Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:25:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083623.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_SRR3083623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083623.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:25:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,834,719
Mapped reads	1,674,775 / 91.28%
Unmapped reads	159,944 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,893 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	93,659 / 5.1%
Duplication rate	4.63%
Clipped reads	765,040 / 41.7%

2.2. ACGT Content

Number/percentage of A's	30,479,217 / 27.4%
Number/percentage of C's	20,228,541 / 18.19%
Number/percentage of T's	35,670,774 / 32.07%
Number/percentage of G's	24,841,344 / 22.33%
Number/percentage of N's	6,034 / 0.01%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3479

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

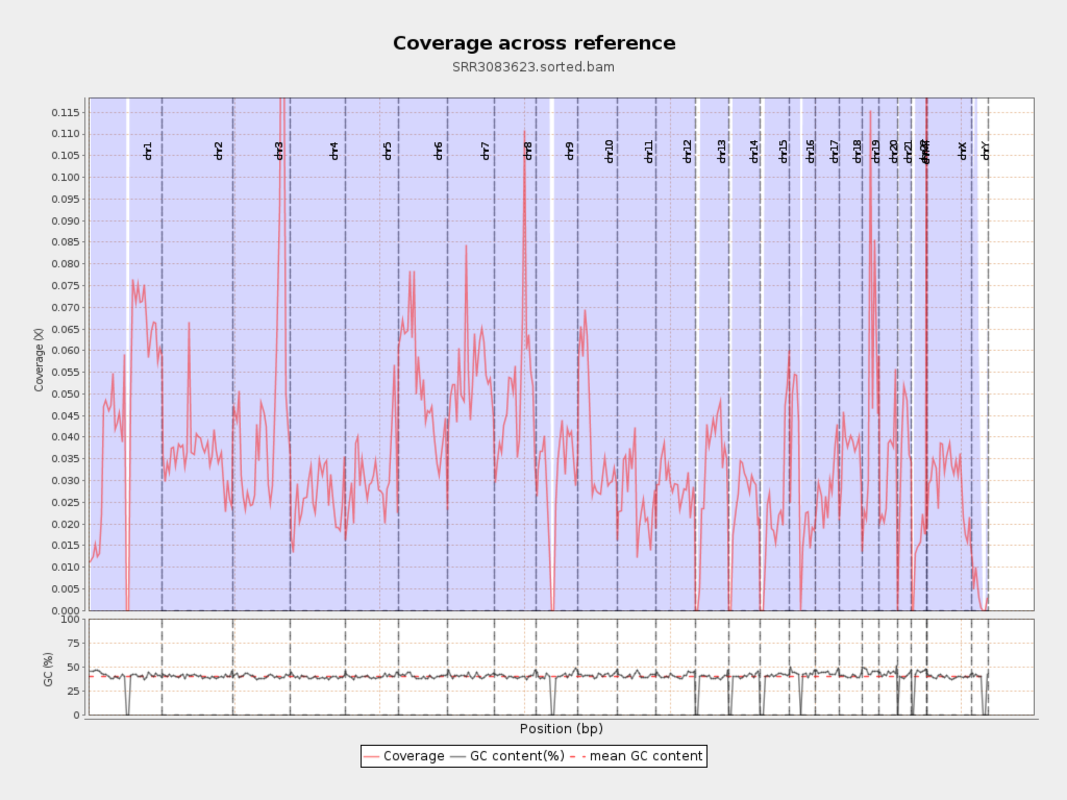
General error rate	0.71%
Mismatches	772,409
Insertions	8,273
Mapped reads with at least one insertion	0.49%
Deletions	25,675
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.11%

2.6. Chromosome stats

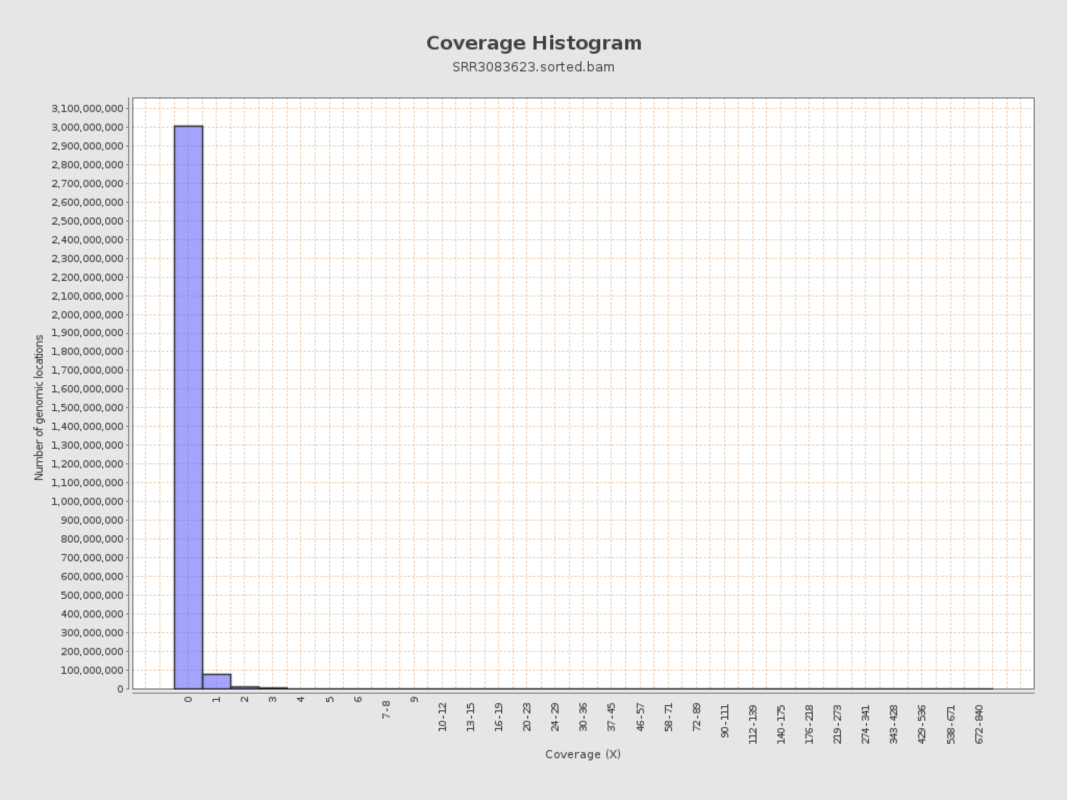
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11636481	0.0467	0.6967
chr2	243199373	8756072	0.036	0.4283
chr3	198022430	9507484	0.048	0.2596
chr4	191154276	4975788	0.026	0.196
chr5	180915260	5591752	0.0309	0.2044
chr6	171115067	8906048	0.052	0.3388
chr7	159138663	8729601	0.0549	0.5702

chr8	146364022	7396542	0.0505	0.4035
chr9	141213431	4328184	0.0306	0.2333
chr10	135534747	5434157	0.0401	0.2844
chr11	135006516	3485121	0.0258	0.2083
chr12	133851895	3901105	0.0291	0.1991
chr13	115169878	3598448	0.0312	0.2083
chr14	107349540	2616542	0.0244	0.183
chr15	102531392	2340743	0.0228	0.1806
chr16	90354753	2565450	0.0284	0.2008
chr17	81195210	2326157	0.0286	0.2006
chr18	78077248	2896851	0.0371	0.3508
chr19	59128983	3009639	0.0509	0.4823
chr20	63025520	2043555	0.0324	0.2149
chr21	48129895	1700250	0.0353	0.2208
chr22	51304566	683134	0.0133	0.1306
chrMT	16571	3385	0.2043	0.5946
chrX	155270560	4611909	0.0297	0.2073
chrY	59373566	222593	0.0037	0.0797

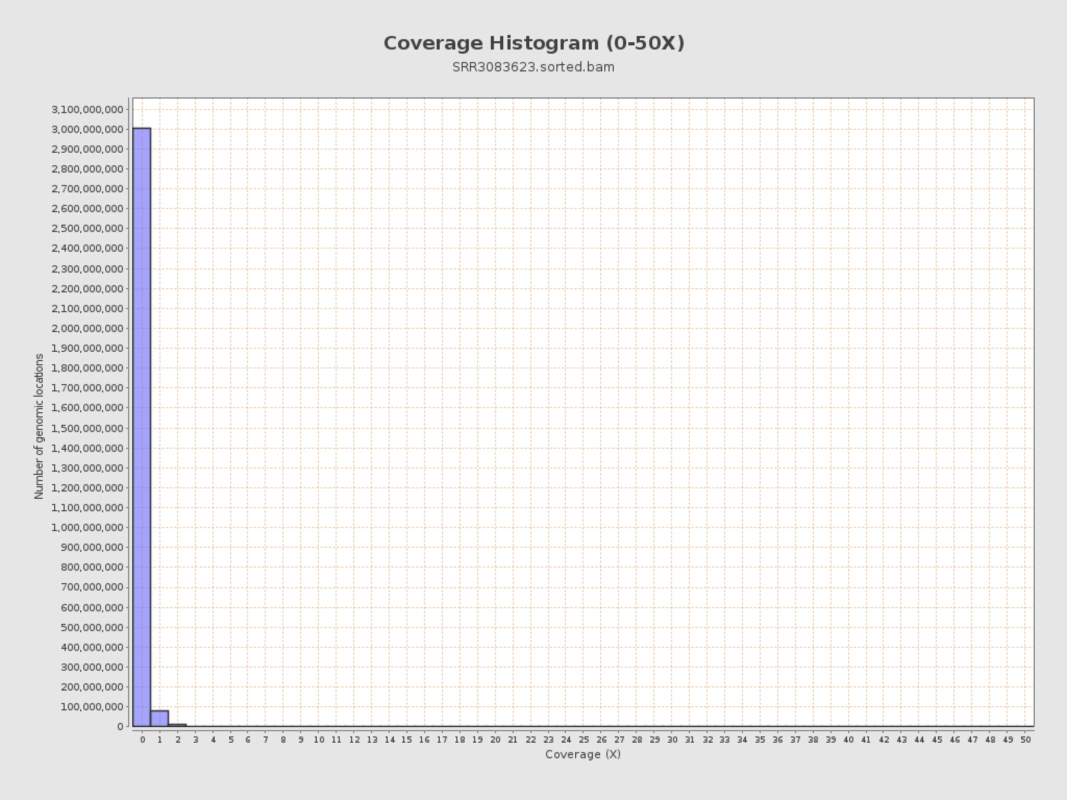
3. Results : Coverage across reference



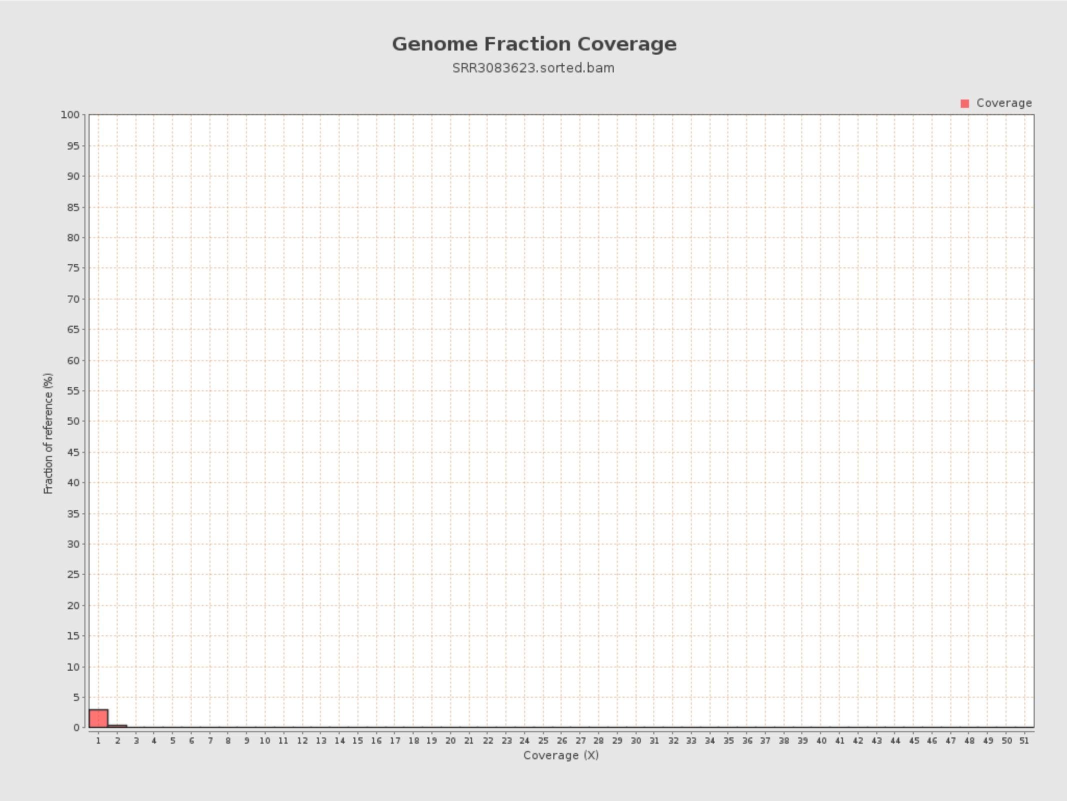
4. Results : Coverage Histogram



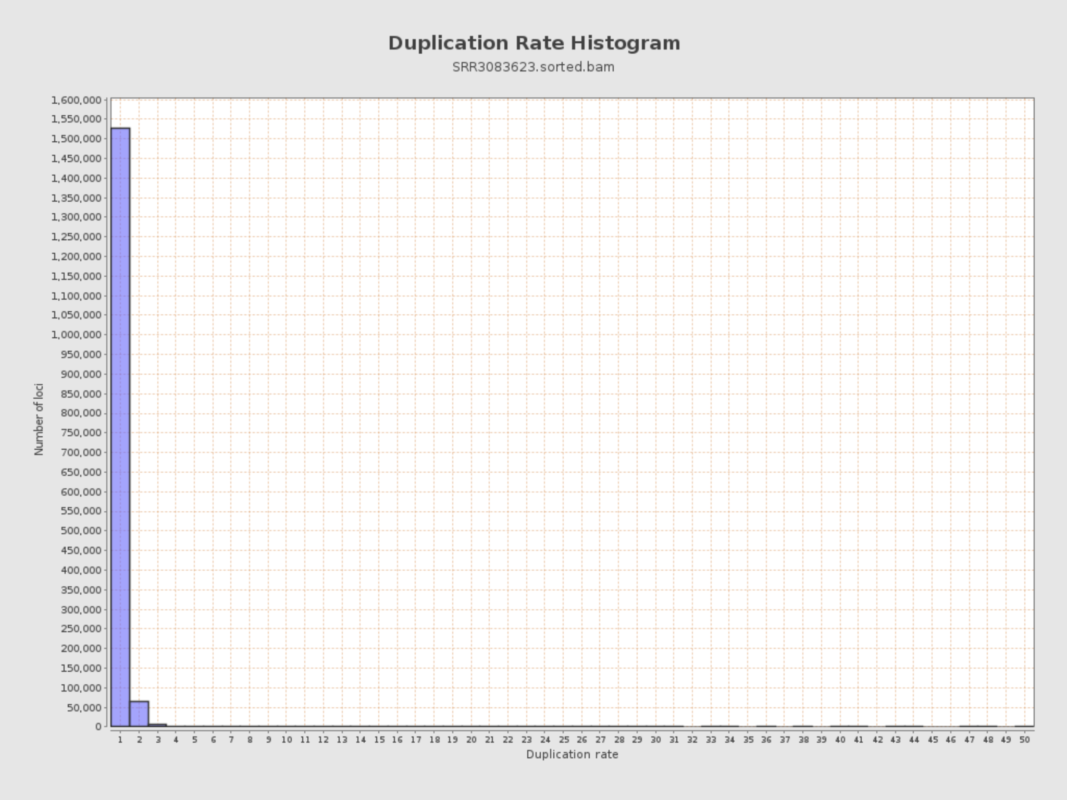
5. Results : Coverage Histogram (0-50X)



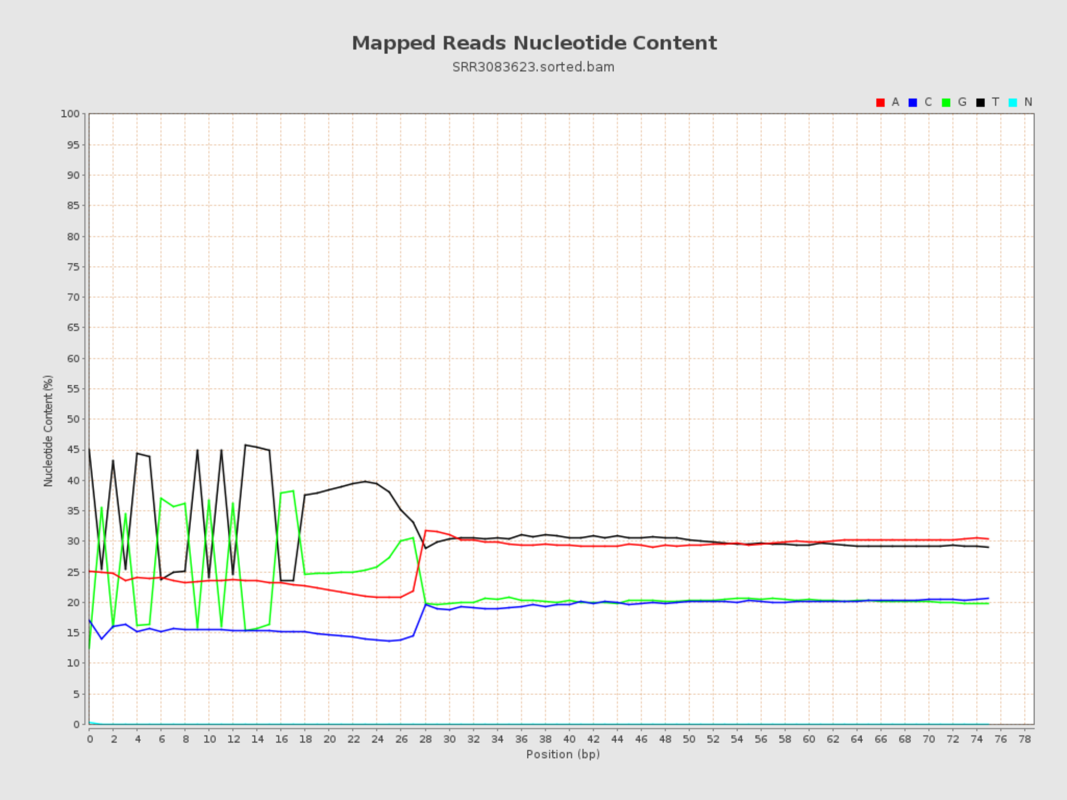
6. Results : Genome Fraction Coverage



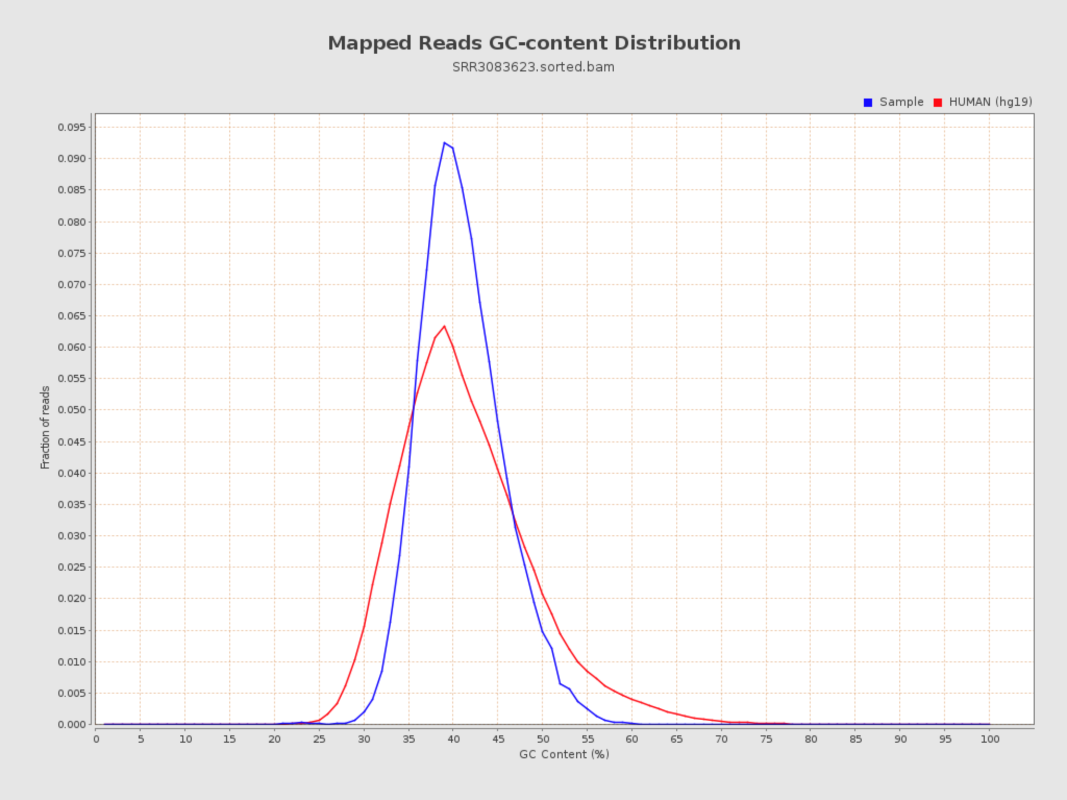
7. Results : Duplication Rate Histogram



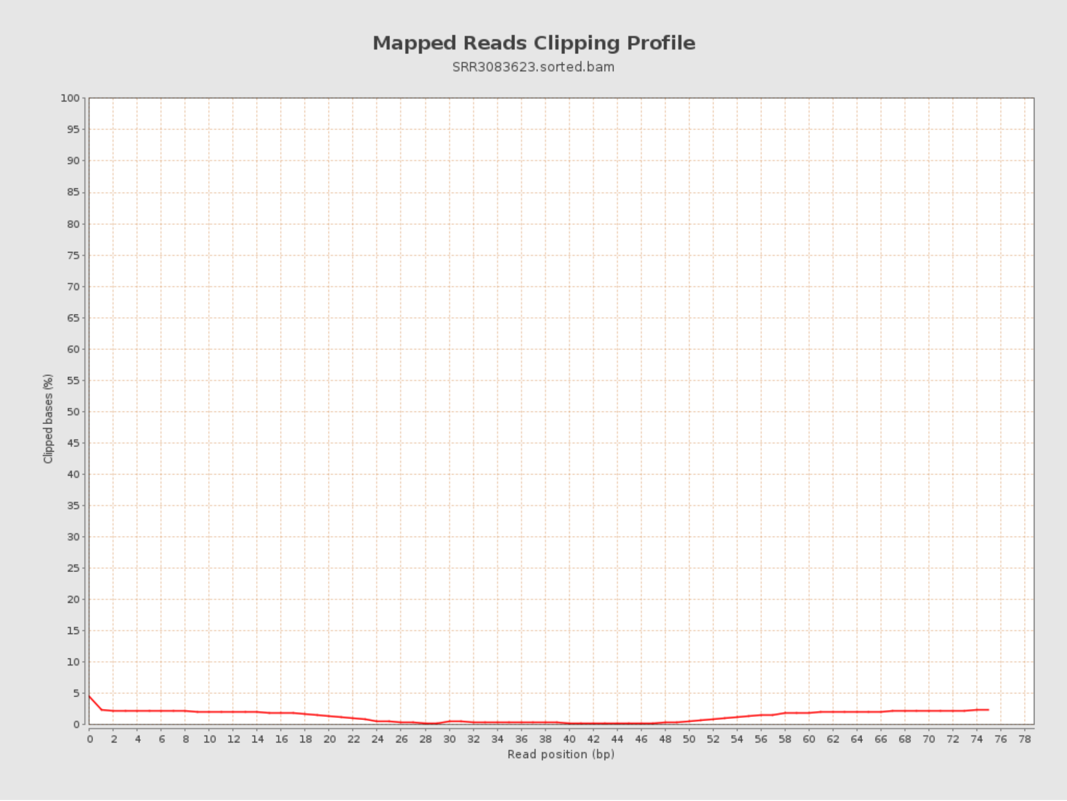
8. Results : Mapped Reads Nucleotide Content



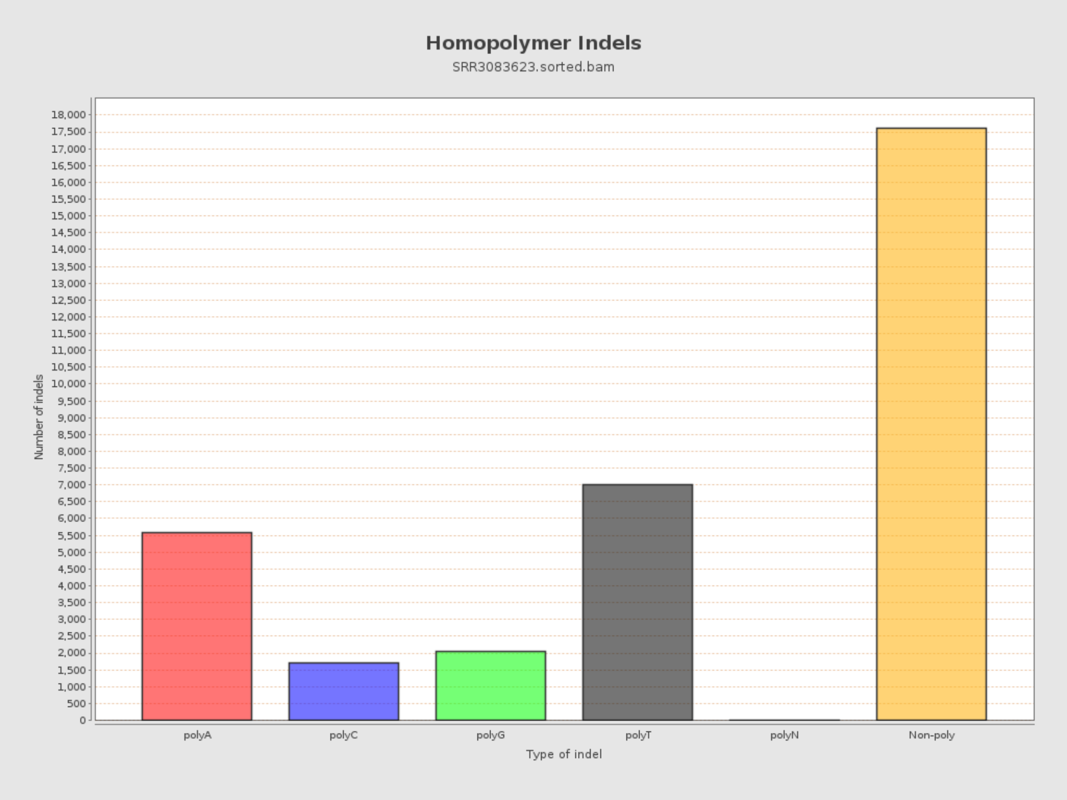
9. Results : Mapped Reads GC-content Distribution



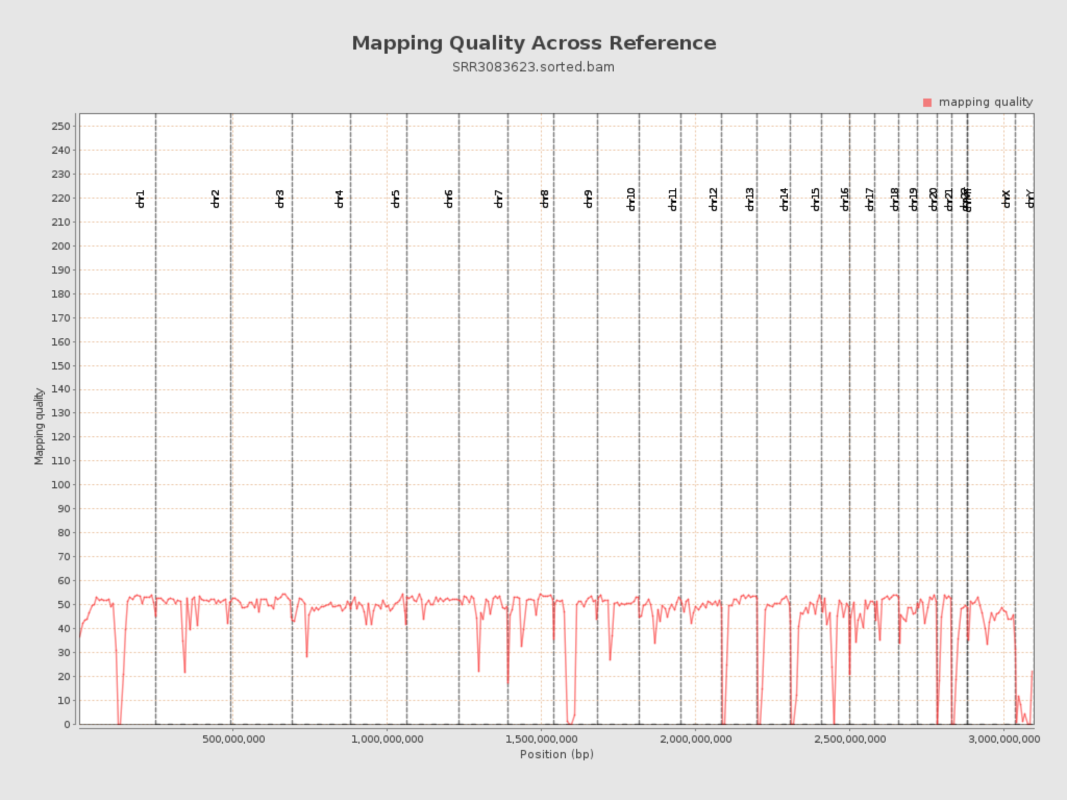
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram