

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 12:19:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867850.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_SRR9867850 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867850.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 12:19:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867850.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,486,163
Mapped reads	12,115,797 / 97.03%
Unmapped reads	370,366 / 2.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,552 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	621,859 / 4.98%
Duplication rate	1.25%
Clipped reads	12,116,437 / 97.04%

2.2. ACGT Content

Number/percentage of A's	307,245,119 / 28.41%
Number/percentage of C's	230,094,550 / 21.27%
Number/percentage of T's	309,459,808 / 28.61%
Number/percentage of G's	234,251,528 / 21.66%
Number/percentage of N's	486,864 / 0.05%
GC Percentage	42.93%

2.3. Coverage

Mean	0.3495

Standard Deviation	5.7837
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2.4. Mapping Quality

Mean Mapping Quality	50.42
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2.5. Mismatches and indels

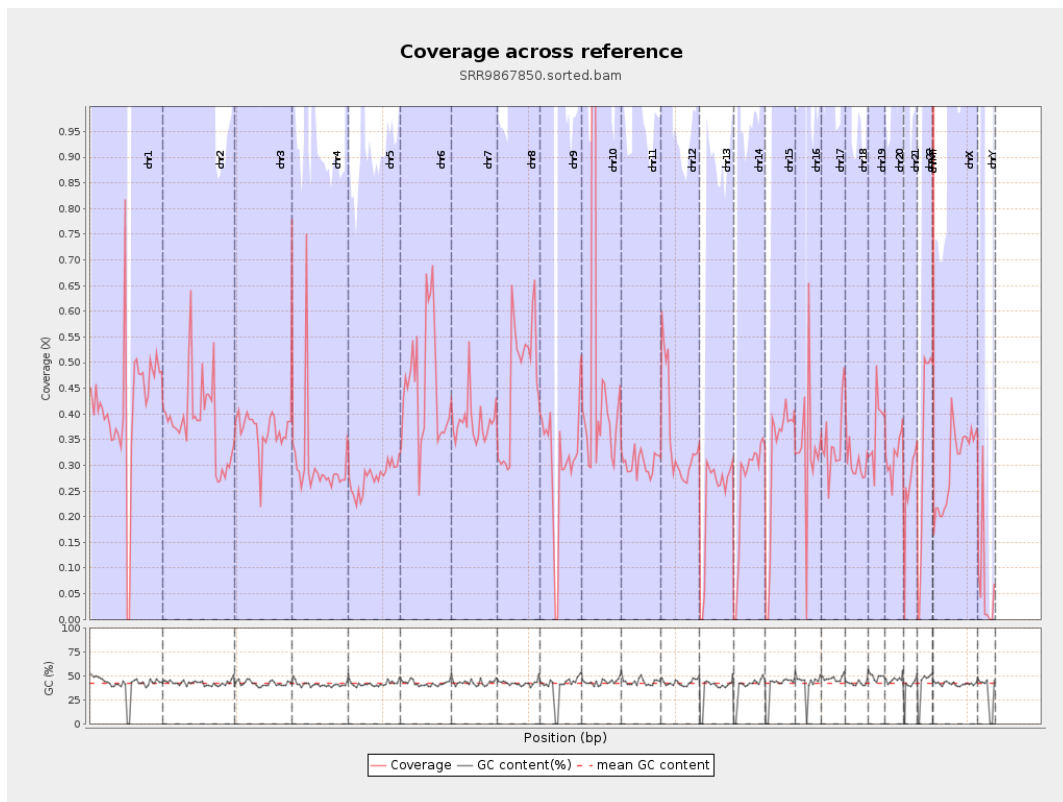
General error rate	0.46%
Mismatches	4,728,816
Insertions	104,185
Mapped reads with at least one insertion	0.84%
Deletions	112,795
Mapped reads with at least one deletion	0.91%
Homopolymer indels	35.88%

2.6. Chromosome stats

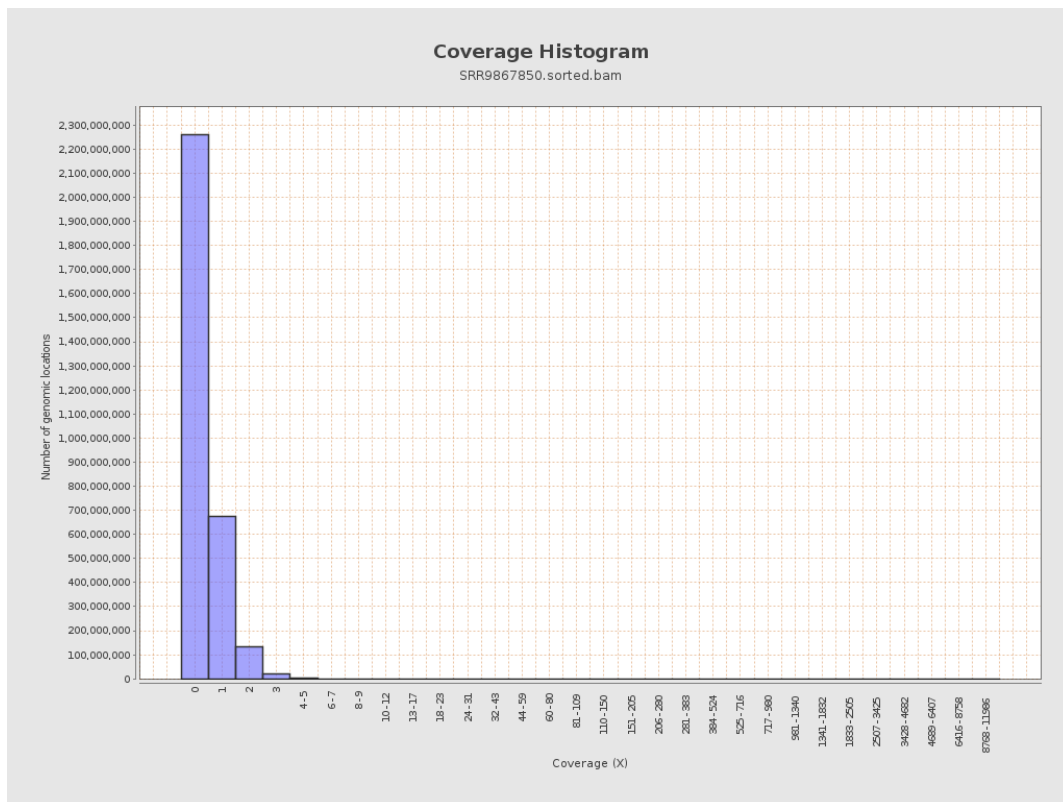
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	103379593	0.4148	9.2257
chr2	243199373	93527797	0.3846	2.2997
chr3	198022430	73534887	0.3713	4.3908
chr4	191154276	57946518	0.3031	2.5816
chr5	180915260	50227273	0.2776	0.6343
chr6	171115067	78011473	0.4559	2.2933
chr7	159138663	61529056	0.3866	3.3382

chr8	146364022	68090867	0.4652	1.6546
chr9	141213431	43011908	0.3046	2.0876
chr10	135534747	70445973	0.5198	22.163
chr11	135006516	40975546	0.3035	1.5002
chr12	133851895	47579946	0.3555	0.6985
chr13	115169878	27116263	0.2354	0.5133
chr14	107349540	27843509	0.2594	0.6987
chr15	102531392	31763155	0.3098	0.5962
chr16	90354753	30077825	0.3329	3.3207
chr17	81195210	27601398	0.3399	1.1982
chr18	78077248	23971672	0.307	3.9152
chr19	59128983	21975267	0.3716	5.196
chr20	63025520	20107535	0.319	0.9202
chr21	48129895	12569275	0.2612	1.8986
chr22	51304566	17702760	0.3451	0.6957
chrMT	16571	1677929	101.257	34.6278
chrX	155270560	47071270	0.3032	1.0414
chrY	59373566	4075523	0.0686	3.1876

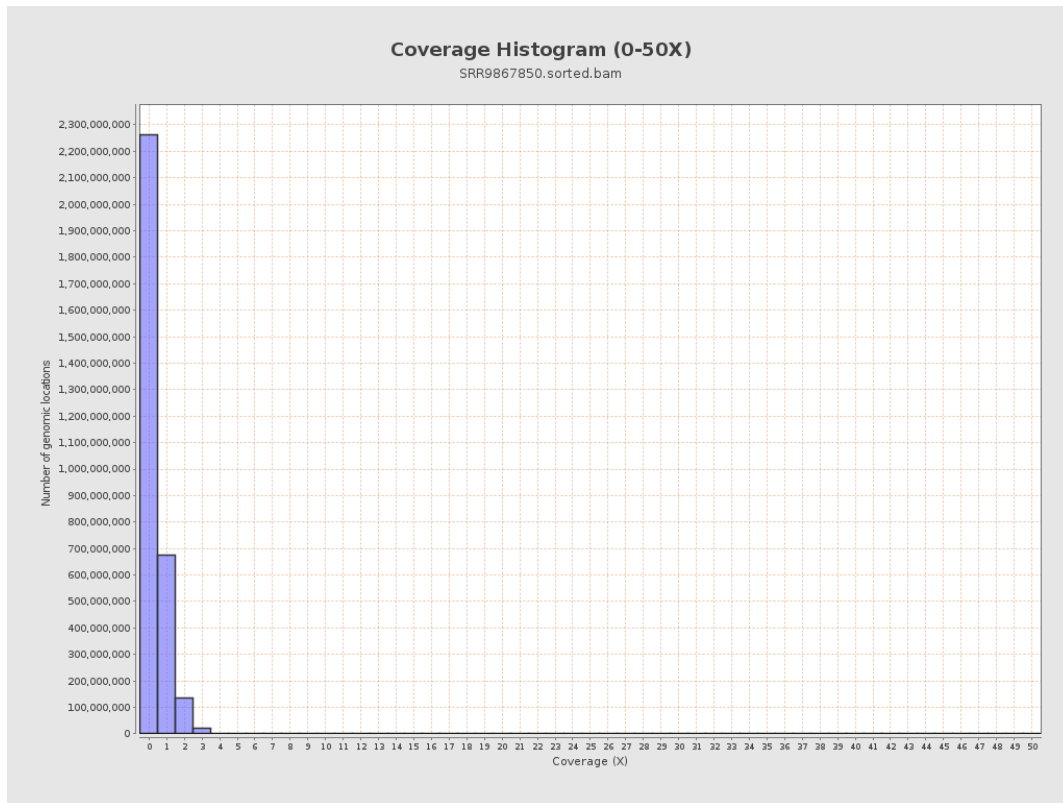
3. Results : Coverage across reference



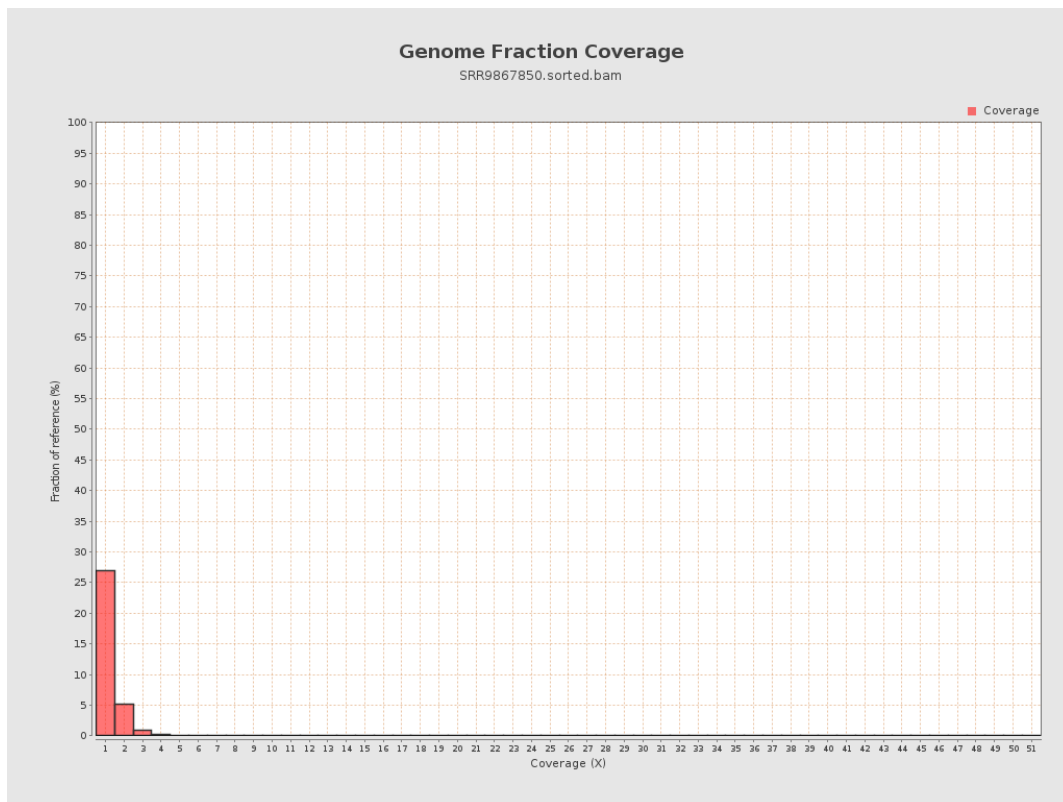
4. Results : Coverage Histogram



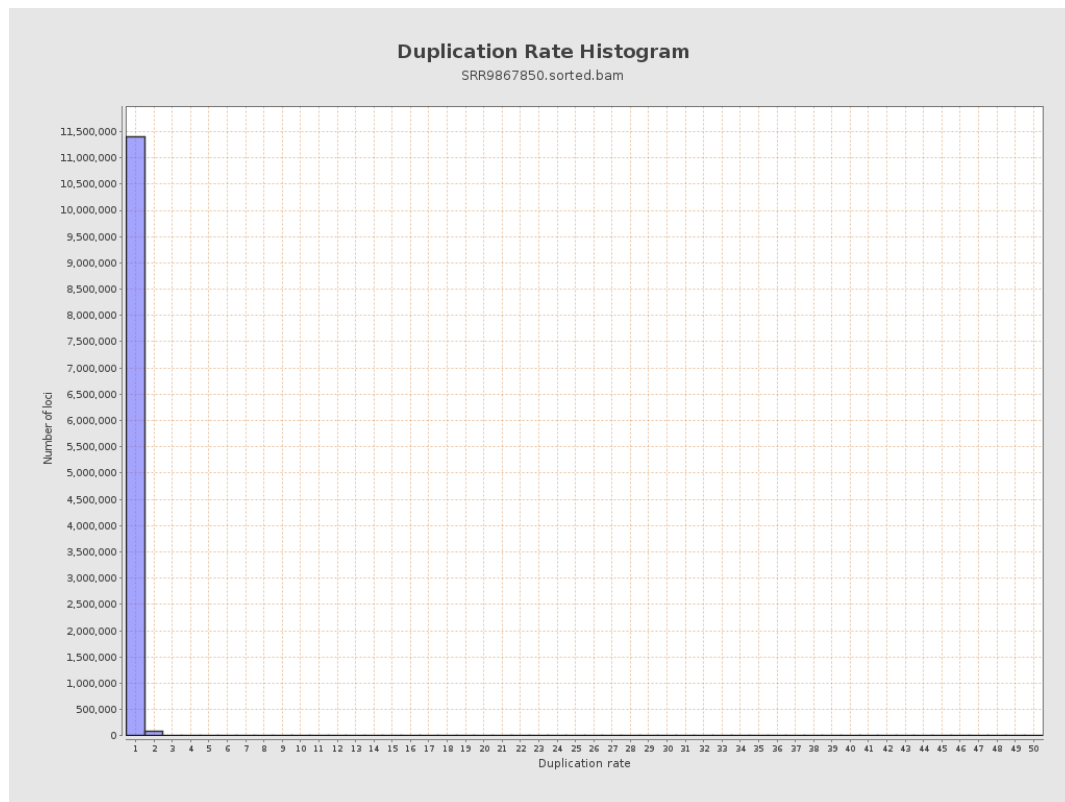
5. Results : Coverage Histogram (0-50X)



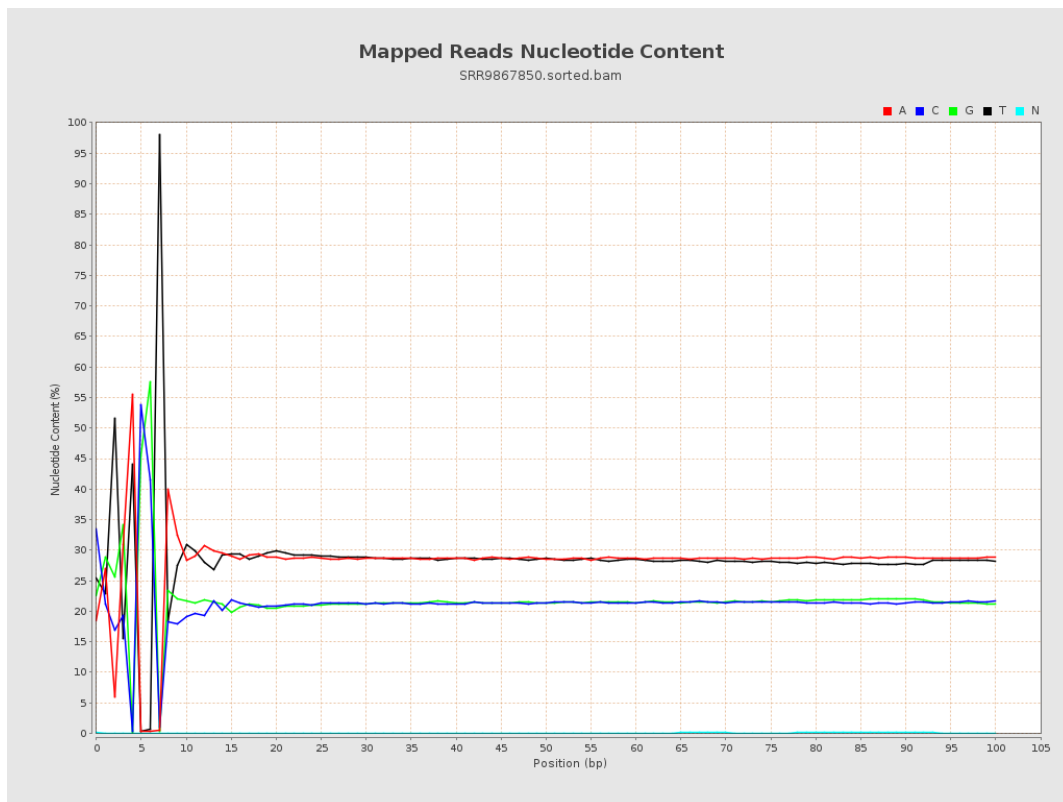
6. Results : Genome Fraction Coverage



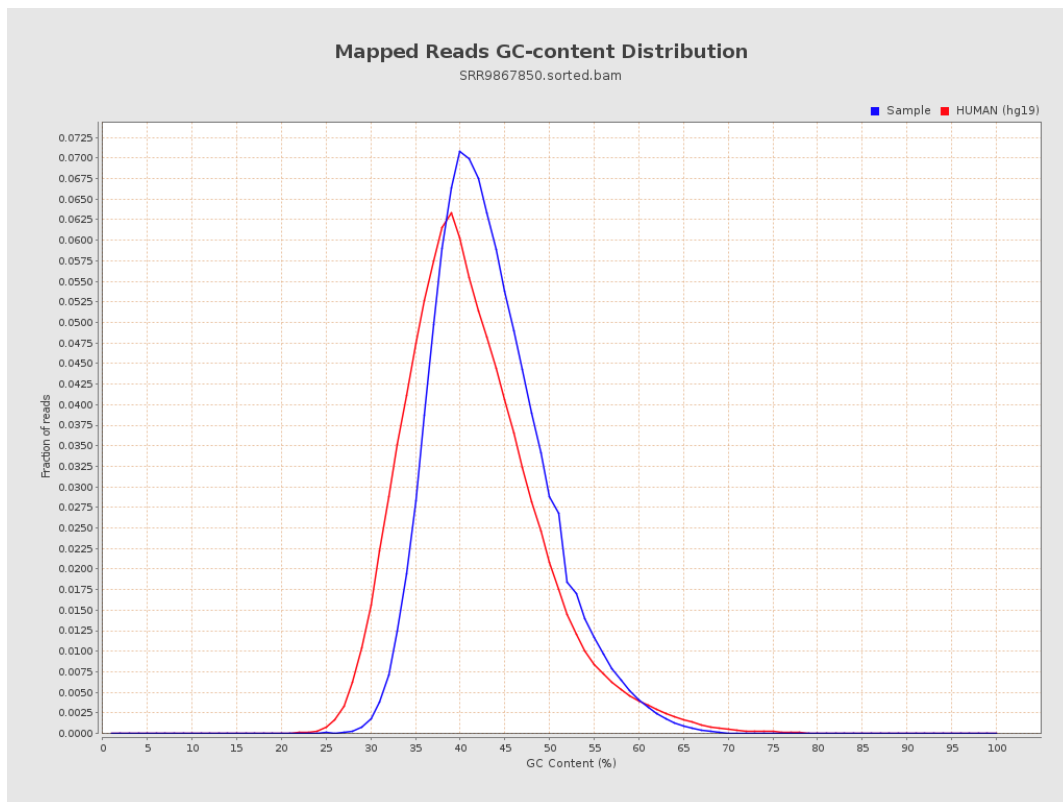
7. Results : Duplication Rate Histogram



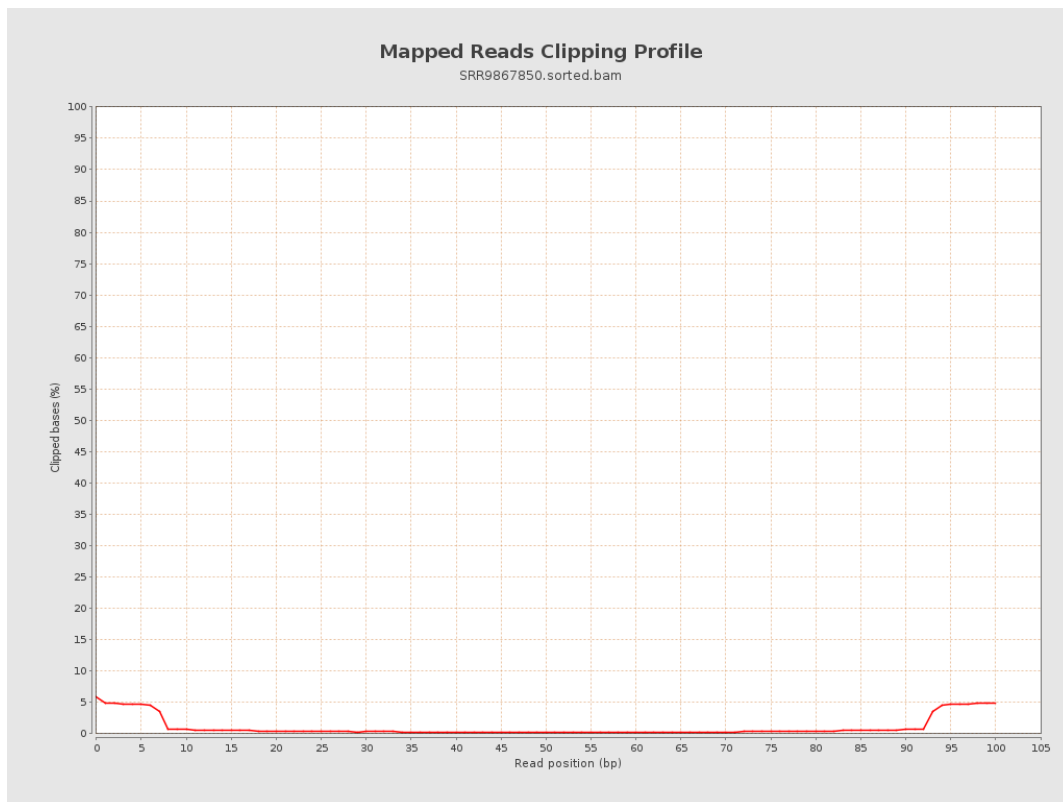
8. Results : Mapped Reads Nucleotide Content



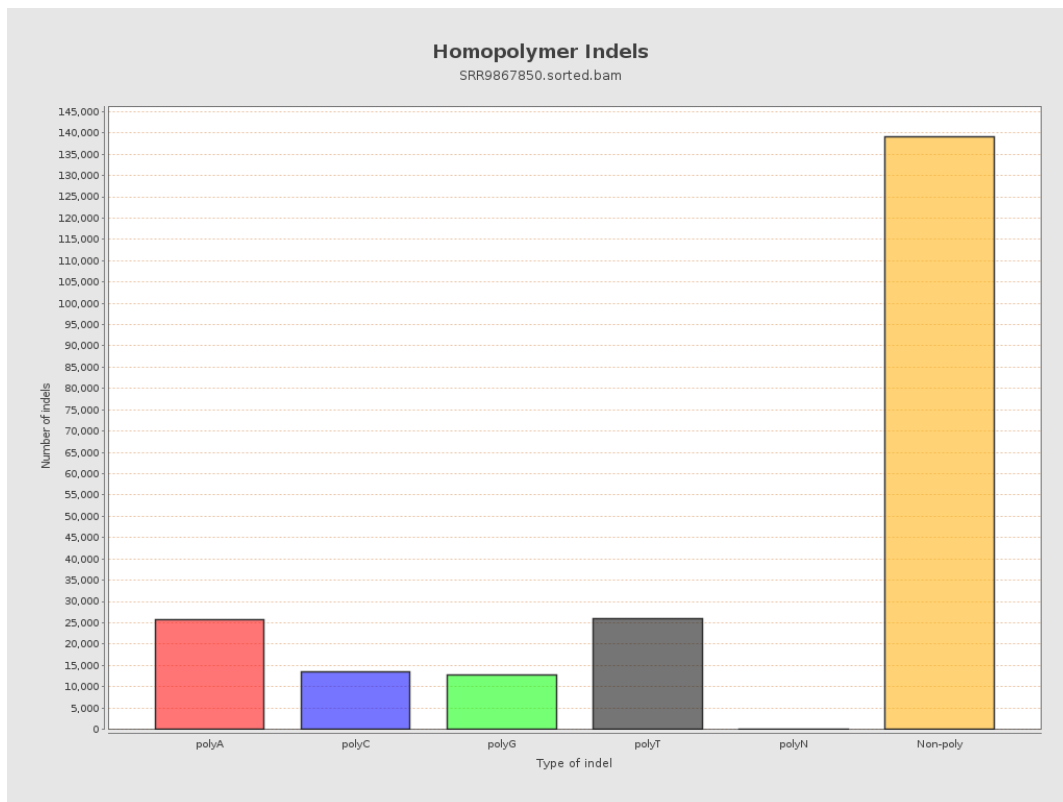
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

