Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:33:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867868.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_SRR9867868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:33:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,532,261
Mapped reads	1,420,390 / 92.7%
Unmapped reads	111,871 / 7.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,724 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	54,483 / 3.56%
Duplication rate	2.85%
Clipped reads	1,422,125 / 92.81%

2.2. ACGT Content

Number/percentage of A's	22,446,073 / 26.7%
Number/percentage of C's	17,223,334 / 20.49%
Number/percentage of T's	25,465,109 / 30.3%
Number/percentage of G's	18,907,087 / 22.49%
Number/percentage of N's	11,696 / 0.01%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2655

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

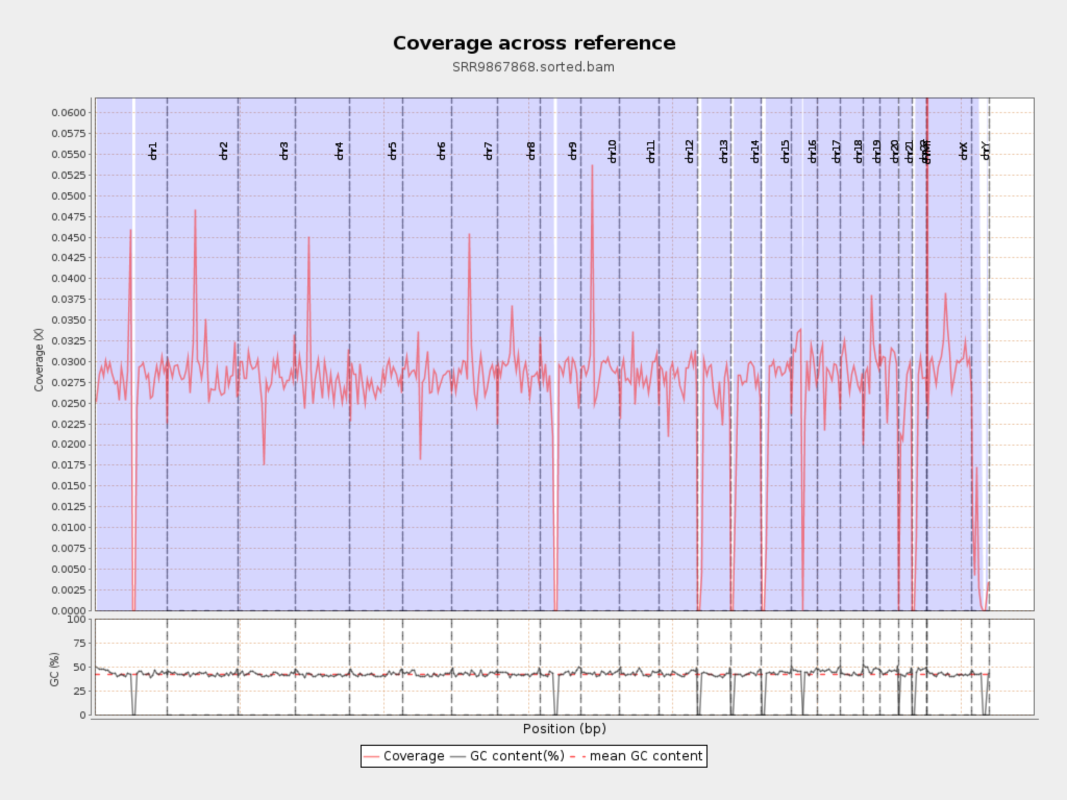
General error rate	0.52%
Mismatches	419,985
Insertions	6,677
Mapped reads with at least one insertion	0.47%
Deletions	15,651
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.64%

2.6. Chromosome stats

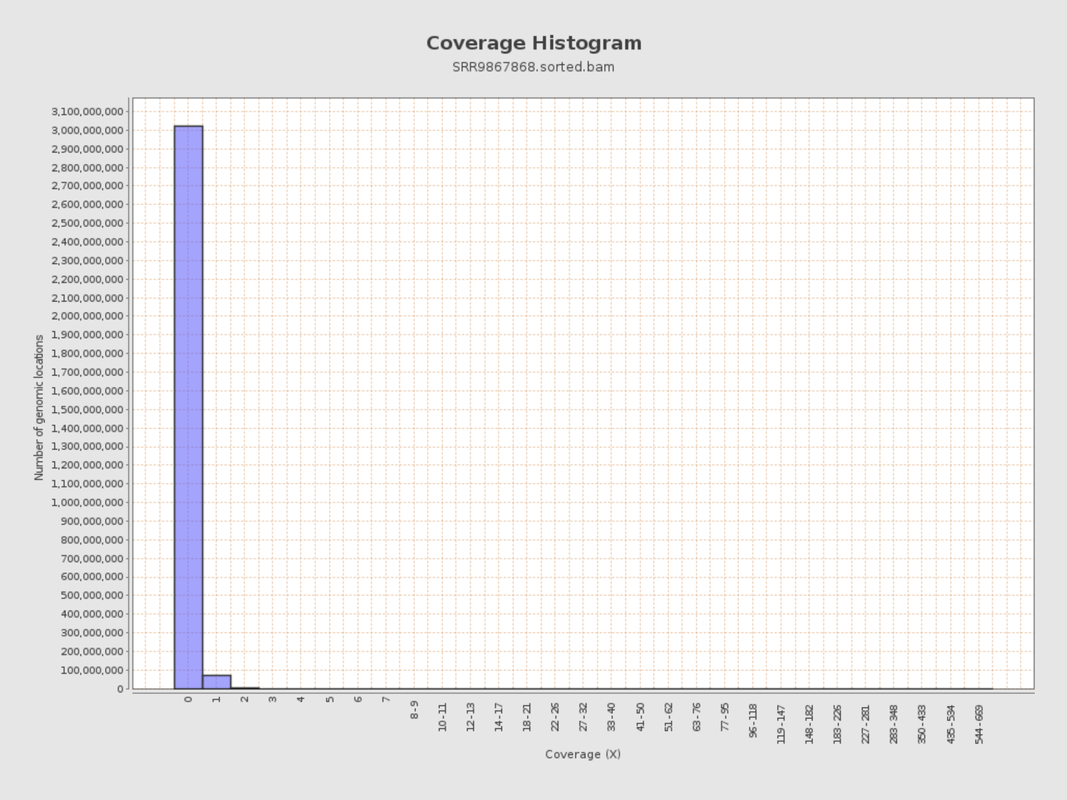
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6706725	0.0269	0.4751
chr2	243199373	7110446	0.0292	0.355
chr3	198022430	5562118	0.0281	0.1813
chr4	191154276	5425587	0.0284	0.2029
chr5	180915260	5020865	0.0278	0.1809
chr6	171115067	4814887	0.0281	0.1999
chr7	159138663	4646728	0.0292	0.3092

chr8	146364022	4287912	0.0293	0.2741
chr9	141213431	3556122	0.0252	0.2202
chr10	135534747	4099327	0.0302	0.2733
chr11	135006516	3851053	0.0285	0.2356
chr12	133851895	3783976	0.0283	0.1827
chr13	115169878	2622320	0.0228	0.162
chr14	107349540	2490406	0.0232	0.1682
chr15	102531392	2410016	0.0235	0.1663
chr16	90354753	2444365	0.0271	0.1912
chr17	81195210	2306797	0.0284	0.194
chr18	78077248	2249175	0.0288	0.3941
chr19	59128983	1777922	0.0301	0.3795
chr20	63025520	1831825	0.0291	0.187
chr21	48129895	1098914	0.0228	0.1846
chr22	51304566	1009843	0.0197	0.152
chrMT	16571	12372	0.7466	0.9711
chrX	155270560	4681220	0.0301	0.2029
chrY	59373566	277212	0.0047	0.1692

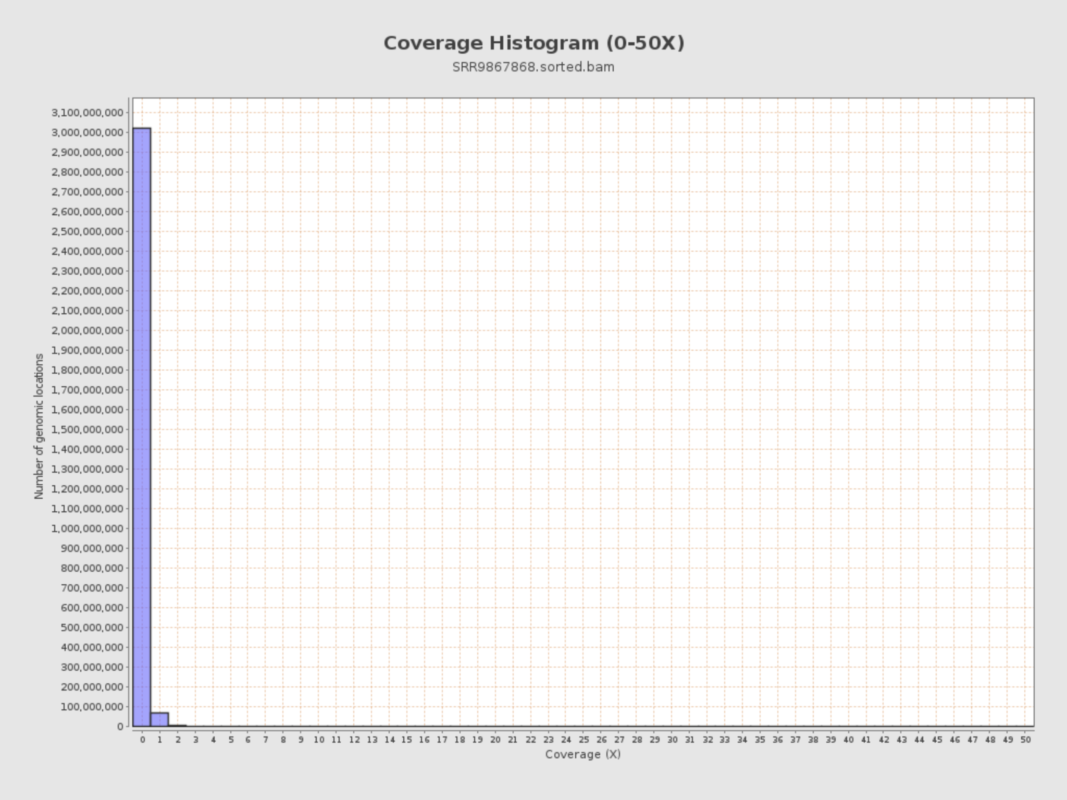
3. Results : Coverage across reference



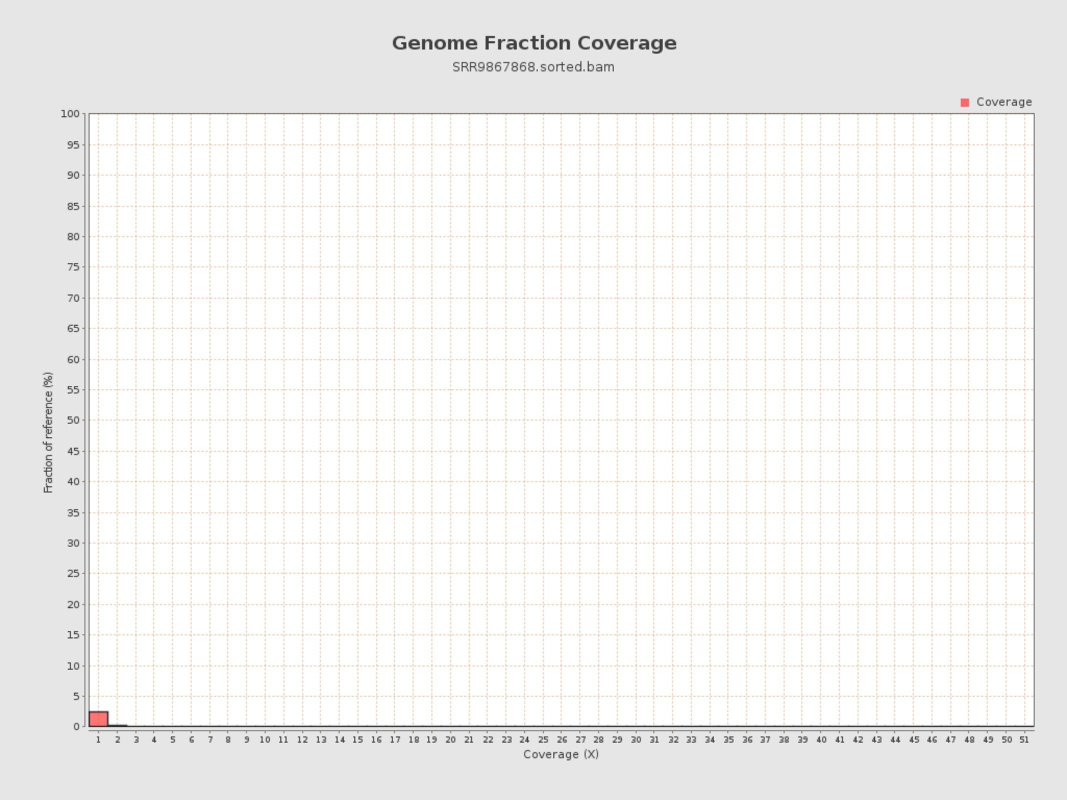
4. Results : Coverage Histogram



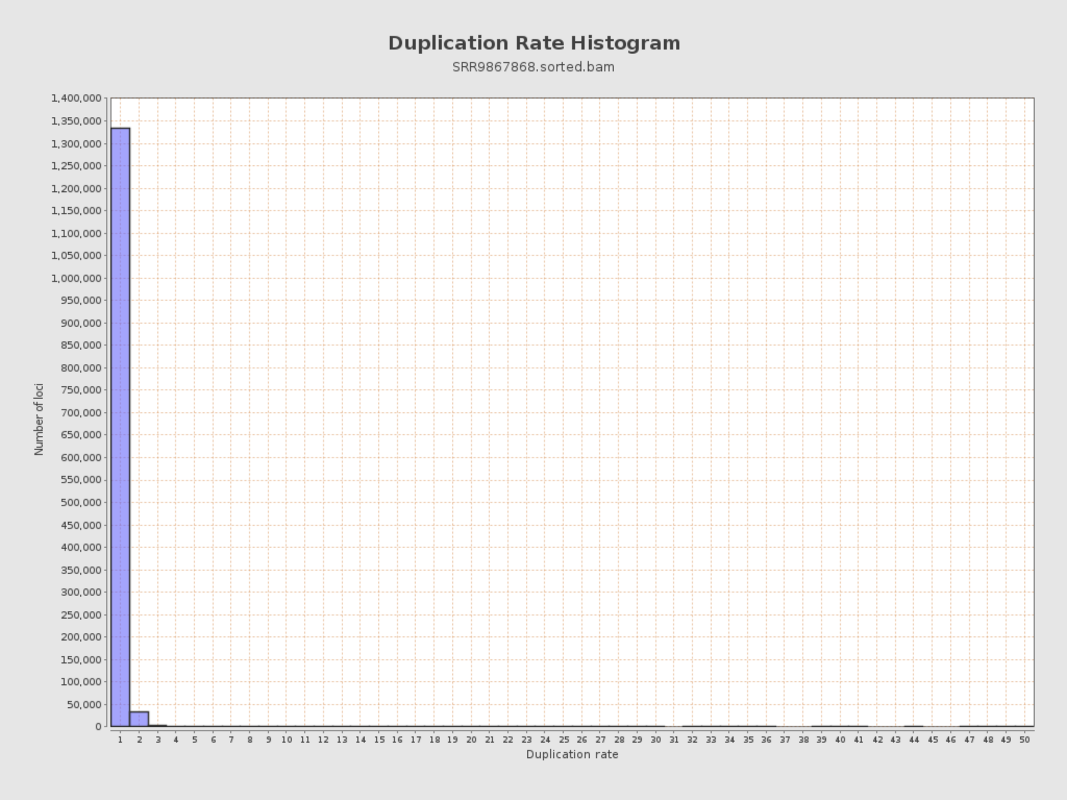
5. Results : Coverage Histogram (0-50X)



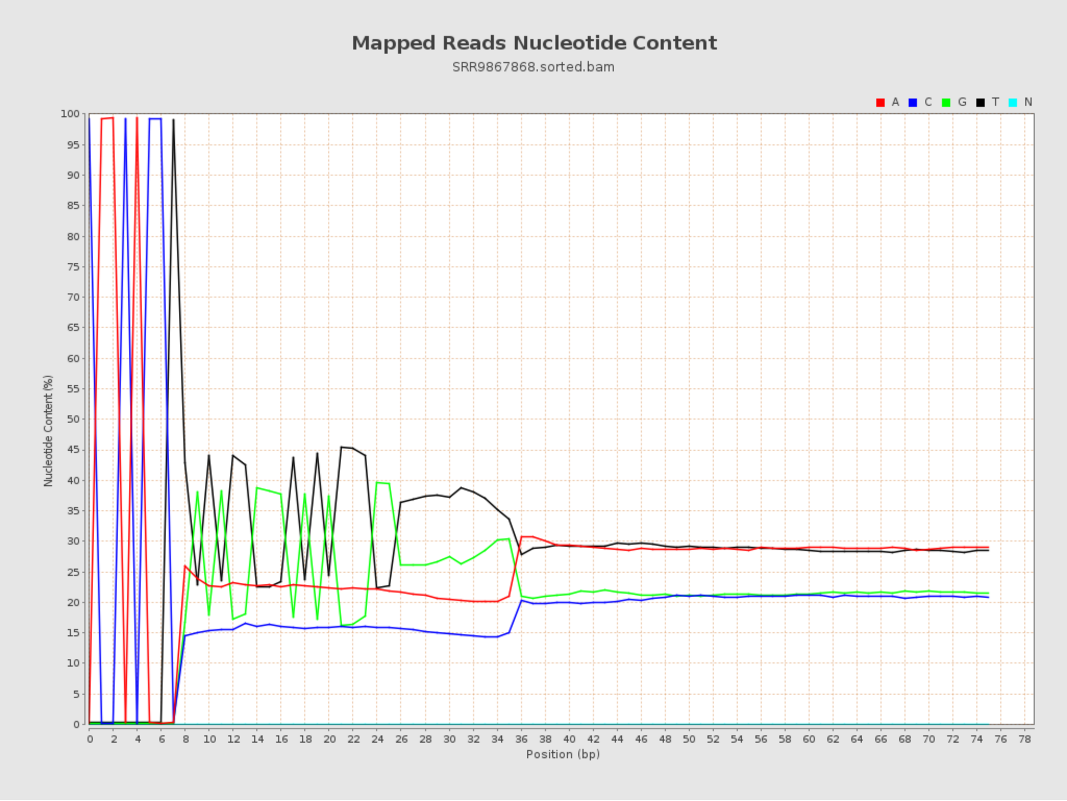
6. Results : Genome Fraction Coverage



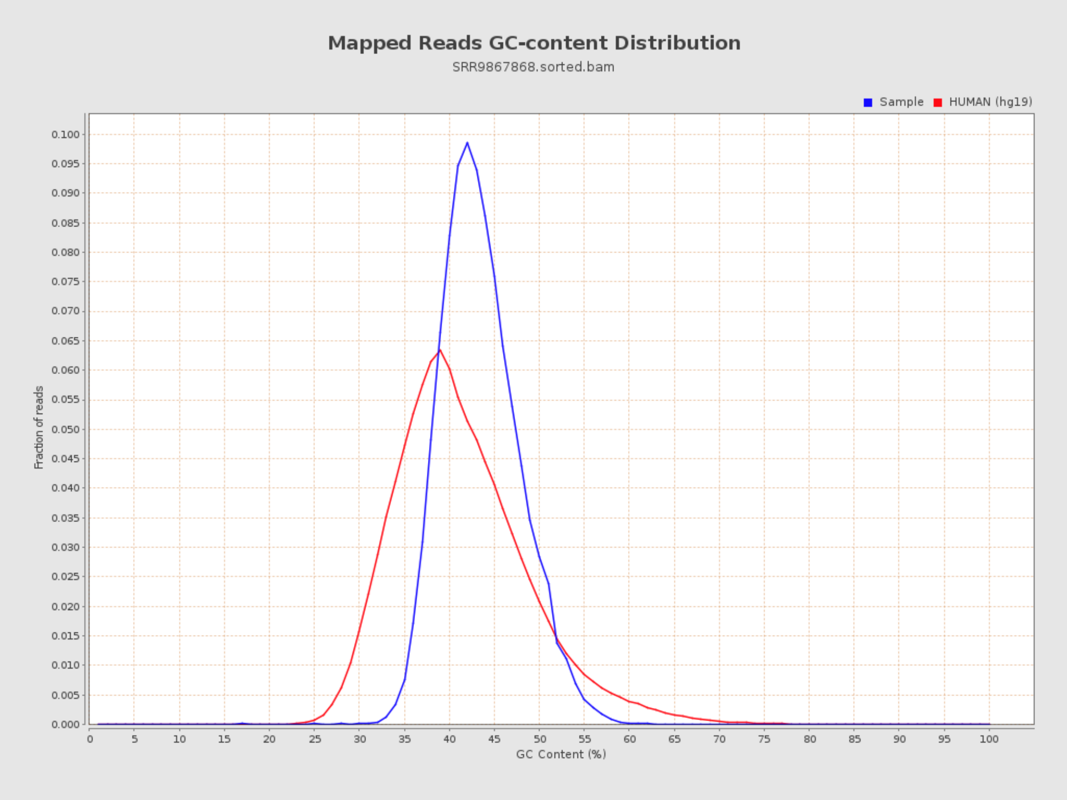
7. Results : Duplication Rate Histogram



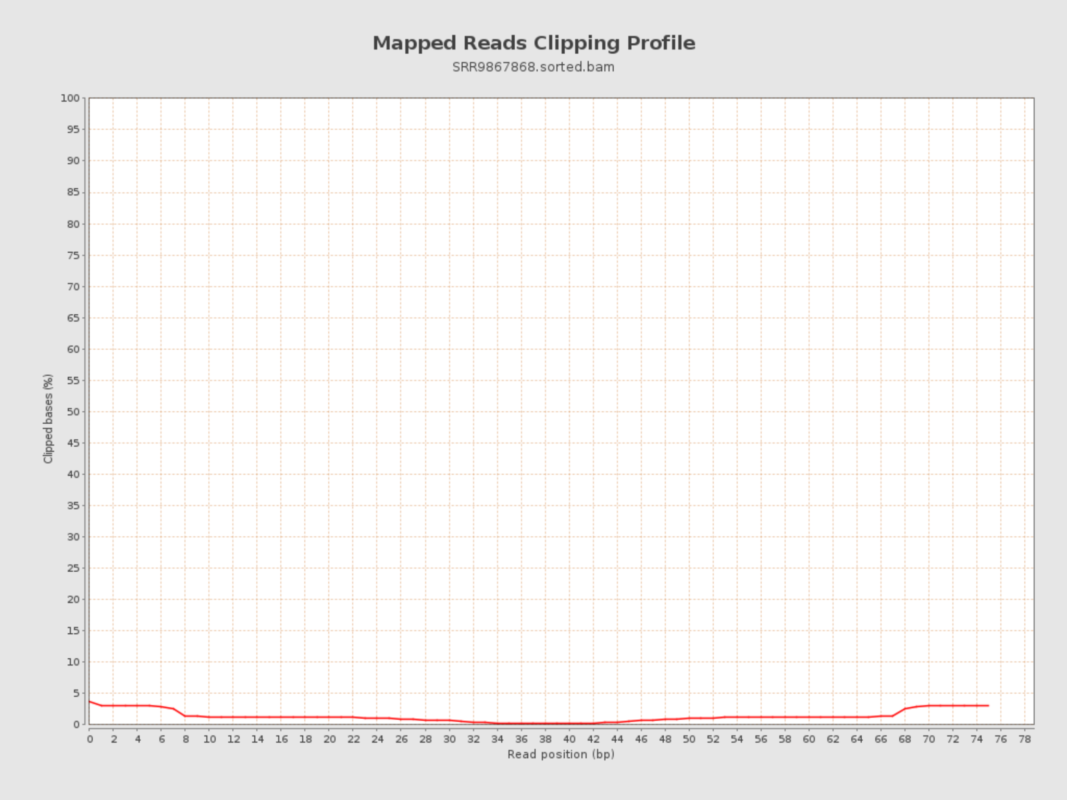
8. Results : Mapped Reads Nucleotide Content



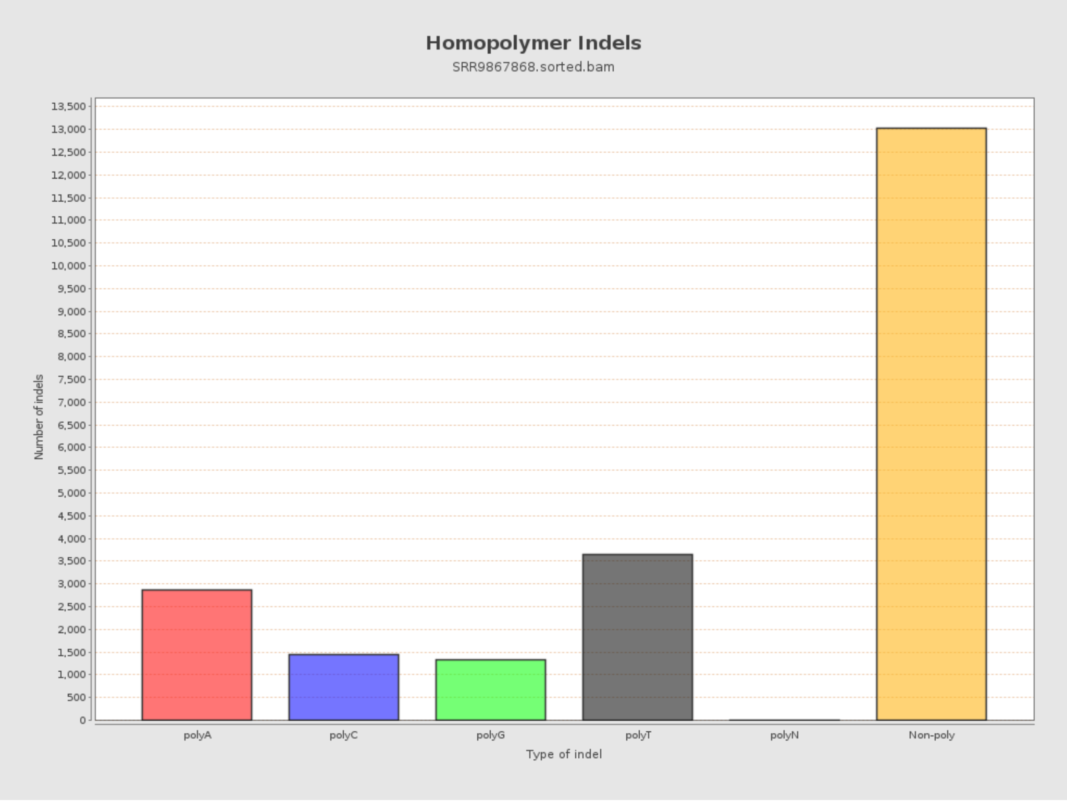
9. Results : Mapped Reads GC-content Distribution



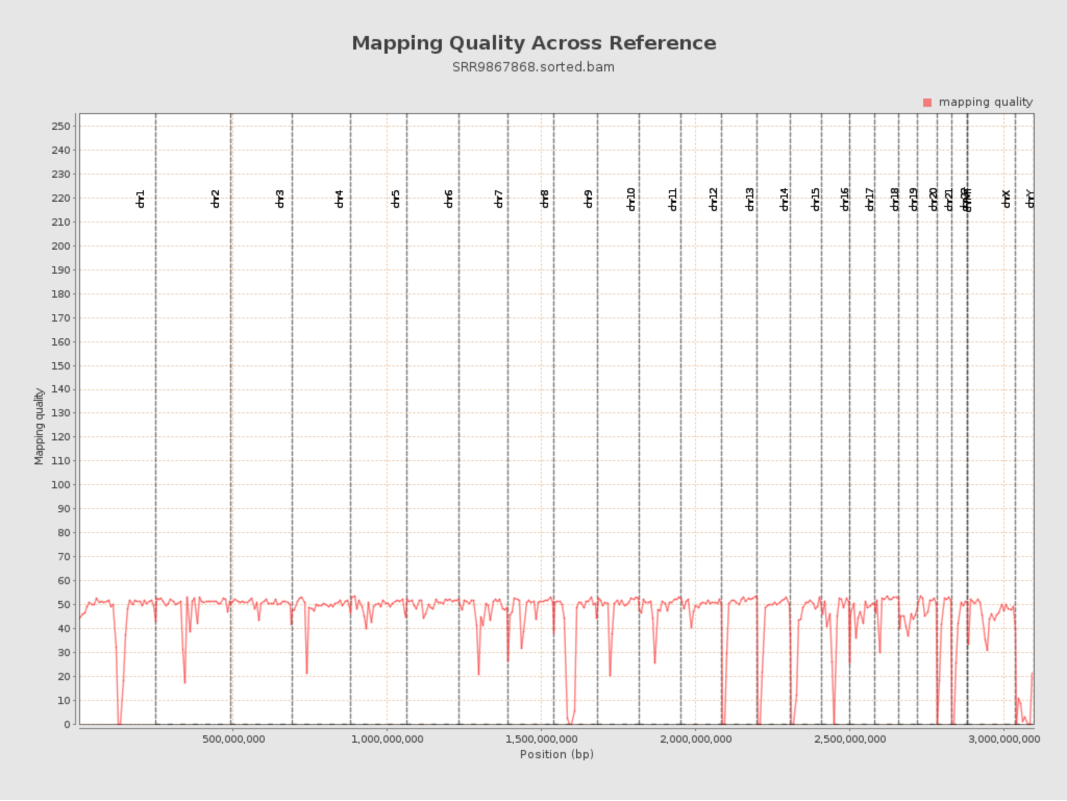
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram