Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:44:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083659.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_SRR3083659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:44:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,801
Mapped reads	1,671,095 / 81.45%
Unmapped reads	380,706 / 18.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,094 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	40,680 / 1.98%
Duplication rate	2%
Clipped reads	1,115,763 / 54.38%

2.2. ACGT Content

Number/percentage of A's	30,542,044 / 30%
Number/percentage of C's	19,587,202 / 19.24%
Number/percentage of T's	29,844,928 / 29.32%
Number/percentage of G's	21,818,647 / 21.43%
Number/percentage of N's	13,956 / 0.01%
GC Percentage	40.67%

2.3. Coverage

Mean	0.0329

Standard Deviation	0.2846

2.4. Mapping Quality

Mean Mapping Quality	45.57

2.5. Mismatches and indels

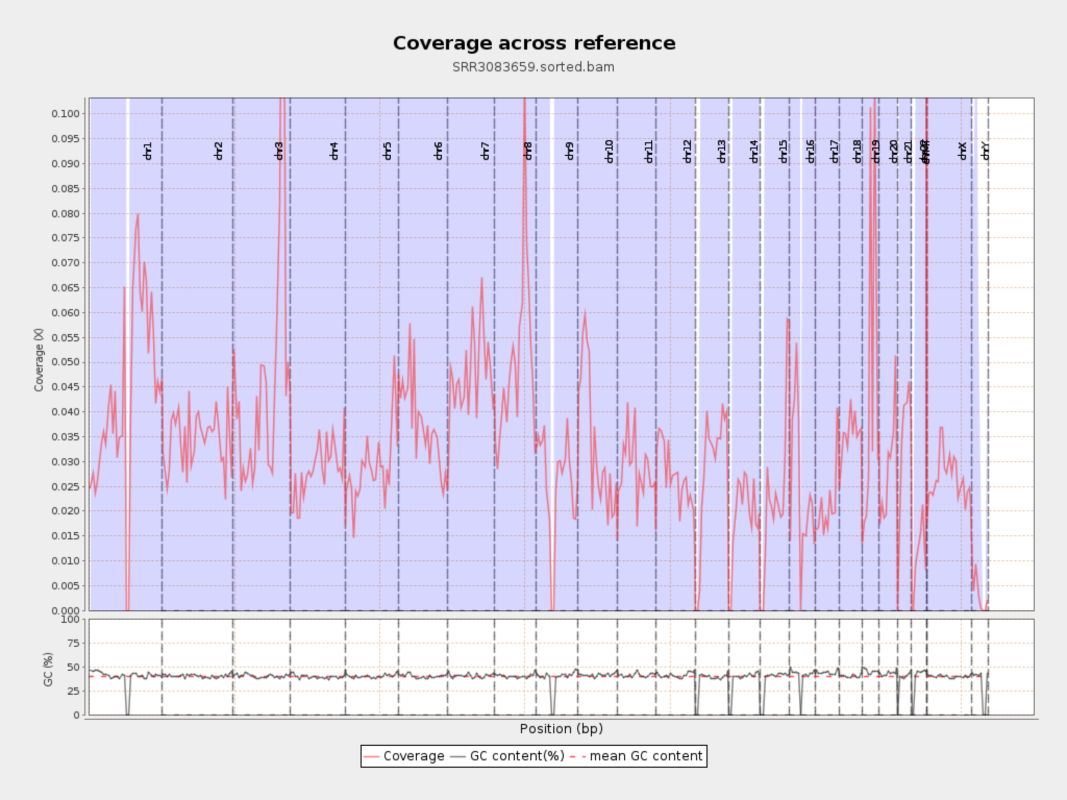
General error rate	0.83%
Mismatches	837,024
Insertions	7,052
Mapped reads with at least one insertion	0.42%
Deletions	20,011
Mapped reads with at least one deletion	1.19%
Homopolymer indels	45.76%

2.6. Chromosome stats

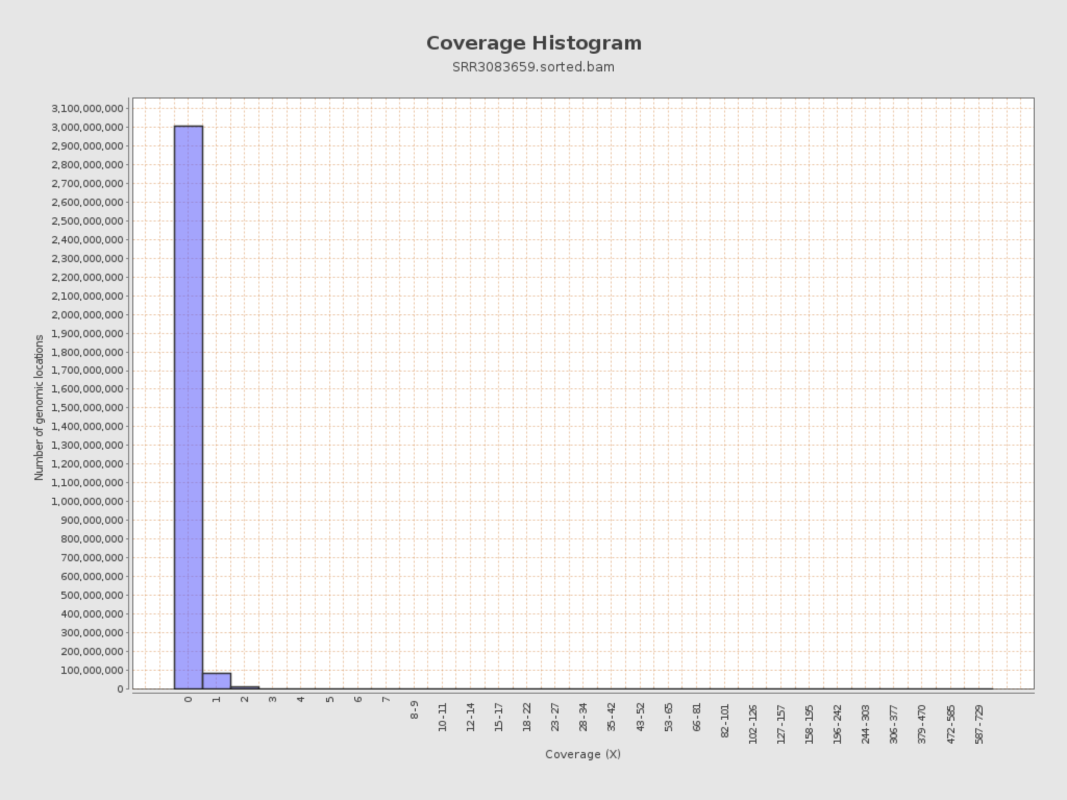
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10862107	0.0436	0.644
chr2	243199373	8393279	0.0345	0.2318
chr3	198022430	9379178	0.0474	0.2381
chr4	191154276	5421813	0.0284	0.1827
chr5	180915260	5232320	0.0289	0.1839
chr6	171115067	6431023	0.0376	0.238
chr7	159138663	7692003	0.0483	0.3474

chr8	146364022	7367322	0.0503	0.3505
chr9	141213431	3591140	0.0254	0.1909
chr10	135534747	4631480	0.0342	0.257
chr11	135006516	3830223	0.0284	0.1967
chr12	133851895	3638532	0.0272	0.1791
chr13	115169878	3240037	0.0281	0.1803
chr14	107349540	2026561	0.0189	0.1494
chr15	102531392	2294347	0.0224	0.1614
chr16	90354753	2256814	0.025	0.1752
chr17	81195210	1788834	0.022	0.1654
chr18	78077248	2767016	0.0354	0.2772
chr19	59128983	2697616	0.0456	0.4083
chr20	63025520	1817968	0.0288	0.186
chr21	48129895	1595370	0.0331	0.1984
chr22	51304566	553478	0.0108	0.1104
chrMT	16571	5134	0.3098	0.6063
chrX	155270560	4143560	0.0267	0.1801
chrY	59373566	181811	0.0031	0.0668

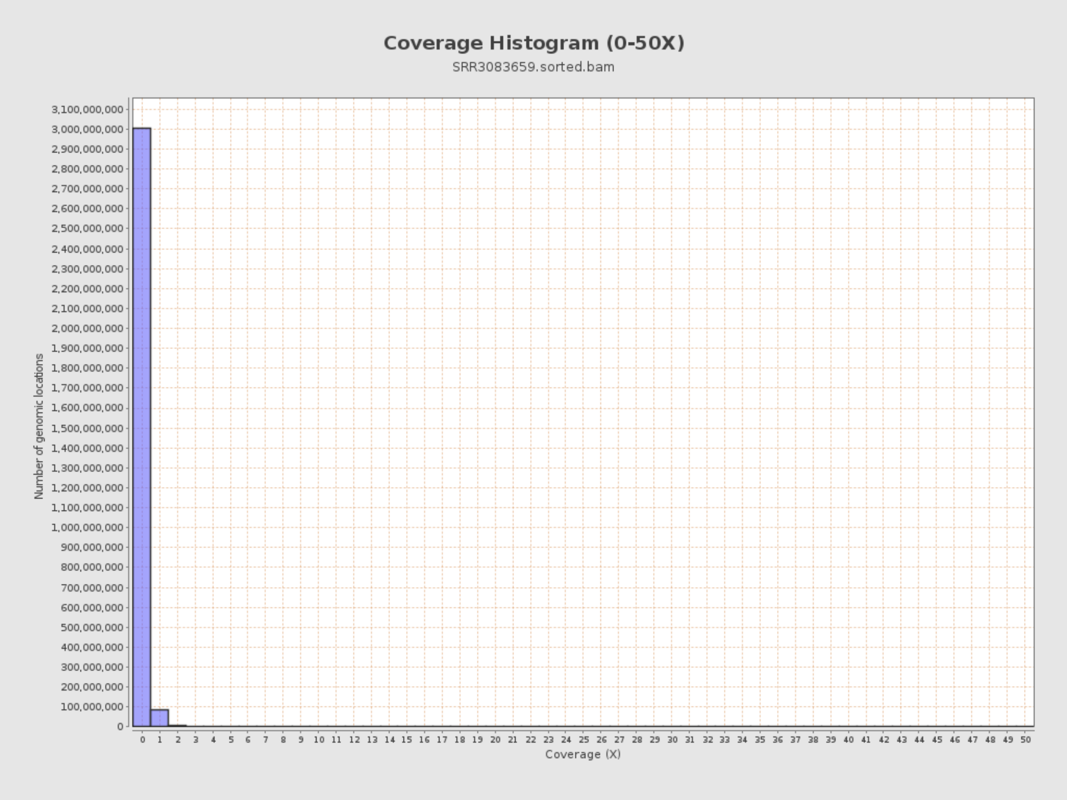
3. Results : Coverage across reference



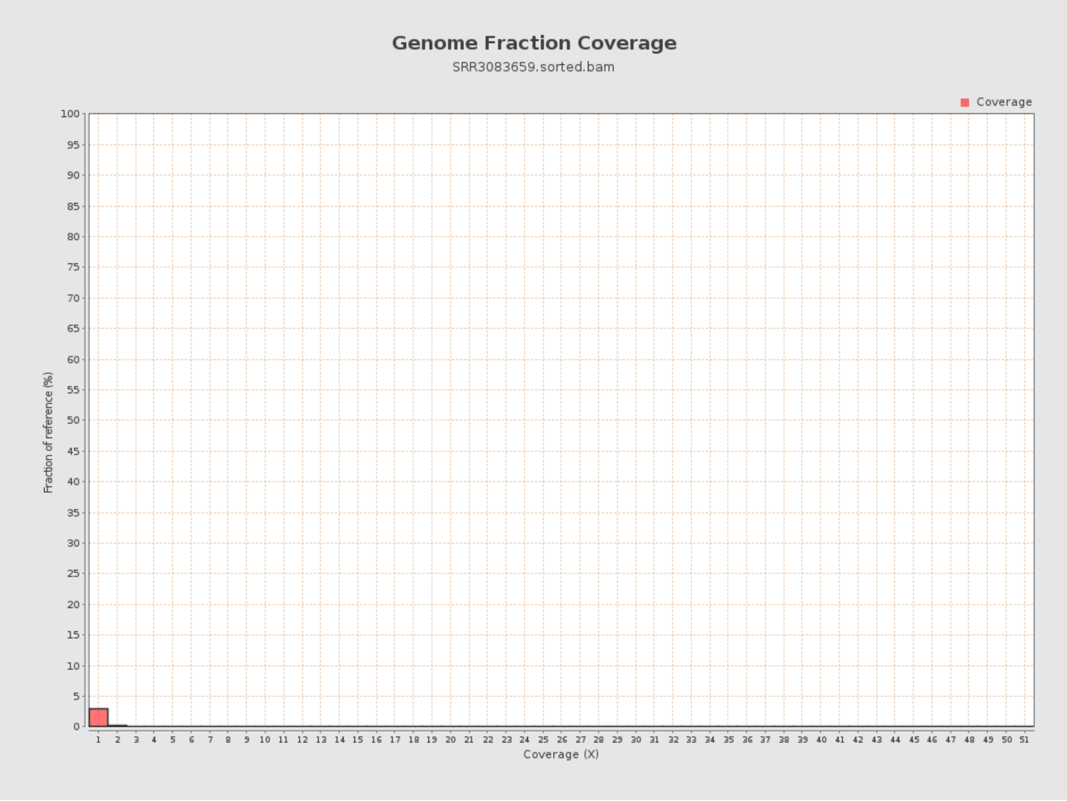
4. Results : Coverage Histogram



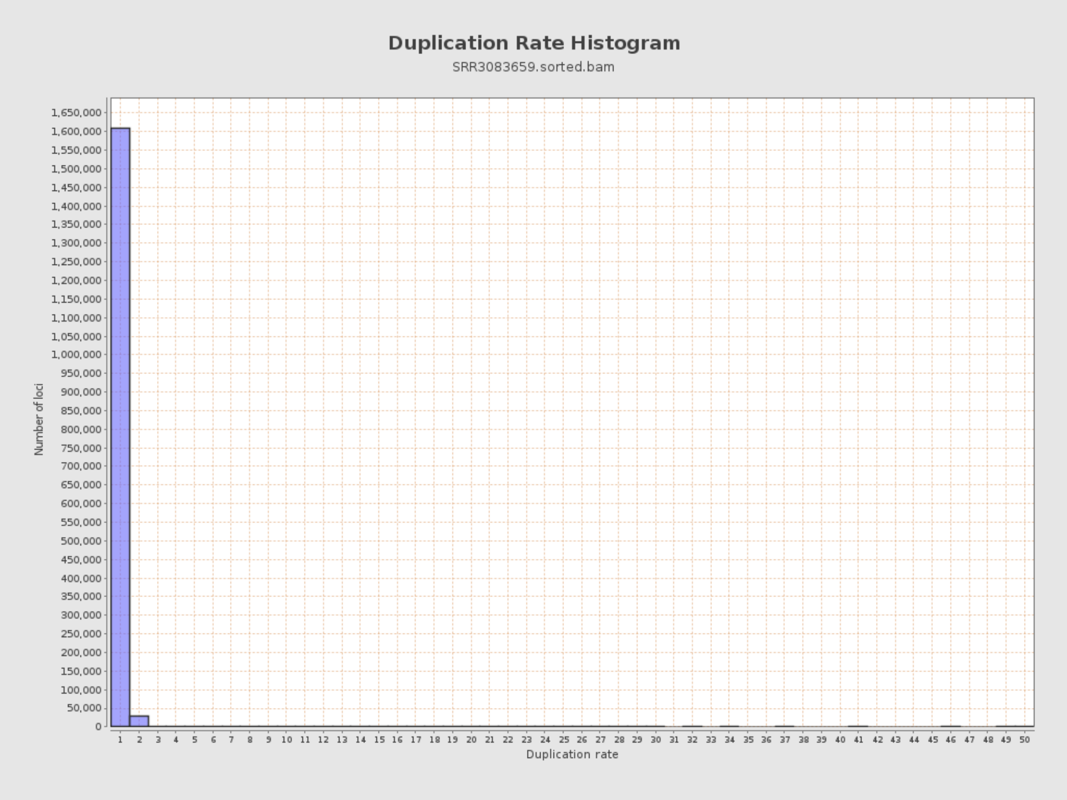
5. Results : Coverage Histogram (0-50X)



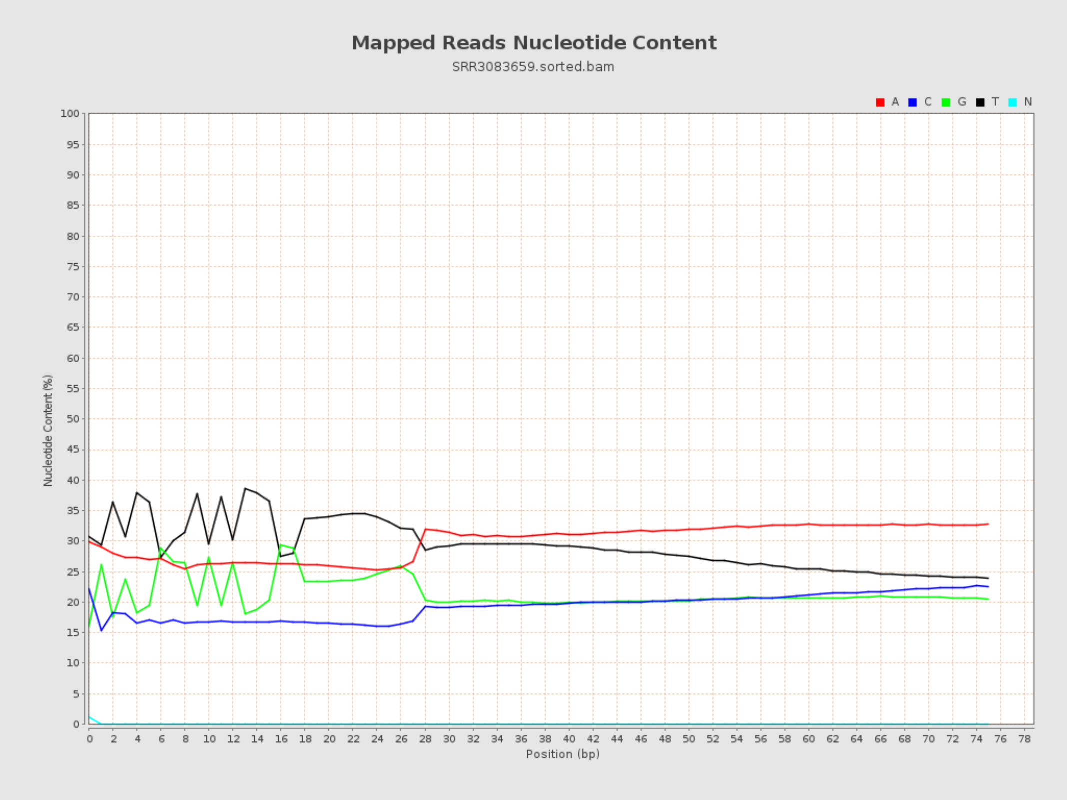
6. Results : Genome Fraction Coverage



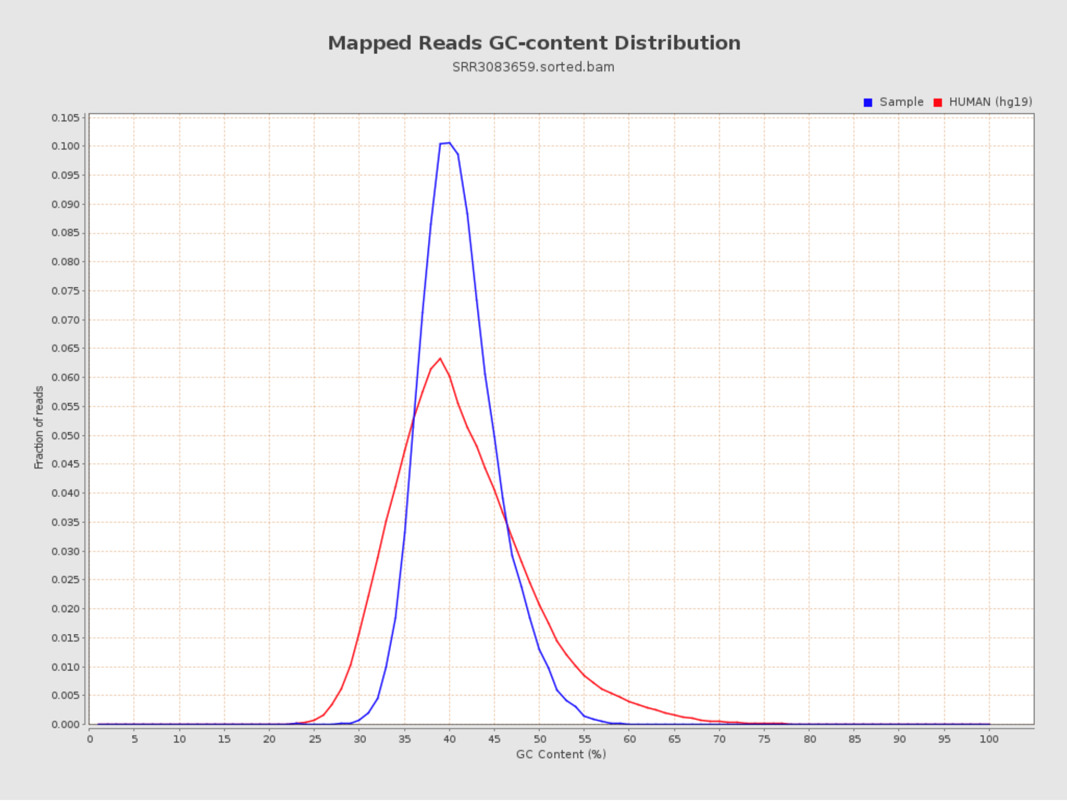
7. Results : Duplication Rate Histogram



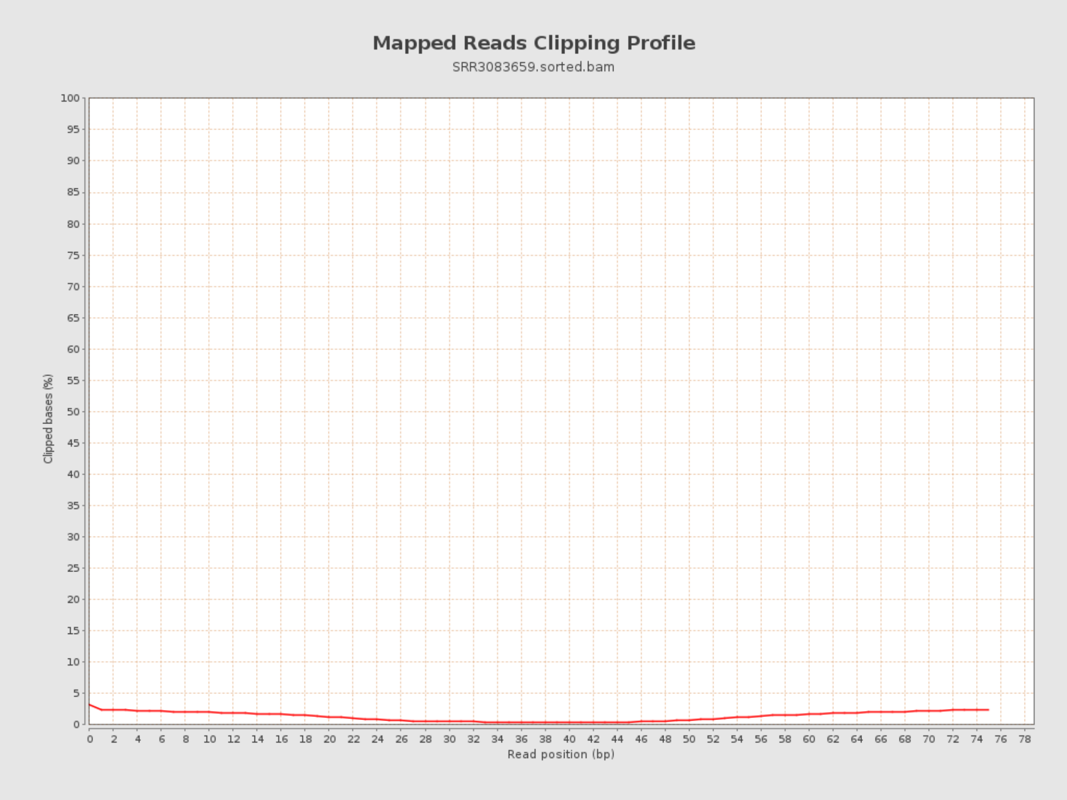
8. Results : Mapped Reads Nucleotide Content



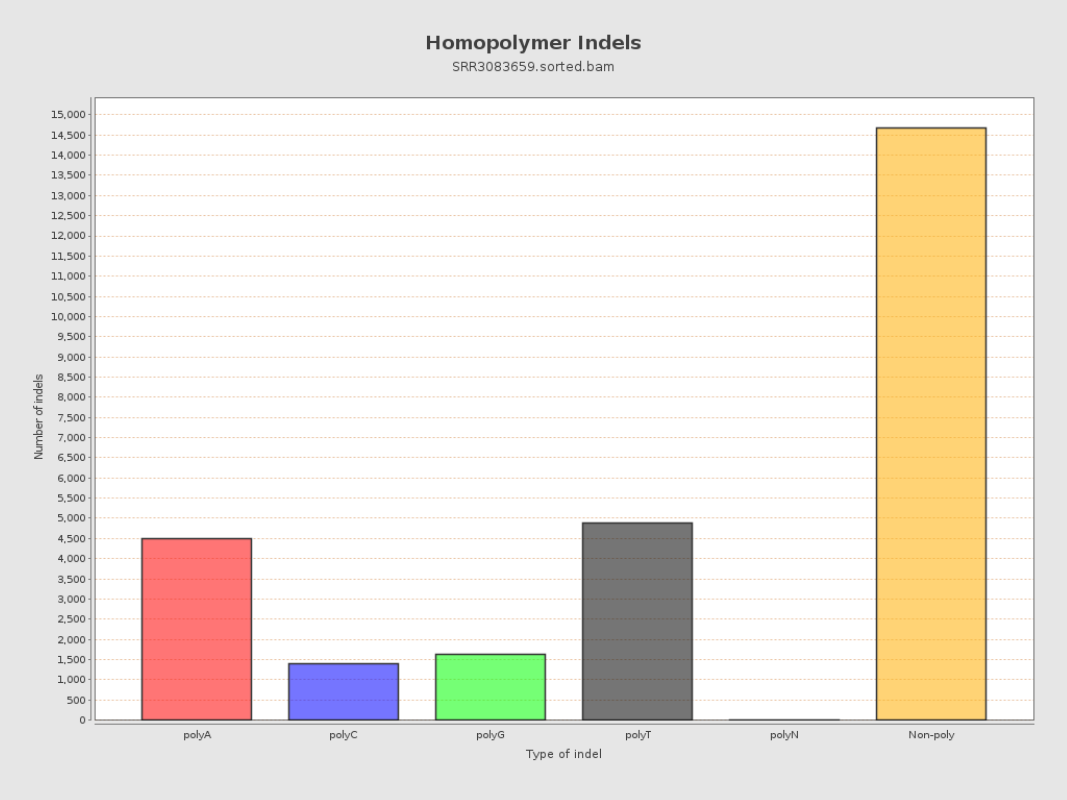
9. Results : Mapped Reads GC-content Distribution



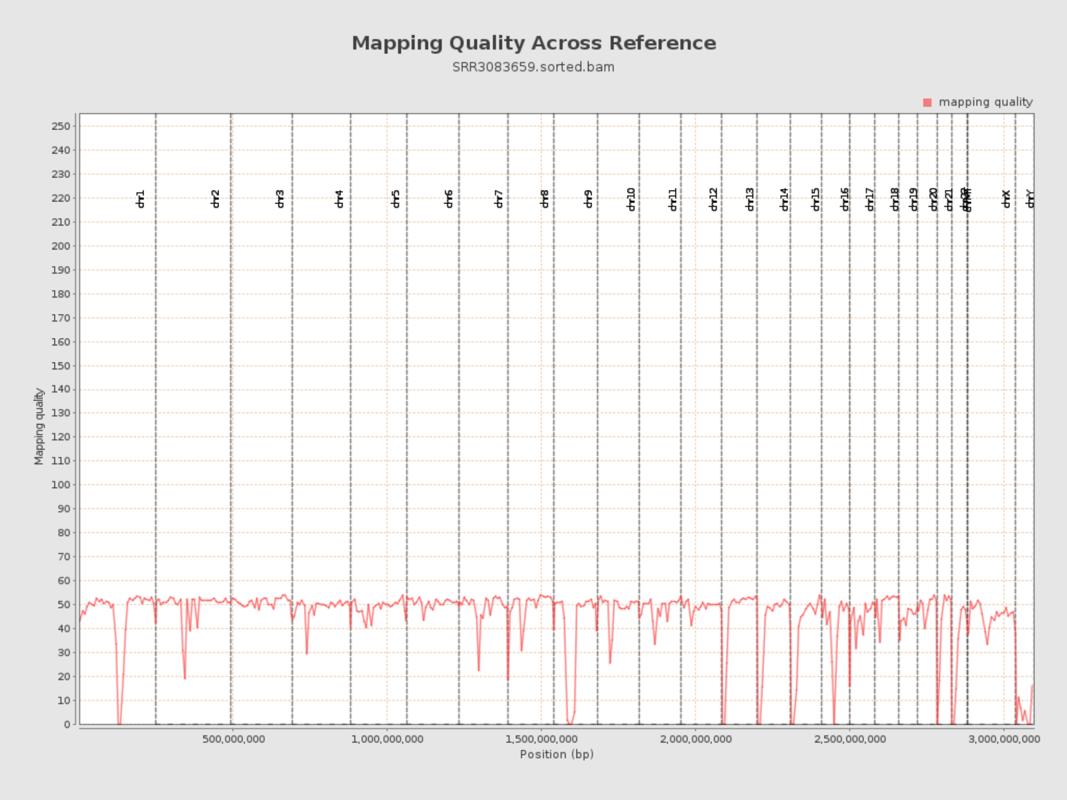
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram