

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:25:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237820.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_SRR6237820 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237820.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:25:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237820.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,468,109
Mapped reads	3,333,837 / 96.13%
Unmapped reads	134,272 / 3.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	49,433 / 1.43%
Read min/max/mean length	30 / 76 / 76.5
Duplicated reads (estimated)	156,818 / 4.52%
Duplication rate	3.14%
Clipped reads	743,600 / 21.44%

2.2. ACGT Content

Number/percentage of A's	73,986,744 / 30.44%
Number/percentage of C's	48,104,672 / 19.79%
Number/percentage of T's	72,447,263 / 29.81%
Number/percentage of G's	48,062,283 / 19.78%
Number/percentage of N's	430,920 / 0.18%
GC Percentage	39.57%

2.3. Coverage

Mean	0.0786

Standard Deviation	0.751
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2.4. Mapping Quality

Mean Mapping Quality	49.13
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2.5. Mismatches and indels

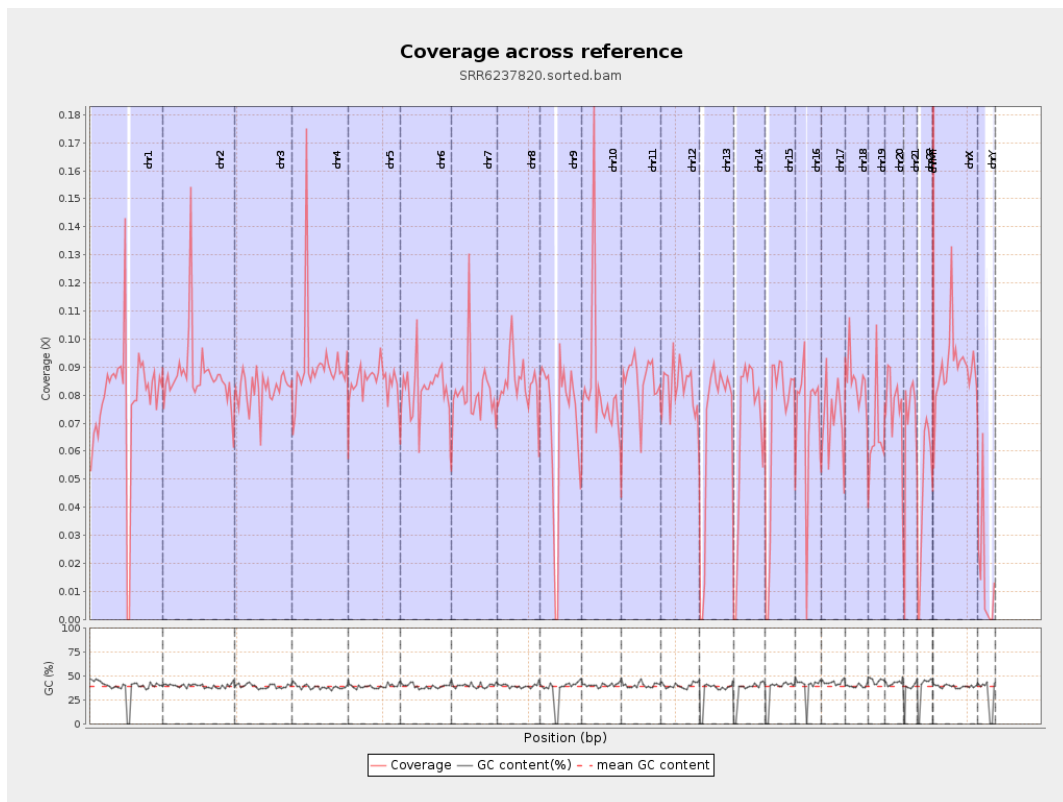
General error rate	0.93%
Mismatches	2,202,283
Insertions	20,819
Mapped reads with at least one insertion	0.62%
Deletions	80,093
Mapped reads with at least one deletion	2.37%
Homopolymer indels	44.55%

2.6. Chromosome stats

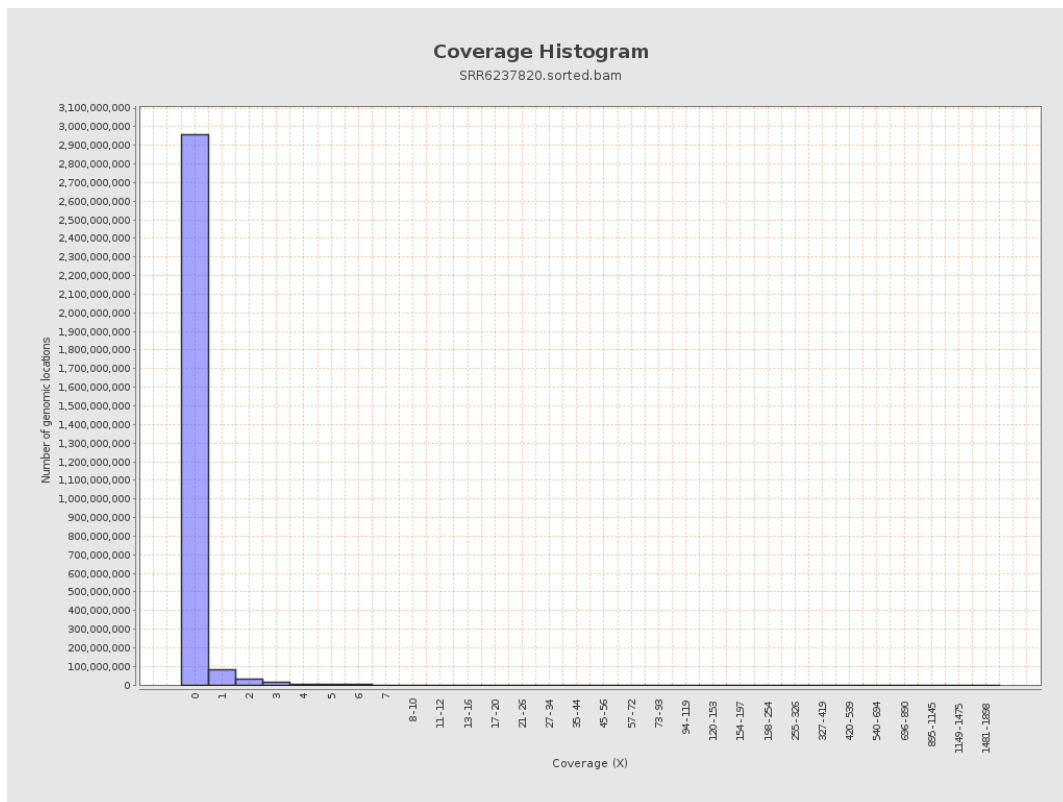
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19445355	0.078	1.4217
chr2	243199373	21290323	0.0875	0.8028
chr3	198022430	16262730	0.0821	0.453
chr4	191154276	17399022	0.091	0.6327
chr5	180915260	15294353	0.0845	0.4606
chr6	171115067	14076056	0.0823	0.5326
chr7	159138663	12837437	0.0807	0.8329

chr8	146364022	12326730	0.0842	0.8012
chr9	141213431	9957190	0.0705	0.7005
chr10	135534747	11110845	0.082	0.911
chr11	135006516	11439746	0.0847	0.6798
chr12	133851895	11066382	0.0827	0.464
chr13	115169878	7963049	0.0691	0.4151
chr14	107349540	7320086	0.0682	0.4435
chr15	102531392	7047358	0.0687	0.4097
chr16	90354753	6392584	0.0707	0.5121
chr17	81195210	5887984	0.0725	0.562
chr18	78077248	6668792	0.0854	1.3416
chr19	59128983	3934024	0.0665	0.933
chr20	63025520	4875604	0.0774	0.4695
chr21	48129895	3322154	0.069	0.5487
chr22	51304566	2374106	0.0463	0.3342
chrMT	16571	55343	3.3398	3.3258
chrX	155270560	13934719	0.0897	0.532
chrY	59373566	897122	0.0151	0.6569

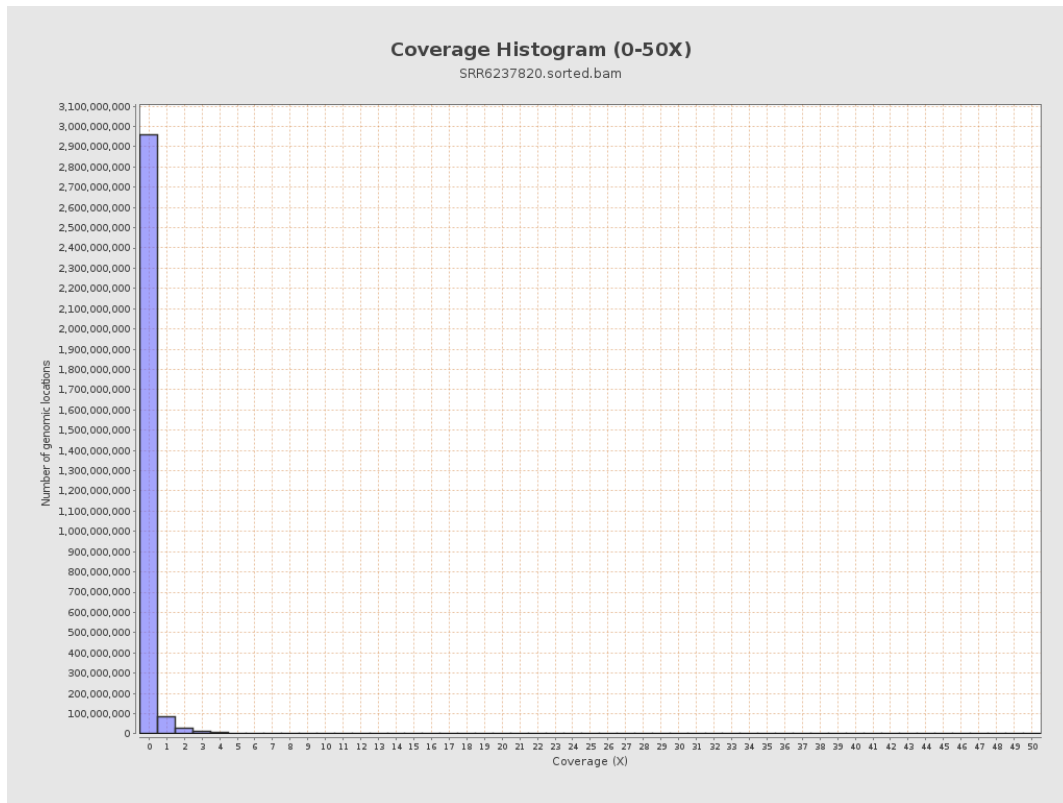
3. Results : Coverage across reference



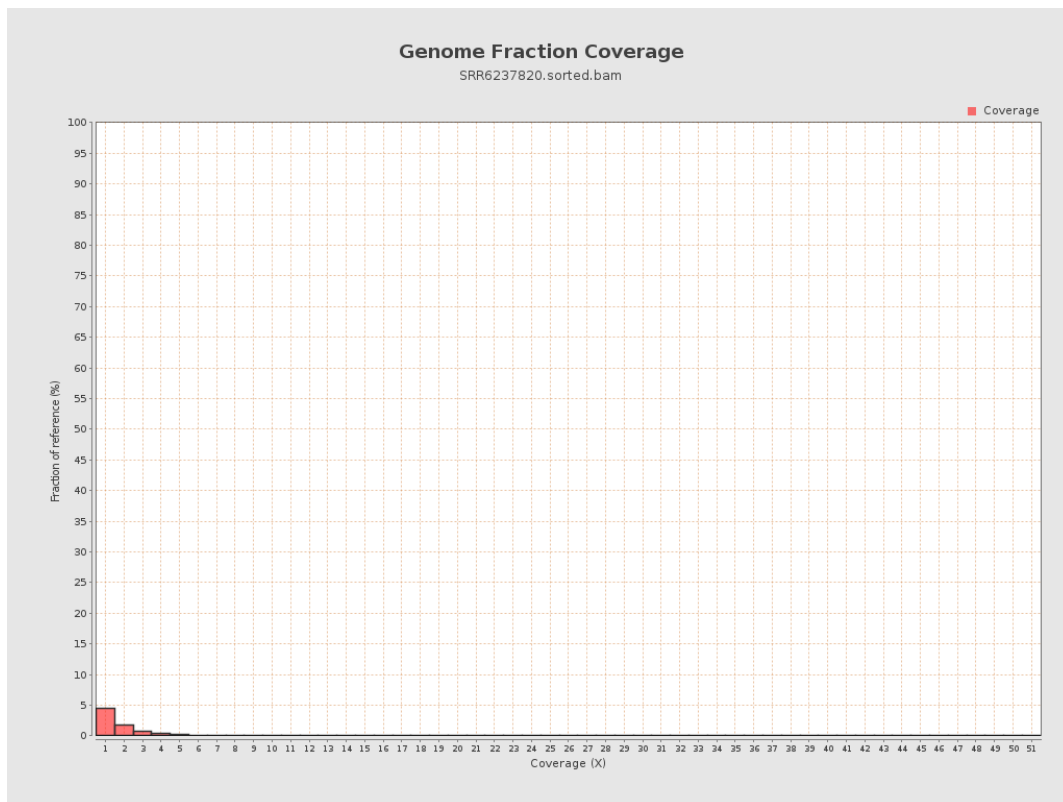
4. Results : Coverage Histogram



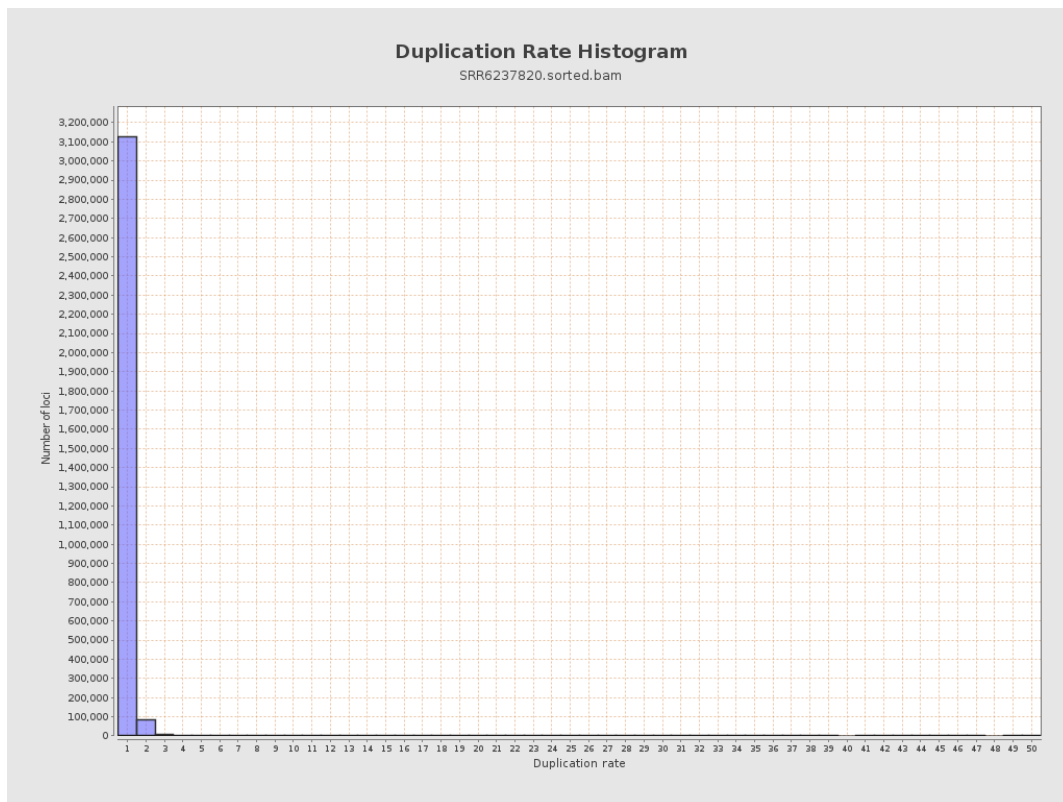
5. Results : Coverage Histogram (0-50X)



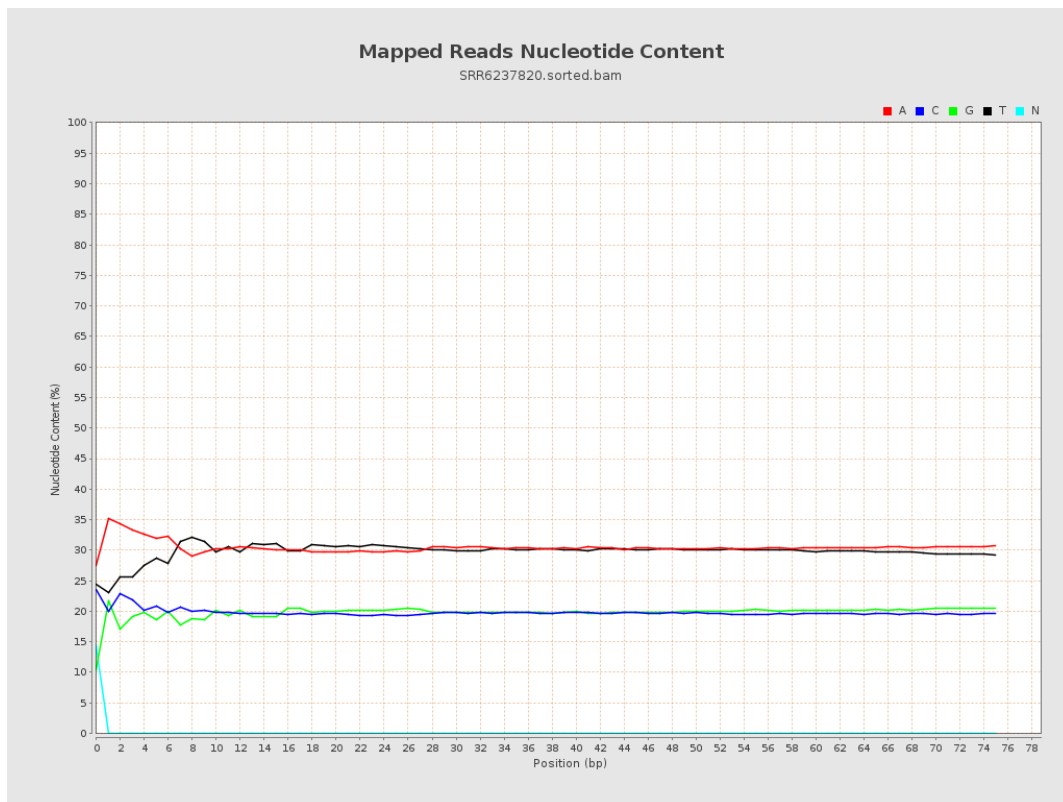
6. Results : Genome Fraction Coverage



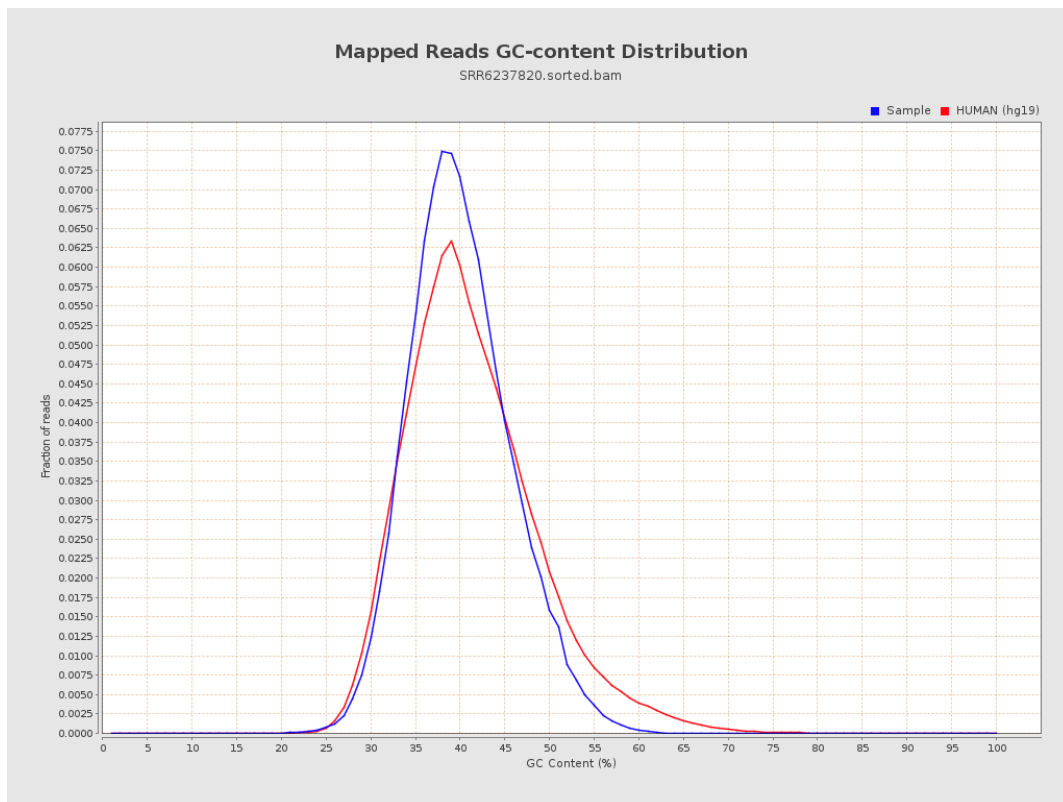
7. Results : Duplication Rate Histogram



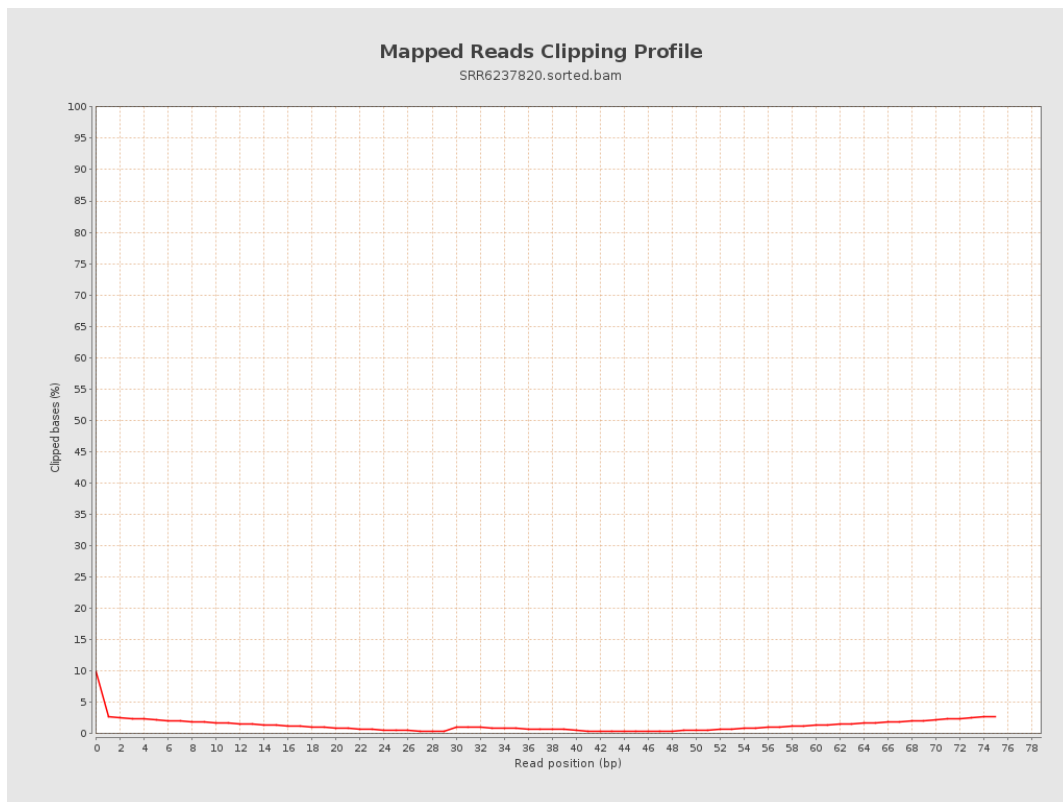
8. Results : Mapped Reads Nucleotide Content



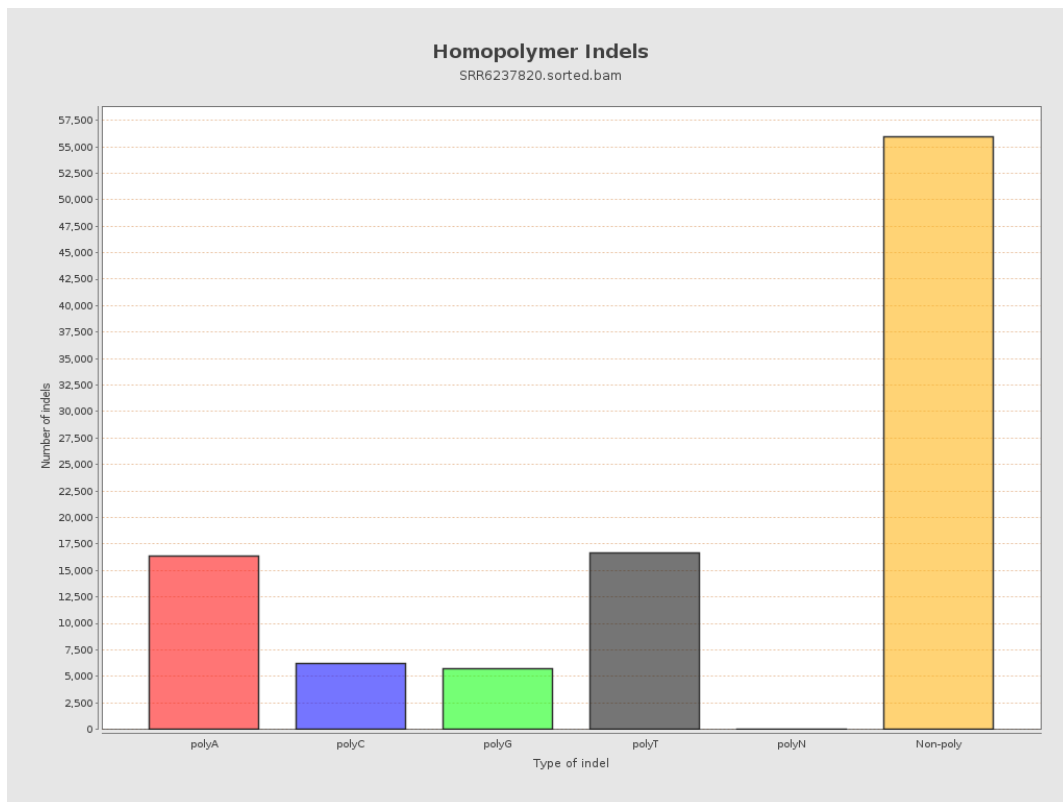
9. Results : Mapped Reads GC-content Distribution



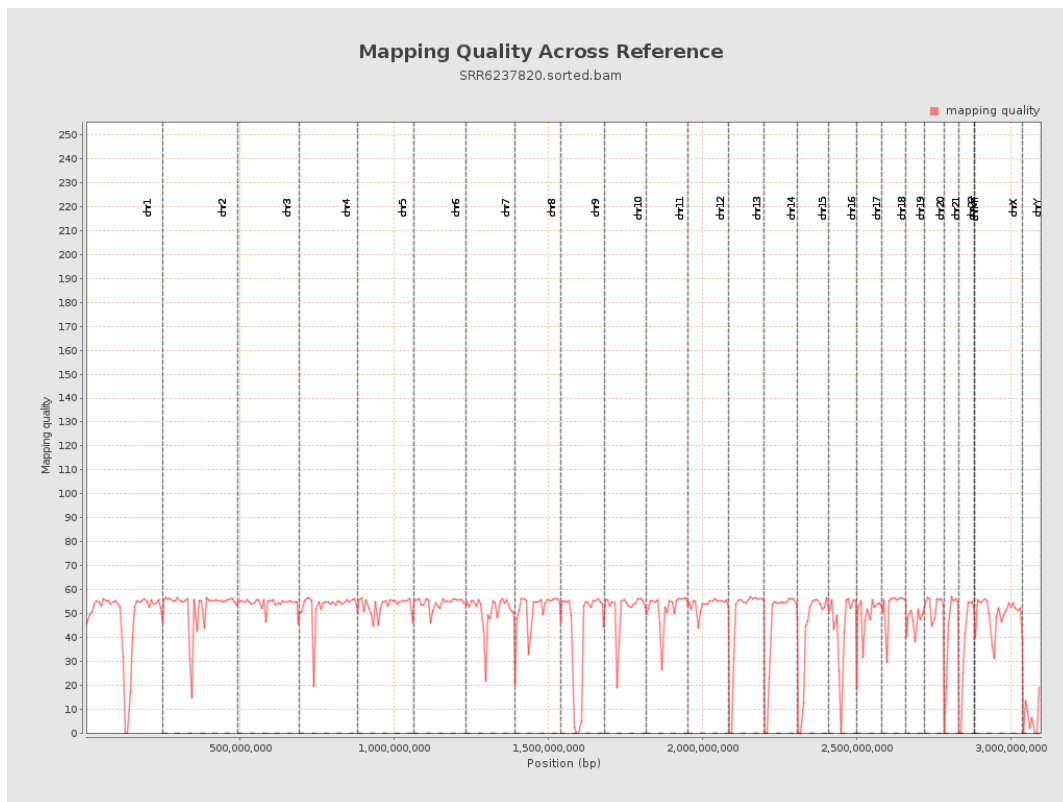
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

