Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:32:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238322.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_SRR6238322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:32:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,067,160
Mapped reads	1,854,658 / 89.72%
Unmapped reads	212,502 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,970 / 1.16%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	100,142 / 4.84%
Duplication rate	4.15%
Clipped reads	860,256 / 41.62%

2.2. ACGT Content

Number/percentage of A's	34,735,019 / 28.18%
Number/percentage of C's	22,884,067 / 18.56%
Number/percentage of T's	38,941,280 / 31.59%
Number/percentage of G's	26,669,095 / 21.63%
Number/percentage of N's	38,931 / 0.03%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0398

Standard Deviation	0.4179

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

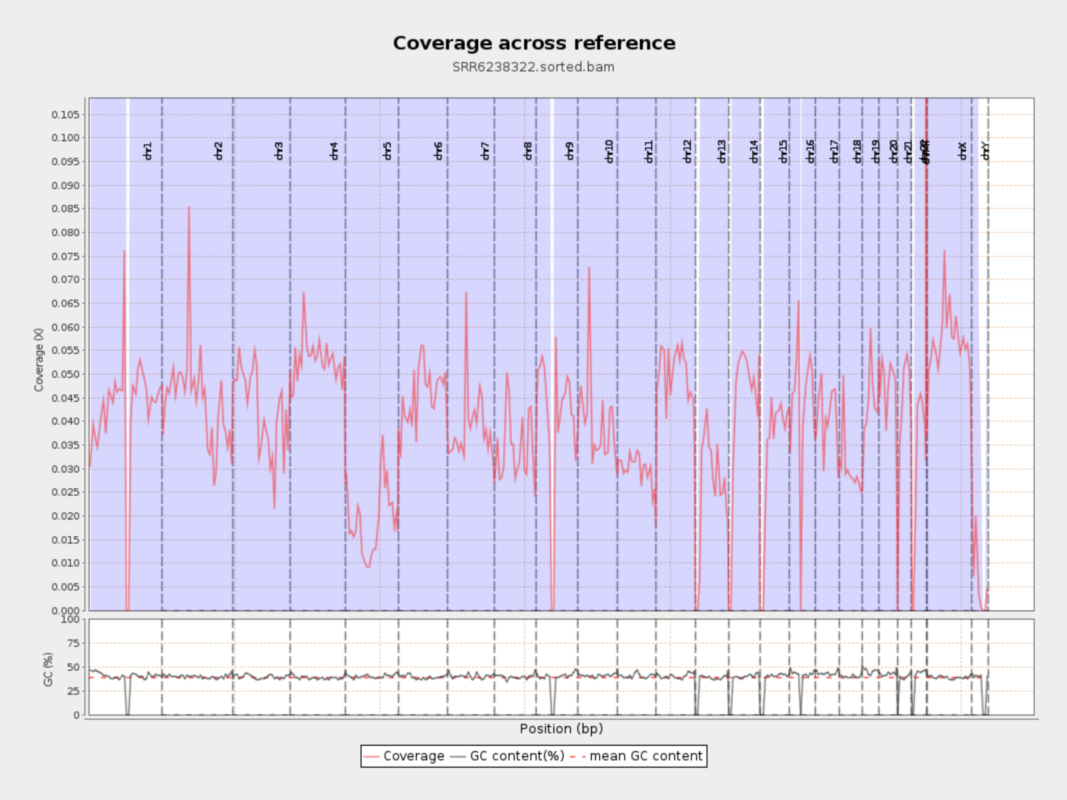
General error rate	0.84%
Mismatches	1,019,405
Insertions	9,488
Mapped reads with at least one insertion	0.51%
Deletions	32,776
Mapped reads with at least one deletion	1.75%
Homopolymer indels	46.73%

2.6. Chromosome stats

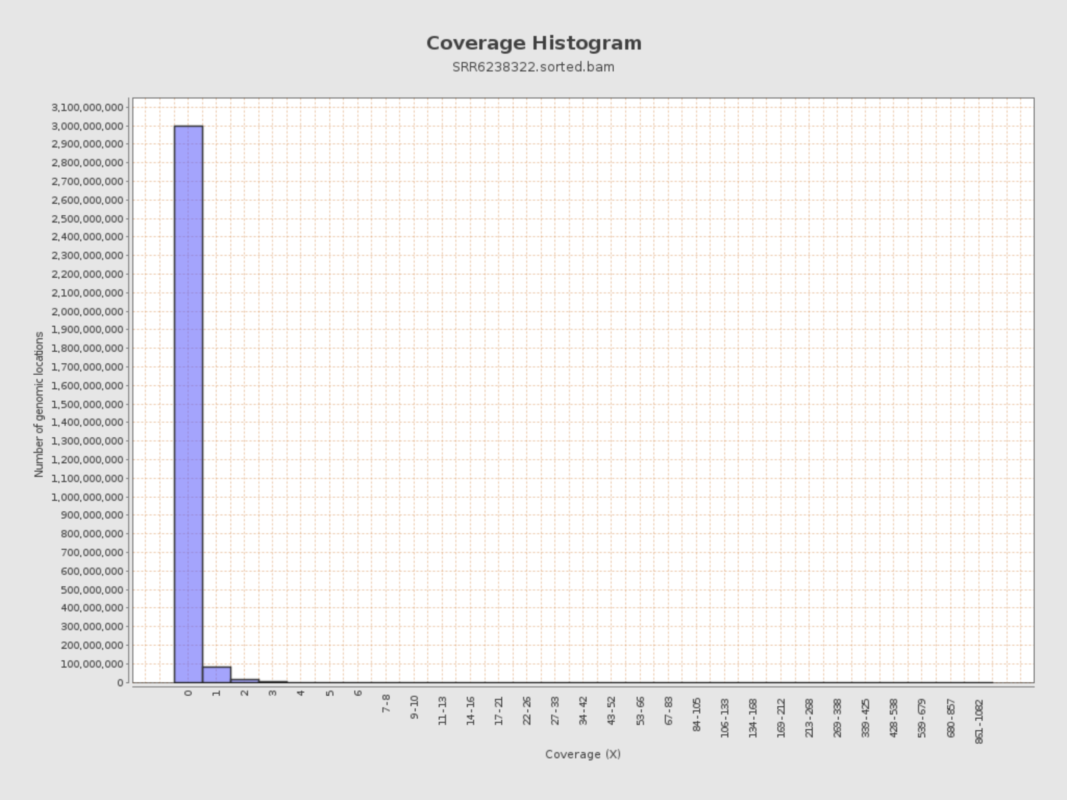
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10567906	0.0424	0.8121
chr2	243199373	10852149	0.0446	0.4288
chr3	198022430	8405384	0.0424	0.2481
chr4	191154276	10138114	0.053	0.3043
chr5	180915260	3484424	0.0193	0.1724
chr6	171115067	7806215	0.0456	0.2862
chr7	159138663	6200605	0.039	0.4475

chr8	146364022	5026762	0.0343	0.6818
chr9	141213431	5714642	0.0405	0.3987
chr10	135534747	5441072	0.0401	0.3889
chr11	135006516	4054302	0.03	0.2744
chr12	133851895	6738038	0.0503	0.2828
chr13	115169878	2925675	0.0254	0.19
chr14	107349540	4528064	0.0422	0.2897
chr15	102531392	3402734	0.0332	0.221
chr16	90354753	3985566	0.0441	0.2886
chr17	81195210	3306808	0.0407	0.2665
chr18	78077248	2377264	0.0304	0.7405
chr19	59128983	2623795	0.0444	0.5155
chr20	63025520	2981482	0.0473	0.2745
chr21	48129895	2007548	0.0417	0.2767
chr22	51304566	1542063	0.0301	0.2062
chrMT	16571	10373	0.626	0.9471
chrX	155270560	8832549	0.0569	0.3188
chrY	59373566	371877	0.0063	0.1682

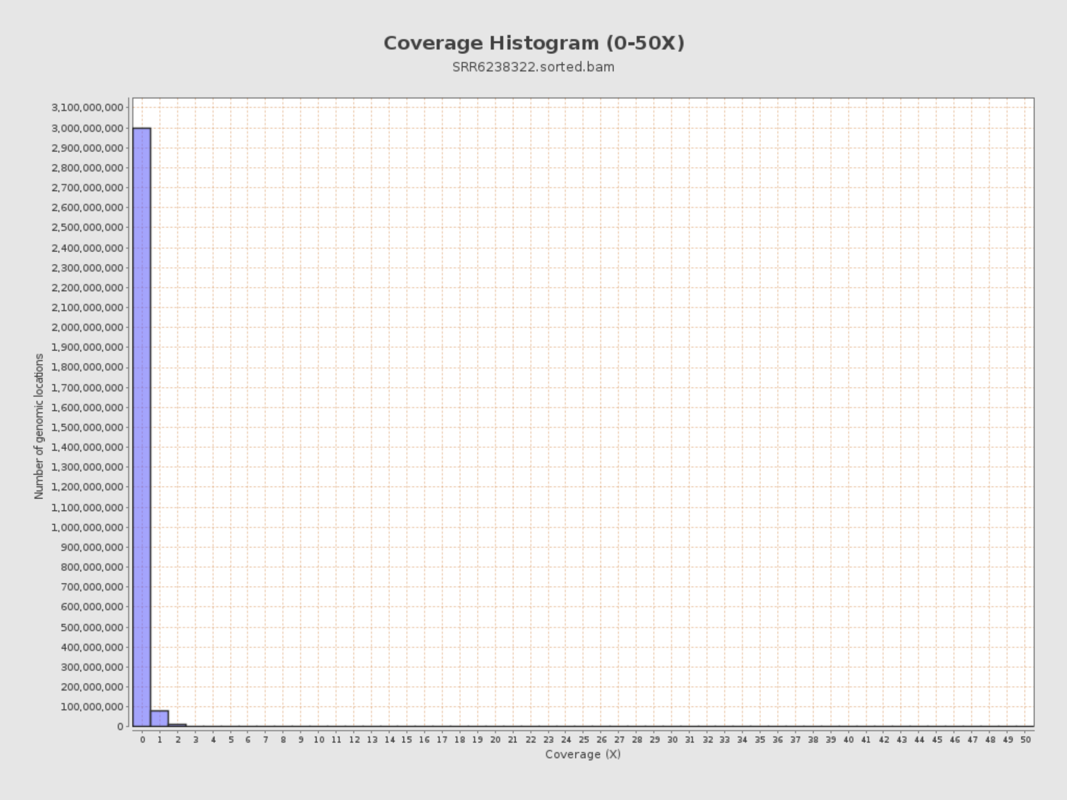
3. Results : Coverage across reference



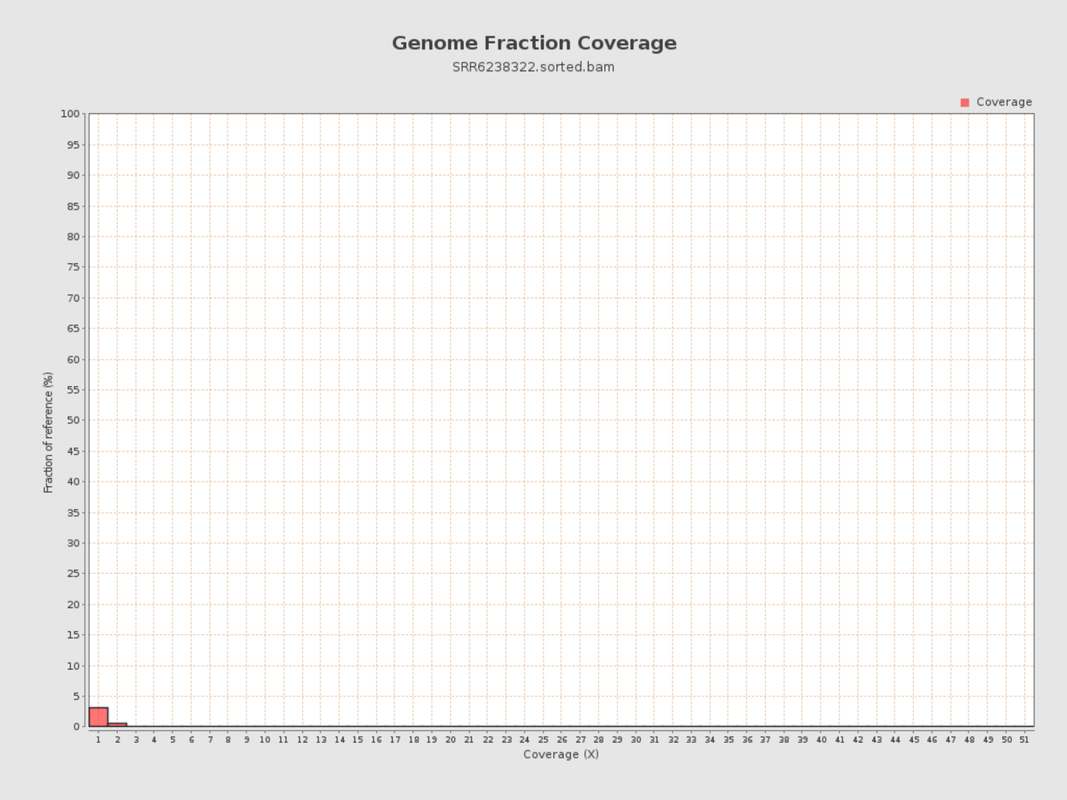
4. Results : Coverage Histogram



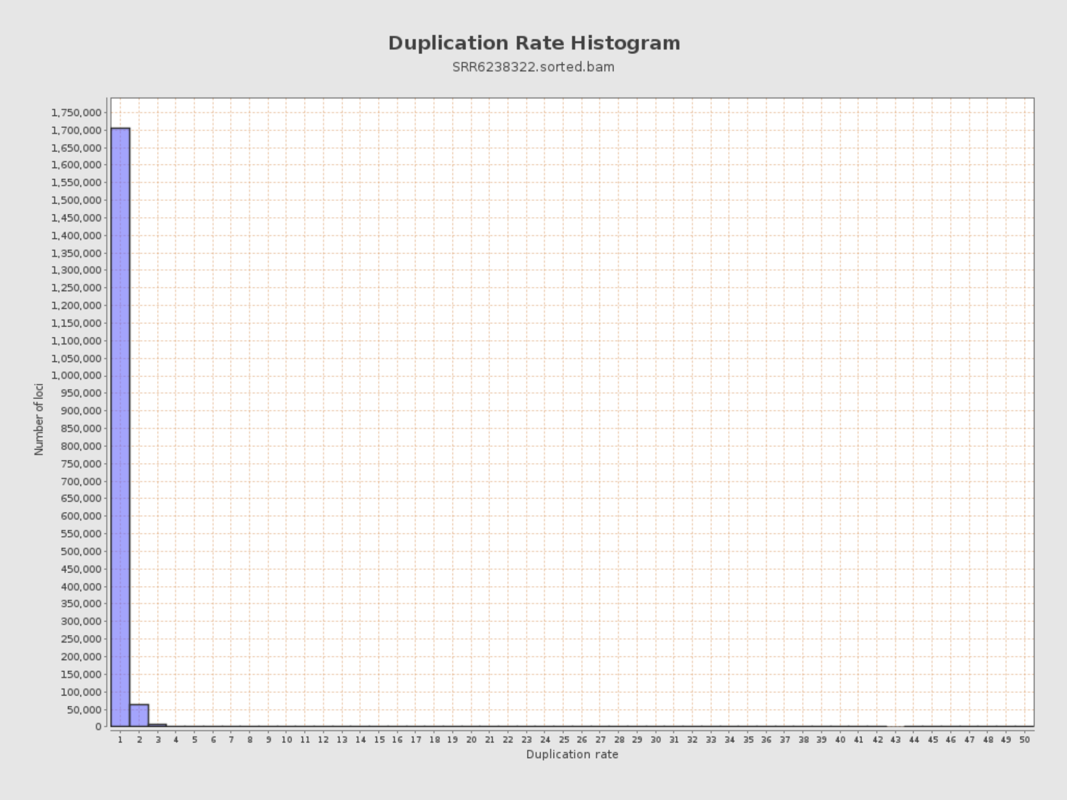
5. Results : Coverage Histogram (0-50X)



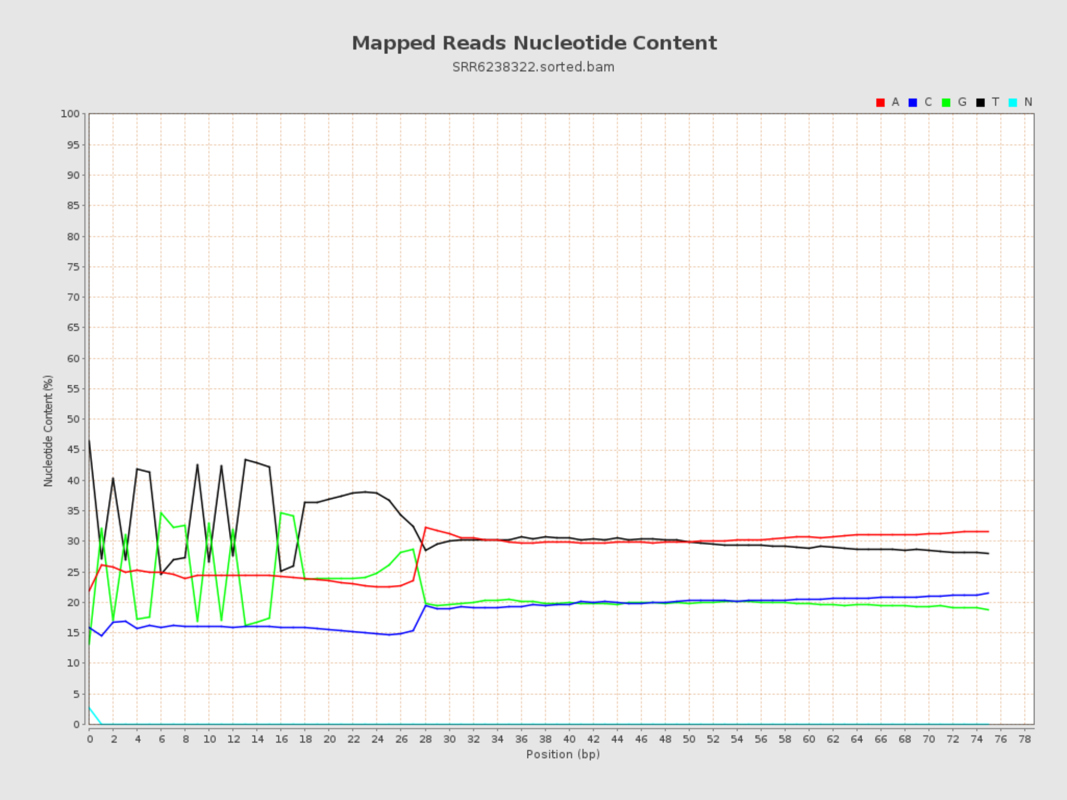
6. Results : Genome Fraction Coverage



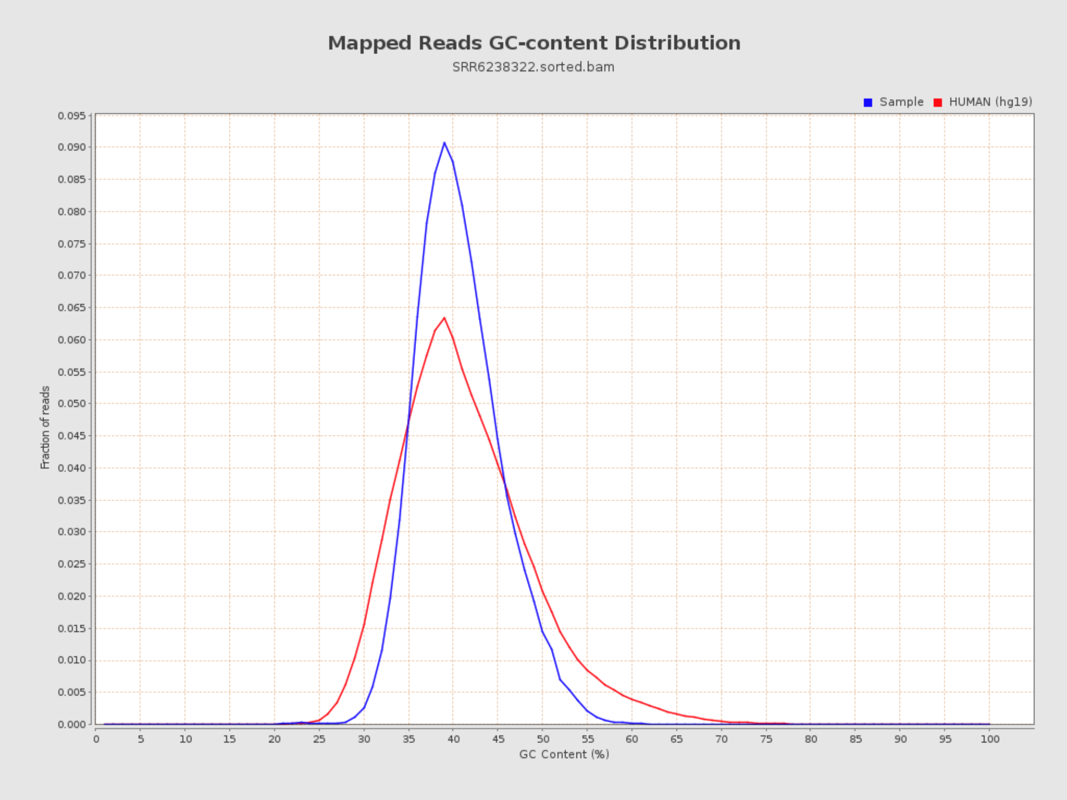
7. Results : Duplication Rate Histogram



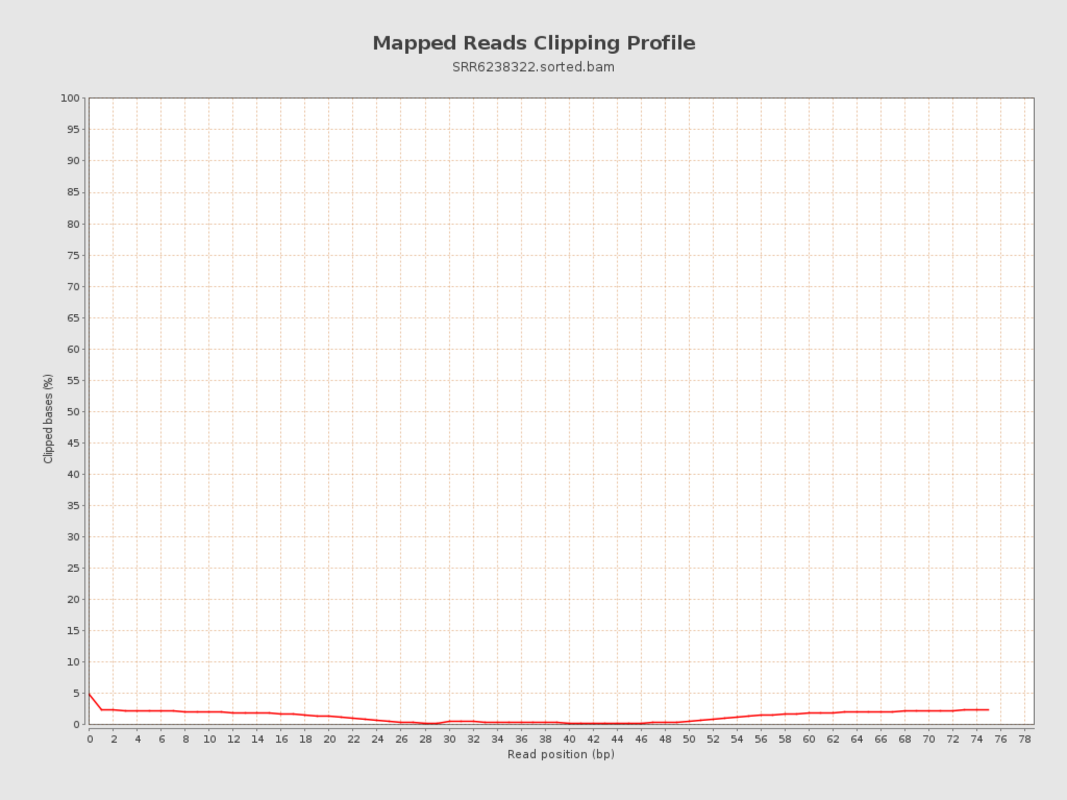
8. Results : Mapped Reads Nucleotide Content



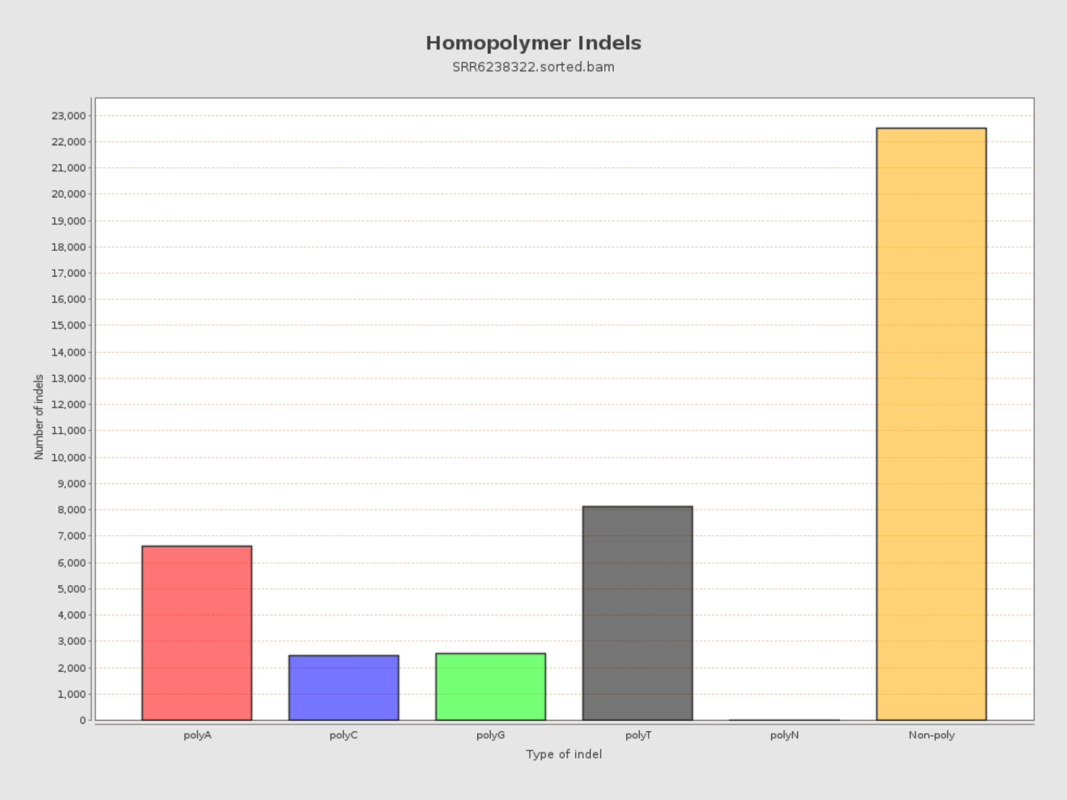
9. Results : Mapped Reads GC-content Distribution



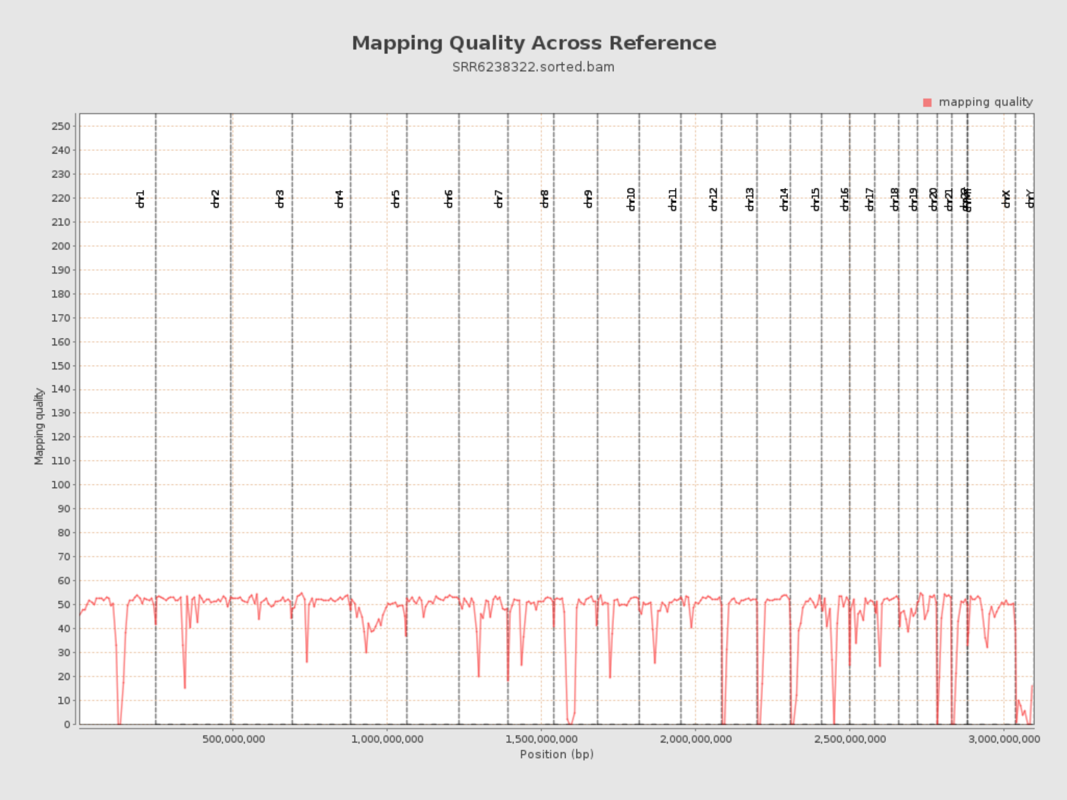
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram