Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:27:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212678.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_SRR3212678 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212678.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:27:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212678.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,477,658
Mapped reads	684,589 / 46.33%
Unmapped reads	793,069 / 53.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,310 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	177,902 / 12.04%
Duplication rate	13.52%
Clipped reads	352,414 / 23.85%

2.2. ACGT Content

Number/percentage of A's	12,322,883 / 27.79%
Number/percentage of C's	8,371,059 / 18.88%
Number/percentage of T's	13,941,115 / 31.44%
Number/percentage of G's	9,703,625 / 21.89%
Number/percentage of N's	428 / 0%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0143

Standard Deviation	0.4467

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

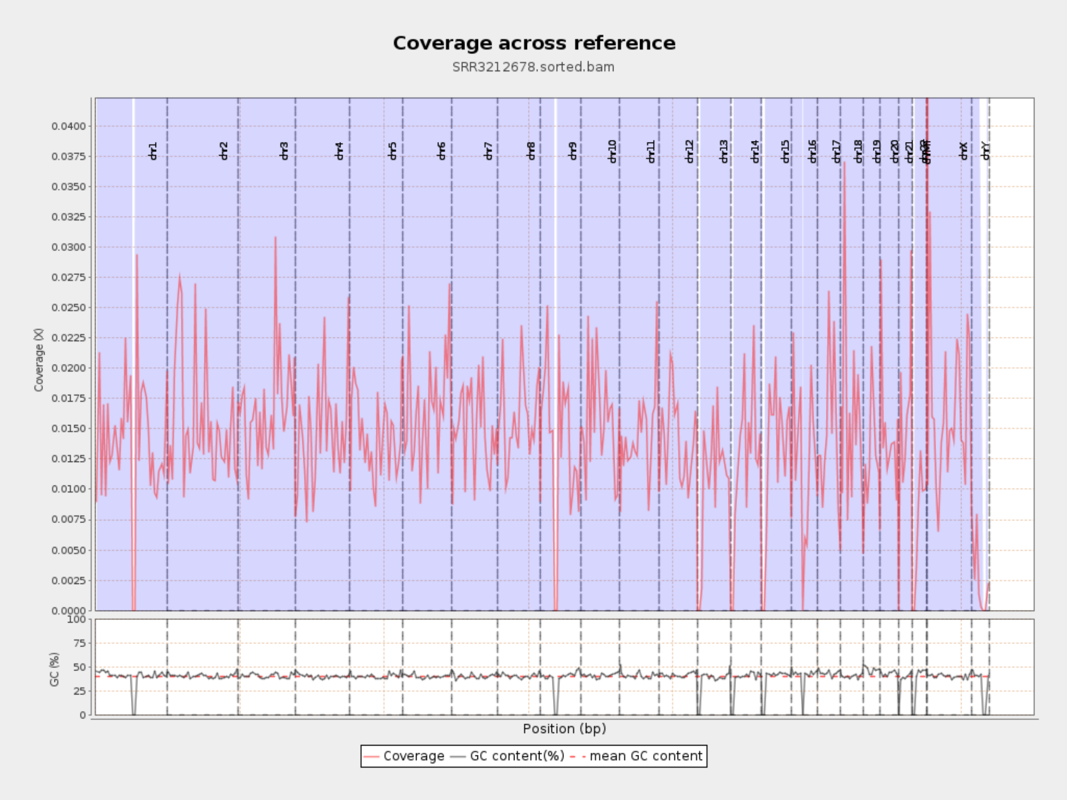
General error rate	0.95%
Mismatches	415,241
Insertions	3,912
Mapped reads with at least one insertion	0.56%
Deletions	9,584
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.11%

2.6. Chromosome stats

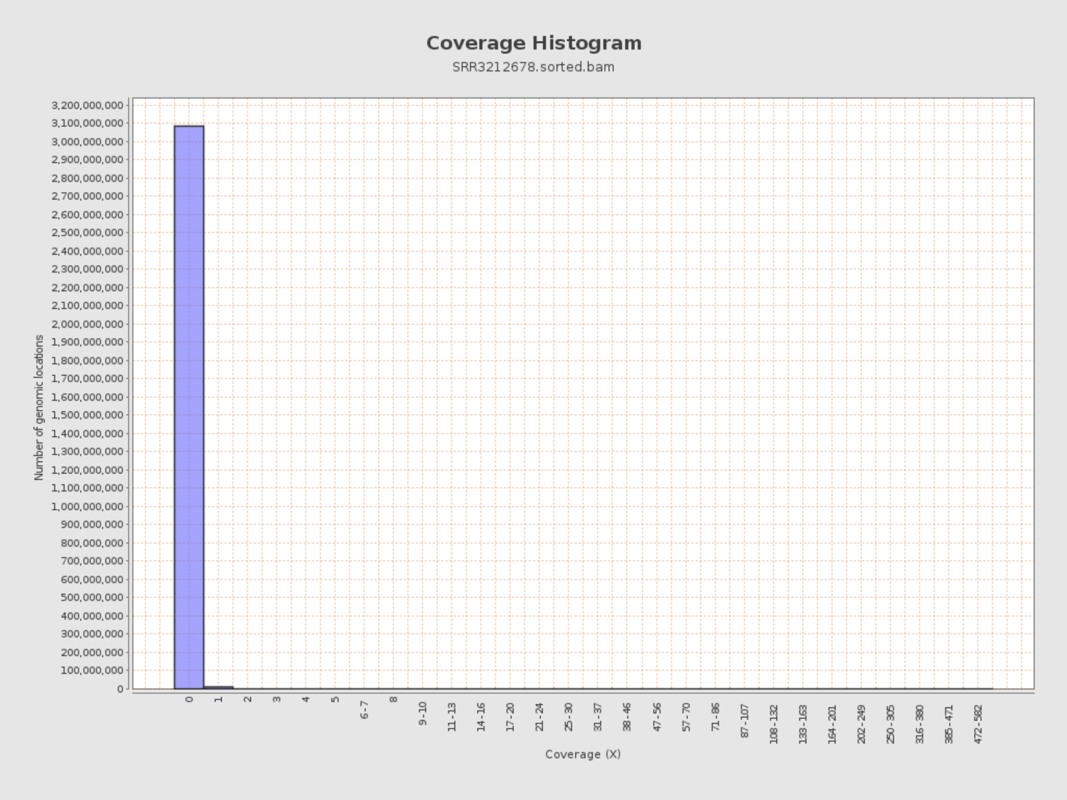
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3451731	0.0138	0.4718
chr2	243199373	3776606	0.0155	0.4927
chr3	198022430	3283779	0.0166	0.447
chr4	191154276	2792123	0.0146	0.466
chr5	180915260	2601661	0.0144	0.4563
chr6	171115067	2865363	0.0167	0.4552
chr7	159138663	2407229	0.0151	0.4492

chr8	146364022	2348782	0.016	0.4372
chr9	141213431	1945125	0.0138	0.4123
chr10	135534747	2143595	0.0158	0.4372
chr11	135006516	1961271	0.0145	0.4433
chr12	133851895	1904818	0.0142	0.4121
chr13	115169878	1208655	0.0105	0.3524
chr14	107349540	1333087	0.0124	0.4988
chr15	102531392	1318277	0.0129	0.522
chr16	90354753	1099134	0.0122	0.3571
chr17	81195210	1174869	0.0145	0.43
chr18	78077248	1263691	0.0162	0.5472
chr19	59128983	770371	0.013	0.3738
chr20	63025520	909867	0.0144	0.4381
chr21	48129895	738241	0.0153	0.4033
chr22	51304566	373694	0.0073	0.2488
chrMT	16571	10864	0.6556	3.1032
chrX	155270560	2527513	0.0163	0.4853
chrY	59373566	145162	0.0024	0.2112

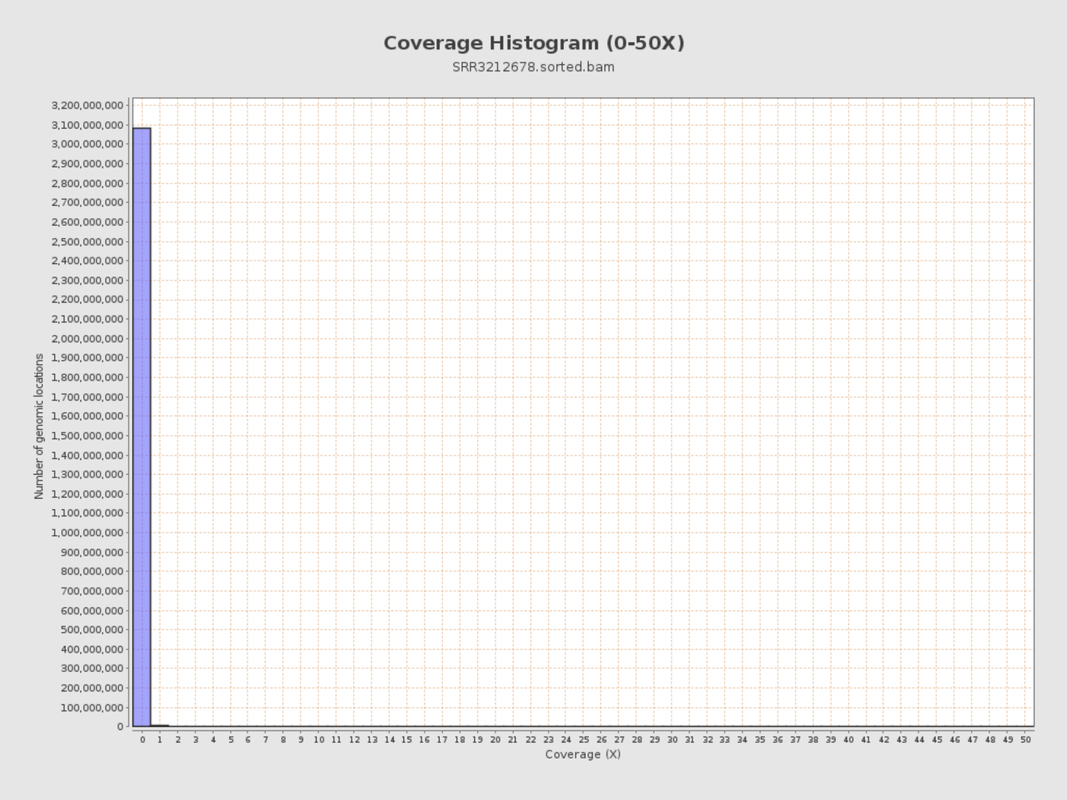
3. Results : Coverage across reference



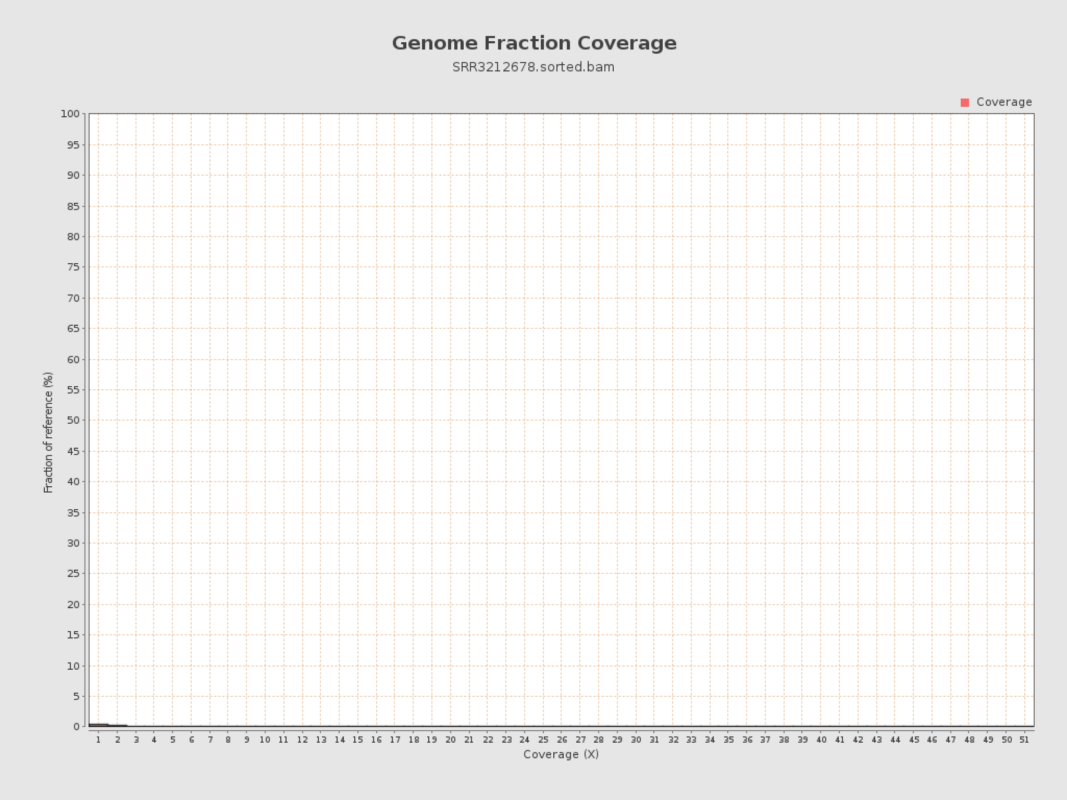
4. Results : Coverage Histogram



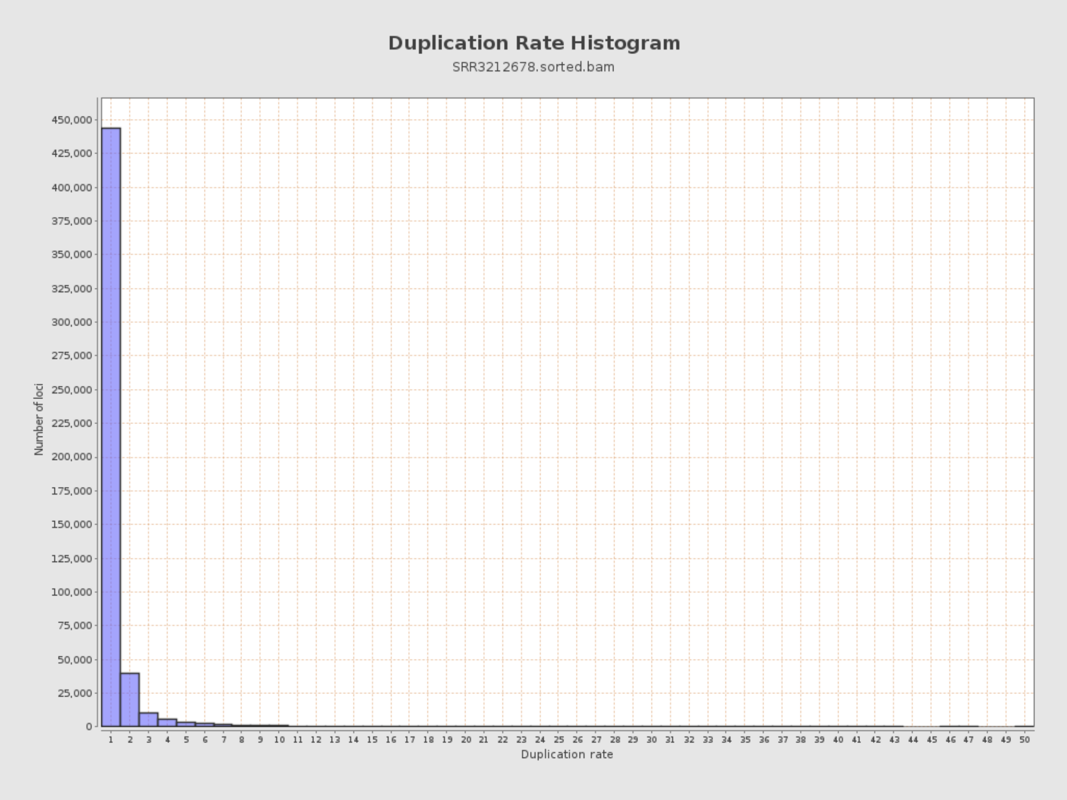
5. Results : Coverage Histogram (0-50X)



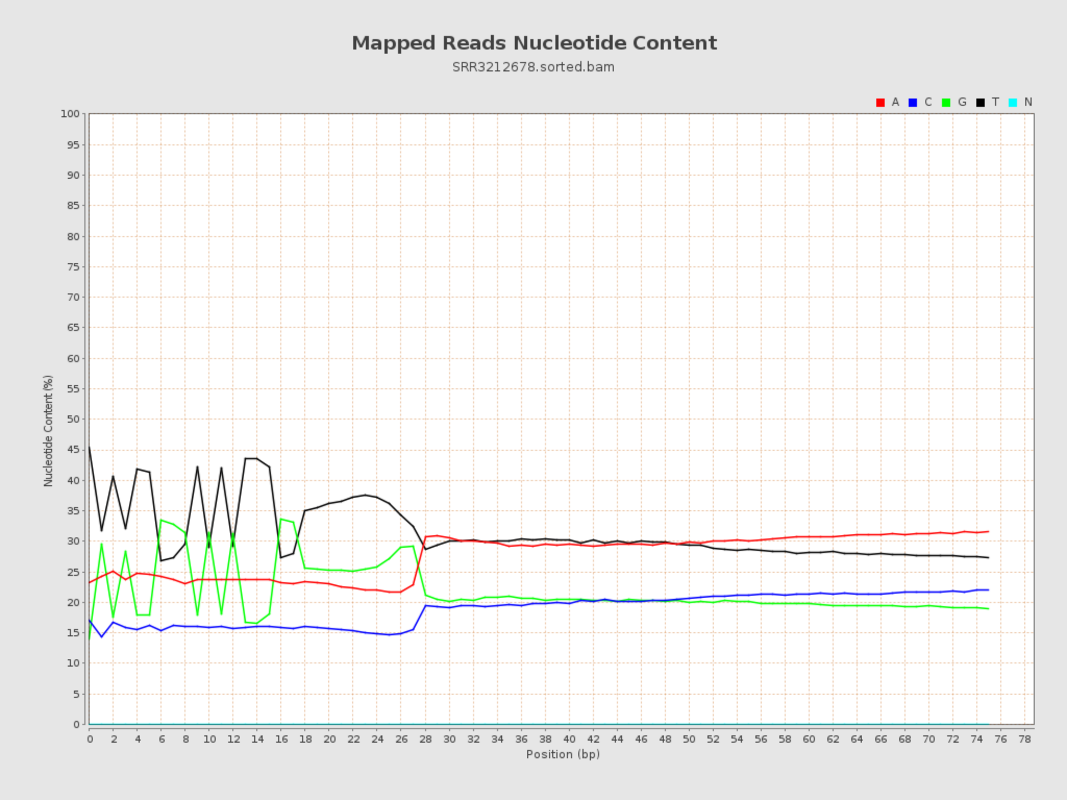
6. Results : Genome Fraction Coverage



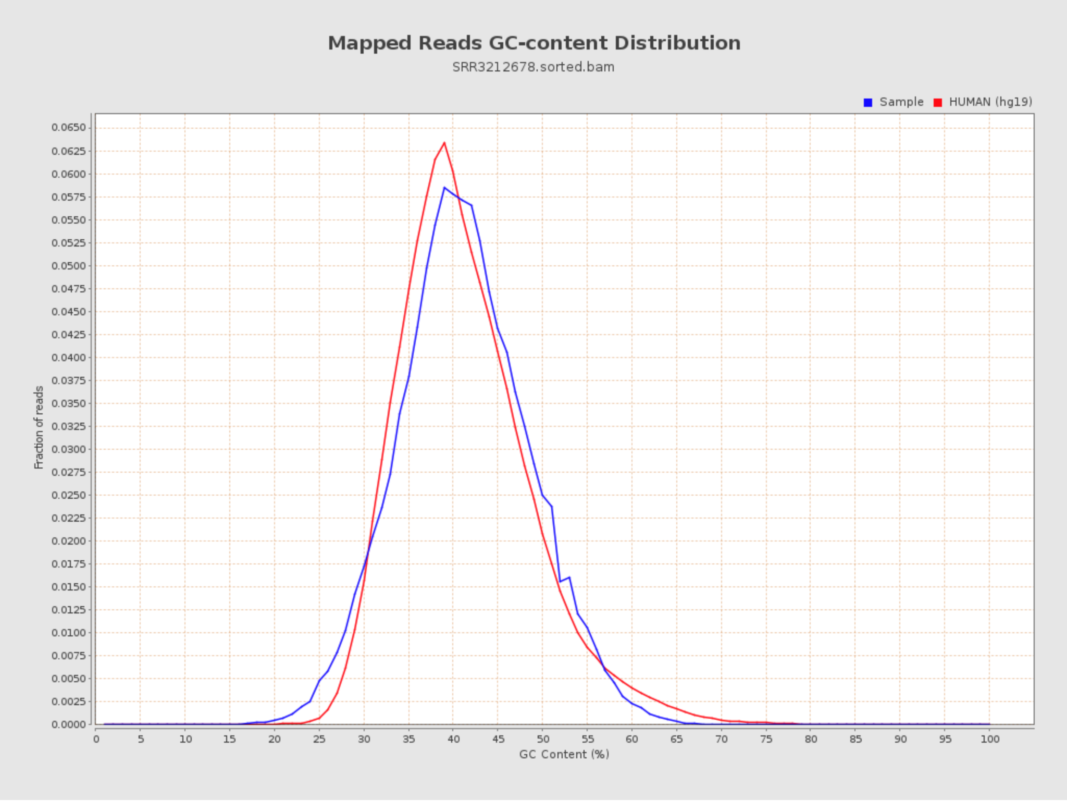
7. Results : Duplication Rate Histogram



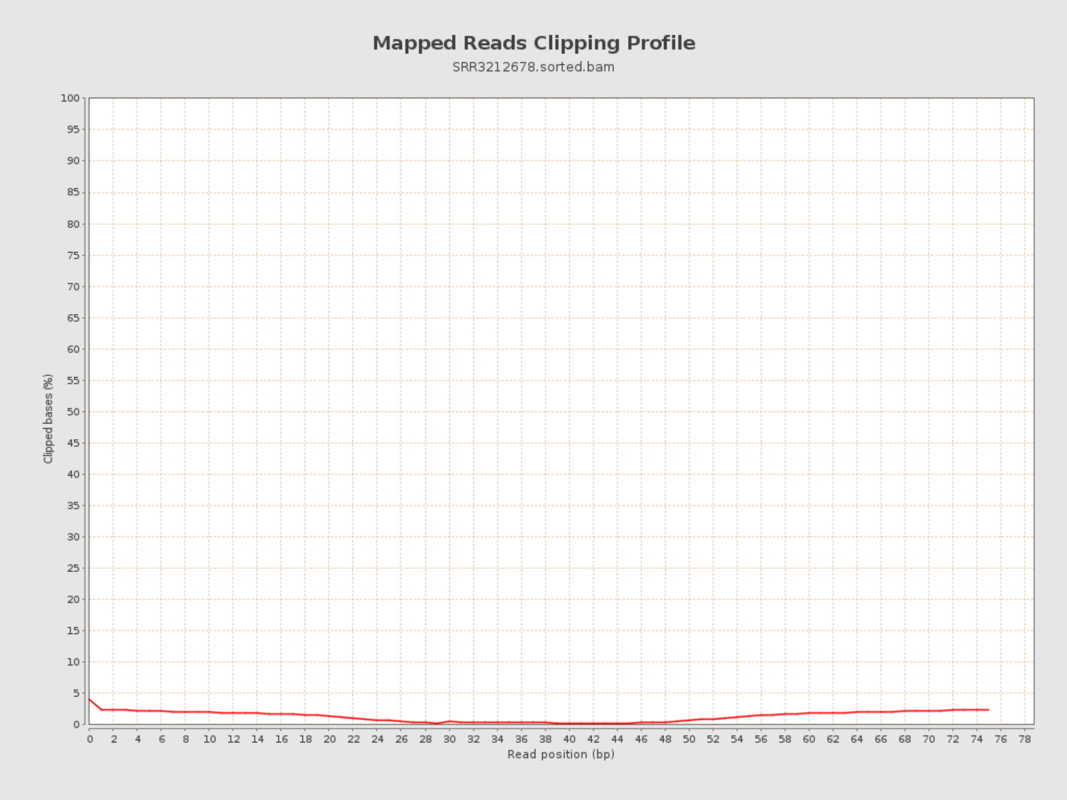
8. Results : Mapped Reads Nucleotide Content



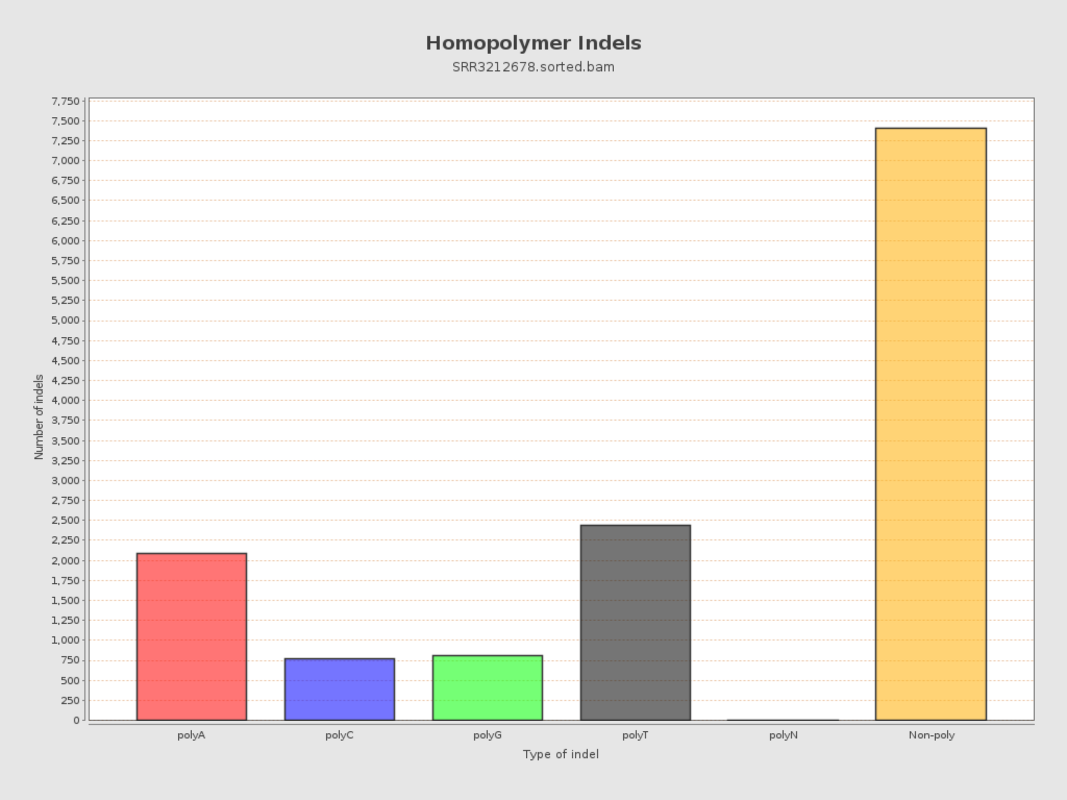
9. Results : Mapped Reads GC-content Distribution



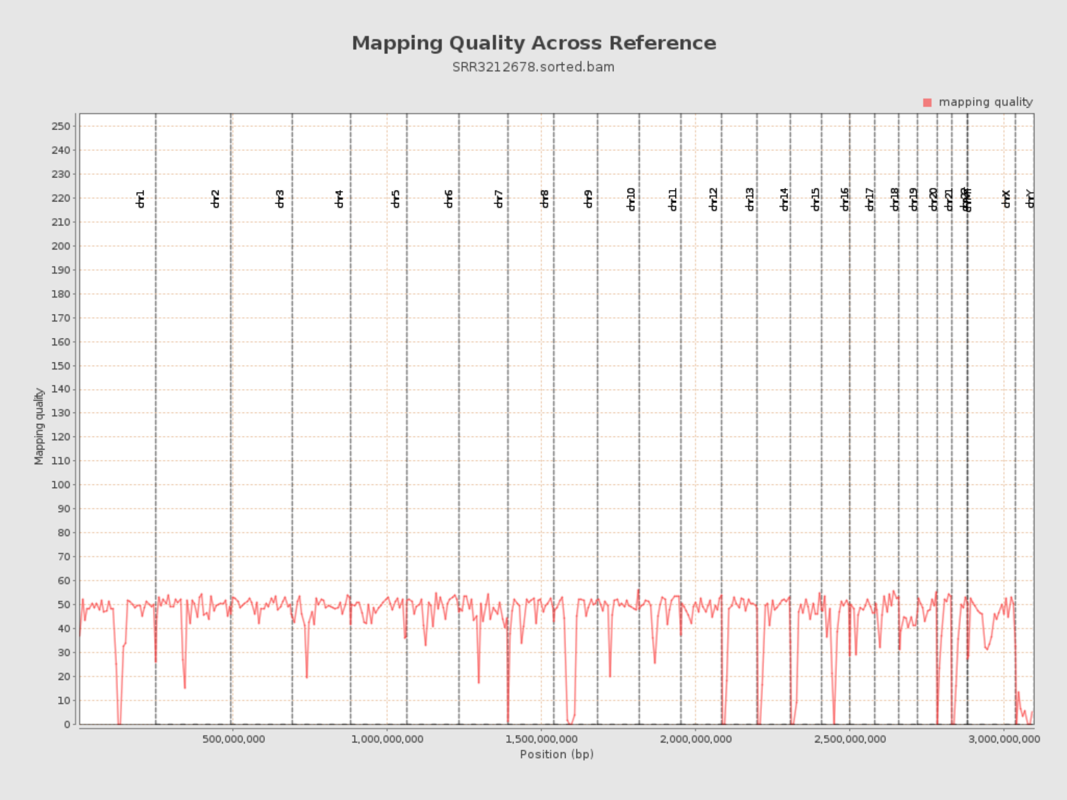
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram