Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:33:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238663.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_SRR6238663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:33:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,541,919
Mapped reads	2,320,952 / 91.31%
Unmapped reads	220,967 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,546 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	336,355 / 13.23%
Duplication rate	12.47%
Clipped reads	1,463,999 / 57.59%

2.2. ACGT Content

Number/percentage of A's	35,561,151 / 24.82%
Number/percentage of C's	24,785,958 / 17.3%
Number/percentage of T's	48,489,312 / 33.84%
Number/percentage of G's	34,425,300 / 24.03%
Number/percentage of N's	7,361 / 0.01%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0463

Standard Deviation	0.5231

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

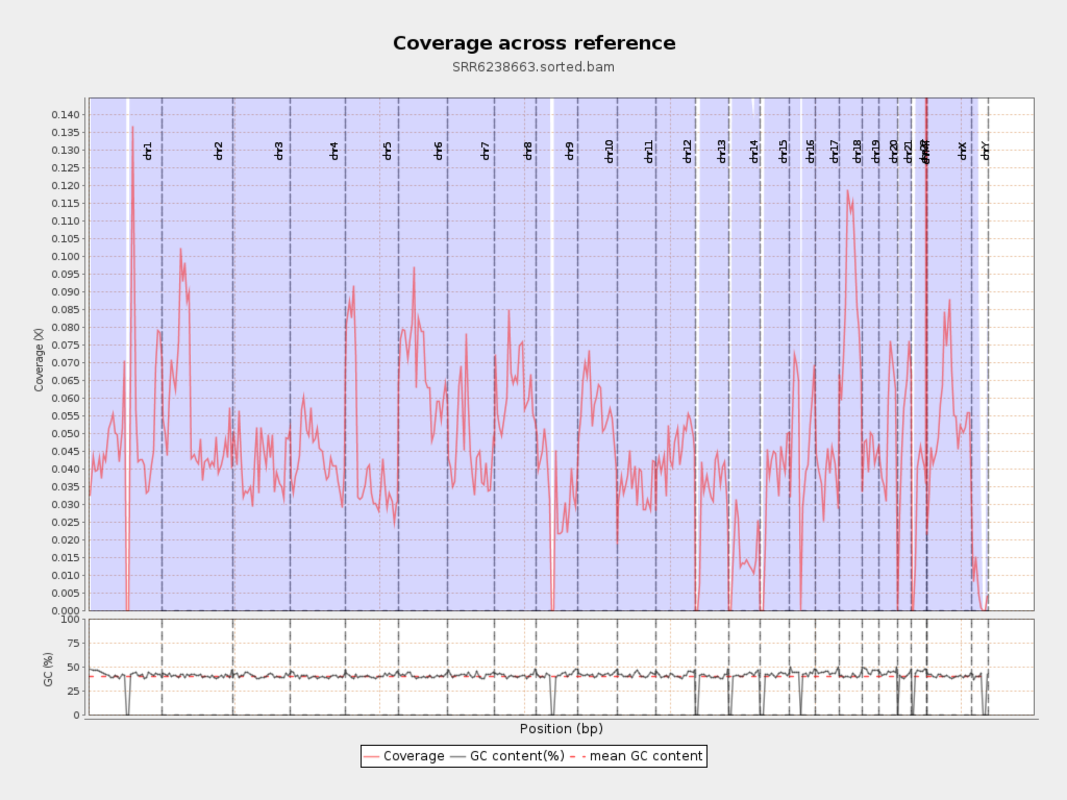
General error rate	0.59%
Mismatches	823,400
Insertions	9,095
Mapped reads with at least one insertion	0.39%
Deletions	40,322
Mapped reads with at least one deletion	1.72%
Homopolymer indels	42.67%

2.6. Chromosome stats

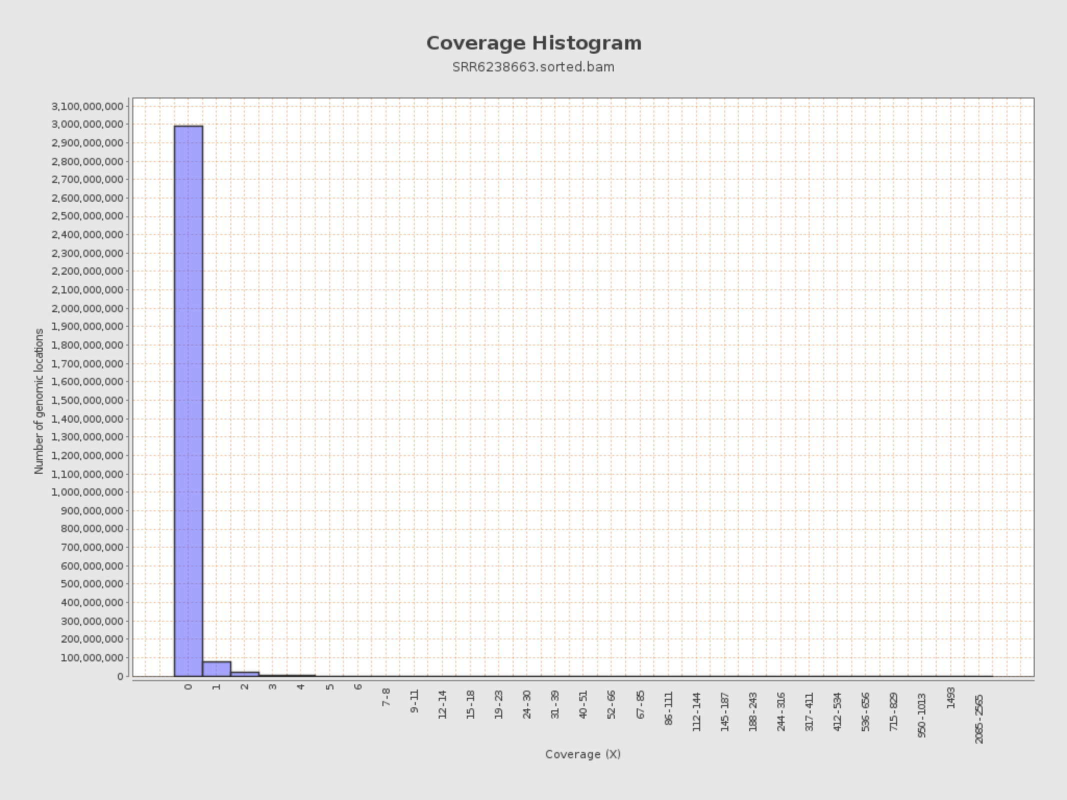
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12173166	0.0488	0.6046
chr2	243199373	13577268	0.0558	1.1707
chr3	198022430	8212757	0.0415	0.2724
chr4	191154276	8299576	0.0434	0.2786
chr5	180915260	7932036	0.0438	0.2812
chr6	171115067	11746499	0.0686	0.5541
chr7	159138663	7208103	0.0453	0.5364

chr8	146364022	9175838	0.0627	0.5907
chr9	141213431	4343085	0.0308	0.3593
chr10	135534747	7818623	0.0577	0.3948
chr11	135006516	4756966	0.0352	0.3001
chr12	133851895	6149625	0.0459	0.2971
chr13	115169878	3582867	0.0311	0.3082
chr14	107349540	1557524	0.0145	0.1991
chr15	102531392	3582080	0.0349	0.3394
chr16	90354753	4452704	0.0493	0.3263
chr17	81195210	3120594	0.0384	0.267
chr18	78077248	6975962	0.0893	0.9996
chr19	59128983	2681323	0.0453	0.4633
chr20	63025520	3219263	0.0511	0.307
chr21	48129895	2422900	0.0503	0.3101
chr22	51304566	1485554	0.029	0.2243
chrMT	16571	18480	1.1152	1.4854
chrX	155270560	8511174	0.0548	0.33
chrY	59373566	335033	0.0056	0.1875

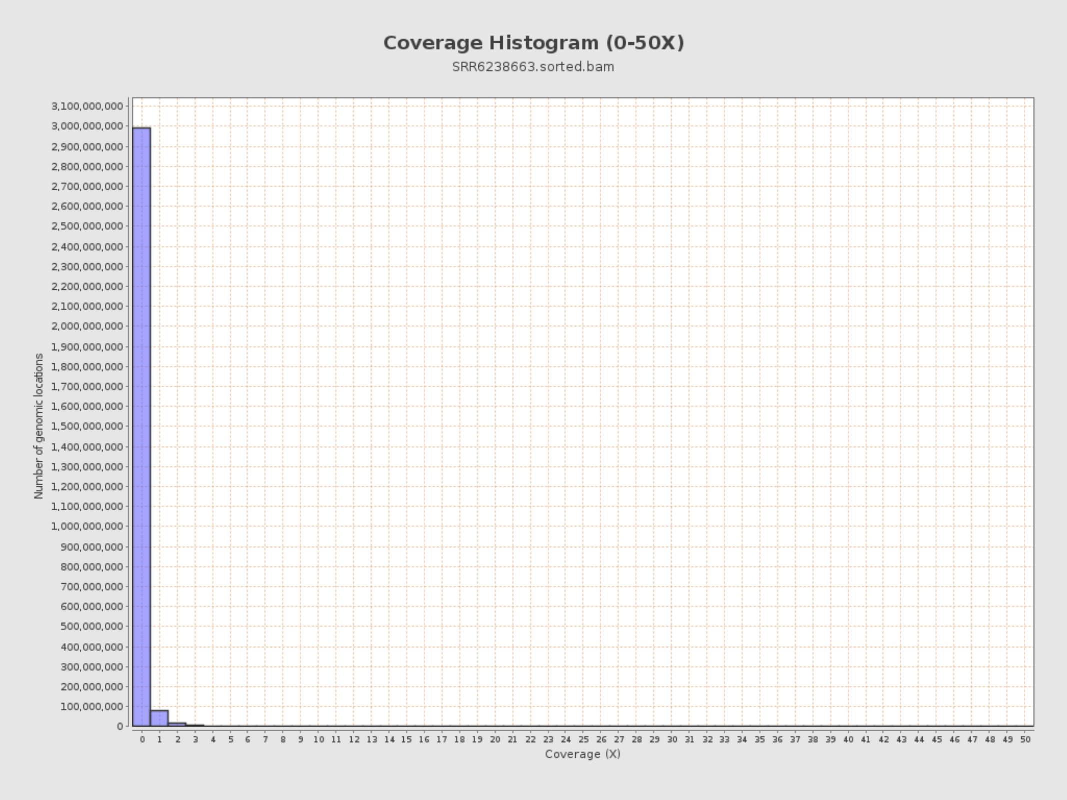
3. Results : Coverage across reference



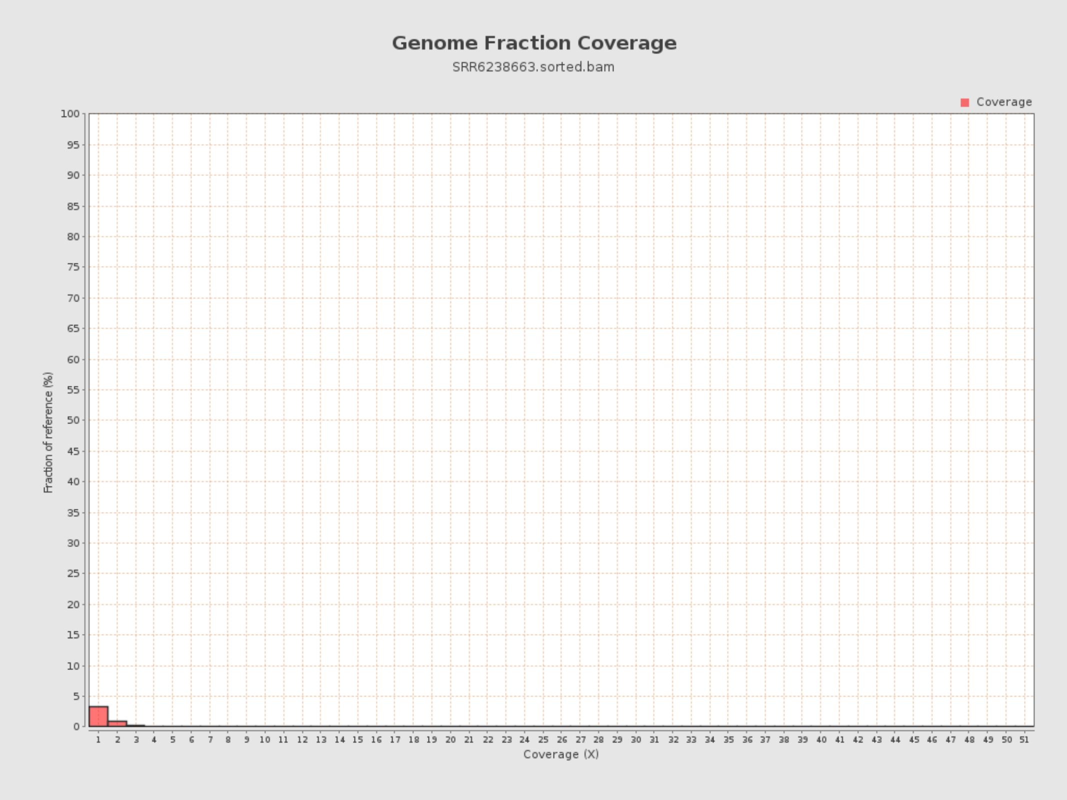
4. Results : Coverage Histogram



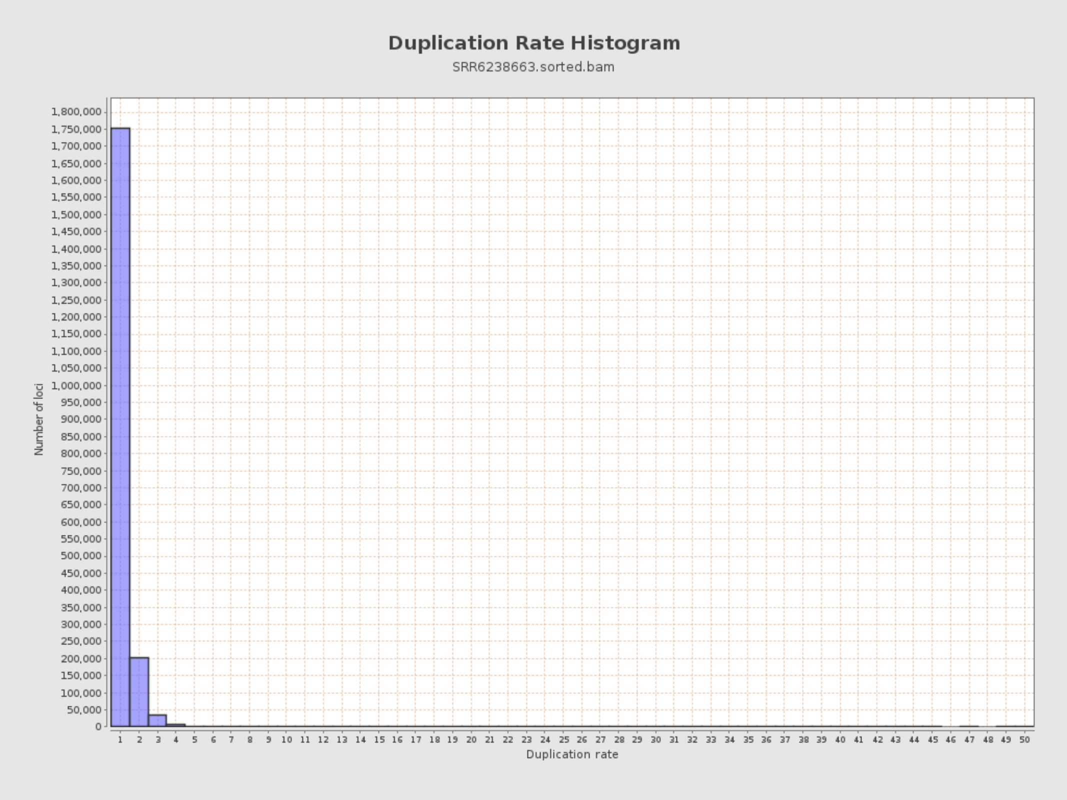
5. Results : Coverage Histogram (0-50X)



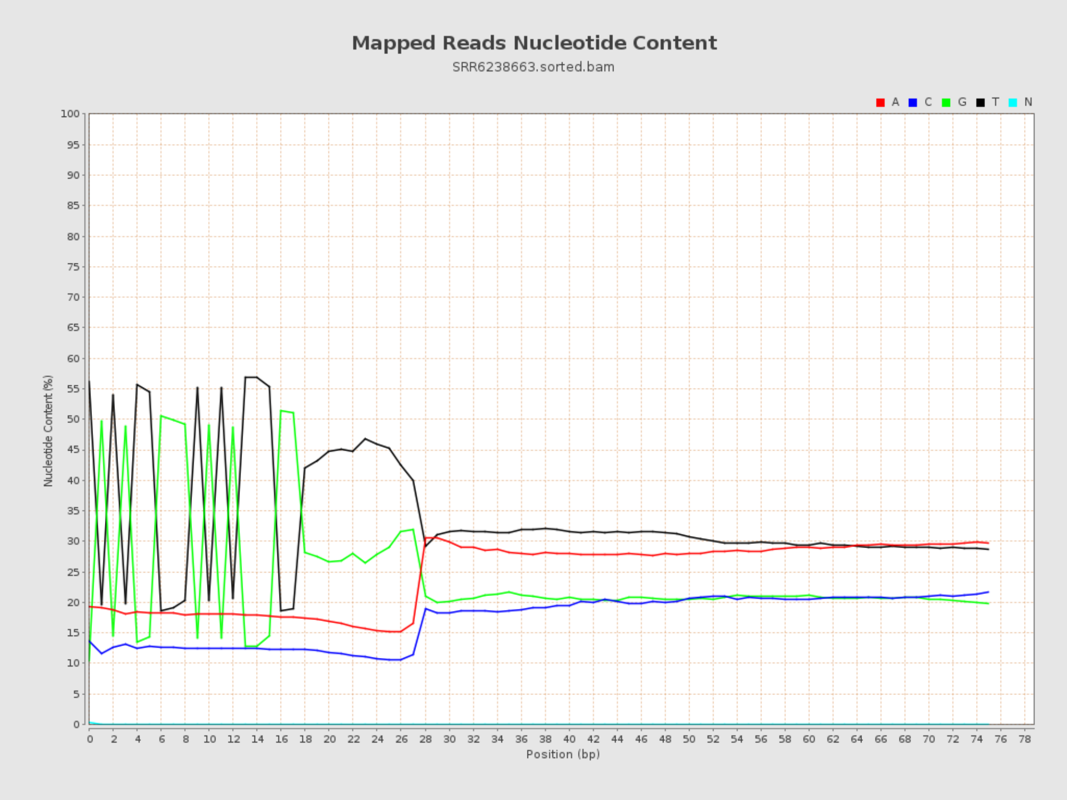
6. Results : Genome Fraction Coverage



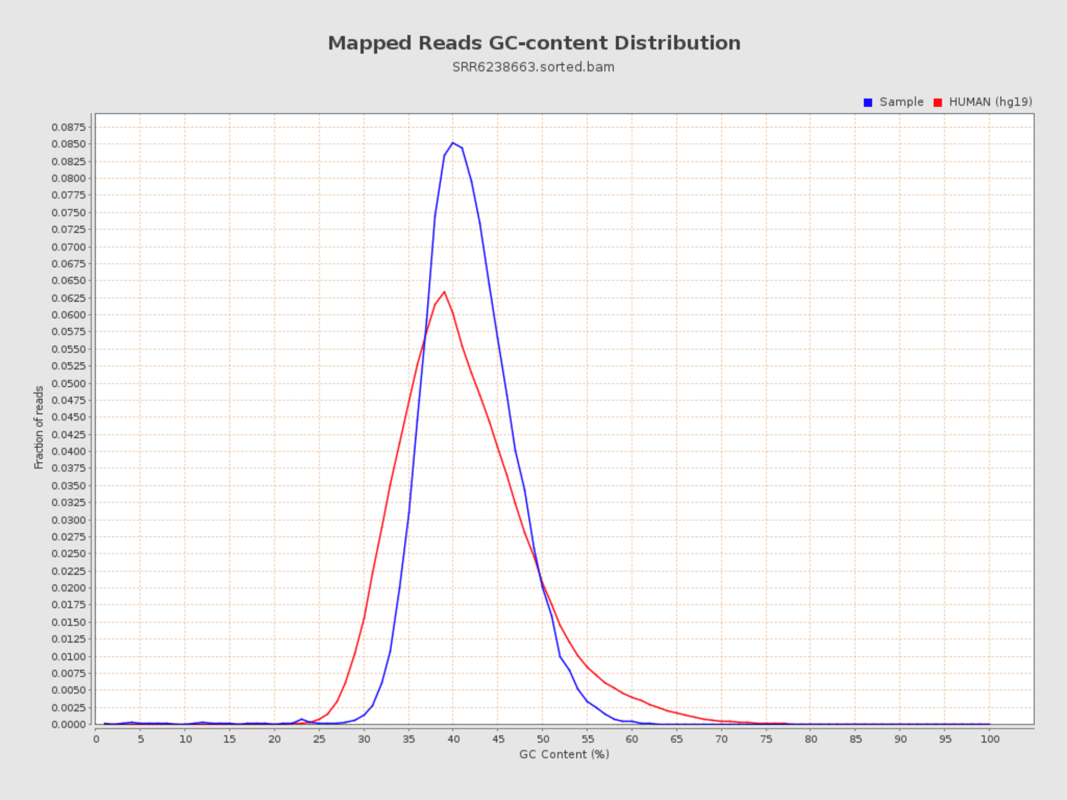
7. Results : Duplication Rate Histogram



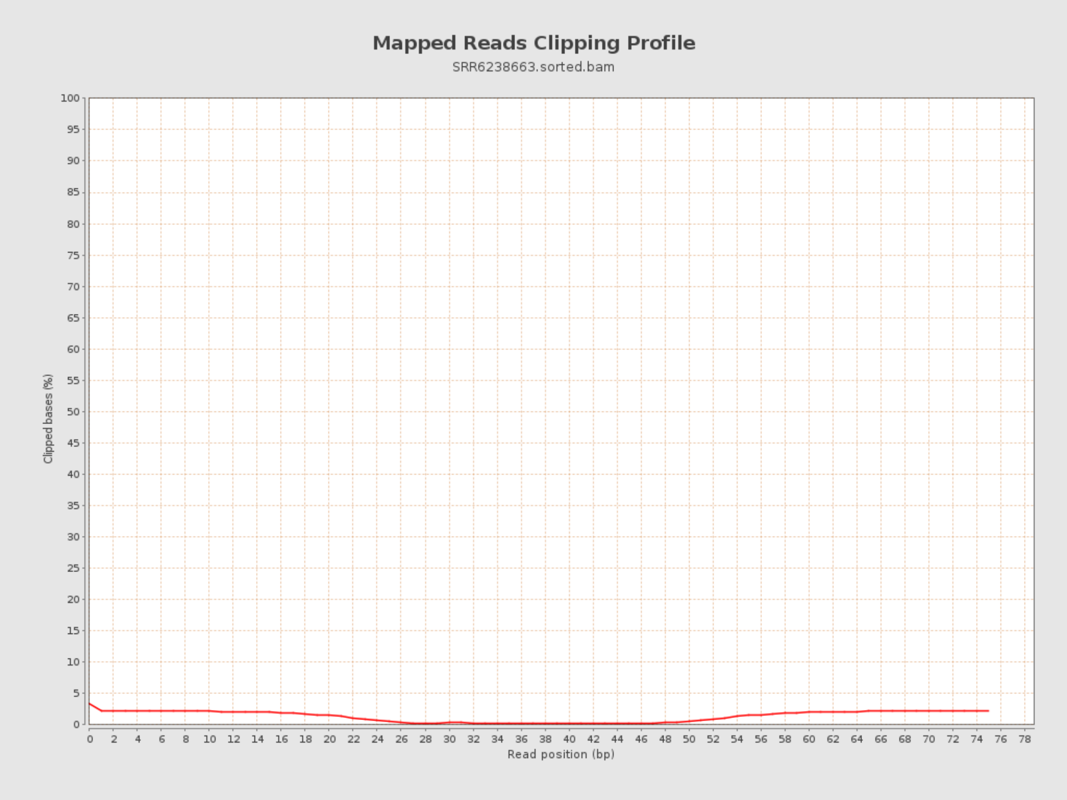
8. Results : Mapped Reads Nucleotide Content



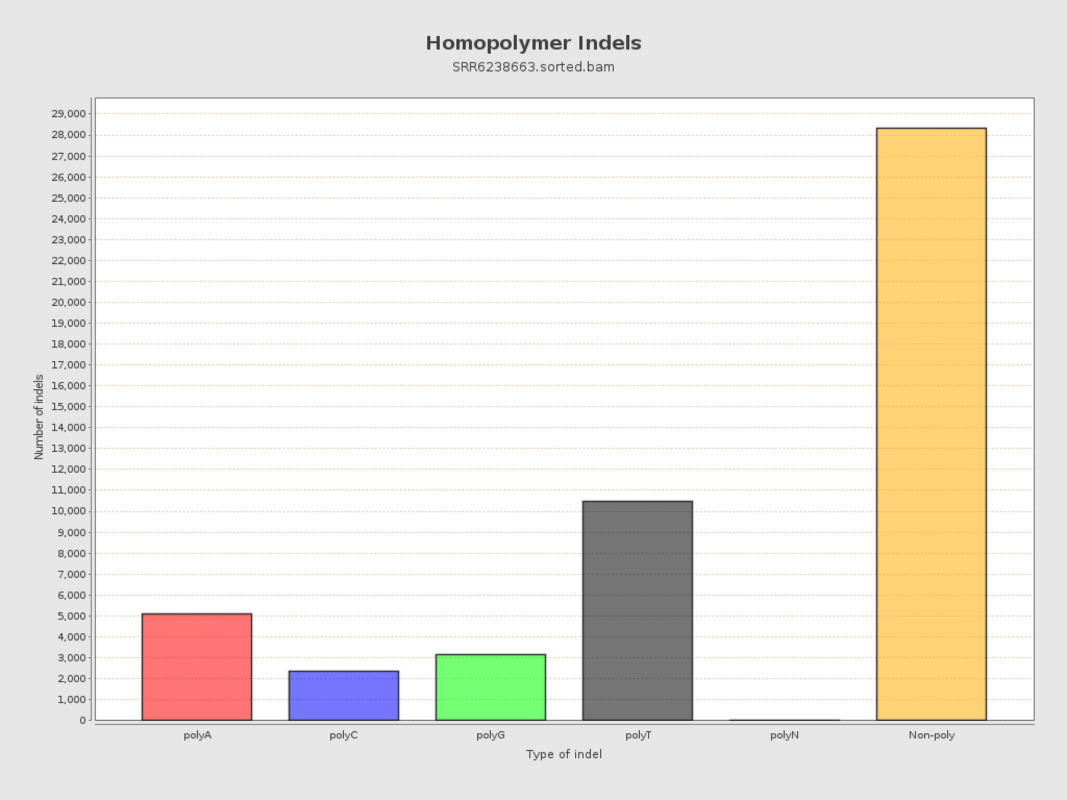
9. Results : Mapped Reads GC-content Distribution



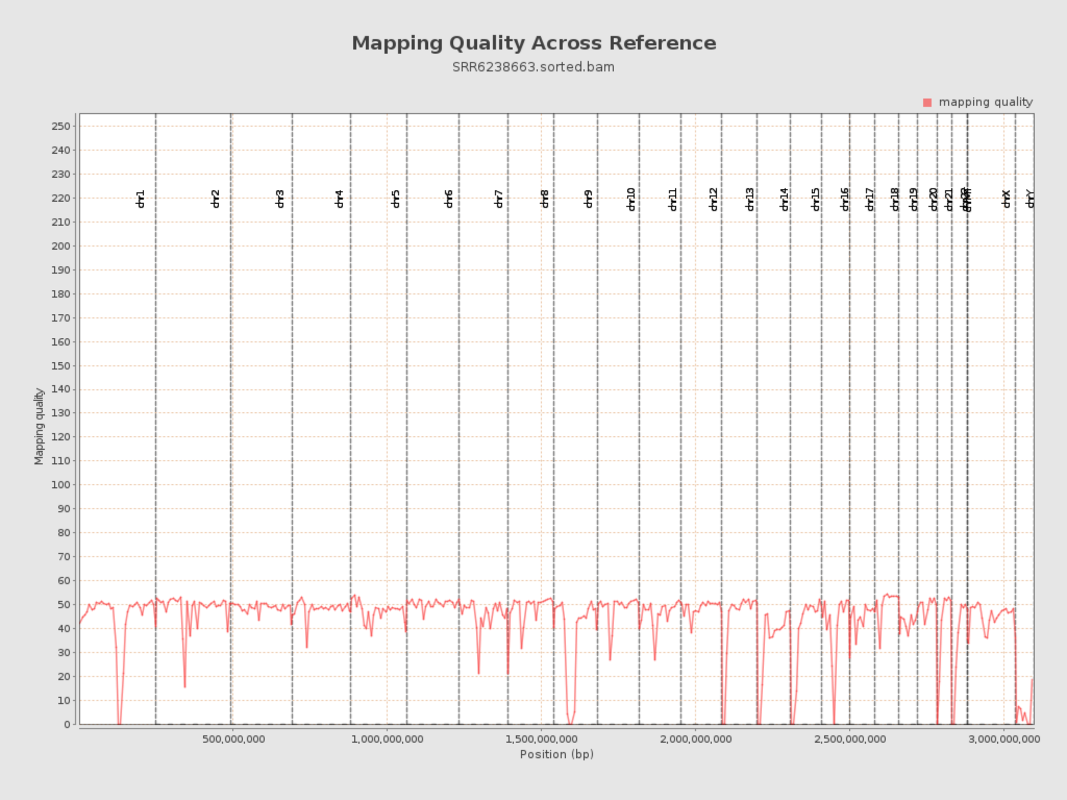
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram