Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 12:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238245.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_SRR6238245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 12:38:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,265,244
Mapped reads	823,242 / 65.07%
Unmapped reads	442,002 / 34.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,154 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	91,579 / 7.24%
Duplication rate	8.3%
Clipped reads	472,710 / 37.36%

2.2. ACGT Content

Number/percentage of A's	14,585,908 / 27.85%
Number/percentage of C's	10,251,056 / 19.57%
Number/percentage of T's	15,902,011 / 30.36%
Number/percentage of G's	11,627,128 / 22.2%
Number/percentage of N's	12,246 / 0.02%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.2718

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

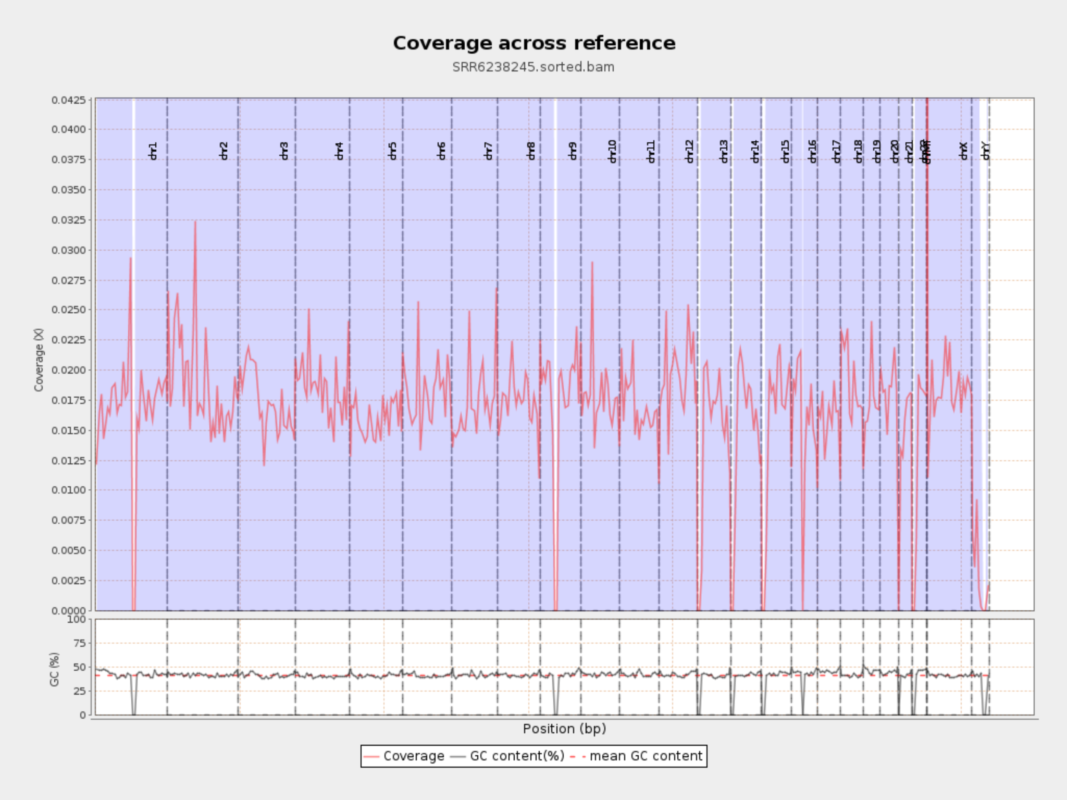
General error rate	0.9%
Mismatches	462,869
Insertions	4,465
Mapped reads with at least one insertion	0.54%
Deletions	13,848
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.36%

2.6. Chromosome stats

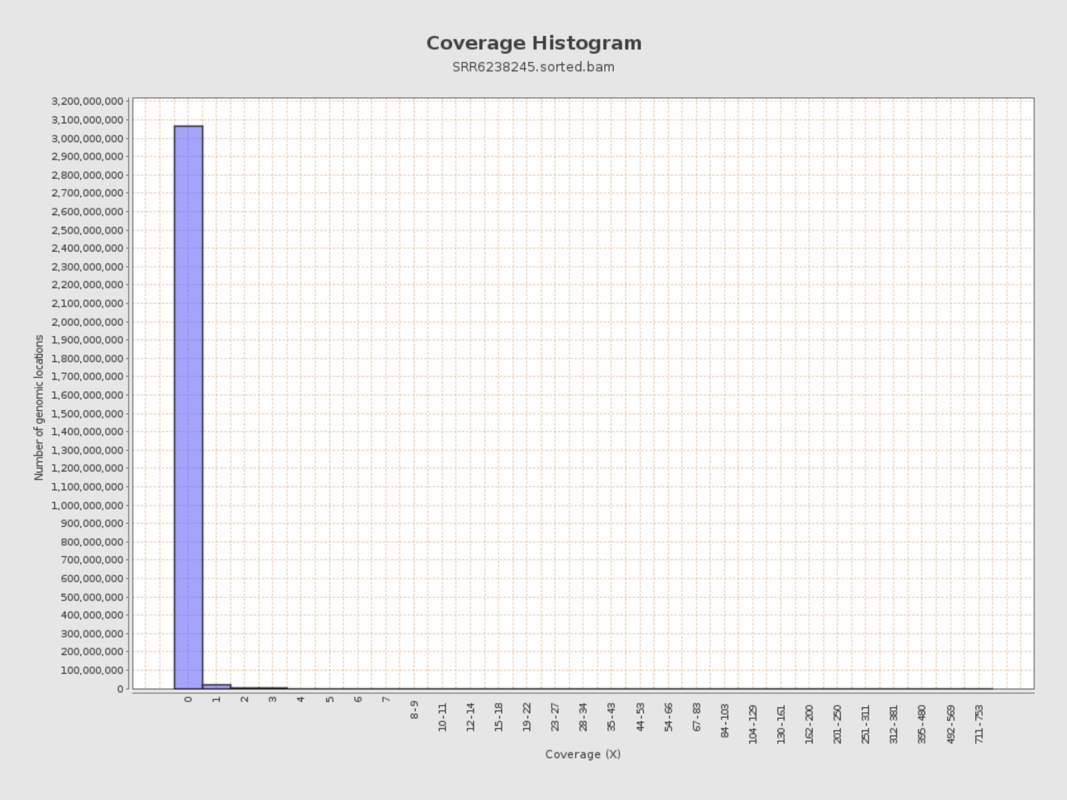
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4143871	0.0166	0.3509
chr2	243199373	4596238	0.0189	0.3713
chr3	198022430	3447063	0.0174	0.2134
chr4	191154276	3573735	0.0187	0.2347
chr5	180915260	2904007	0.0161	0.2083
chr6	171115067	3114444	0.0182	0.2639
chr7	159138663	2771192	0.0174	0.2409

chr8	146364022	2541345	0.0174	0.2475
chr9	141213431	2418255	0.0171	0.2281
chr10	135534747	2422052	0.0179	0.2337
chr11	135006516	2306654	0.0171	0.2188
chr12	133851895	2627069	0.0196	0.2289
chr13	115169878	1653349	0.0144	0.2296
chr14	107349540	1573853	0.0147	0.3758
chr15	102531392	1567400	0.0153	0.4747
chr16	90354753	1392952	0.0154	0.1963
chr17	81195210	1300678	0.016	0.2045
chr18	78077248	1501376	0.0192	0.2865
chr19	59128983	1032524	0.0175	0.2681
chr20	63025520	1140366	0.0181	0.2112
chr21	48129895	692797	0.0144	0.1875
chr22	51304566	658740	0.0128	0.1791
chrMT	16571	10282	0.6205	1.3508
chrX	155270560	2846362	0.0183	0.2549
chrY	59373566	164442	0.0028	0.0988

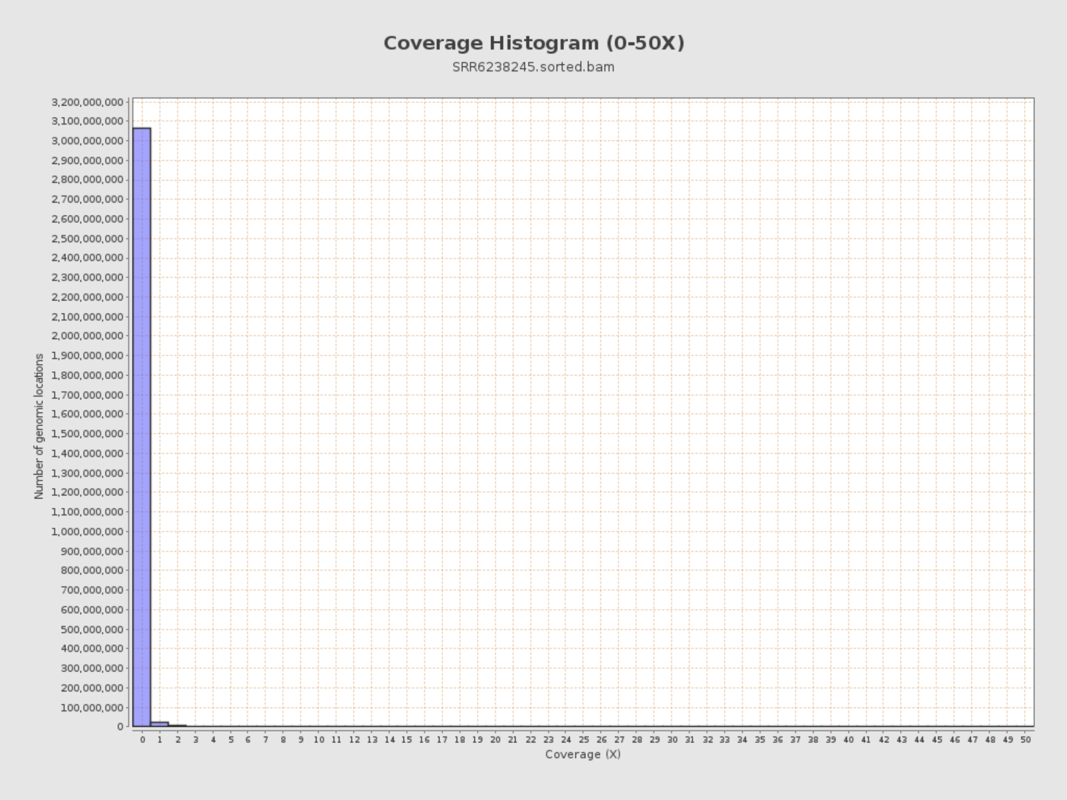
3. Results : Coverage across reference



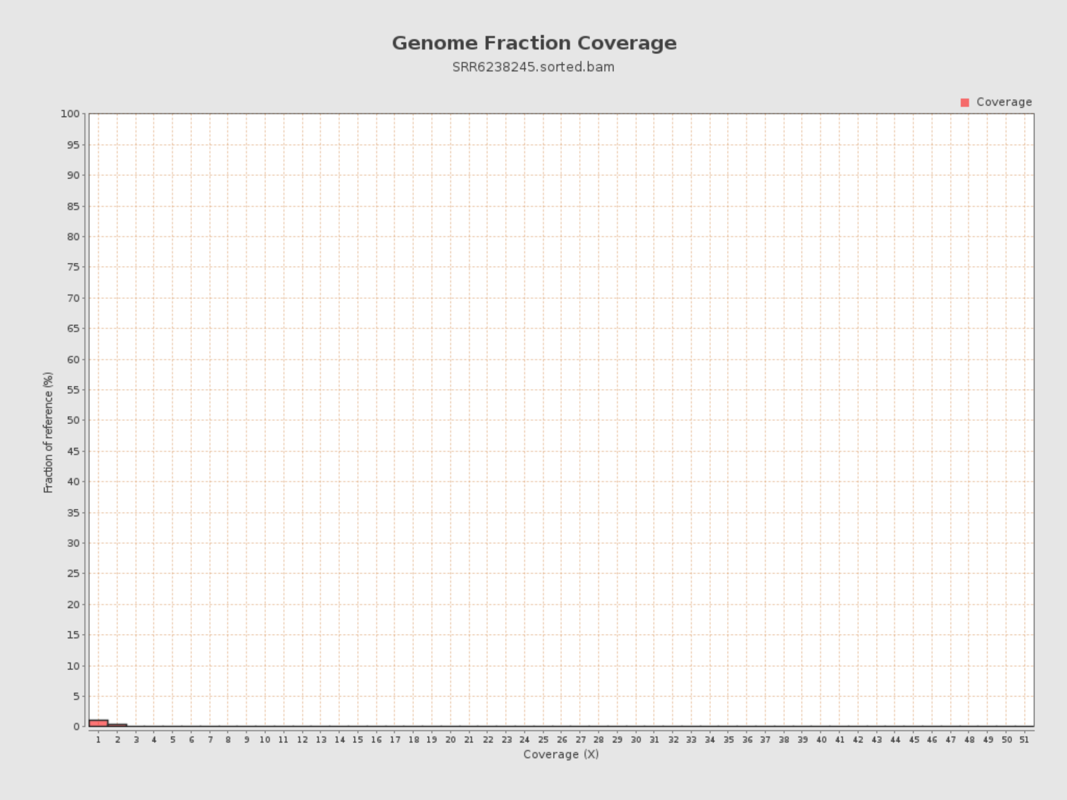
4. Results : Coverage Histogram



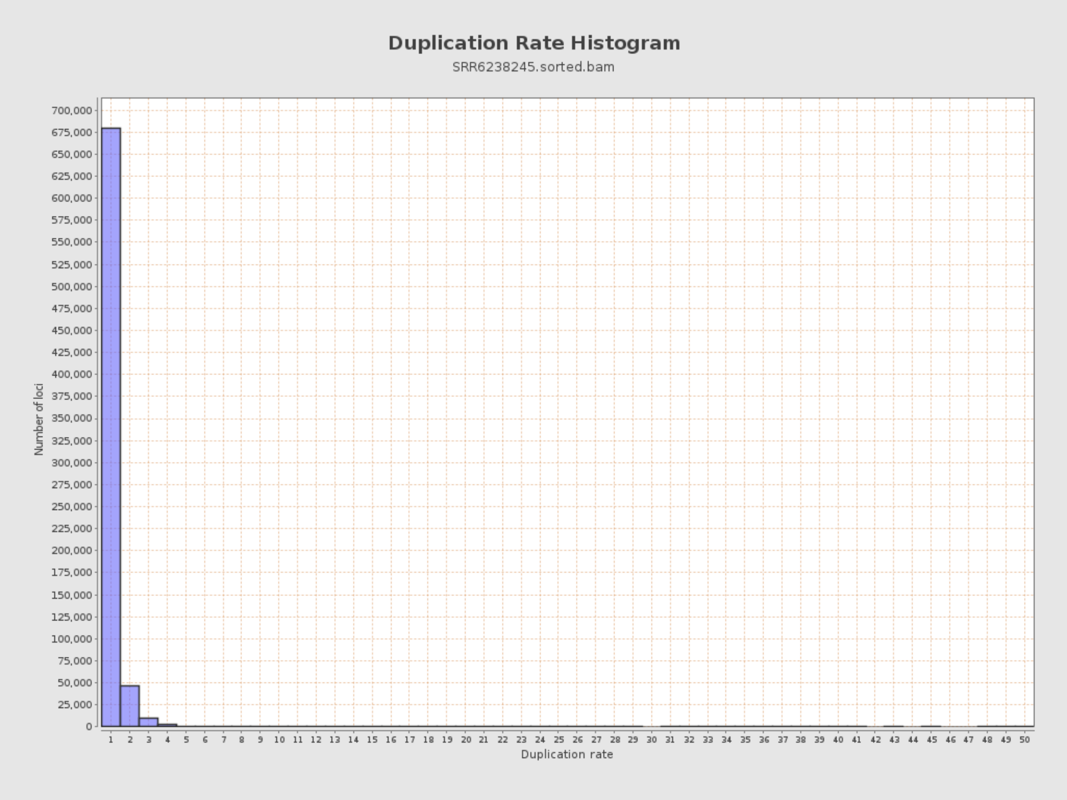
5. Results : Coverage Histogram (0-50X)



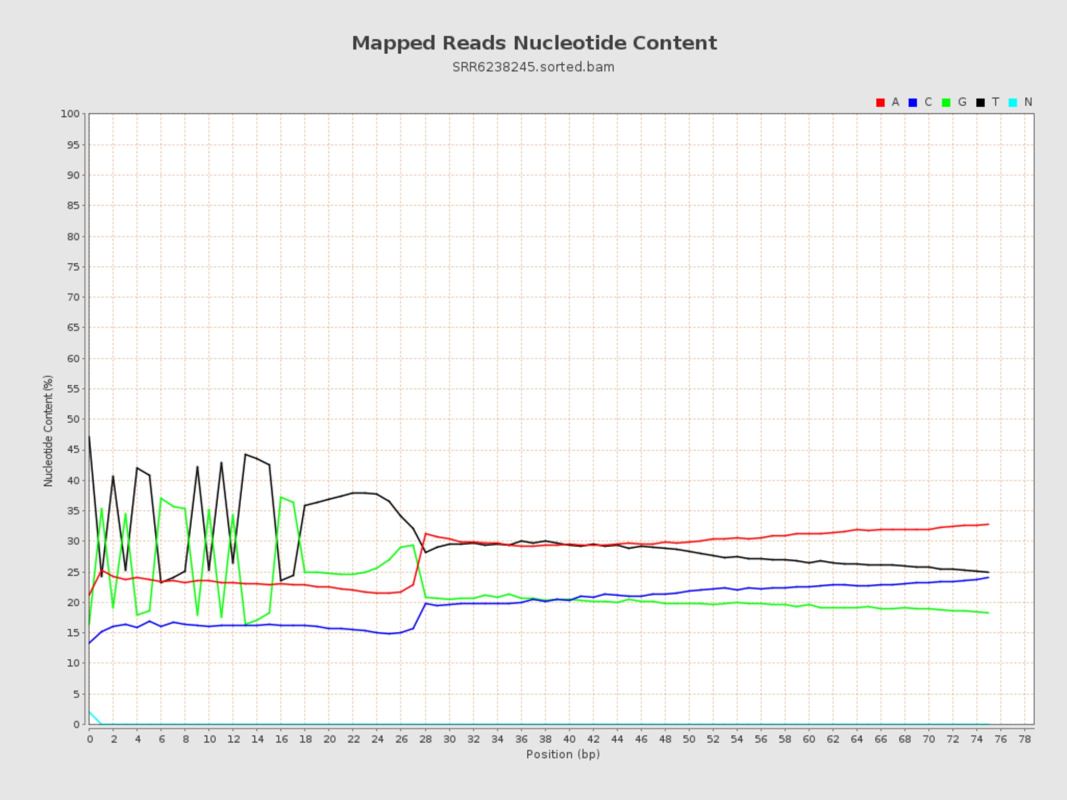
6. Results : Genome Fraction Coverage



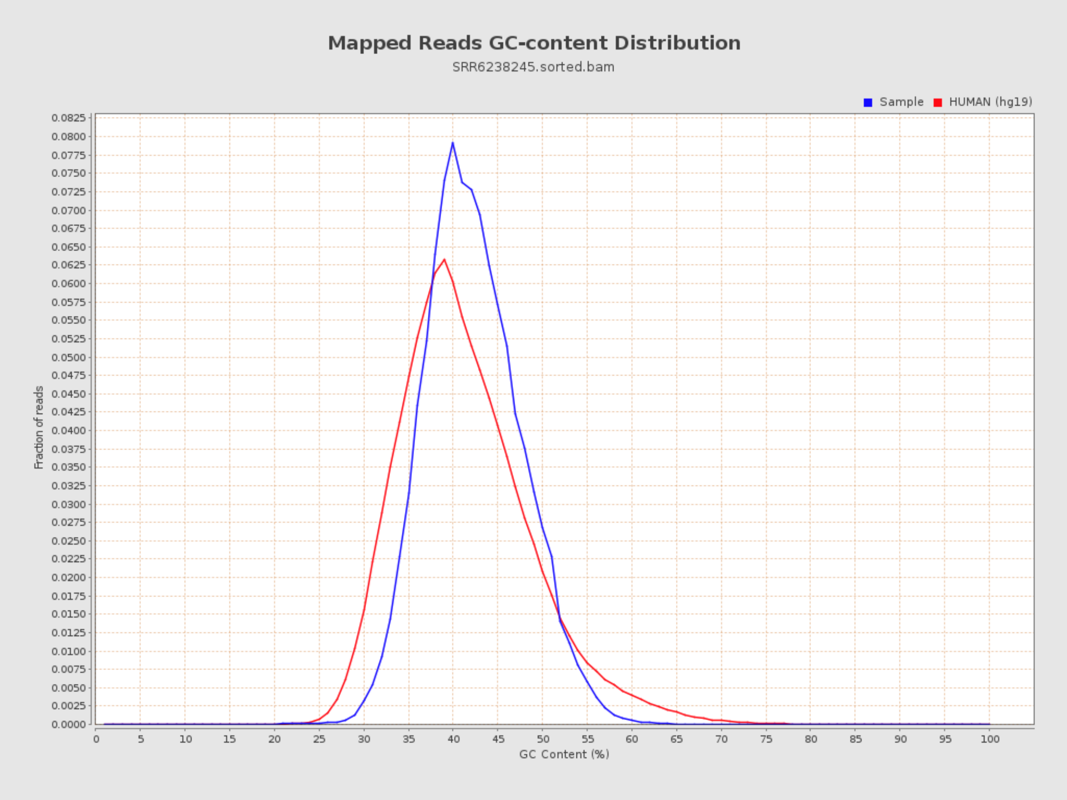
7. Results : Duplication Rate Histogram



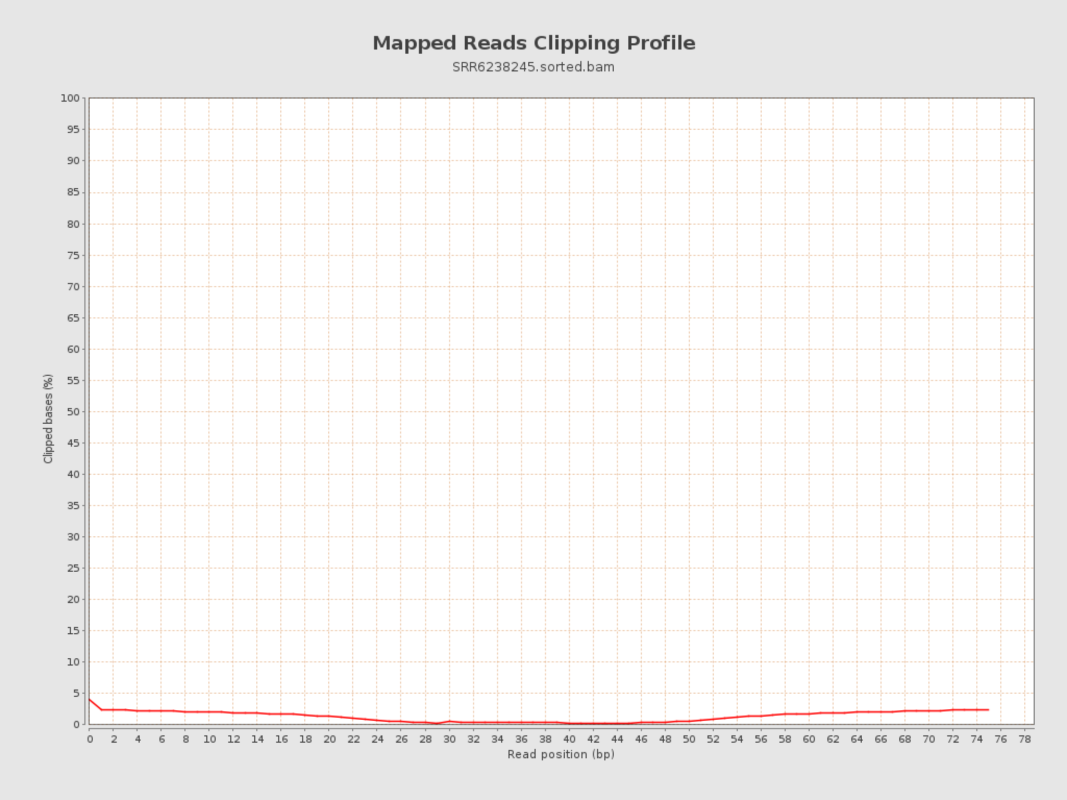
8. Results : Mapped Reads Nucleotide Content



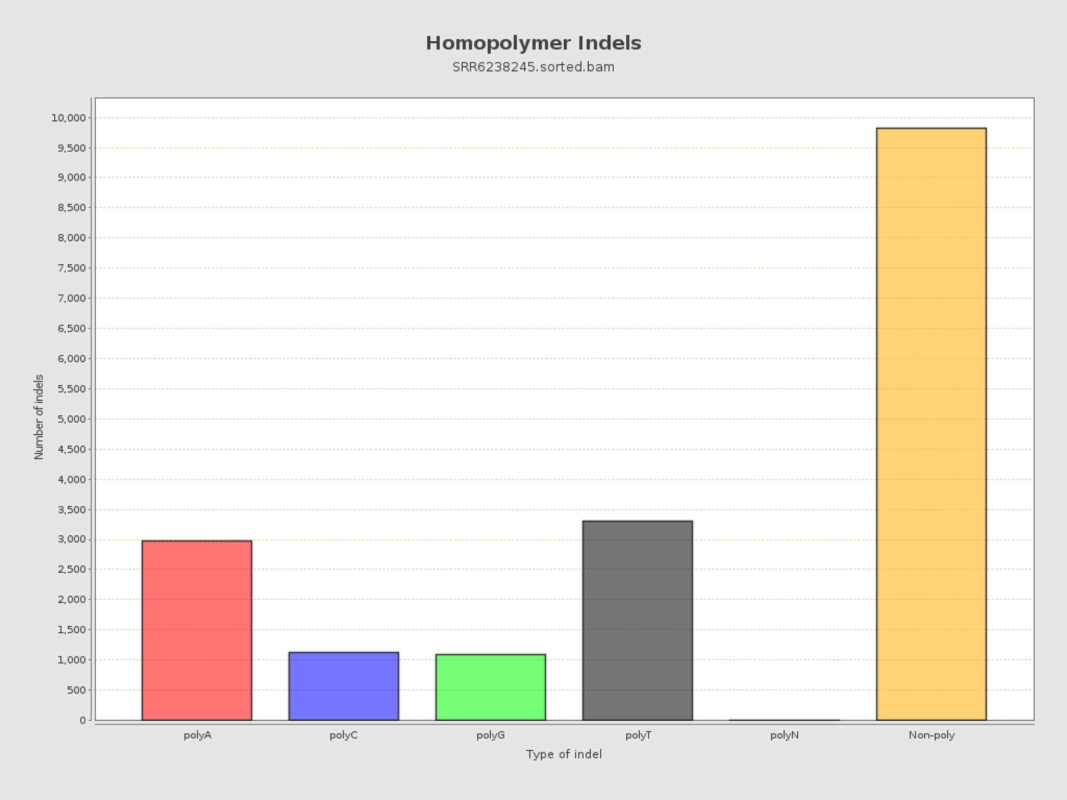
9. Results : Mapped Reads GC-content Distribution



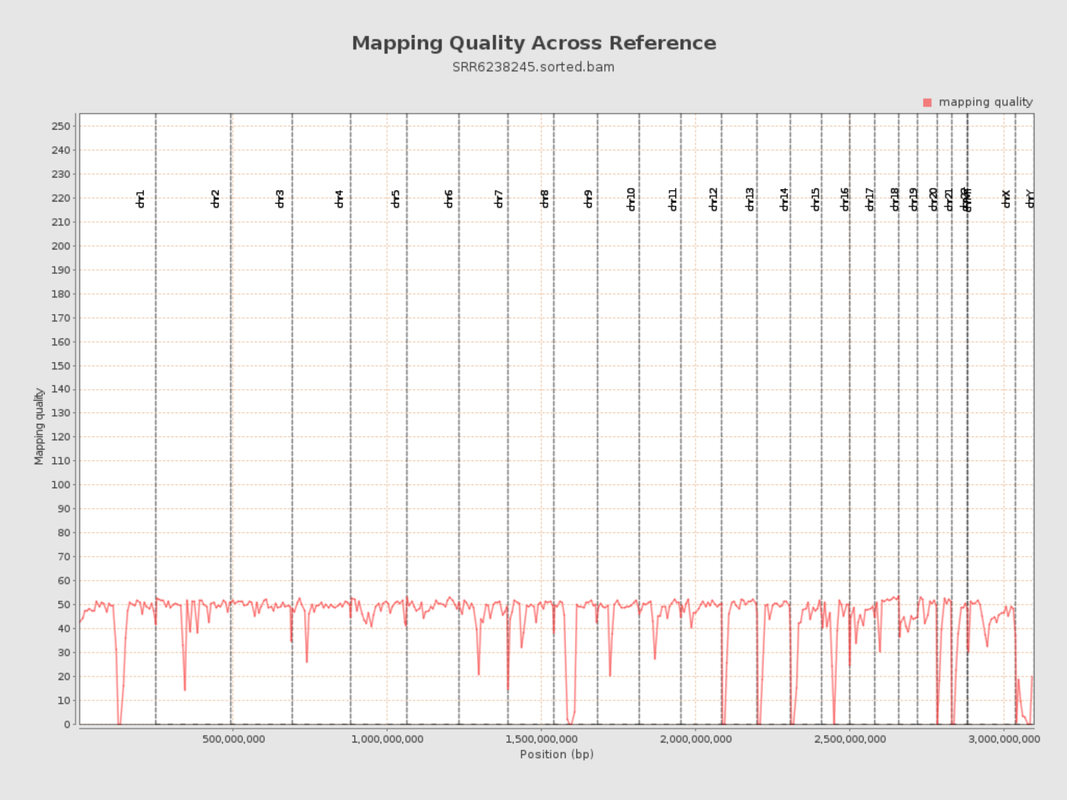
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram