Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:02:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083762.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_SRR3083762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:02:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,033
Mapped reads	1,611,167 / 72.94%
Unmapped reads	597,866 / 27.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,215 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	48,175 / 2.18%
Duplication rate	2.4%
Clipped reads	854,674 / 38.69%

2.2. ACGT Content

Number/percentage of A's	29,020,116 / 28.23%
Number/percentage of C's	19,790,413 / 19.25%
Number/percentage of T's	30,037,344 / 29.22%
Number/percentage of G's	23,956,519 / 23.3%
Number/percentage of N's	1,123 / 0%
GC Percentage	42.55%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.2562

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

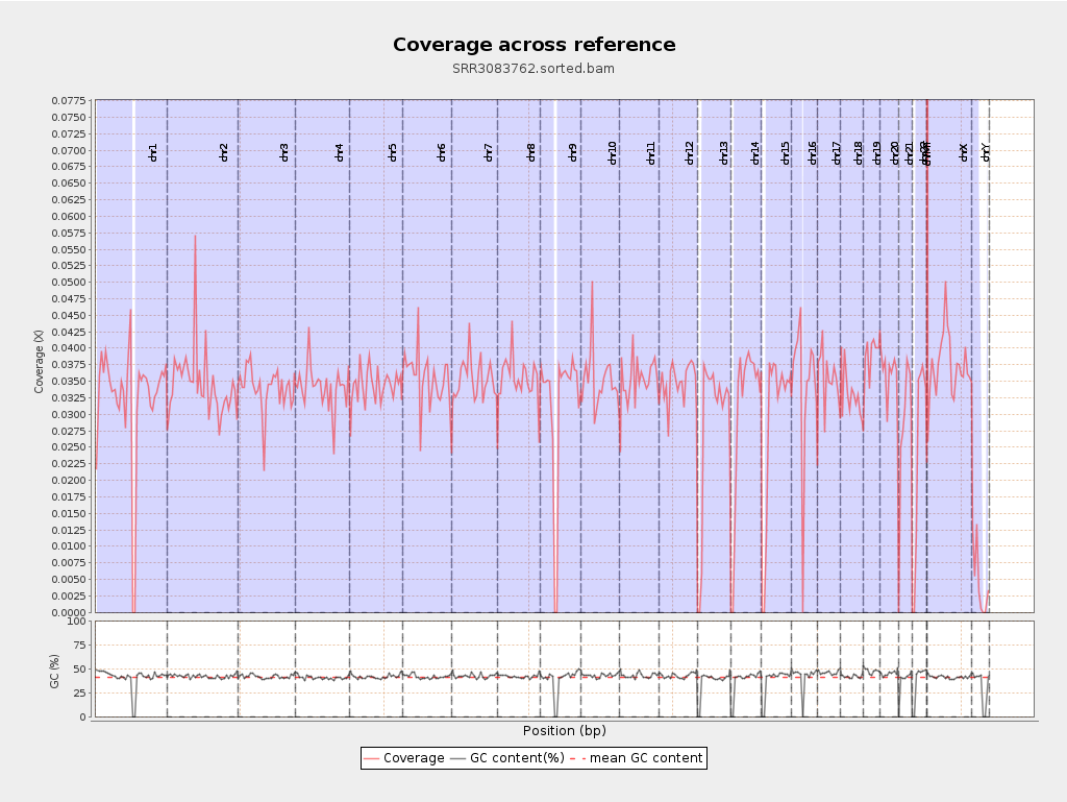
General error rate	0.9%
Mismatches	909,684
Insertions	7,260
Mapped reads with at least one insertion	0.45%
Deletions	22,585
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.76%

2.6. Chromosome stats

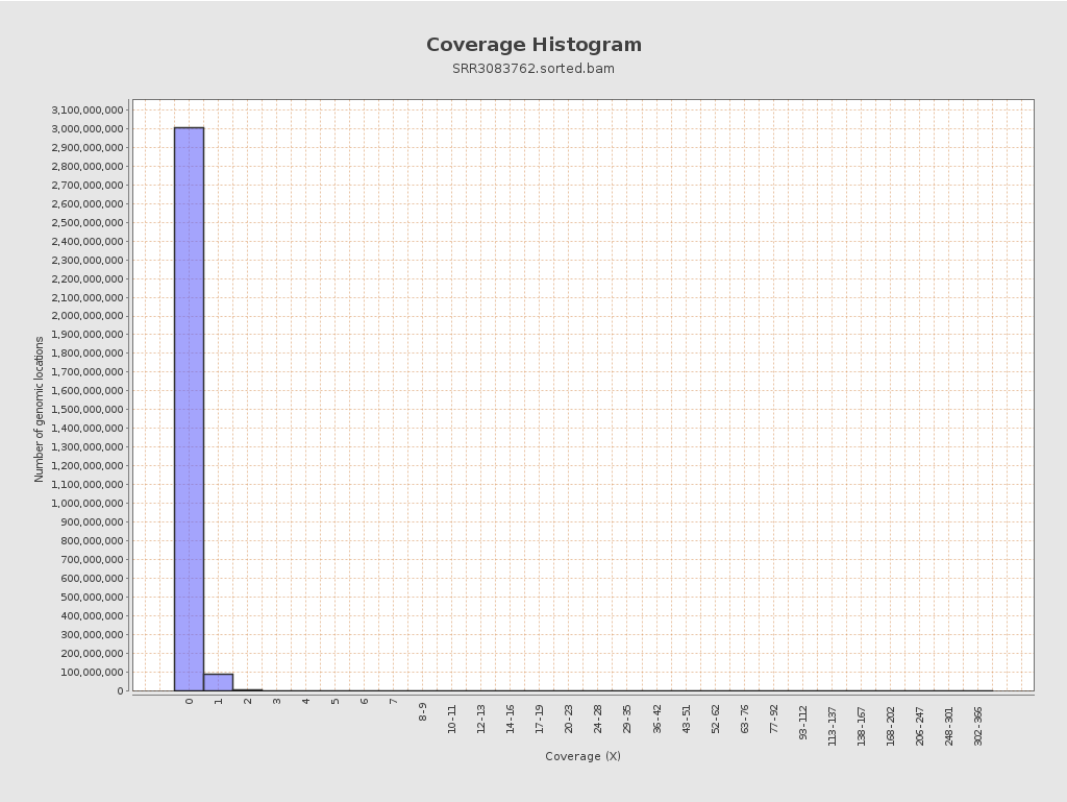
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8047543	0.0323	0.3602
chr2	243199373	8420148	0.0346	0.3189
chr3	198022430	6725238	0.034	0.2008
chr4	191154276	6543477	0.0342	0.2106
chr5	180915260	6256173	0.0346	0.2021
chr6	171115067	6042078	0.0353	0.2332
chr7	159138663	5635727	0.0354	0.2837

chr8	146364022	5184298	0.0354	0.254
chr9	141213431	4425587	0.0313	0.2516
chr10	135534747	4783588	0.0353	0.2676
chr11	135006516	4796713	0.0355	0.2458
chr12	133851895	4669742	0.0349	0.2042
chr13	115169878	3266324	0.0284	0.1819
chr14	107349540	3260038	0.0304	0.1991
chr15	102531392	2944190	0.0287	0.1924
chr16	90354753	3073591	0.034	0.2203
chr17	81195210	2896821	0.0357	0.2295
chr18	78077248	2569142	0.0329	0.4663
chr19	59128983	2302479	0.0389	0.3115
chr20	63025520	2262656	0.0359	0.2115
chr21	48129895	1372526	0.0285	0.193
chr22	51304566	1244538	0.0243	0.1692
chrMT	16571	34726	2.0956	1.7592
chrX	155270560	5819256	0.0375	0.2296
chrY	59373566	266028	0.0045	0.1015

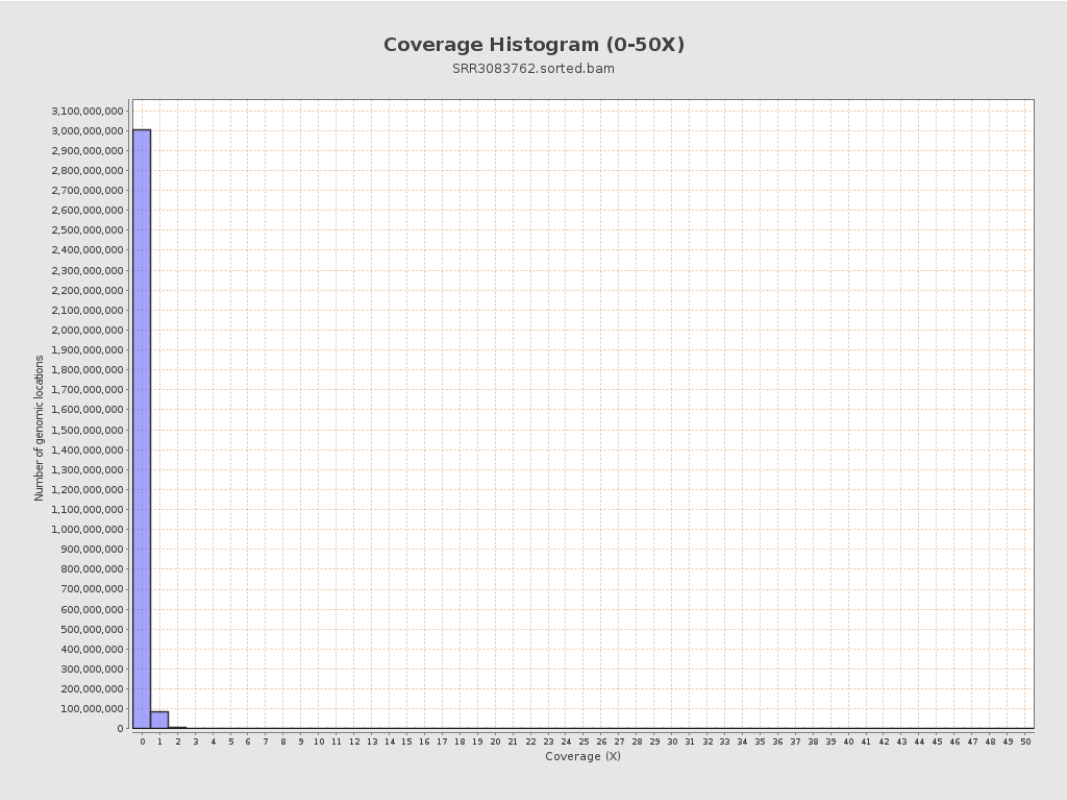
3. Results : Coverage across reference



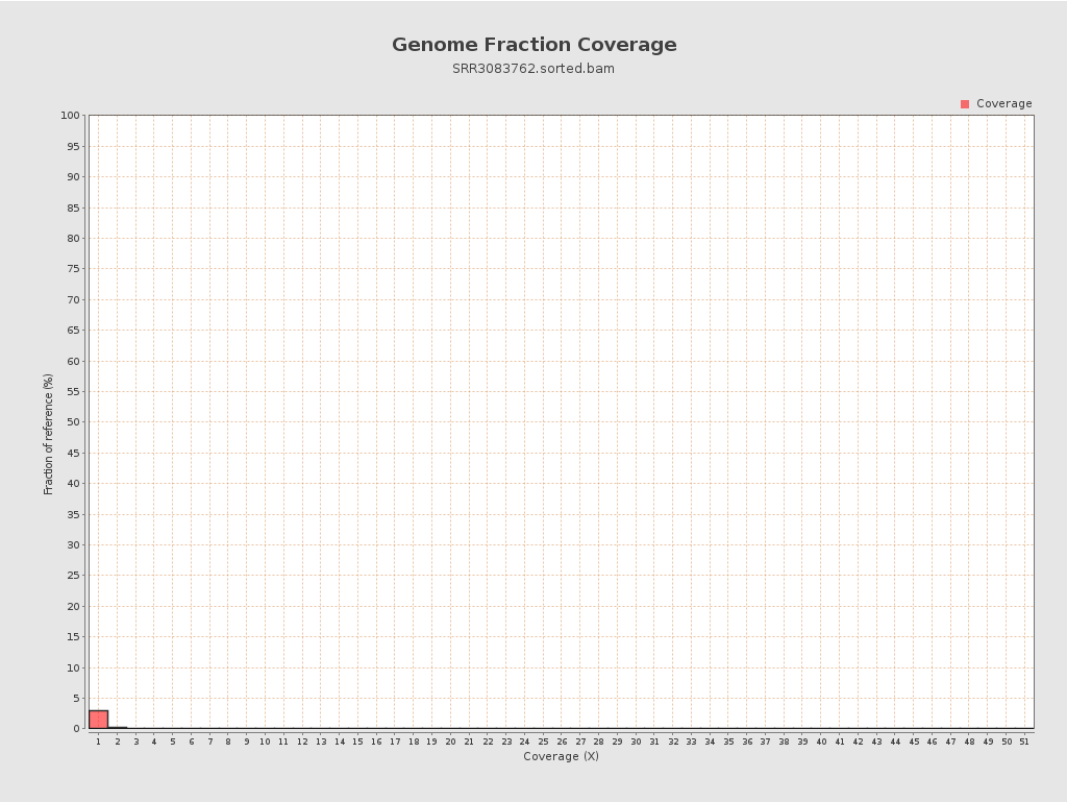
4. Results : Coverage Histogram



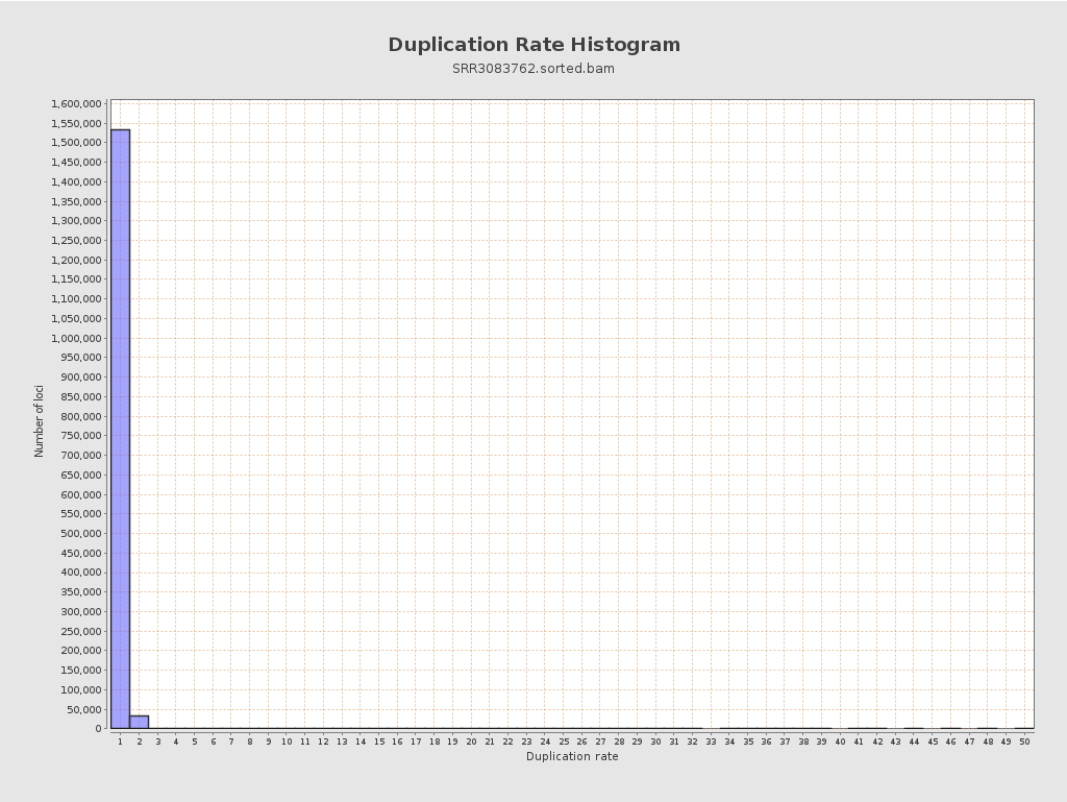
5. Results : Coverage Histogram (0-50X)



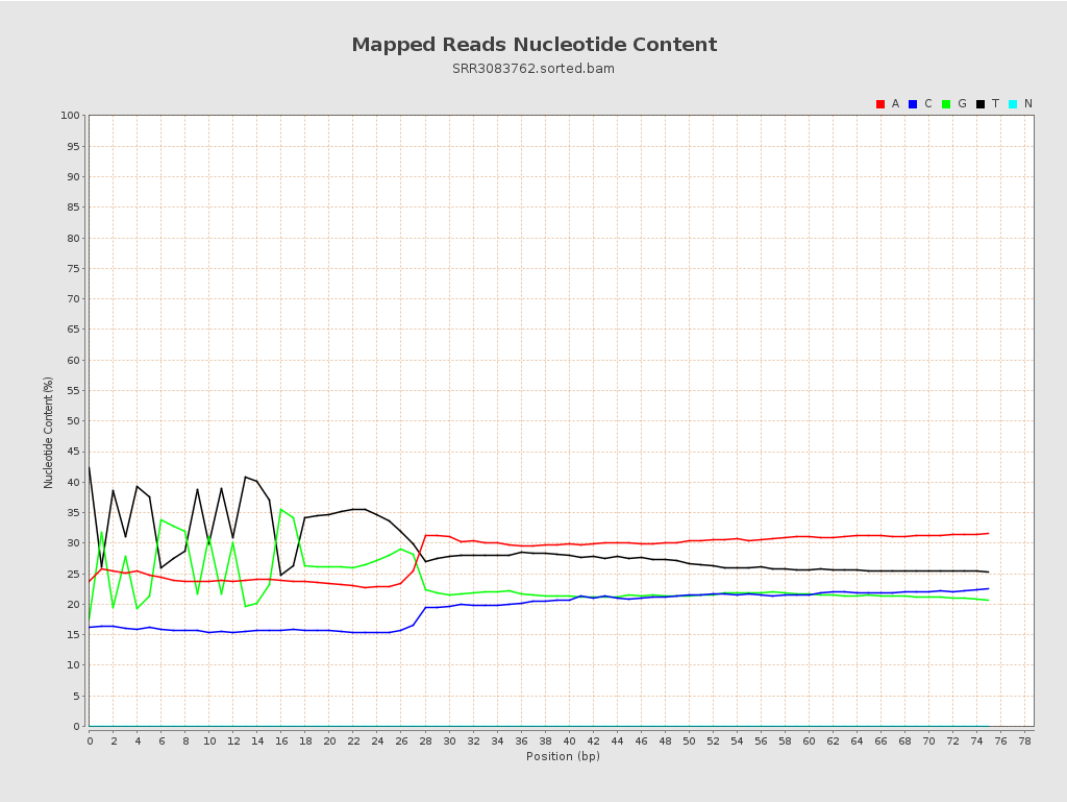
6. Results : Genome Fraction Coverage



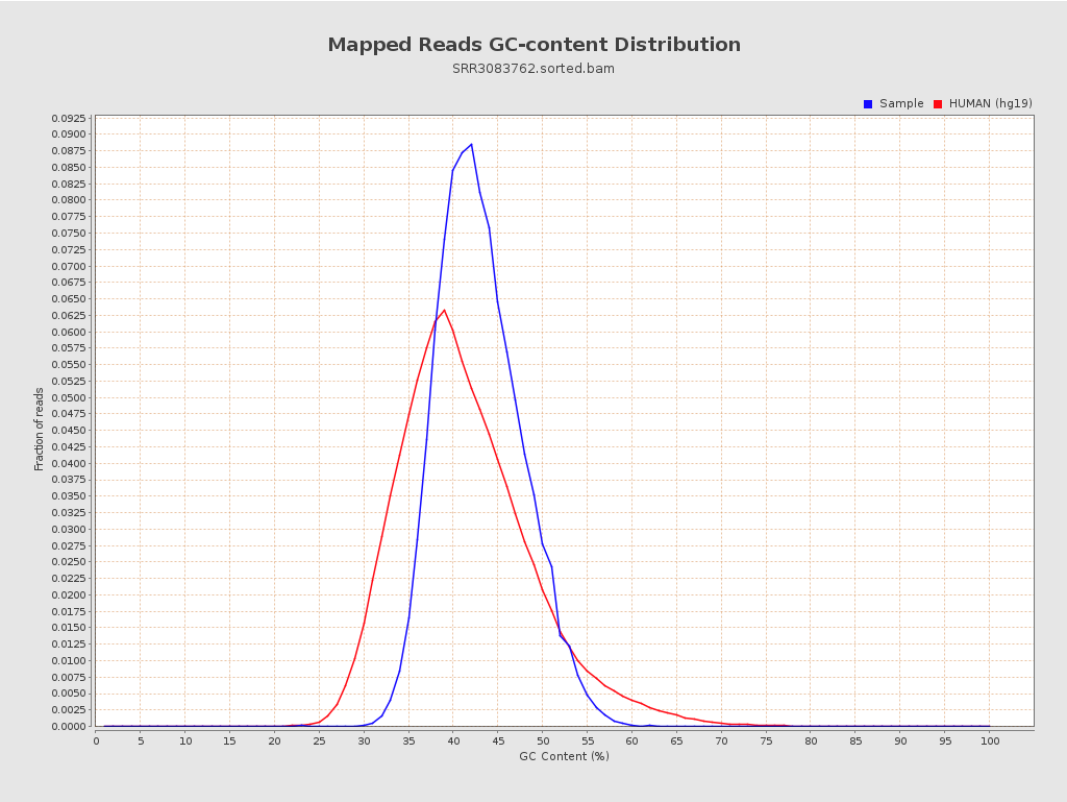
7. Results : Duplication Rate Histogram



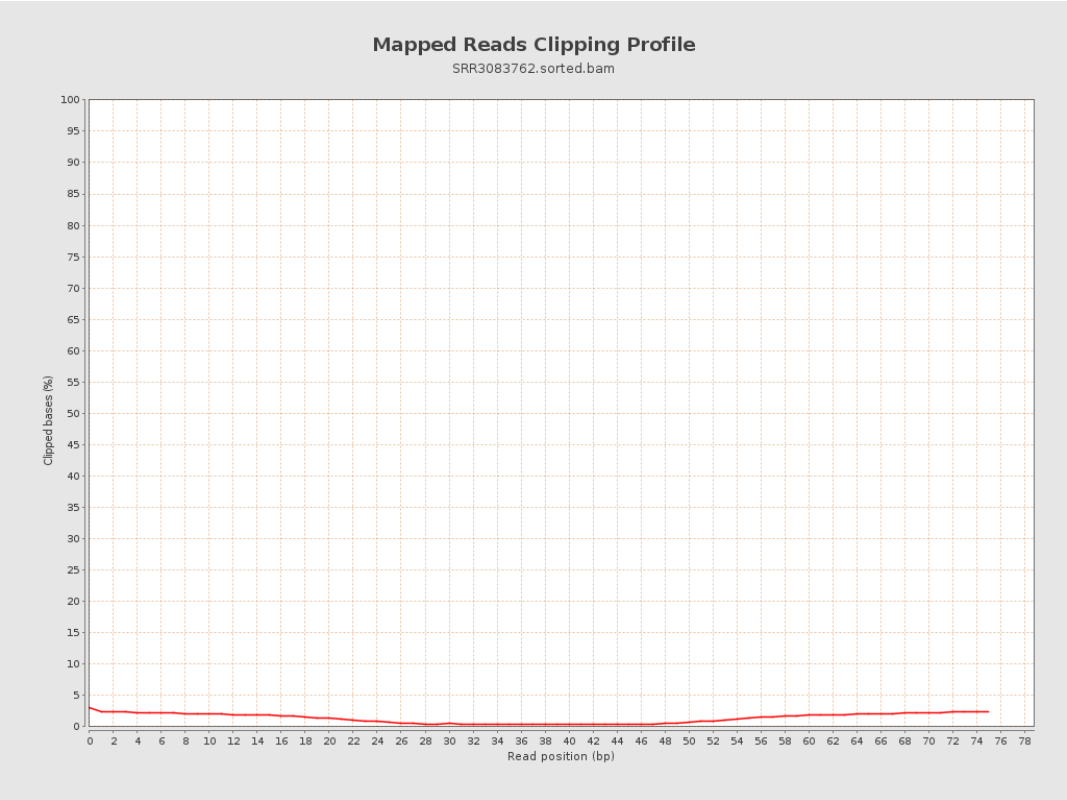
8. Results : Mapped Reads Nucleotide Content



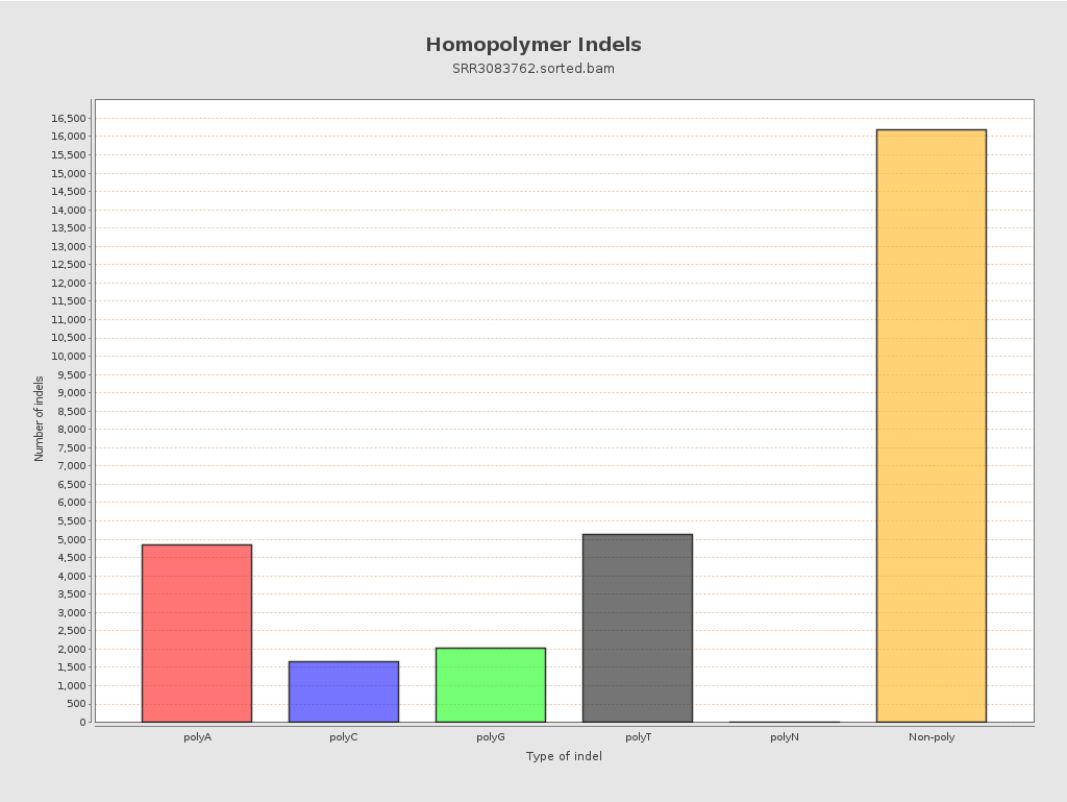
9. Results : Mapped Reads GC-content Distribution



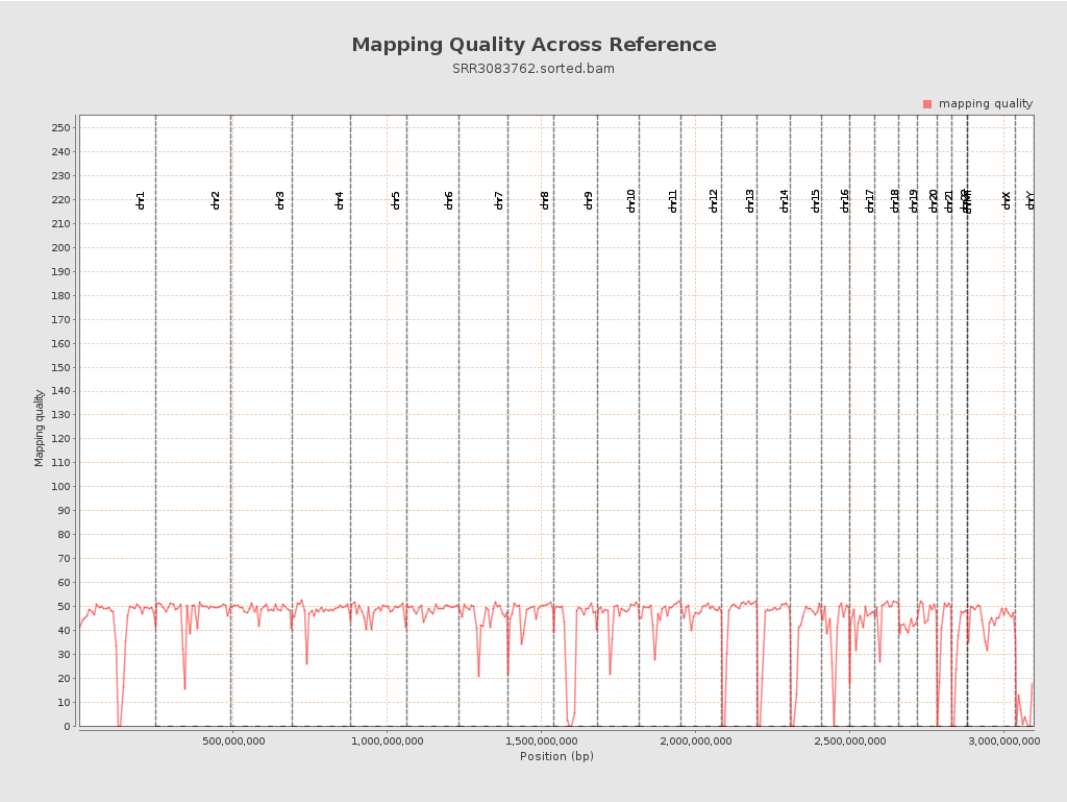
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram