Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:18:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238515.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_SRR6238515 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238515.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:18:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238515.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,434,339
Mapped reads	2,043,871 / 59.51%
Unmapped reads	1,390,468 / 40.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,804 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	933,491 / 27.18%
Duplication rate	23.15%
Clipped reads	1,417,089 / 41.26%

2.2. ACGT Content

Number/percentage of A's	29,645,733 / 24.12%
Number/percentage of C's	21,043,944 / 17.12%
Number/percentage of T's	42,135,265 / 34.28%
Number/percentage of G's	30,086,096 / 24.48%
Number/percentage of N's	7,749 / 0.01%
GC Percentage	41.6%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.7594

2.4. Mapping Quality

Mean Mapping Quality	41.95

2.5. Mismatches and indels

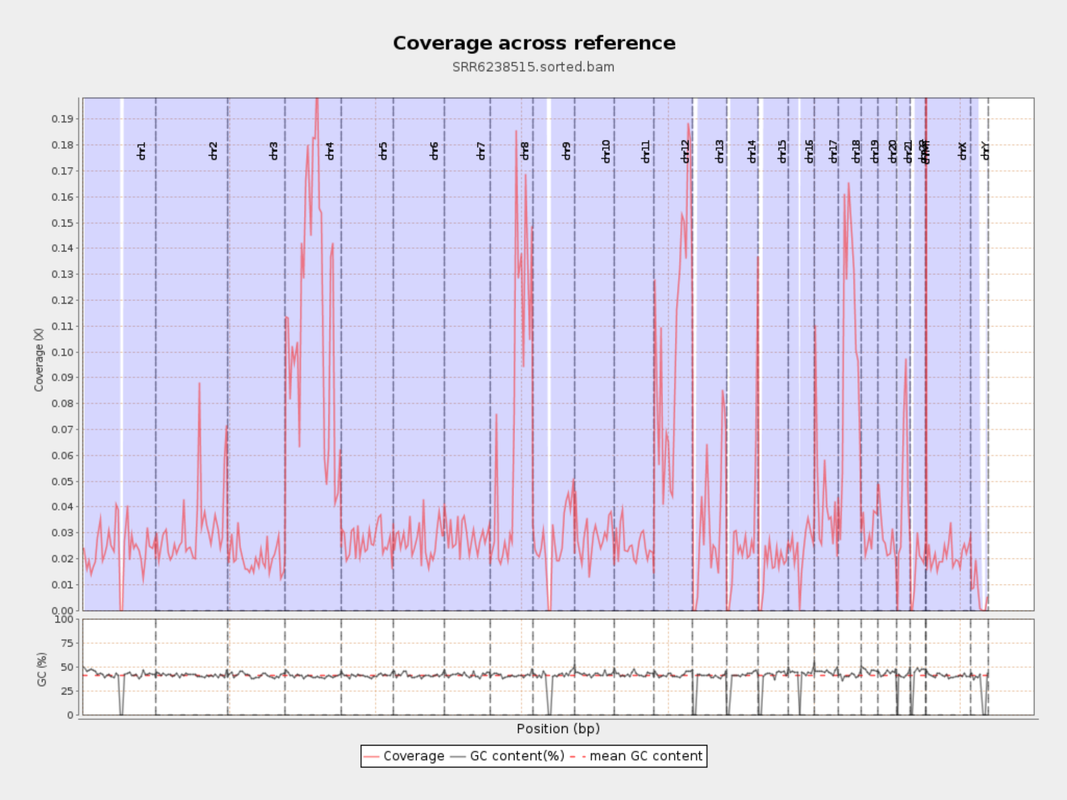
General error rate	0.62%
Mismatches	748,005
Insertions	7,576
Mapped reads with at least one insertion	0.37%
Deletions	39,169
Mapped reads with at least one deletion	1.89%
Homopolymer indels	40.96%

2.6. Chromosome stats

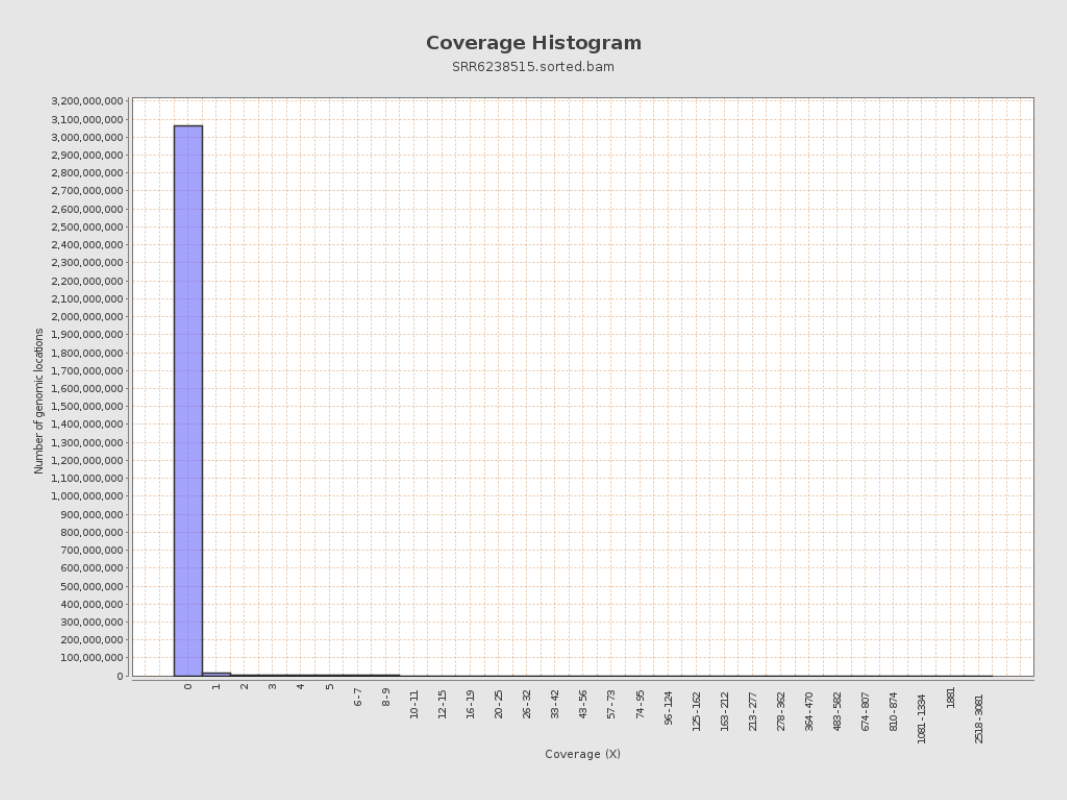
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5819595	0.0233	0.5772
chr2	243199373	7655823	0.0315	1.4491
chr3	198022430	4033851	0.0204	0.419
chr4	191154276	22350664	0.1169	1.0379
chr5	180915260	4863739	0.0269	0.4952
chr6	171115067	4622429	0.027	0.6659
chr7	159138663	4628163	0.0291	0.569

chr8	146364022	11205155	0.0766	0.8769
chr9	141213431	3772107	0.0267	0.5067
chr10	135534747	3861005	0.0285	0.5169
chr11	135006516	3434853	0.0254	0.4805
chr12	133851895	14082007	0.1052	1.0356
chr13	115169878	3926254	0.0341	0.6473
chr14	107349540	2651649	0.0247	0.5179
chr15	102531392	1714493	0.0167	0.4481
chr16	90354753	2155708	0.0239	0.4758
chr17	81195210	3575055	0.044	0.6507
chr18	78077248	8275385	0.106	1.4802
chr19	59128983	1838698	0.0311	0.5474
chr20	63025520	1794084	0.0285	0.5107
chr21	48129895	2177828	0.0452	0.6367
chr22	51304566	806944	0.0157	0.3606
chrMT	16571	9095	0.5489	1.7782
chrX	155270560	3353000	0.0216	0.4239
chrY	59373566	376875	0.0063	0.2775

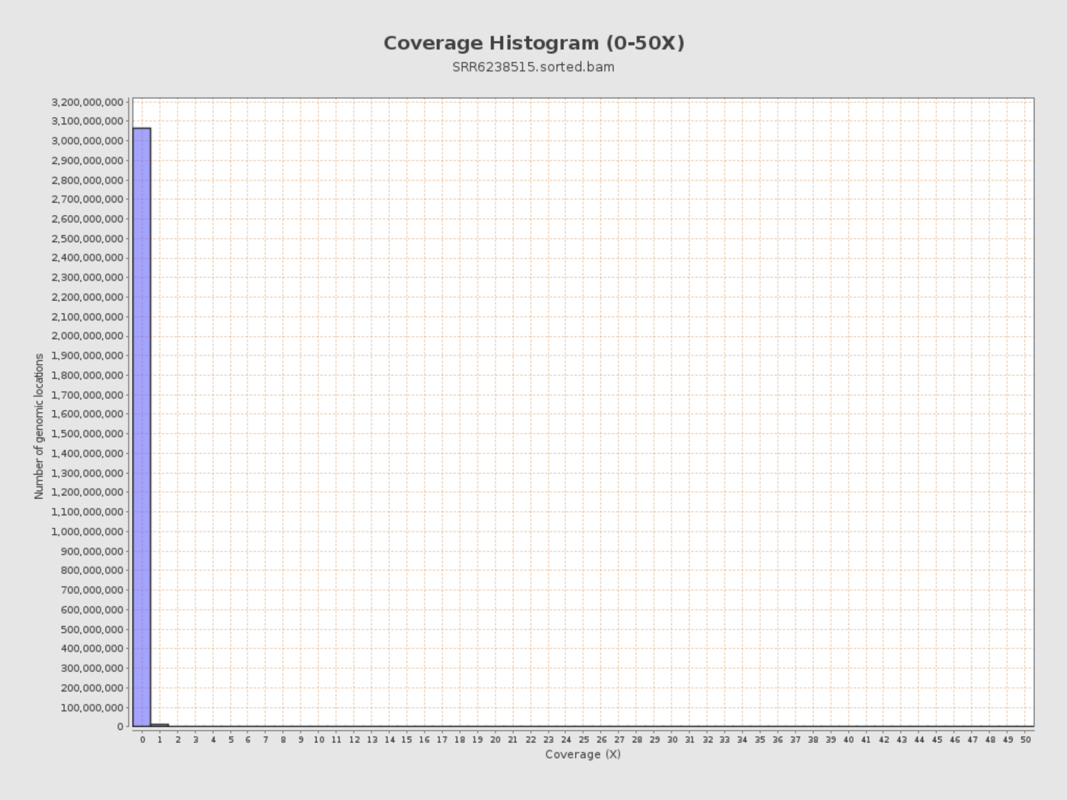
3. Results : Coverage across reference



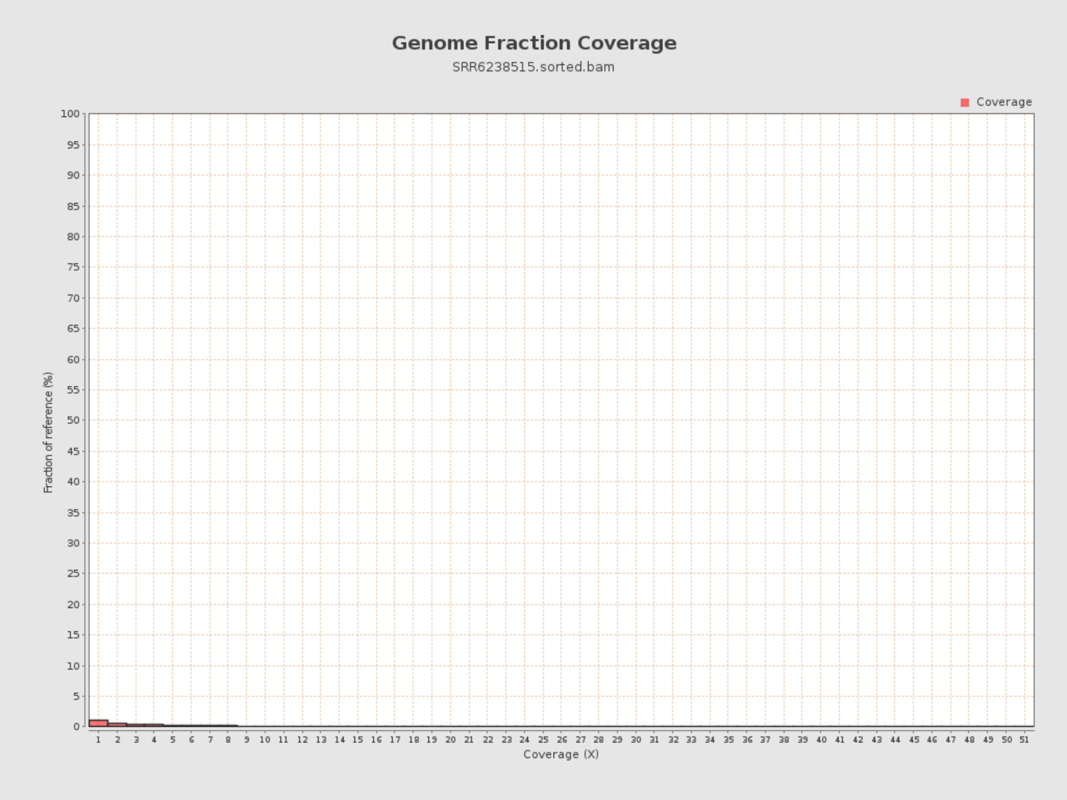
4. Results : Coverage Histogram



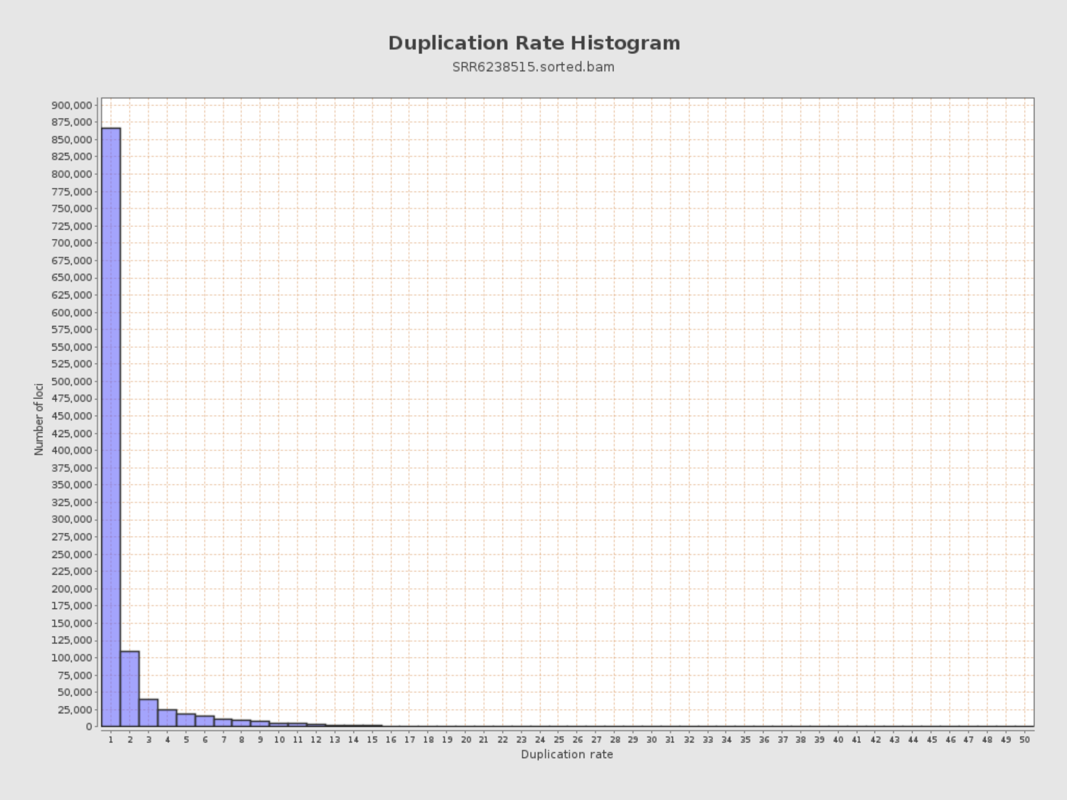
5. Results : Coverage Histogram (0-50X)



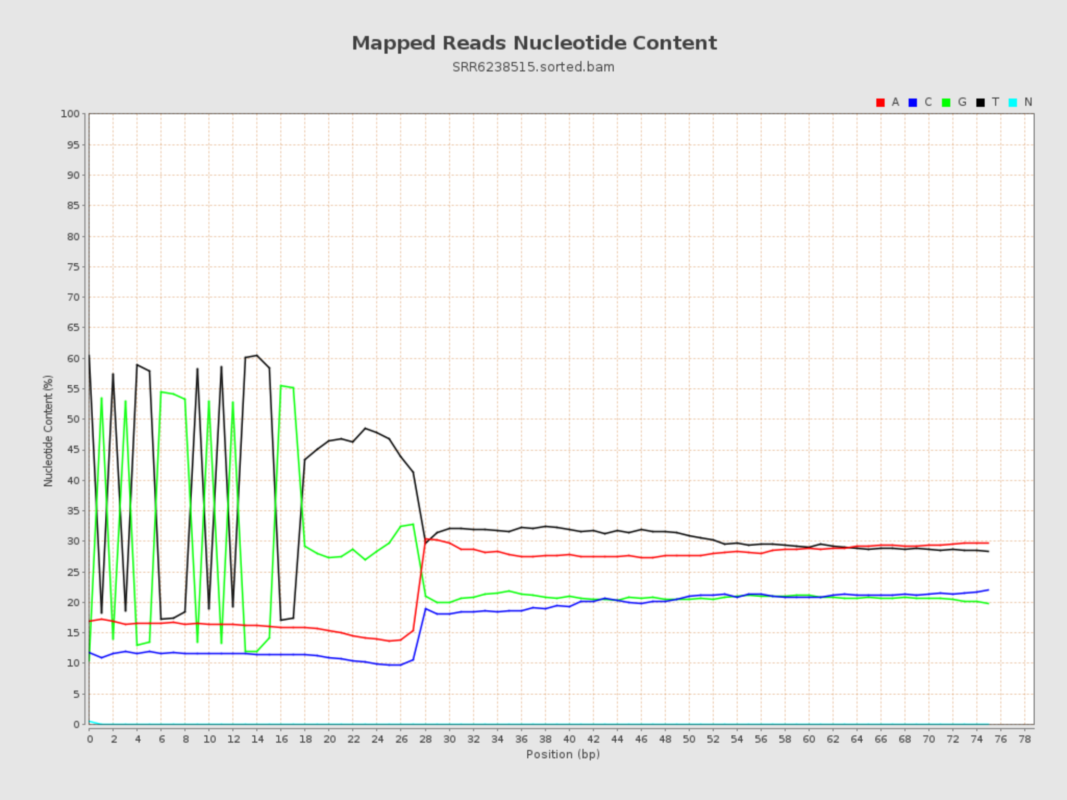
6. Results : Genome Fraction Coverage



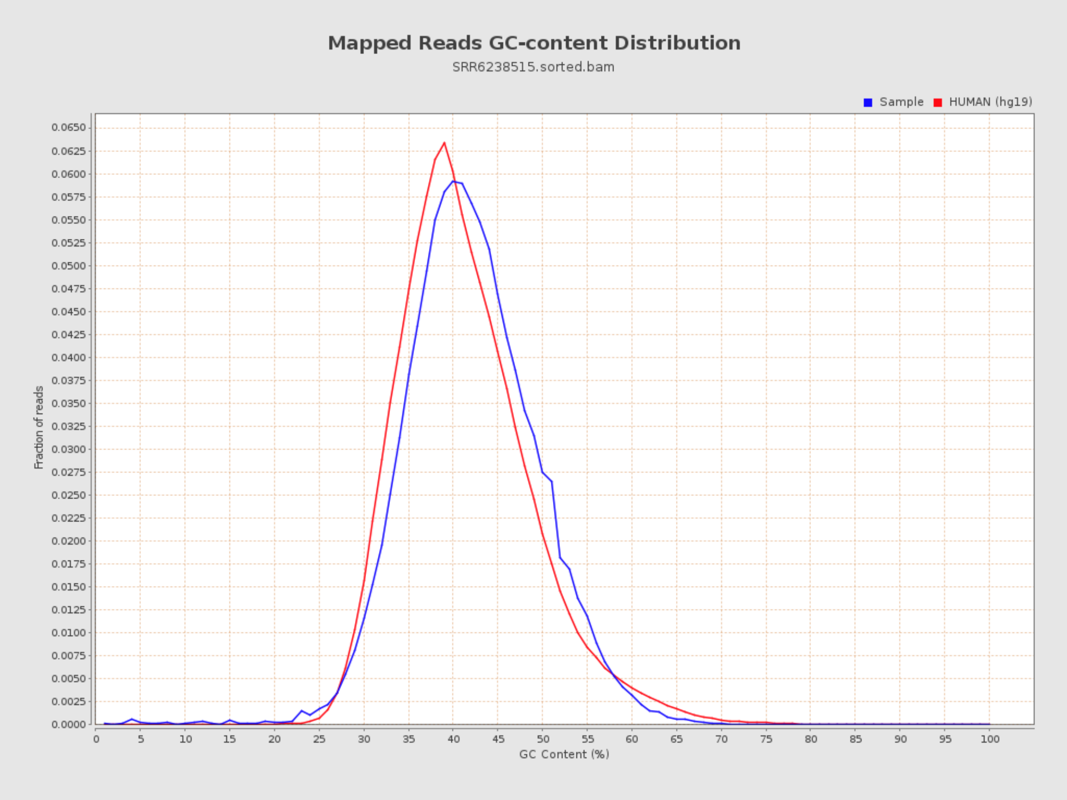
7. Results : Duplication Rate Histogram



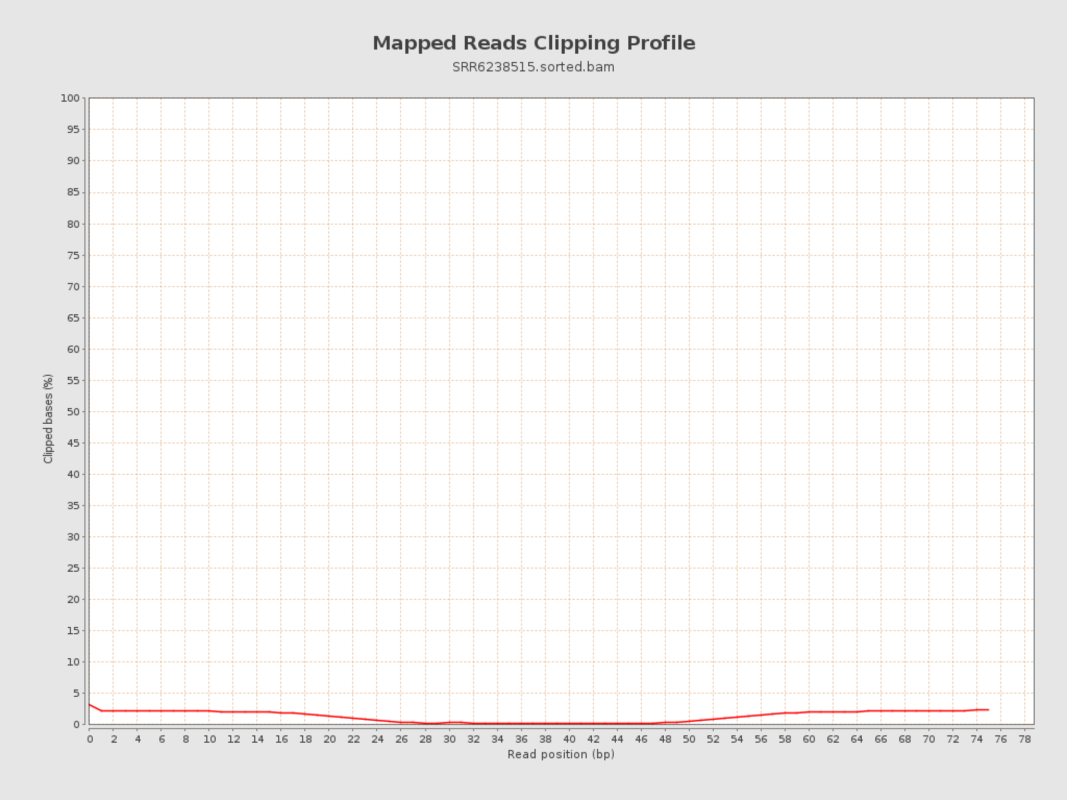
8. Results : Mapped Reads Nucleotide Content



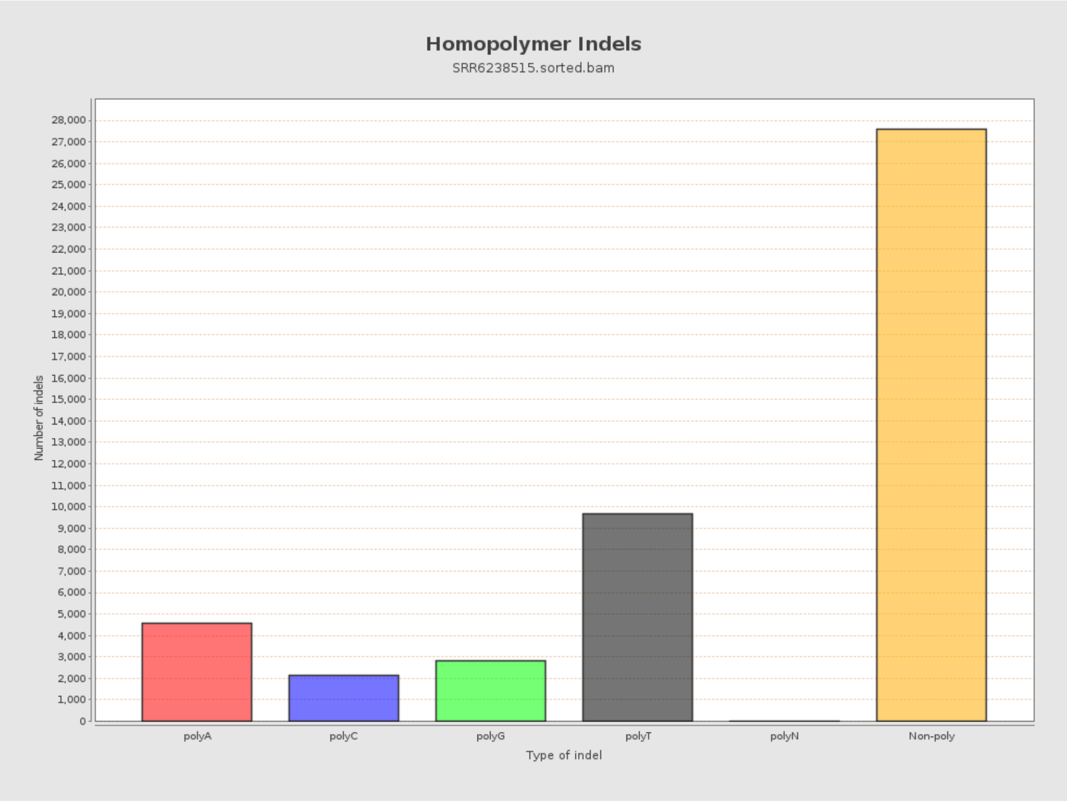
9. Results : Mapped Reads GC-content Distribution



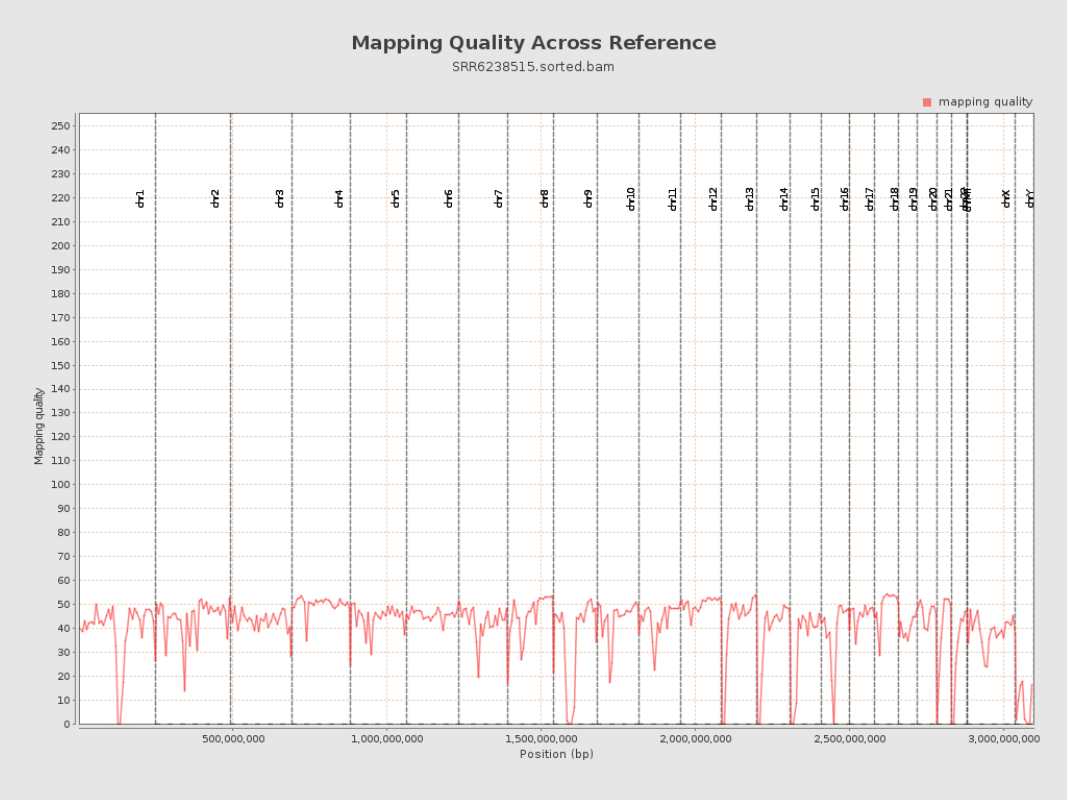
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram