

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:35:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231837.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_SRR6231837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:35:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,456,816
Mapped reads	3,865,052 / 86.72%
Unmapped reads	591,764 / 13.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,899 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	713,795 / 16.02%
Duplication rate	14.51%
Clipped reads	2,161,577 / 48.5%

2.2. ACGT Content

Number/percentage of A's	61,637,055 / 25.25%
Number/percentage of C's	43,519,515 / 17.83%
Number/percentage of T's	80,592,824 / 33.02%
Number/percentage of G's	58,249,240 / 23.86%
Number/percentage of N's	90,954 / 0.04%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0789

Standard Deviation	0.8773
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2.4. Mapping Quality

Mean Mapping Quality	45.66
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2.5. Mismatches and indels

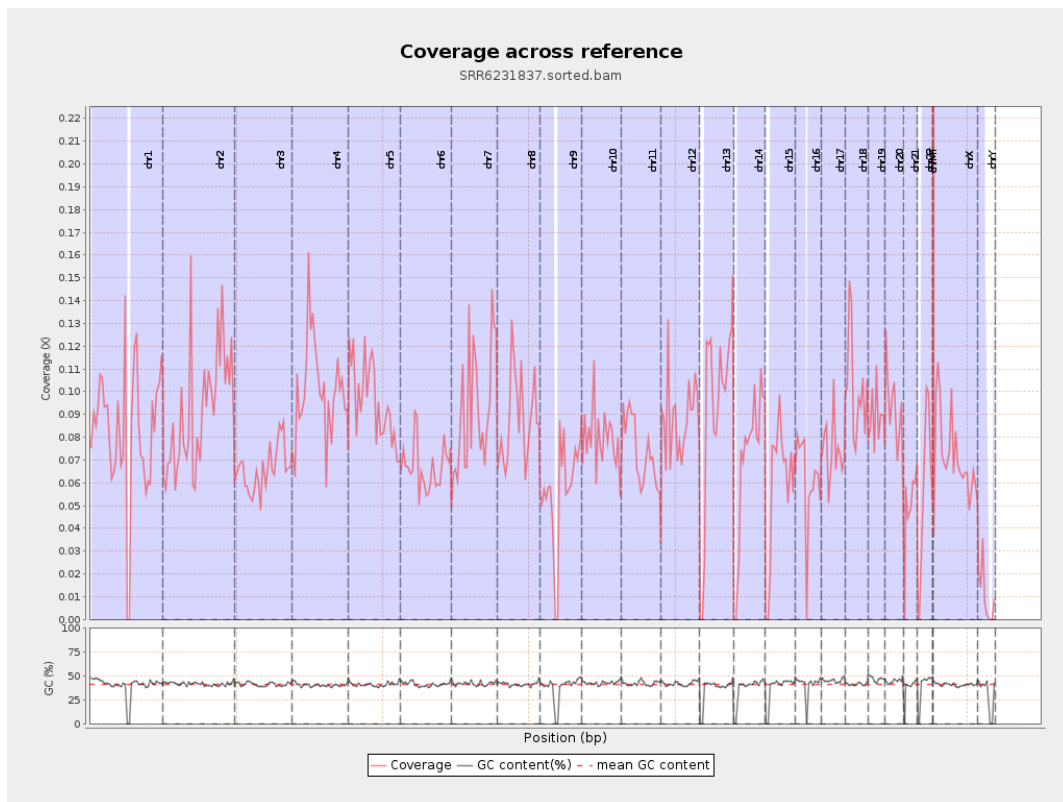
General error rate	0.63%
Mismatches	1,502,545
Insertions	15,188
Mapped reads with at least one insertion	0.39%
Deletions	53,176
Mapped reads with at least one deletion	1.36%
Homopolymer indels	44.45%

2.6. Chromosome stats

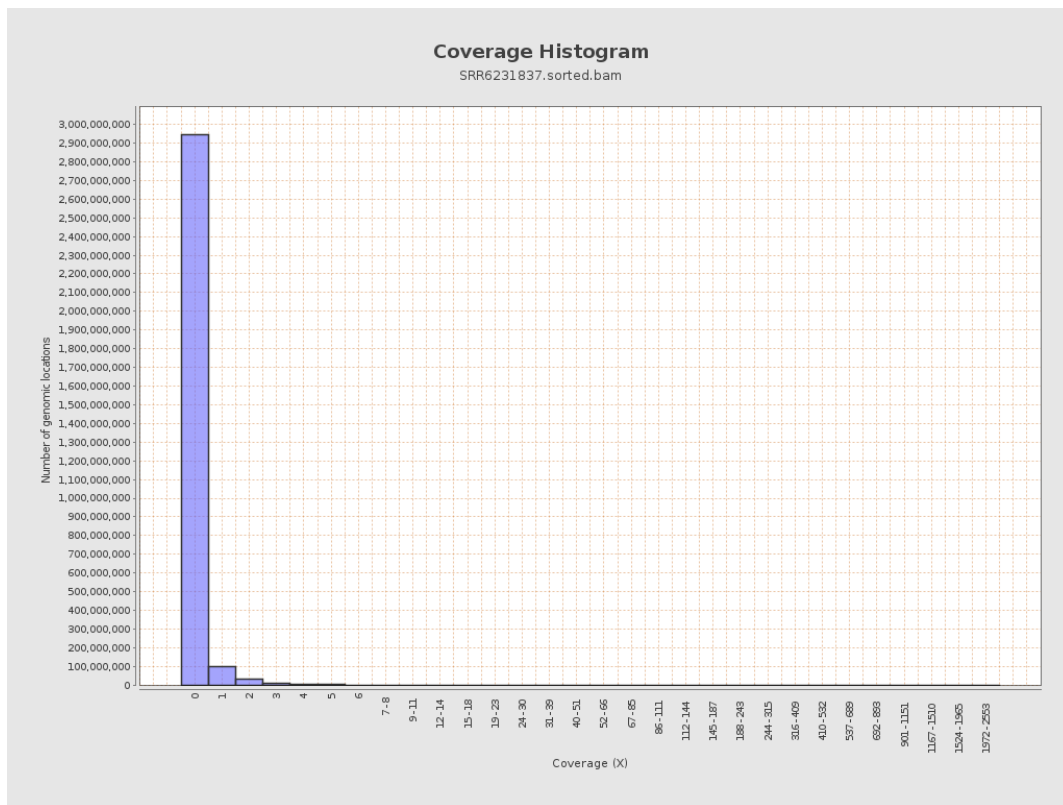
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20542052	0.0824	1.8599
chr2	243199373	22252354	0.0915	1.4301
chr3	198022430	13101819	0.0662	0.3882
chr4	191154276	19315335	0.101	0.5044
chr5	180915260	17240668	0.0953	0.4682
chr6	171115067	11458048	0.067	0.6433
chr7	159138663	14565738	0.0915	0.9284

chr8	146364022	12912665	0.0882	0.8244
chr9	141213431	8052647	0.057	0.6608
chr10	135534747	10694506	0.0789	0.6113
chr11	135006516	9920810	0.0735	0.5626
chr12	133851895	11827502	0.0884	0.465
chr13	115169878	10649738	0.0925	0.497
chr14	107349540	7525866	0.0701	0.4233
chr15	102531392	5960115	0.0581	0.4059
chr16	90354753	5451303	0.0603	0.4234
chr17	81195210	6056569	0.0746	0.4847
chr18	78077248	8007341	0.1026	1.4289
chr19	59128983	5245573	0.0887	1.114
chr20	63025520	5878398	0.0933	0.5053
chr21	48129895	2446878	0.0508	0.3771
chr22	51304566	2961902	0.0577	0.3607
chrMT	16571	390034	23.5371	13.52
chrX	155270560	11100651	0.0715	0.4663
chrY	59373566	627212	0.0106	0.2748

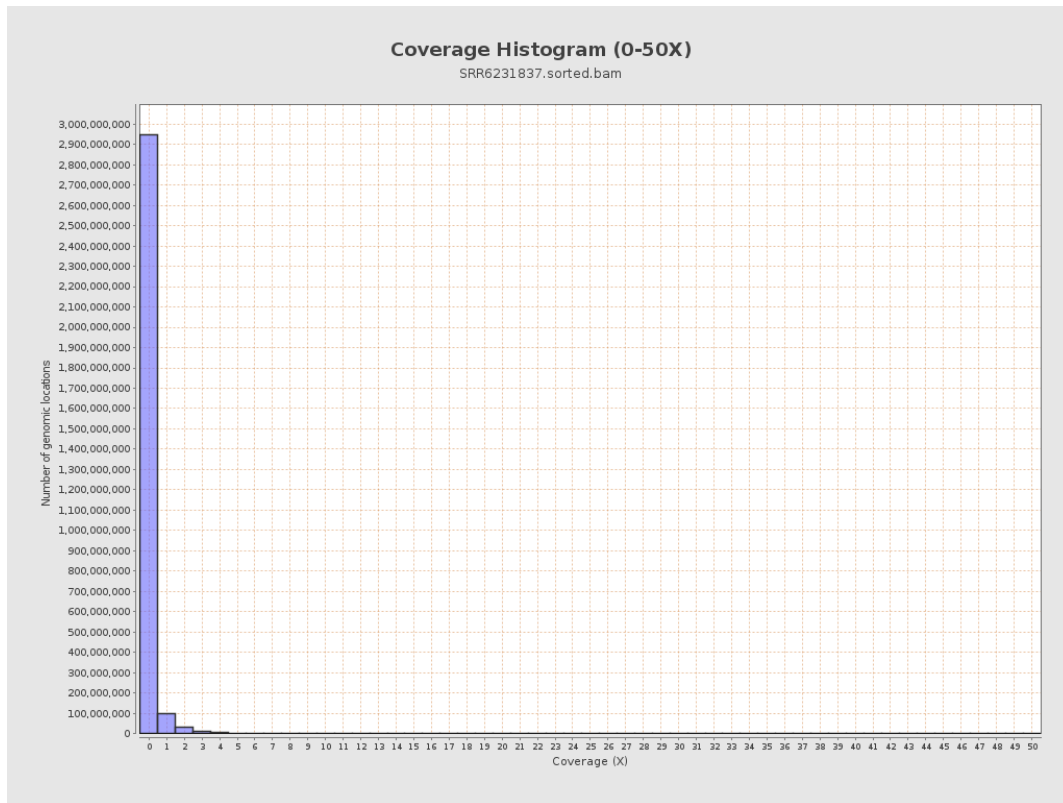
3. Results : Coverage across reference



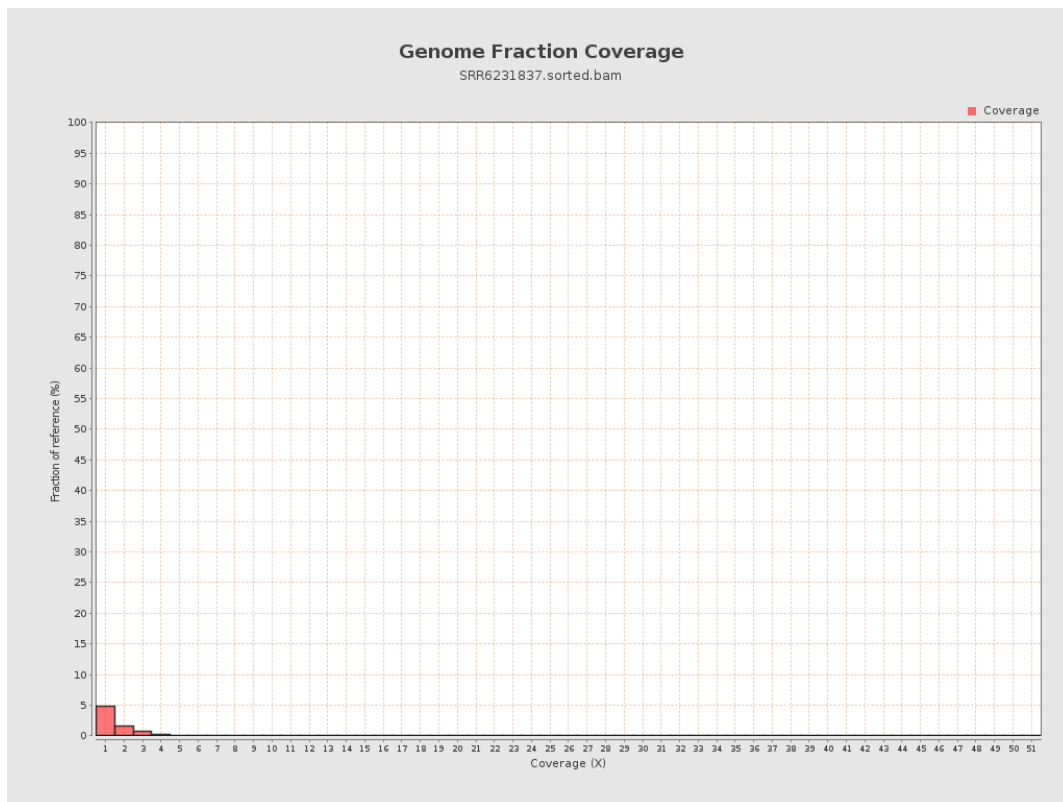
4. Results : Coverage Histogram



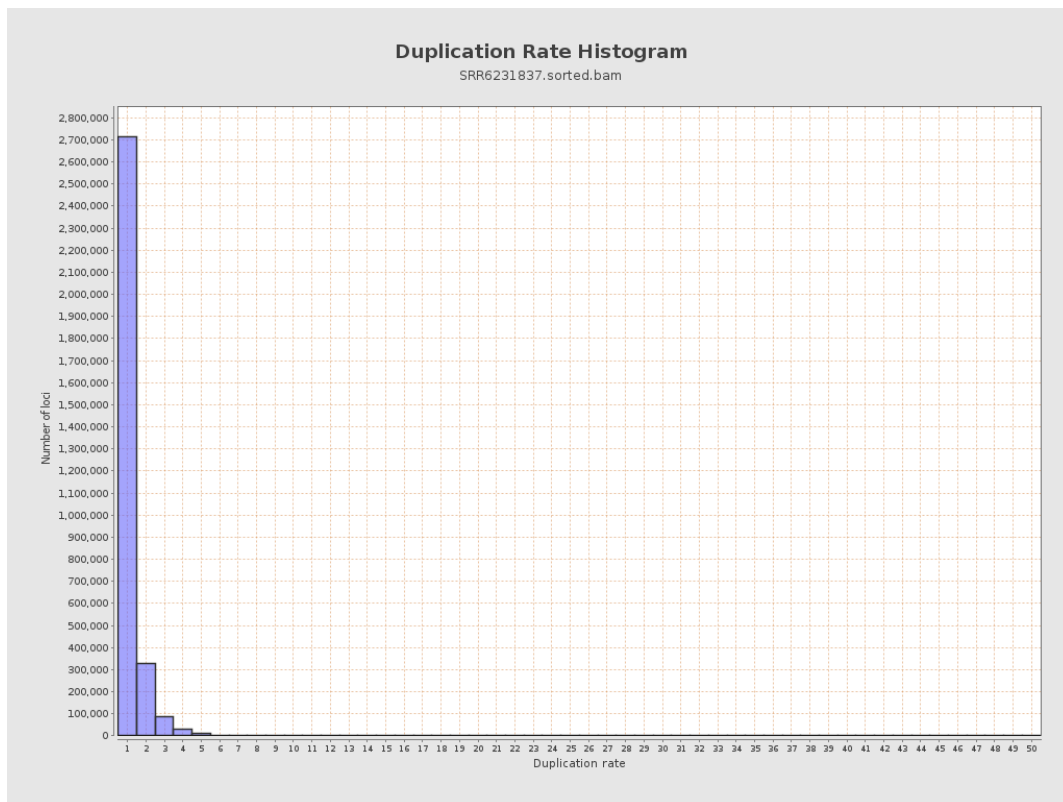
5. Results : Coverage Histogram (0-50X)



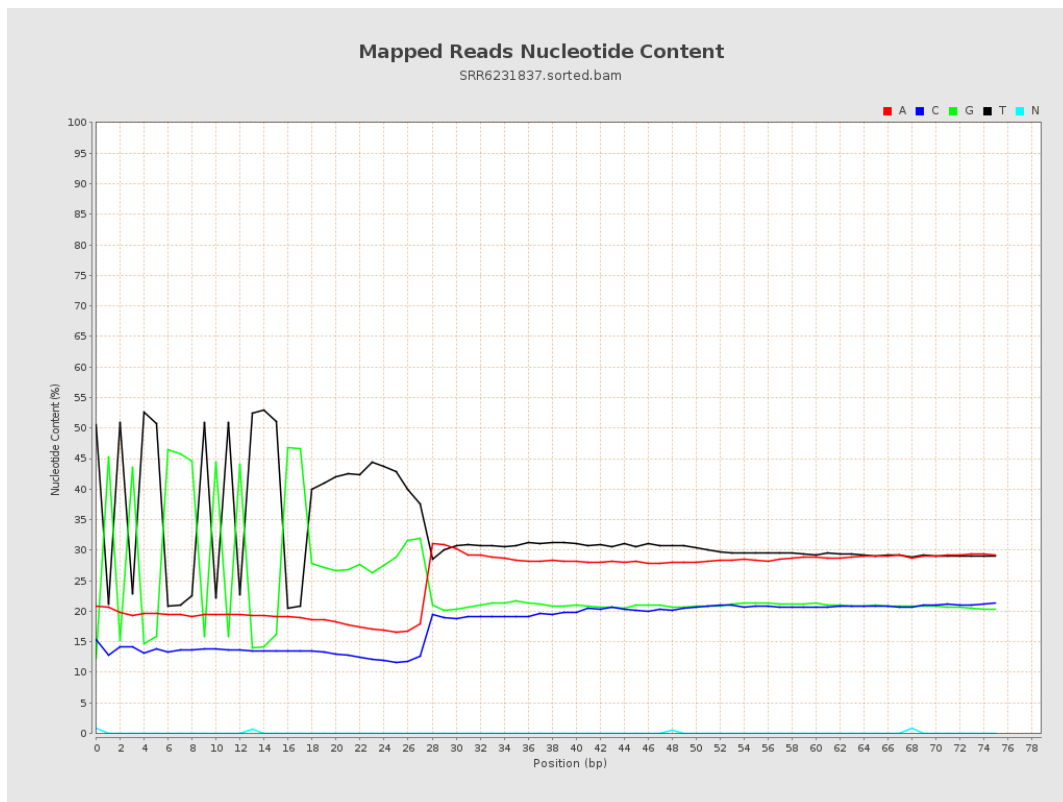
6. Results : Genome Fraction Coverage



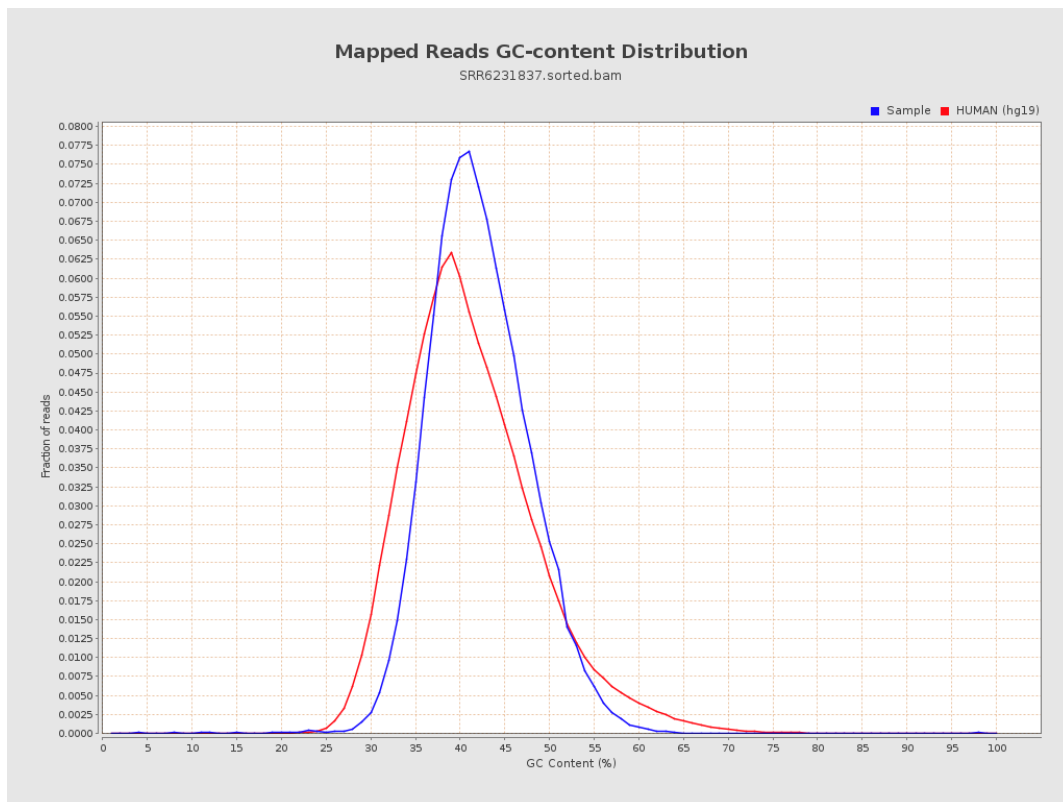
7. Results : Duplication Rate Histogram



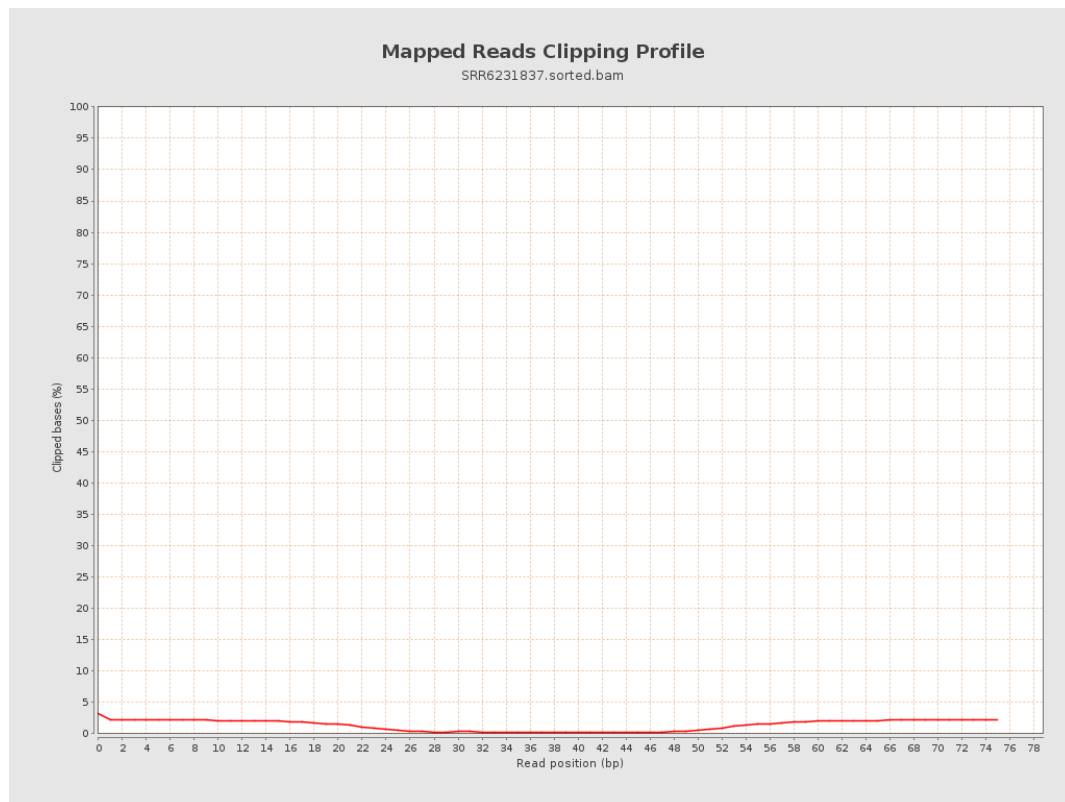
8. Results : Mapped Reads Nucleotide Content



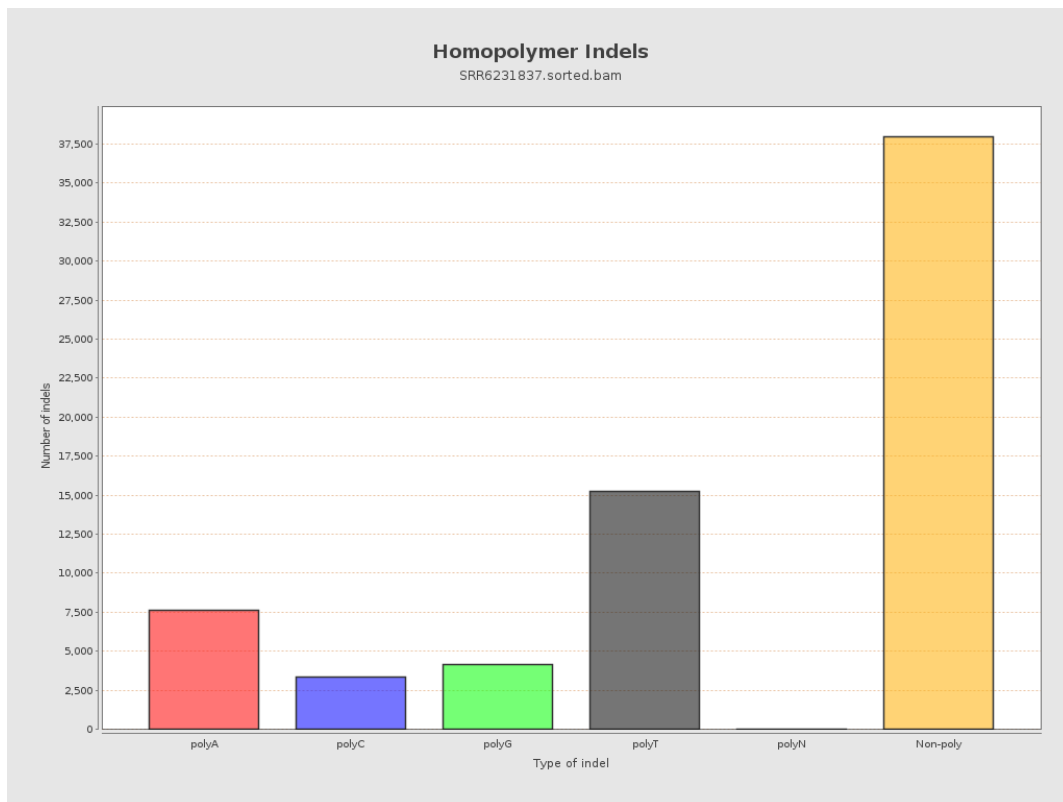
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

