Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:50:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083662.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_SRR3083662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:50:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,366,196
Mapped reads	1,034,103 / 75.69%
Unmapped reads	332,093 / 24.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,893 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	23,089 / 1.69%
Duplication rate	1.85%
Clipped reads	575,757 / 42.14%

2.2. ACGT Content

Number/percentage of A's	19,375,581 / 29.6%
Number/percentage of C's	12,133,281 / 18.54%
Number/percentage of T's	19,428,110 / 29.68%
Number/percentage of G's	14,508,238 / 22.17%
Number/percentage of N's	9,033 / 0.01%
GC Percentage	40.7%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2061

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

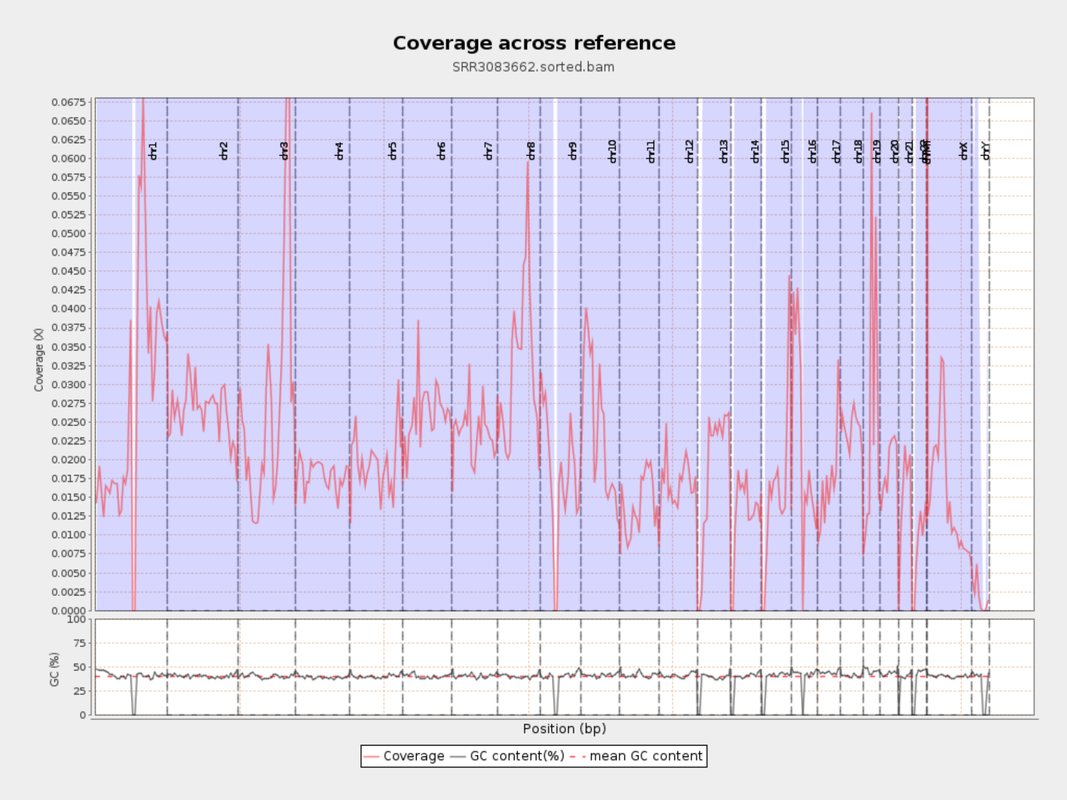
General error rate	0.9%
Mismatches	582,454
Insertions	4,826
Mapped reads with at least one insertion	0.46%
Deletions	14,305
Mapped reads with at least one deletion	1.37%
Homopolymer indels	46.11%

2.6. Chromosome stats

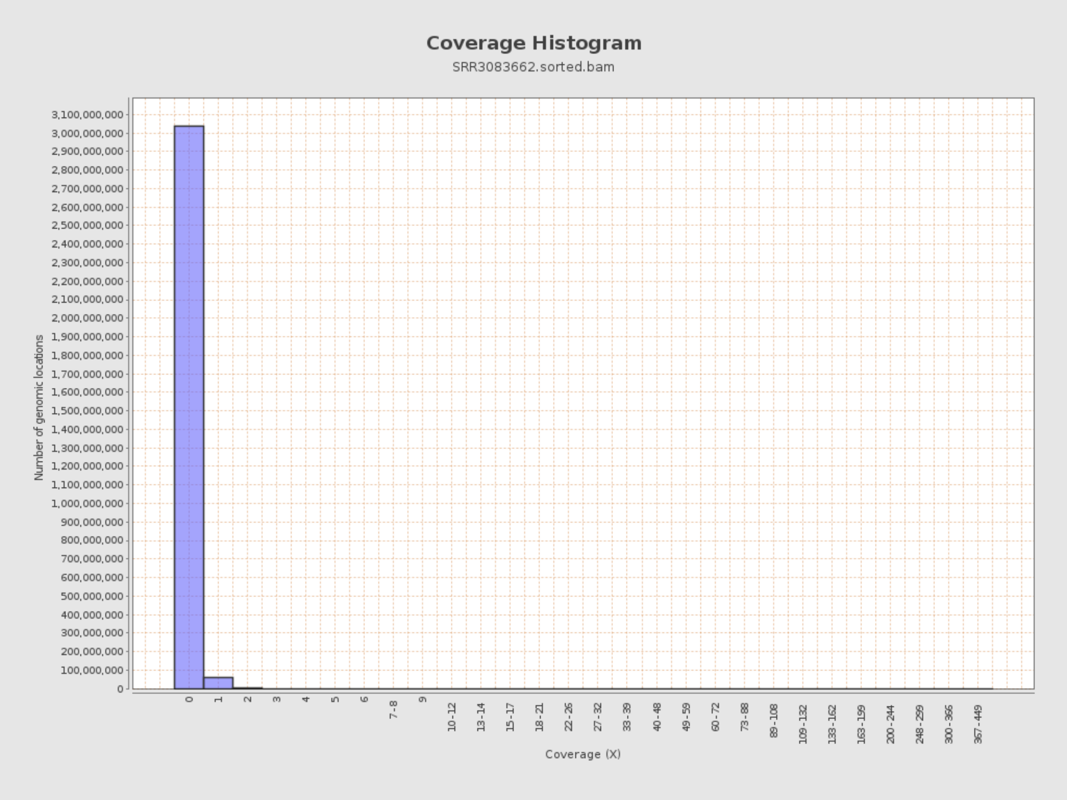
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6742175	0.027	0.4292
chr2	243199373	6432150	0.0264	0.1968
chr3	198022430	5379921	0.0272	0.1748
chr4	191154276	3408682	0.0178	0.1408
chr5	180915260	3607202	0.0199	0.1481
chr6	171115067	4454954	0.026	0.1902
chr7	159138663	3772340	0.0237	0.2317

chr8	146364022	4804732	0.0328	0.2292
chr9	141213431	2555987	0.0181	0.1569
chr10	135534747	3284567	0.0242	0.2213
chr11	135006516	1915688	0.0142	0.1372
chr12	133851895	2287472	0.0171	0.1375
chr13	115169878	2145138	0.0186	0.1425
chr14	107349540	1365438	0.0127	0.1193
chr15	102531392	1699344	0.0166	0.1355
chr16	90354753	1946995	0.0215	0.1601
chr17	81195210	1406274	0.0173	0.1437
chr18	78077248	1897678	0.0243	0.2316
chr19	59128983	1527362	0.0258	0.2968
chr20	63025520	1198044	0.019	0.1462
chr21	48129895	729115	0.0151	0.1303
chr22	51304566	445631	0.0087	0.0973
chrMT	16571	6587	0.3975	0.6625
chrX	155270560	2349443	0.0151	0.1323
chrY	59373566	114088	0.0019	0.0517

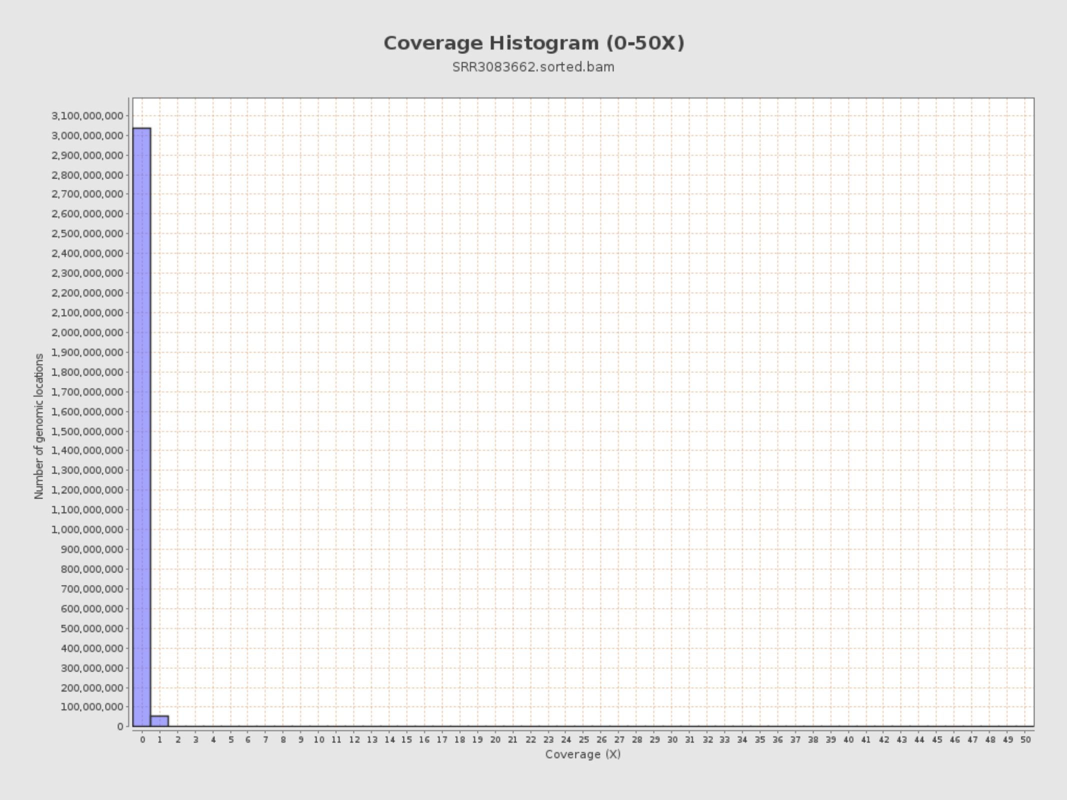
3. Results : Coverage across reference



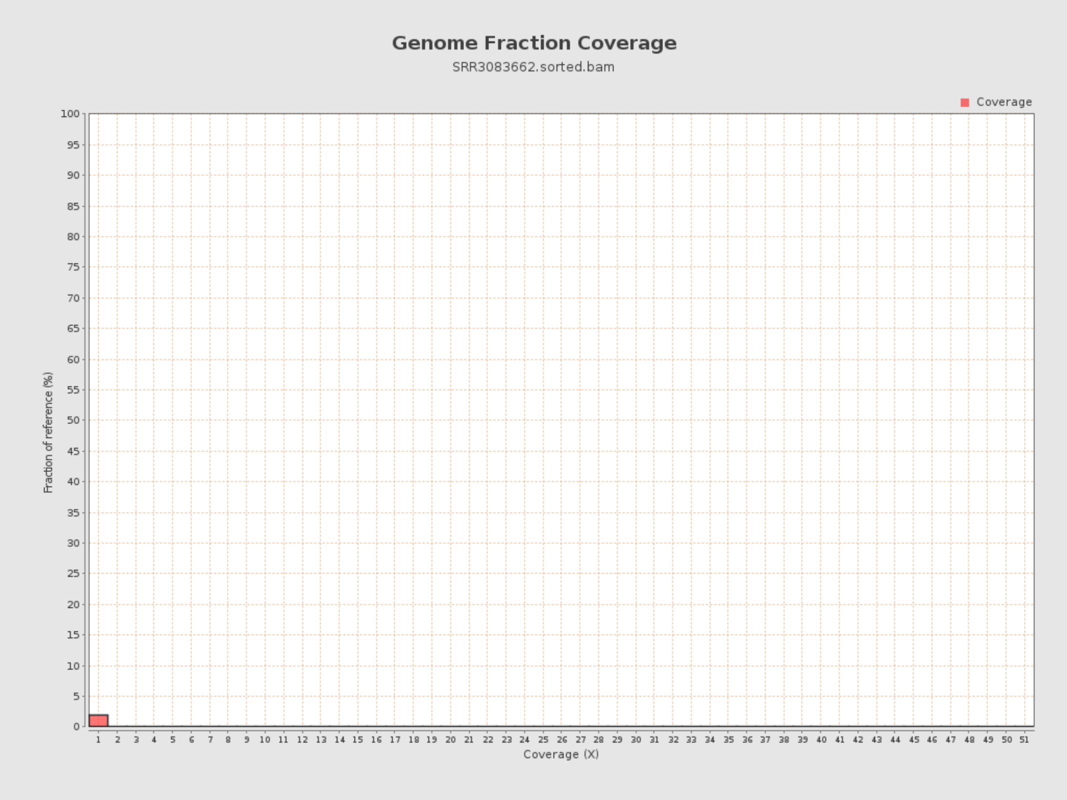
4. Results : Coverage Histogram



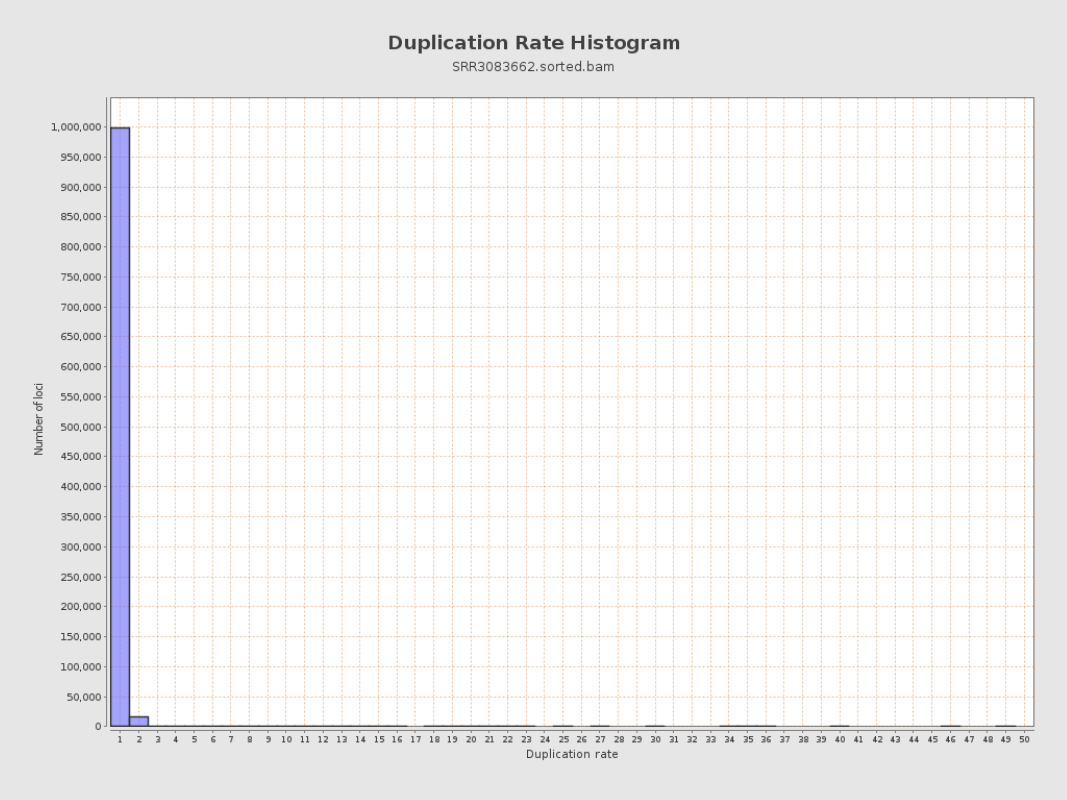
5. Results : Coverage Histogram (0-50X)



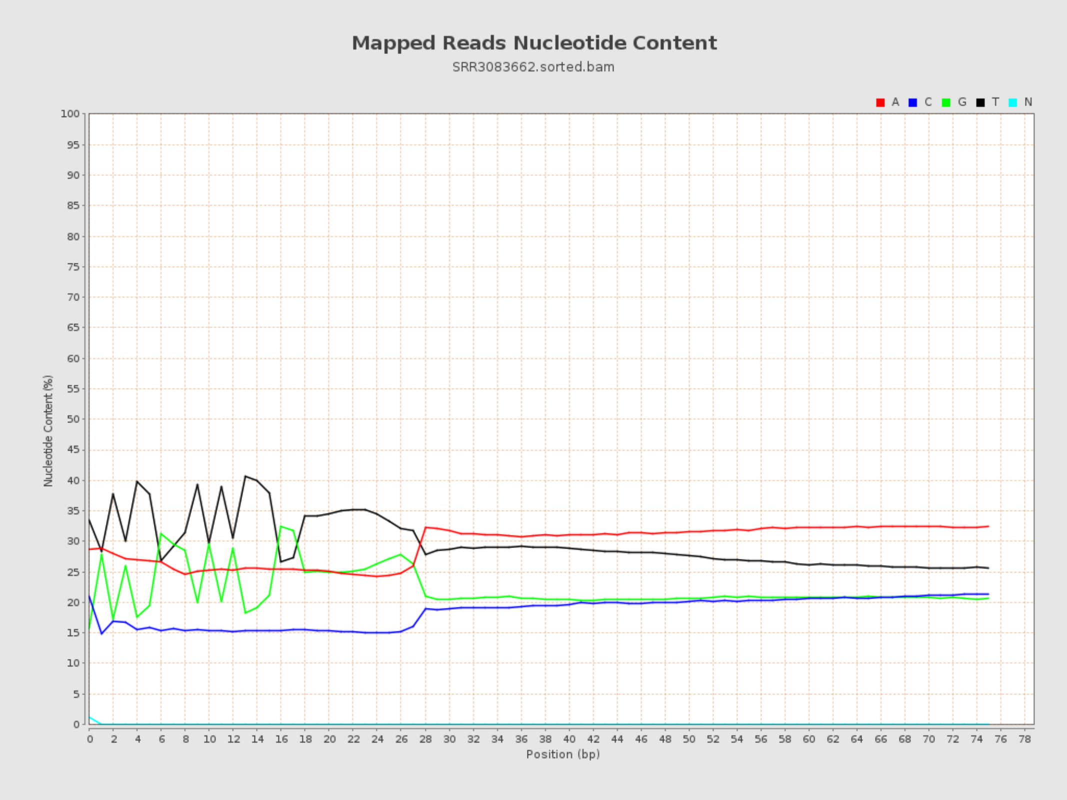
6. Results : Genome Fraction Coverage



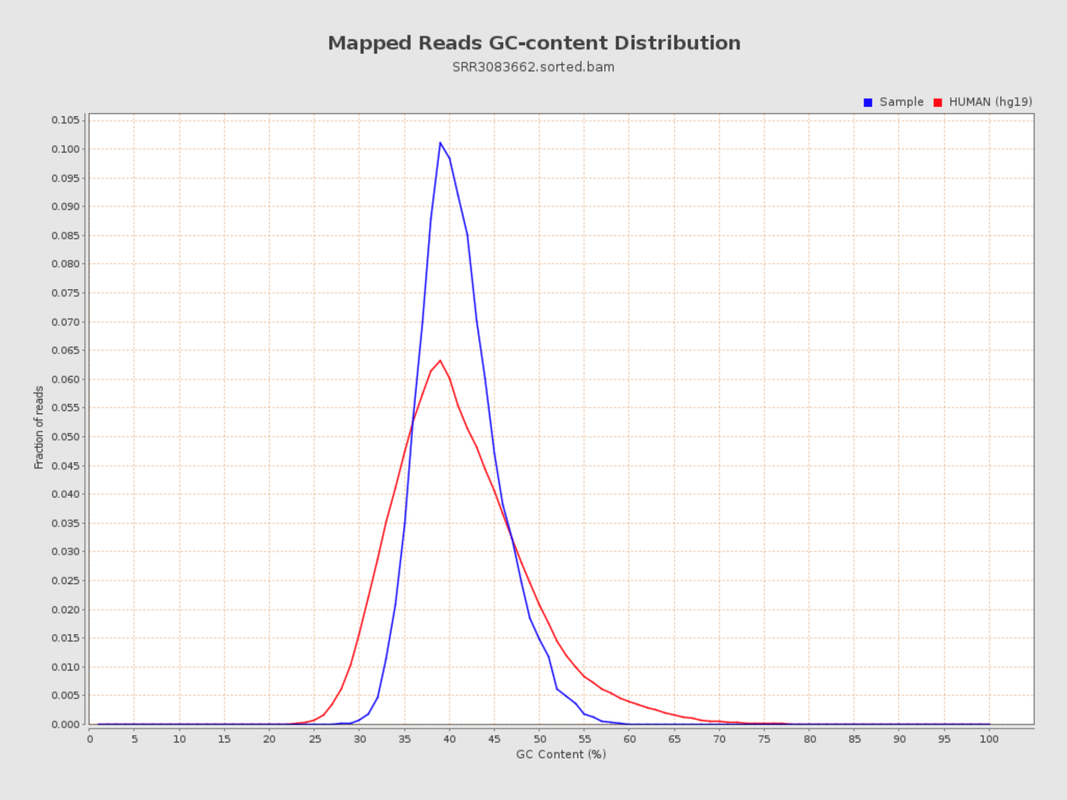
7. Results : Duplication Rate Histogram



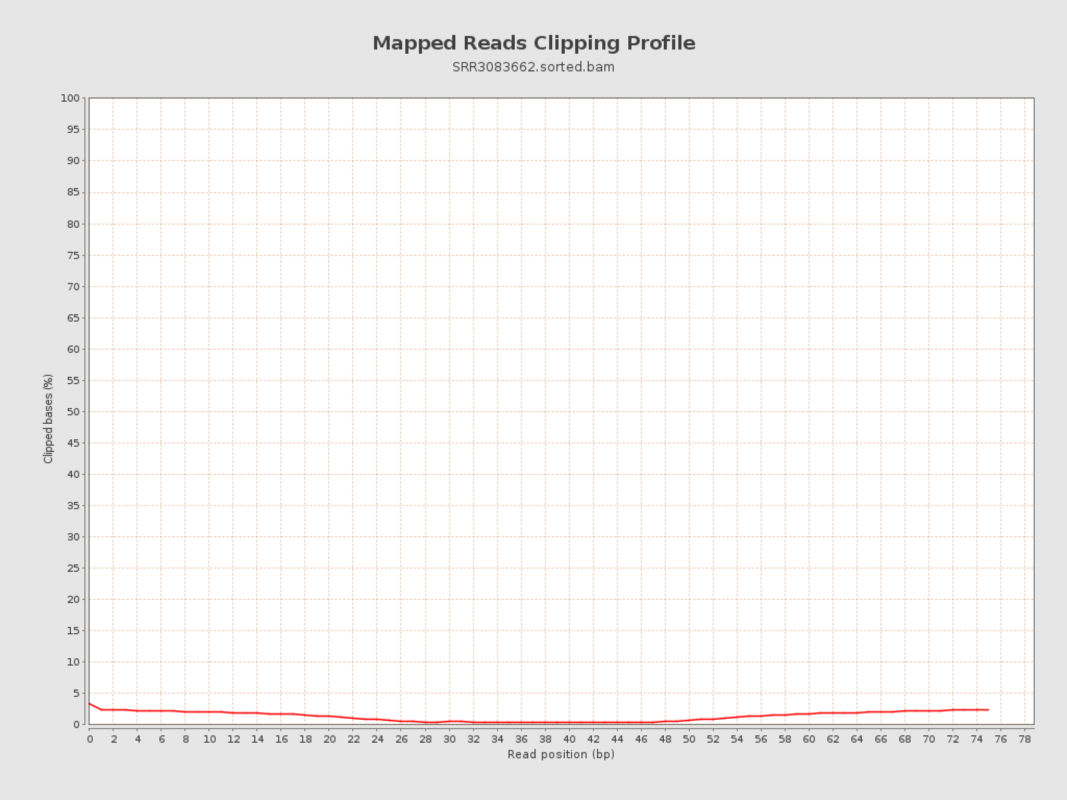
8. Results : Mapped Reads Nucleotide Content



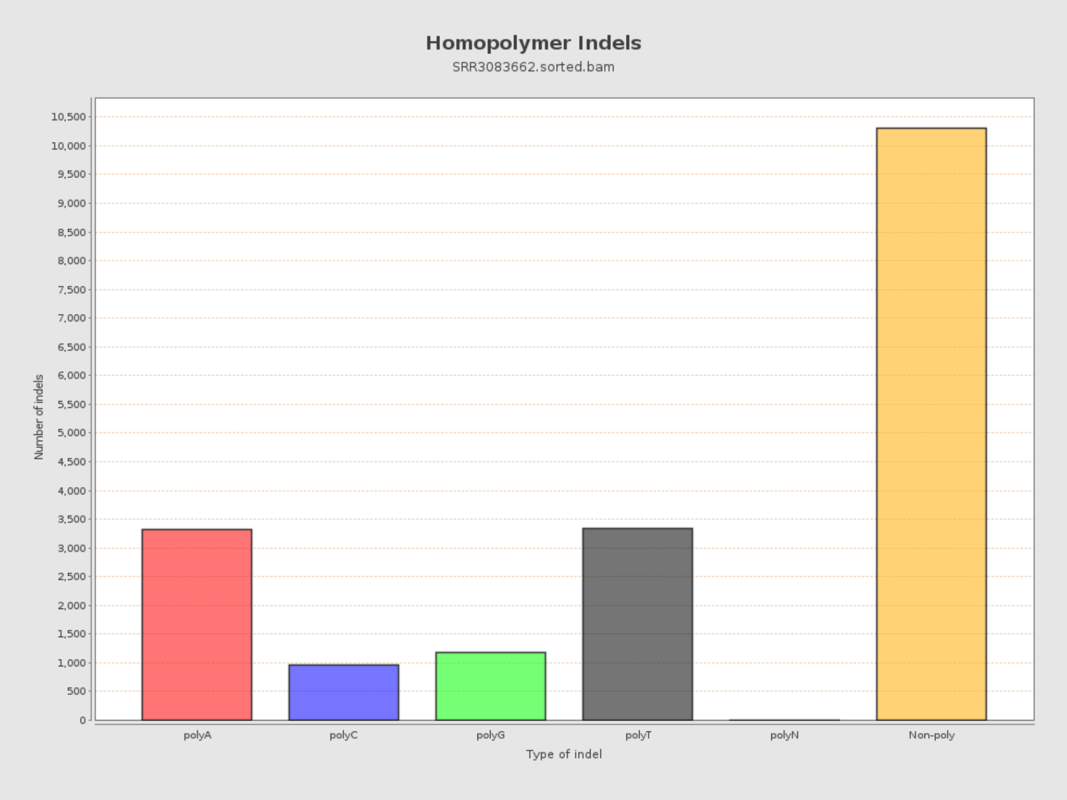
9. Results : Mapped Reads GC-content Distribution



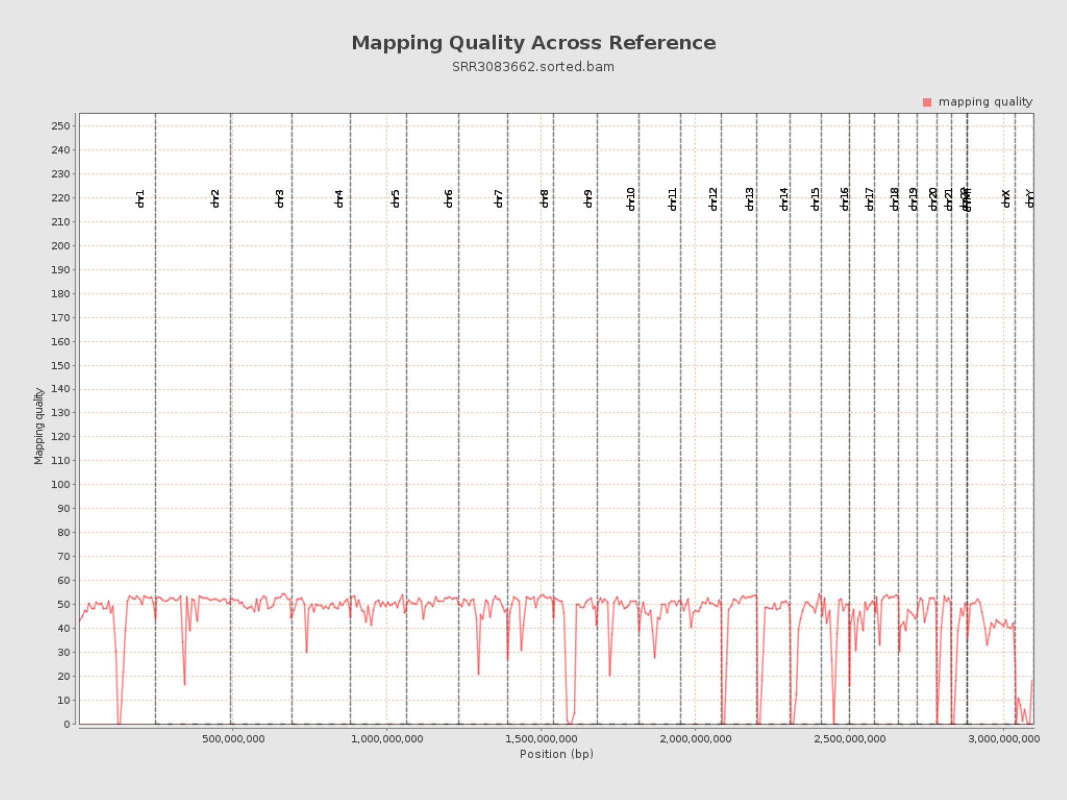
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram