Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:12:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238058.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_SRR6238058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:12:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,233,914
Mapped reads	994,487 / 80.6%
Unmapped reads	239,427 / 19.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,196 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	107,730 / 8.73%
Duplication rate	8.1%
Clipped reads	477,087 / 38.66%

2.2. ACGT Content

Number/percentage of A's	17,671,529 / 27.01%
Number/percentage of C's	12,646,377 / 19.33%
Number/percentage of T's	20,188,888 / 30.86%
Number/percentage of G's	14,906,676 / 22.79%
Number/percentage of N's	8,107 / 0.01%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.3369

2.4. Mapping Quality

Mean Mapping Quality	44.19

2.5. Mismatches and indels

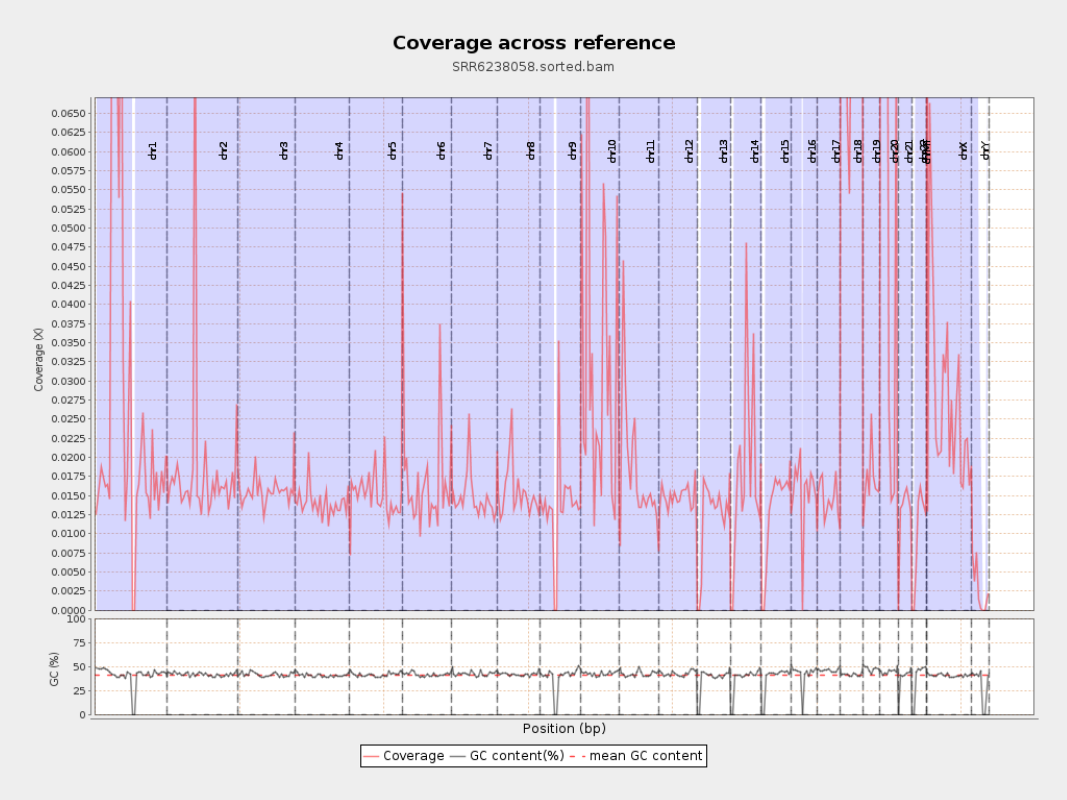
General error rate	0.82%
Mismatches	526,054
Insertions	4,574
Mapped reads with at least one insertion	0.45%
Deletions	16,229
Mapped reads with at least one deletion	1.61%
Homopolymer indels	45.32%

2.6. Chromosome stats

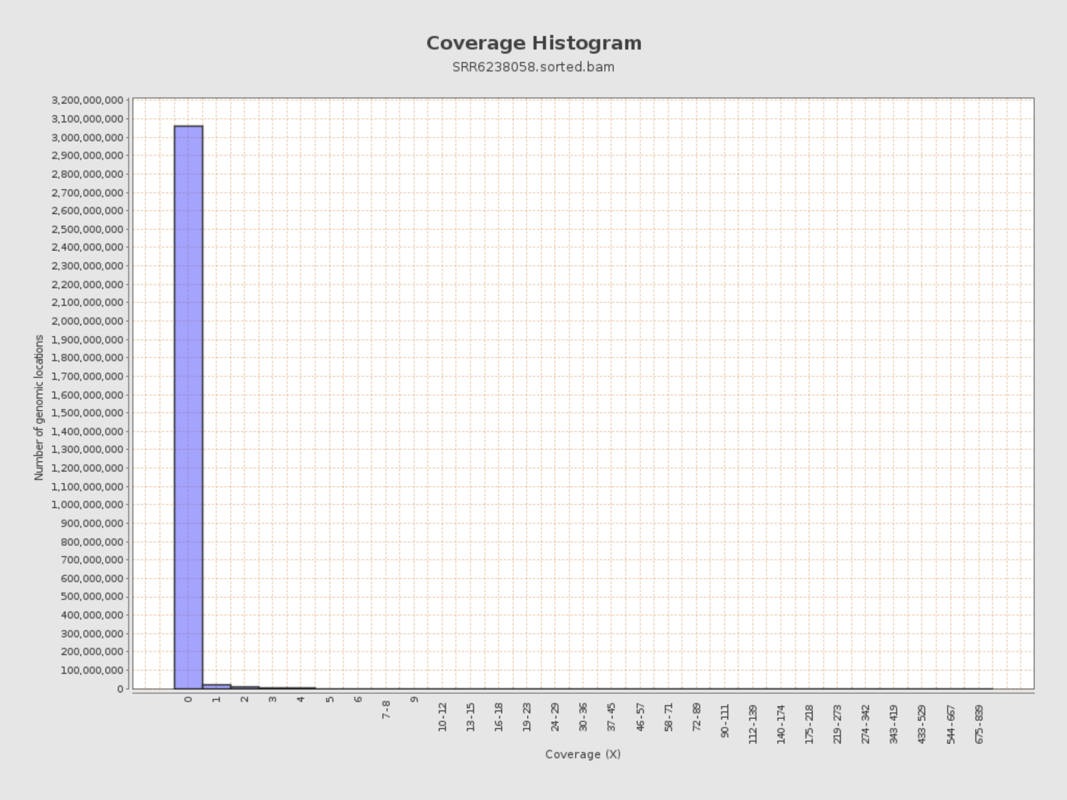
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6984084	0.028	0.4342
chr2	243199373	4472150	0.0184	0.6595
chr3	198022430	3076448	0.0155	0.2007
chr4	191154276	2693881	0.0141	0.1883
chr5	180915260	2769017	0.0153	0.1974
chr6	171115067	2925299	0.0171	0.2206
chr7	159138663	2348817	0.0148	0.2494

chr8	146364022	2271552	0.0155	0.3644
chr9	141213431	1919109	0.0136	0.3841
chr10	135534747	4607407	0.034	0.3274
chr11	135006516	2531756	0.0188	0.2991
chr12	133851895	1992581	0.0149	0.1991
chr13	115169878	1375355	0.0119	0.1751
chr14	107349540	1915007	0.0178	0.2234
chr15	102531392	1325446	0.0129	0.1951
chr16	90354753	1374088	0.0152	0.2003
chr17	81195210	1185968	0.0146	0.2072
chr18	78077248	9336492	0.1196	0.6176
chr19	59128983	1022342	0.0173	0.352
chr20	63025520	3681593	0.0584	0.4161
chr21	48129895	620631	0.0129	0.1822
chr22	51304566	524519	0.0102	0.1665
chrMT	16571	21164	1.2772	1.8462
chrX	155270560	4317798	0.0278	0.2987
chrY	59373566	157048	0.0026	0.0871

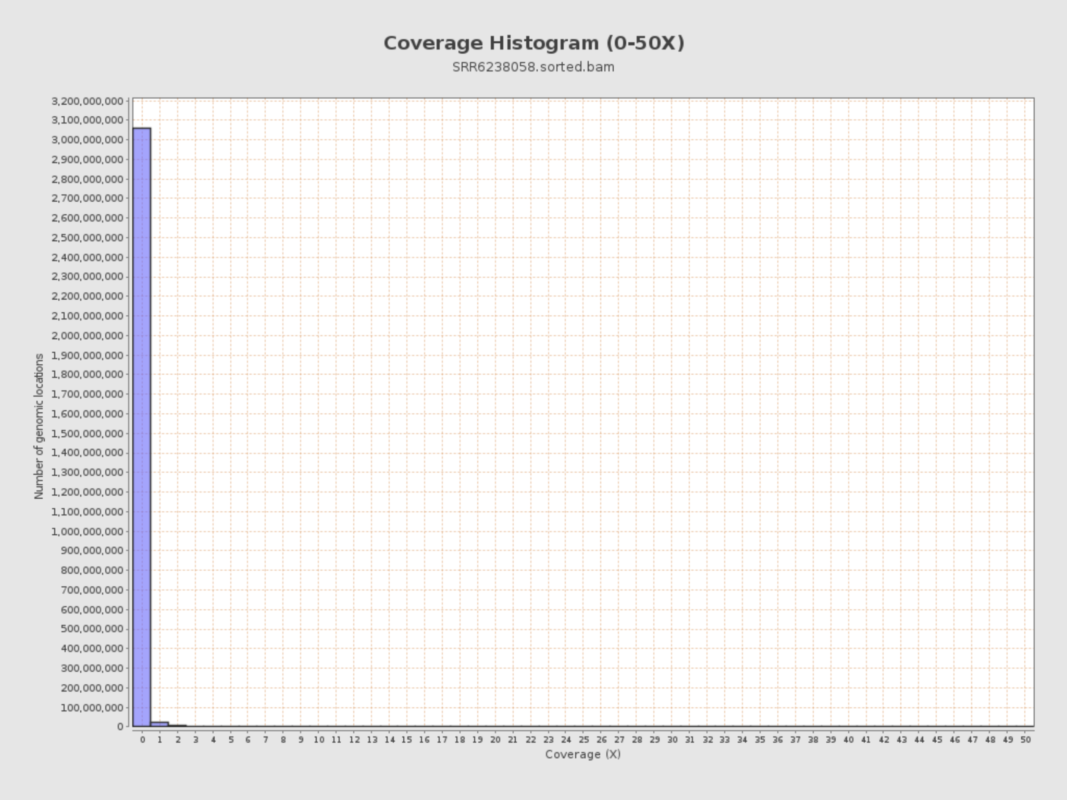
3. Results : Coverage across reference



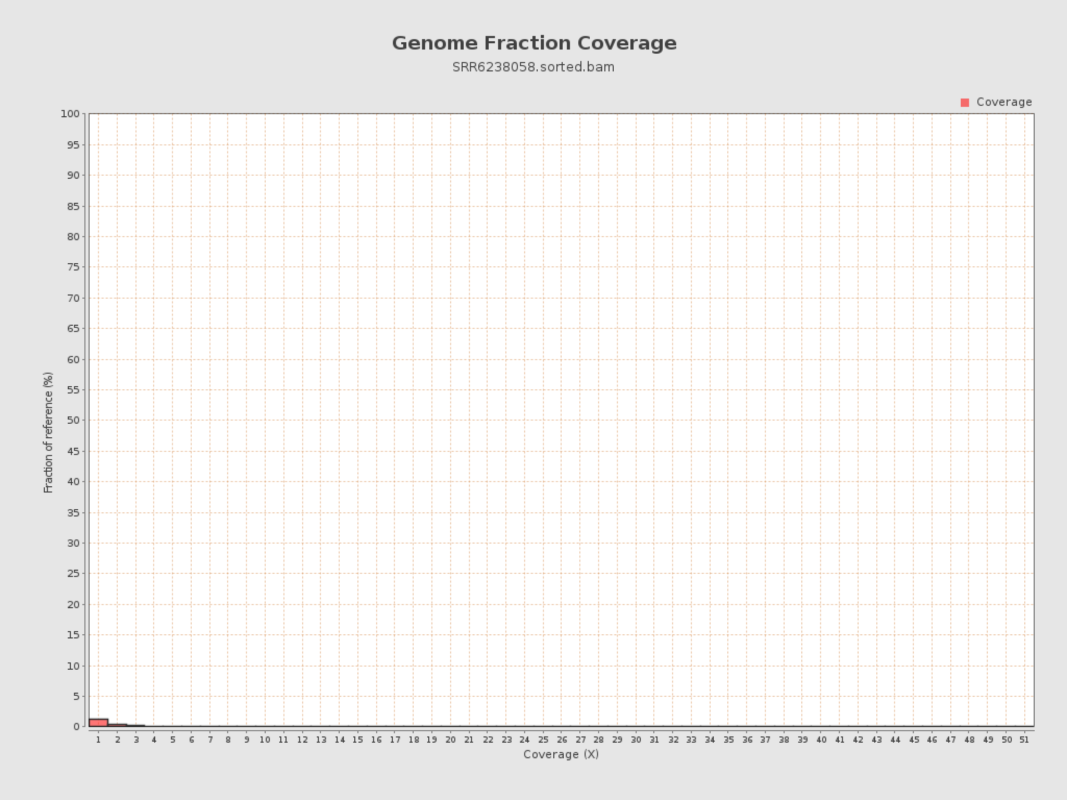
4. Results : Coverage Histogram



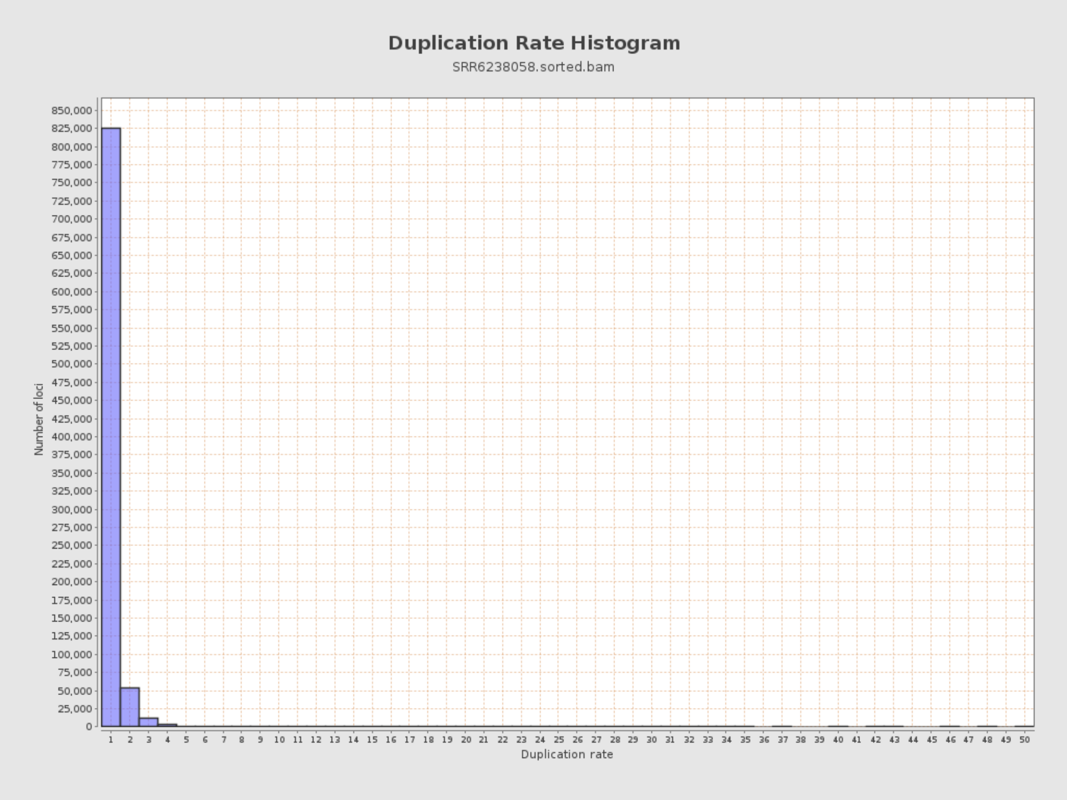
5. Results : Coverage Histogram (0-50X)



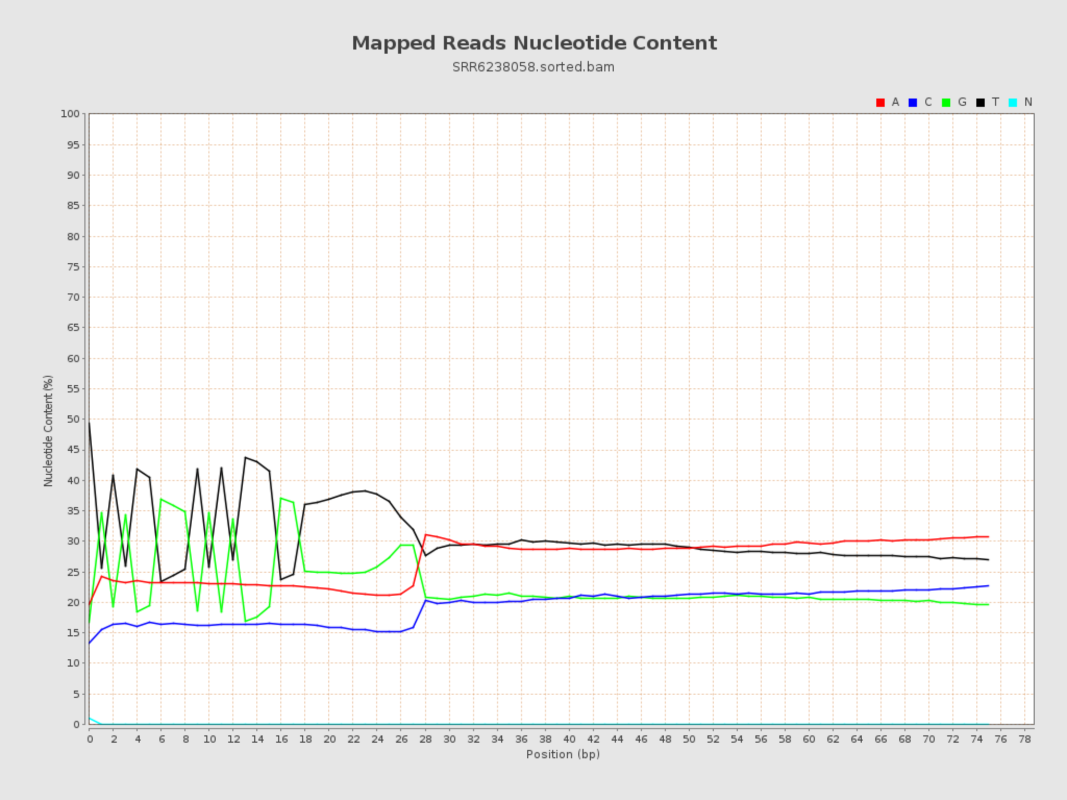
6. Results : Genome Fraction Coverage



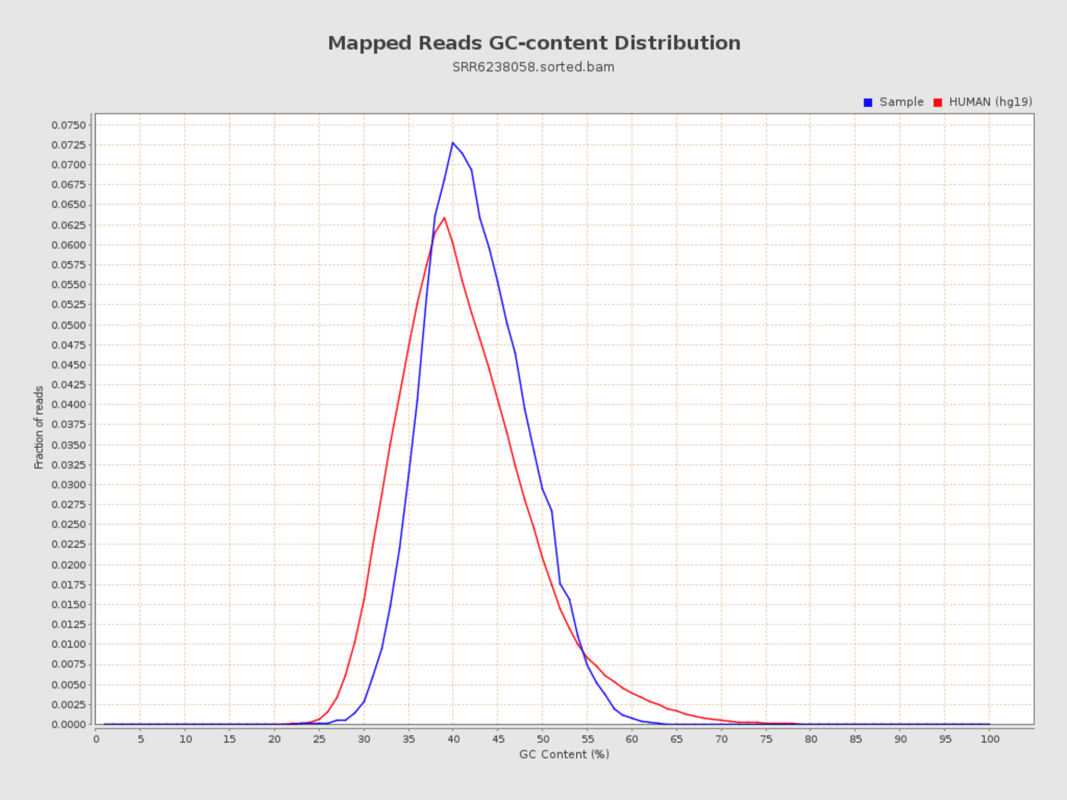
7. Results : Duplication Rate Histogram



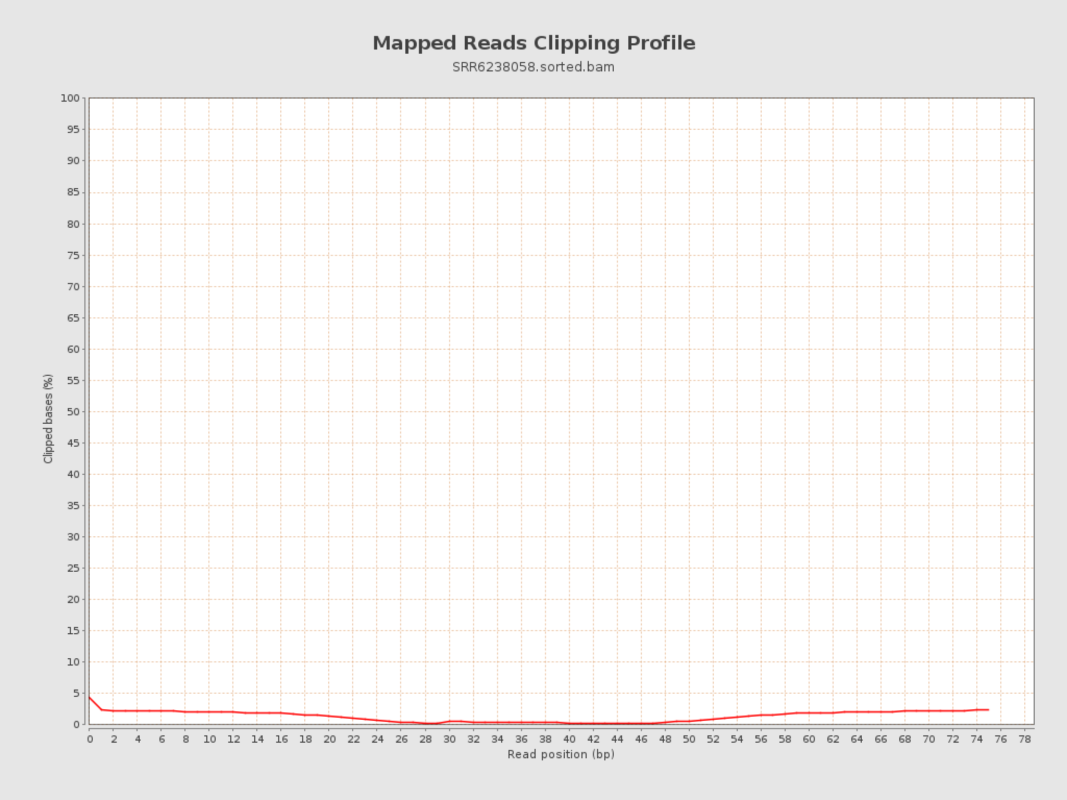
8. Results : Mapped Reads Nucleotide Content



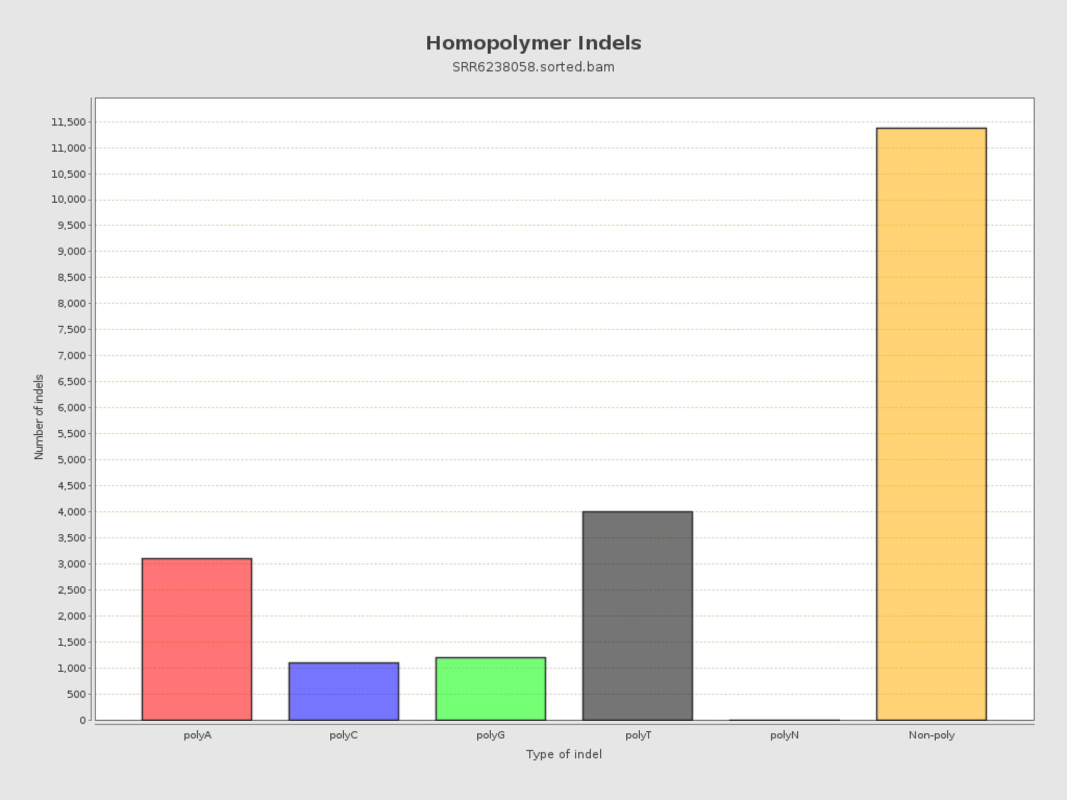
9. Results : Mapped Reads GC-content Distribution



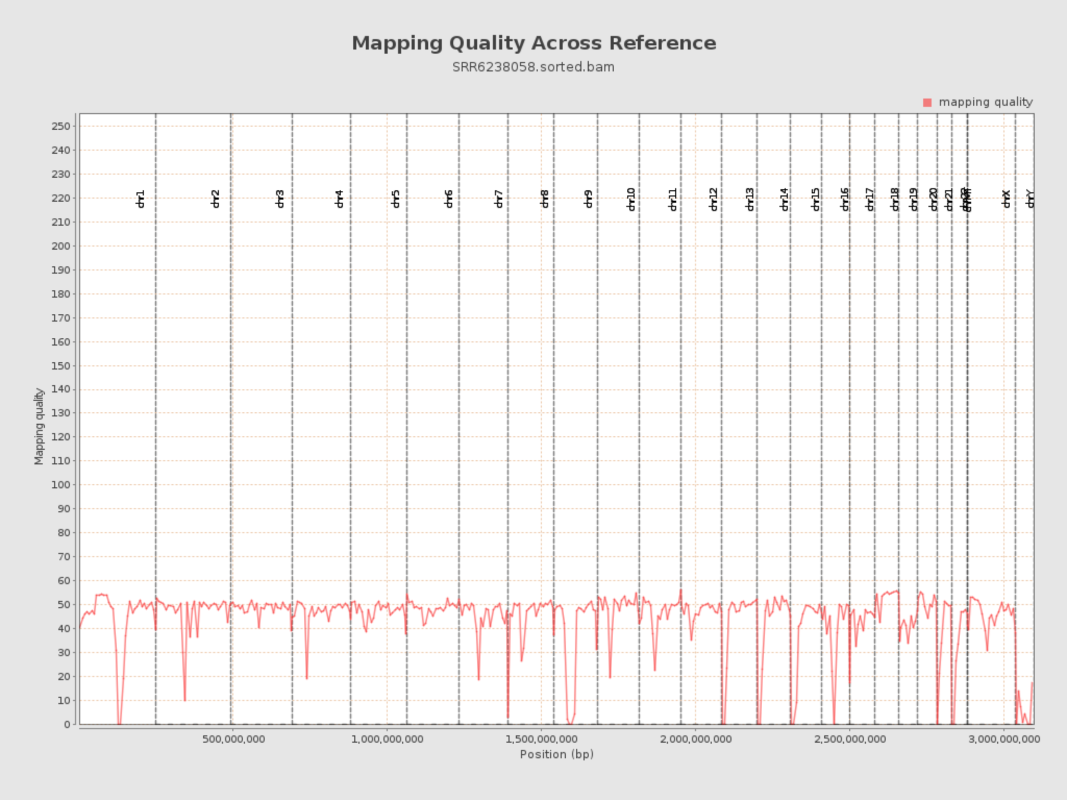
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram