Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:52:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238329.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_SRR6238329 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238329.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:52:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238329.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,048,811
Mapped reads	1,870,058 / 91.28%
Unmapped reads	178,753 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,752 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	74,860 / 3.65%
Duplication rate	3.02%
Clipped reads	858,514 / 41.9%

2.2. ACGT Content

Number/percentage of A's	35,468,383 / 28.41%
Number/percentage of C's	23,653,031 / 18.95%
Number/percentage of T's	38,837,209 / 31.11%
Number/percentage of G's	26,846,470 / 21.51%
Number/percentage of N's	30,312 / 0.02%
GC Percentage	40.45%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3889

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

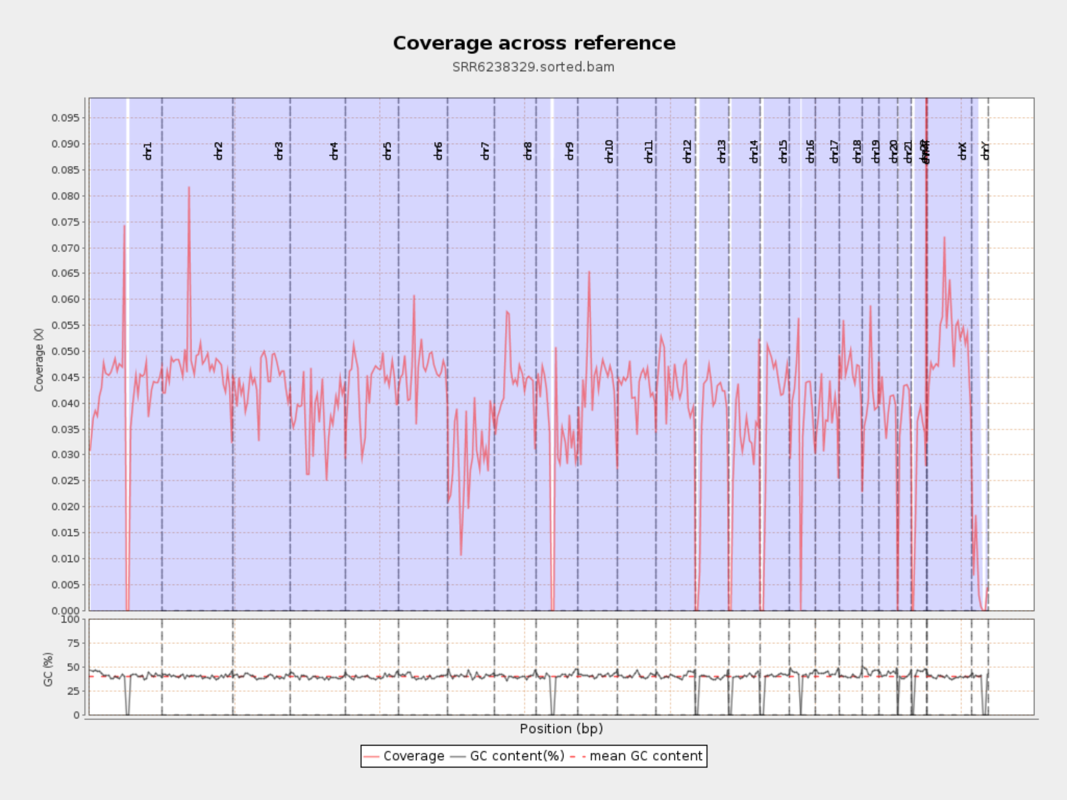
General error rate	0.85%
Mismatches	1,039,687
Insertions	9,603
Mapped reads with at least one insertion	0.51%
Deletions	32,732
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.27%

2.6. Chromosome stats

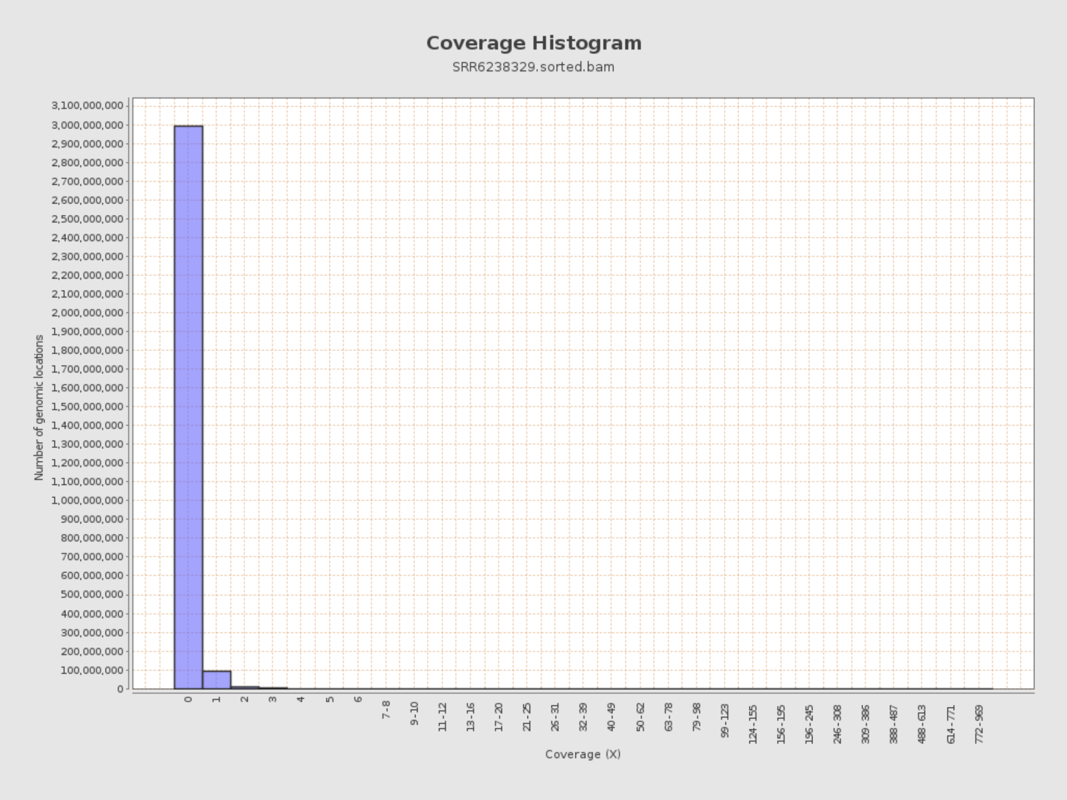
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10348042	0.0415	0.7948
chr2	243199373	11598599	0.0477	0.4039
chr3	198022430	8764923	0.0443	0.2389
chr4	191154276	7205610	0.0377	0.2405
chr5	180915260	7912823	0.0437	0.2404
chr6	171115067	7966661	0.0466	0.2942
chr7	159138663	4729549	0.0297	0.2938

chr8	146364022	6402821	0.0437	0.6488
chr9	141213431	4670082	0.0331	0.3347
chr10	135534747	6008939	0.0443	0.3449
chr11	135006516	5818478	0.0431	0.3118
chr12	133851895	5857419	0.0438	0.248
chr13	115169878	4034788	0.035	0.2131
chr14	107349540	3223739	0.03	0.2267
chr15	102531392	3877148	0.0378	0.2232
chr16	90354753	3442543	0.0381	0.2538
chr17	81195210	3033349	0.0374	0.2621
chr18	78077248	3678287	0.0471	0.6279
chr19	59128983	2435757	0.0412	0.4922
chr20	63025520	2455646	0.039	0.2319
chr21	48129895	1716633	0.0357	0.2362
chr22	51304566	1316622	0.0257	0.1796
chrMT	16571	4818	0.2907	0.6268
chrX	155270560	8052136	0.0519	0.2917
chrY	59373566	336525	0.0057	0.1496

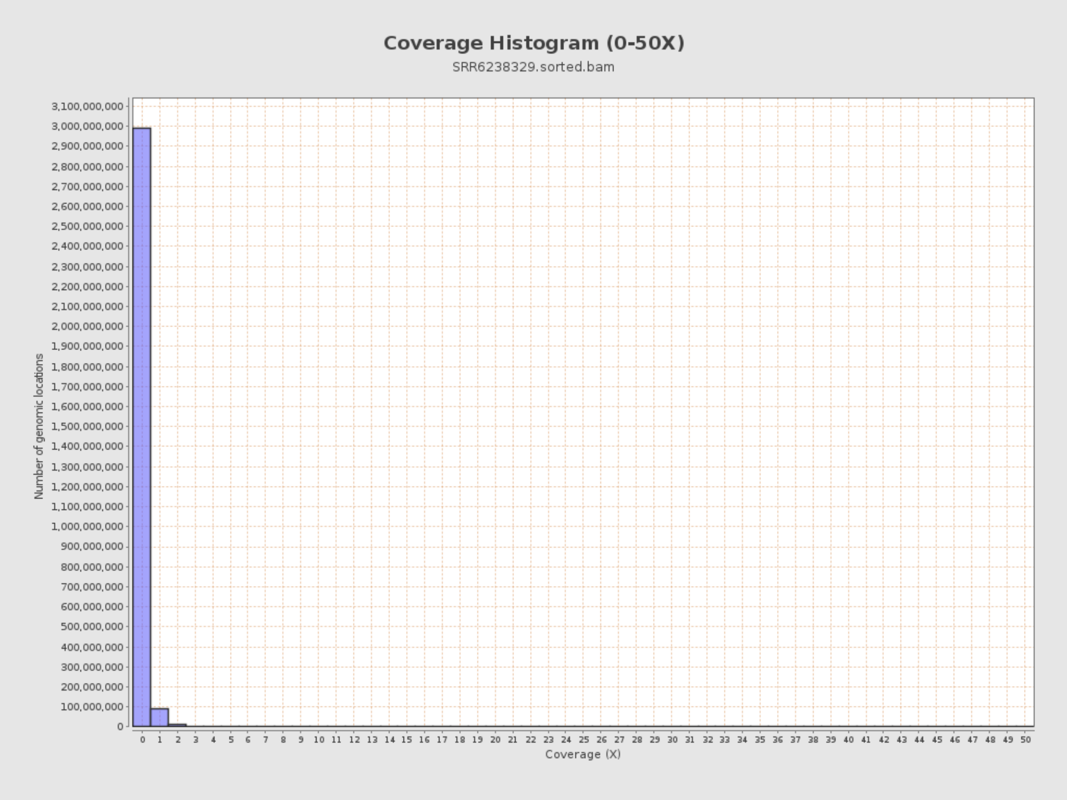
3. Results : Coverage across reference



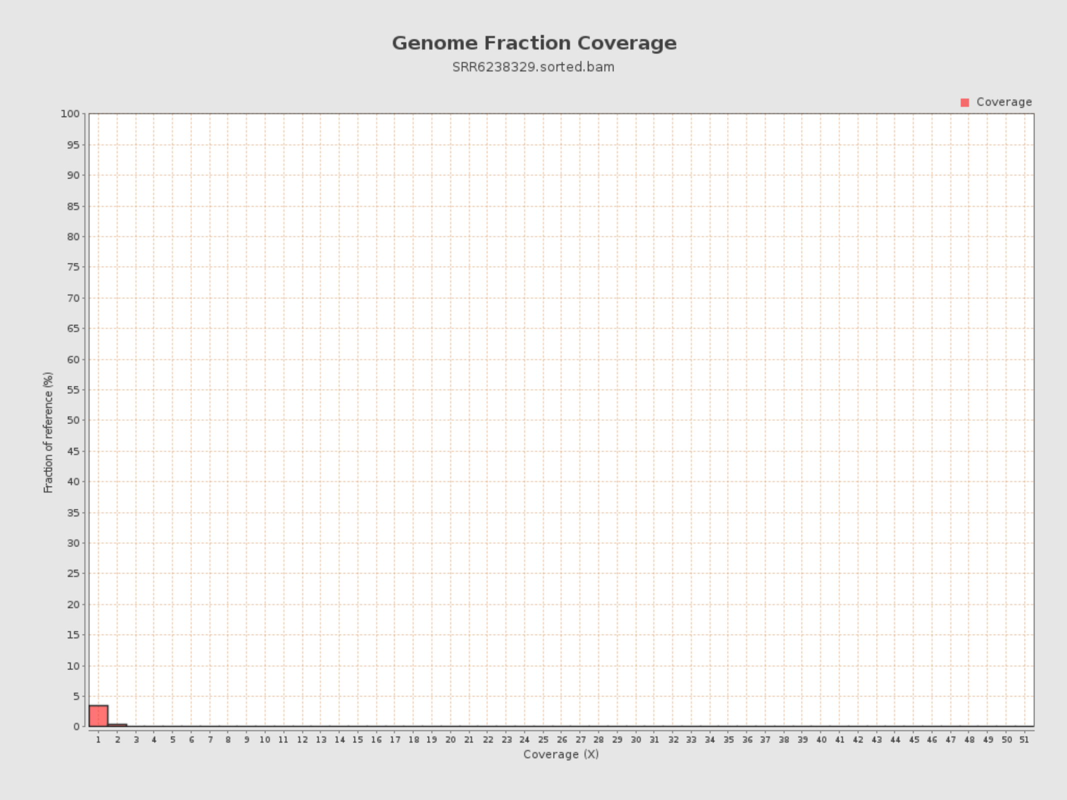
4. Results : Coverage Histogram



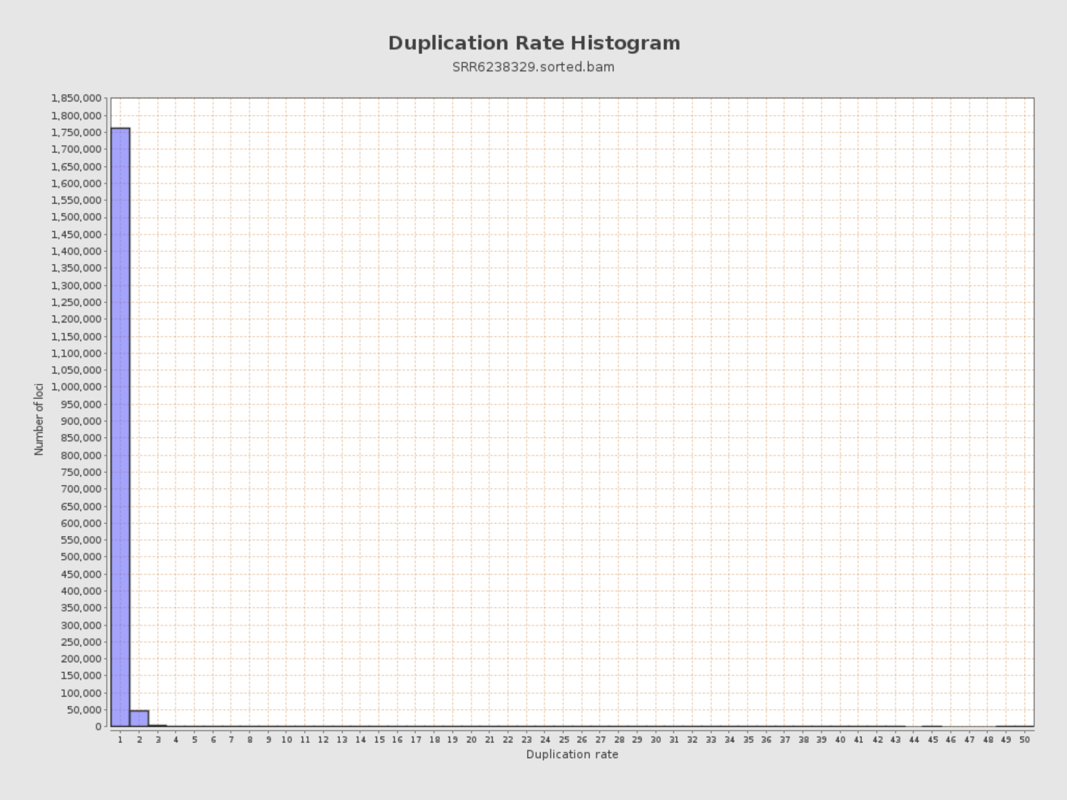
5. Results : Coverage Histogram (0-50X)



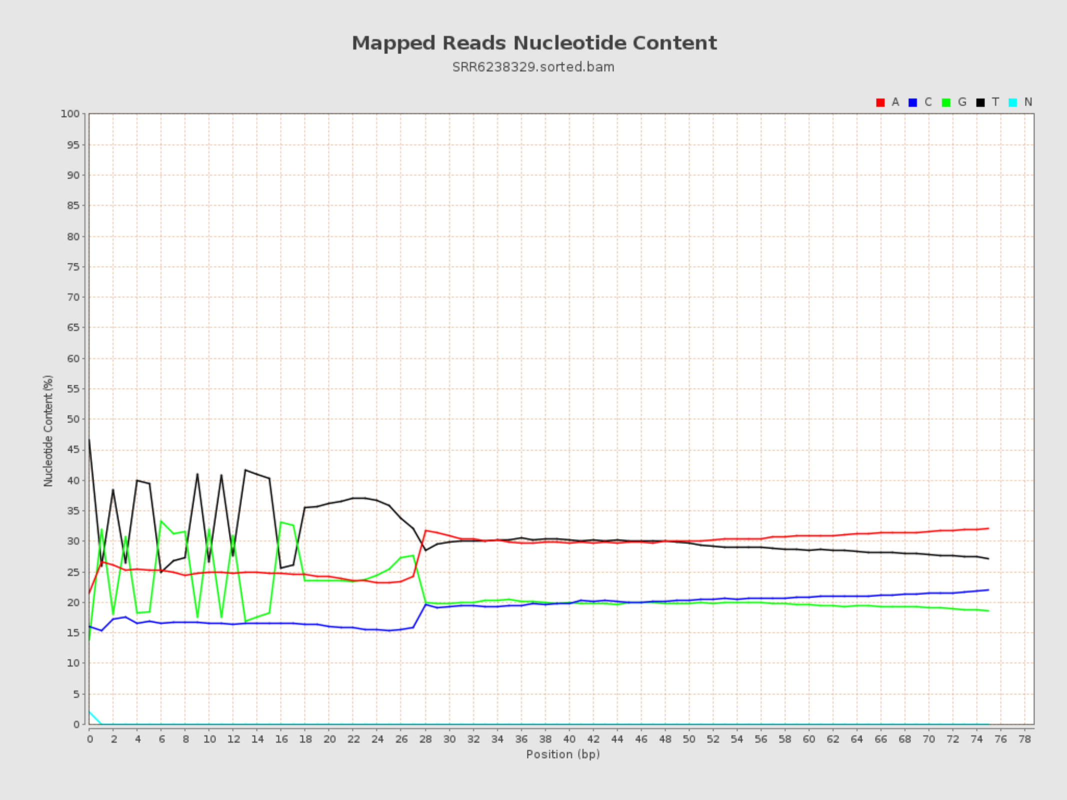
6. Results : Genome Fraction Coverage



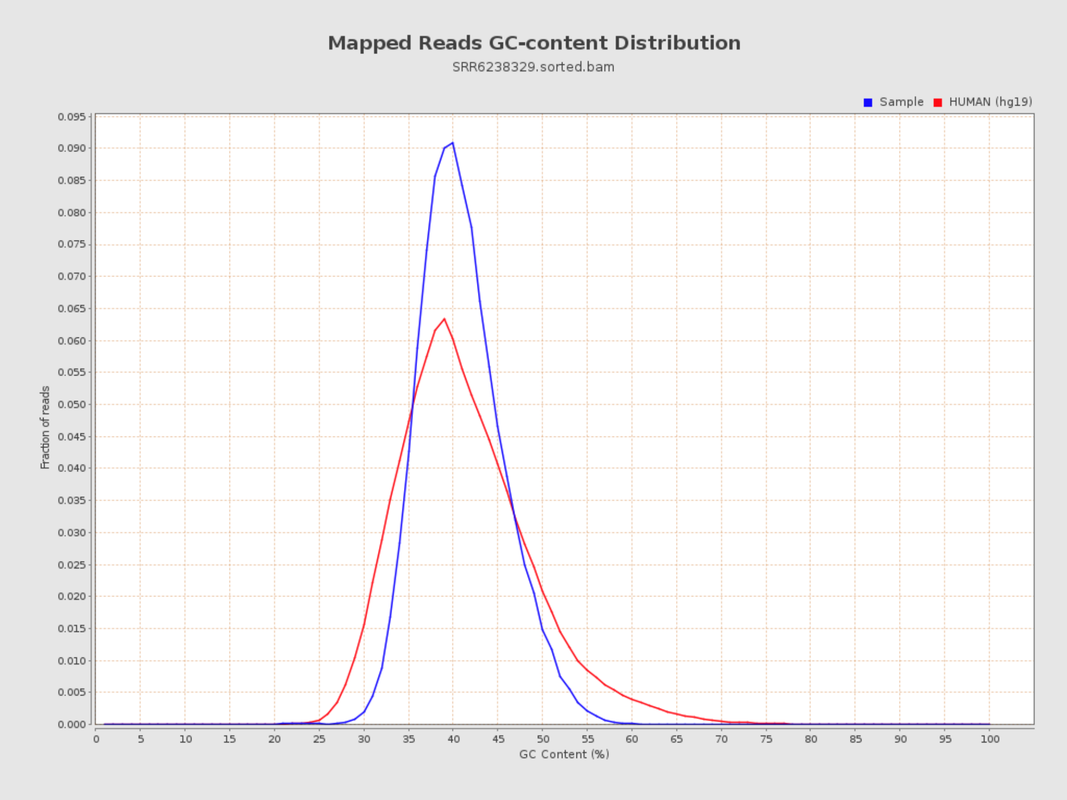
7. Results : Duplication Rate Histogram



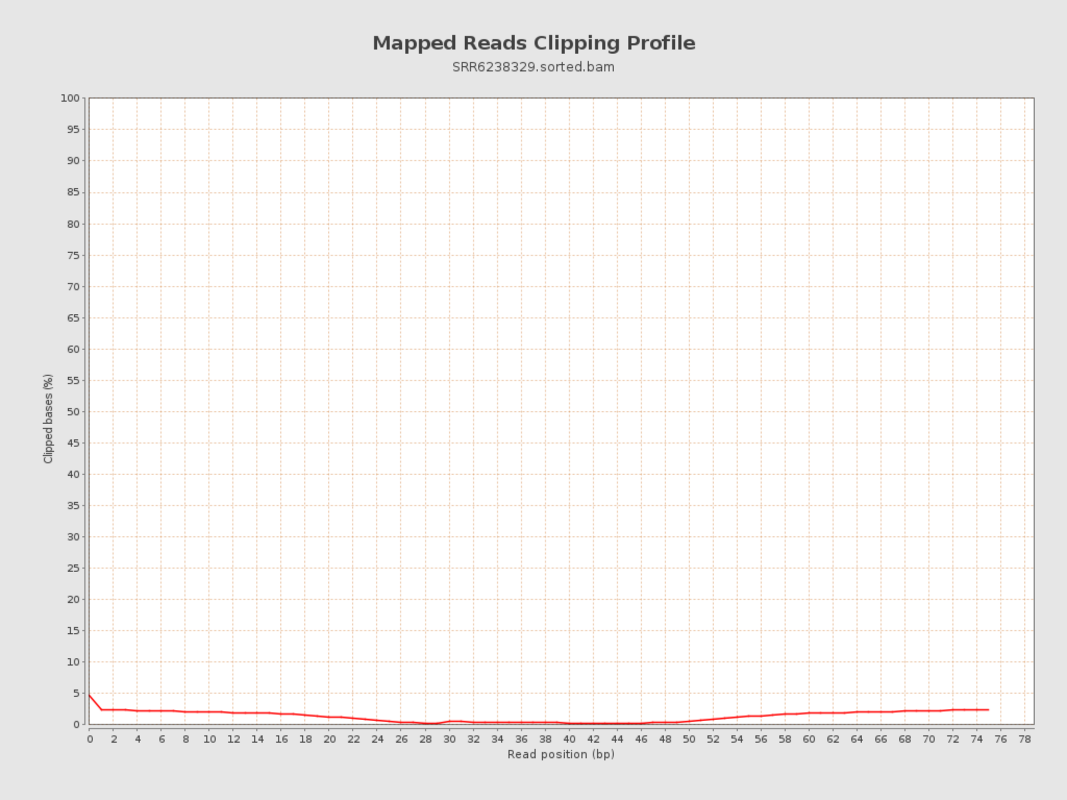
8. Results : Mapped Reads Nucleotide Content



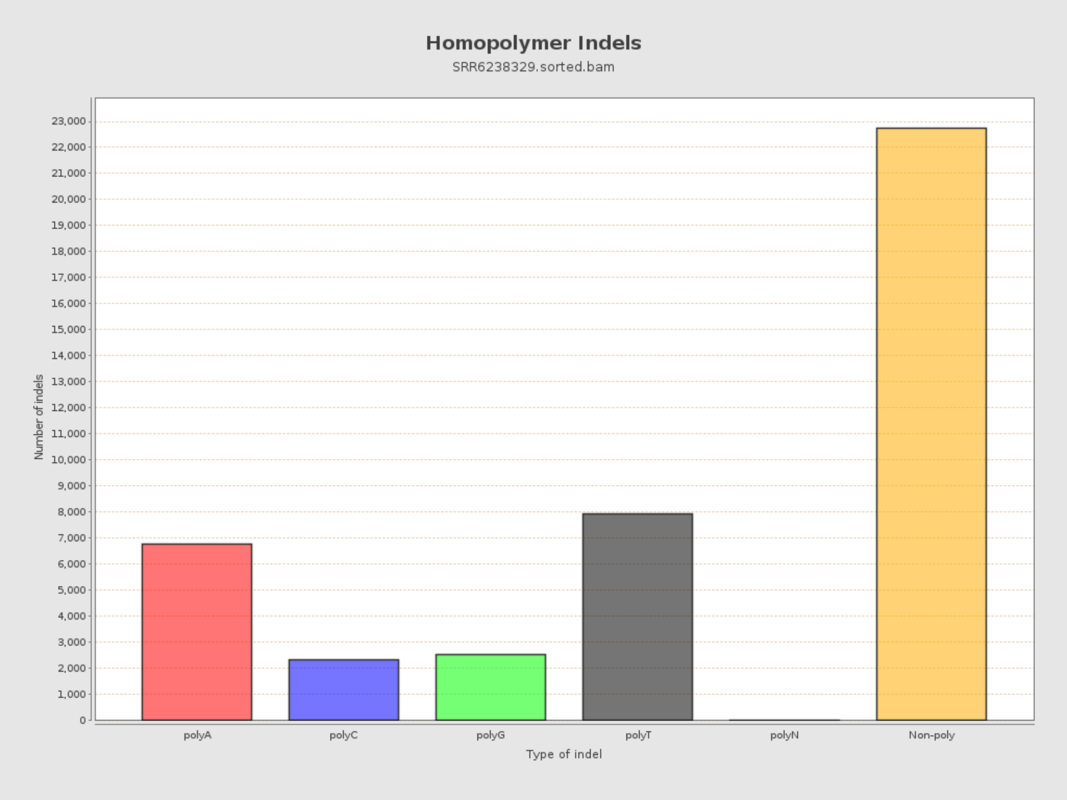
9. Results : Mapped Reads GC-content Distribution



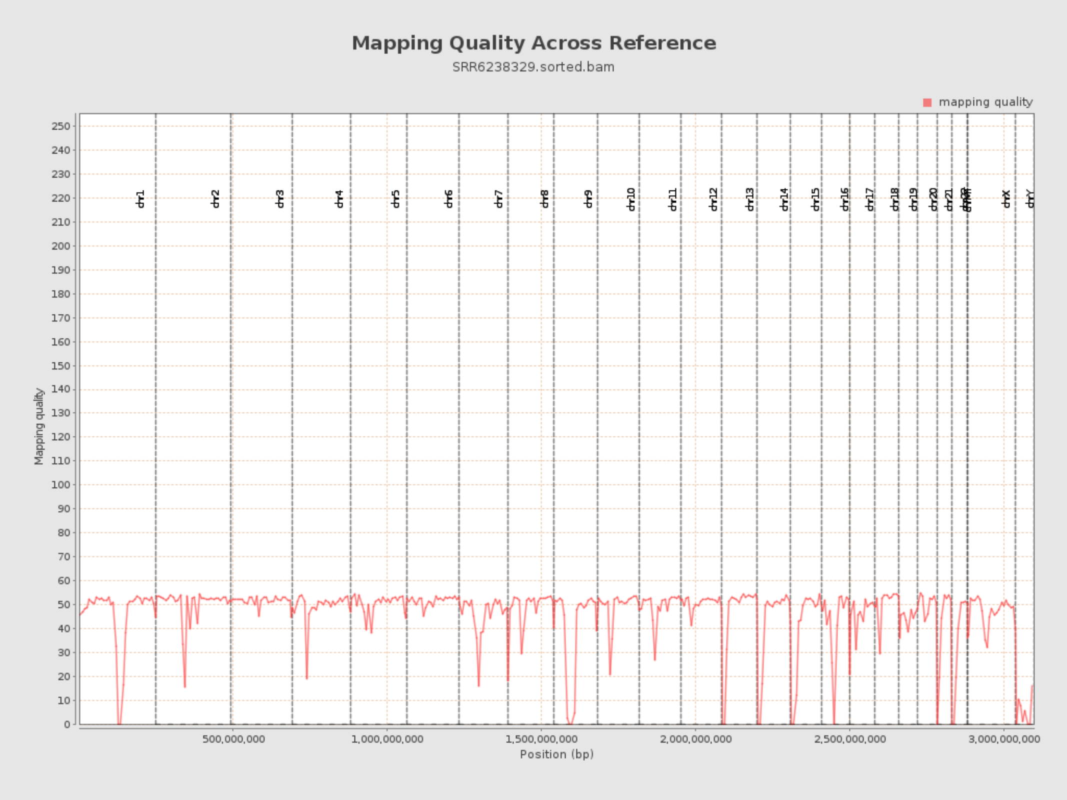
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram