Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 16:46:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867862.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_SRR9867862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 16:46:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,016,942
Mapped reads	21,626,266 / 98.23%
Unmapped reads	390,676 / 1.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	90,343 / 0.41%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	1,424,829 / 6.47%
Duplication rate	1.61%
Clipped reads	21,638,112 / 98.28%

2.2. ACGT Content

Number/percentage of A's	515,397,412 / 27.19%
Number/percentage of C's	421,759,195 / 22.25%
Number/percentage of T's	524,699,085 / 27.68%
Number/percentage of G's	433,168,211 / 22.85%
Number/percentage of N's	400,220 / 0.02%
GC Percentage	45.1%

2.3. Coverage

Mean	0.6125

Standard Deviation	8.6901

2.4. Mapping Quality

Mean Mapping Quality	49.84

2.5. Mismatches and indels

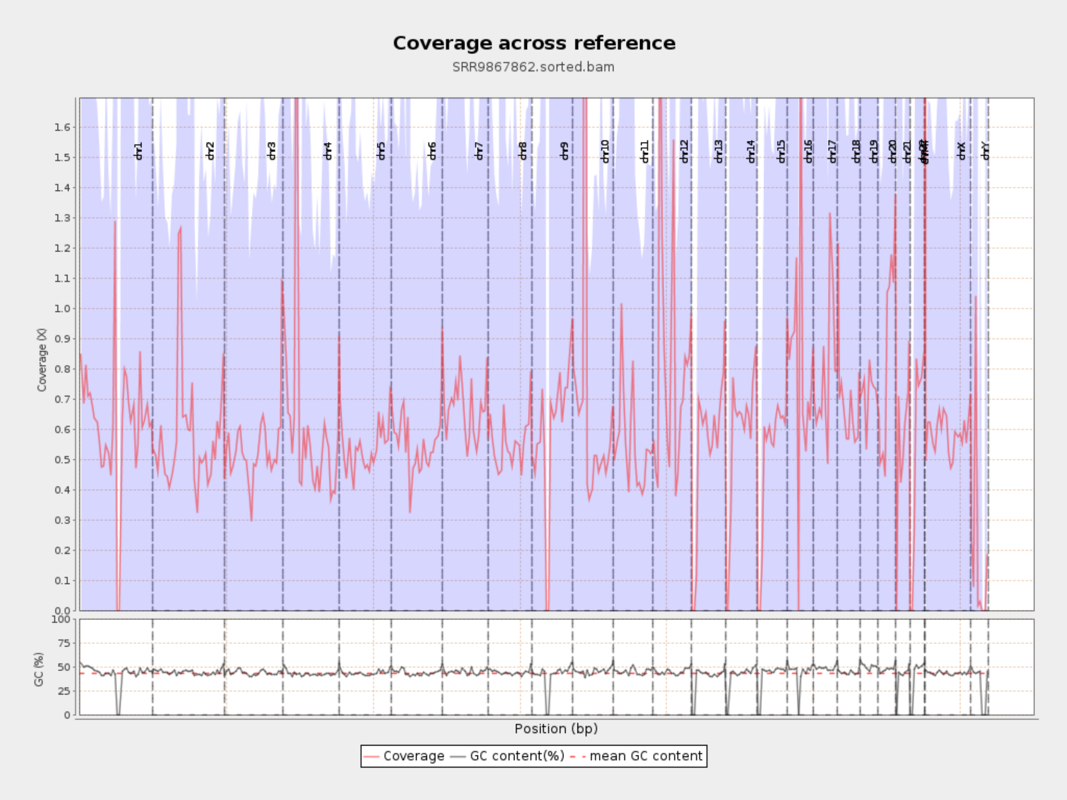
General error rate	0.54%
Mismatches	9,499,387
Insertions	213,732
Mapped reads with at least one insertion	0.96%
Deletions	199,237
Mapped reads with at least one deletion	0.89%
Homopolymer indels	33.19%

2.6. Chromosome stats

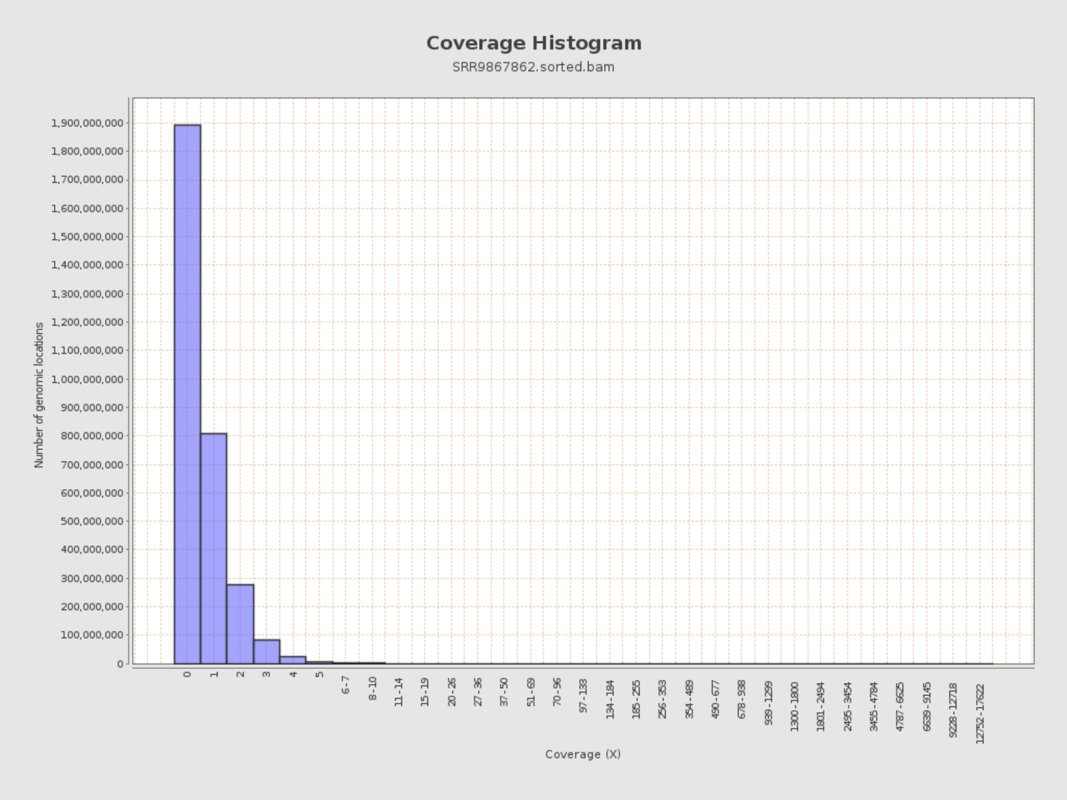
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	154855517	0.6213	15.3848
chr2	243199373	141055920	0.58	5.652
chr3	198022430	103748386	0.5239	5.3388
chr4	191154276	117148691	0.6128	8.6334
chr5	180915260	98569237	0.5448	0.9345
chr6	171115067	93557300	0.5468	1.8241
chr7	159138663	107285826	0.6742	4.1733

chr8	146364022	81335321	0.5557	2.3162
chr9	141213431	84284889	0.5969	3.3983
chr10	135534747	103093204	0.7606	28.528
chr11	135006516	76113492	0.5638	1.9698
chr12	133851895	111516117	0.8331	1.5191
chr13	115169878	61941614	0.5378	0.8703
chr14	107349540	61520039	0.5731	1.213
chr15	102531392	50526003	0.4928	0.821
chr16	90354753	76009221	0.8412	9.2709
chr17	81195210	63756953	0.7852	1.9965
chr18	78077248	52504937	0.6725	8.5714
chr19	59128983	42935031	0.7261	9.4747
chr20	63025520	53336897	0.8463	2.6271
chr21	48129895	27384005	0.569	6.3884
chr22	51304566	28457367	0.5547	1.0459
chrMT	16571	2554042	154.1272	71.6384
chrX	155270560	90801844	0.5848	1.5903
chrY	59373566	11681067	0.1967	11.0596

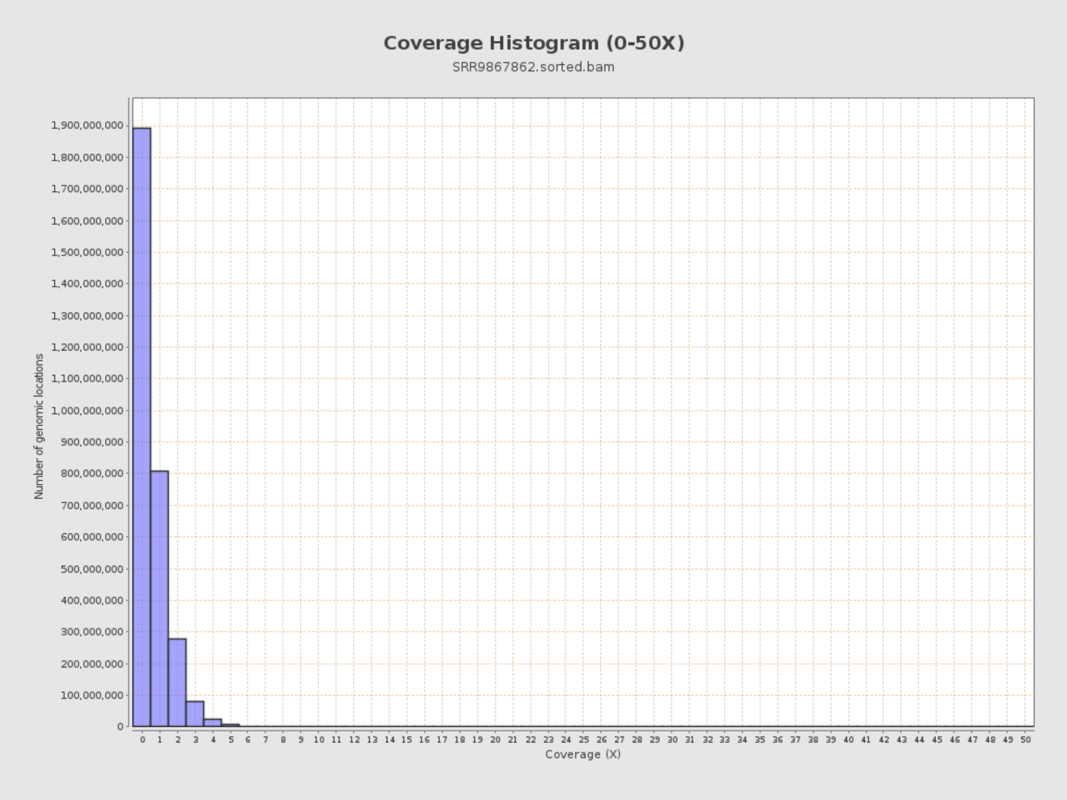
3. Results : Coverage across reference



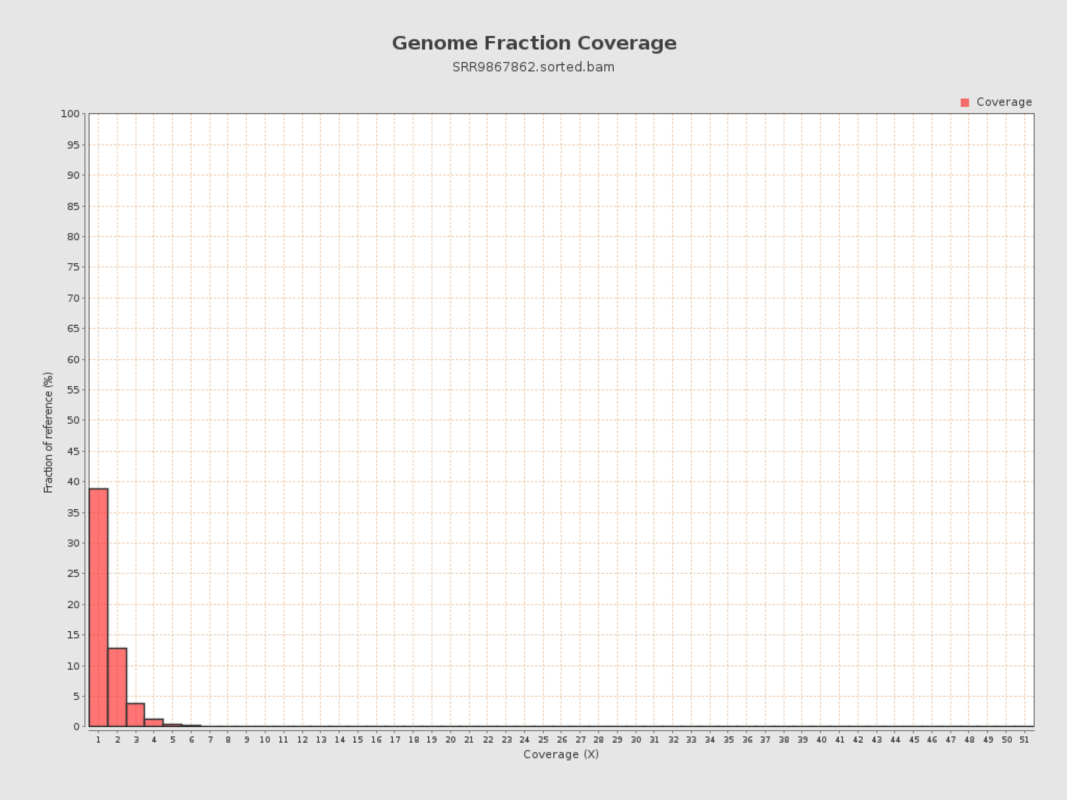
4. Results : Coverage Histogram



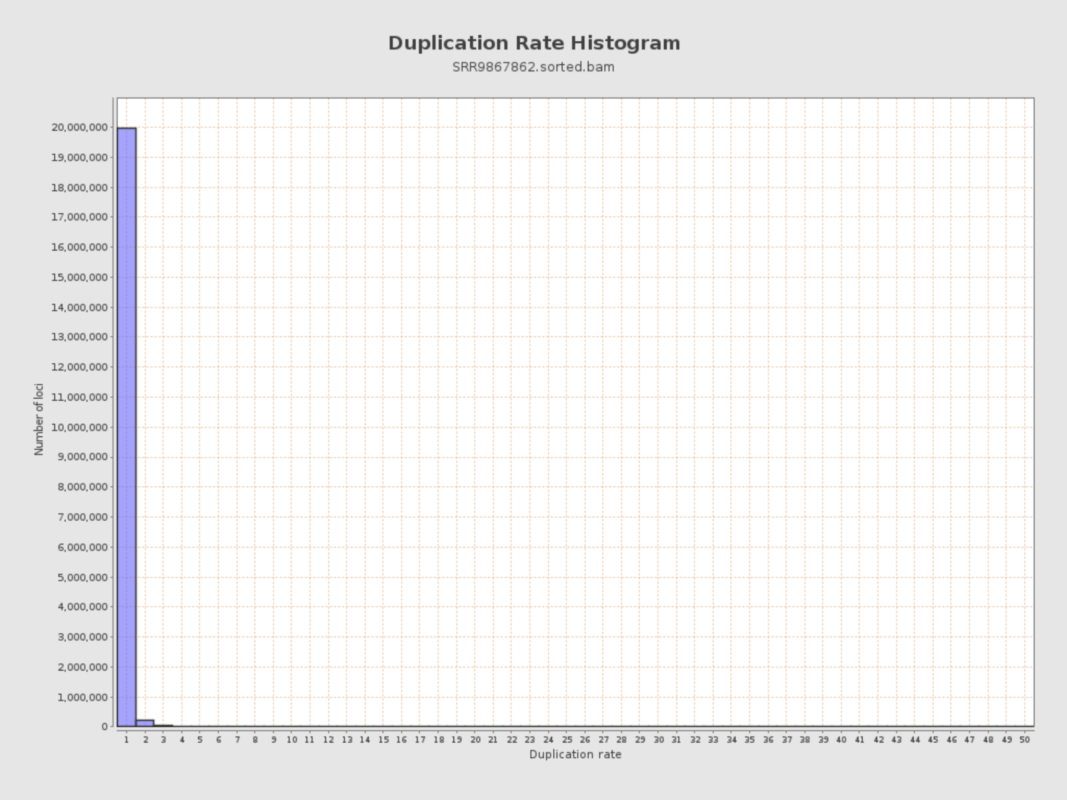
5. Results : Coverage Histogram (0-50X)



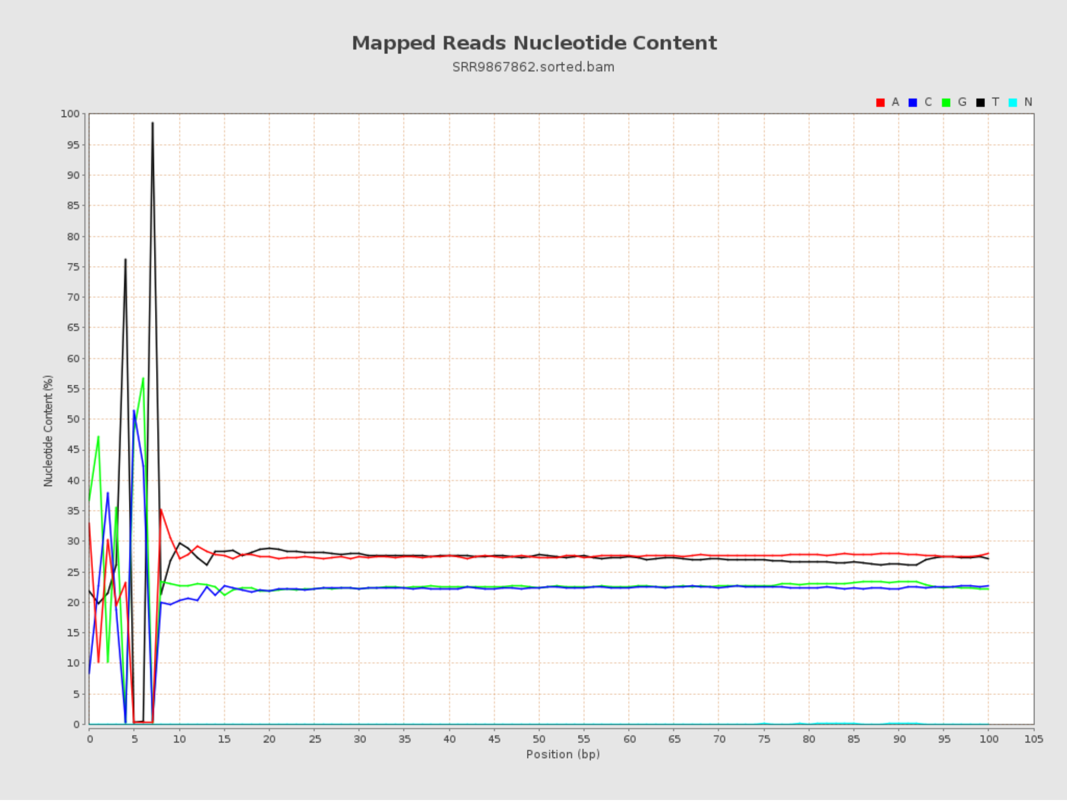
6. Results : Genome Fraction Coverage



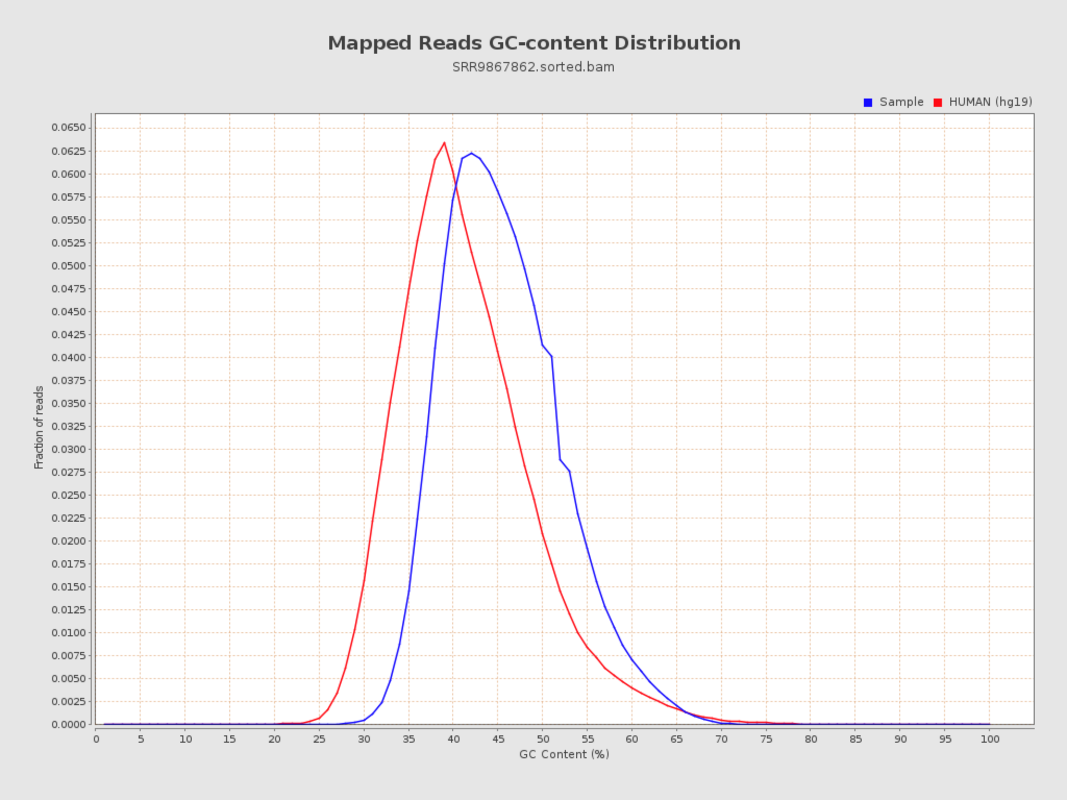
7. Results : Duplication Rate Histogram



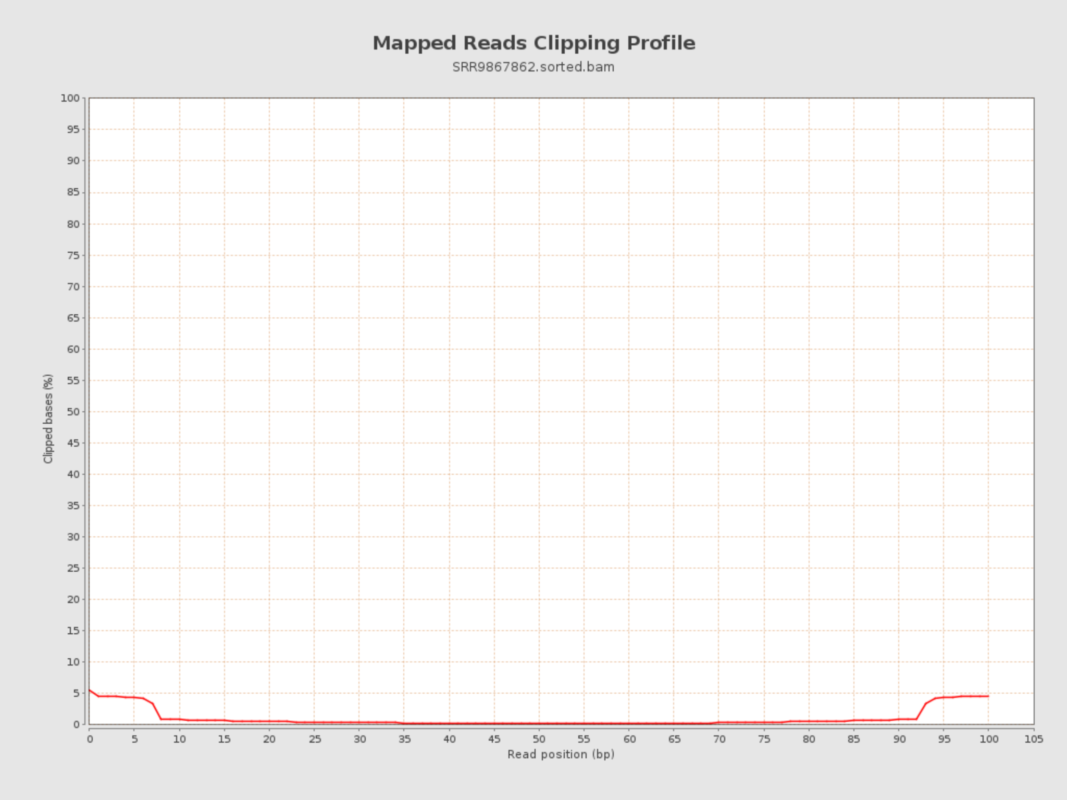
8. Results : Mapped Reads Nucleotide Content



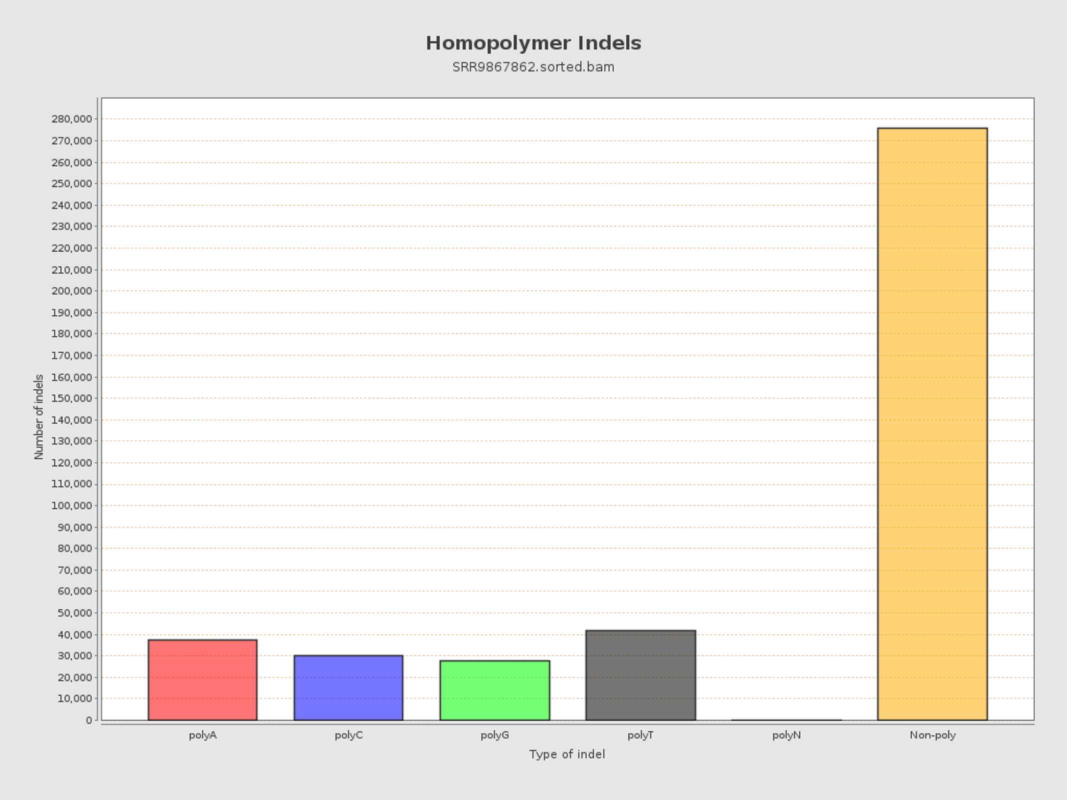
9. Results : Mapped Reads GC-content Distribution



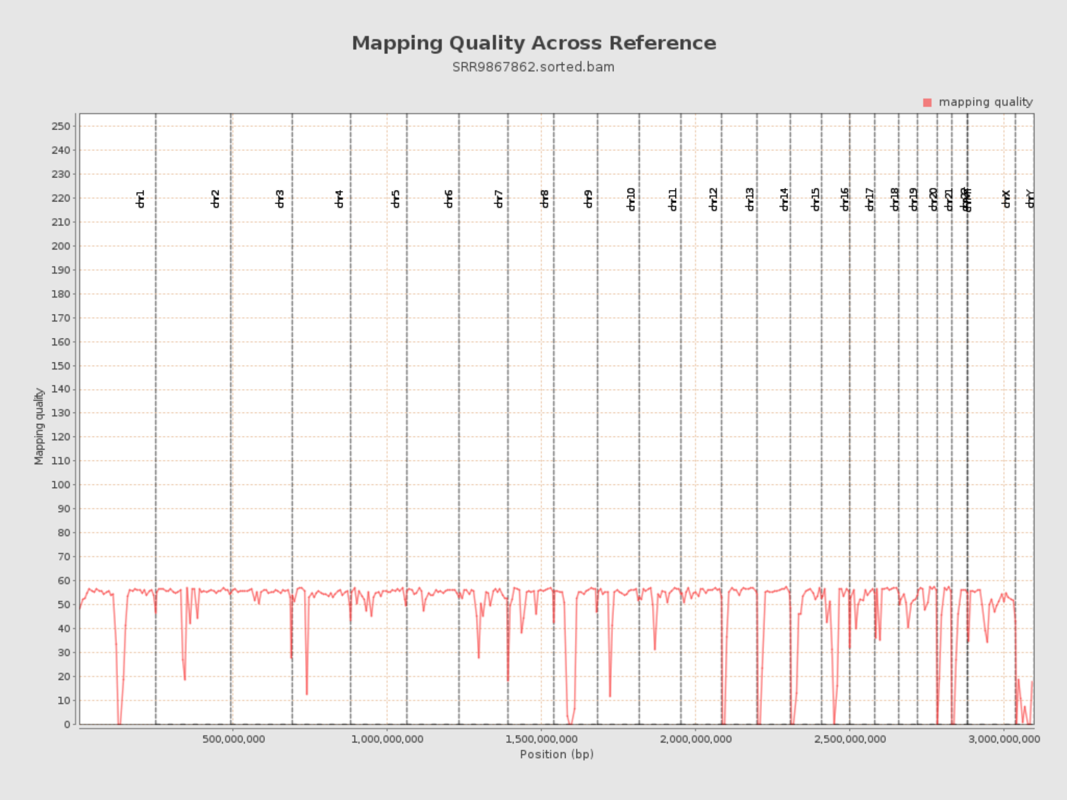
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram