Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:49:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238071.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_SRR6238071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:49:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,276,302
Mapped reads	647,438 / 50.73%
Unmapped reads	628,864 / 49.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,107 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	38,804 / 3.04%
Duplication rate	5.22%
Clipped reads	492,414 / 38.58%

2.2. ACGT Content

Number/percentage of A's	9,702,007 / 25.66%
Number/percentage of C's	6,281,973 / 16.62%
Number/percentage of T's	12,540,749 / 33.17%
Number/percentage of G's	9,279,223 / 24.54%
Number/percentage of N's	1,429 / 0%
GC Percentage	41.16%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1494

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

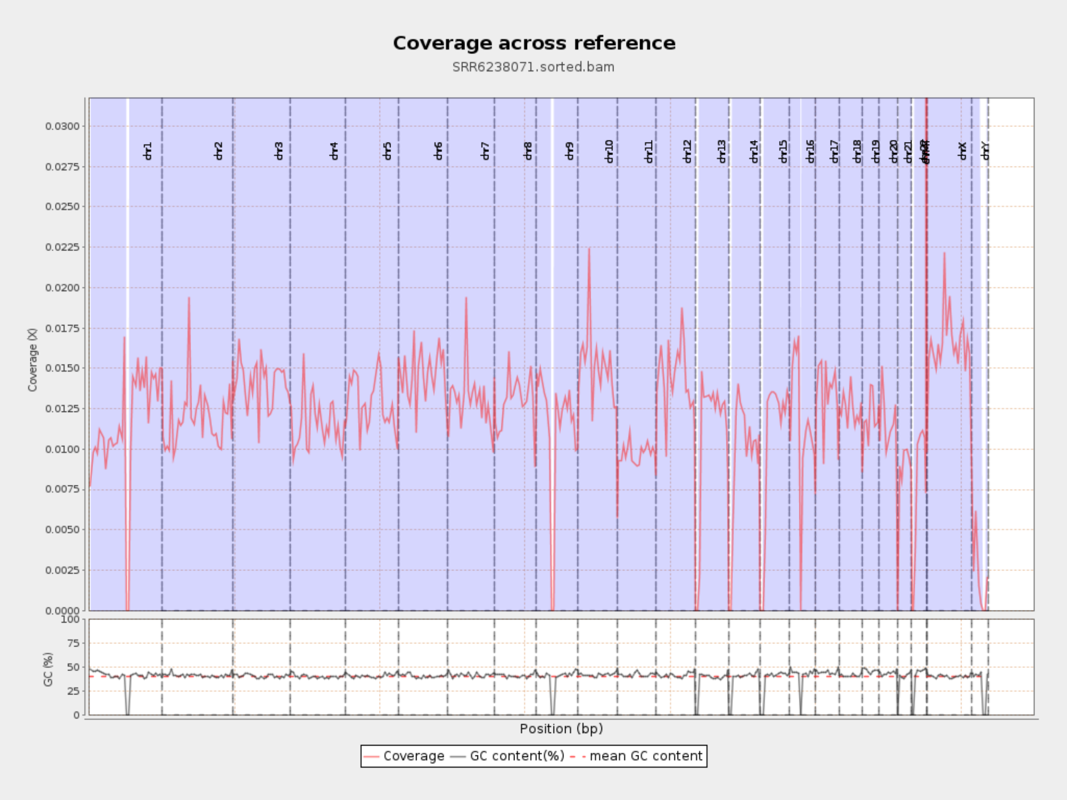
General error rate	0.86%
Mismatches	321,352
Insertions	2,868
Mapped reads with at least one insertion	0.44%
Deletions	15,163
Mapped reads with at least one deletion	2.31%
Homopolymer indels	44.11%

2.6. Chromosome stats

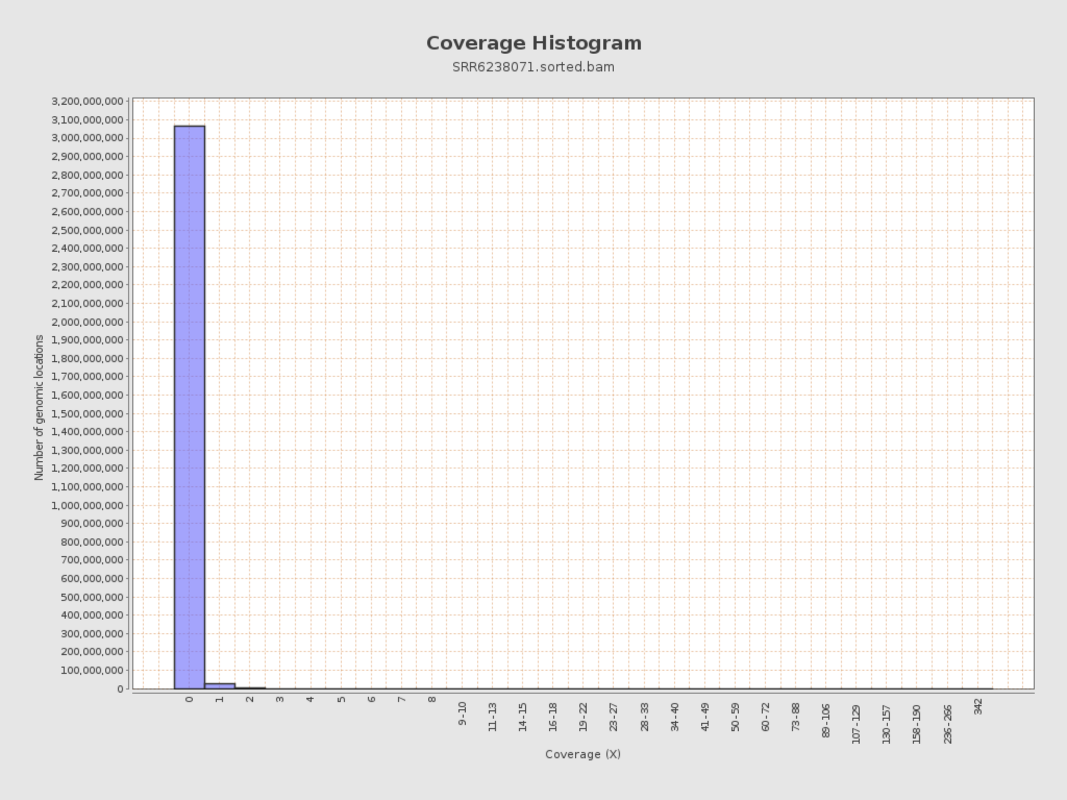
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2853015	0.0114	0.1817
chr2	243199373	2900545	0.0119	0.2046
chr3	198022430	2797708	0.0141	0.1356
chr4	191154276	2196054	0.0115	0.1278
chr5	180915260	2329237	0.0129	0.1297
chr6	171115067	2503236	0.0146	0.1499
chr7	159138663	2086658	0.0131	0.1791

chr8	146364022	1892343	0.0129	0.1621
chr9	141213431	1595190	0.0113	0.1351
chr10	135534747	2067245	0.0153	0.1627
chr11	135006516	1304172	0.0097	0.1178
chr12	133851895	1943701	0.0145	0.1439
chr13	115169878	1242175	0.0108	0.1202
chr14	107349540	1017796	0.0095	0.1136
chr15	102531392	1079916	0.0105	0.1184
chr16	90354753	1047610	0.0116	0.1266
chr17	81195210	1089299	0.0134	0.1336
chr18	78077248	973287	0.0125	0.1832
chr19	59128983	705818	0.0119	0.1567
chr20	63025520	733640	0.0116	0.1238
chr21	48129895	401805	0.0083	0.1073
chr22	51304566	377896	0.0074	0.0973
chrMT	16571	19479	1.1755	1.3305
chrX	155270560	2545359	0.0164	0.1507
chrY	59373566	126668	0.0021	0.0599

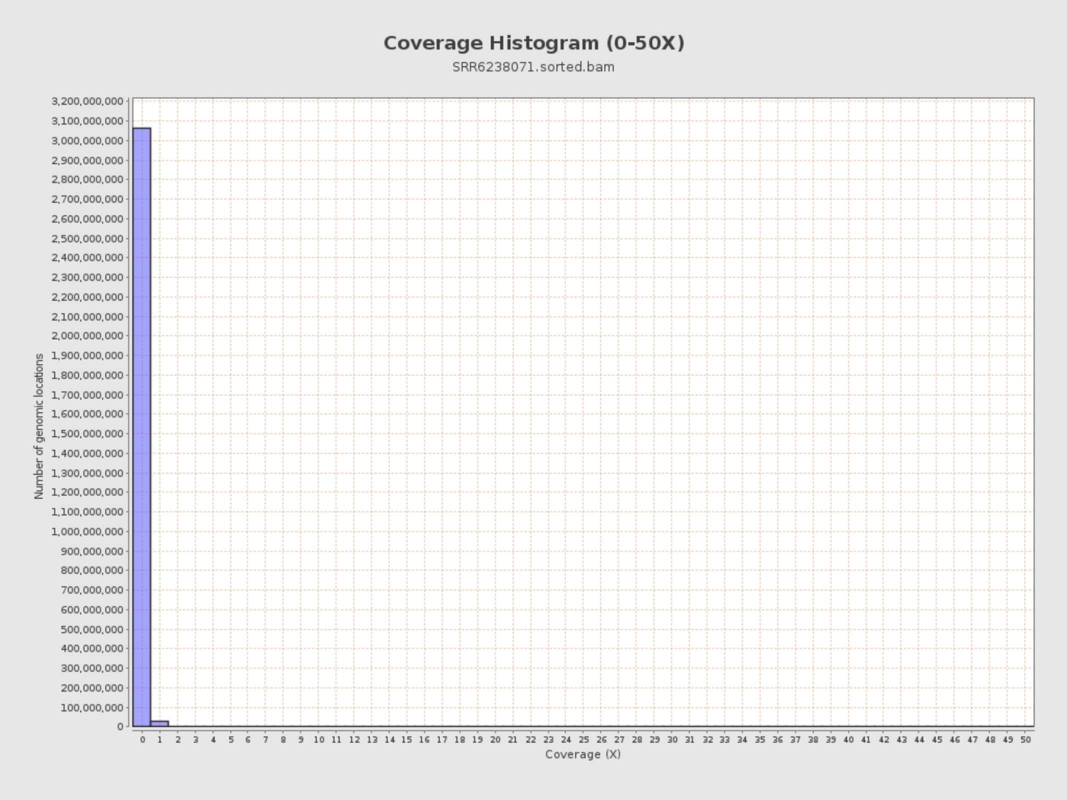
3. Results : Coverage across reference



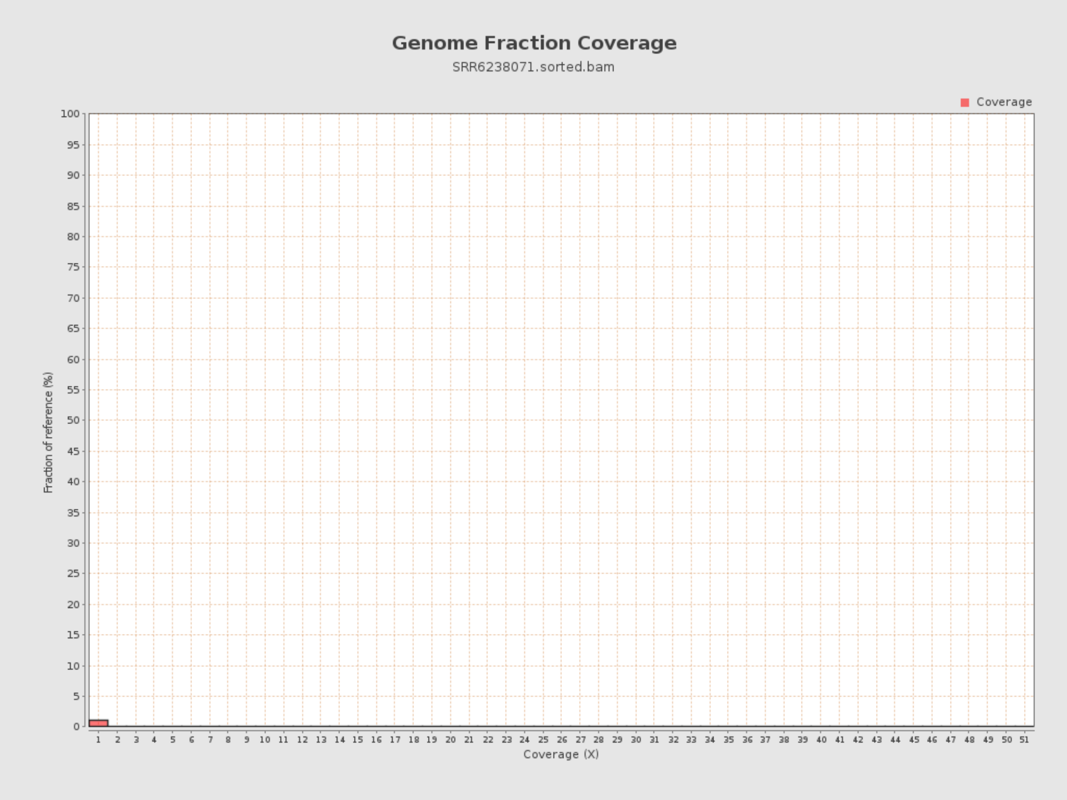
4. Results : Coverage Histogram



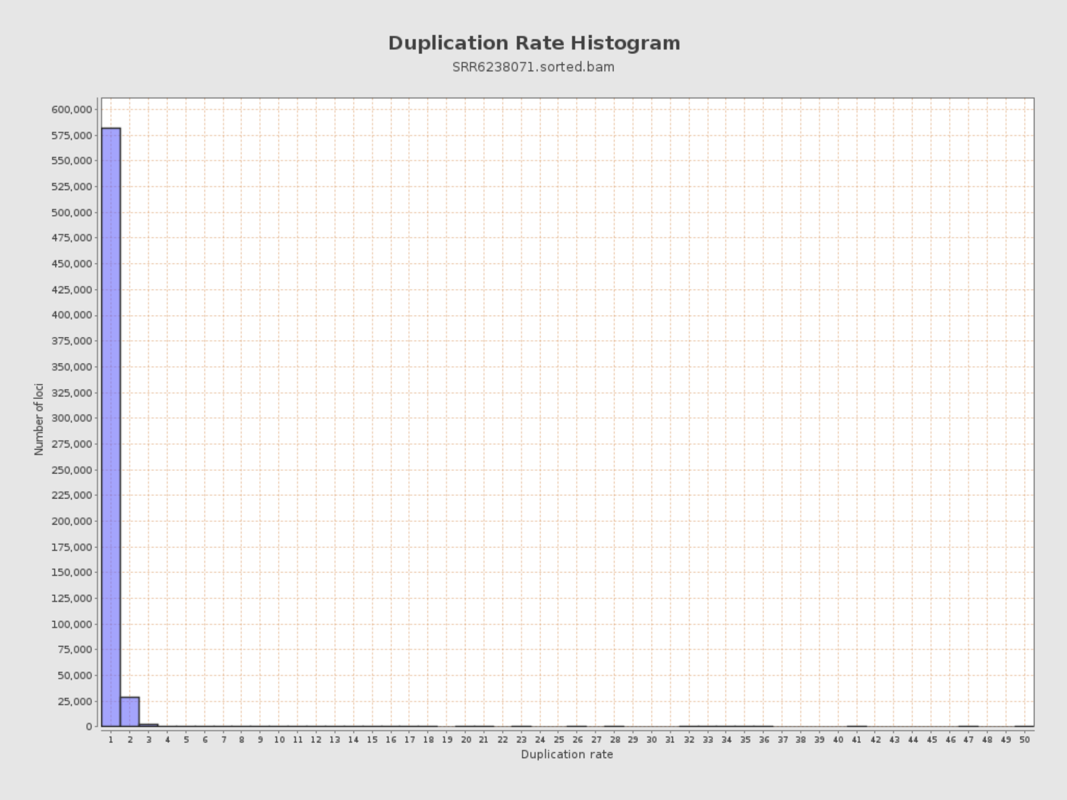
5. Results : Coverage Histogram (0-50X)



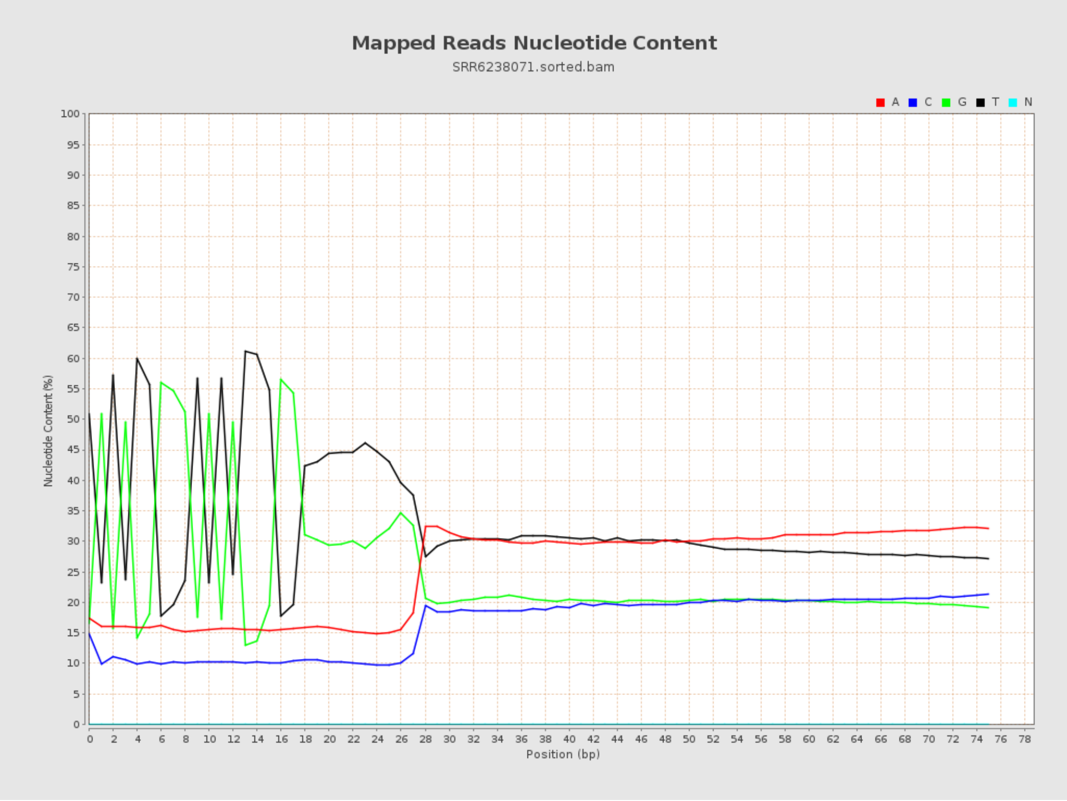
6. Results : Genome Fraction Coverage



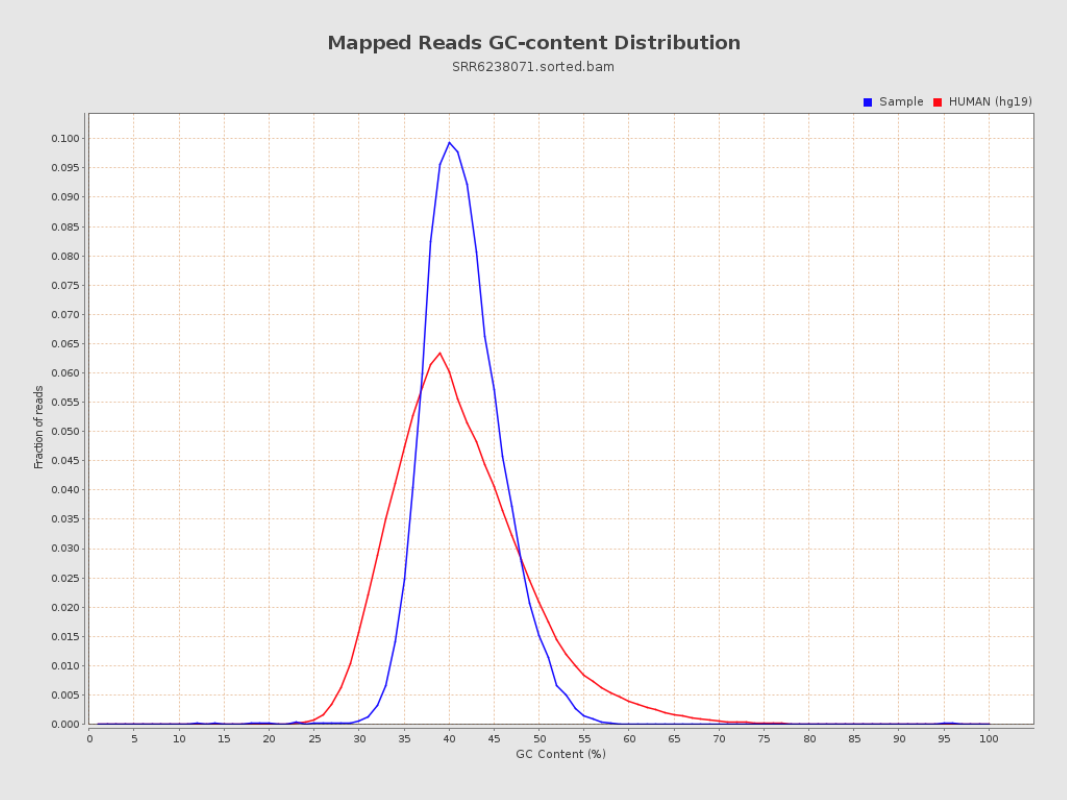
7. Results : Duplication Rate Histogram



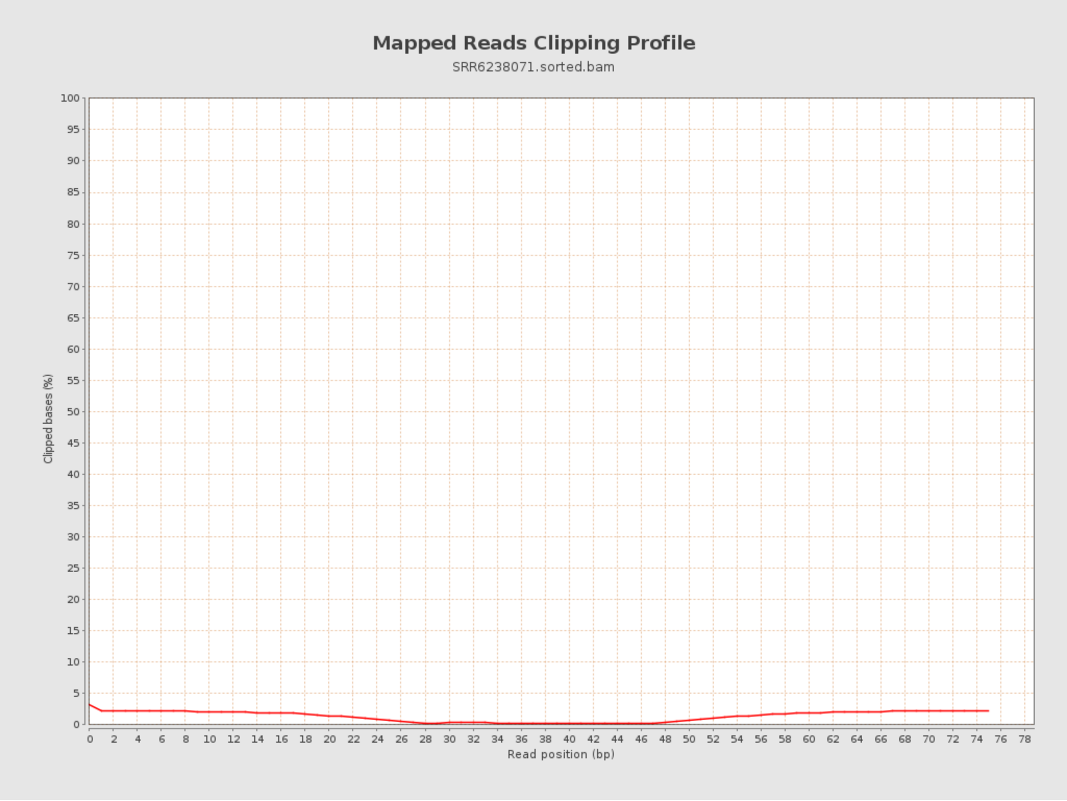
8. Results : Mapped Reads Nucleotide Content



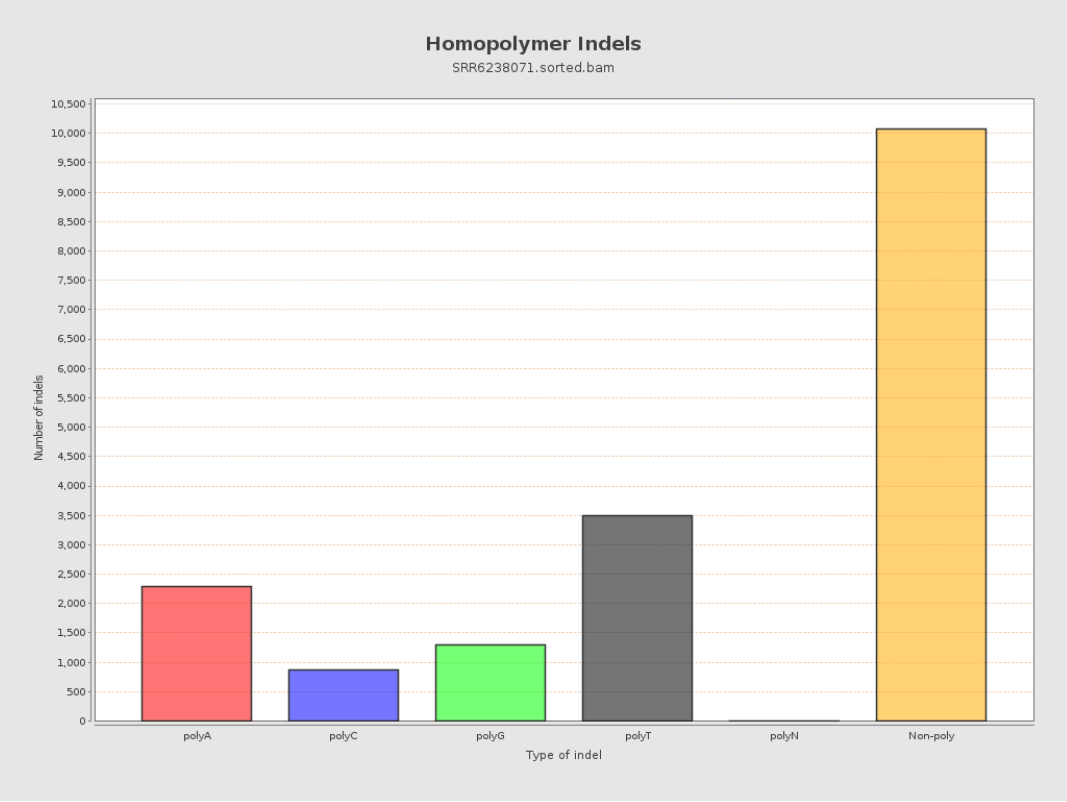
9. Results : Mapped Reads GC-content Distribution



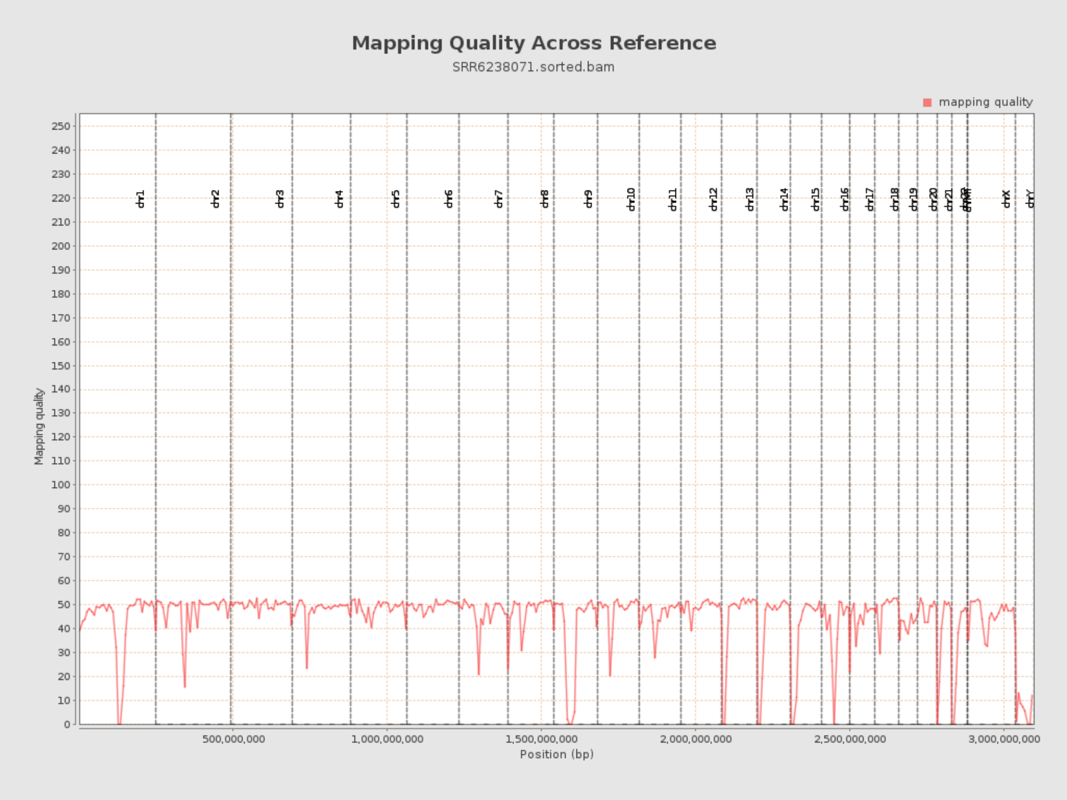
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram