Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:07:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083632.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_SRR3083632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:07:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,414,425
Mapped reads	2,021,267 / 83.72%
Unmapped reads	393,158 / 16.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,896 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	49,751 / 2.06%
Duplication rate	1.94%
Clipped reads	1,398,473 / 57.92%

2.2. ACGT Content

Number/percentage of A's	36,693,899 / 30.05%
Number/percentage of C's	24,011,217 / 19.67%
Number/percentage of T's	35,573,880 / 29.14%
Number/percentage of G's	25,802,962 / 21.13%
Number/percentage of N's	16,701 / 0.01%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0395

Standard Deviation	0.2949

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

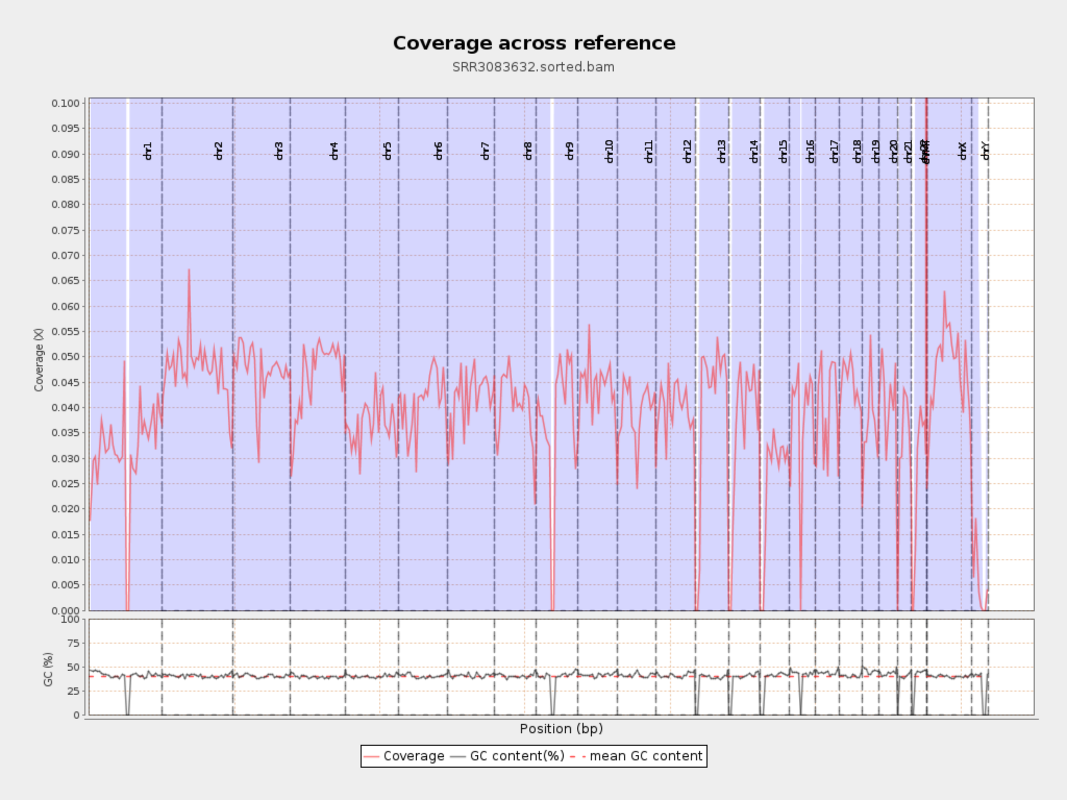
General error rate	0.85%
Mismatches	1,018,224
Insertions	8,749
Mapped reads with at least one insertion	0.43%
Deletions	25,966
Mapped reads with at least one deletion	1.27%
Homopolymer indels	45.77%

2.6. Chromosome stats

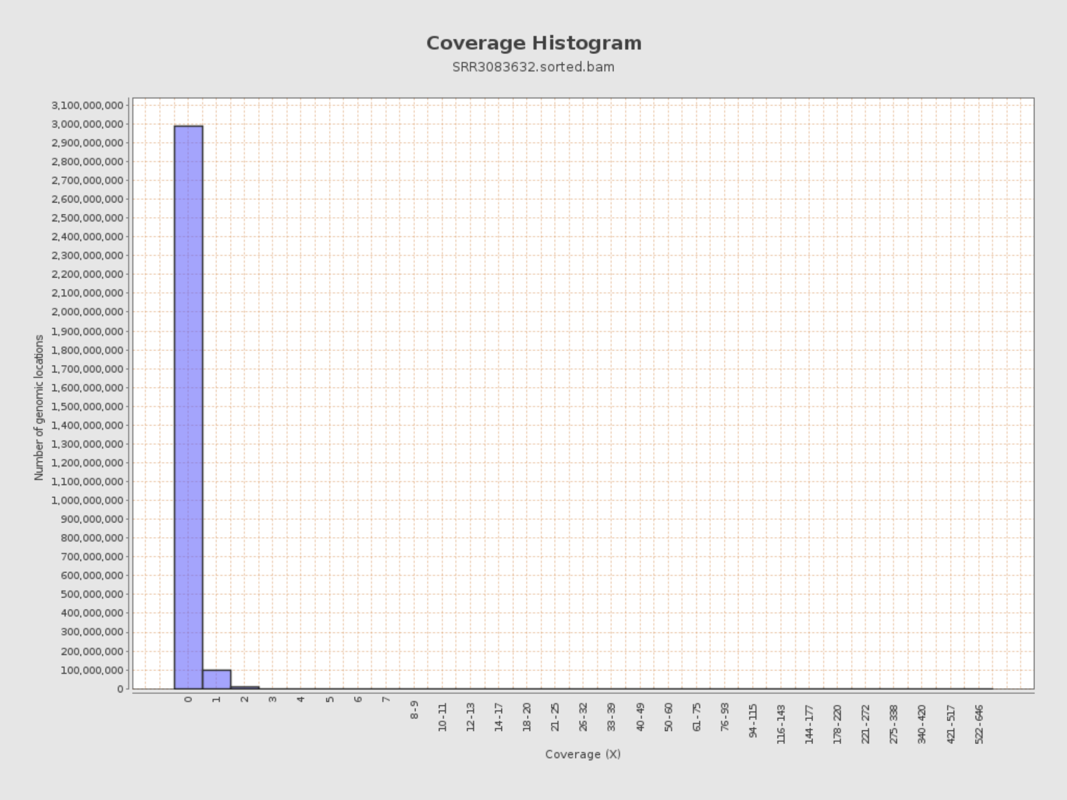
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7836260	0.0314	0.4917
chr2	243199373	11615203	0.0478	0.319
chr3	198022430	9369279	0.0473	0.2349
chr4	191154276	8839858	0.0462	0.2415
chr5	180915260	6639482	0.0367	0.2077
chr6	171115067	7043079	0.0412	0.2333
chr7	159138663	6723919	0.0423	0.3118

chr8	146364022	5861324	0.04	0.451
chr9	141213431	5204836	0.0369	0.2639
chr10	135534747	5987852	0.0442	0.2945
chr11	135006516	5321859	0.0394	0.2491
chr12	133851895	5349904	0.04	0.2186
chr13	115169878	4546411	0.0395	0.2139
chr14	107349540	3766333	0.0351	0.2101
chr15	102531392	2630805	0.0257	0.1733
chr16	90354753	3369808	0.0373	0.23
chr17	81195210	3197121	0.0394	0.2446
chr18	78077248	3508171	0.0449	0.4406
chr19	59128983	2202565	0.0373	0.361
chr20	63025520	2606211	0.0414	0.2251
chr21	48129895	1527817	0.0317	0.2034
chr22	51304566	1286313	0.0251	0.1697
chrMT	16571	26083	1.574	1.4879
chrX	155270560	7359227	0.0474	0.2519
chrY	59373566	320226	0.0054	0.1331

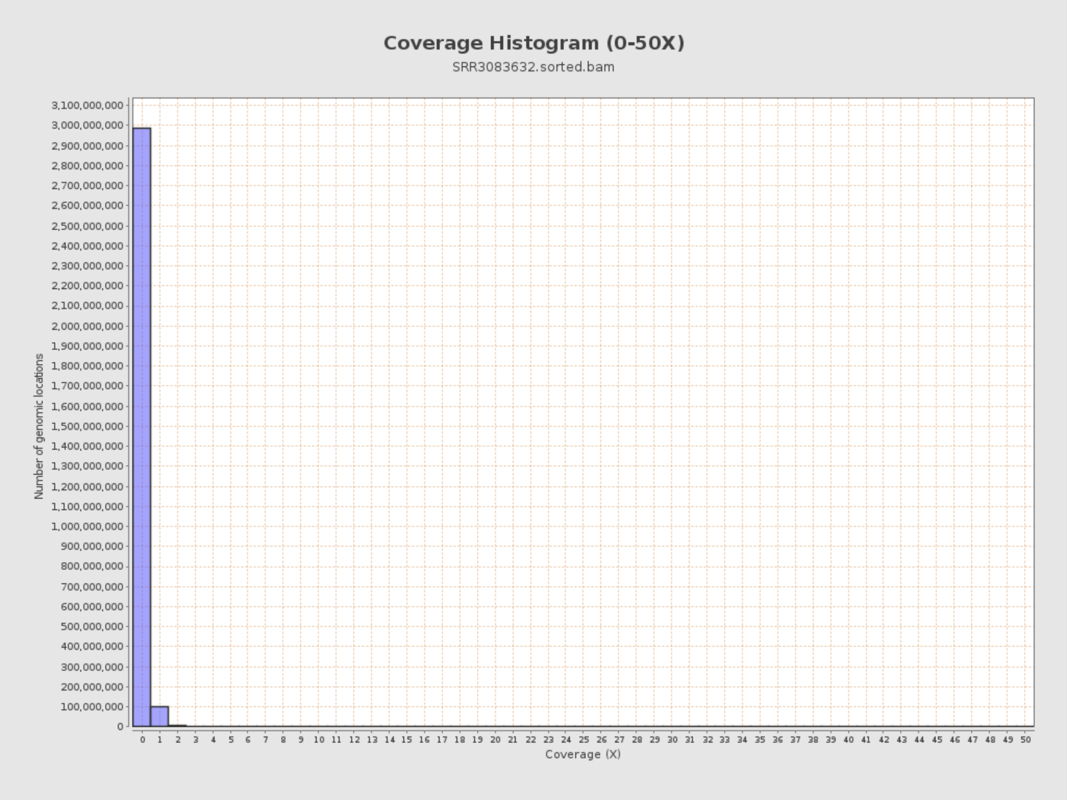
3. Results : Coverage across reference



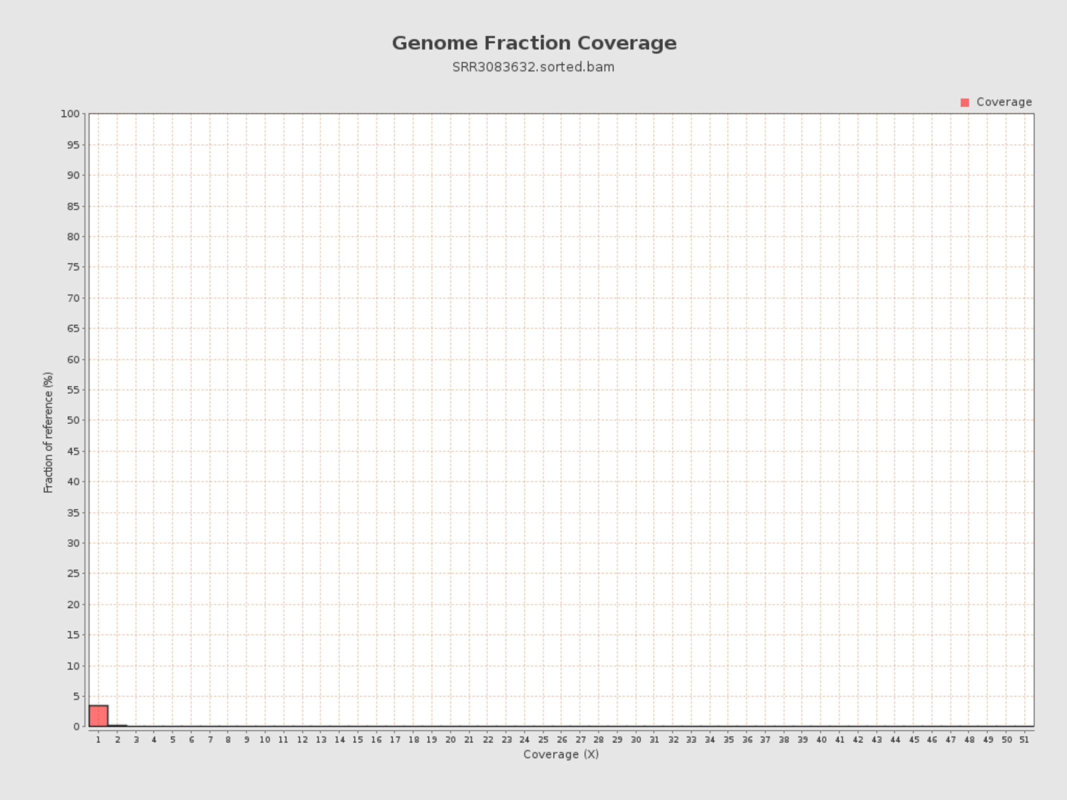
4. Results : Coverage Histogram



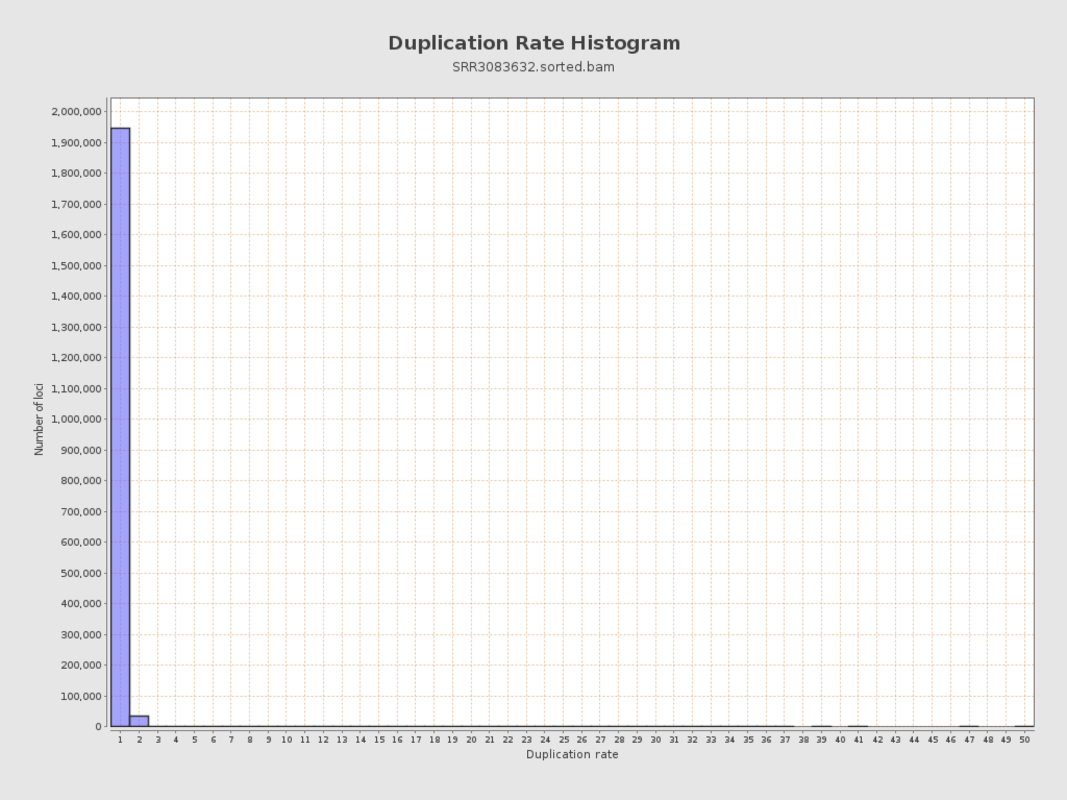
5. Results : Coverage Histogram (0-50X)



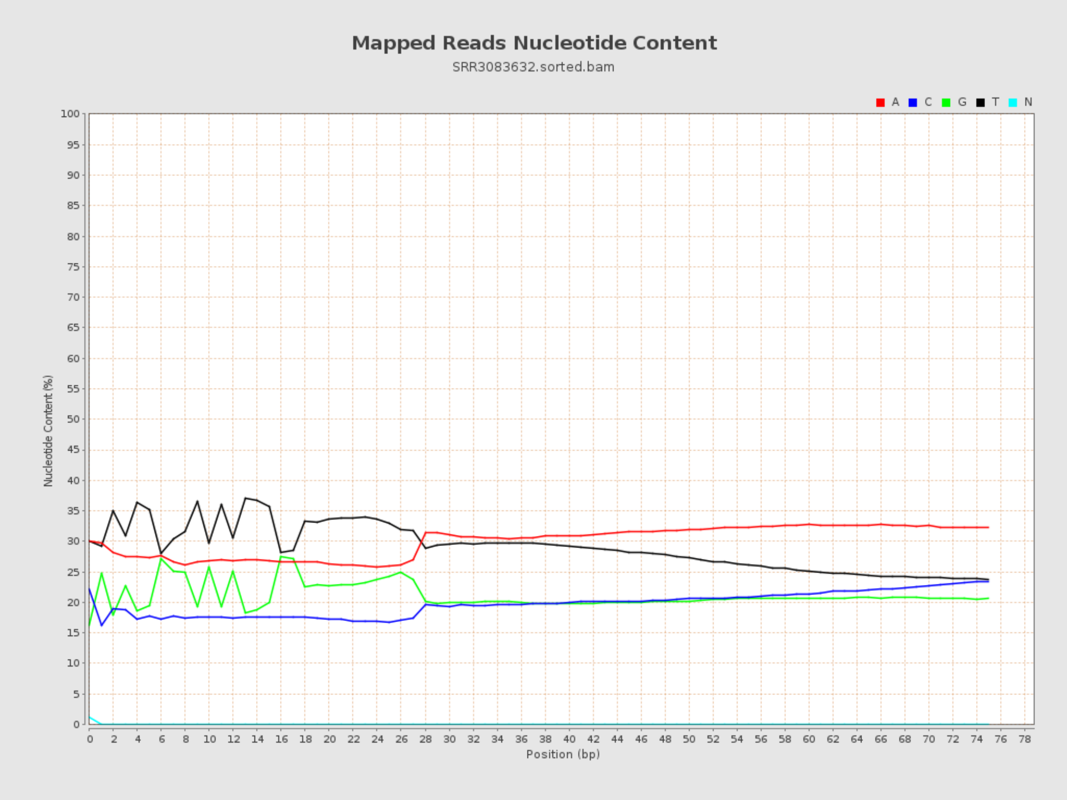
6. Results : Genome Fraction Coverage



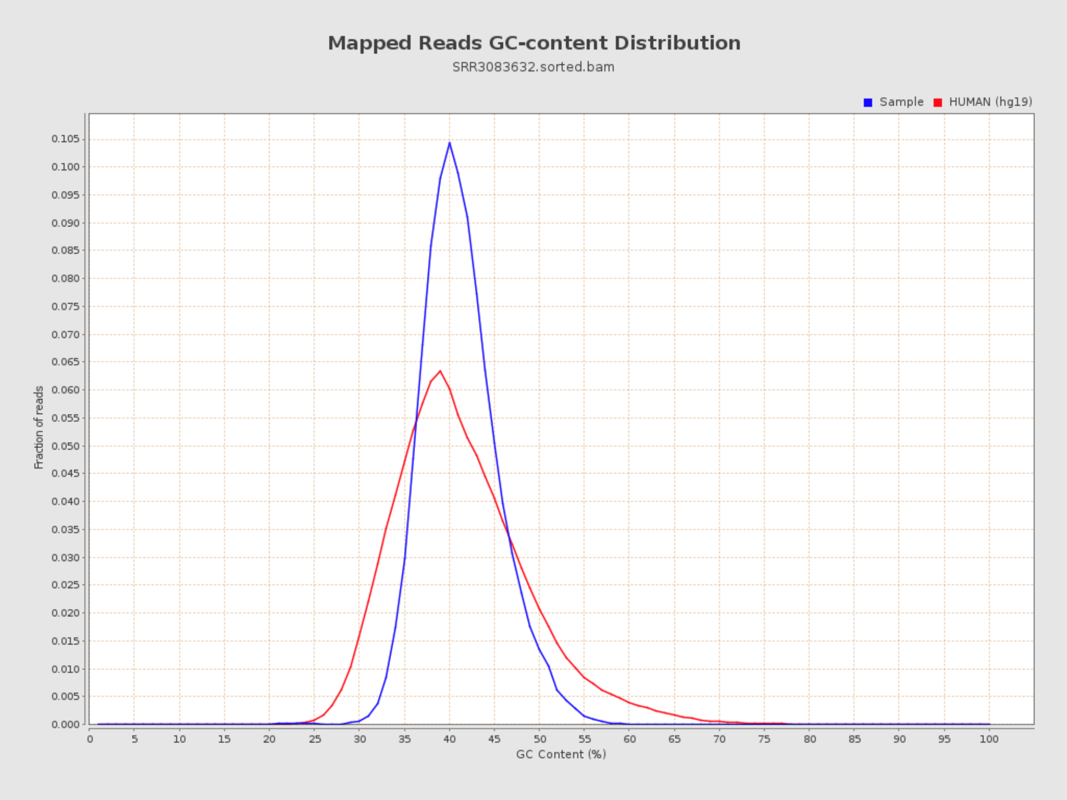
7. Results : Duplication Rate Histogram



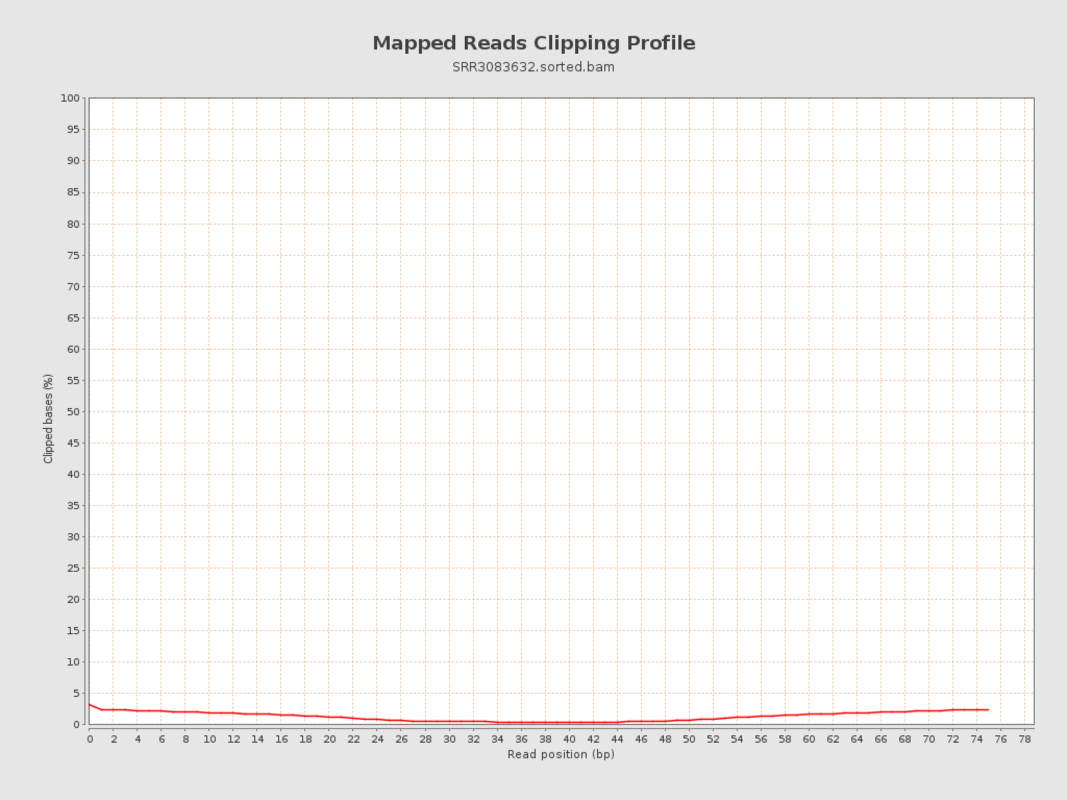
8. Results : Mapped Reads Nucleotide Content



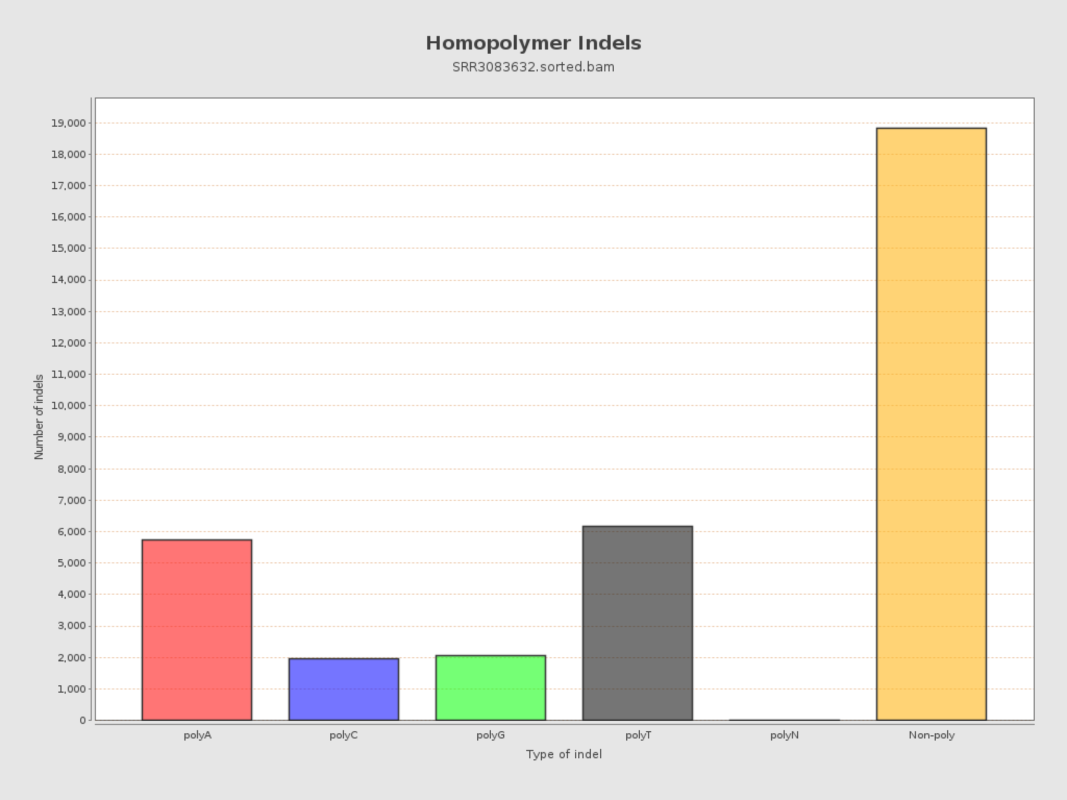
9. Results : Mapped Reads GC-content Distribution



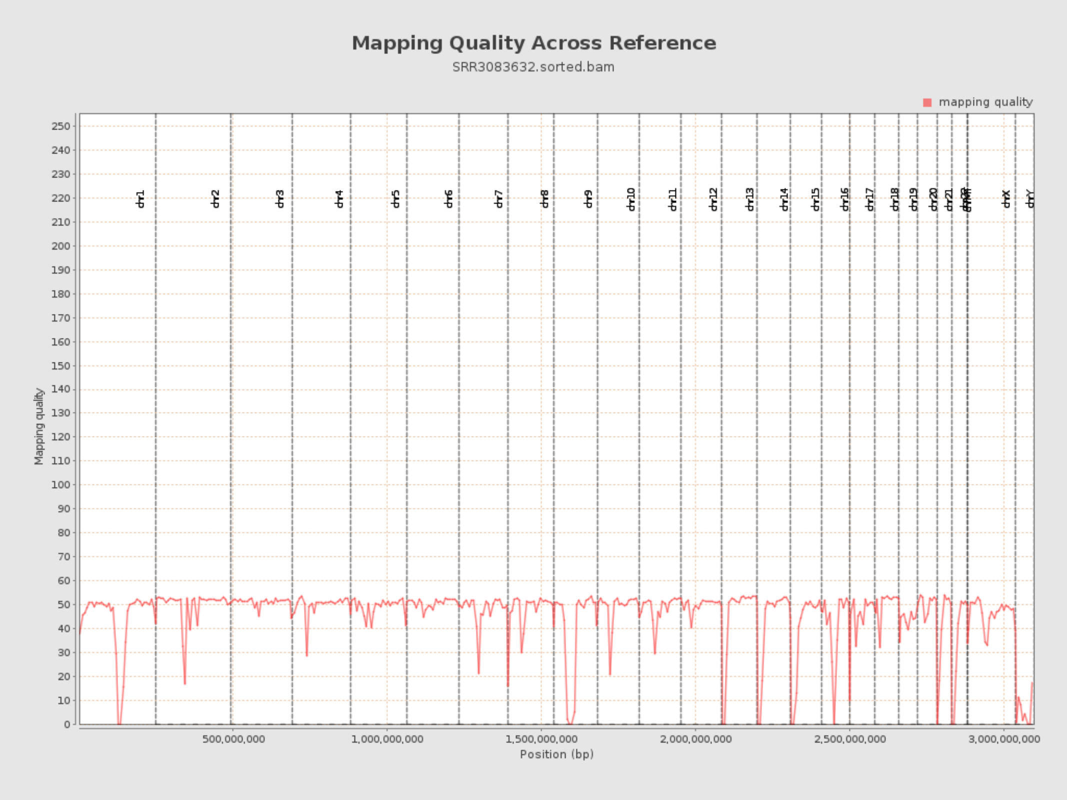
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram