

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:13:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237817.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_SRR6237817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:13:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,469,743
Mapped reads	3,108,796 / 89.6%
Unmapped reads	360,947 / 10.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,267 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	313,205 / 9.03%
Duplication rate	7.87%
Clipped reads	860,031 / 24.79%

2.2. ACGT Content

Number/percentage of A's	67,760,821 / 30.36%
Number/percentage of C's	43,732,113 / 19.59%
Number/percentage of T's	67,015,699 / 30.02%
Number/percentage of G's	44,326,361 / 19.86%
Number/percentage of N's	369,347 / 0.17%
GC Percentage	39.45%

2.3. Coverage

Mean	0.0721

Standard Deviation	1.1322
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2.4. Mapping Quality

Mean Mapping Quality	49.07
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2.5. Mismatches and indels

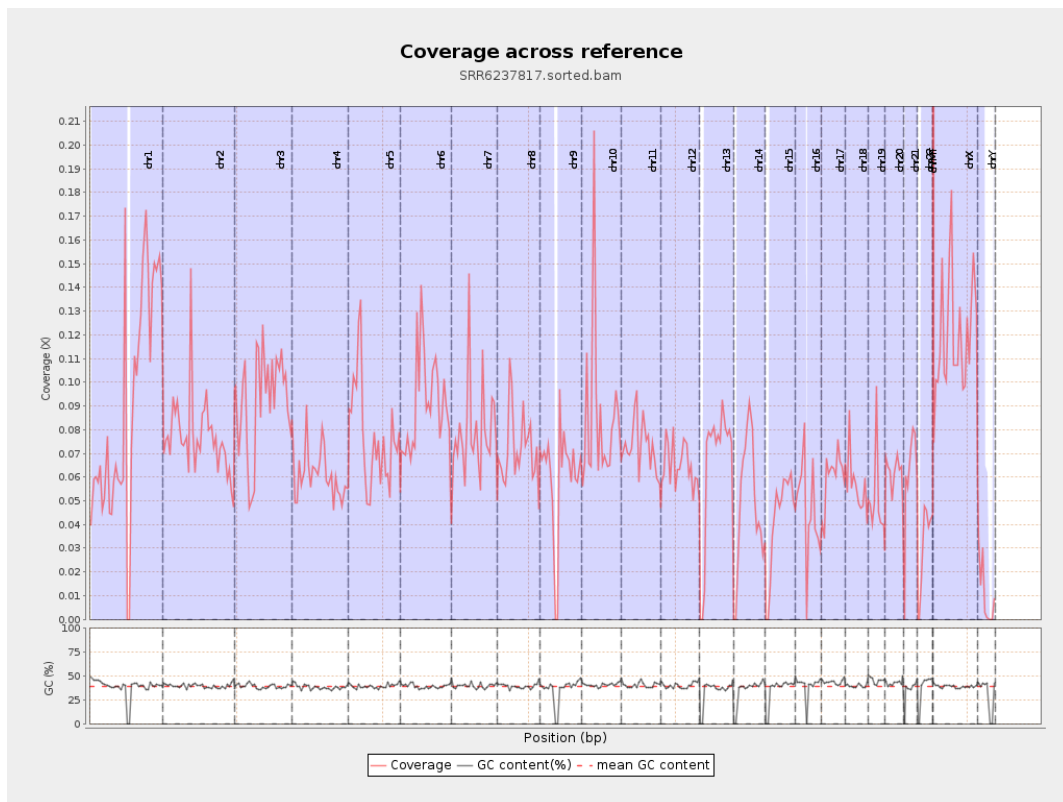
General error rate	0.89%
Mismatches	1,948,766
Insertions	16,226
Mapped reads with at least one insertion	0.52%
Deletions	53,844
Mapped reads with at least one deletion	1.71%
Homopolymer indels	46.08%

2.6. Chromosome stats

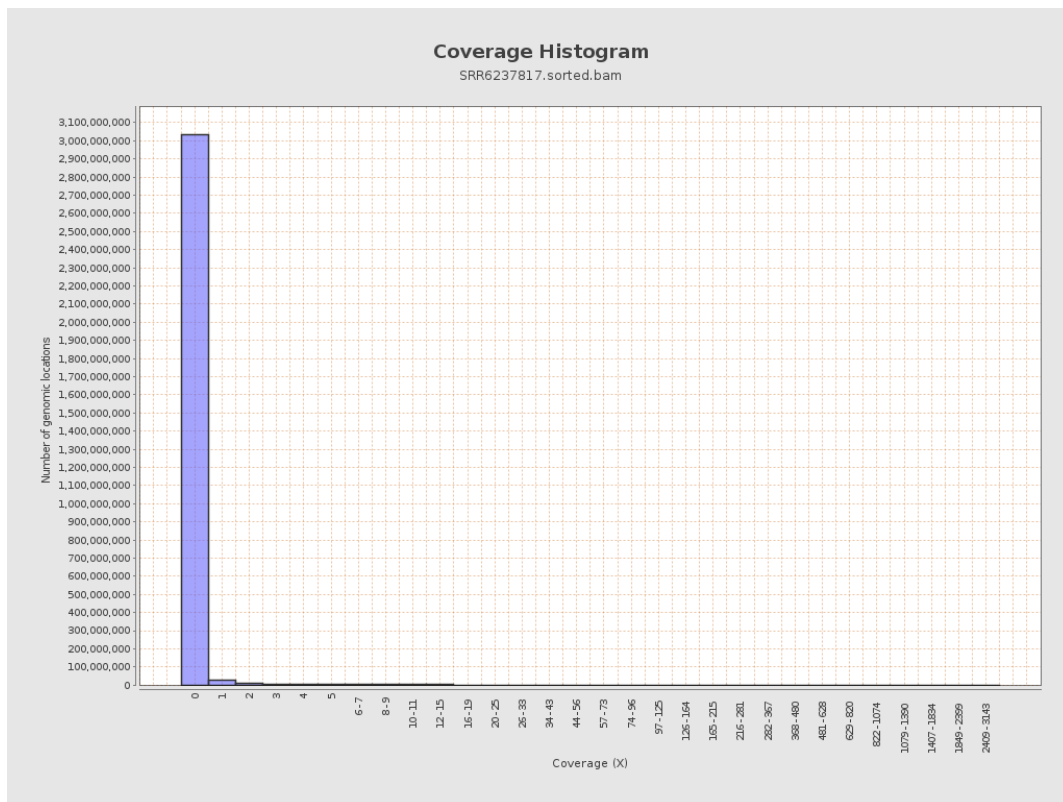
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22343836	0.0896	2.3684
chr2	243199373	18749103	0.0771	0.9624
chr3	198022430	18328852	0.0926	0.8638
chr4	191154276	11691955	0.0612	0.7073
chr5	180915260	13988721	0.0773	0.798
chr6	171115067	15482091	0.0905	0.9234
chr7	159138663	12565015	0.079	1.2493

chr8	146364022	10511401	0.0718	1.4764
chr9	141213431	8529853	0.0604	0.8753
chr10	135534747	11414409	0.0842	1.1941
chr11	135006516	9825107	0.0728	0.9921
chr12	133851895	8671872	0.0648	0.7147
chr13	115169878	7485987	0.065	0.7277
chr14	107349540	5329023	0.0496	0.6795
chr15	102531392	4259904	0.0415	0.5753
chr16	90354753	4150120	0.0459	0.6519
chr17	81195210	4866547	0.0599	0.8222
chr18	78077248	4450841	0.057	1.5156
chr19	59128983	3008171	0.0509	1.3358
chr20	63025520	3921496	0.0622	0.698
chr21	48129895	2990146	0.0621	0.7217
chr22	51304566	1574846	0.0307	0.5031
chrMT	16571	109745	6.6227	5.985
chrX	155270560	18433274	0.1187	1.047
chrY	59373566	618617	0.0104	0.3278

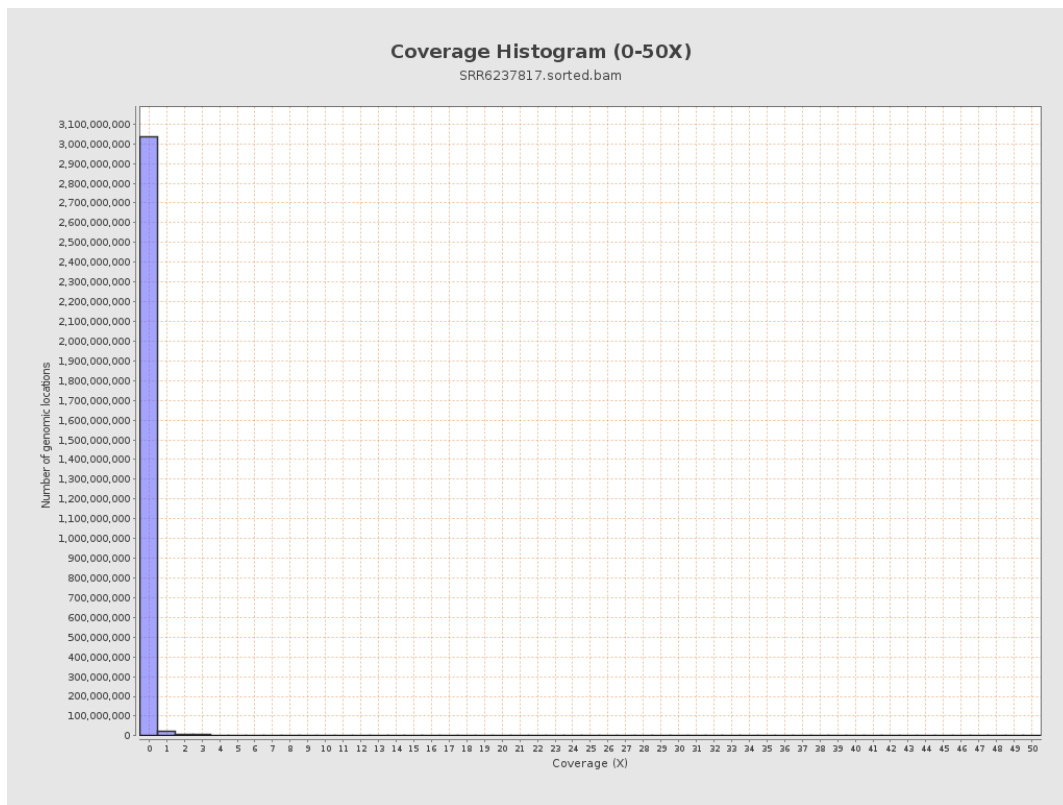
3. Results : Coverage across reference



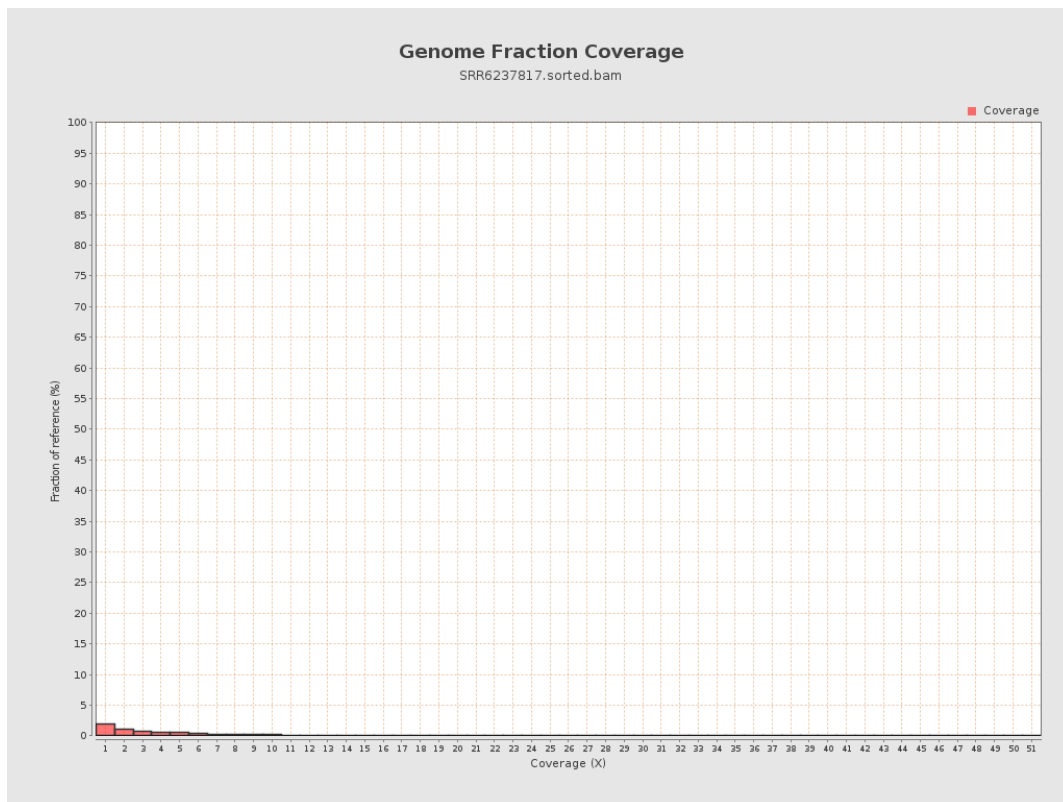
4. Results : Coverage Histogram



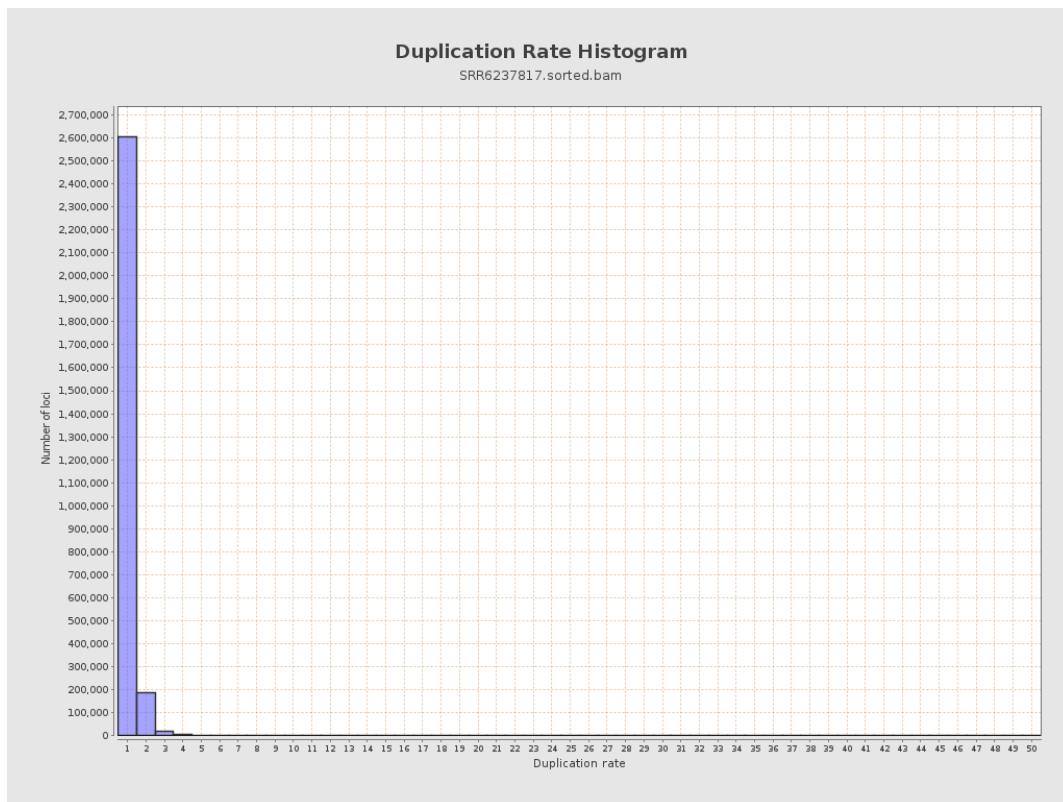
5. Results : Coverage Histogram (0-50X)



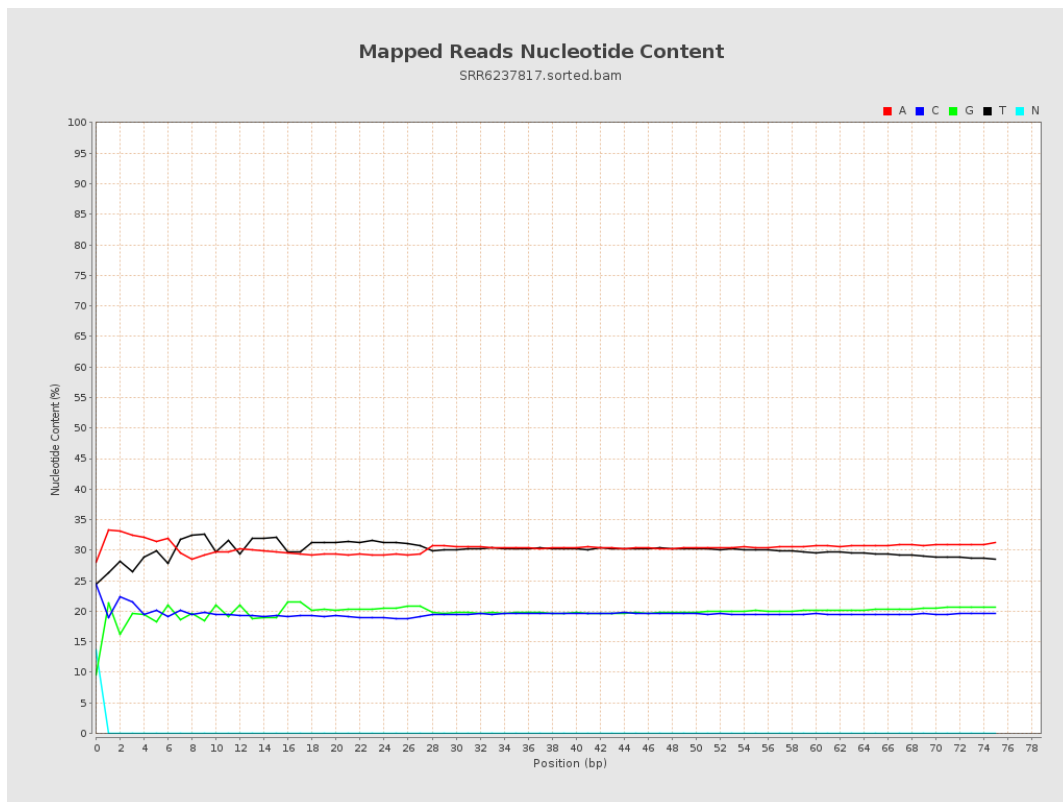
6. Results : Genome Fraction Coverage



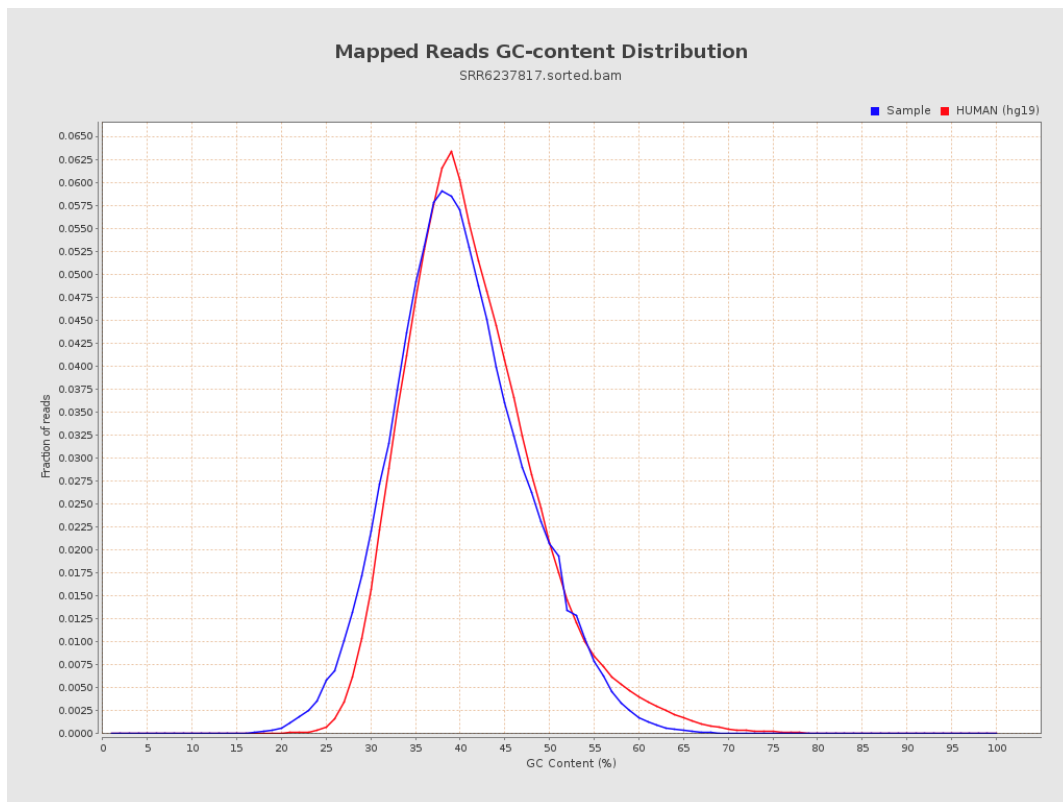
7. Results : Duplication Rate Histogram



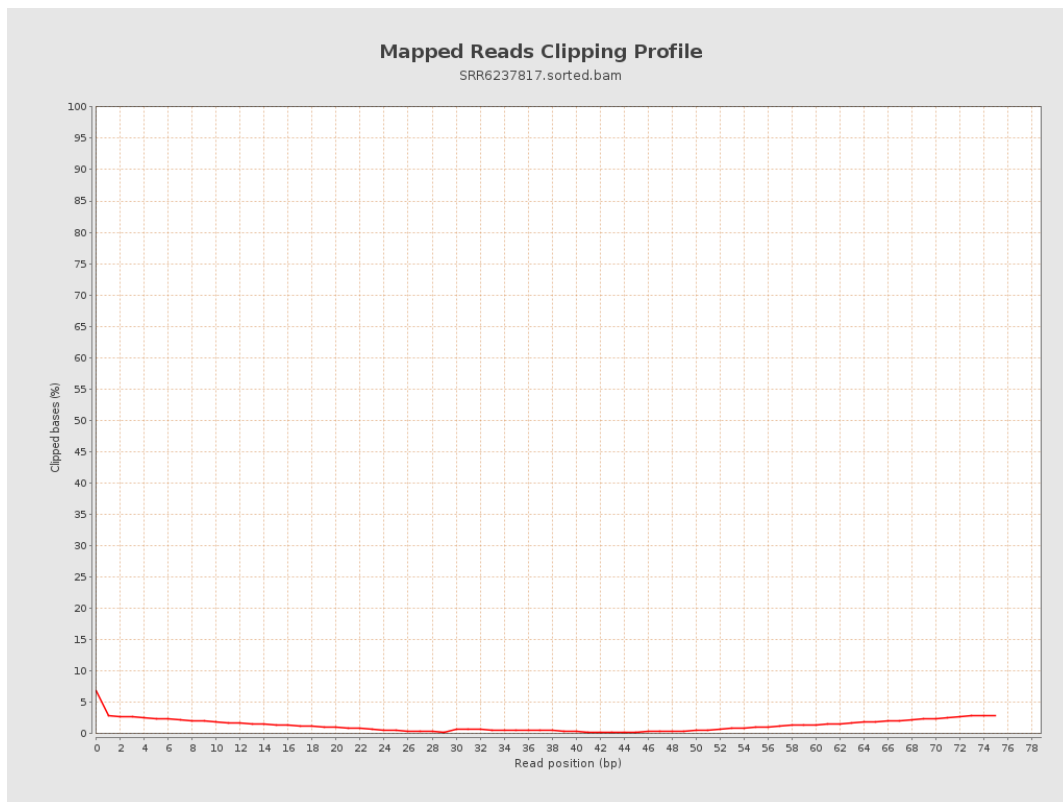
8. Results : Mapped Reads Nucleotide Content



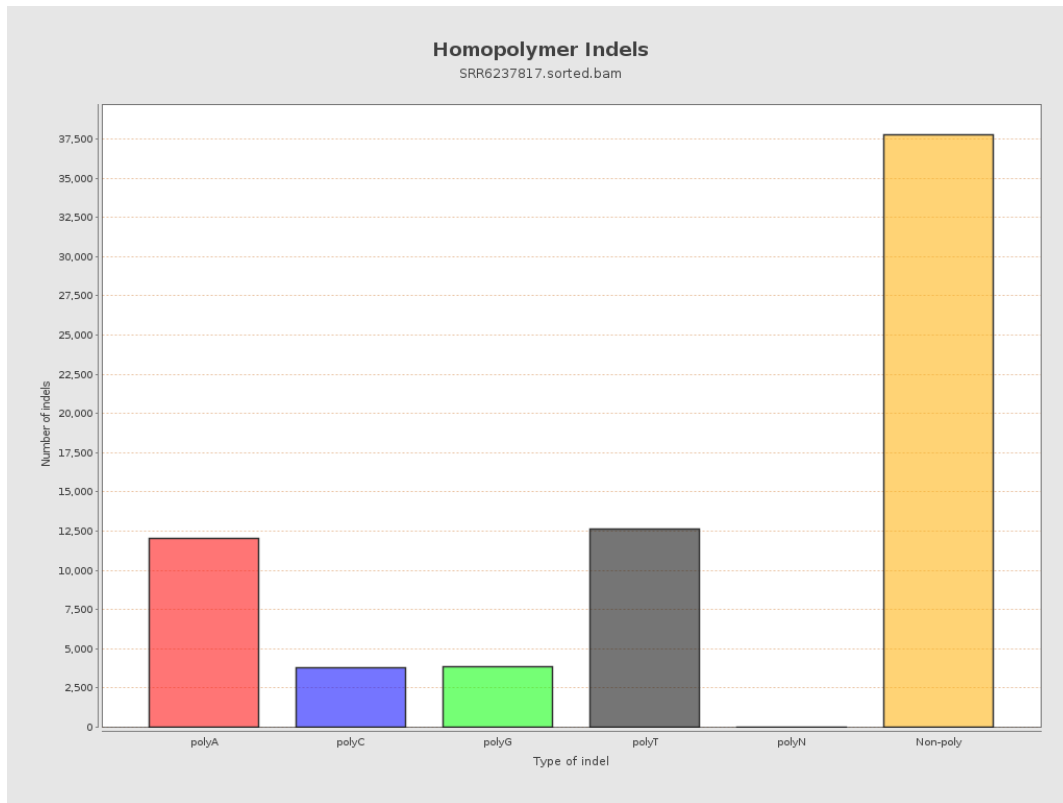
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

