Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:20:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238039.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_SRR6238039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:20:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,005,845
Mapped reads	1,787,283 / 89.1%
Unmapped reads	218,562 / 10.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,146 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	91,948 / 4.58%
Duplication rate	3.98%
Clipped reads	862,781 / 43.01%

2.2. ACGT Content

Number/percentage of A's	31,250,802 / 26.68%
Number/percentage of C's	21,503,325 / 18.36%
Number/percentage of T's	36,940,854 / 31.54%
Number/percentage of G's	27,194,423 / 23.22%
Number/percentage of N's	227,230 / 0.19%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0379

Standard Deviation	0.369

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

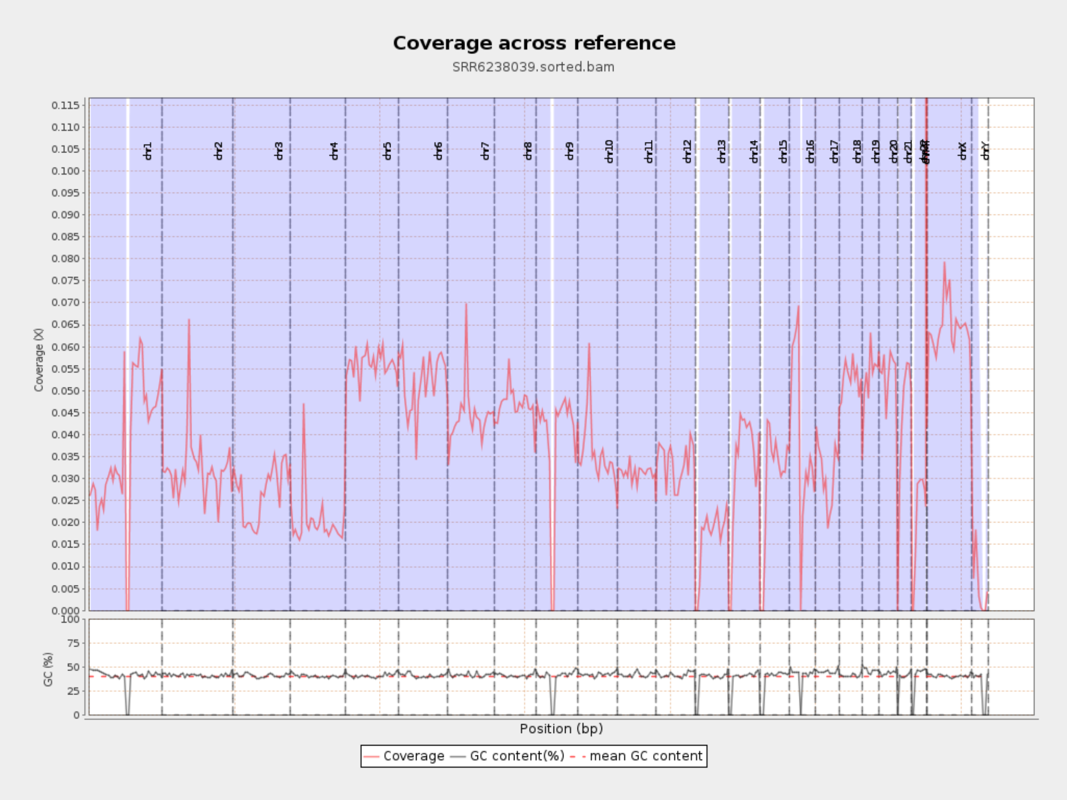
General error rate	0.88%
Mismatches	1,013,328
Insertions	9,576
Mapped reads with at least one insertion	0.53%
Deletions	36,231
Mapped reads with at least one deletion	2%
Homopolymer indels	46.03%

2.6. Chromosome stats

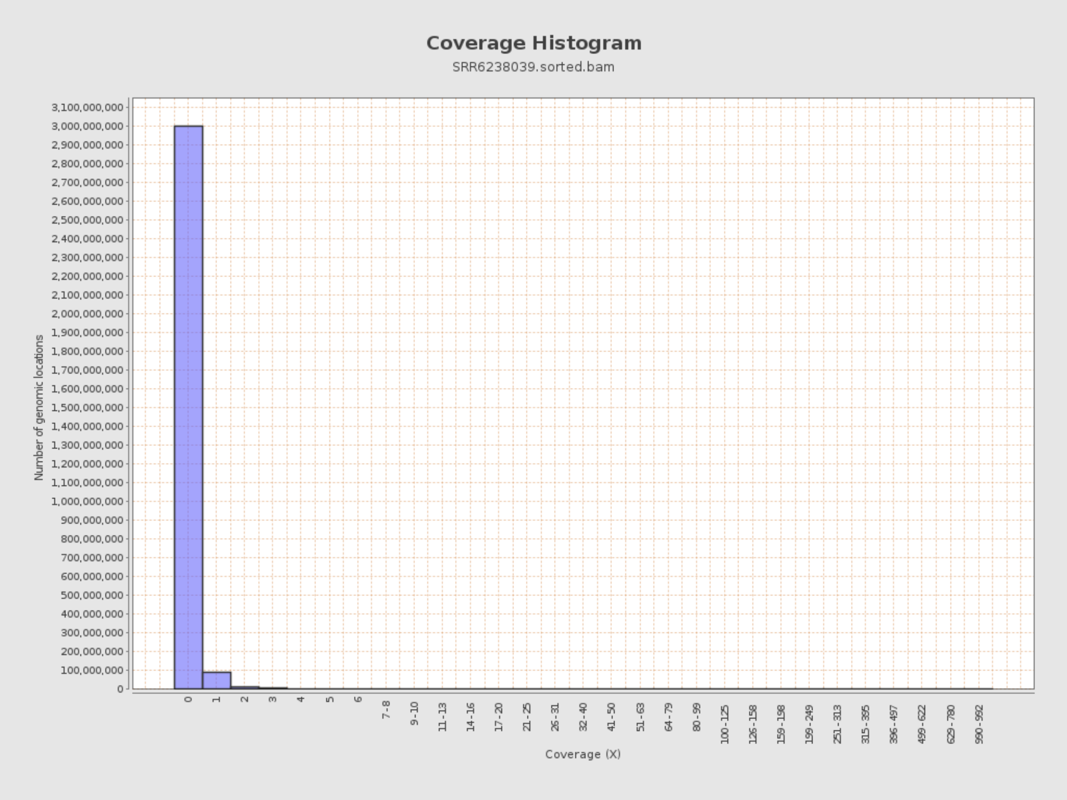
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9239384	0.0371	0.6754
chr2	243199373	7896826	0.0325	0.5247
chr3	198022430	5319854	0.0269	0.1902
chr4	191154276	3825970	0.02	0.2122
chr5	180915260	10141049	0.0561	0.275
chr6	171115067	8956574	0.0523	0.3314
chr7	159138663	7072888	0.0444	0.4918

chr8	146364022	6847875	0.0468	0.3569
chr9	141213431	5482886	0.0388	0.3127
chr10	135534747	4896504	0.0361	0.3152
chr11	135006516	4217206	0.0312	0.2419
chr12	133851895	4498434	0.0336	0.2168
chr13	115169878	1916876	0.0166	0.1639
chr14	107349540	3499737	0.0326	0.2202
chr15	102531392	3019418	0.0294	0.2028
chr16	90354753	3574518	0.0396	0.246
chr17	81195210	2517787	0.031	0.2234
chr18	78077248	4129676	0.0529	0.6083
chr19	59128983	3169620	0.0536	0.4654
chr20	63025520	3379877	0.0536	0.2699
chr21	48129895	2065182	0.0429	0.2615
chr22	51304566	1036416	0.0202	0.1618
chrMT	16571	198257	11.9641	7.2142
chrX	155270560	9914065	0.0639	0.3172
chrY	59373566	359780	0.0061	0.1648

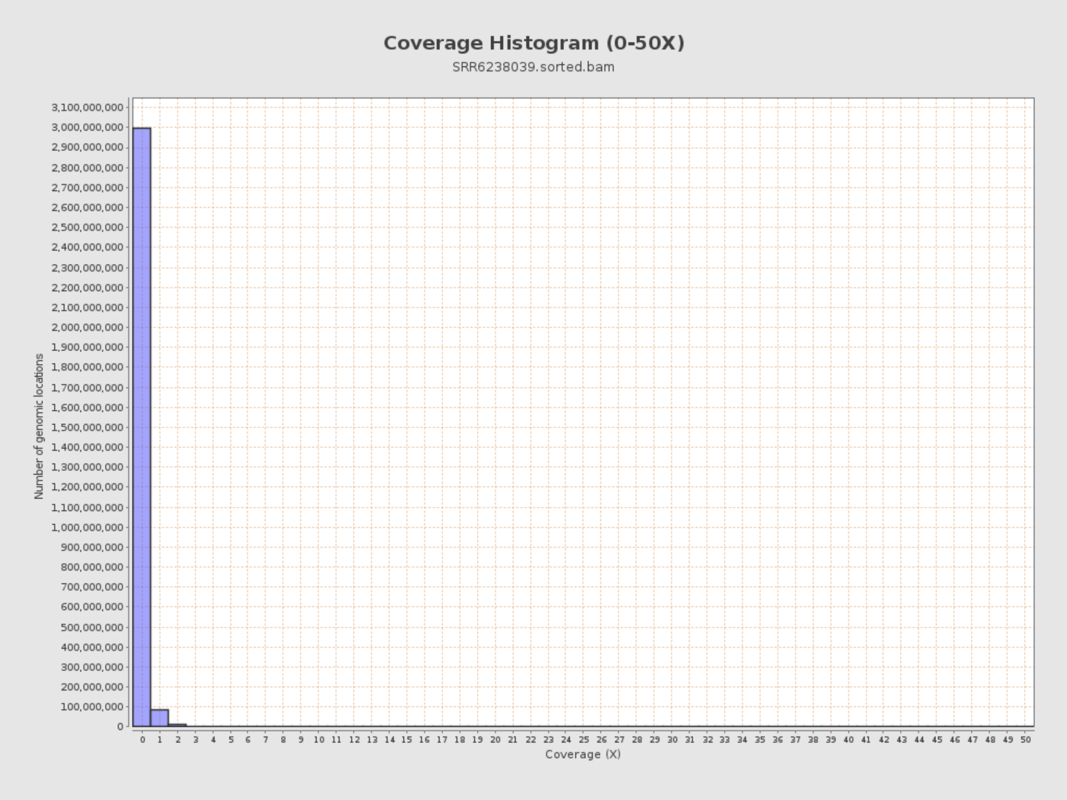
3. Results : Coverage across reference



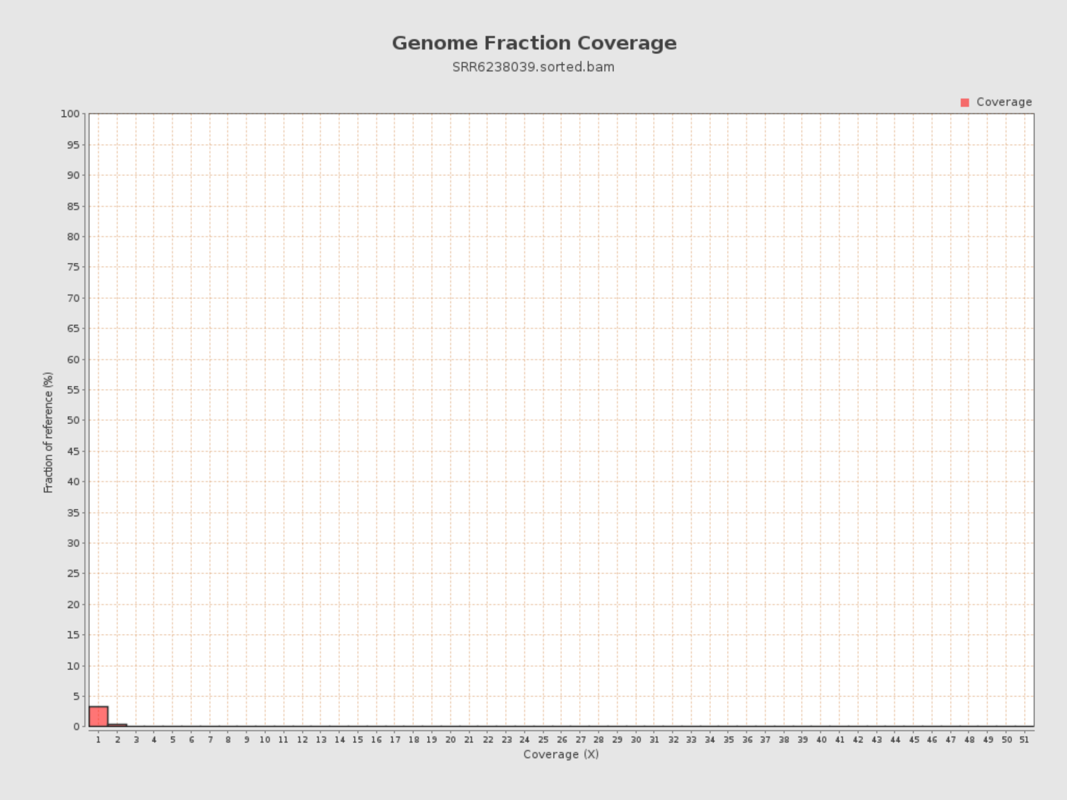
4. Results : Coverage Histogram



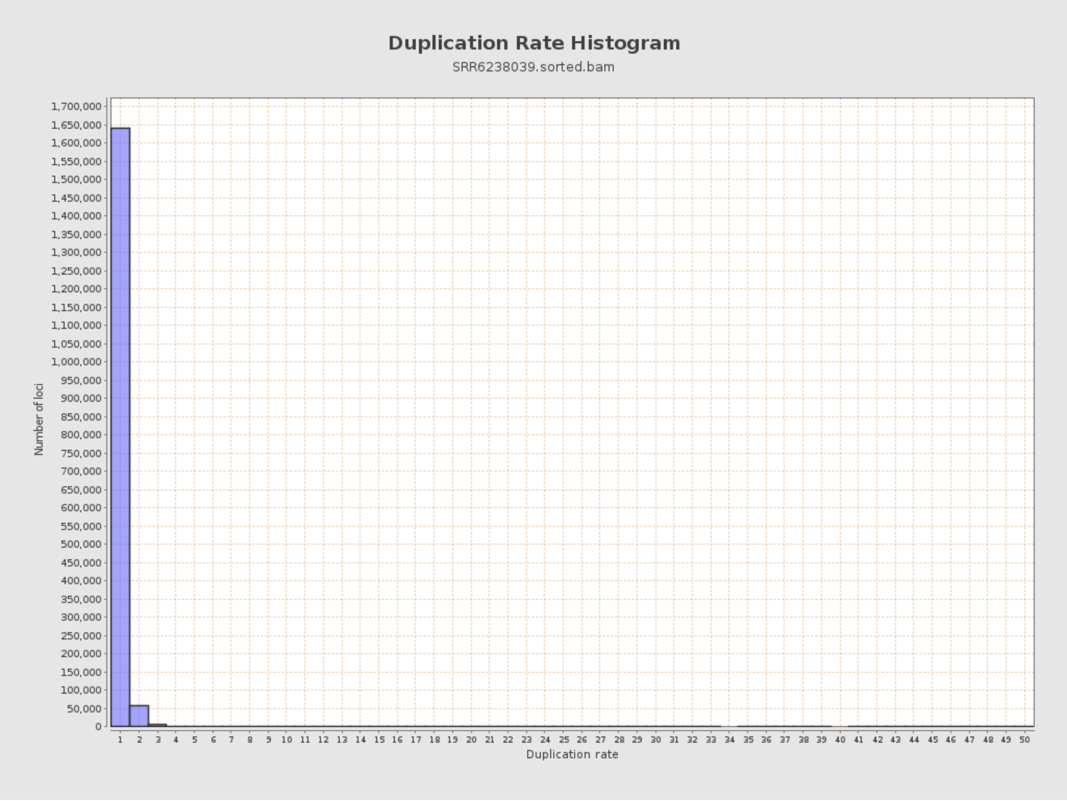
5. Results : Coverage Histogram (0-50X)



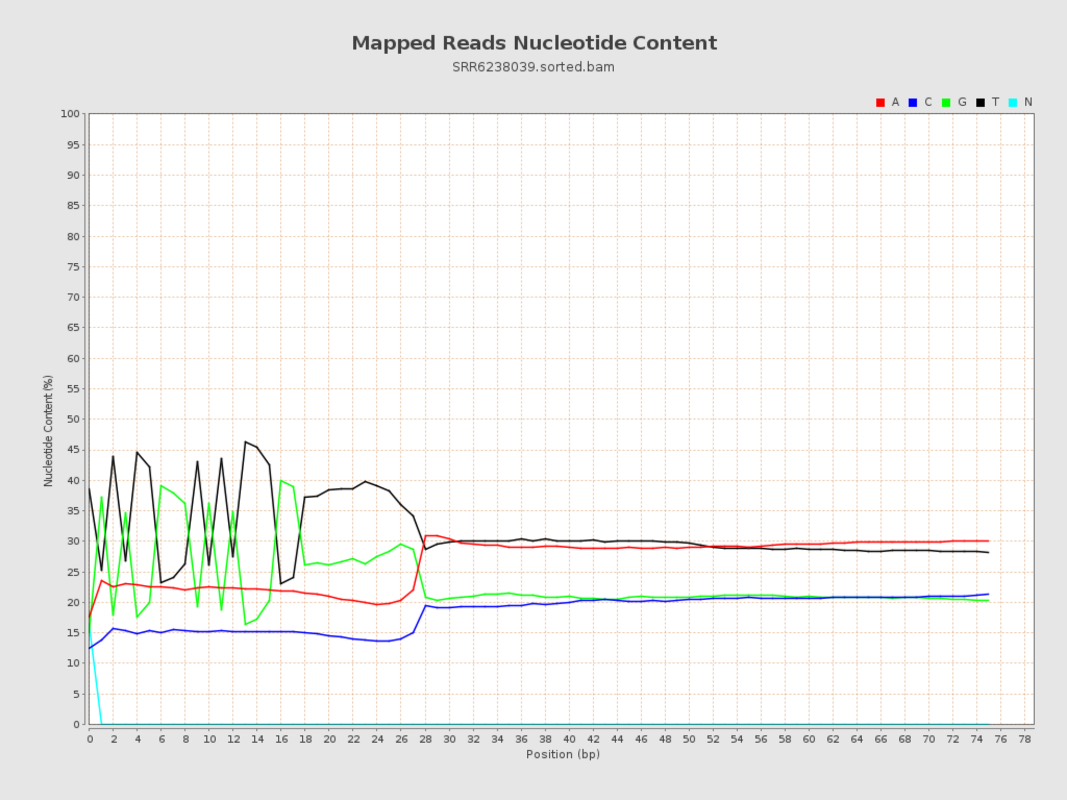
6. Results : Genome Fraction Coverage



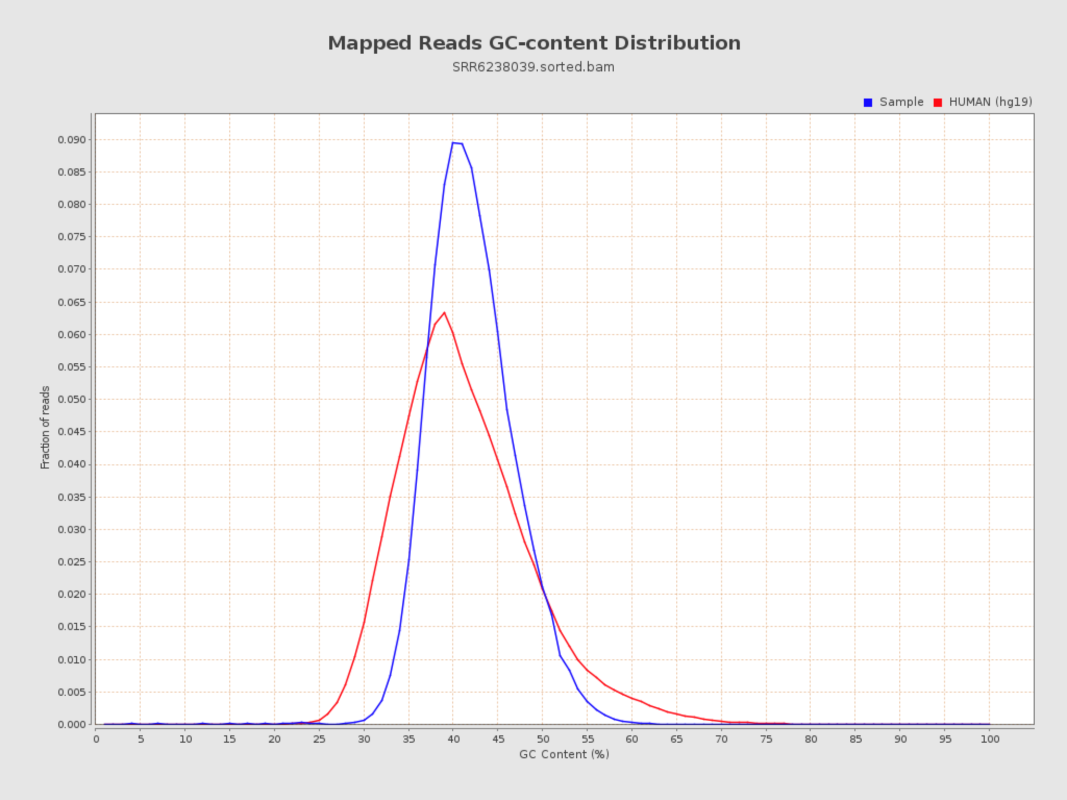
7. Results : Duplication Rate Histogram



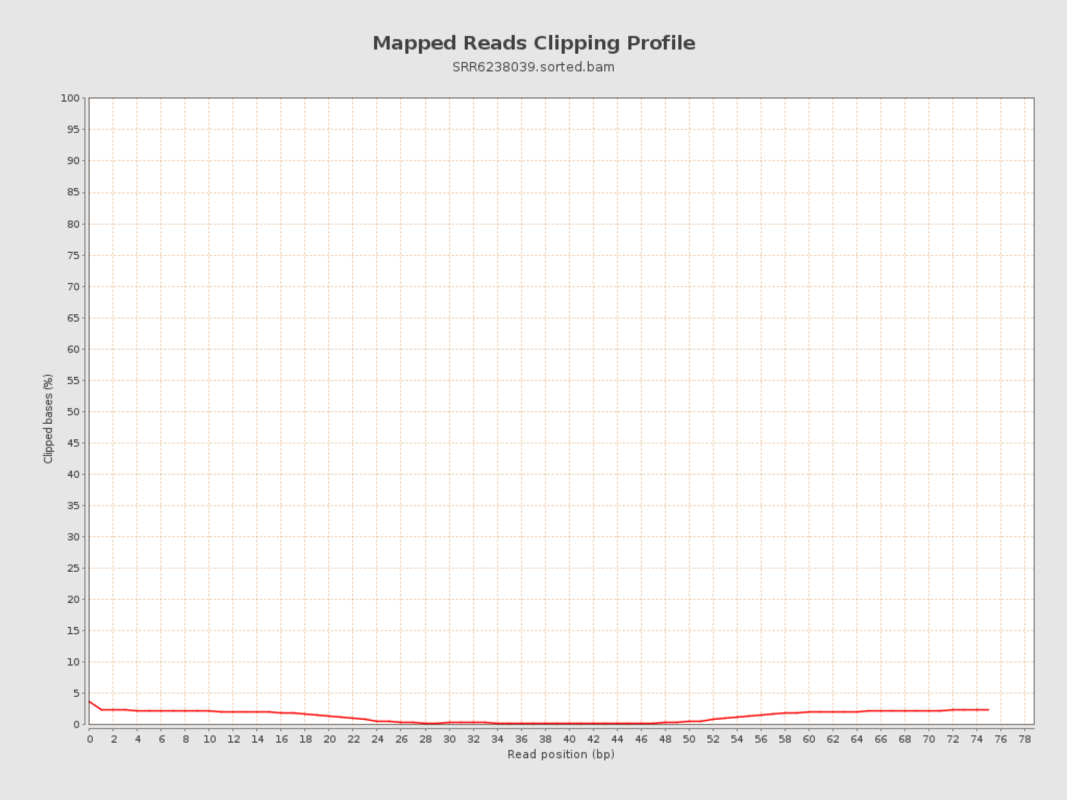
8. Results : Mapped Reads Nucleotide Content



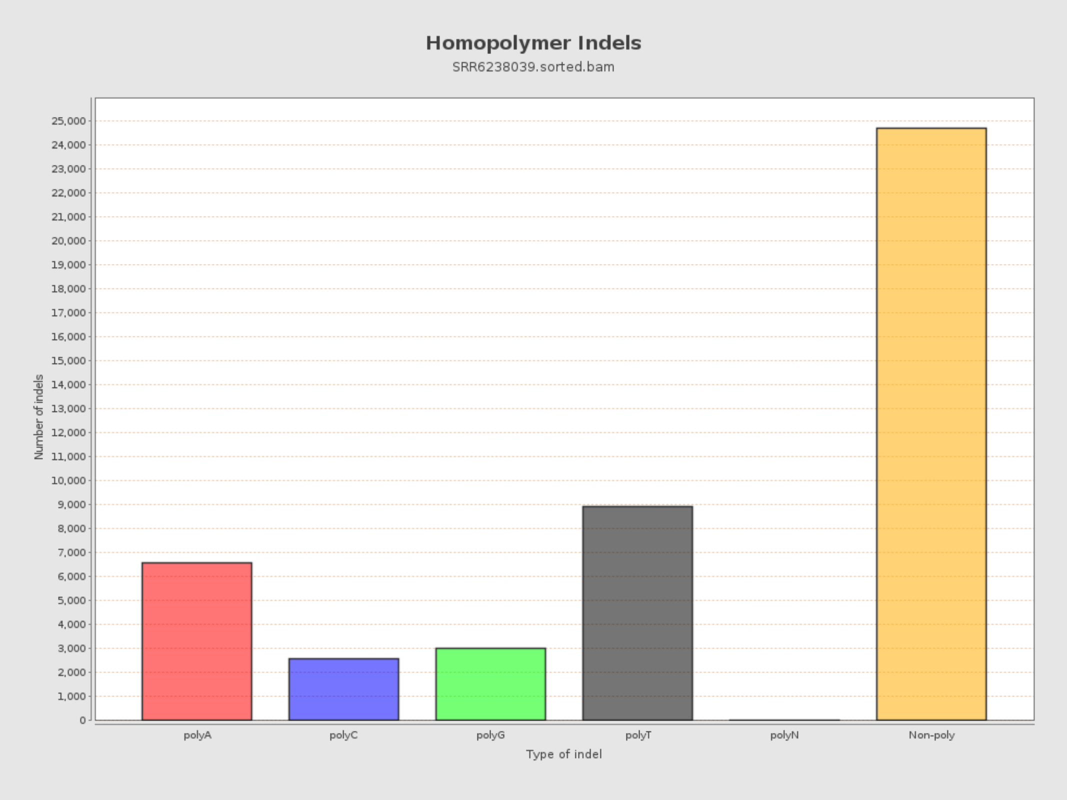
9. Results : Mapped Reads GC-content Distribution



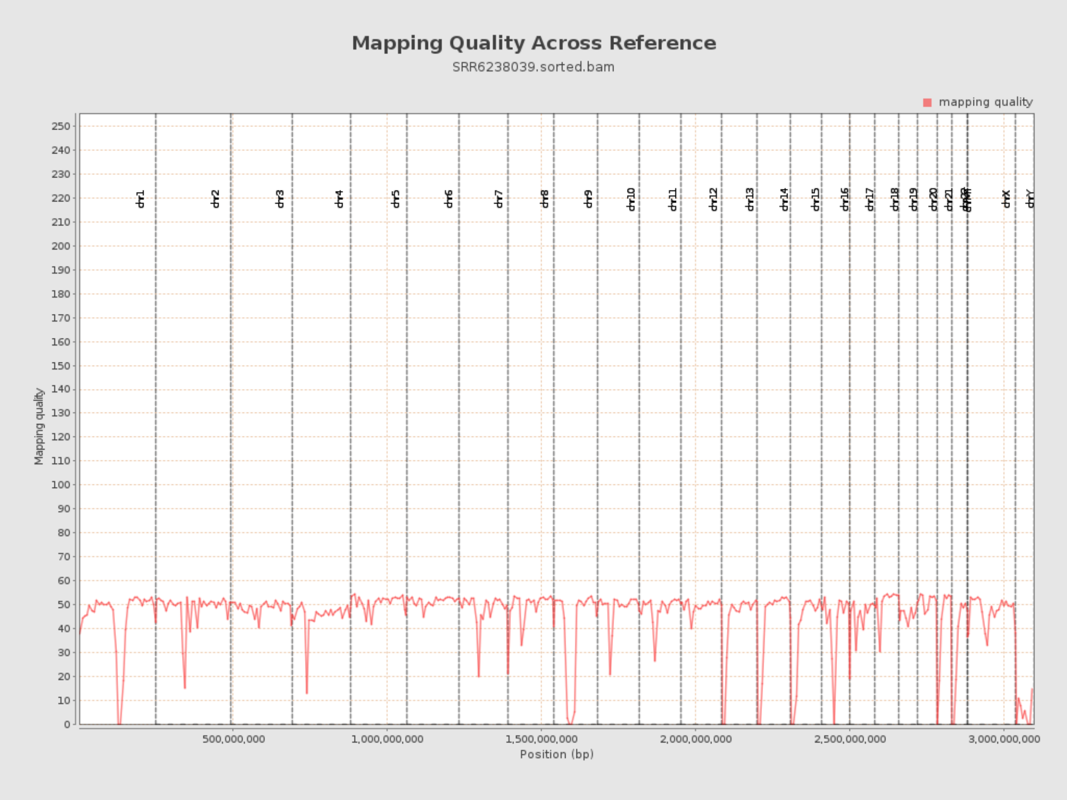
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram