

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:30:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238263.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_SRR6238263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:30:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,485,513
Mapped reads	1,163,420 / 78.32%
Unmapped reads	322,093 / 21.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,789 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	133,522 / 8.99%
Duplication rate	9.07%
Clipped reads	668,143 / 44.98%

2.2. ACGT Content

Number/percentage of A's	20,515,788 / 27.61%
Number/percentage of C's	14,322,834 / 19.27%
Number/percentage of T's	22,832,499 / 30.72%
Number/percentage of G's	16,629,055 / 22.38%
Number/percentage of N's	16,458 / 0.02%
GC Percentage	41.65%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2783
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.1
----------------------	------

2.5. Mismatches and indels

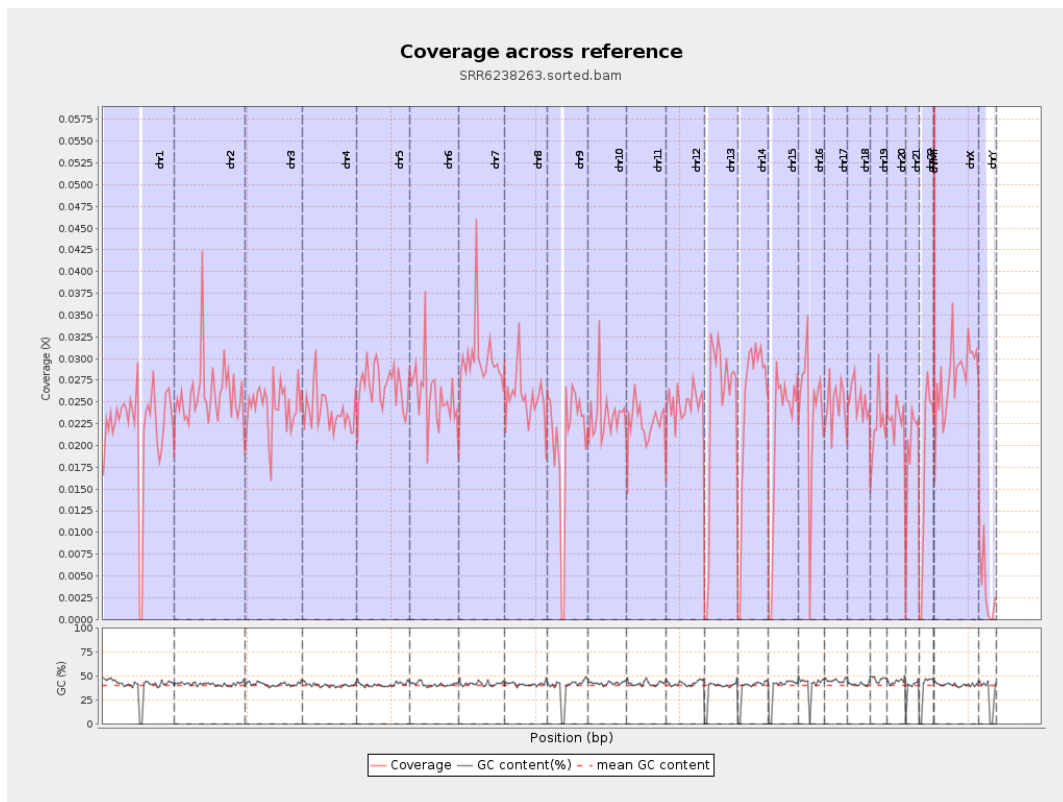
General error rate	1.03%
Mismatches	752,242
Insertions	6,014
Mapped reads with at least one insertion	0.51%
Deletions	29,373
Mapped reads with at least one deletion	2.49%
Homopolymer indels	46.76%

2.6. Chromosome stats

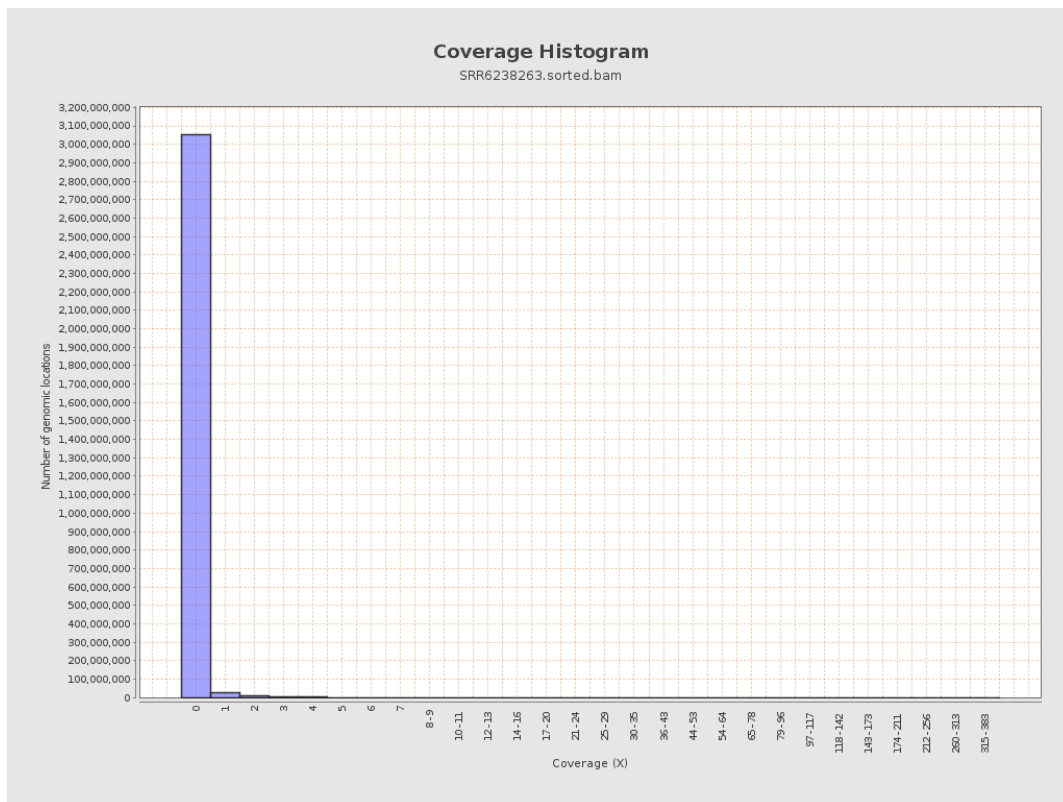
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5445015	0.0218	0.3234
chr2	243199373	6302148	0.0259	0.3357
chr3	198022430	4845687	0.0245	0.2328
chr4	191154276	4577804	0.0239	0.252
chr5	180915260	4876894	0.027	0.2459
chr6	171115067	4402893	0.0257	0.2813
chr7	159138663	4755346	0.0299	0.3861

chr8	146364022	3733310	0.0255	0.3325
chr9	141213431	2903032	0.0206	0.2467
chr10	135534747	3176130	0.0234	0.2632
chr11	135006516	3073235	0.0228	0.2445
chr12	133851895	3330484	0.0249	0.2374
chr13	115169878	2765915	0.024	0.2369
chr14	107349540	2650170	0.0247	0.2821
chr15	102531392	2186659	0.0213	0.2788
chr16	90354753	2148822	0.0238	0.2355
chr17	81195210	1998499	0.0246	0.2412
chr18	78077248	1964688	0.0252	0.3397
chr19	59128983	1329489	0.0225	0.2789
chr20	63025520	1450964	0.023	0.2284
chr21	48129895	951146	0.0198	0.2131
chr22	51304566	924949	0.018	0.1995
chrMT	16571	9948	0.6003	1.1696
chrX	155270560	4359535	0.0281	0.2658
chrY	59373566	202186	0.0034	0.1042

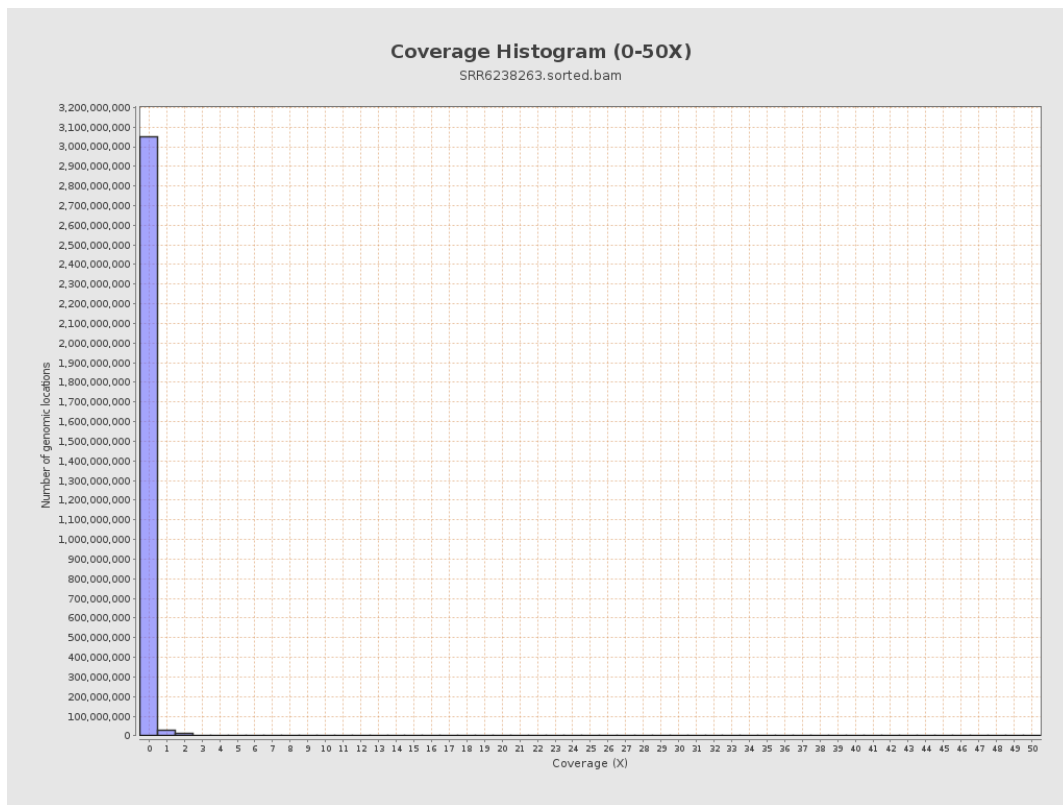
3. Results : Coverage across reference



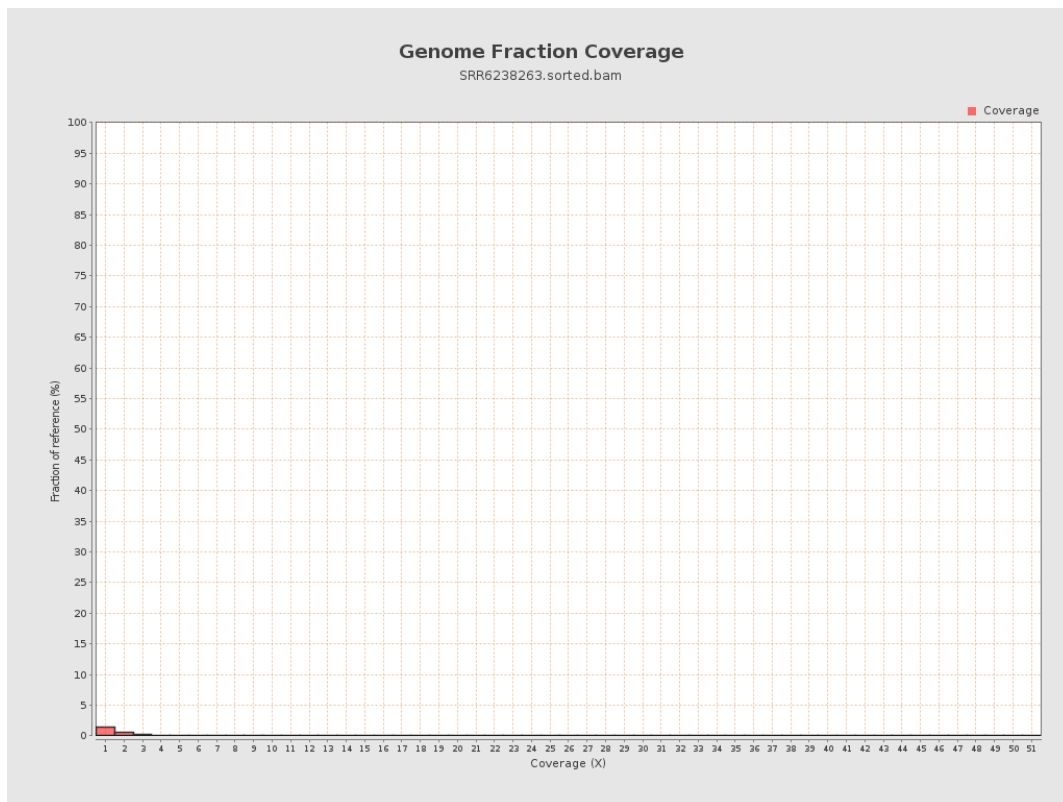
4. Results : Coverage Histogram



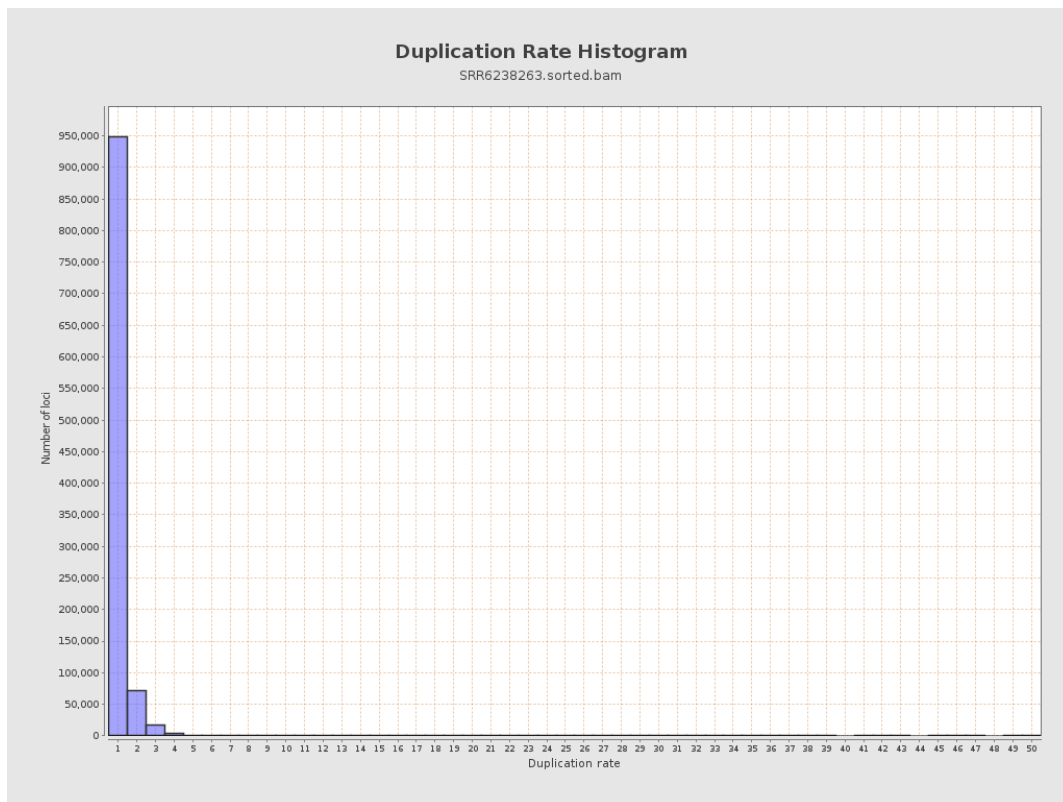
5. Results : Coverage Histogram (0-50X)



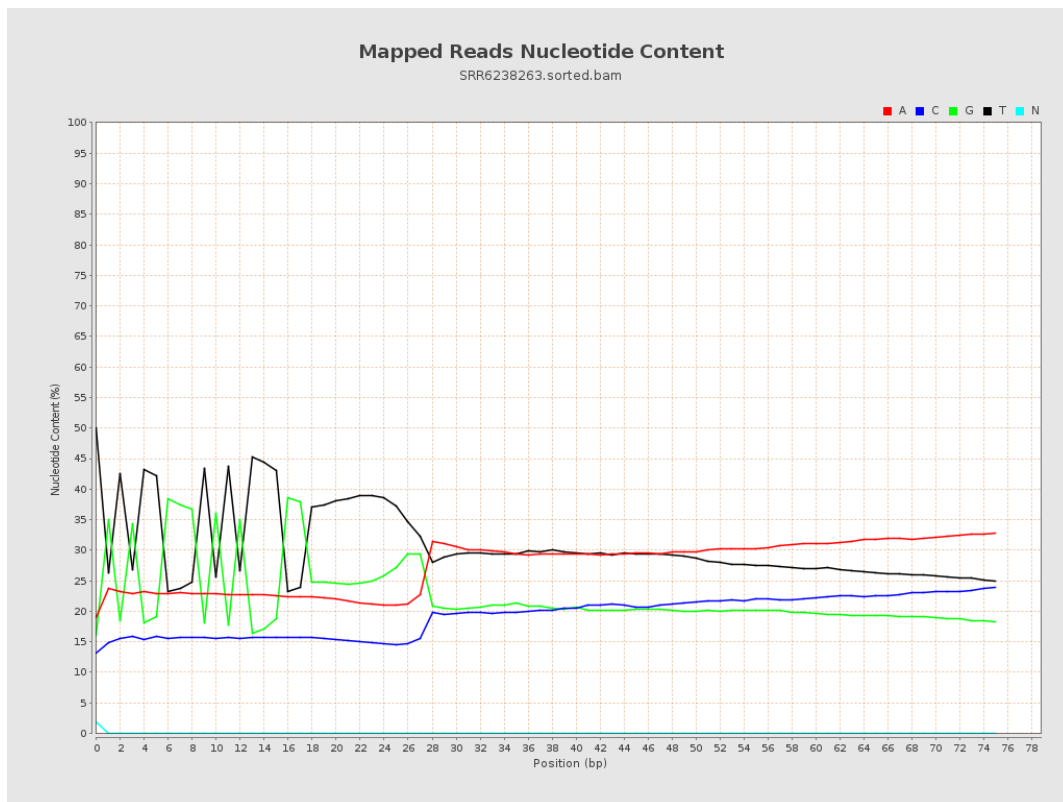
6. Results : Genome Fraction Coverage



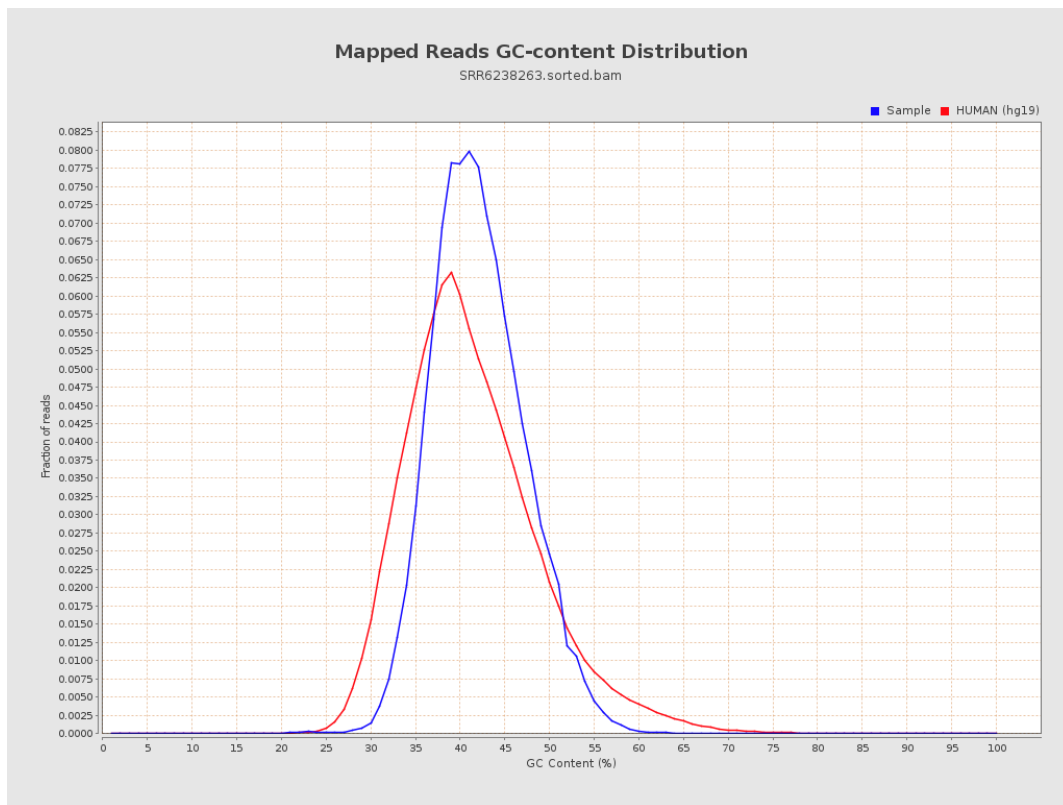
7. Results : Duplication Rate Histogram



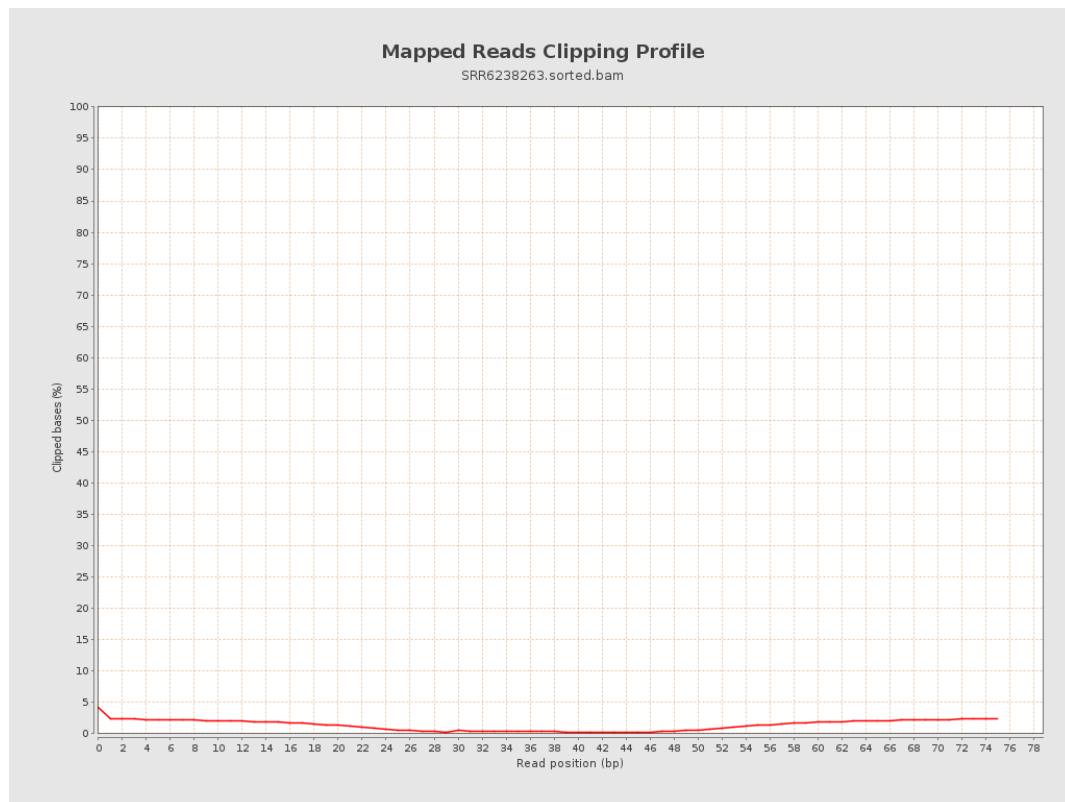
8. Results : Mapped Reads Nucleotide Content



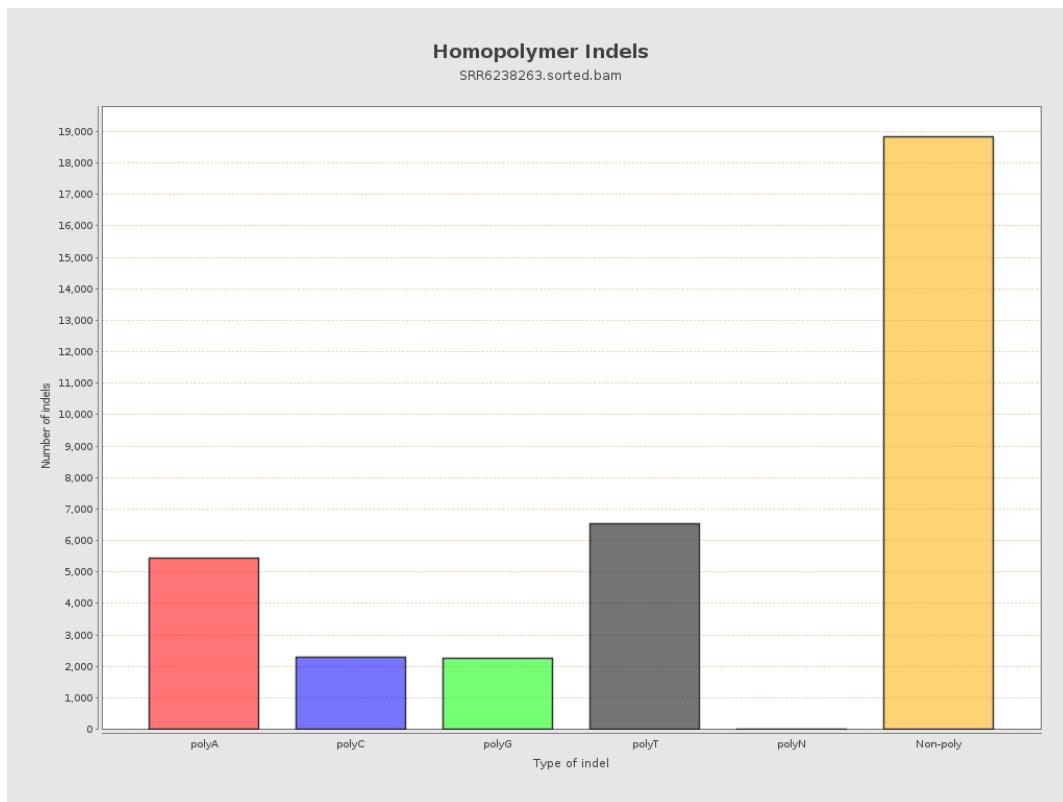
9. Results : Mapped Reads GC-content Distribution



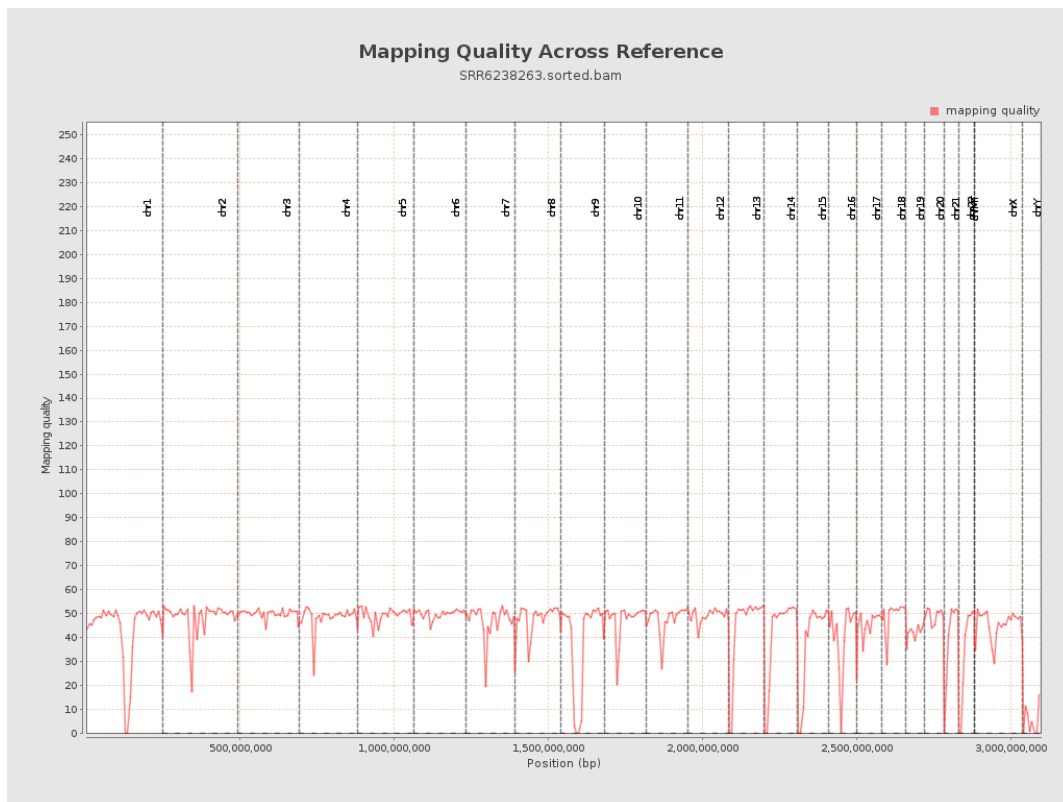
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

