Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:12:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083633.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_SRR3083633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:12:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,538,261
Mapped reads	2,113,379 / 83.26%
Unmapped reads	424,882 / 16.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,396 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	71,883 / 2.83%
Duplication rate	2.72%
Clipped reads	1,477,246 / 58.2%

2.2. ACGT Content

Number/percentage of A's	37,826,584 / 29.74%
Number/percentage of C's	24,783,871 / 19.49%
Number/percentage of T's	37,533,717 / 29.51%
Number/percentage of G's	27,032,445 / 21.25%
Number/percentage of N's	17,127 / 0.01%
GC Percentage	40.74%

2.3. Coverage

Mean	0.0411

Standard Deviation	0.3463

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

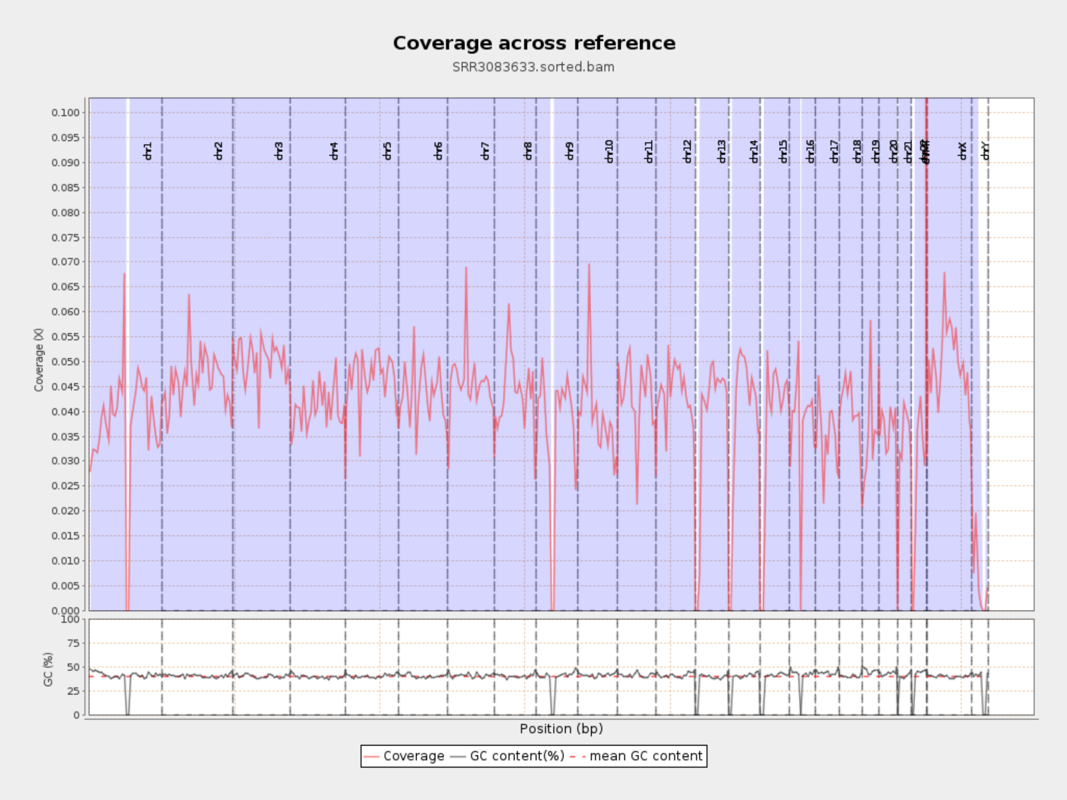
General error rate	0.84%
Mismatches	1,057,158
Insertions	9,150
Mapped reads with at least one insertion	0.43%
Deletions	26,129
Mapped reads with at least one deletion	1.23%
Homopolymer indels	45.74%

2.6. Chromosome stats

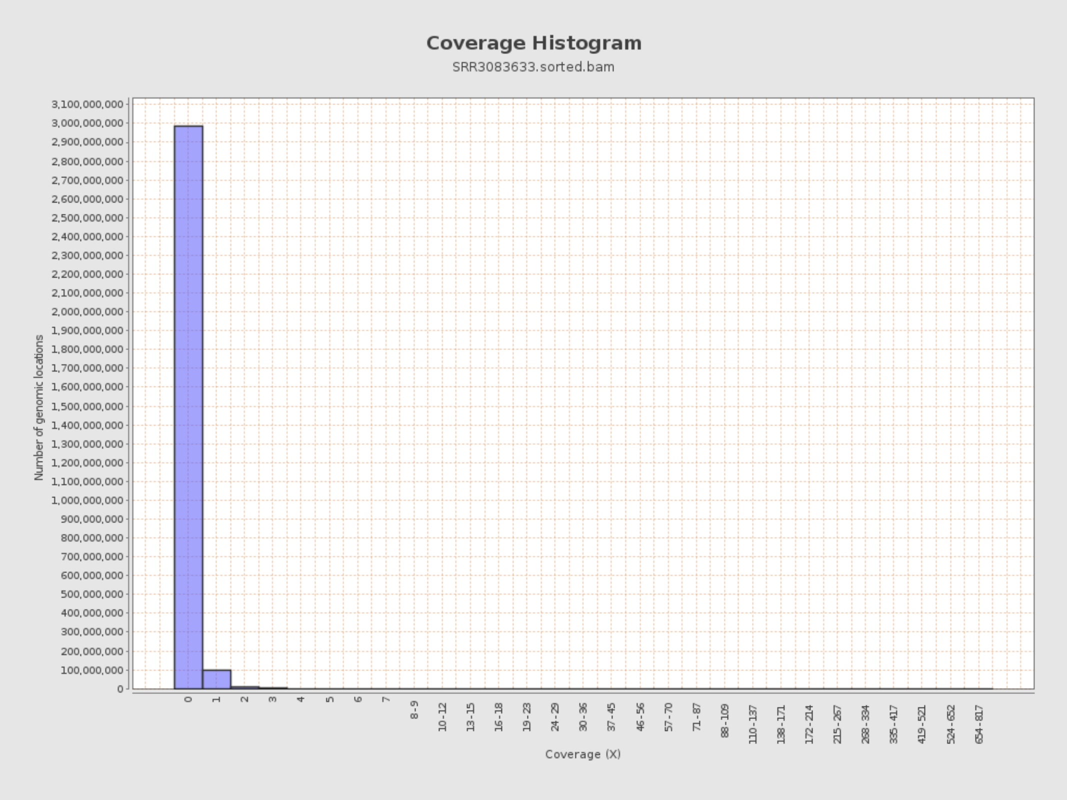
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9375742	0.0376	0.6873
chr2	243199373	11230339	0.0462	0.313
chr3	198022430	9952875	0.0503	0.2467
chr4	191154276	7784896	0.0407	0.2341
chr5	180915260	8481099	0.0469	0.239
chr6	171115067	7447044	0.0435	0.2644
chr7	159138663	7374736	0.0463	0.4754

chr8	146364022	6454784	0.0441	0.4989
chr9	141213431	5132071	0.0363	0.2672
chr10	135534747	5400717	0.0398	0.3296
chr11	135006516	5805323	0.043	0.2513
chr12	133851895	5853468	0.0437	0.2331
chr13	115169878	4320353	0.0375	0.2125
chr14	107349540	4155029	0.0387	0.2244
chr15	102531392	3768798	0.0368	0.2111
chr16	90354753	3371058	0.0373	0.2312
chr17	81195210	2792085	0.0344	0.21
chr18	78077248	3229250	0.0414	0.4451
chr19	59128983	2103368	0.0356	0.4854
chr20	63025520	2280142	0.0362	0.2138
chr21	48129895	1551192	0.0322	0.2094
chr22	51304566	1294204	0.0252	0.1737
chrMT	16571	23186	1.3992	1.5041
chrX	155270560	7690511	0.0495	0.2635
chrY	59373566	363034	0.0061	0.1527

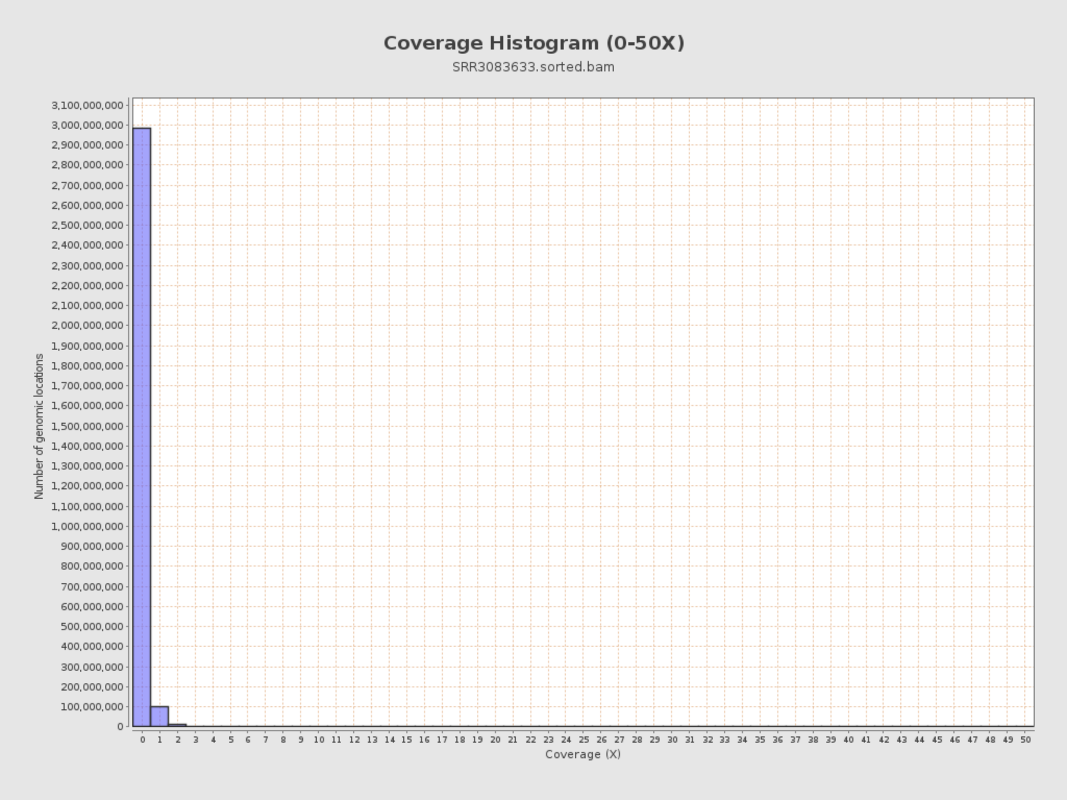
3. Results : Coverage across reference



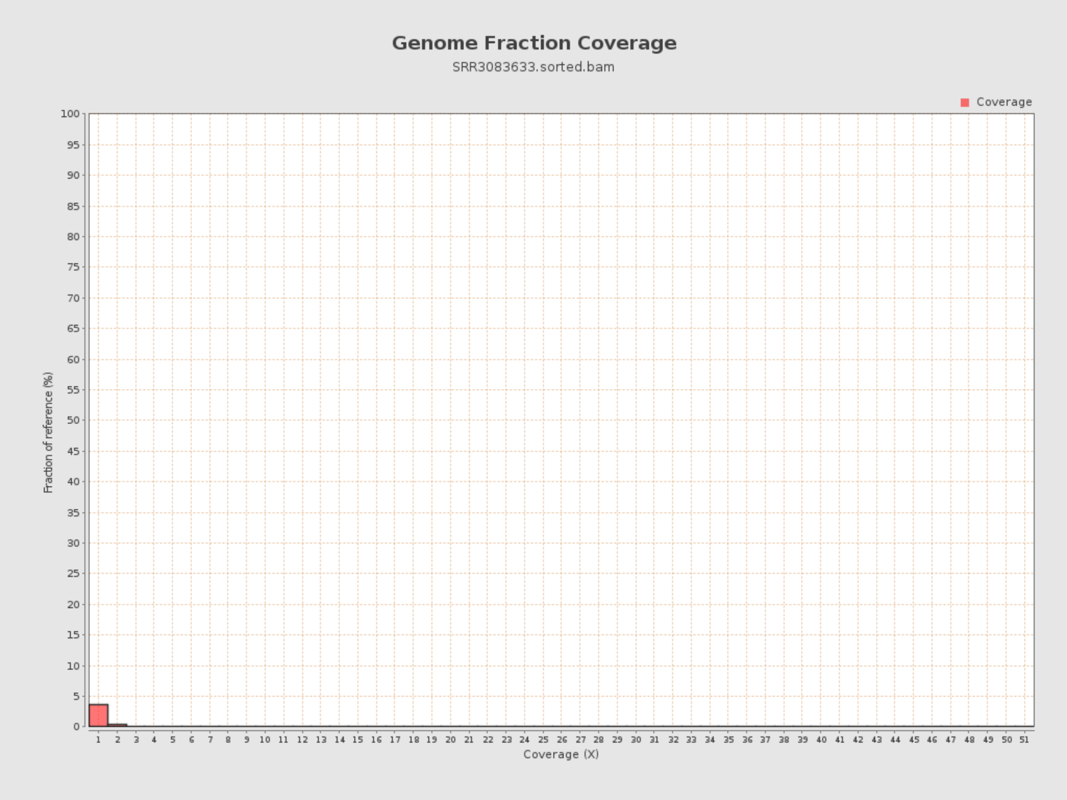
4. Results : Coverage Histogram



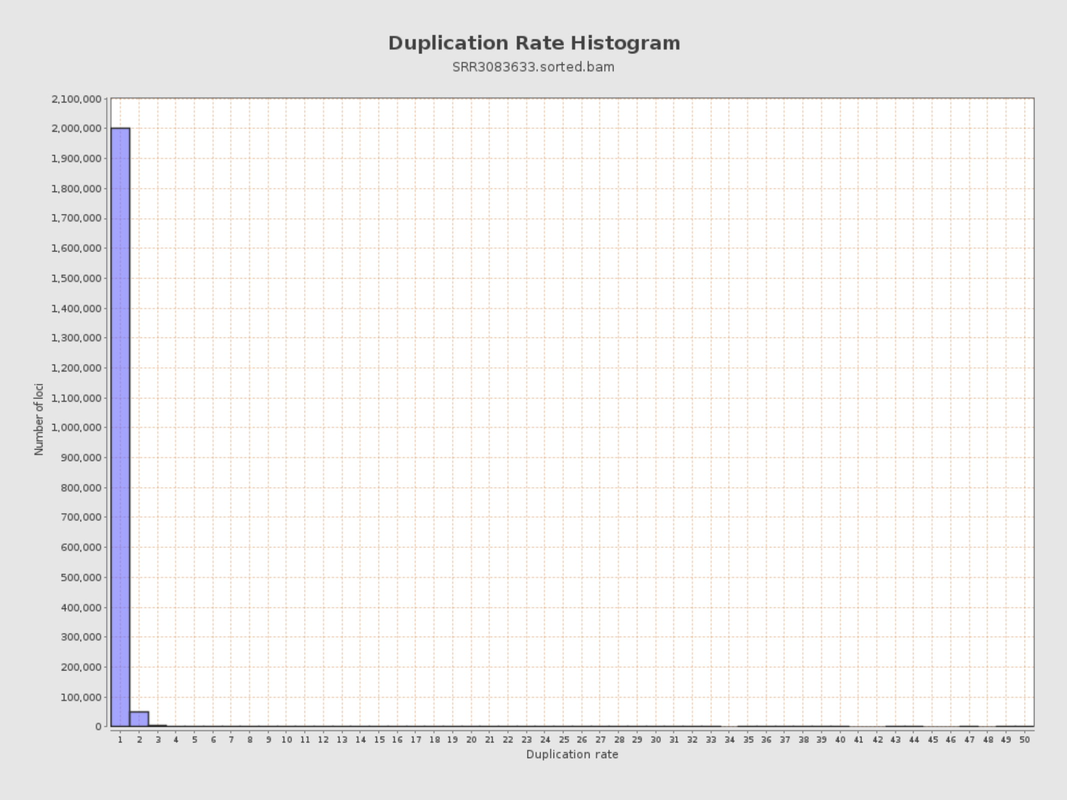
5. Results : Coverage Histogram (0-50X)



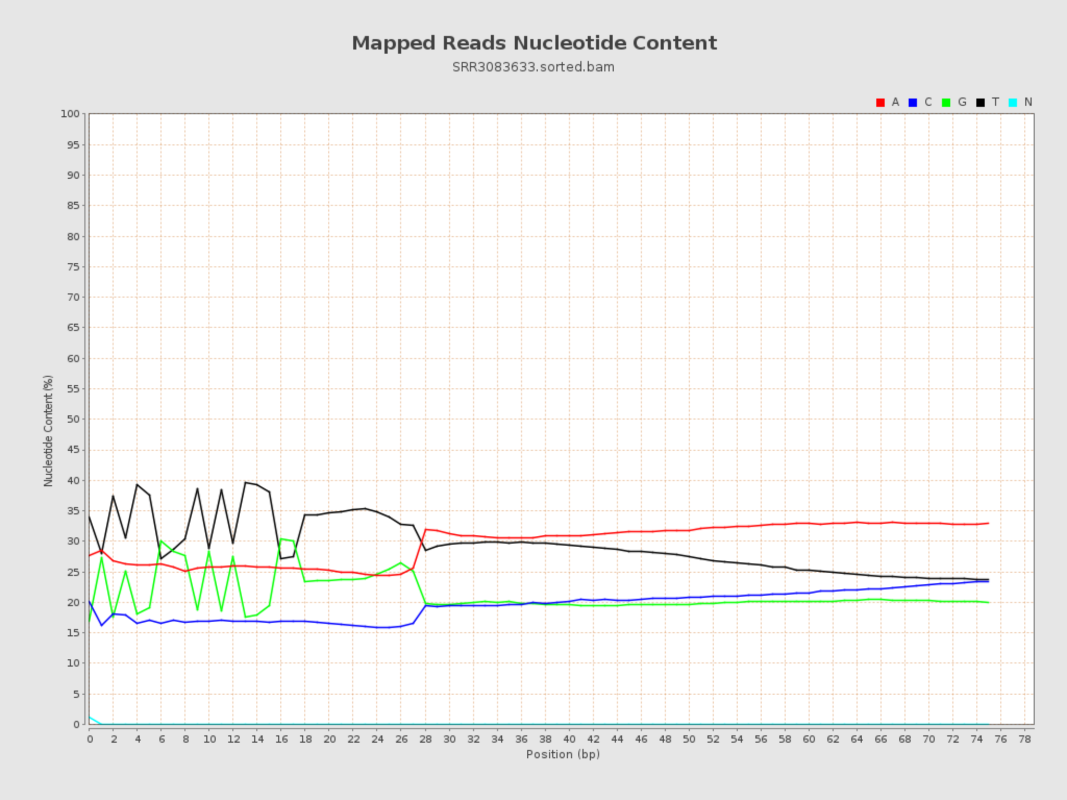
6. Results : Genome Fraction Coverage



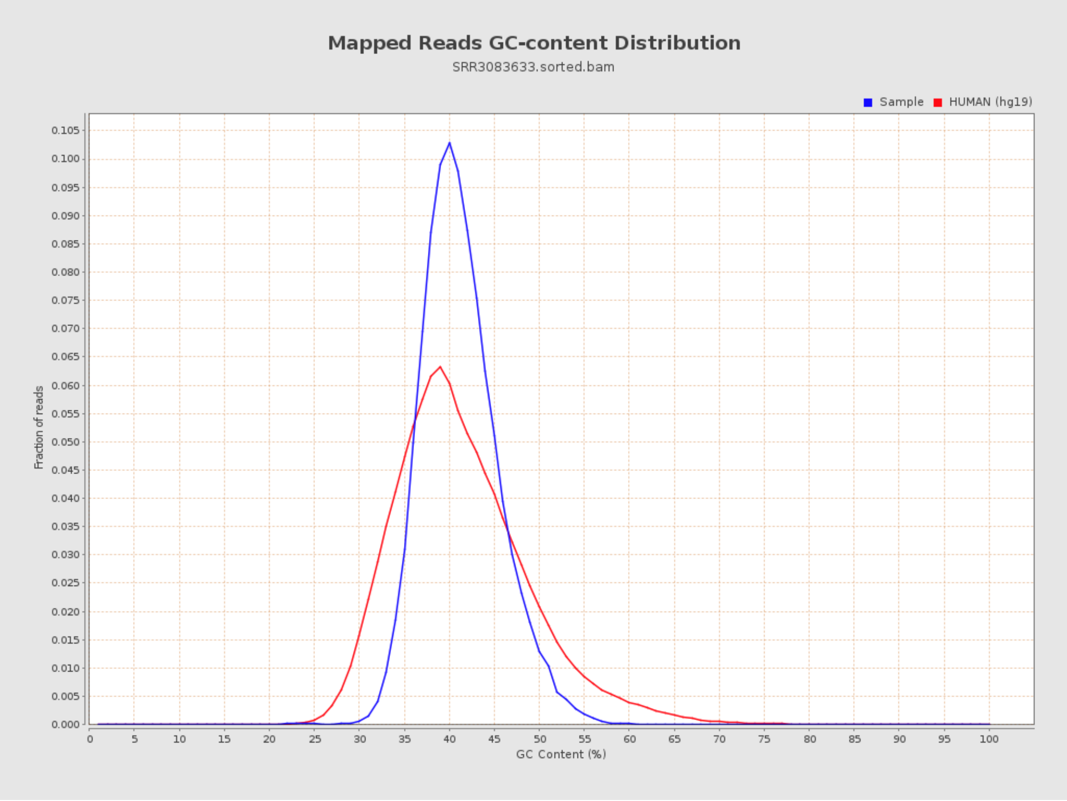
7. Results : Duplication Rate Histogram



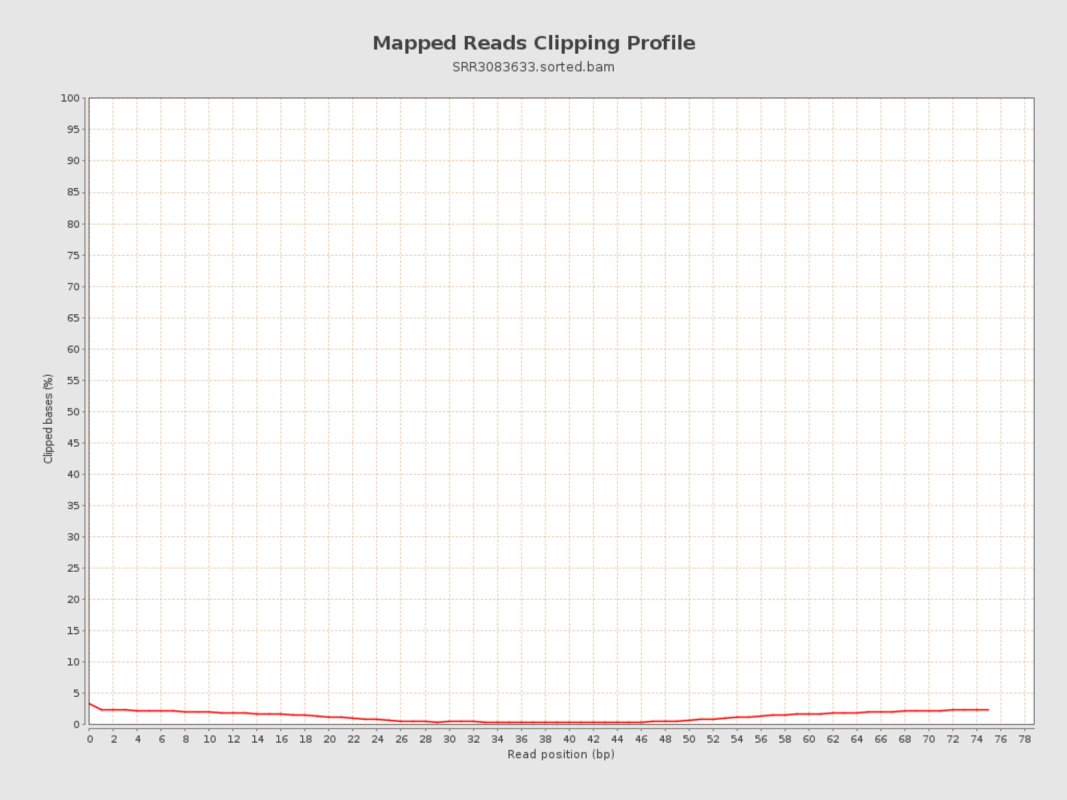
8. Results : Mapped Reads Nucleotide Content



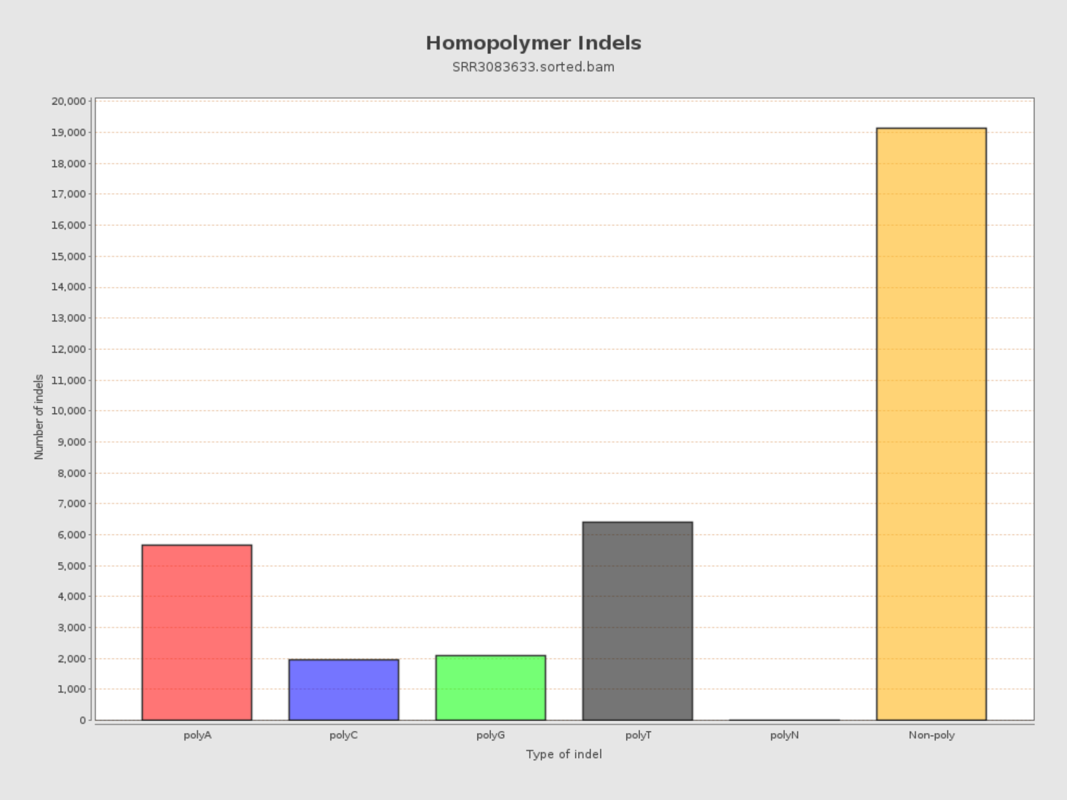
9. Results : Mapped Reads GC-content Distribution



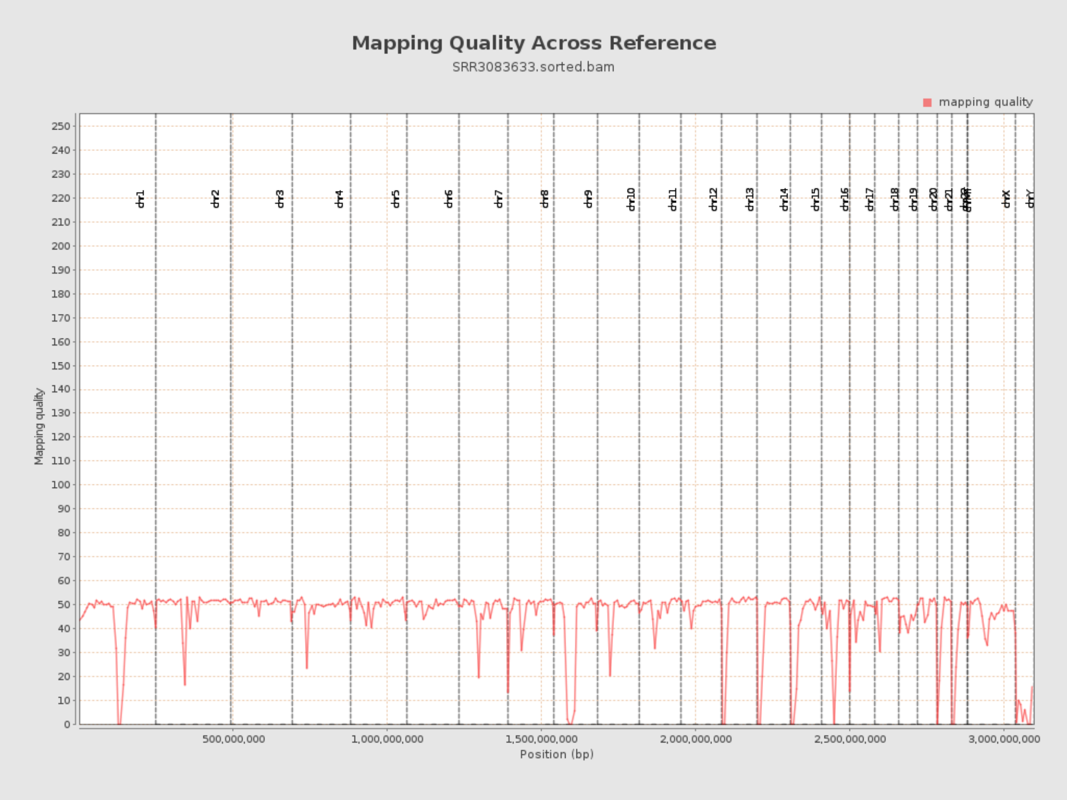
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram