Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:26:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238041.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_SRR6238041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:26:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,168,087
Mapped reads	1,922,656 / 88.68%
Unmapped reads	245,431 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,166 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	84,019 / 3.88%
Duplication rate	3.42%
Clipped reads	993,205 / 45.81%

2.2. ACGT Content

Number/percentage of A's	34,551,021 / 27.66%
Number/percentage of C's	22,692,327 / 18.17%
Number/percentage of T's	39,579,440 / 31.69%
Number/percentage of G's	27,814,464 / 22.27%
Number/percentage of N's	258,984 / 0.21%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.3786

2.4. Mapping Quality

Mean Mapping Quality	45.91

2.5. Mismatches and indels

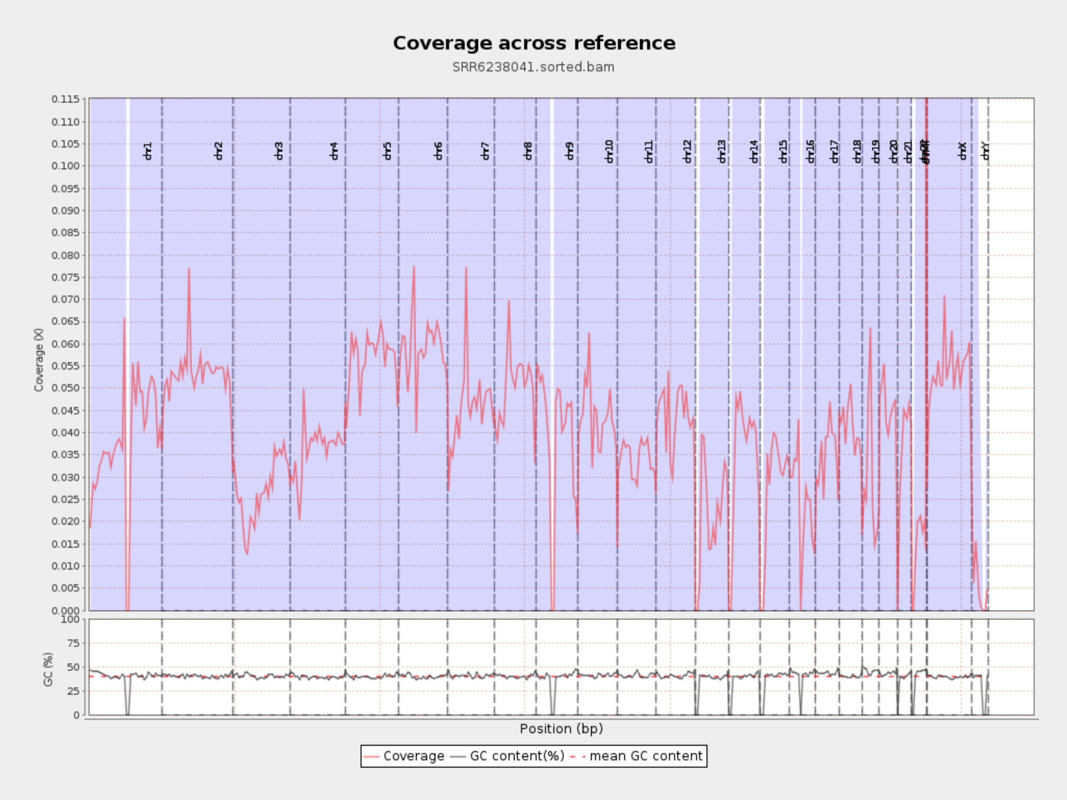
General error rate	0.93%
Mismatches	1,139,394
Insertions	9,752
Mapped reads with at least one insertion	0.5%
Deletions	43,051
Mapped reads with at least one deletion	2.21%
Homopolymer indels	45.31%

2.6. Chromosome stats

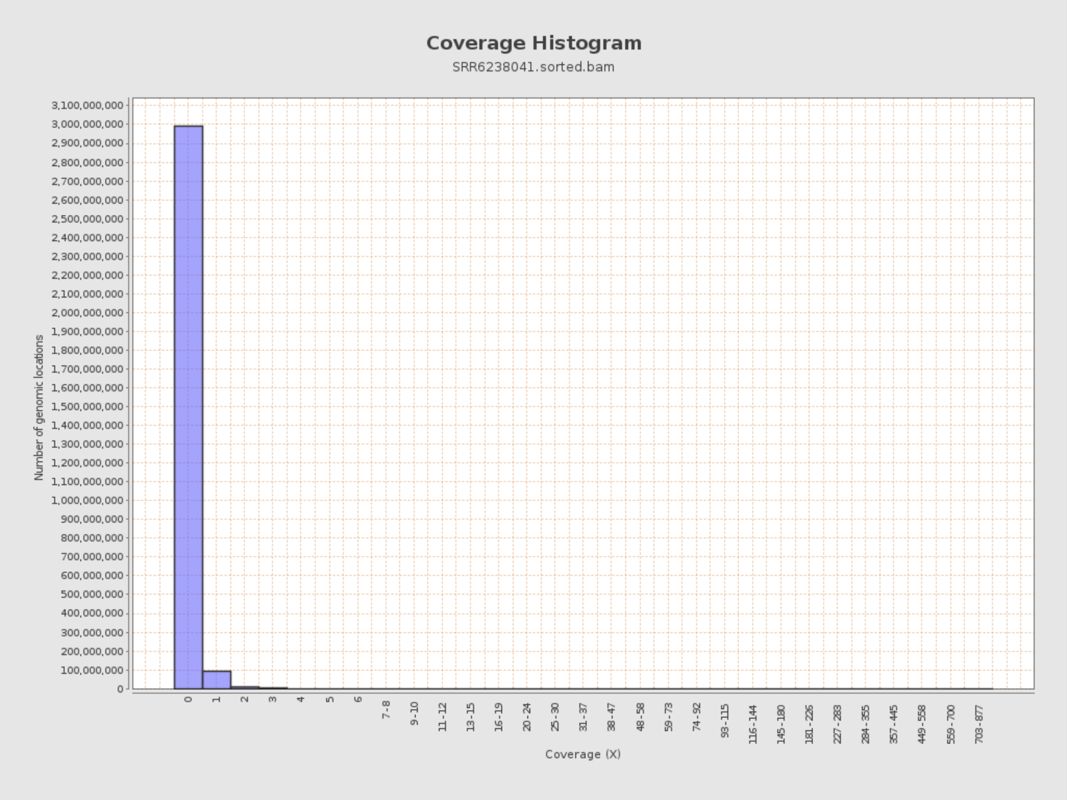
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9457212	0.0379	0.763
chr2	243199373	13040011	0.0536	0.4616
chr3	198022430	5360754	0.0271	0.1869
chr4	191154276	6902085	0.0361	0.2399
chr5	180915260	10339464	0.0572	0.2734
chr6	171115067	10125840	0.0592	0.344
chr7	159138663	7317170	0.046	0.5381

chr8	146364022	7335171	0.0501	0.4402
chr9	141213431	5537144	0.0392	0.3152
chr10	135534747	5942082	0.0438	0.3485
chr11	135006516	4598644	0.0341	0.2564
chr12	133851895	5873994	0.0439	0.2437
chr13	115169878	2438382	0.0212	0.1663
chr14	107349540	3750525	0.0349	0.2299
chr15	102531392	2832527	0.0276	0.1942
chr16	90354753	2180987	0.0241	0.1969
chr17	81195210	2858170	0.0352	0.2251
chr18	78077248	3228989	0.0414	0.4987
chr19	59128983	1807776	0.0306	0.4412
chr20	63025520	2884183	0.0458	0.2476
chr21	48129895	1722836	0.0358	0.2369
chr22	51304566	720125	0.014	0.1322
chrMT	16571	66228	3.9966	2.8596
chrX	155270560	8325318	0.0536	0.2844
chrY	59373566	321473	0.0054	0.1375

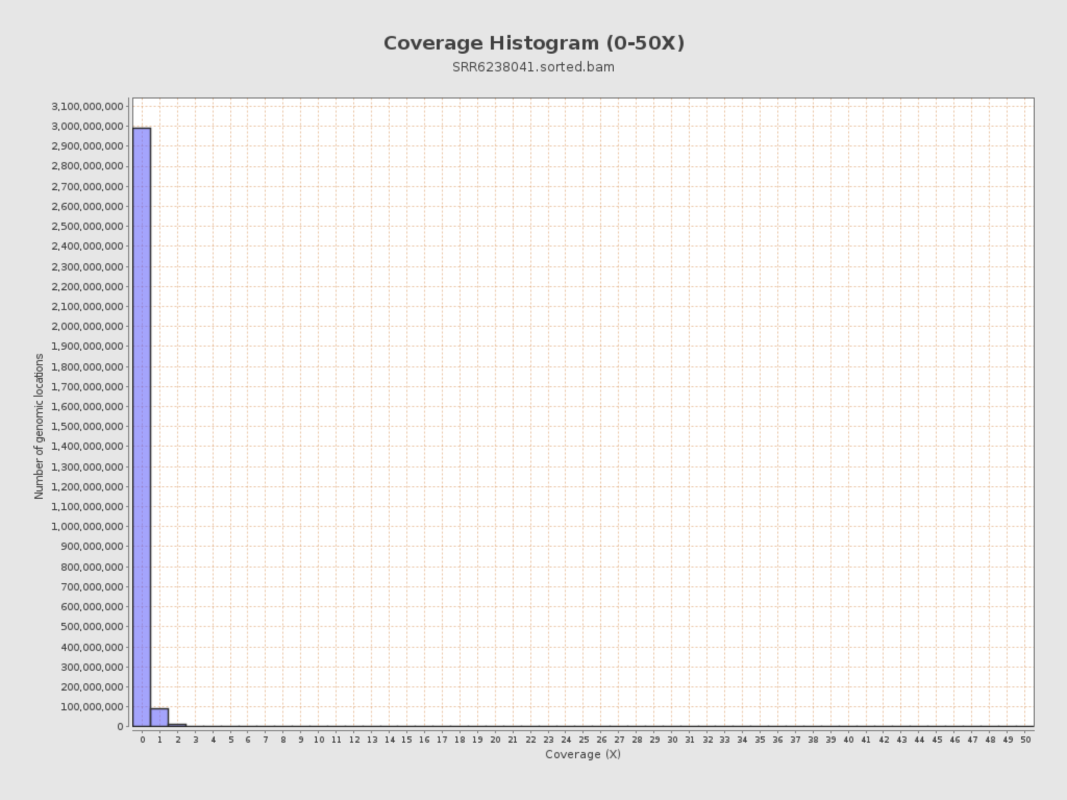
3. Results : Coverage across reference



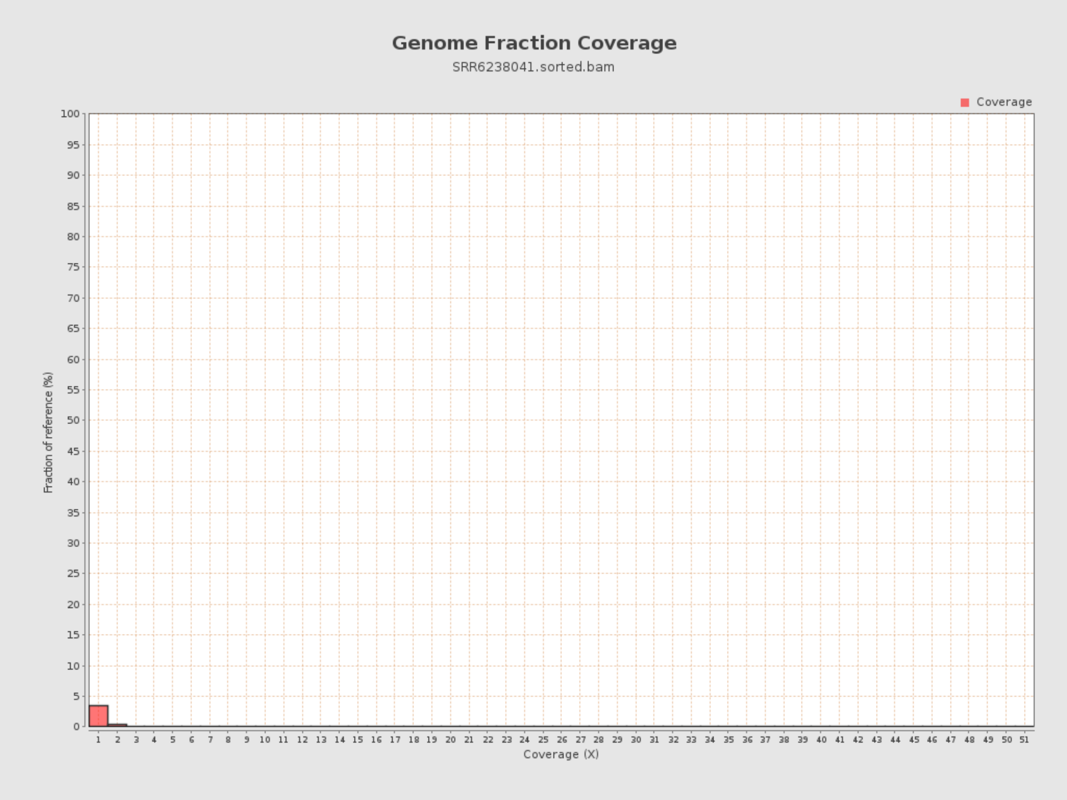
4. Results : Coverage Histogram



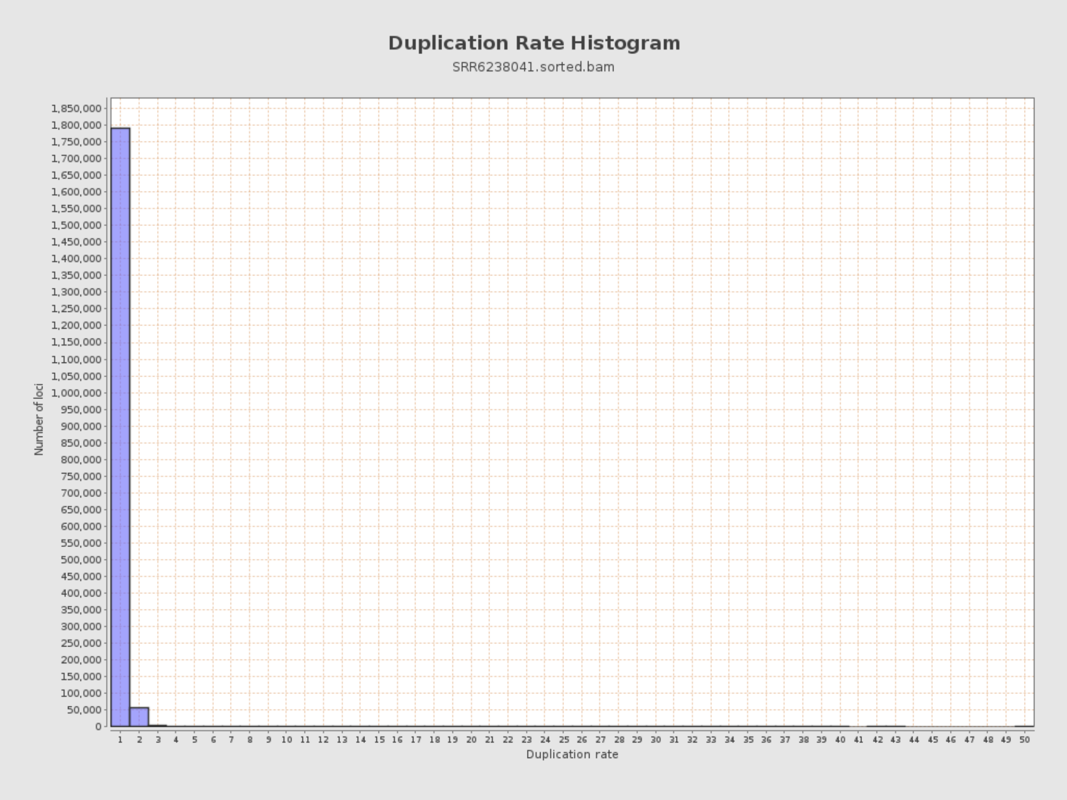
5. Results : Coverage Histogram (0-50X)



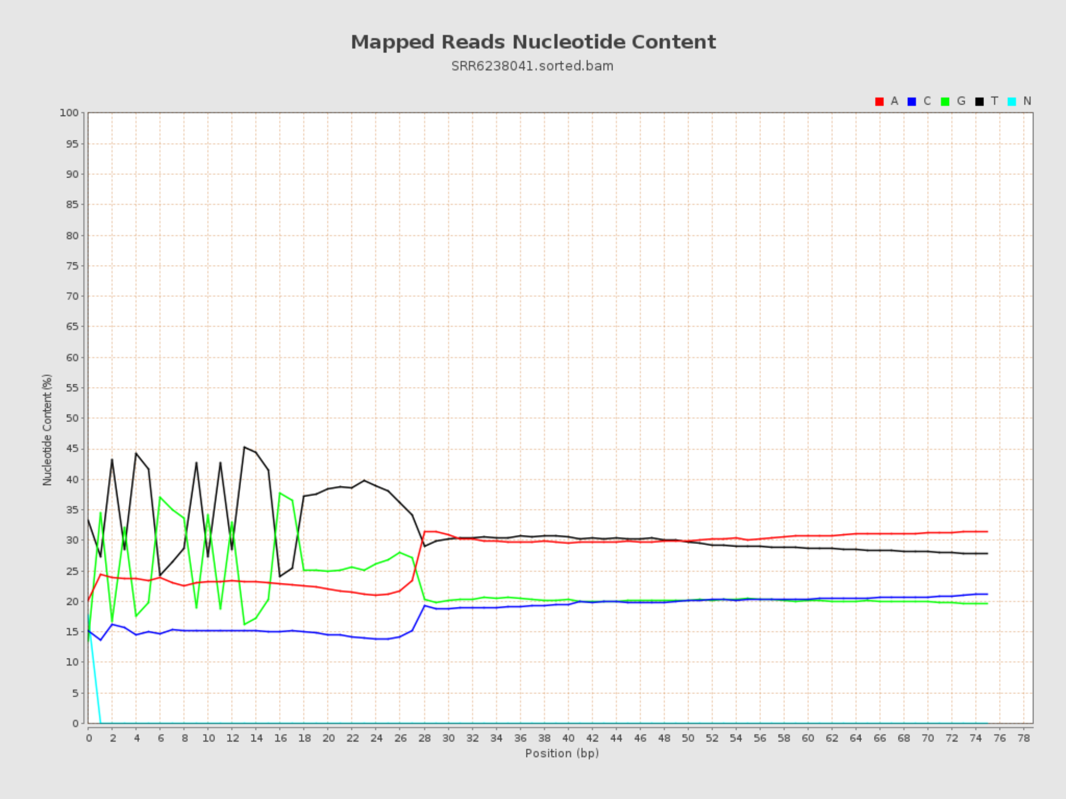
6. Results : Genome Fraction Coverage



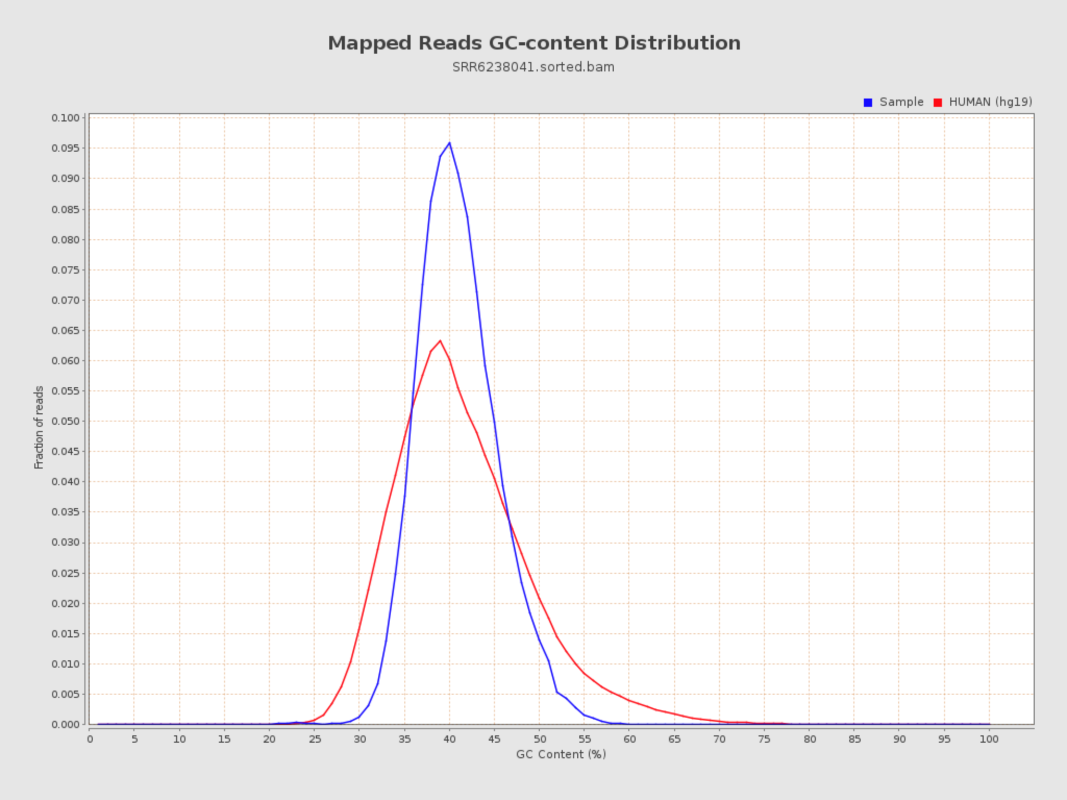
7. Results : Duplication Rate Histogram



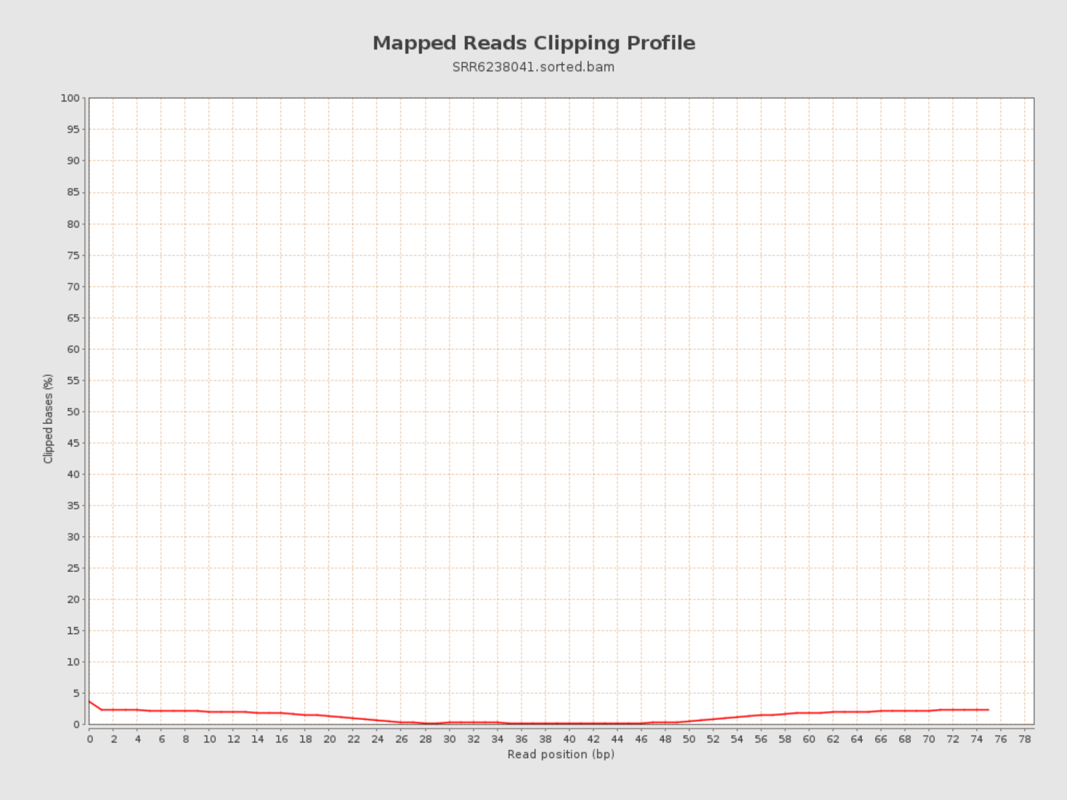
8. Results : Mapped Reads Nucleotide Content



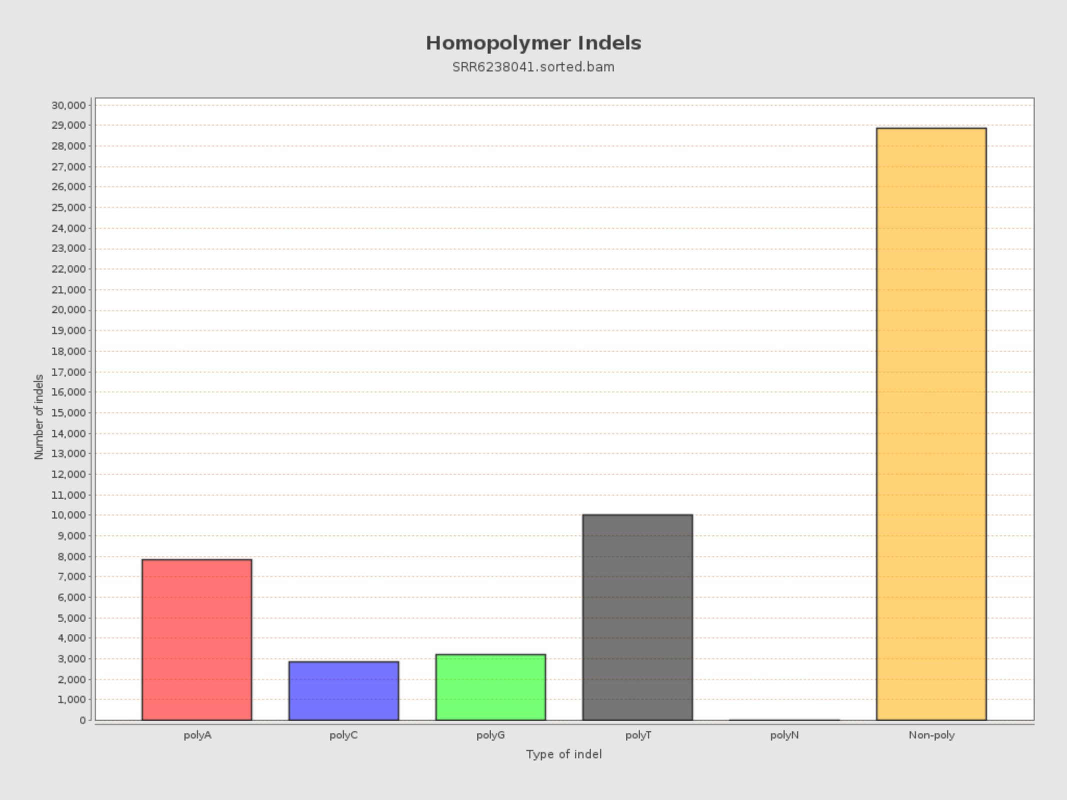
9. Results : Mapped Reads GC-content Distribution



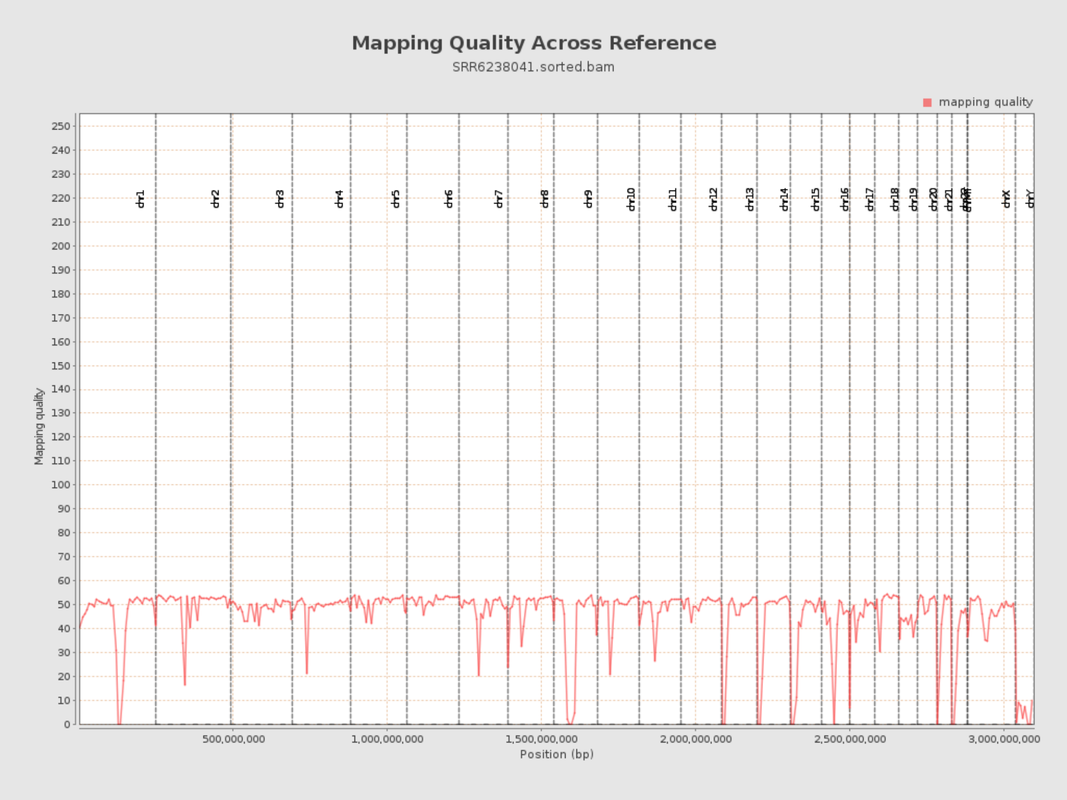
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram