

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:25:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237611.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_SRR6237611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:25:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,651,360
Mapped reads	1,461,306 / 88.49%
Unmapped reads	190,054 / 11.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,126 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	60,065 / 3.64%
Duplication rate	2.76%
Clipped reads	733,398 / 44.41%

2.2. ACGT Content

Number/percentage of A's	25,162,856 / 26.54%
Number/percentage of C's	16,886,848 / 17.81%
Number/percentage of T's	30,458,964 / 32.12%
Number/percentage of G's	22,155,453 / 23.37%
Number/percentage of N's	154,712 / 0.16%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.3678
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2.4. Mapping Quality

Mean Mapping Quality	44.26
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2.5. Mismatches and indels

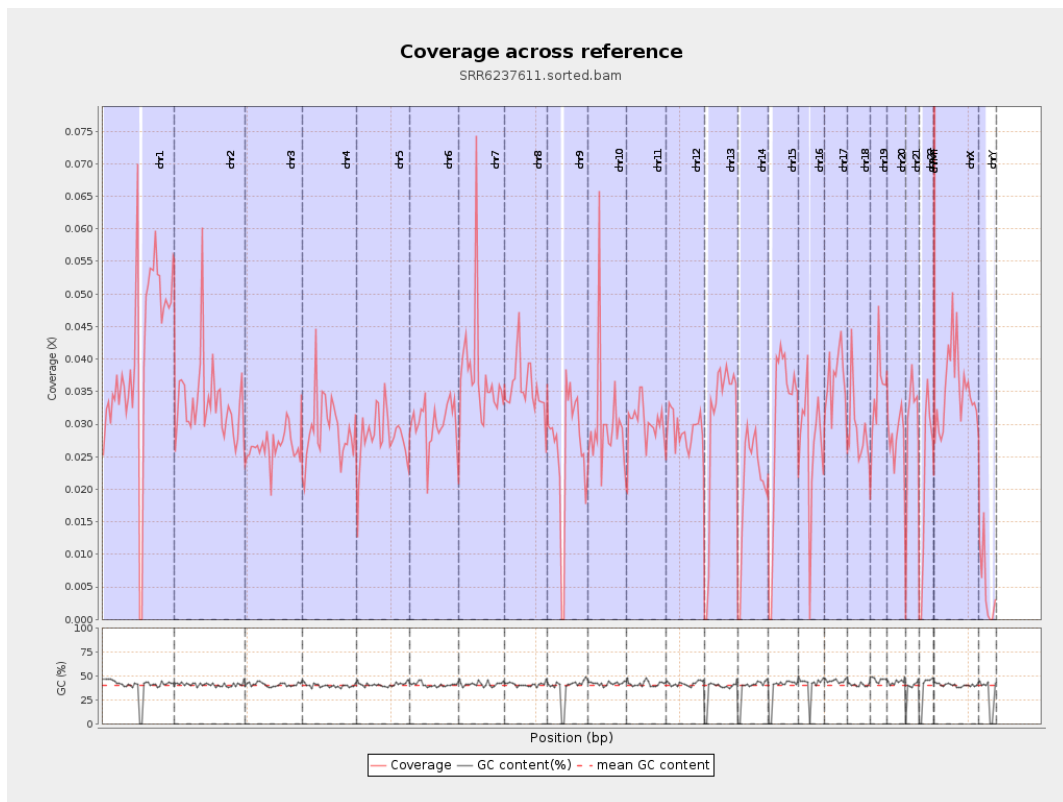
General error rate	0.87%
Mismatches	810,934
Insertions	8,689
Mapped reads with at least one insertion	0.59%
Deletions	26,681
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.43%

2.6. Chromosome stats

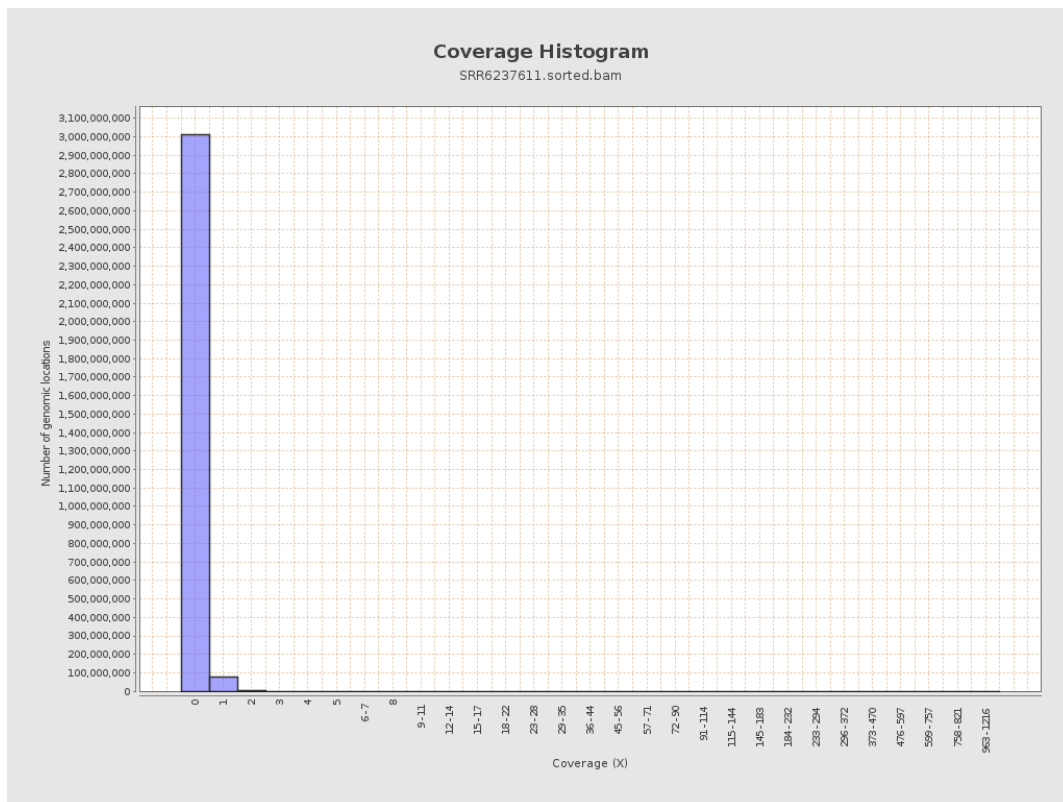
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10048641	0.0403	0.663
chr2	243199373	8055547	0.0331	0.5797
chr3	198022430	5264095	0.0266	0.1838
chr4	191154276	5571619	0.0291	0.2022
chr5	180915260	5112493	0.0283	0.185
chr6	171115067	5150098	0.0301	0.2664
chr7	159138663	5967949	0.0375	0.5826

chr8	146364022	5205406	0.0356	0.3967
chr9	141213431	3691773	0.0261	0.2931
chr10	135534747	4053168	0.0299	0.35
chr11	135006516	4112357	0.0305	0.2809
chr12	133851895	3892897	0.0291	0.1893
chr13	115169878	3442542	0.0299	0.195
chr14	107349540	2239138	0.0209	0.1786
chr15	102531392	3168590	0.0309	0.1986
chr16	90354753	2419800	0.0268	0.2248
chr17	81195210	2980784	0.0367	0.235
chr18	78077248	2269352	0.0291	0.5762
chr19	59128983	2071449	0.035	0.4235
chr20	63025520	1758478	0.0279	0.1967
chr21	48129895	1465646	0.0305	0.2099
chr22	51304566	1108638	0.0216	0.159
chrMT	16571	43038	2.5972	2.508
chrX	155270560	5481016	0.0353	0.2372
chrY	59373566	288585	0.0049	0.1342

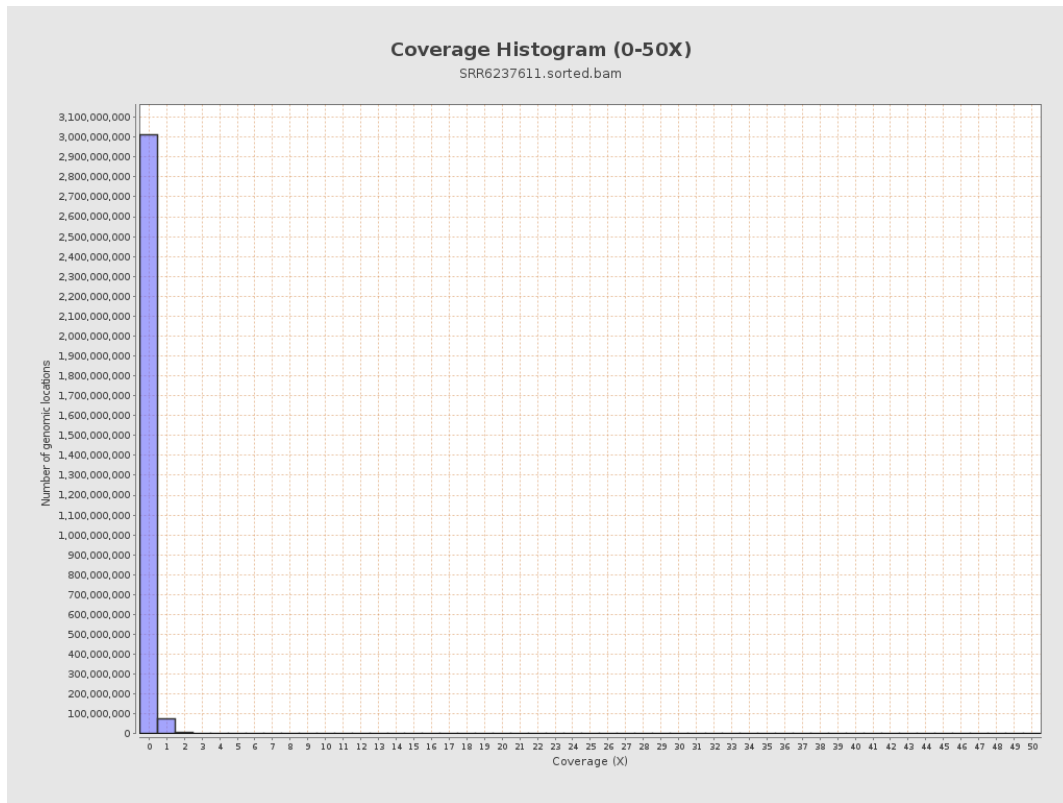
3. Results : Coverage across reference



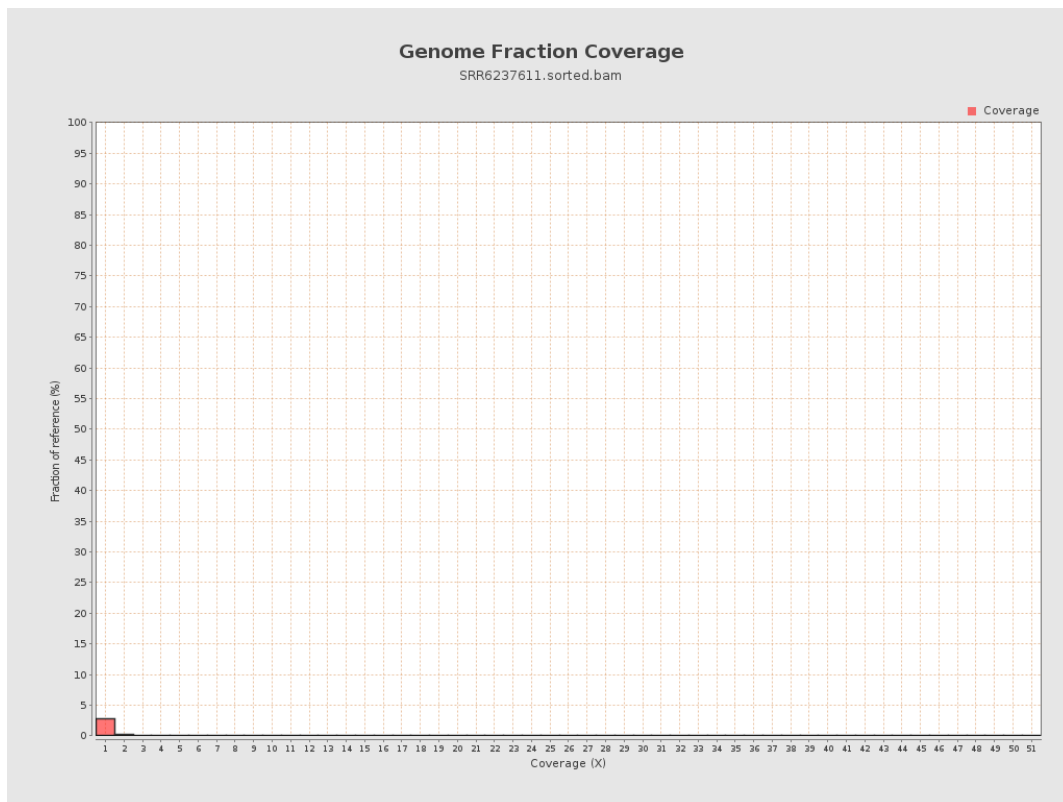
4. Results : Coverage Histogram



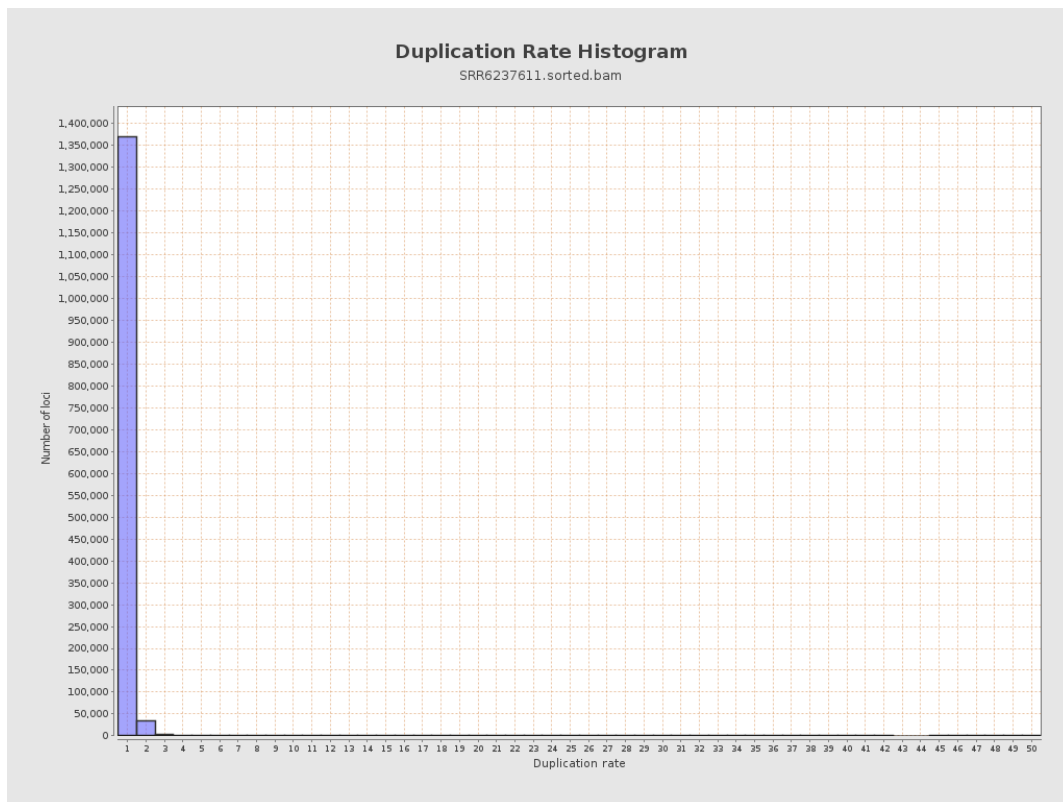
5. Results : Coverage Histogram (0-50X)



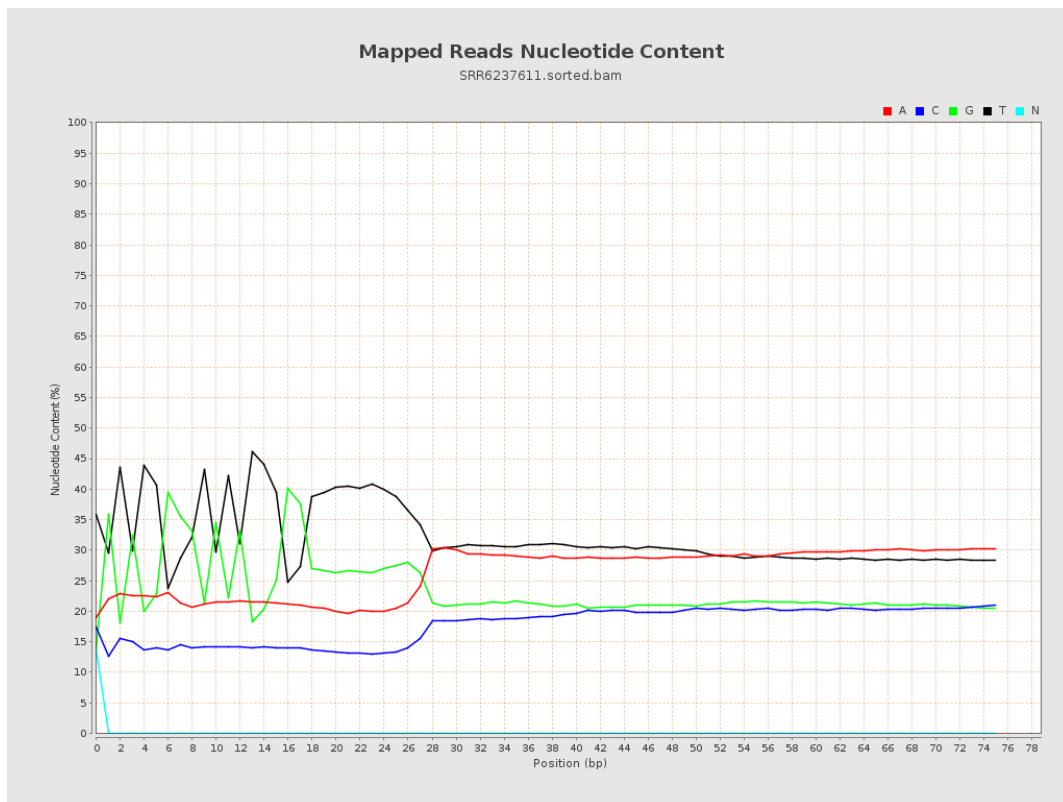
6. Results : Genome Fraction Coverage



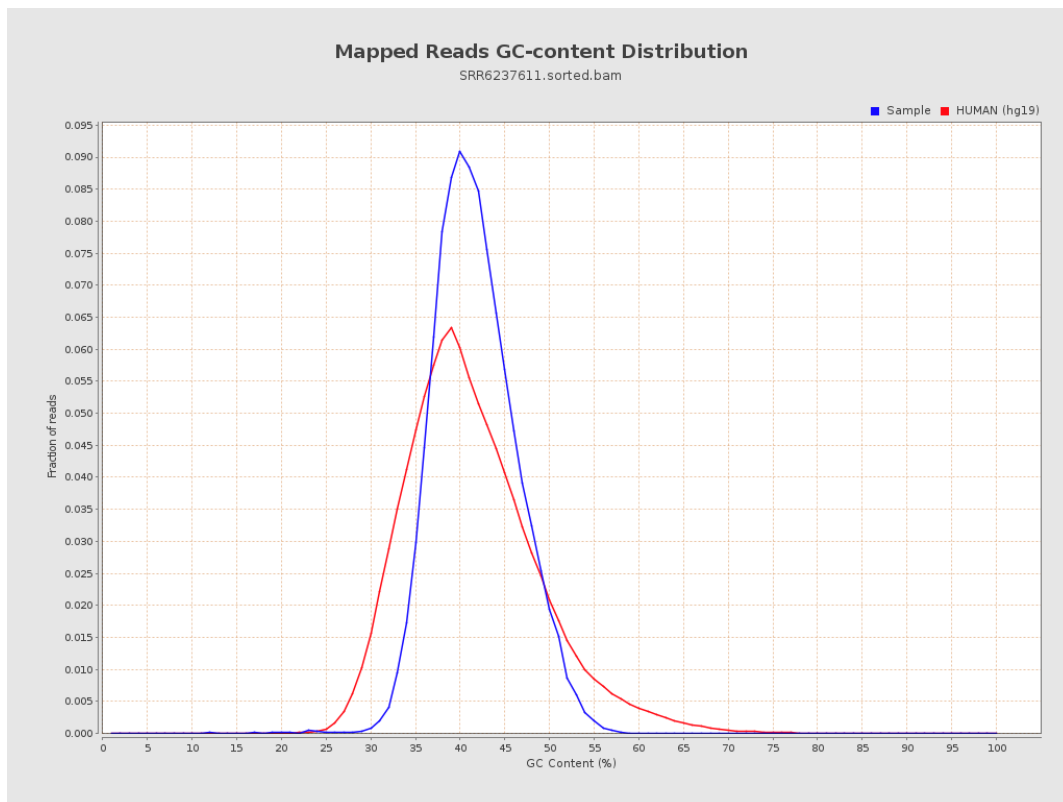
7. Results : Duplication Rate Histogram



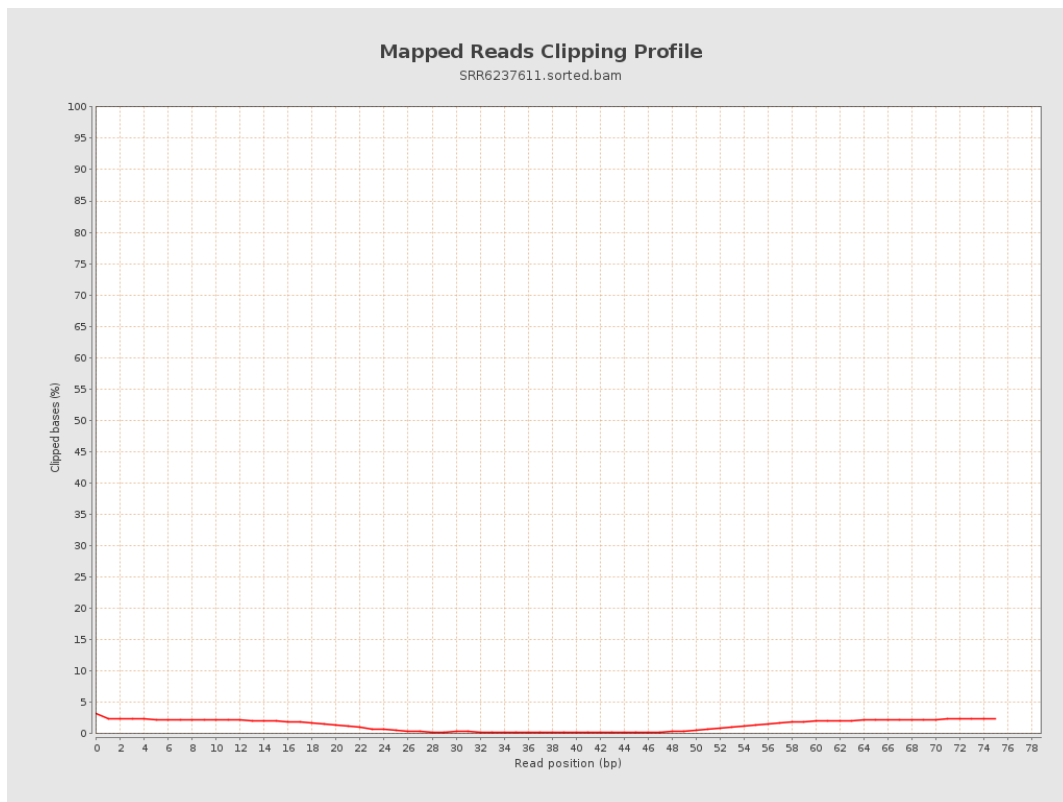
8. Results : Mapped Reads Nucleotide Content



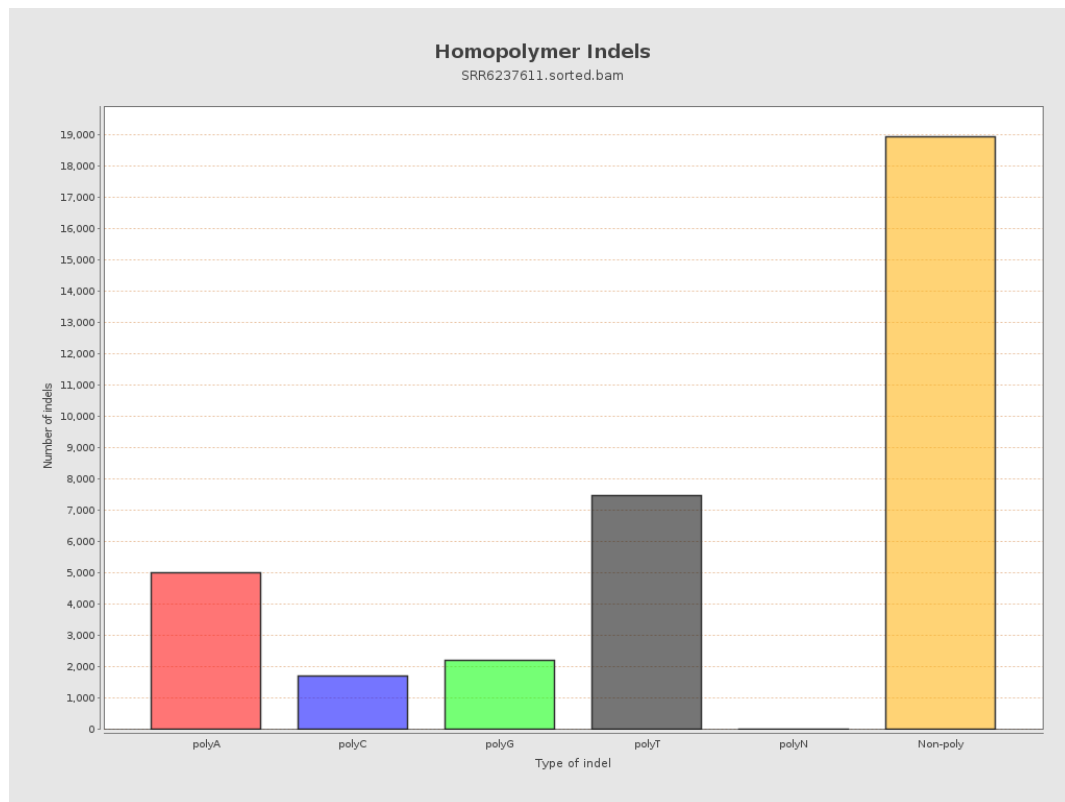
9. Results : Mapped Reads GC-content Distribution



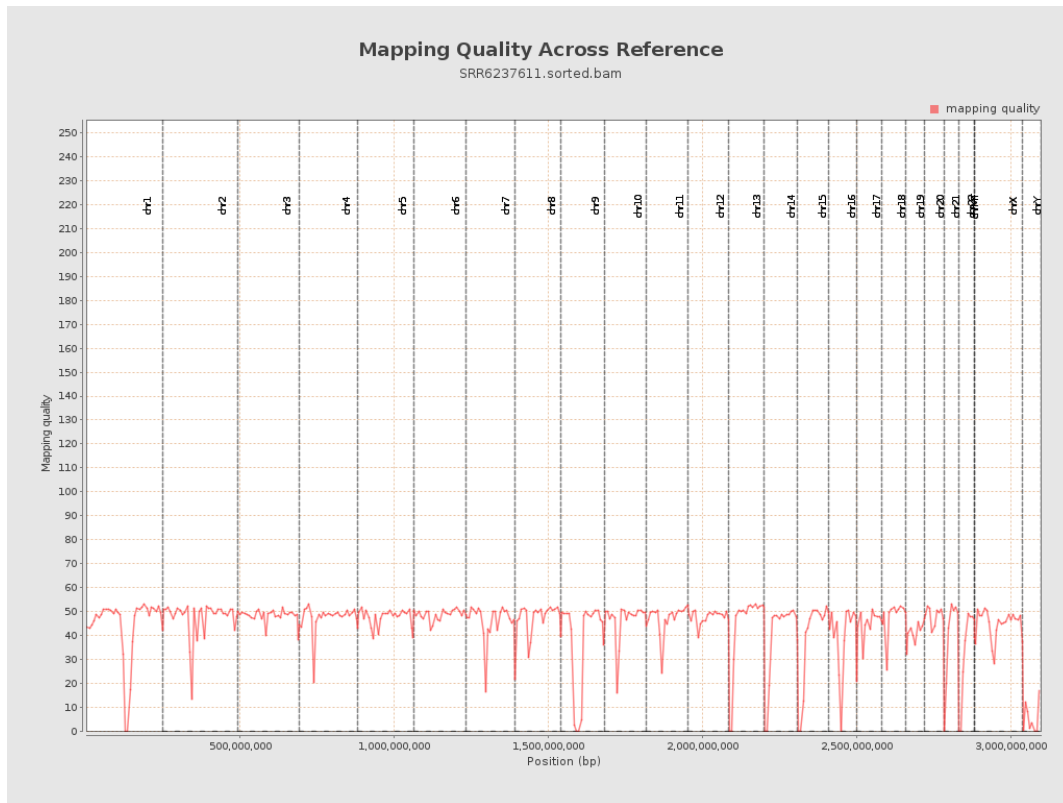
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

