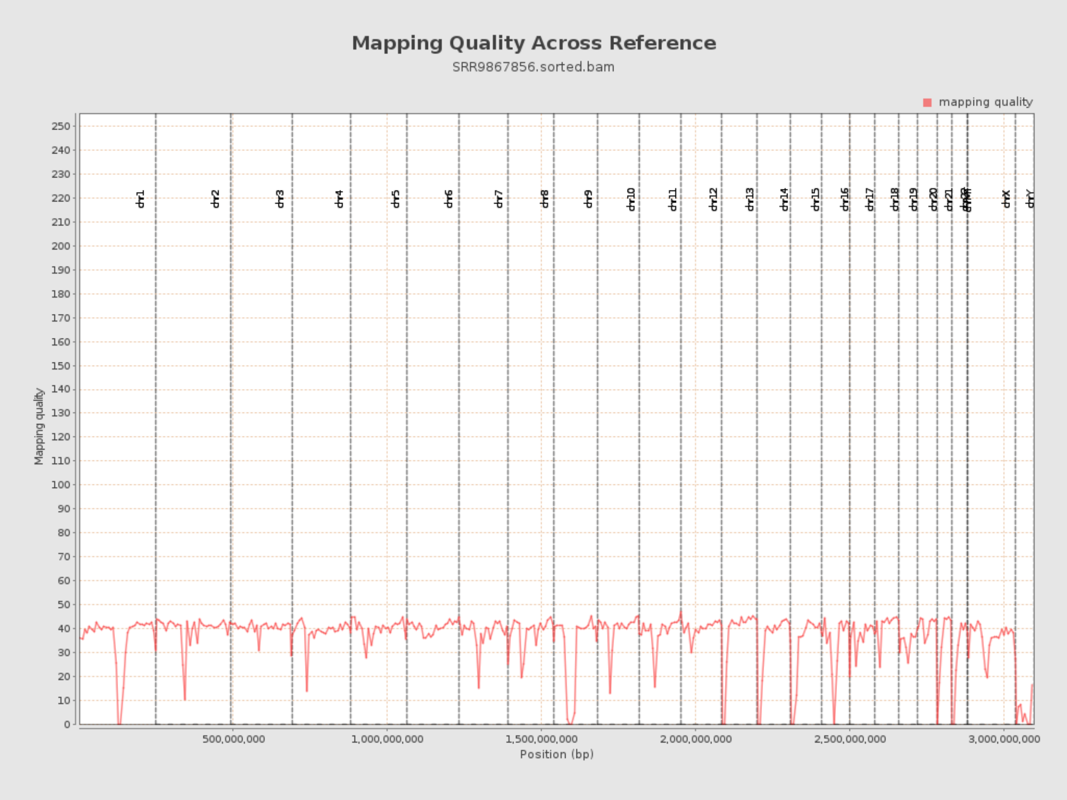
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram