Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:45:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238048.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_SRR6238048 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238048.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:45:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238048.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,836,316
Mapped reads	497,713 / 27.1%
Unmapped reads	1,338,603 / 72.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,498 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	54,292 / 2.96%
Duplication rate	9.18%
Clipped reads	356,888 / 19.43%

2.2. ACGT Content

Number/percentage of A's	7,680,800 / 26.01%
Number/percentage of C's	5,051,306 / 17.1%
Number/percentage of T's	9,590,867 / 32.48%
Number/percentage of G's	7,208,622 / 24.41%
Number/percentage of N's	1,255 / 0%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.148

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

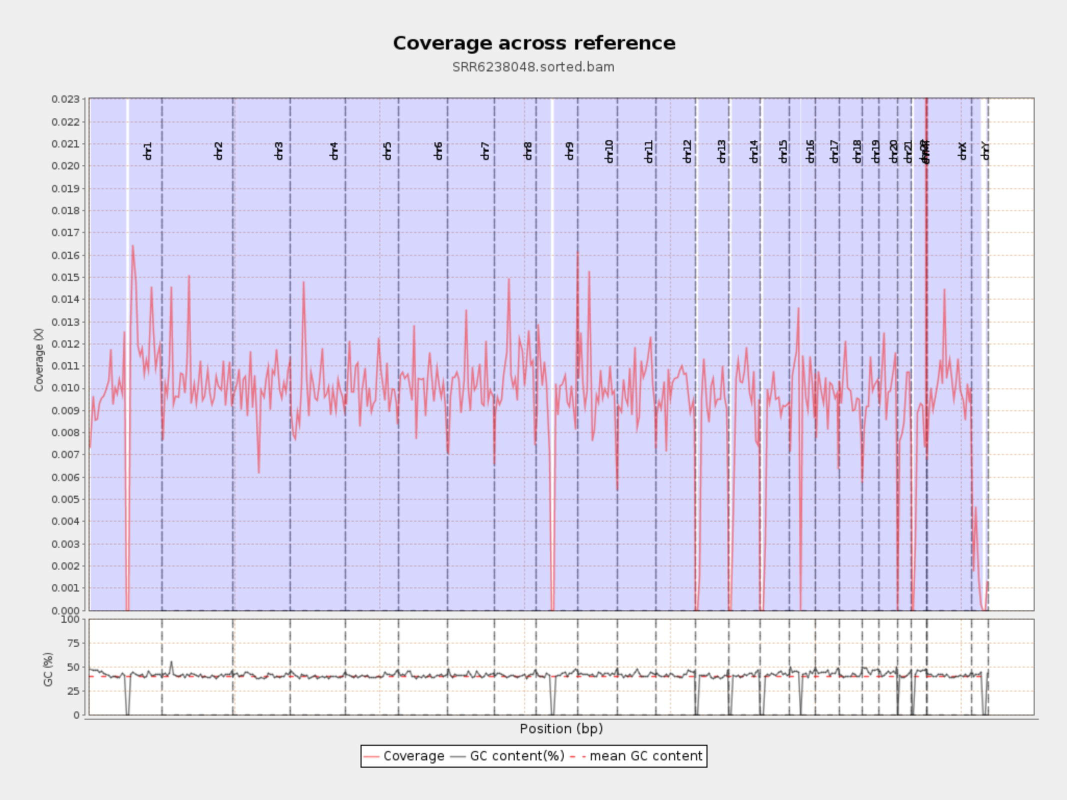
General error rate	0.86%
Mismatches	250,945
Insertions	2,379
Mapped reads with at least one insertion	0.47%
Deletions	9,171
Mapped reads with at least one deletion	1.82%
Homopolymer indels	46.36%

2.6. Chromosome stats

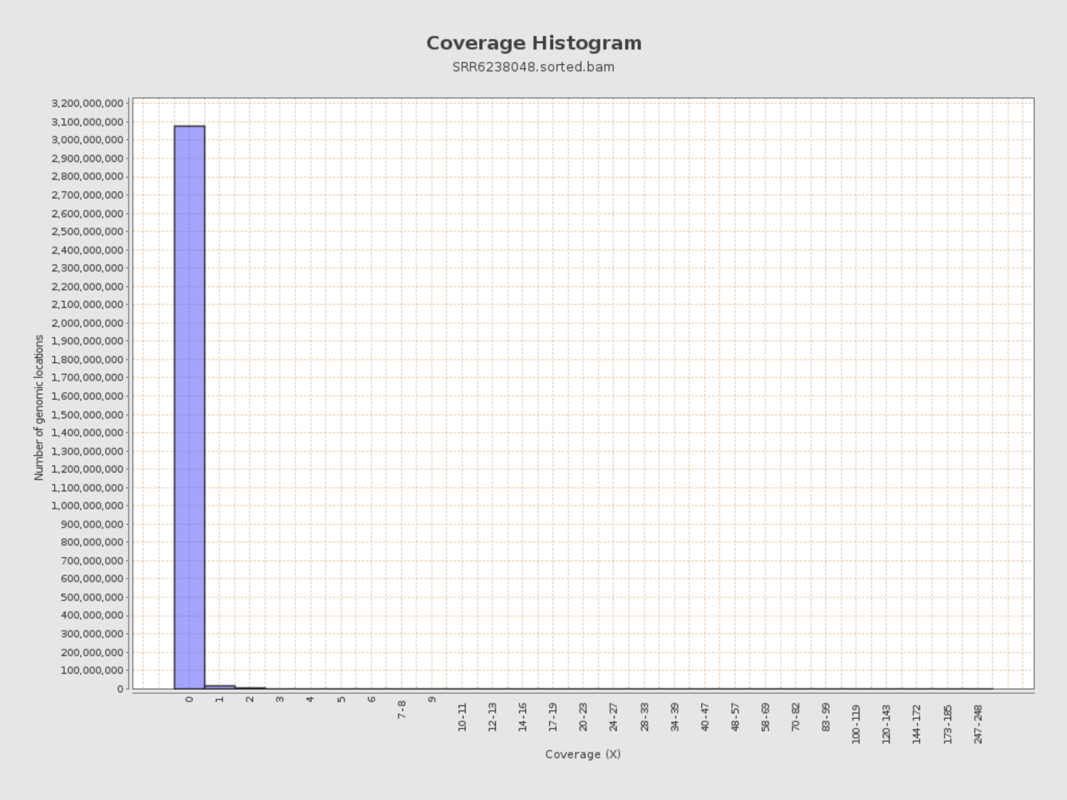
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2568242	0.0103	0.1673
chr2	243199373	2512870	0.0103	0.2151
chr3	198022430	1976923	0.01	0.1372
chr4	191154276	1868204	0.0098	0.1357
chr5	180915260	1816035	0.01	0.136
chr6	171115067	1732954	0.0101	0.1499
chr7	159138663	1619340	0.0102	0.1529

chr8	146364022	1563019	0.0107	0.1579
chr9	141213431	1251832	0.0089	0.1328
chr10	135534747	1362437	0.0101	0.1455
chr11	135006516	1346350	0.01	0.1398
chr12	133851895	1316520	0.0098	0.1365
chr13	115169878	929693	0.0081	0.1237
chr14	107349540	890247	0.0083	0.1255
chr15	102531392	790040	0.0077	0.1199
chr16	90354753	870628	0.0096	0.134
chr17	81195210	767281	0.0094	0.1299
chr18	78077248	764785	0.0098	0.1782
chr19	59128983	566058	0.0096	0.1431
chr20	63025520	650982	0.0103	0.1385
chr21	48129895	388867	0.0081	0.1211
chr22	51304566	307992	0.006	0.1035
chrMT	16571	19526	1.1783	1.8905
chrX	155270560	1572941	0.0101	0.1381
chrY	59373566	93203	0.0016	0.0527

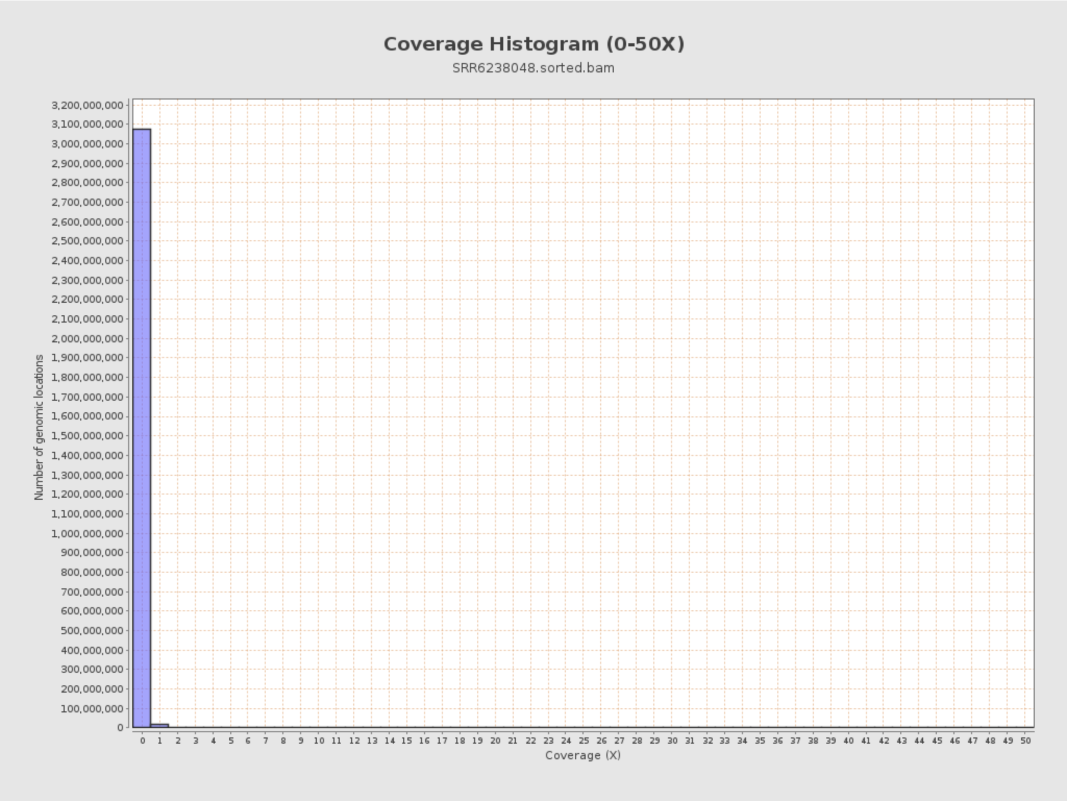
3. Results : Coverage across reference



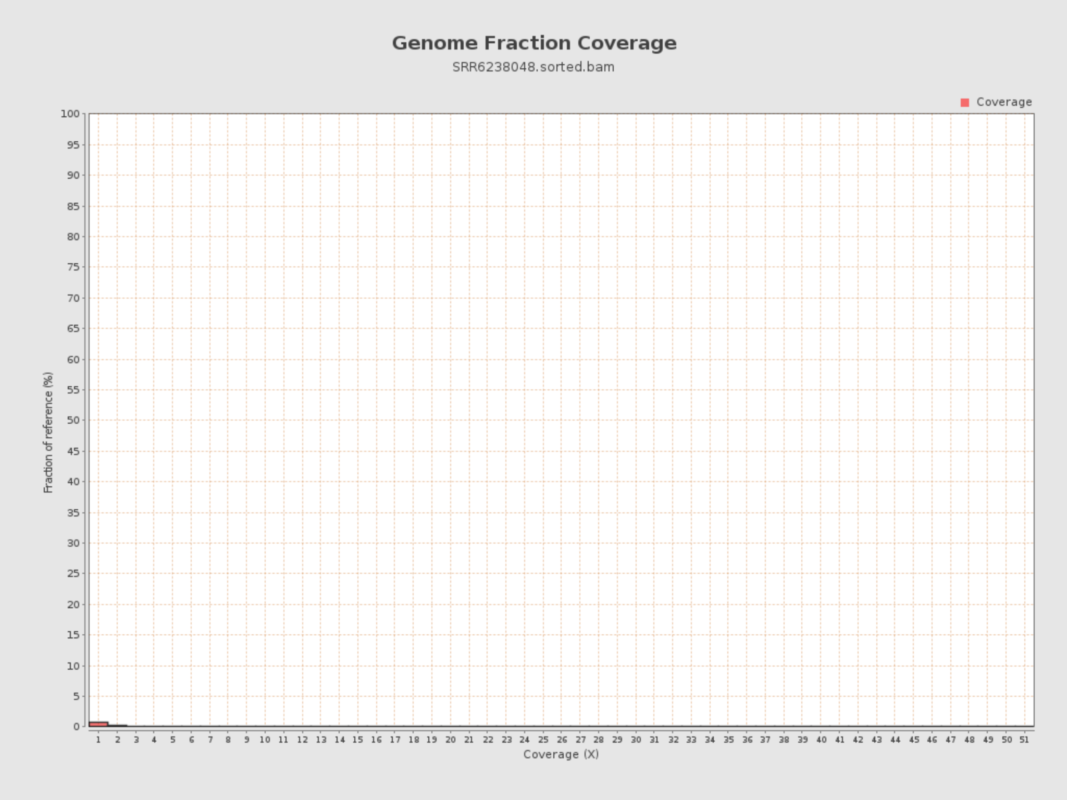
4. Results : Coverage Histogram



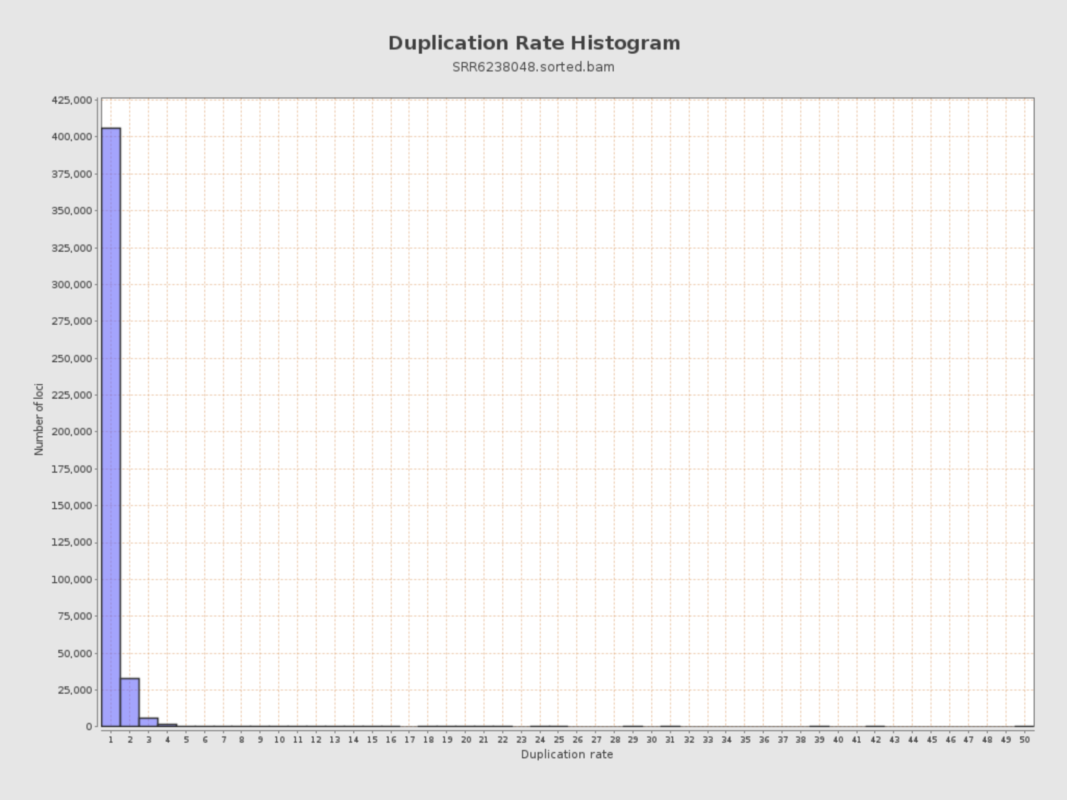
5. Results : Coverage Histogram (0-50X)



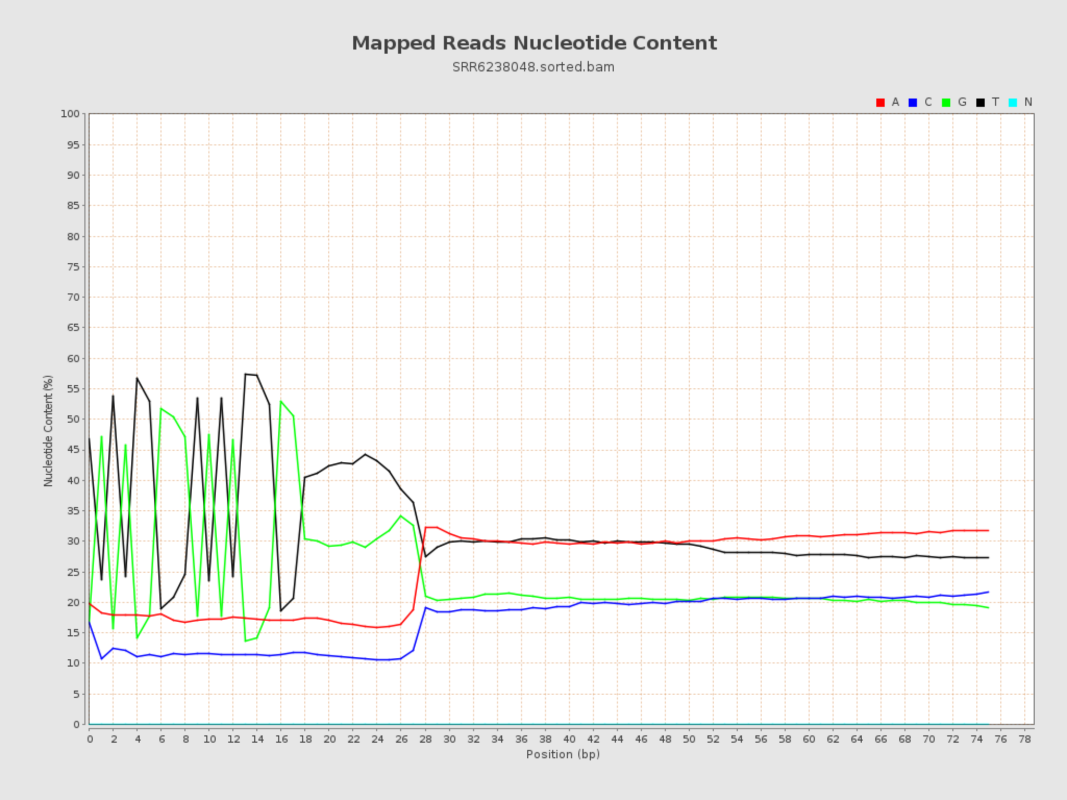
6. Results : Genome Fraction Coverage



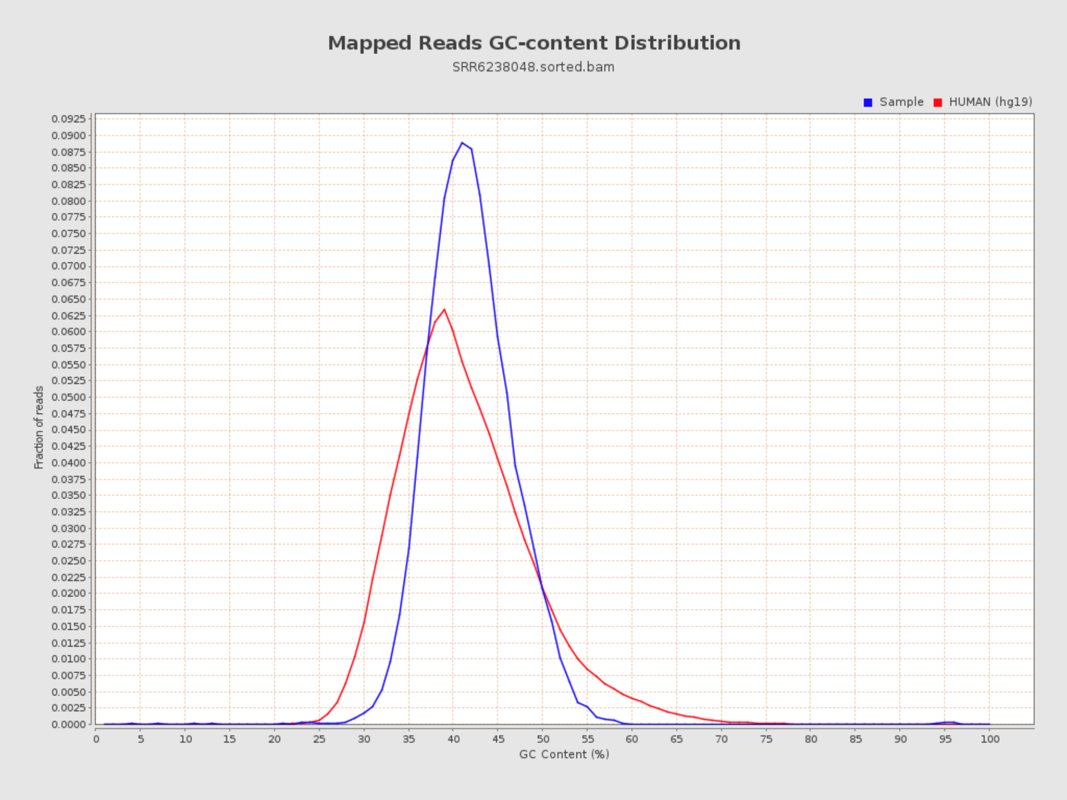
7. Results : Duplication Rate Histogram



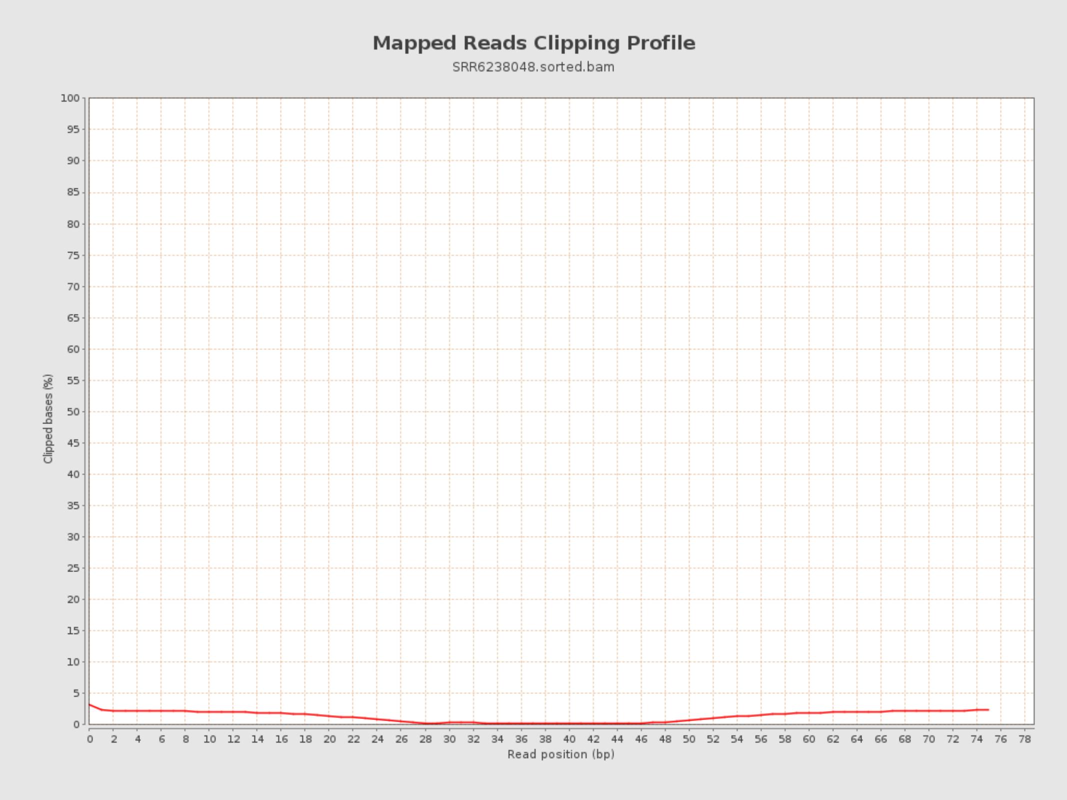
8. Results : Mapped Reads Nucleotide Content



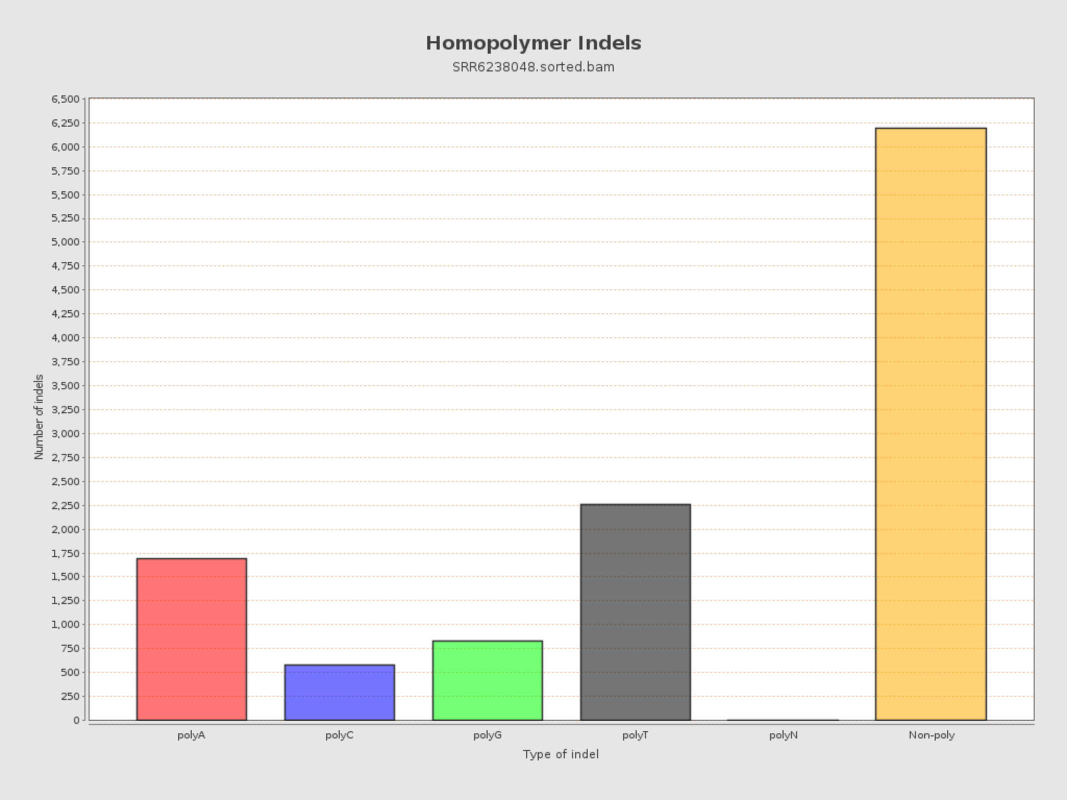
9. Results : Mapped Reads GC-content Distribution



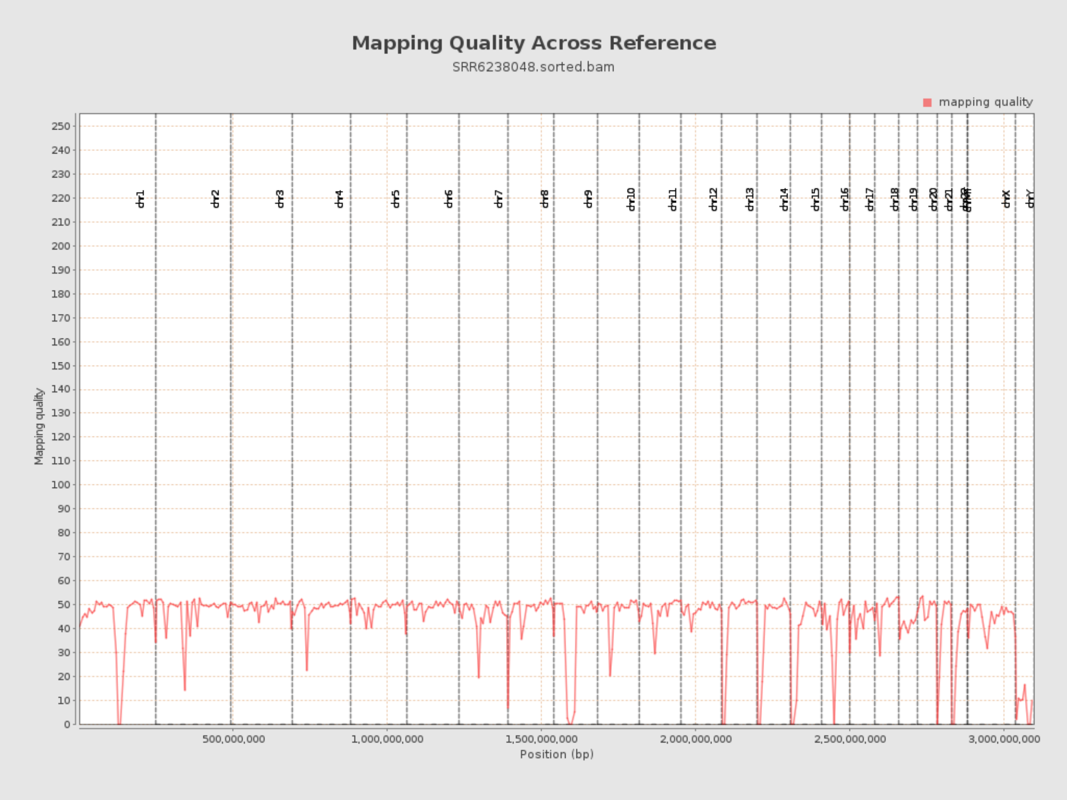
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram