Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:14:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867859.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_SRR9867859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:14:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,329,614
Mapped reads	2,153,338 / 92.43%
Unmapped reads	176,276 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,991 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	99,023 / 4.25%
Duplication rate	3.35%
Clipped reads	2,161,982 / 92.8%

2.2. ACGT Content

Number/percentage of A's	32,860,874 / 25.51%
Number/percentage of C's	25,535,464 / 19.82%
Number/percentage of T's	39,719,966 / 30.83%
Number/percentage of G's	30,694,641 / 23.83%
Number/percentage of N's	16,659 / 0.01%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0416

Standard Deviation	0.38

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

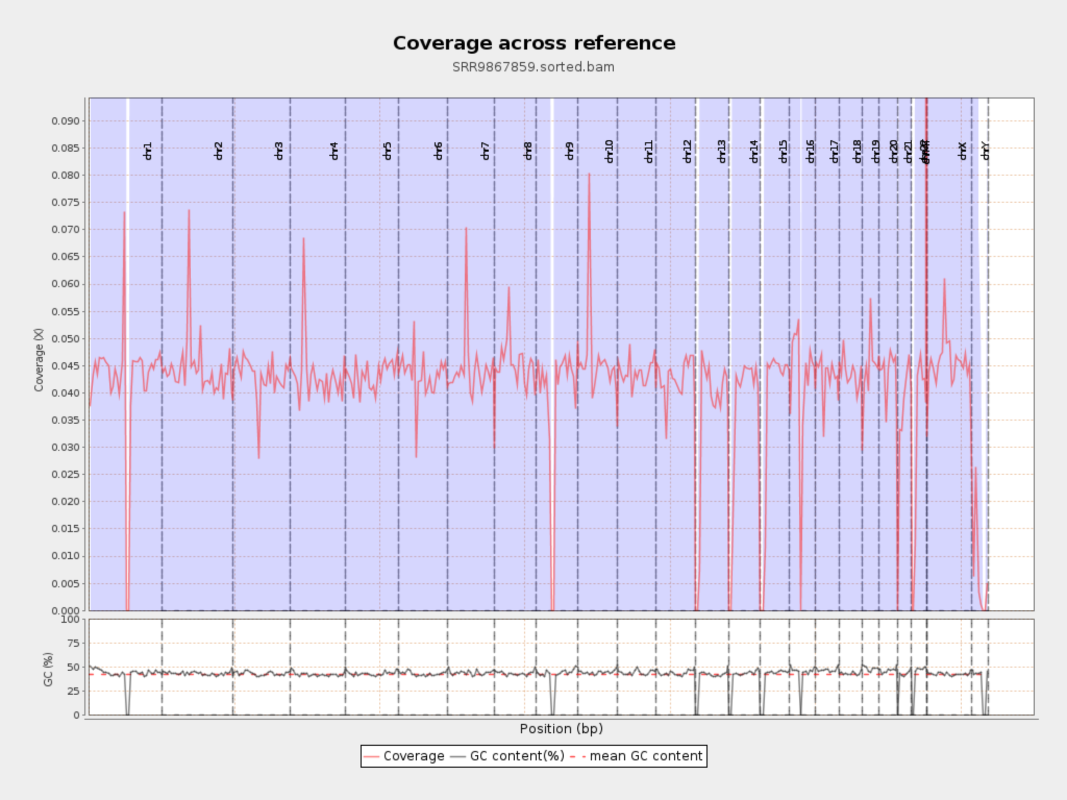
General error rate	0.5%
Mismatches	634,561
Insertions	7,596
Mapped reads with at least one insertion	0.35%
Deletions	23,470
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.16%

2.6. Chromosome stats

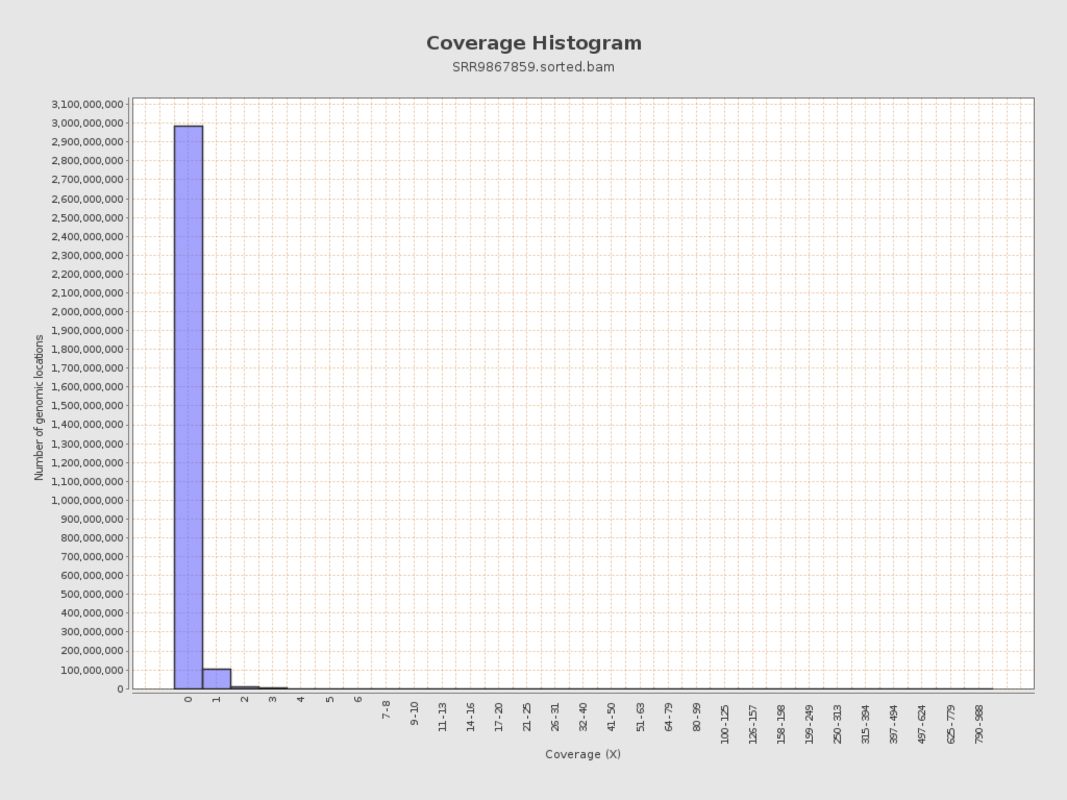
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10515134	0.0422	0.7276
chr2	243199373	10867390	0.0447	0.5073
chr3	198022430	8505347	0.043	0.2291
chr4	191154276	8249559	0.0432	0.2657
chr5	180915260	7829404	0.0433	0.2323
chr6	171115067	7397442	0.0432	0.2706
chr7	159138663	7093140	0.0446	0.4588

chr8	146364022	6648685	0.0454	0.4054
chr9	141213431	5403320	0.0383	0.3134
chr10	135534747	6272225	0.0463	0.3775
chr11	135006516	5888784	0.0436	0.3225
chr12	133851895	5730509	0.0428	0.2342
chr13	115169878	4022990	0.0349	0.2065
chr14	107349540	3833299	0.0357	0.2199
chr15	102531392	3699662	0.0361	0.2095
chr16	90354753	3781034	0.0418	0.2485
chr17	81195210	3482436	0.0429	0.2513
chr18	78077248	3411754	0.0437	0.5972
chr19	59128983	2663359	0.045	0.5377
chr20	63025520	2760772	0.0438	0.2419
chr21	48129895	1719989	0.0357	0.247
chr22	51304566	1532153	0.0299	0.1914
chrMT	16571	63803	3.8503	2.8969
chrX	155270560	7081017	0.0456	0.2625
chrY	59373566	412509	0.0069	0.2678

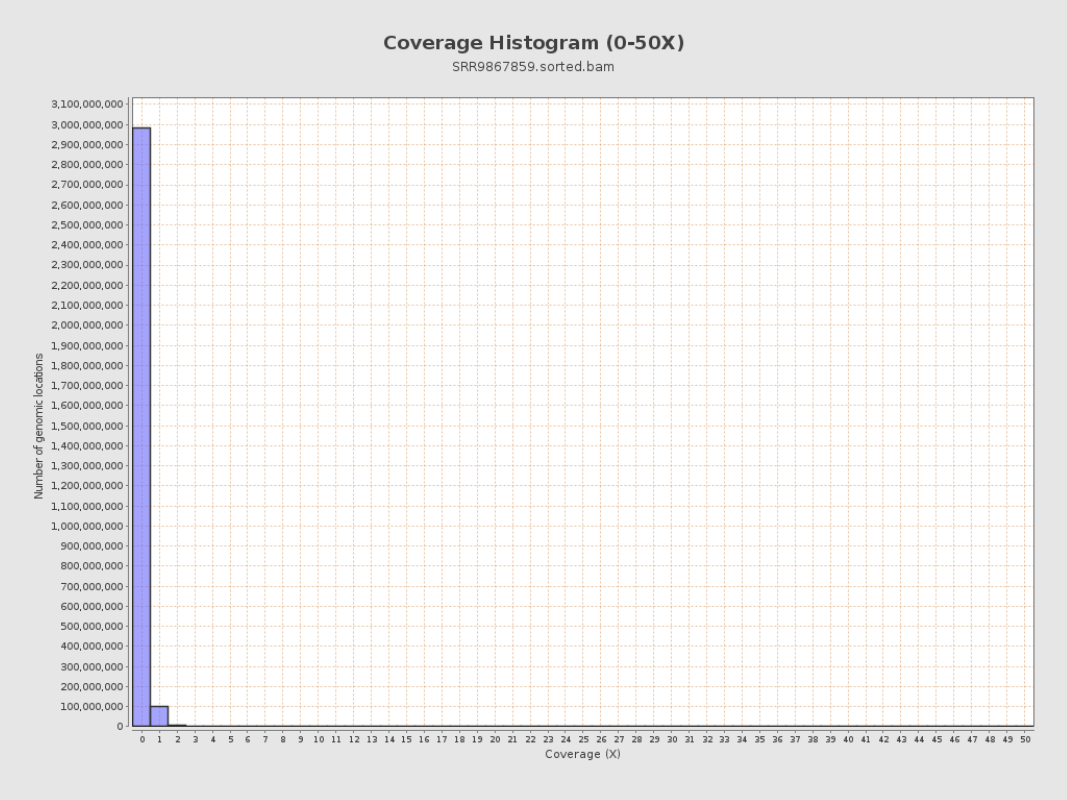
3. Results : Coverage across reference



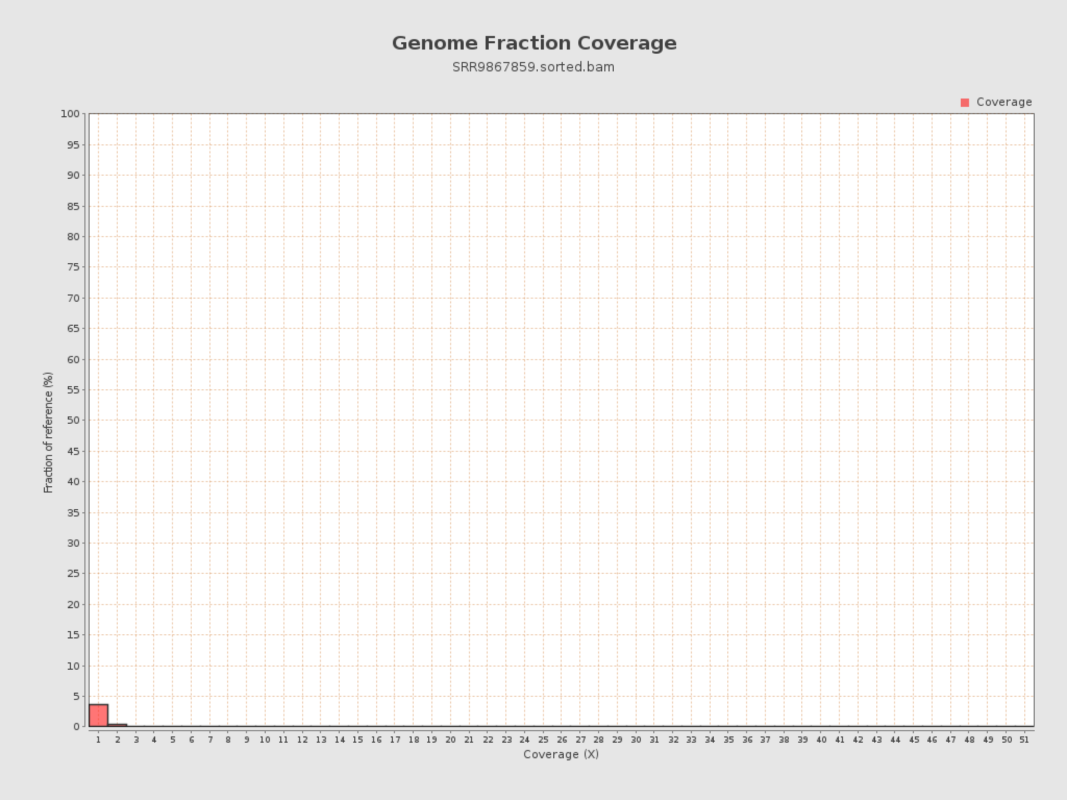
4. Results : Coverage Histogram



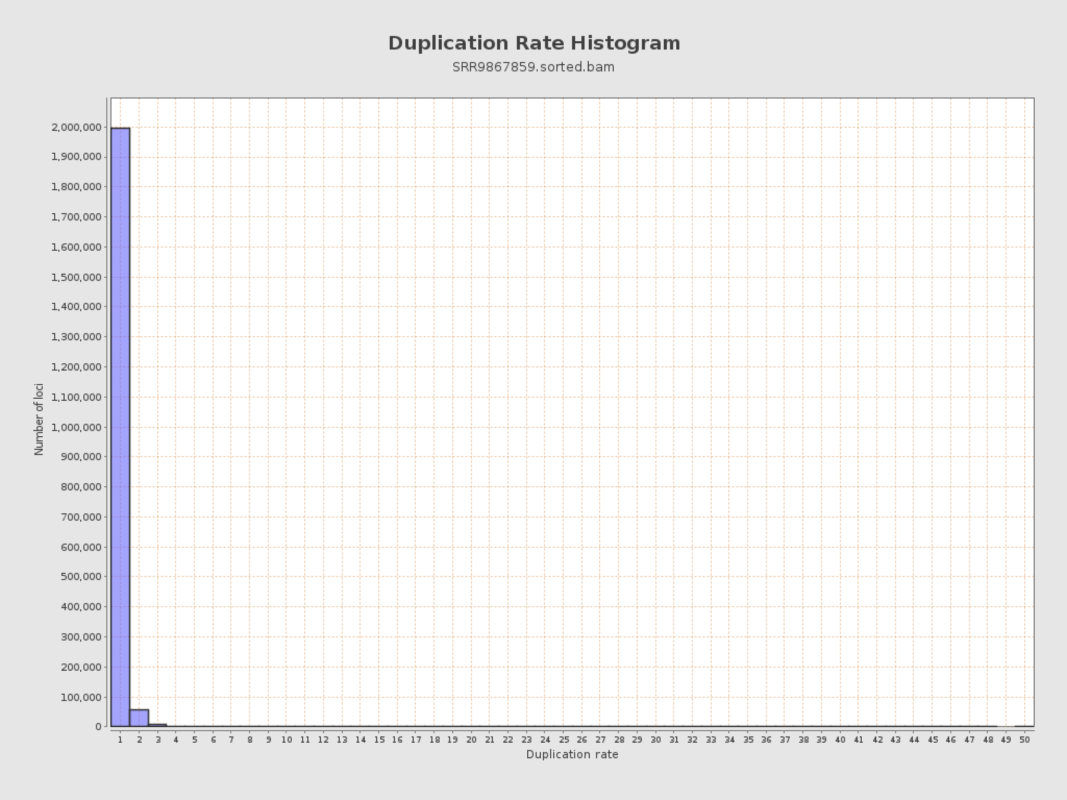
5. Results : Coverage Histogram (0-50X)



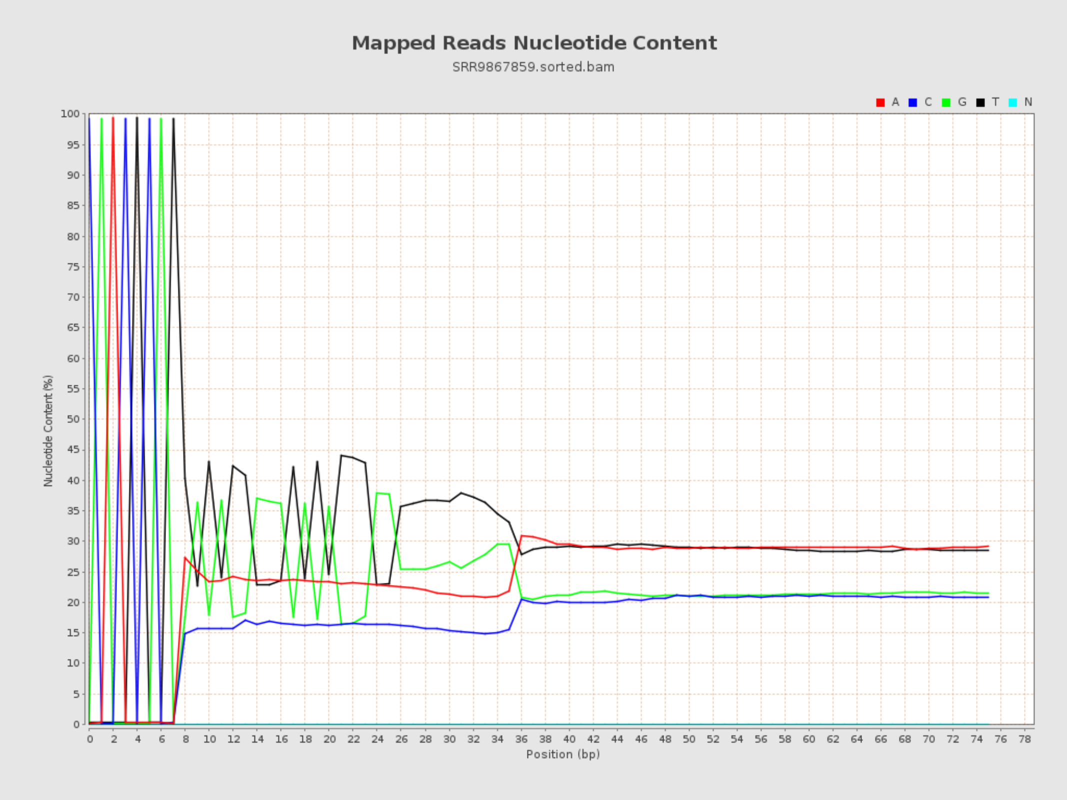
6. Results : Genome Fraction Coverage



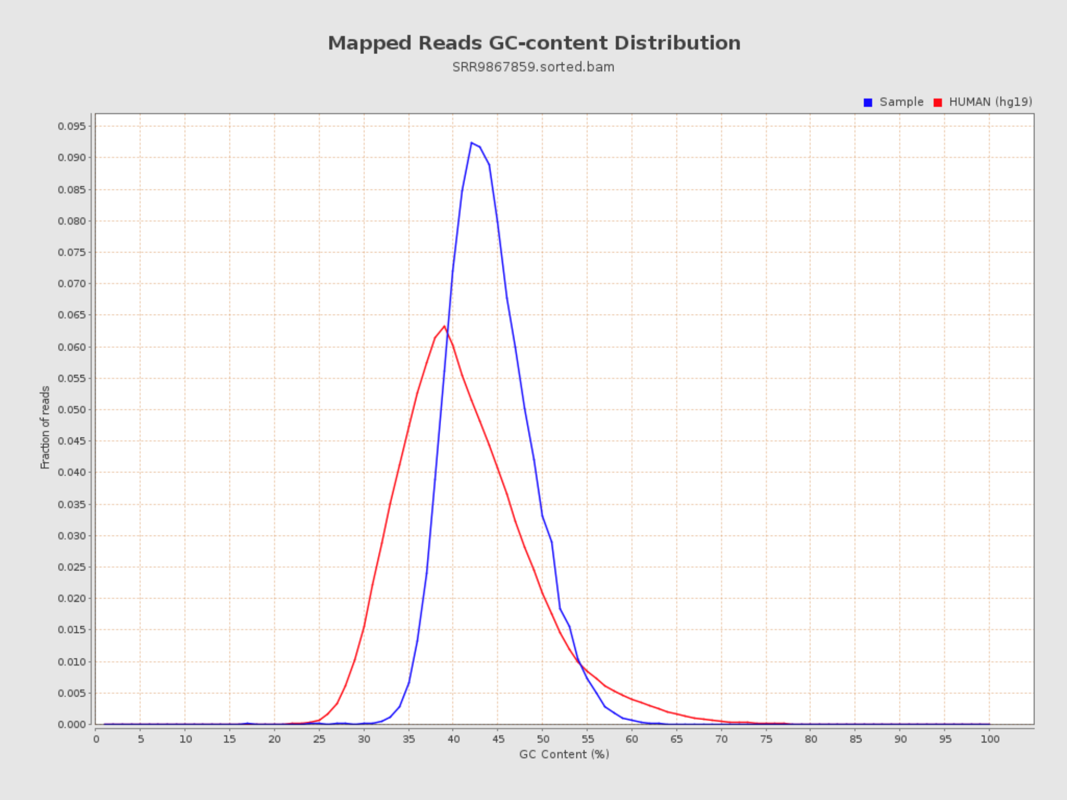
7. Results : Duplication Rate Histogram



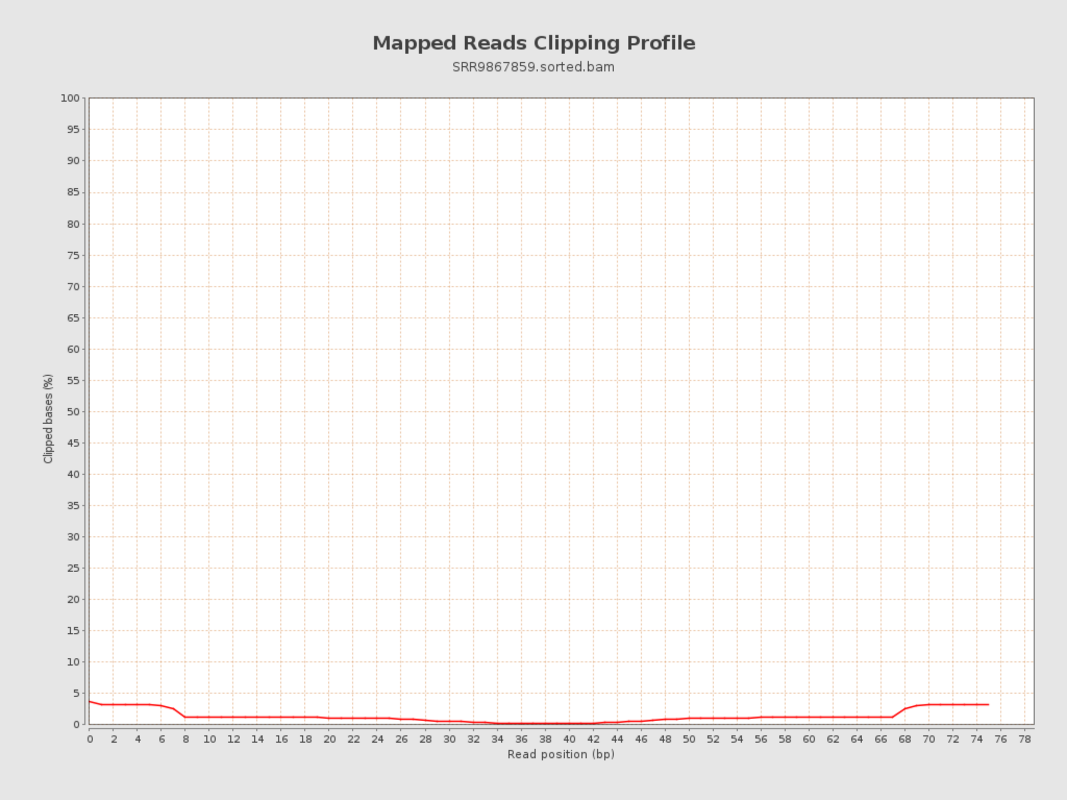
8. Results : Mapped Reads Nucleotide Content



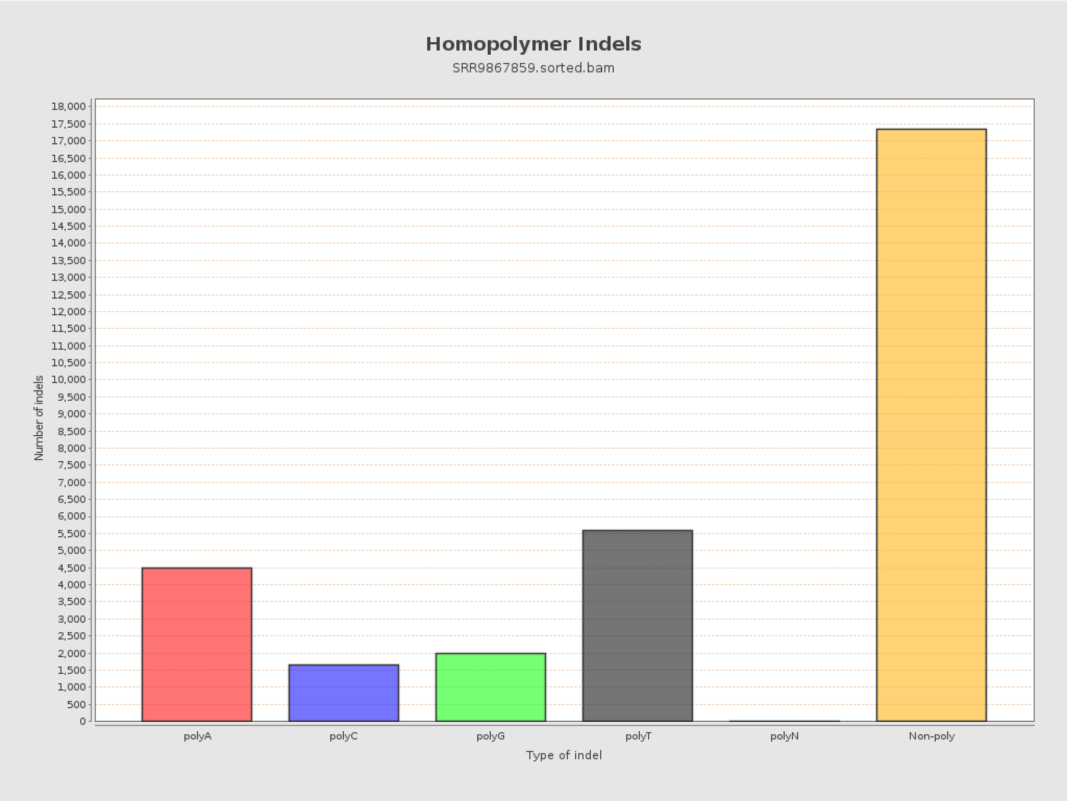
9. Results : Mapped Reads GC-content Distribution



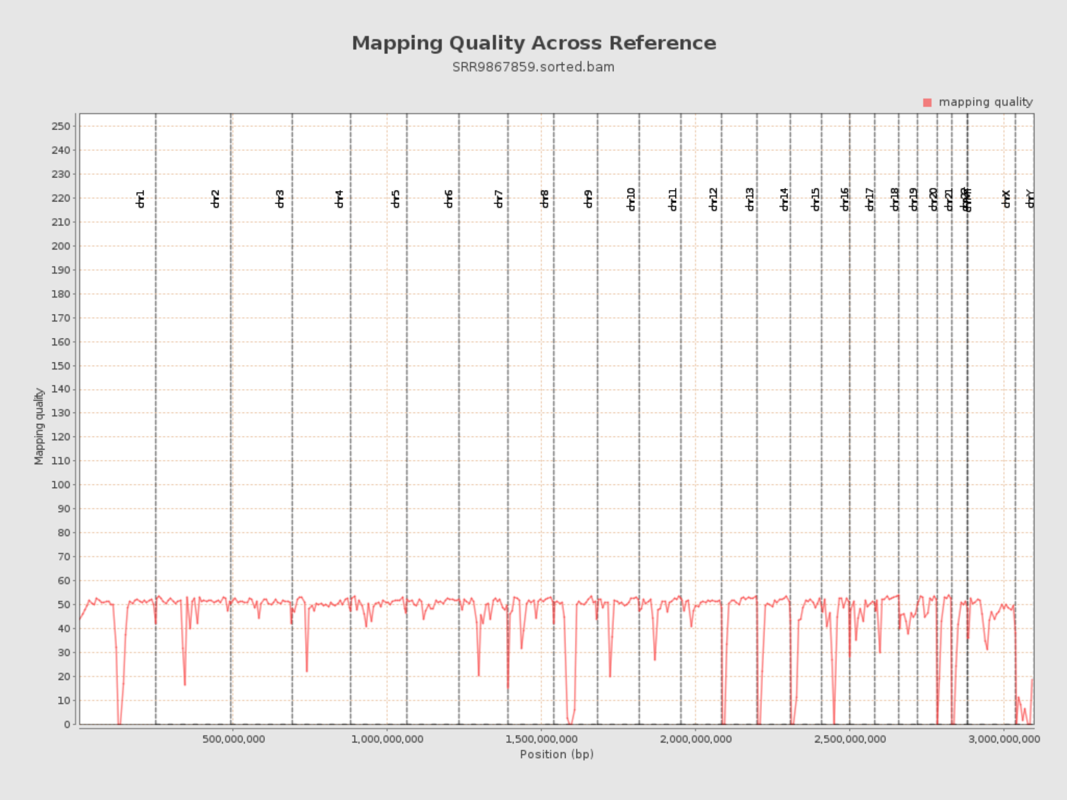
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram