Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 04:16:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867837.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_SRR9867837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 04:16:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,661,723
Mapped reads	24,887,466 / 96.98%
Unmapped reads	774,257 / 3.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	137,656 / 0.54%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	1,429,972 / 5.57%
Duplication rate	1.58%
Clipped reads	24,915,278 / 97.09%

2.2. ACGT Content

Number/percentage of A's	631,793,250 / 28.21%
Number/percentage of C's	483,473,207 / 21.59%
Number/percentage of T's	634,662,295 / 28.34%
Number/percentage of G's	488,609,355 / 21.82%
Number/percentage of N's	1,098,502 / 0.05%
GC Percentage	43.4%

2.3. Coverage

Mean	0.7237

Standard Deviation	8.656

2.4. Mapping Quality

Mean Mapping Quality	50.36

2.5. Mismatches and indels

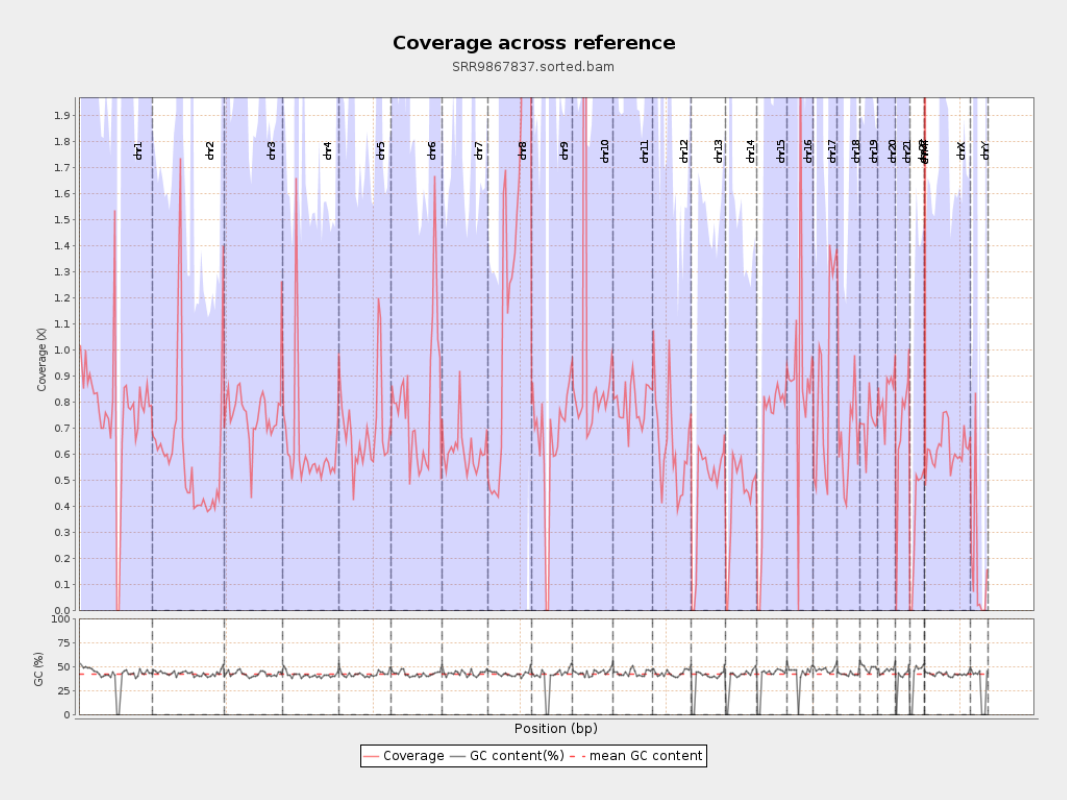
General error rate	0.46%
Mismatches	9,741,875
Insertions	220,633
Mapped reads with at least one insertion	0.87%
Deletions	226,283
Mapped reads with at least one deletion	0.88%
Homopolymer indels	35.91%

2.6. Chromosome stats

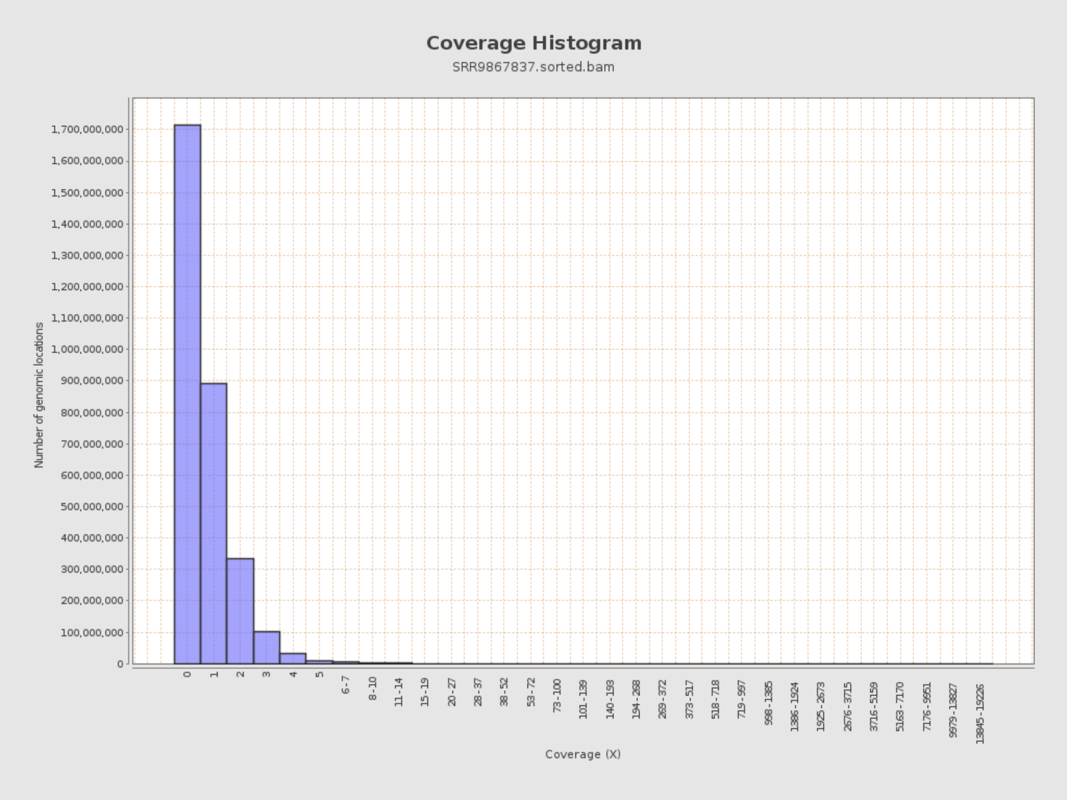
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	192515602	0.7724	16.8639
chr2	243199373	146701662	0.6032	4.7185
chr3	198022430	149198039	0.7534	5.1919
chr4	191154276	118111800	0.6179	5.867
chr5	180915260	125967136	0.6963	1.0362
chr6	171115067	135715783	0.7931	2.3897
chr7	159138663	98173337	0.6169	5.6828

chr8	146364022	220016091	1.5032	4.5666
chr9	141213431	92117374	0.6523	3.8538
chr10	135534747	133687789	0.9864	27.49
chr11	135006516	107707126	0.7978	2.821
chr12	133851895	85650221	0.6399	1.0634
chr13	115169878	54018478	0.469	0.7621
chr14	107349540	46386178	0.4321	1.0862
chr15	102531392	66625640	0.6498	0.9208
chr16	90354753	84304409	0.933	9.3453
chr17	81195210	72153609	0.8886	3.0743
chr18	78077248	51889183	0.6646	7.8073
chr19	59128983	42346910	0.7162	10.5239
chr20	63025520	52260927	0.8292	1.9637
chr21	48129895	33825125	0.7028	4.2965
chr22	51304566	18620694	0.3629	0.7775
chrMT	16571	6186022	373.3041	119.1156
chrX	155270560	96380582	0.6207	1.8765
chrY	59373566	9649862	0.1625	8.1796

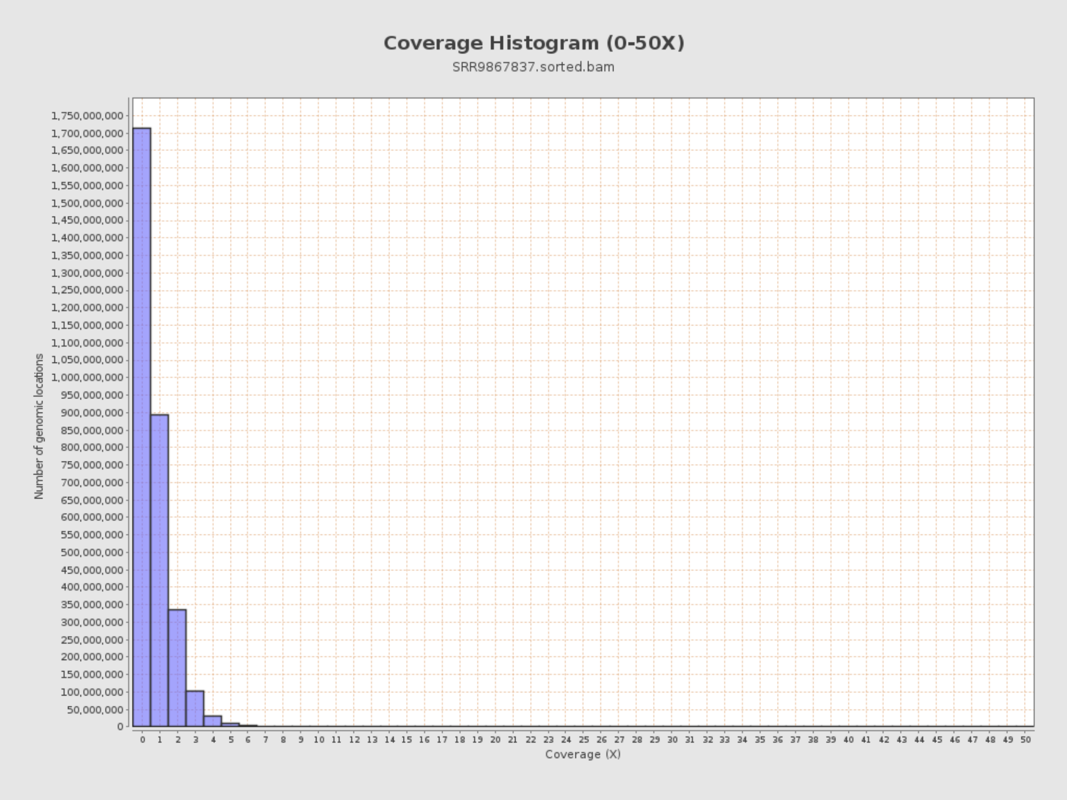
3. Results : Coverage across reference



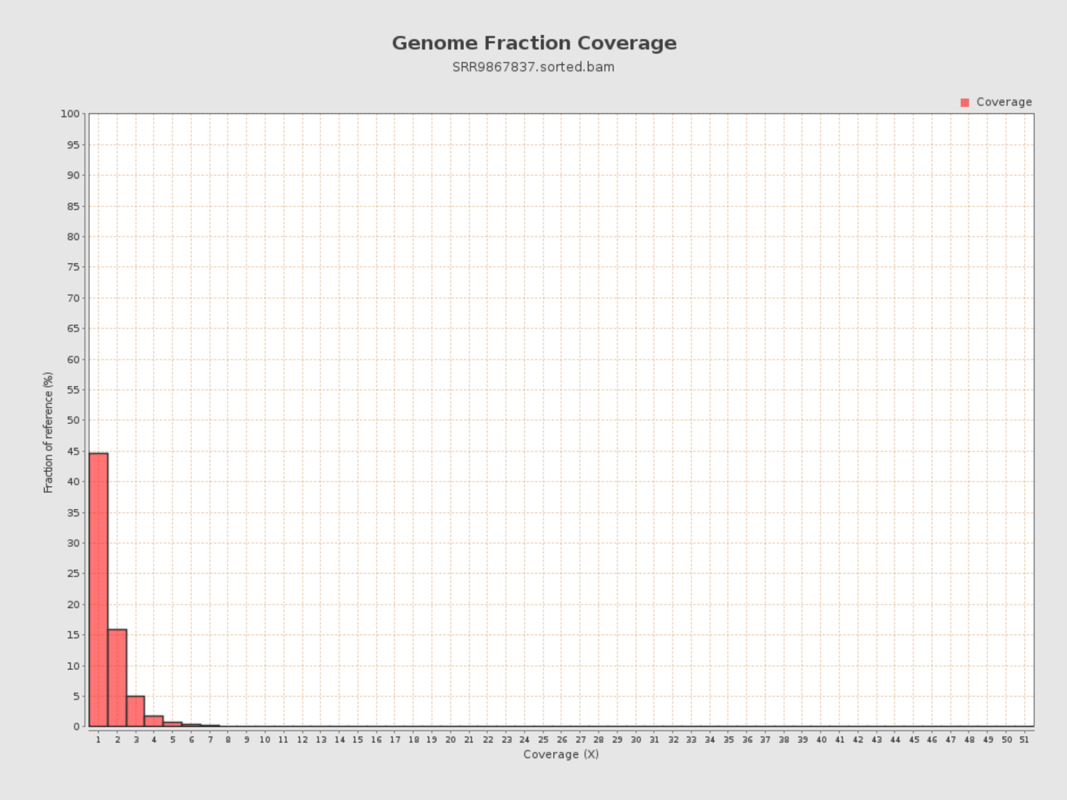
4. Results : Coverage Histogram



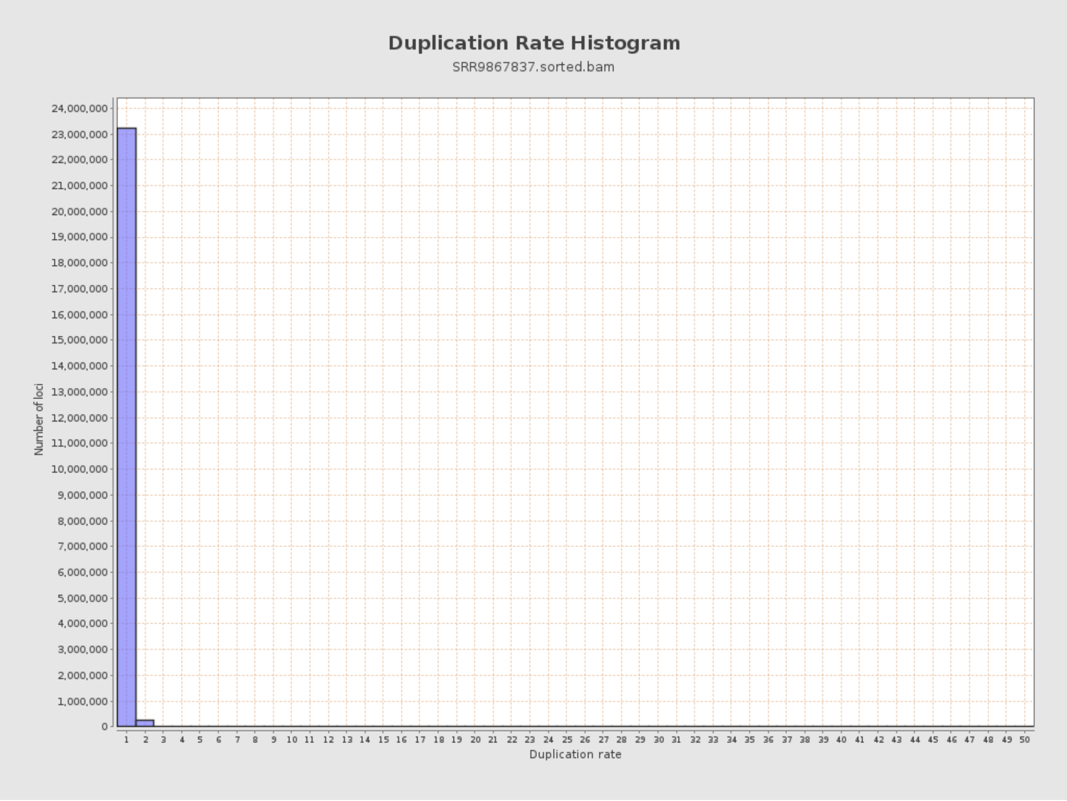
5. Results : Coverage Histogram (0-50X)



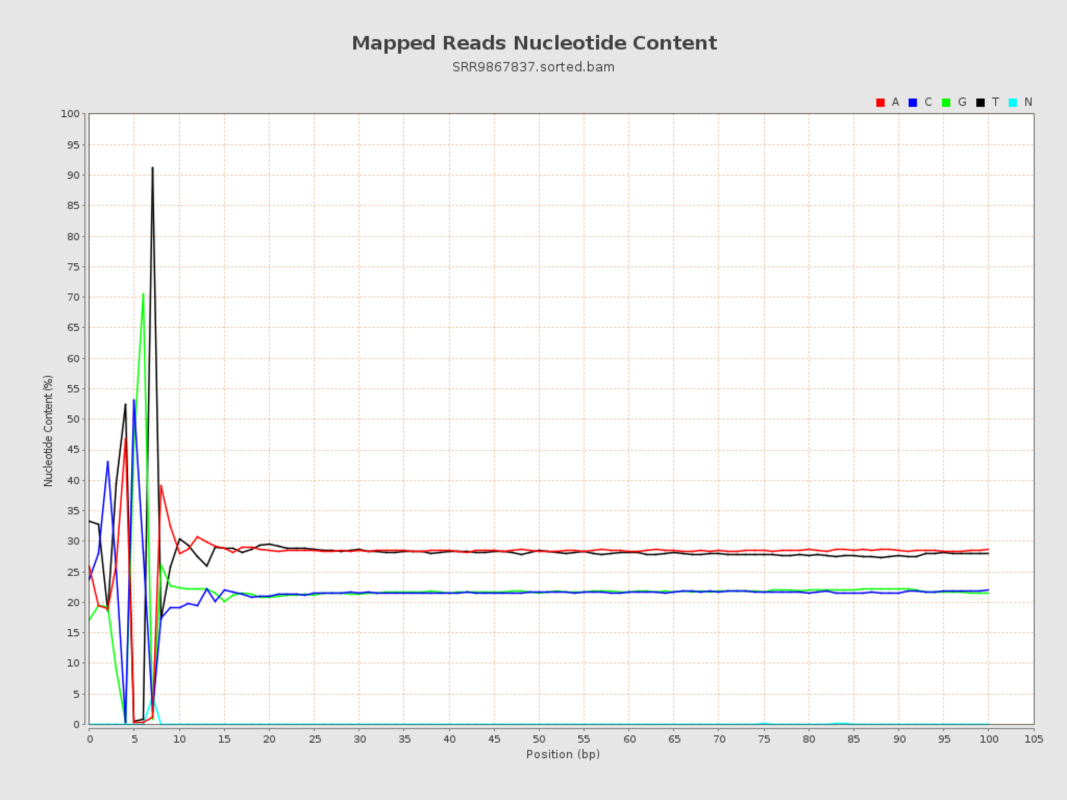
6. Results : Genome Fraction Coverage



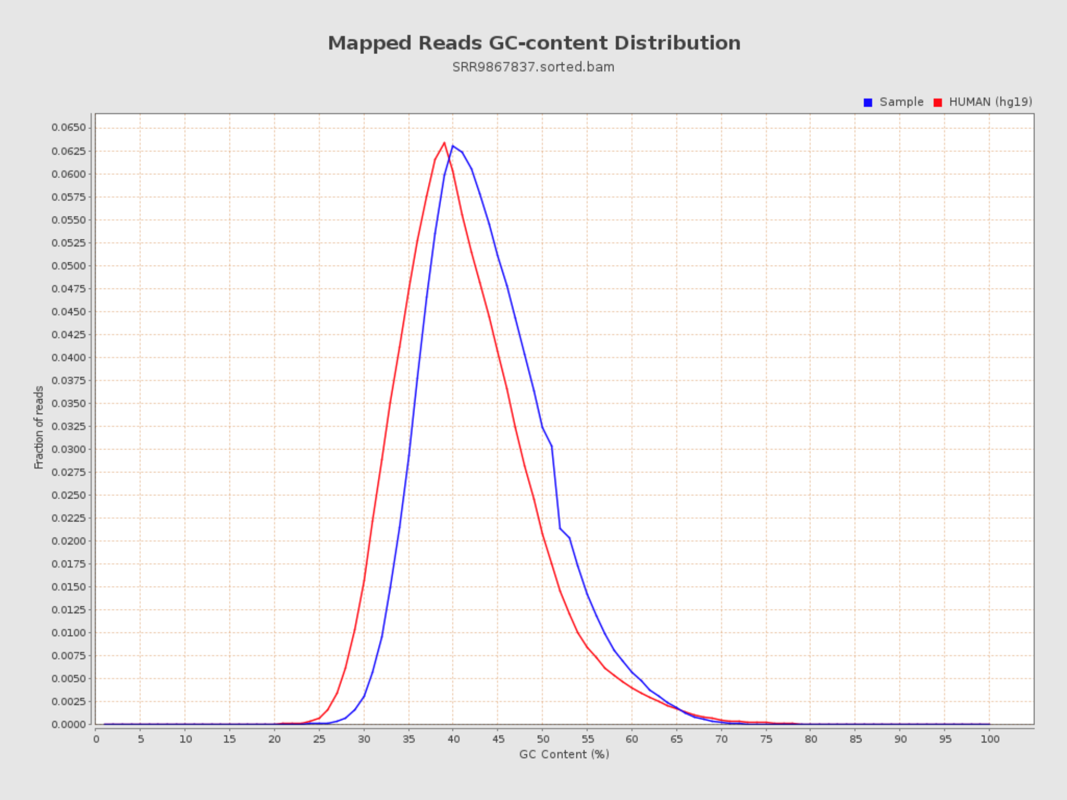
7. Results : Duplication Rate Histogram



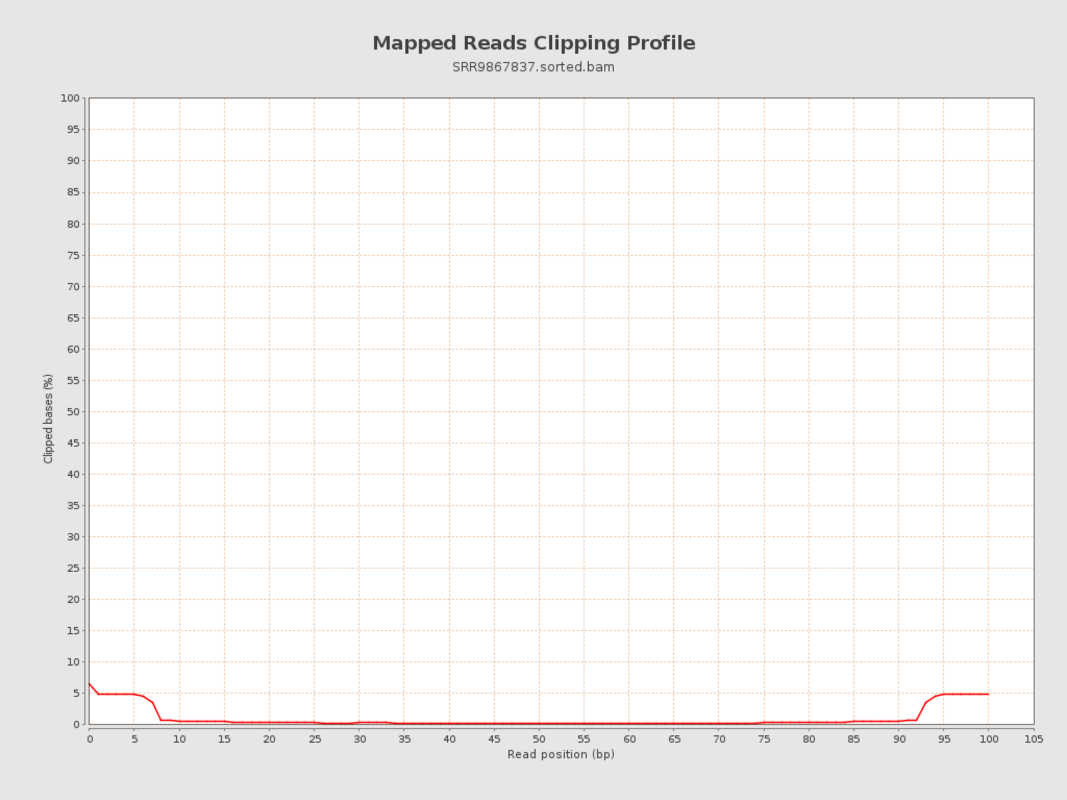
8. Results : Mapped Reads Nucleotide Content



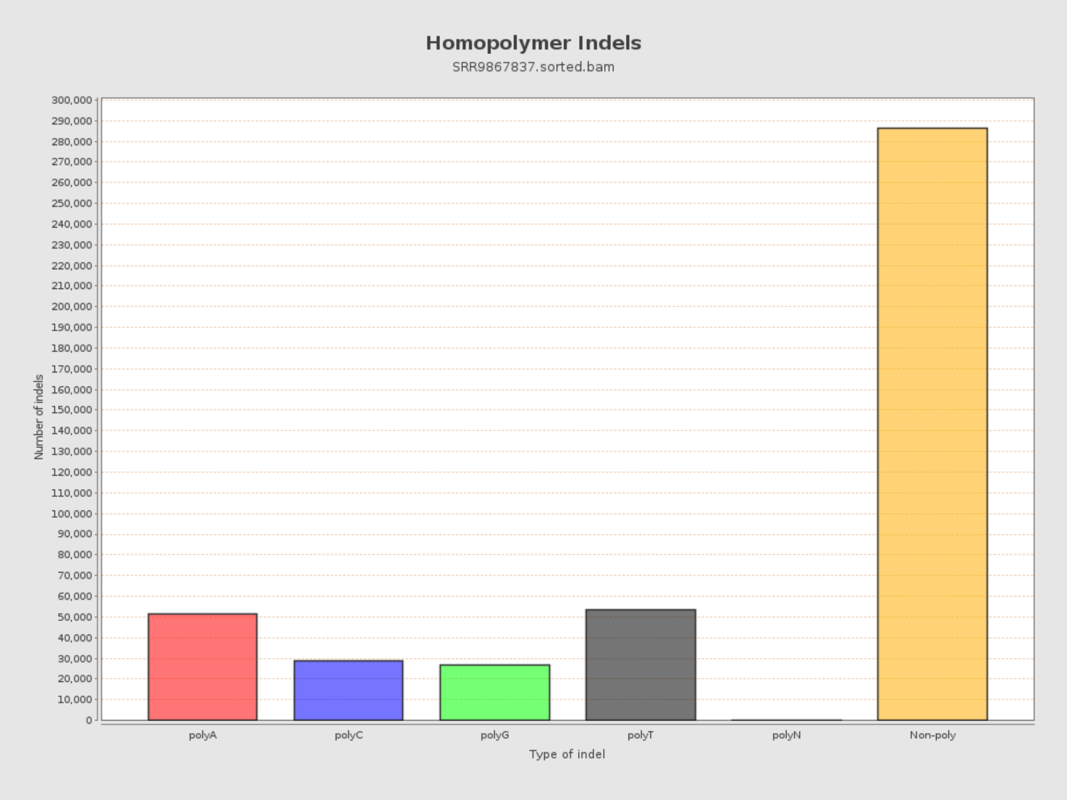
9. Results : Mapped Reads GC-content Distribution



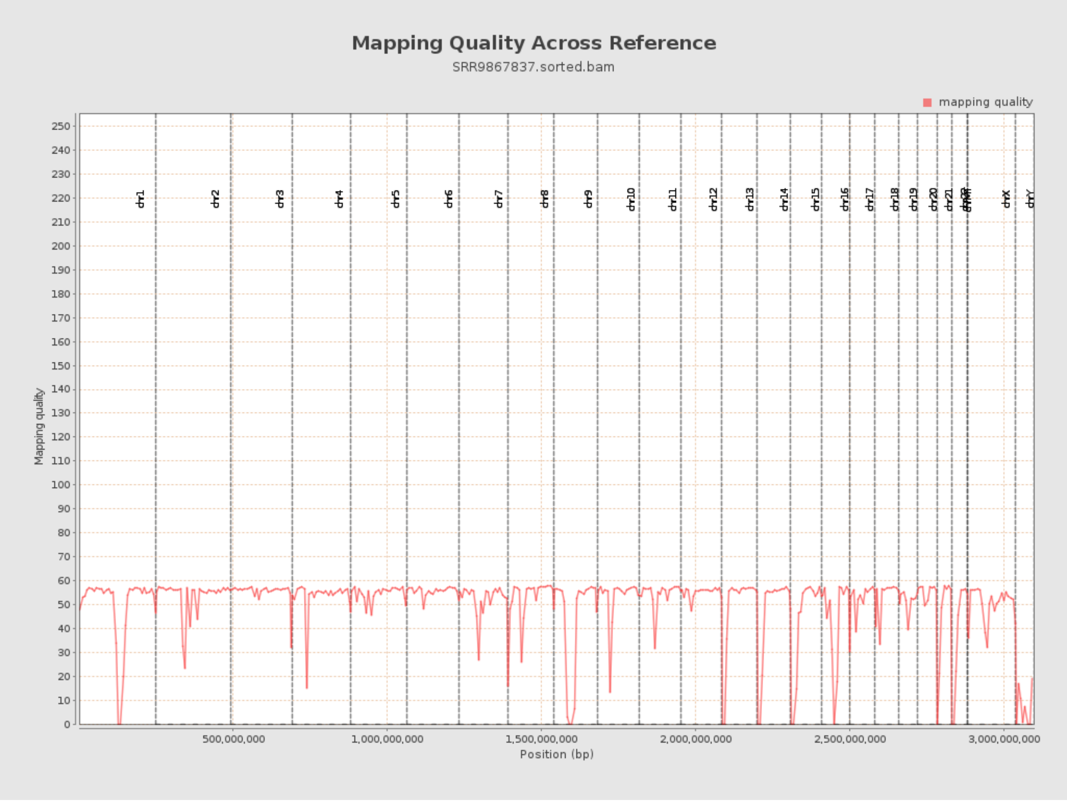
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram