

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:21:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237801.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_SRR6237801 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237801.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:21:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237801.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,610,540
Mapped reads	3,954,178 / 85.76%
Unmapped reads	656,362 / 14.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,860 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	876,190 / 19%
Duplication rate	17.44%
Clipped reads	1,423,055 / 30.87%

2.2. ACGT Content

Number/percentage of A's	81,127,699 / 29.33%
Number/percentage of C's	56,496,206 / 20.43%
Number/percentage of T's	80,189,358 / 28.99%
Number/percentage of G's	58,336,159 / 21.09%
Number/percentage of N's	443,144 / 0.16%
GC Percentage	41.52%

2.3. Coverage

Mean	0.0894

Standard Deviation	1.6522
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2.4. Mapping Quality

Mean Mapping Quality	46.68
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2.5. Mismatches and indels

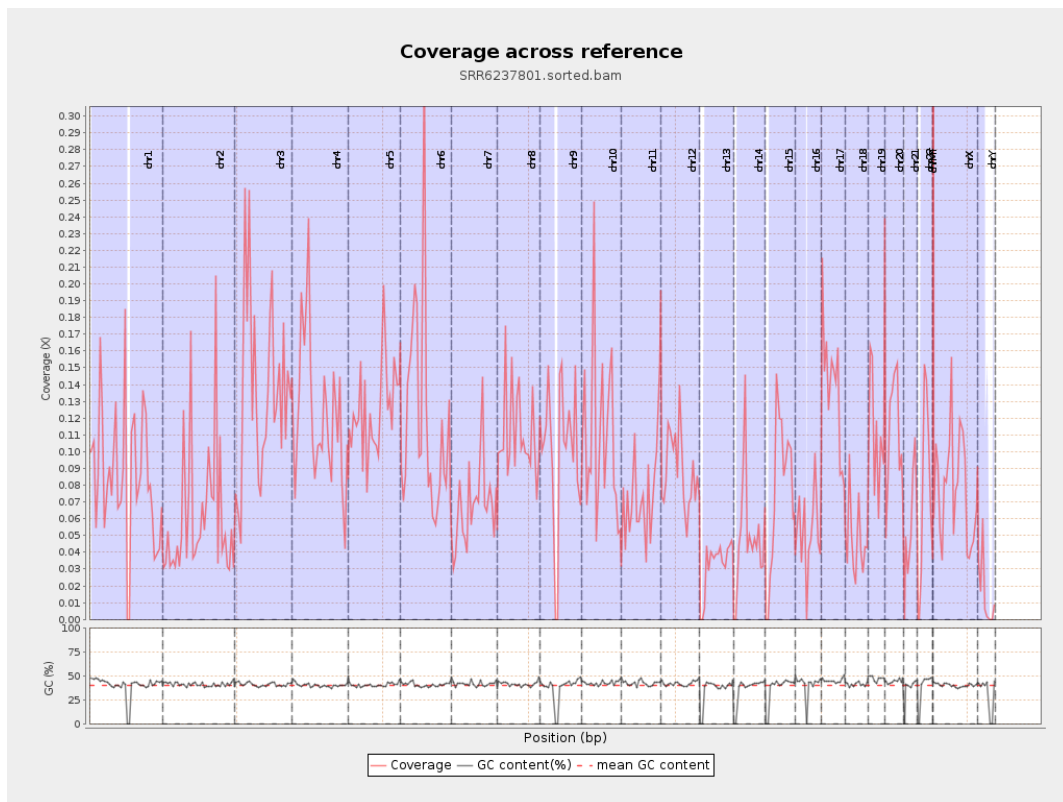
General error rate	0.89%
Mismatches	2,411,260
Insertions	22,805
Mapped reads with at least one insertion	0.57%
Deletions	67,380
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.91%

2.6. Chromosome stats

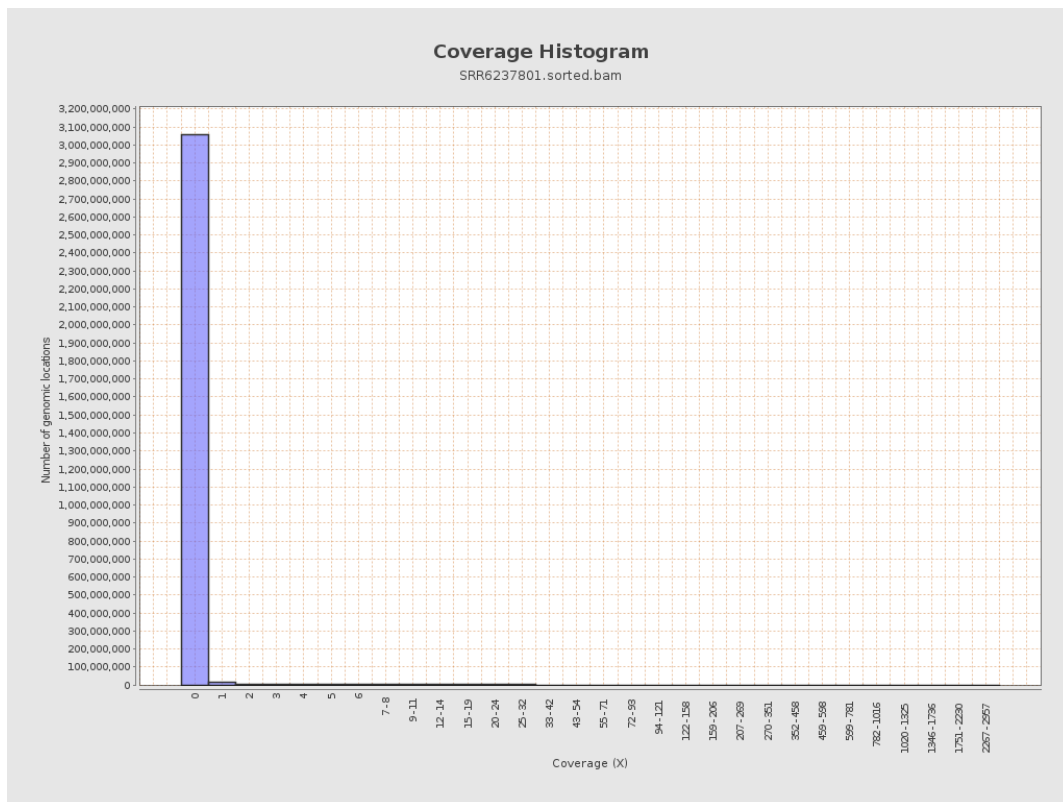
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	21071277	0.0845	2.5178
chr2	243199373	14904008	0.0613	1.4269
chr3	198022430	26728329	0.135	1.7926
chr4	191154276	23619857	0.1236	1.7211
chr5	180915260	22668147	0.1253	1.71
chr6	171115067	20285358	0.1185	1.7751
chr7	159138663	10837666	0.0681	1.3258

chr8	146364022	16140489	0.1103	1.6776
chr9	141213431	14284720	0.1012	1.6446
chr10	135534747	14566749	0.1075	1.9429
chr11	135006516	9983513	0.0739	1.3195
chr12	133851895	11881789	0.0888	1.4206
chr13	115169878	3765276	0.0327	0.8488
chr14	107349540	5312105	0.0495	1.0683
chr15	102531392	7614617	0.0743	1.2366
chr16	90354753	4659974	0.0516	1.1068
chr17	81195210	11356549	0.1399	1.9204
chr18	78077248	3666867	0.047	2.2035
chr19	59128983	6724292	0.1137	2.0313
chr20	63025520	6991536	0.1109	1.6657
chr21	48129895	2784774	0.0579	1.172
chr22	51304566	3934205	0.0767	1.2981
chrMT	16571	23952	1.4454	3.5567
chrX	155270560	12006174	0.0773	1.2888
chrY	59373566	900833	0.0152	0.7084

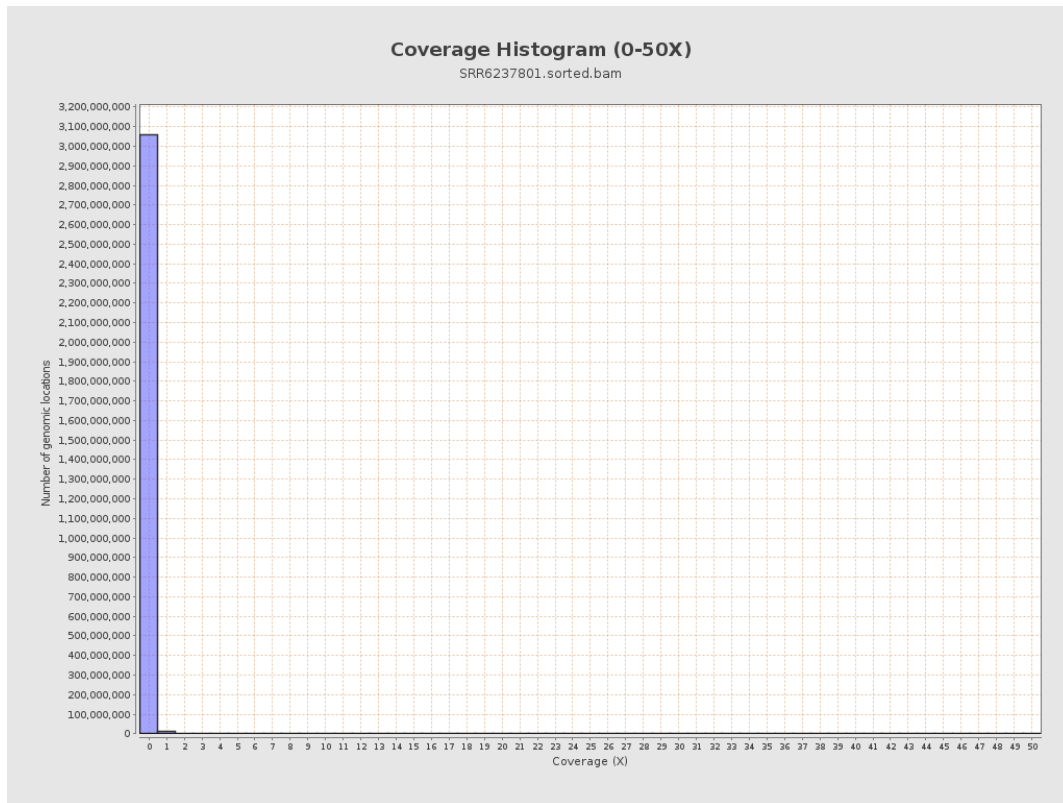
3. Results : Coverage across reference



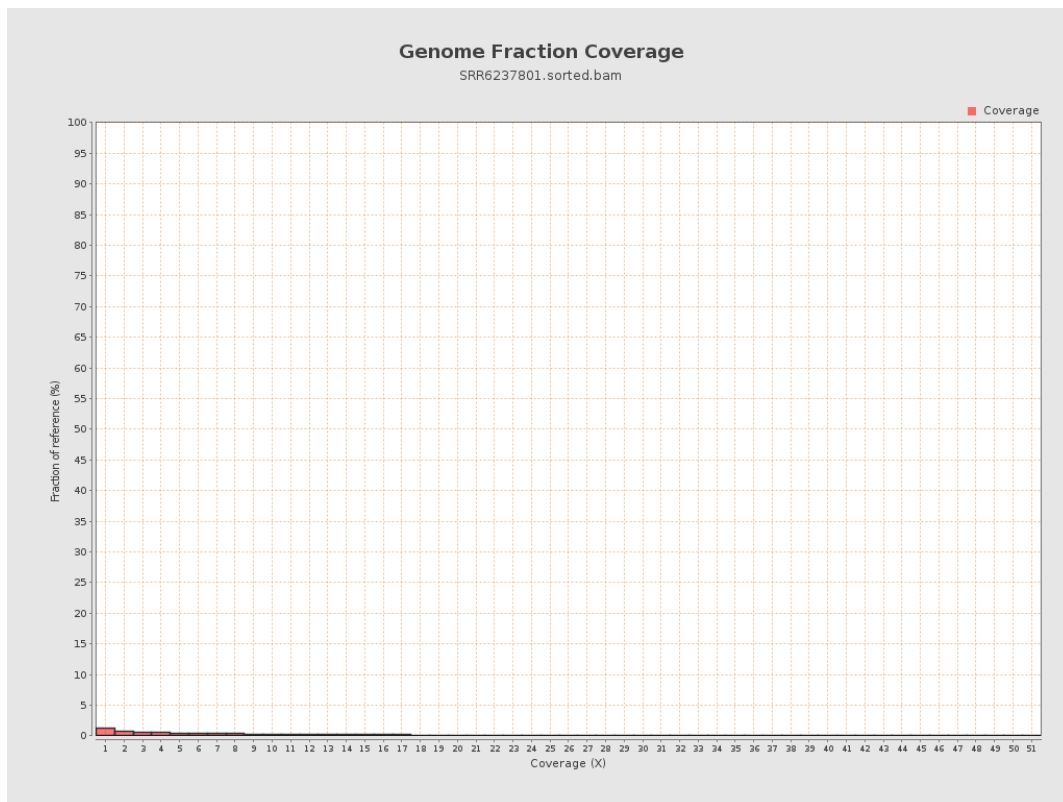
4. Results : Coverage Histogram



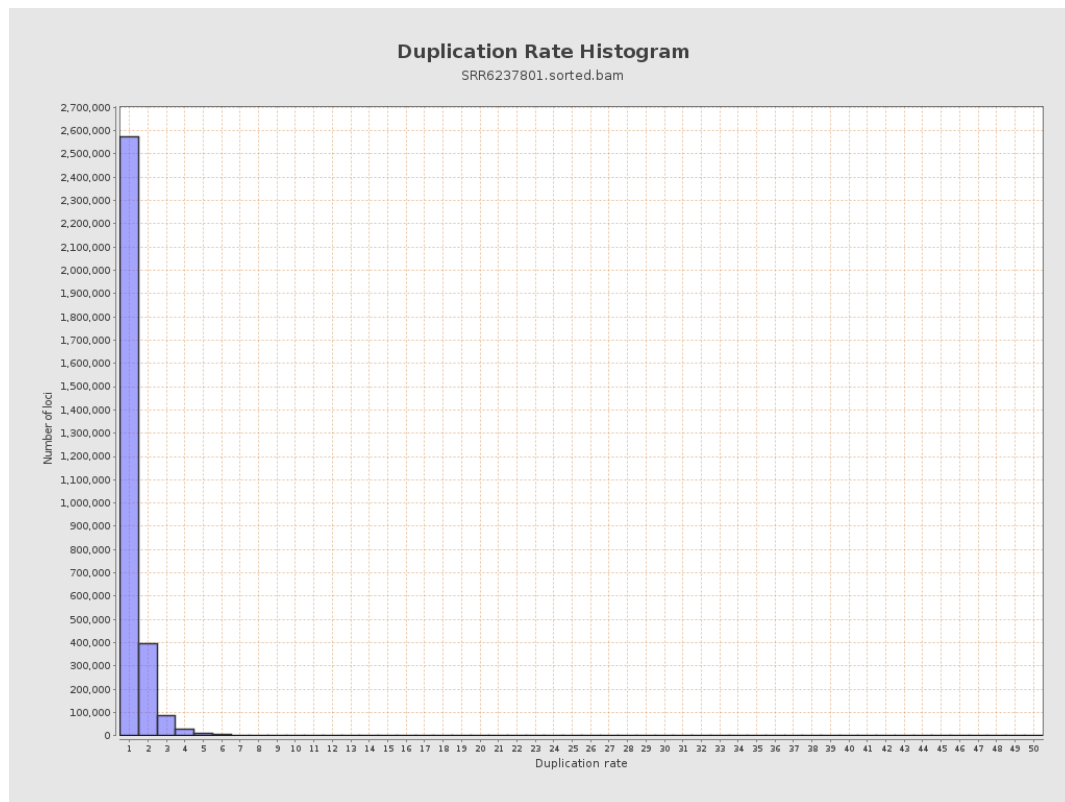
5. Results : Coverage Histogram (0-50X)



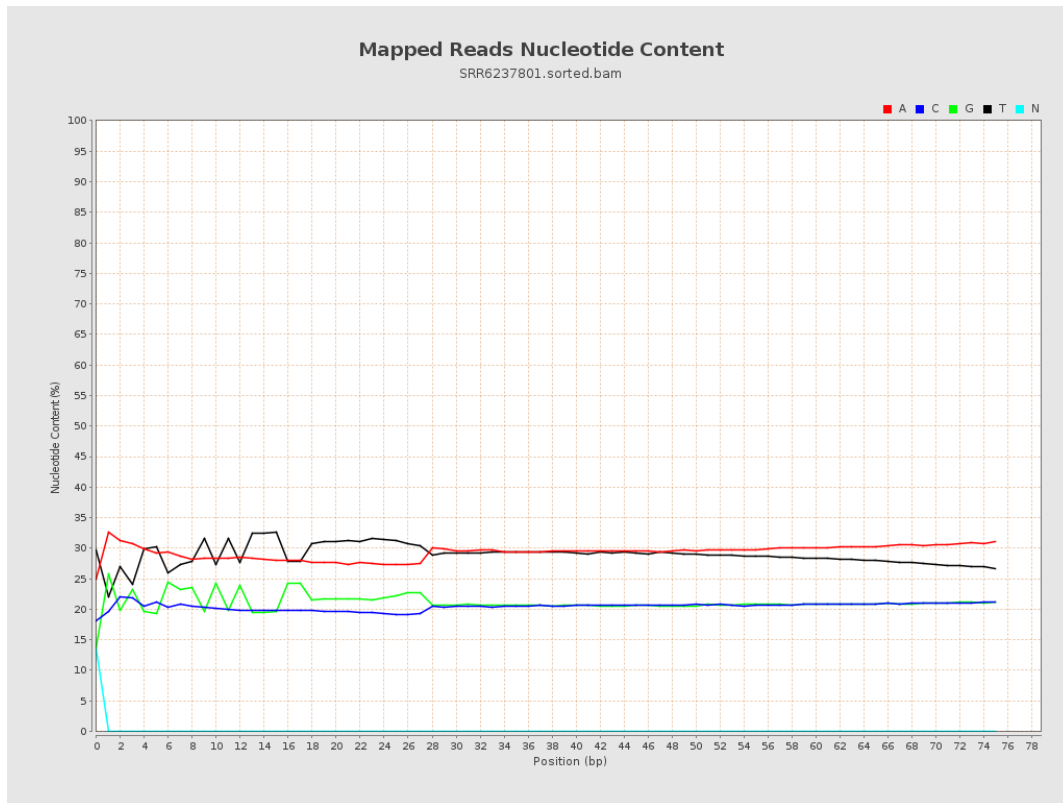
6. Results : Genome Fraction Coverage



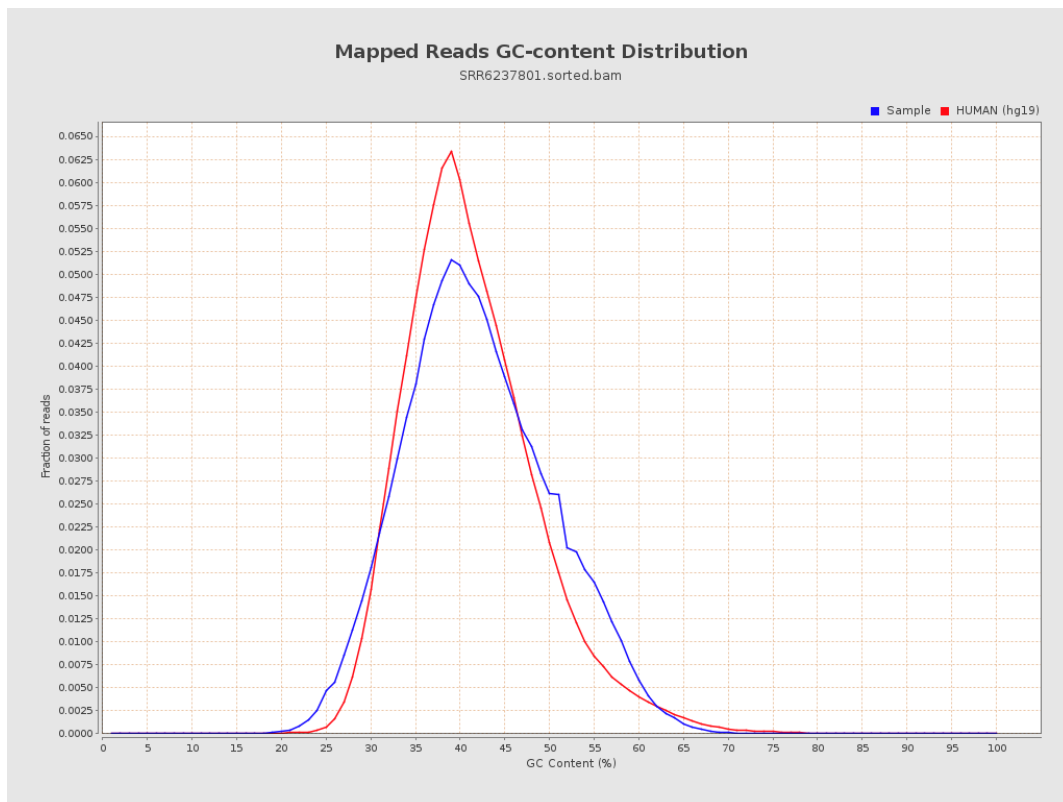
7. Results : Duplication Rate Histogram



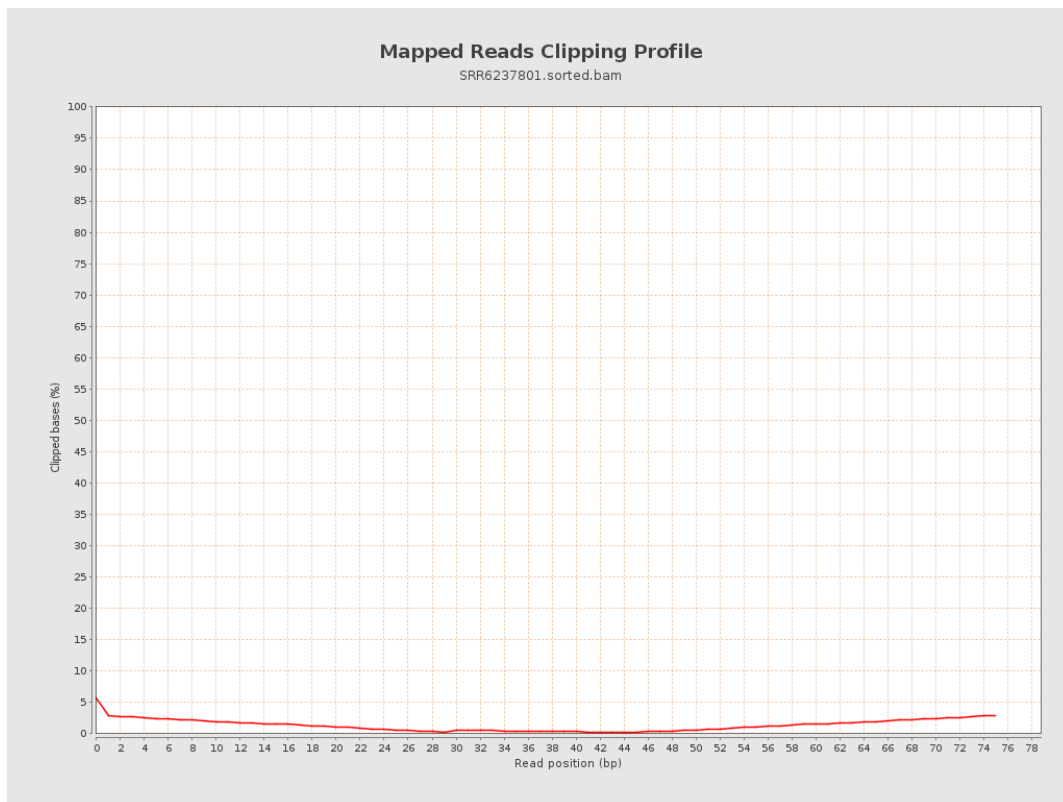
8. Results : Mapped Reads Nucleotide Content



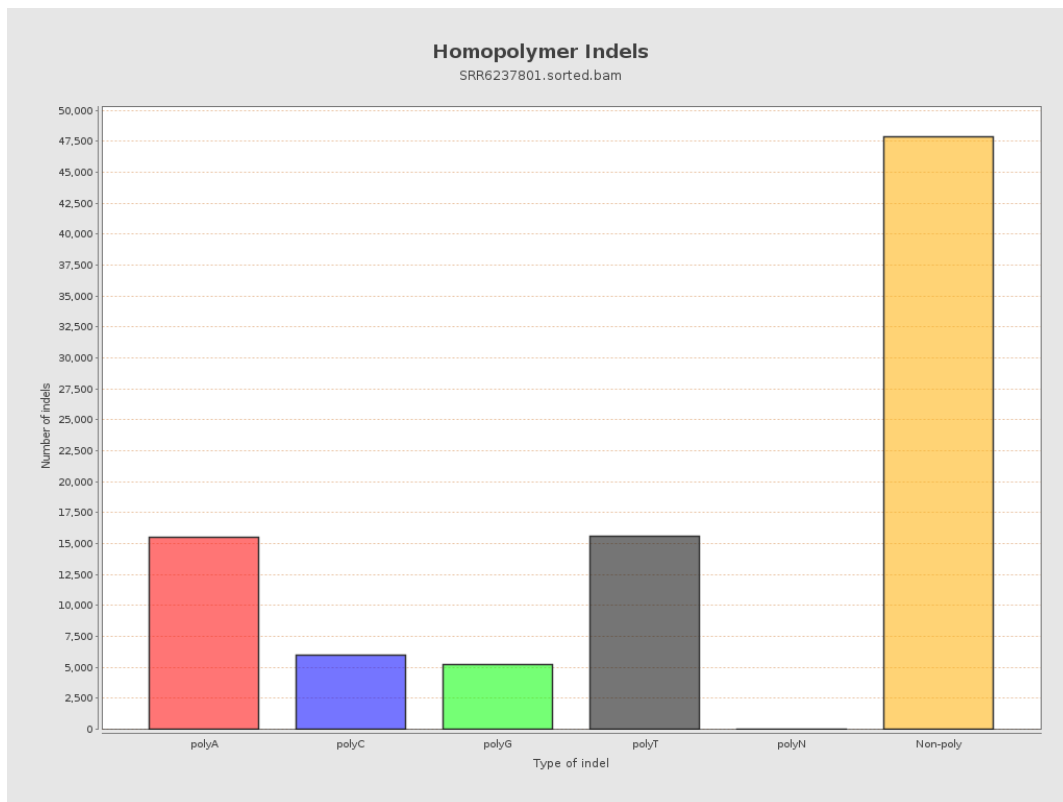
9. Results : Mapped Reads GC-content Distribution



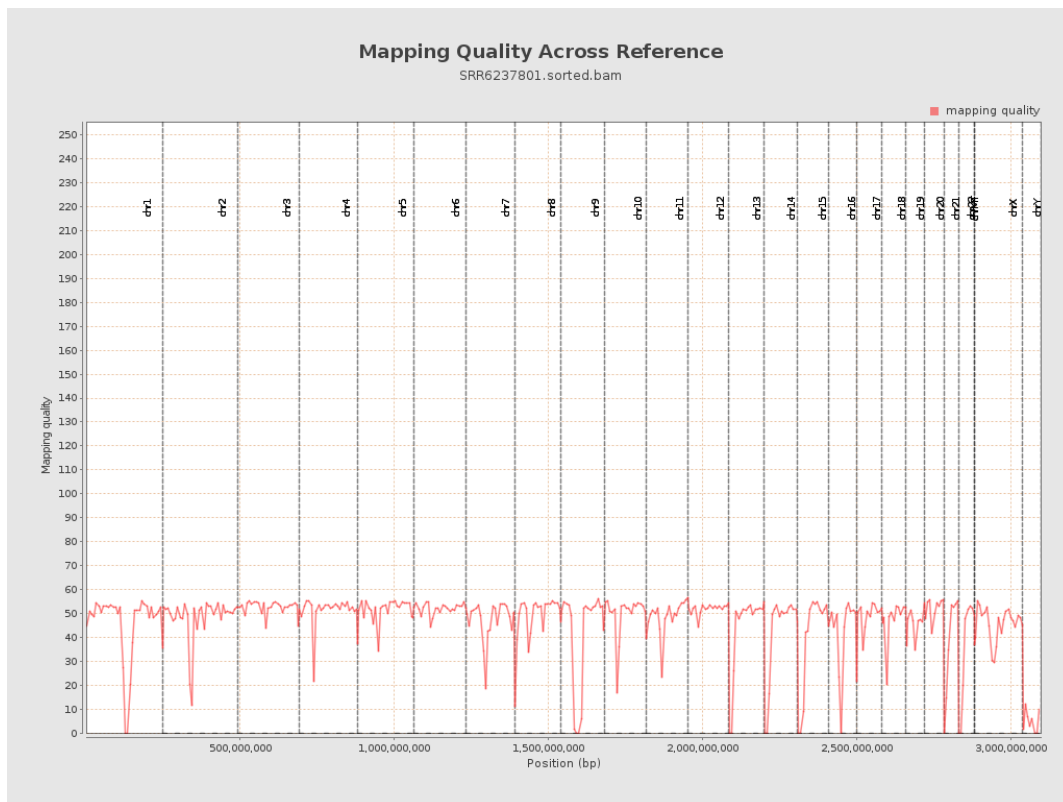
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

