Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:05:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867865.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_SRR9867865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:05:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,861,673
Mapped reads	1,714,045 / 92.07%
Unmapped reads	147,628 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,836 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	71,683 / 3.85%
Duplication rate	3.07%
Clipped reads	1,717,632 / 92.26%

2.2. ACGT Content

Number/percentage of A's	26,266,369 / 25.94%
Number/percentage of C's	19,000,279 / 18.77%
Number/percentage of T's	32,463,503 / 32.06%
Number/percentage of G's	23,502,439 / 23.21%
Number/percentage of N's	15,082 / 0.01%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.3098

2.4. Mapping Quality

Mean Mapping Quality	45.9

2.5. Mismatches and indels

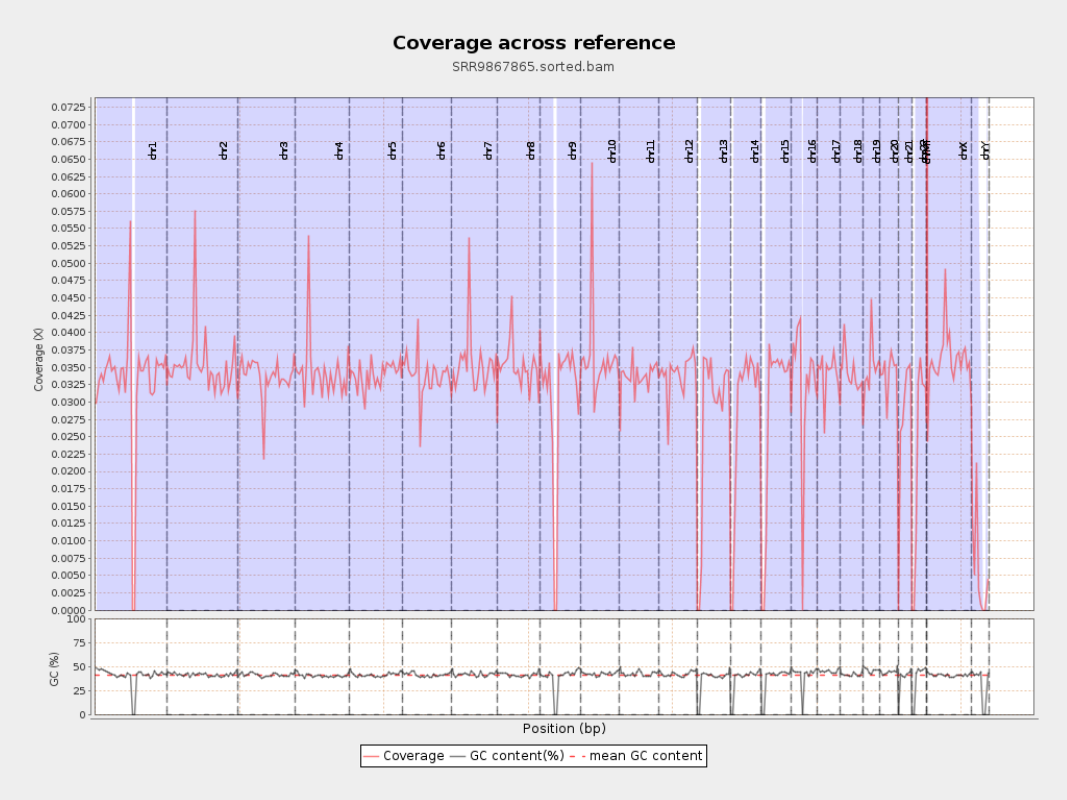
General error rate	0.51%
Mismatches	507,389
Insertions	6,770
Mapped reads with at least one insertion	0.39%
Deletions	18,974
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.5%

2.6. Chromosome stats

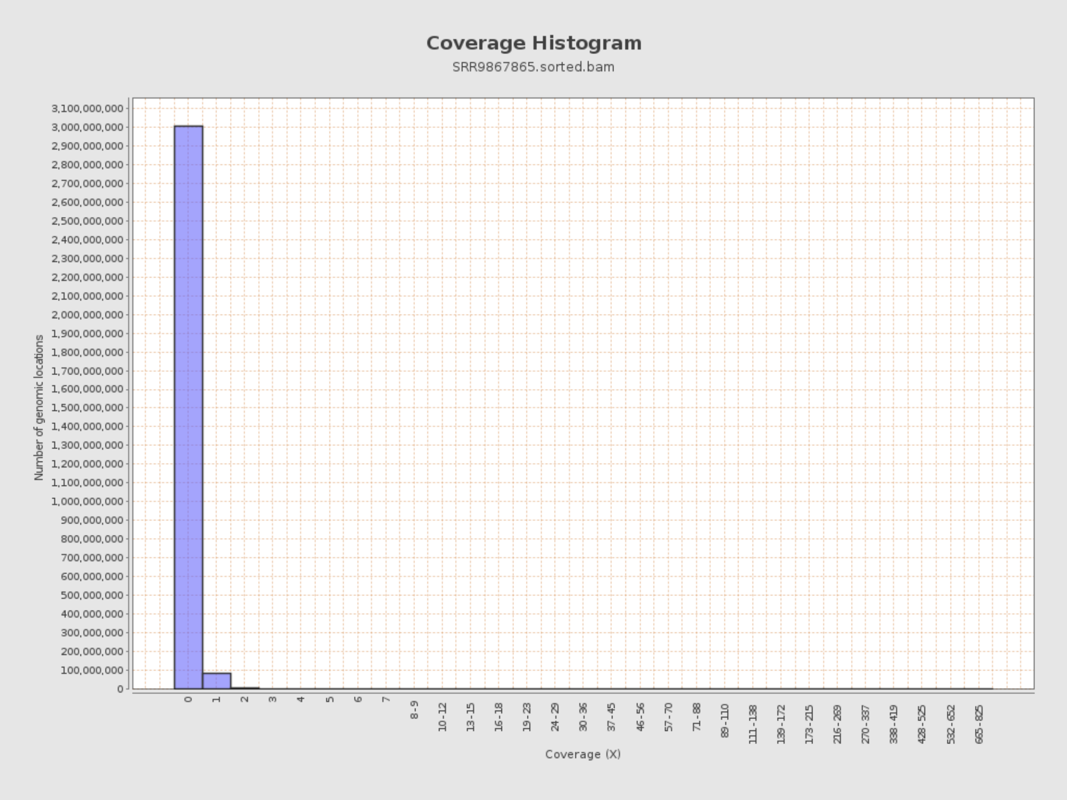
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8148033	0.0327	0.5755
chr2	243199373	8593414	0.0353	0.4228
chr3	198022430	6658079	0.0336	0.1991
chr4	191154276	6576722	0.0344	0.2312
chr5	180915260	6159945	0.034	0.2024
chr6	171115067	5789983	0.0338	0.2269
chr7	159138663	5663464	0.0356	0.3616

chr8	146364022	5149699	0.0352	0.3243
chr9	141213431	4279222	0.0303	0.2557
chr10	135534747	4936201	0.0364	0.3101
chr11	135006516	4561762	0.0338	0.2615
chr12	133851895	4547924	0.034	0.203
chr13	115169878	3175964	0.0276	0.1826
chr14	107349540	3028721	0.0282	0.19
chr15	102531392	2942466	0.0287	0.1848
chr16	90354753	2892938	0.032	0.2159
chr17	81195210	2758730	0.034	0.2143
chr18	78077248	2675429	0.0343	0.4578
chr19	59128983	2079350	0.0352	0.4279
chr20	63025520	2138566	0.0339	0.203
chr21	48129895	1346722	0.028	0.2123
chr22	51304566	1177643	0.023	0.1648
chrMT	16571	34825	2.1016	1.9047
chrX	155270560	5624637	0.0362	0.2298
chrY	59373566	337319	0.0057	0.2095

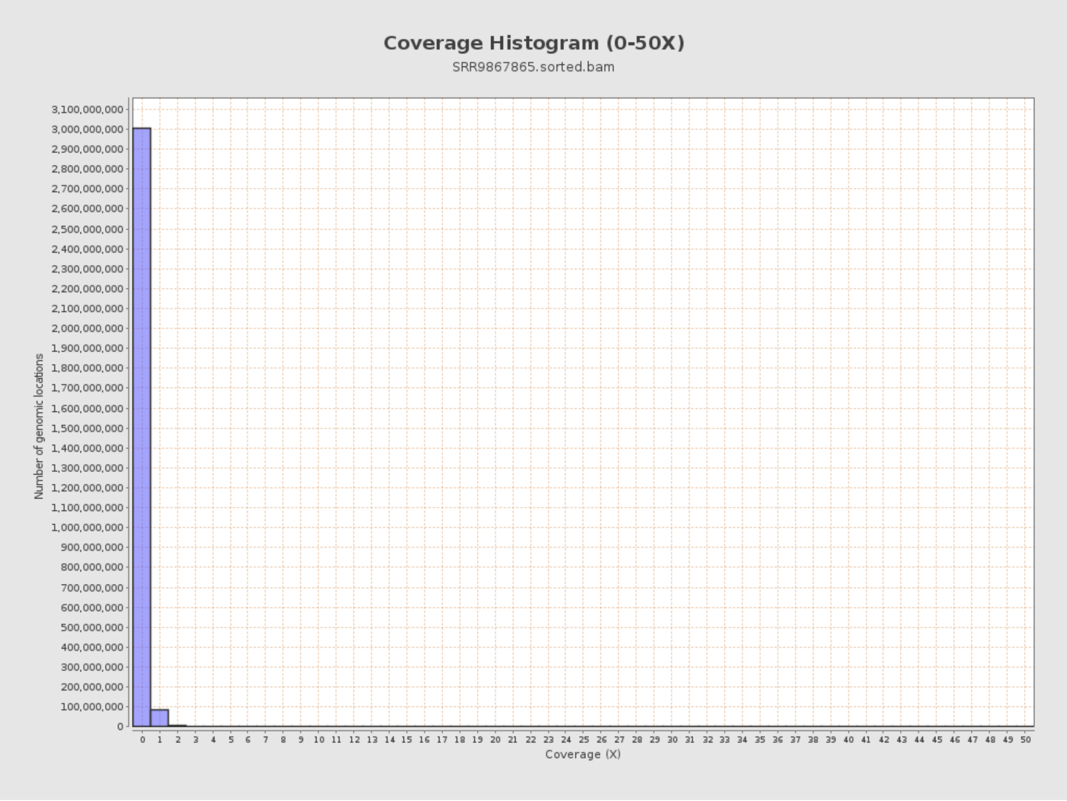
3. Results : Coverage across reference



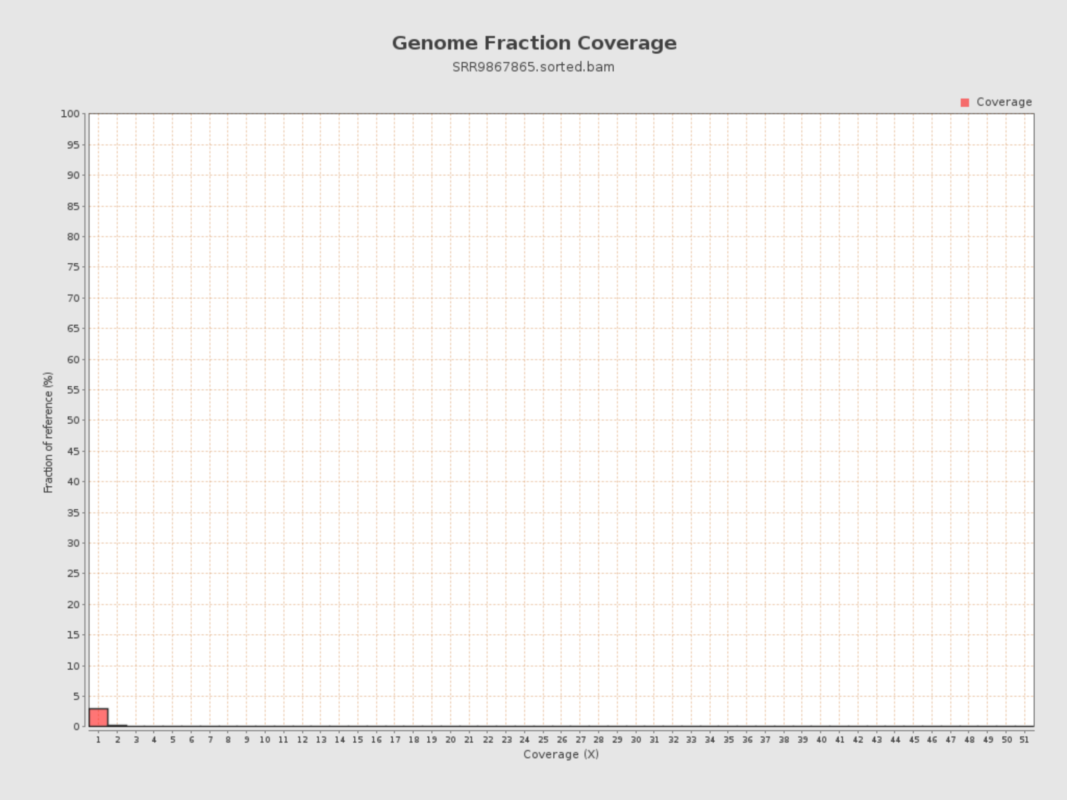
4. Results : Coverage Histogram



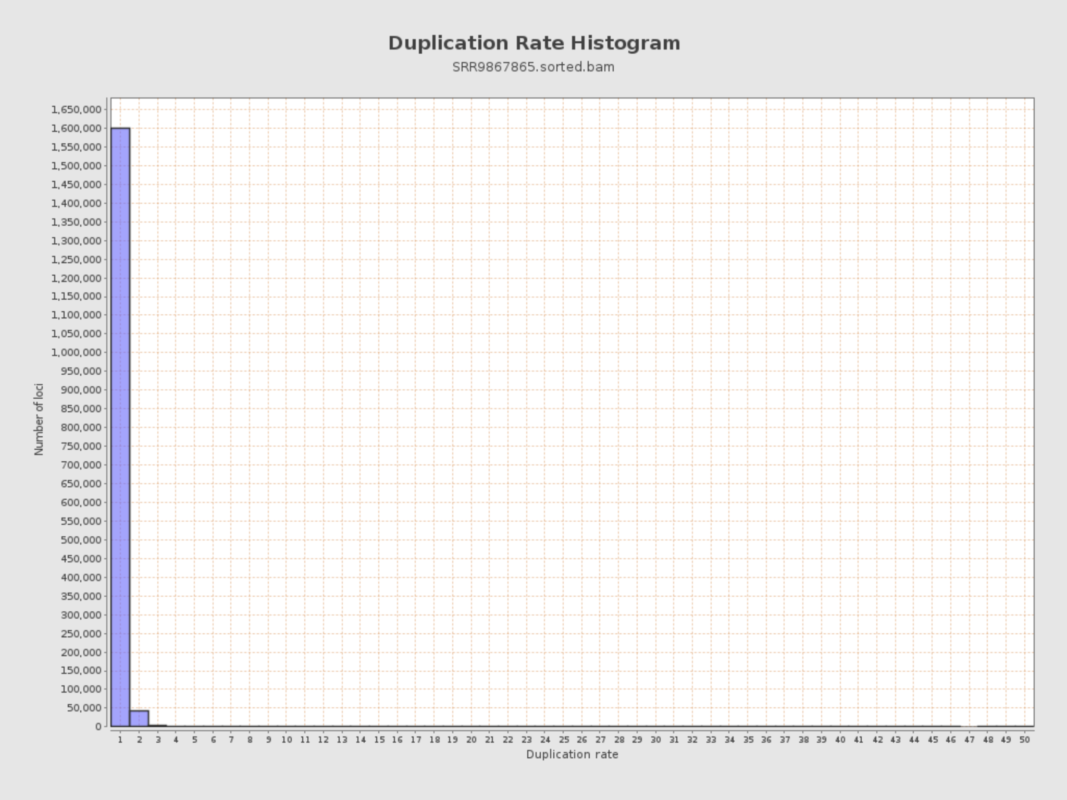
5. Results : Coverage Histogram (0-50X)



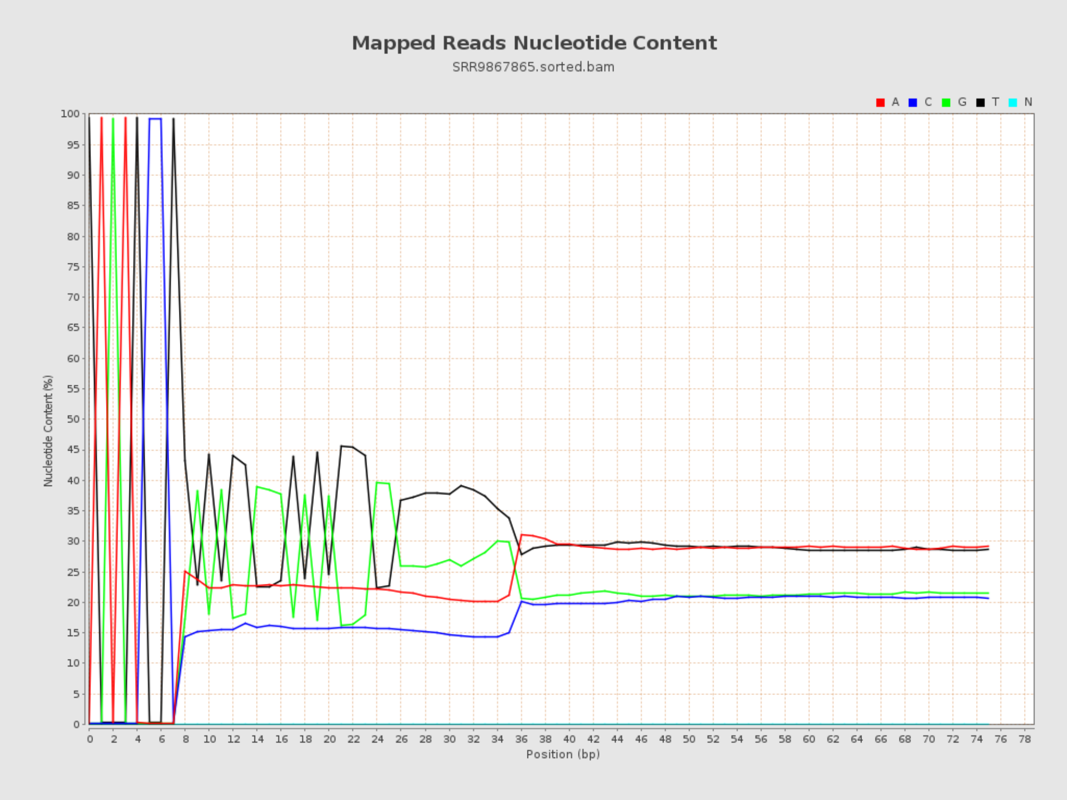
6. Results : Genome Fraction Coverage



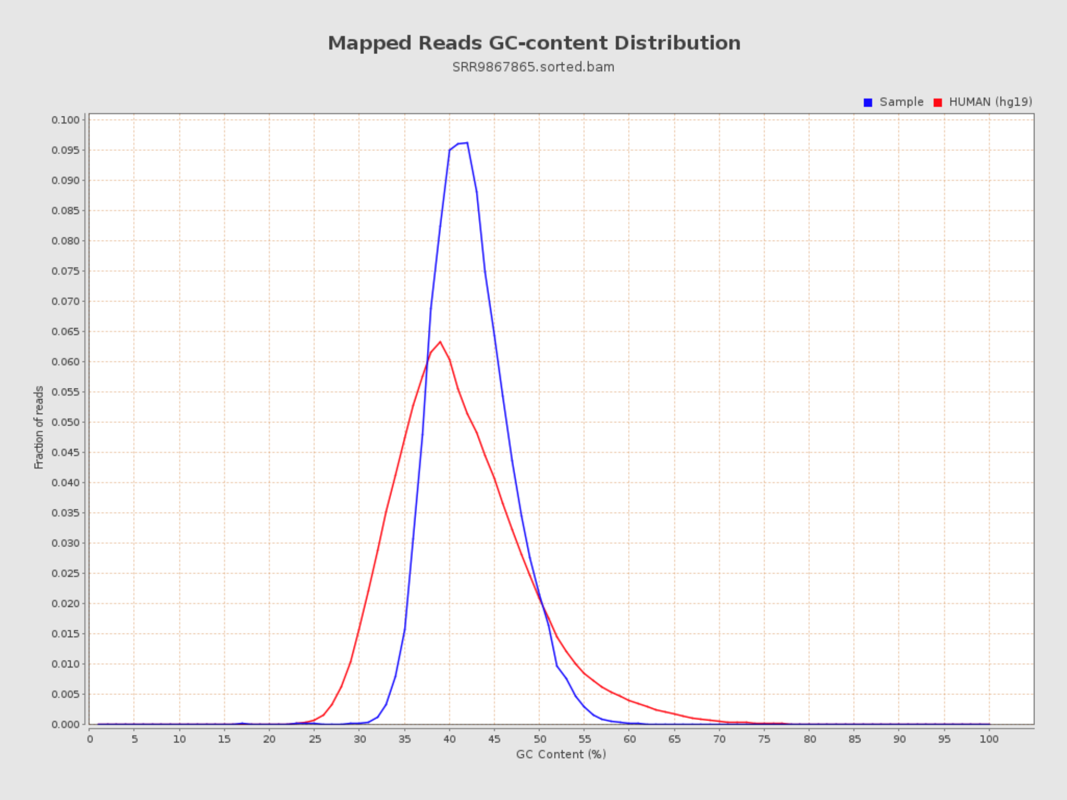
7. Results : Duplication Rate Histogram



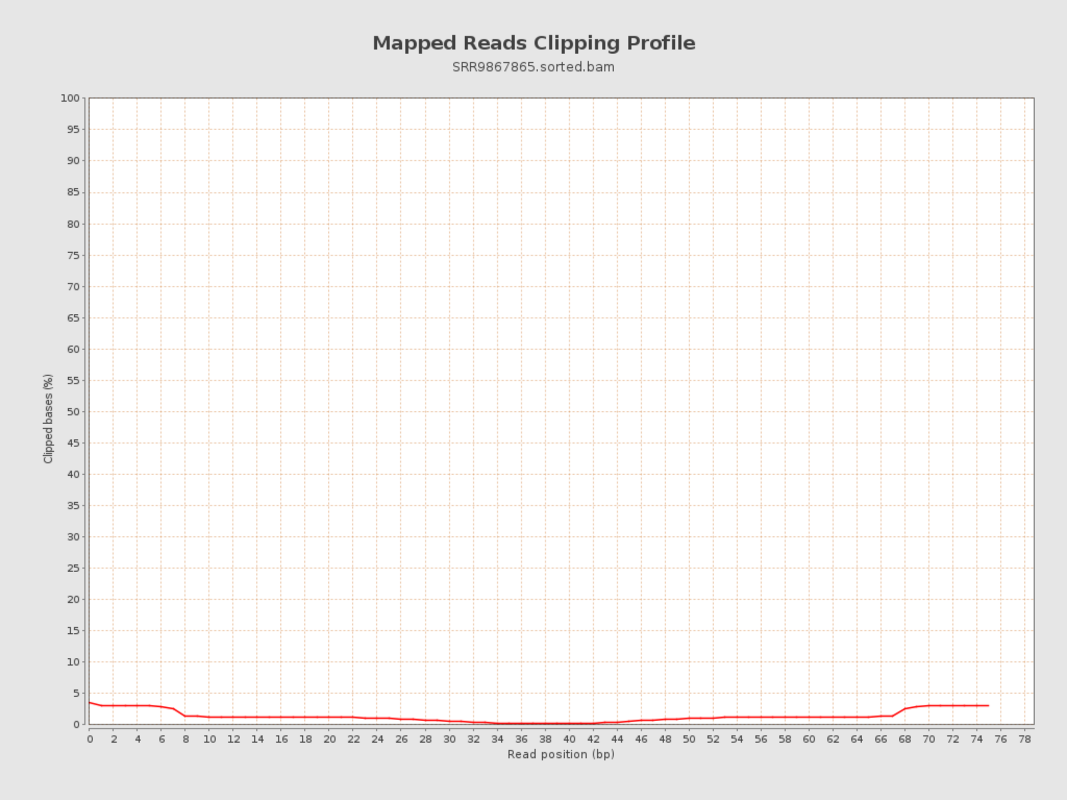
8. Results : Mapped Reads Nucleotide Content



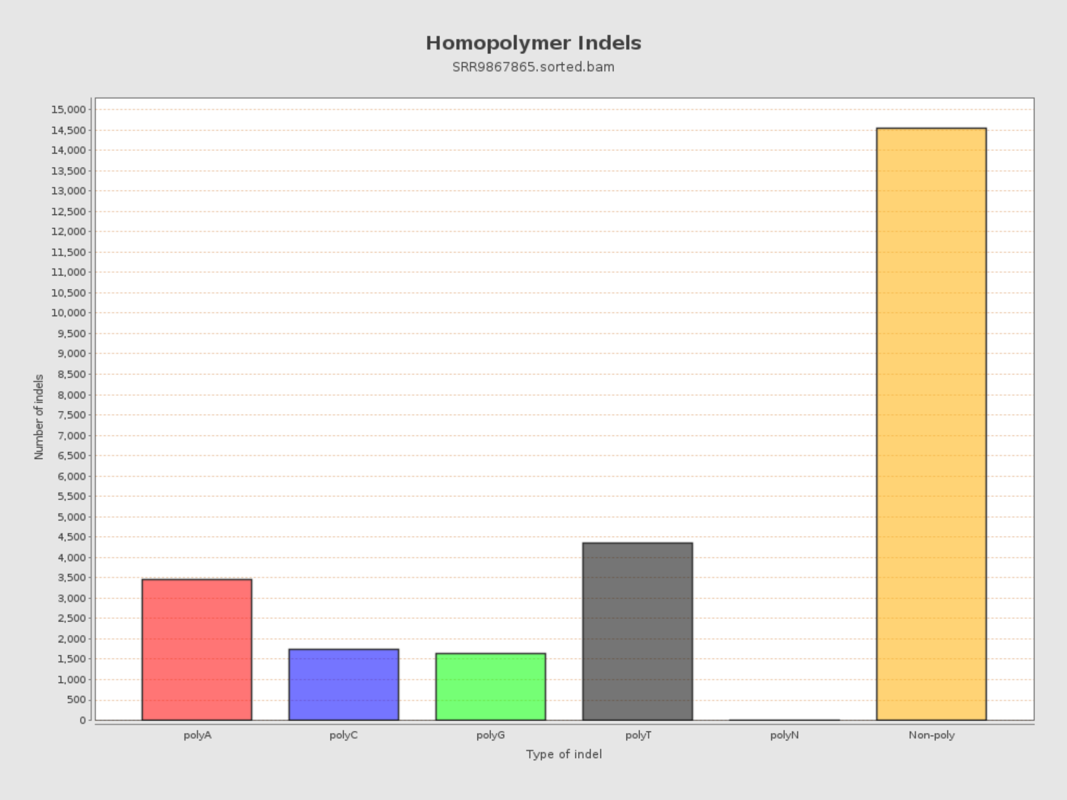
9. Results : Mapped Reads GC-content Distribution



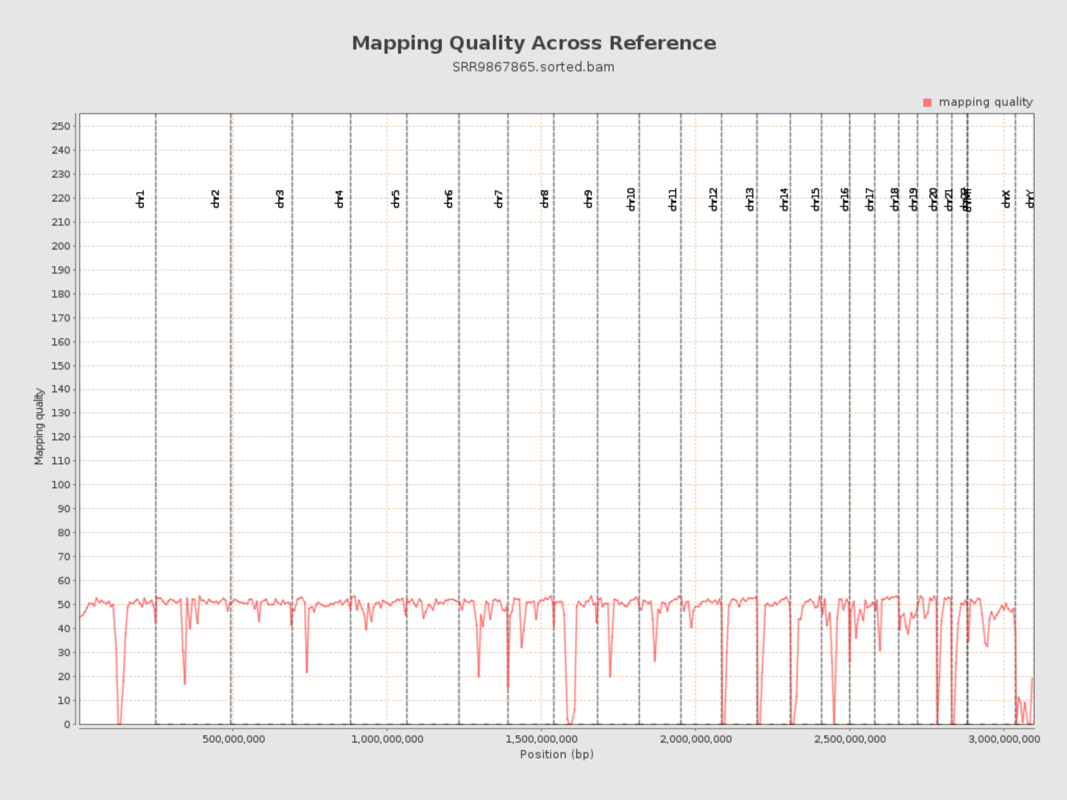
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram