

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 23:02:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237261.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_SRR6237261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237261.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 23:02:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,903,370
Mapped reads	2,617,993 / 90.17%
Unmapped reads	285,377 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,824 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	343,639 / 11.84%
Duplication rate	11.07%
Clipped reads	1,634,284 / 56.29%

2.2. ACGT Content

Number/percentage of A's	42,467,335 / 26.22%
Number/percentage of C's	27,953,873 / 17.26%
Number/percentage of T's	54,138,906 / 33.42%
Number/percentage of G's	37,411,614 / 23.1%
Number/percentage of N's	17,753 / 0.01%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0524

Standard Deviation	0.6034
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2.4. Mapping Quality

Mean Mapping Quality	43.7
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2.5. Mismatches and indels

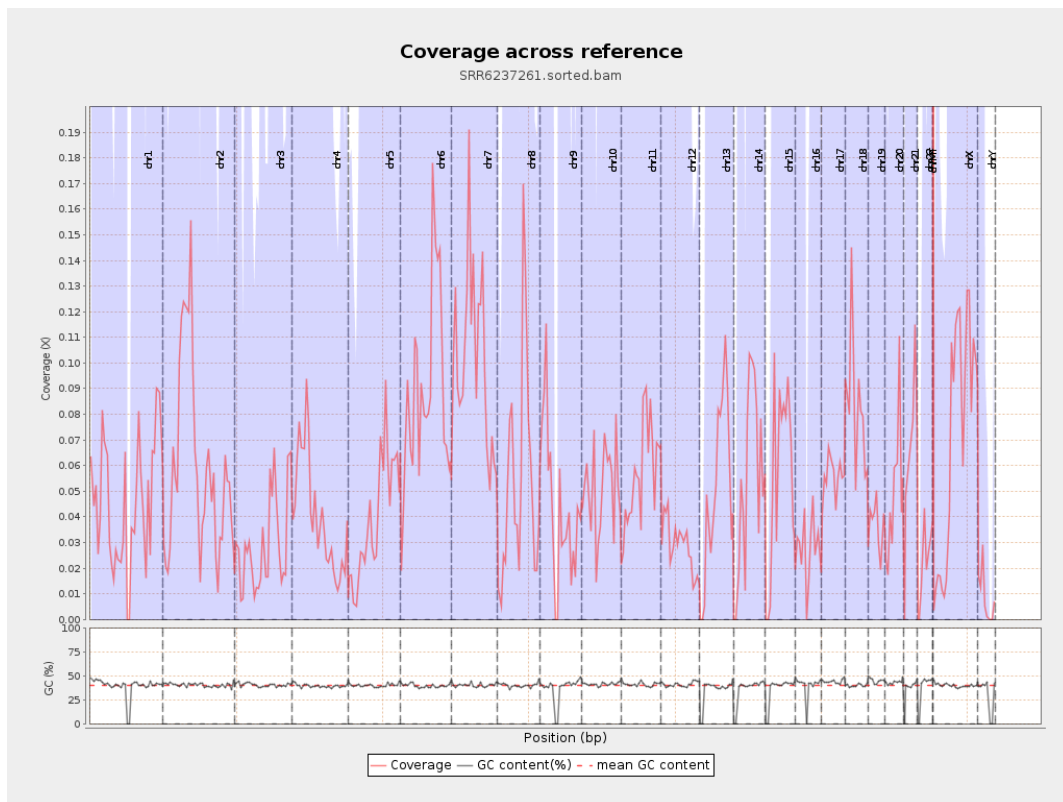
General error rate	0.63%
Mismatches	1,000,121
Insertions	11,309
Mapped reads with at least one insertion	0.43%
Deletions	56,296
Mapped reads with at least one deletion	2.12%
Homopolymer indels	42.34%

2.6. Chromosome stats

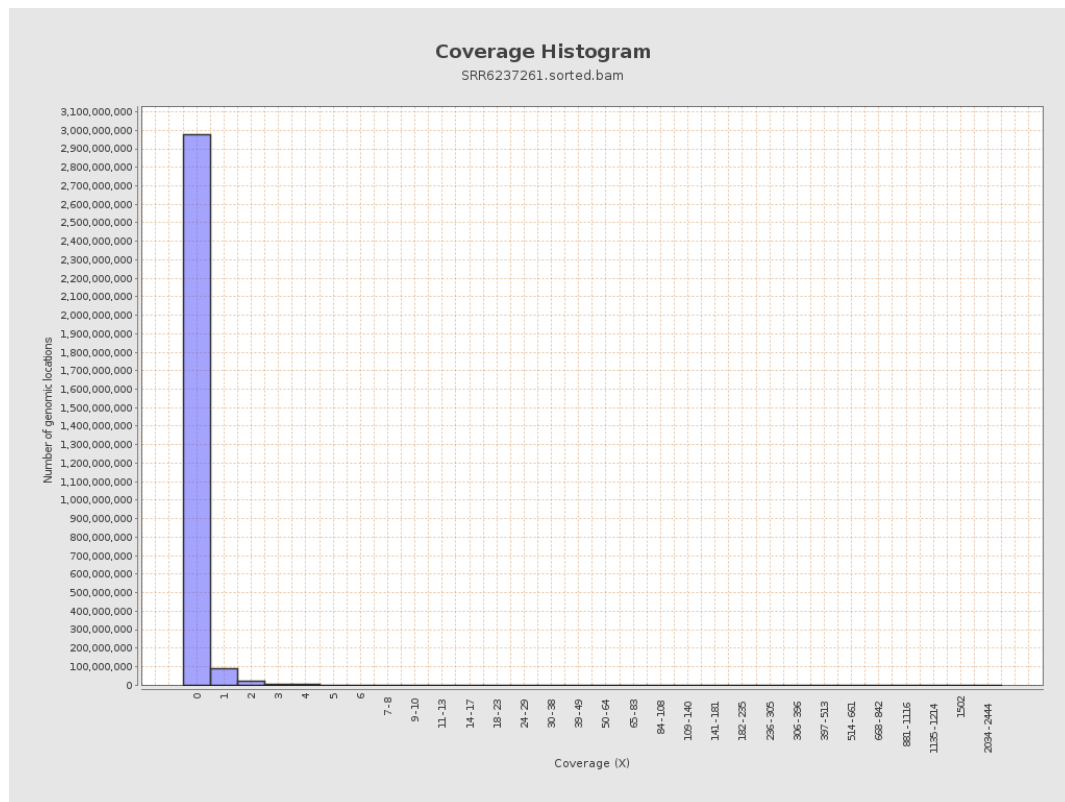
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11358767	0.0456	0.6239
chr2	243199373	14459725	0.0595	1.2034
chr3	198022430	5702442	0.0288	0.2263
chr4	191154276	7698270	0.0403	0.3496
chr5	180915260	7168887	0.0396	0.2674
chr6	171115067	15268254	0.0892	0.5735
chr7	159138663	16156438	0.1015	1.0525

chr8	146364022	7699189	0.0526	0.8264
chr9	141213431	6107556	0.0433	0.4227
chr10	135534747	6857010	0.0506	0.4807
chr11	135006516	7624357	0.0565	0.4089
chr12	133851895	3887618	0.029	0.2569
chr13	115169878	5912310	0.0513	0.3458
chr14	107349540	5858758	0.0546	0.3304
chr15	102531392	5626959	0.0549	0.3409
chr16	90354753	2467473	0.0273	0.2777
chr17	81195210	4496585	0.0554	0.3754
chr18	78077248	6625251	0.0849	1.1334
chr19	59128983	2201894	0.0372	0.4152
chr20	63025520	3104019	0.0493	0.3003
chr21	48129895	3208196	0.0667	0.3846
chr22	51304566	1110040	0.0216	0.1844
chrMT	16571	14444	0.8716	1.2537
chrX	155270560	10961170	0.0706	0.3938
chrY	59373566	511855	0.0086	0.282

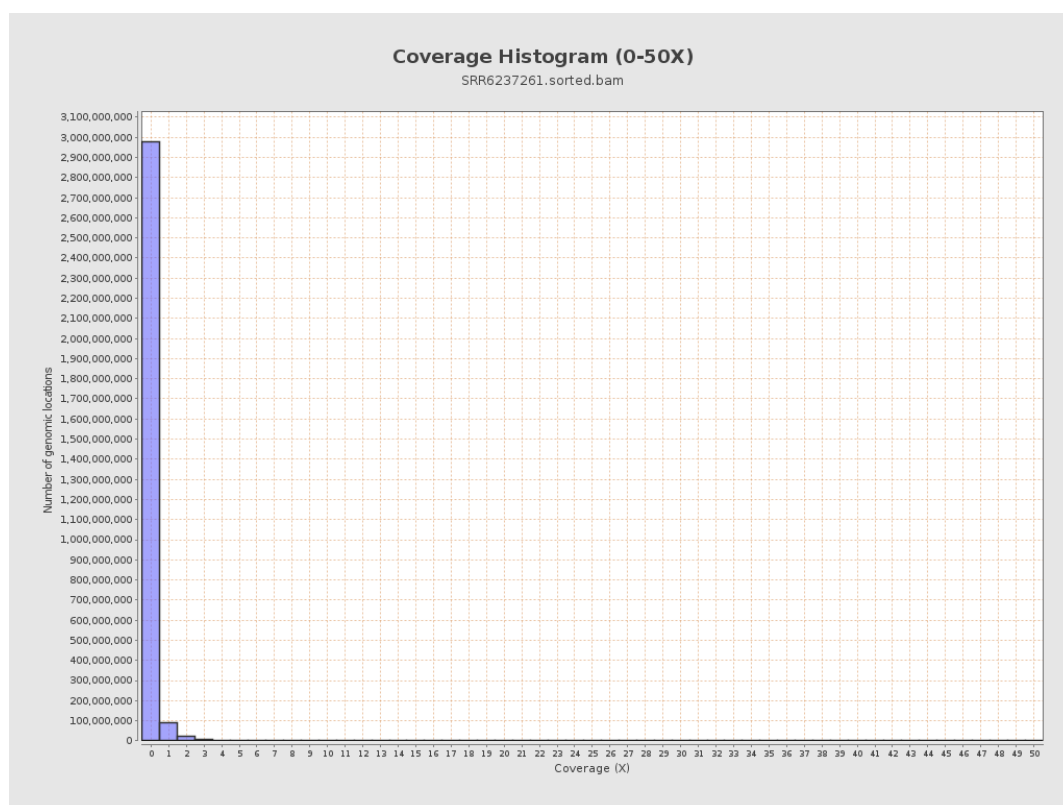
3. Results : Coverage across reference



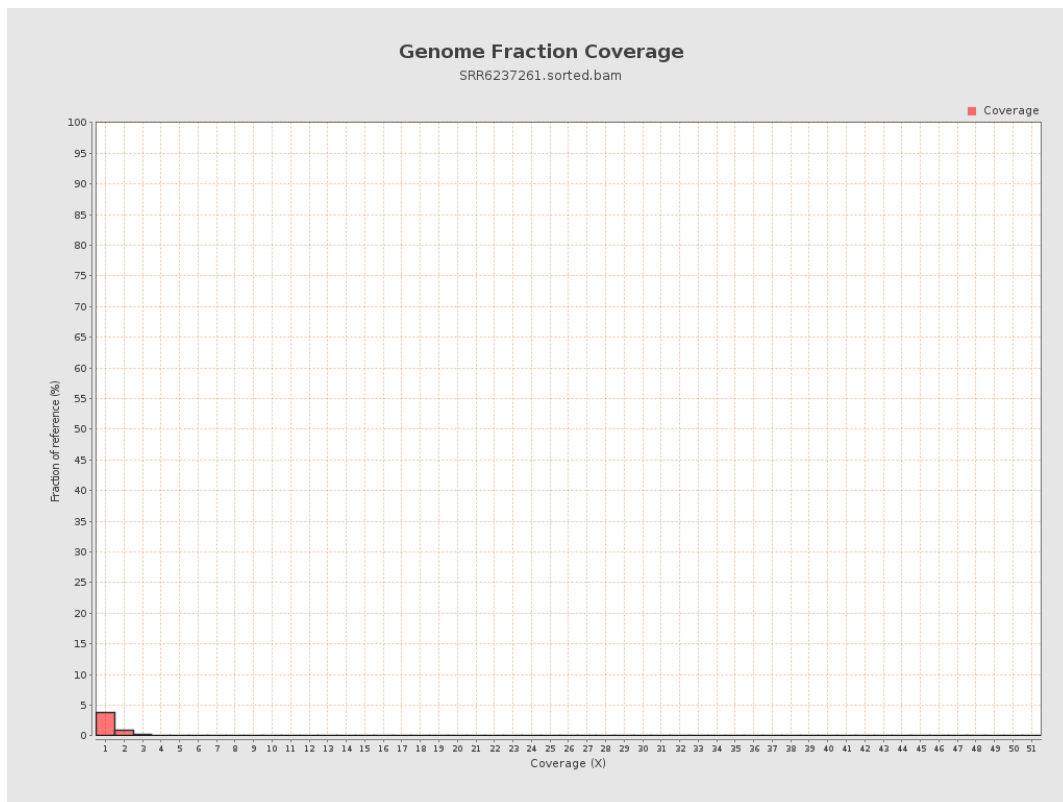
4. Results : Coverage Histogram



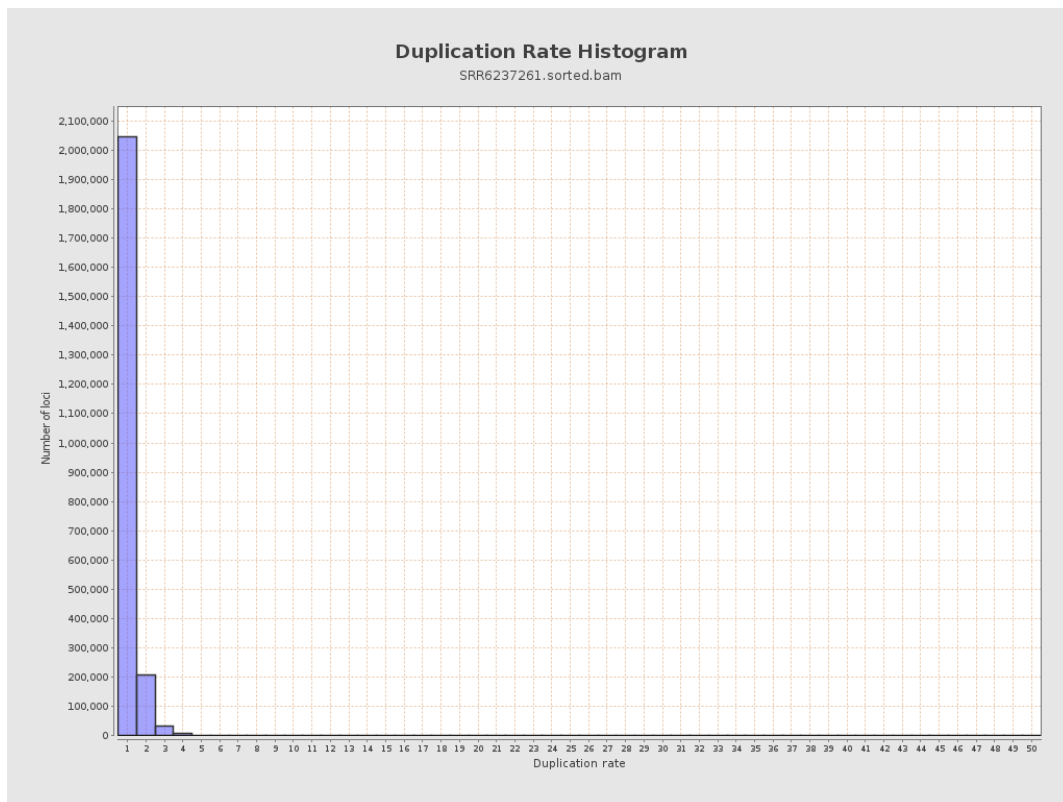
5. Results : Coverage Histogram (0-50X)



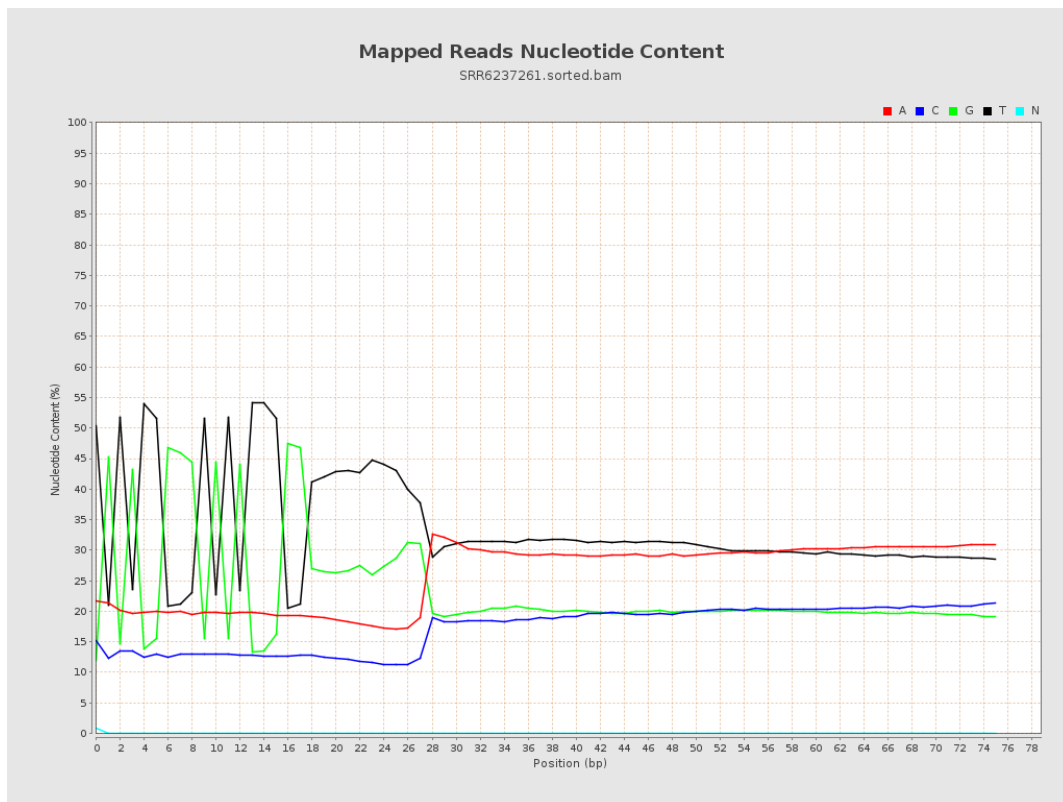
6. Results : Genome Fraction Coverage



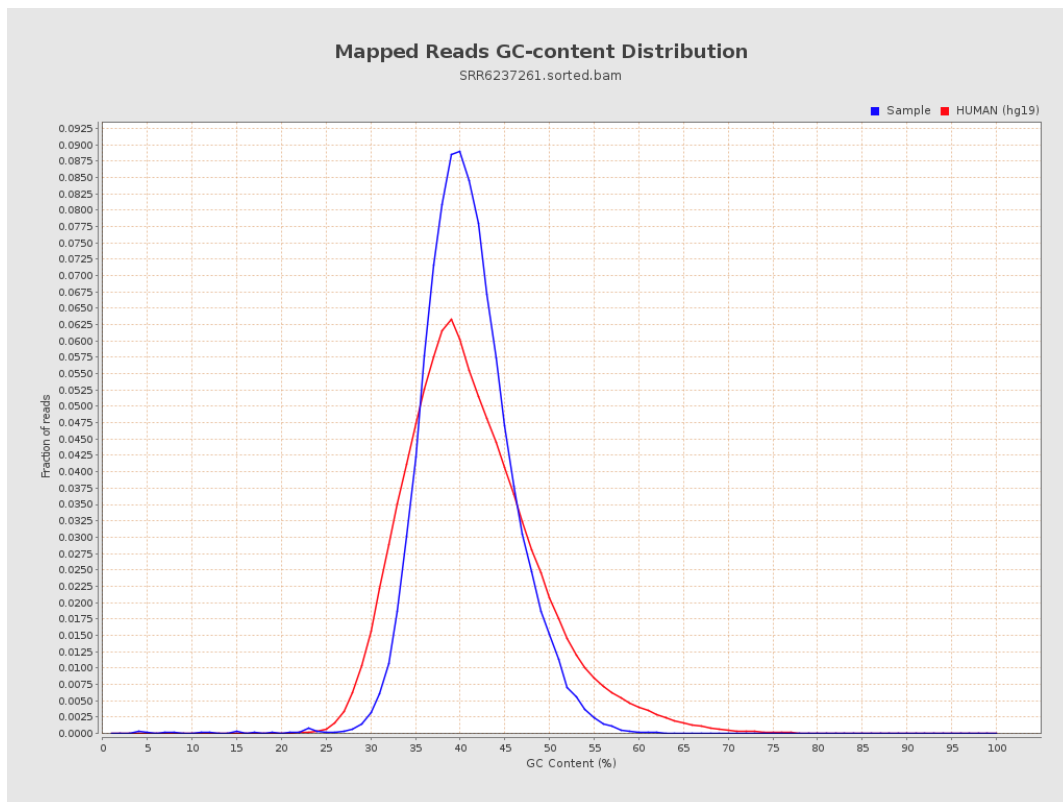
7. Results : Duplication Rate Histogram



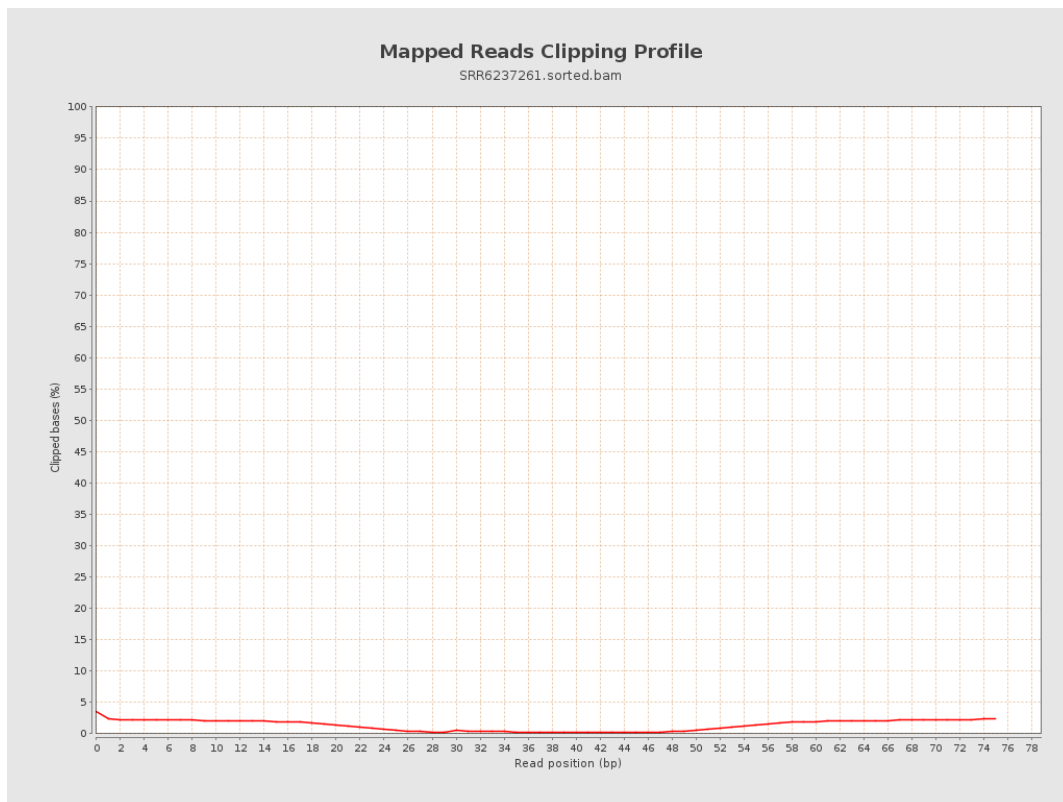
8. Results : Mapped Reads Nucleotide Content



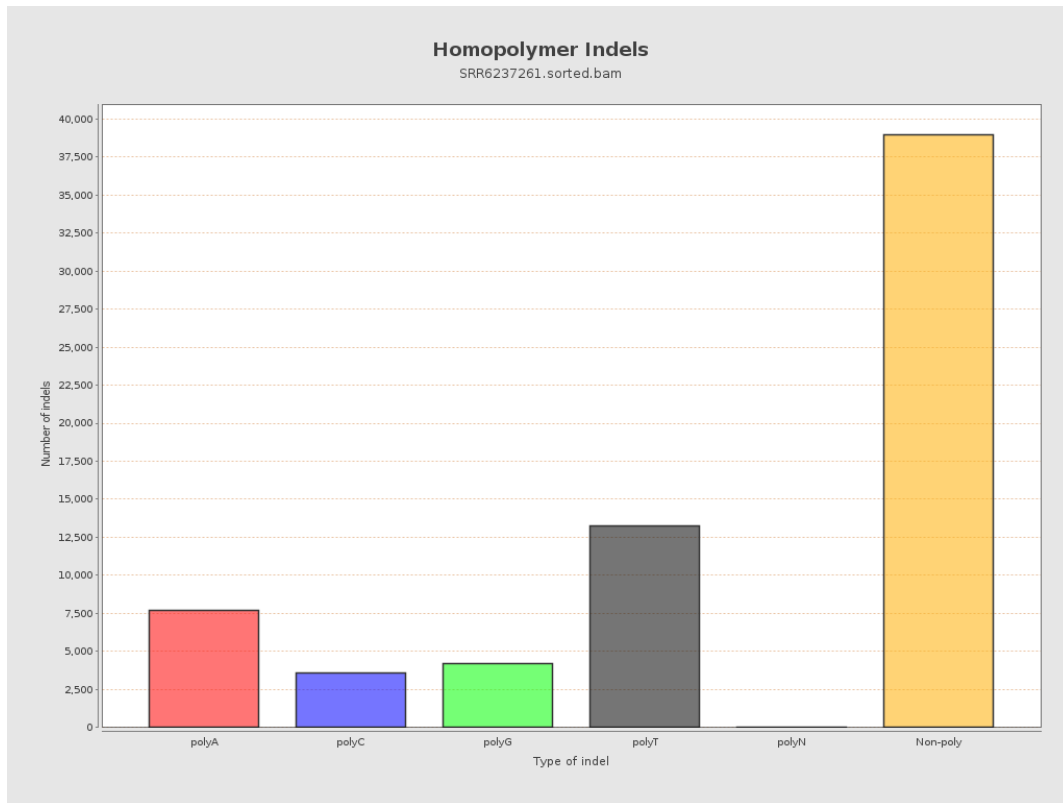
9. Results : Mapped Reads GC-content Distribution



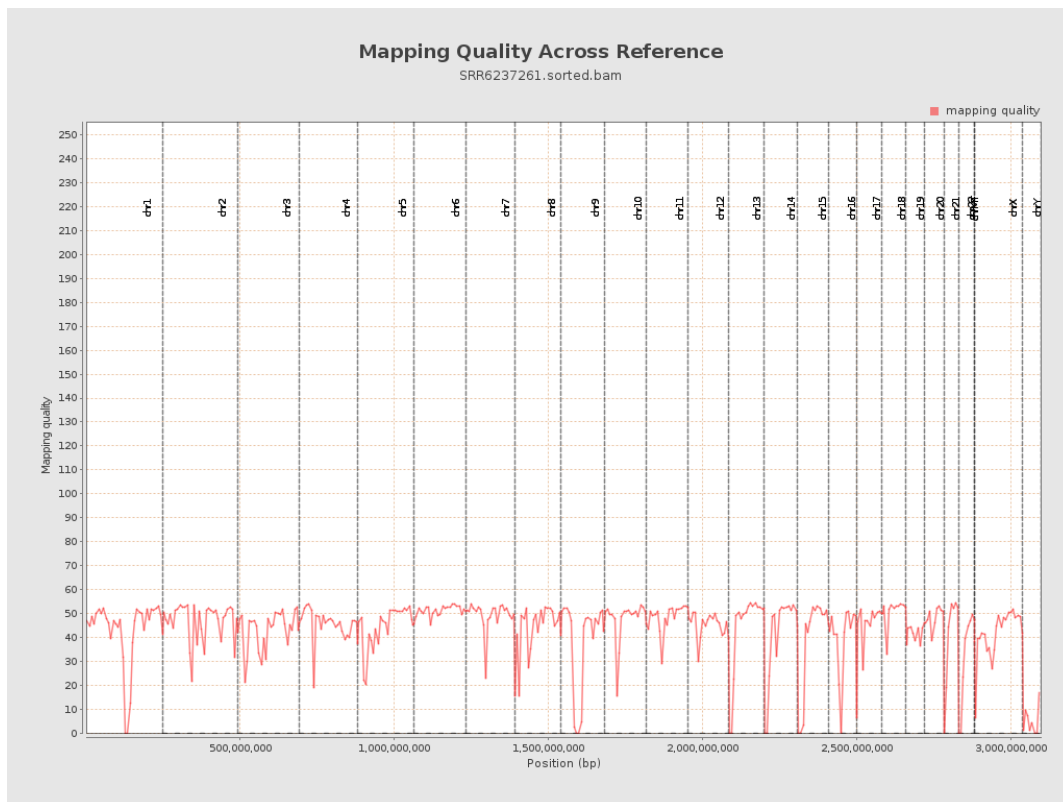
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

