

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:51:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238524.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_SRR6238524 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238524.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:51:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238524.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,441,791
Mapped reads	2,163,074 / 88.59%
Unmapped reads	278,717 / 11.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,125 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	458,153 / 18.76%
Duplication rate	16.48%
Clipped reads	1,336,431 / 54.73%

2.2. ACGT Content

Number/percentage of A's	33,536,233 / 25.01%
Number/percentage of C's	23,917,414 / 17.84%
Number/percentage of T's	44,235,813 / 32.99%
Number/percentage of G's	32,383,947 / 24.15%
Number/percentage of N's	9,305 / 0.01%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.5112
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2.4. Mapping Quality

Mean Mapping Quality	44.39
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2.5. Mismatches and indels

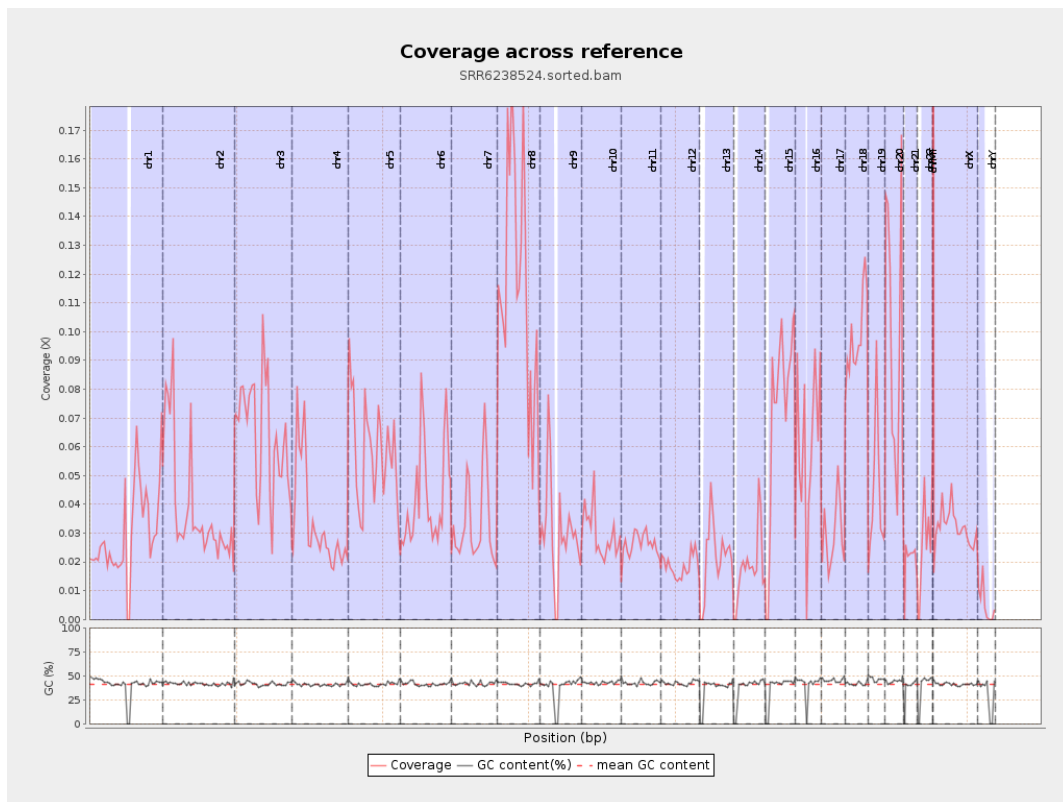
General error rate	0.57%
Mismatches	752,762
Insertions	8,092
Mapped reads with at least one insertion	0.37%
Deletions	33,716
Mapped reads with at least one deletion	1.54%
Homopolymer indels	43.49%

2.6. Chromosome stats

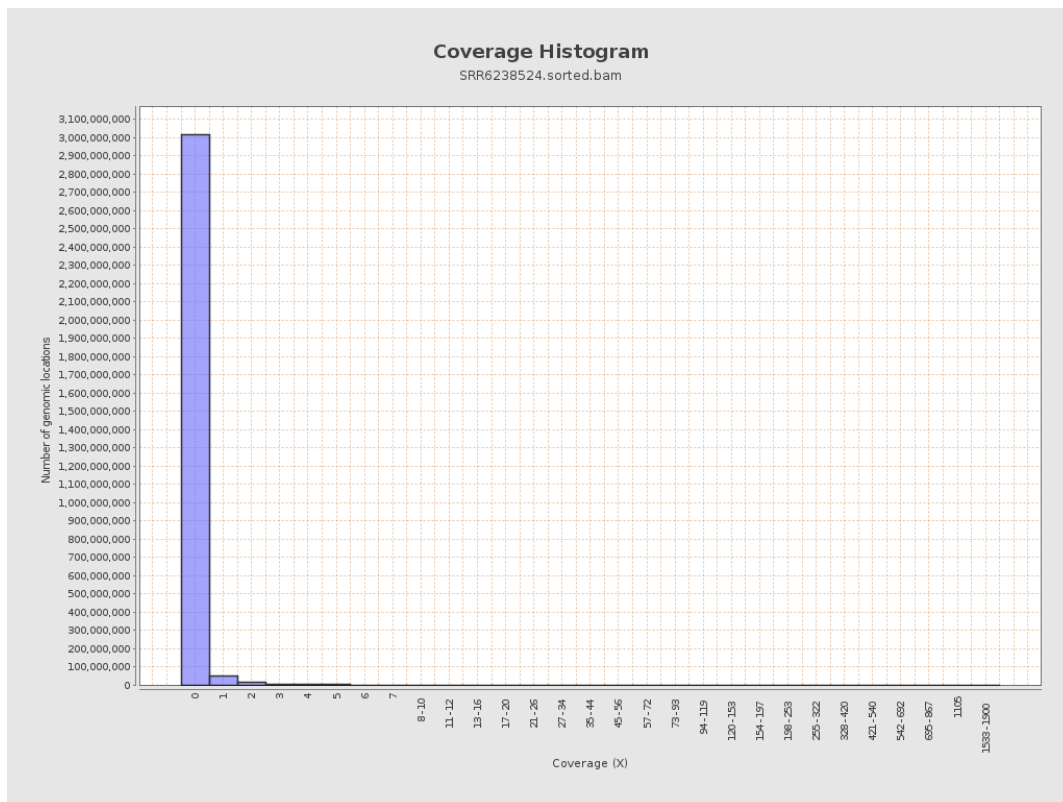
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7524859	0.0302	0.746
chr2	243199373	9342390	0.0384	0.9715
chr3	198022430	12585571	0.0636	0.3959
chr4	191154276	6469396	0.0338	0.292
chr5	180915260	10372864	0.0573	0.3732
chr6	171115067	7238912	0.0423	0.4442
chr7	159138663	5332570	0.0335	0.4051

chr8	146364022	16874674	0.1153	0.7325
chr9	141213431	4359712	0.0309	0.3958
chr10	135534747	4003214	0.0295	0.3558
chr11	135006516	3519558	0.0261	0.3066
chr12	133851895	2498873	0.0187	0.2291
chr13	115169878	2477943	0.0215	0.2861
chr14	107349540	2009352	0.0187	0.2189
chr15	102531392	7336389	0.0716	0.4459
chr16	90354753	5416515	0.0599	0.4052
chr17	81195210	2455194	0.0302	0.2814
chr18	78077248	7725069	0.0989	0.8558
chr19	59128983	2676854	0.0453	0.533
chr20	63025520	6360787	0.1009	0.5091
chr21	48129895	982132	0.0204	0.2341
chr22	51304566	1296847	0.0253	0.2522
chrMT	16571	19659	1.1863	1.9344
chrX	155270560	4945983	0.0319	0.2997
chrY	59373566	316404	0.0053	0.2002

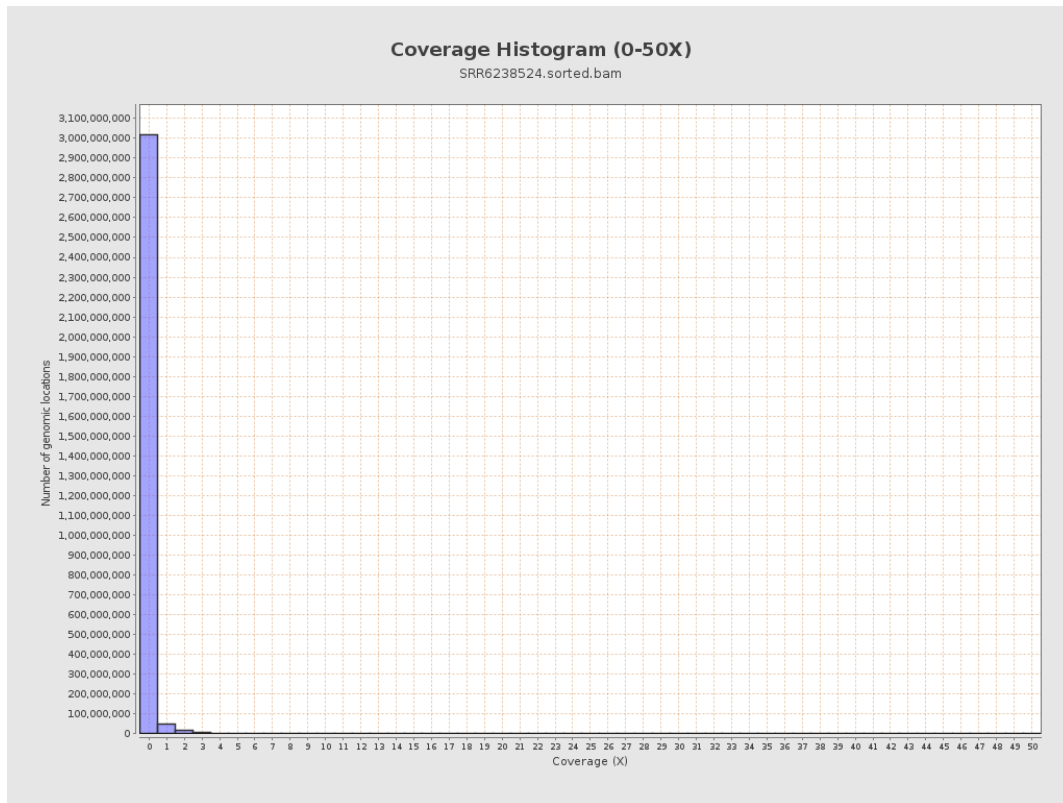
3. Results : Coverage across reference



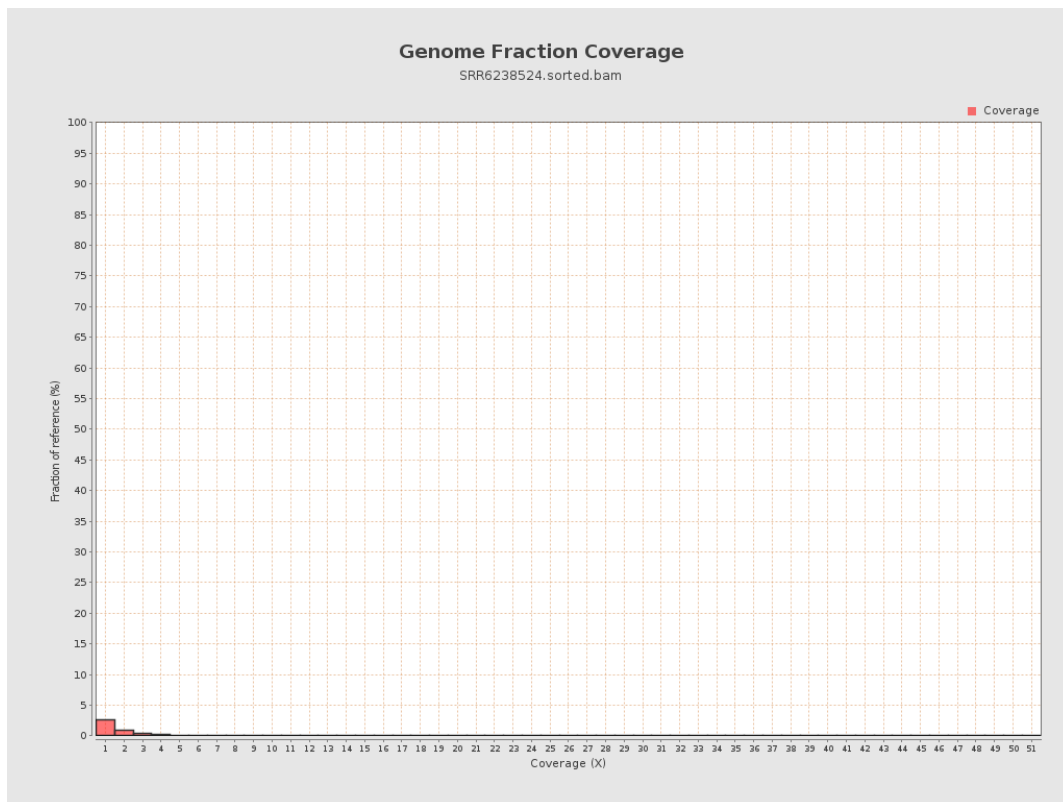
4. Results : Coverage Histogram



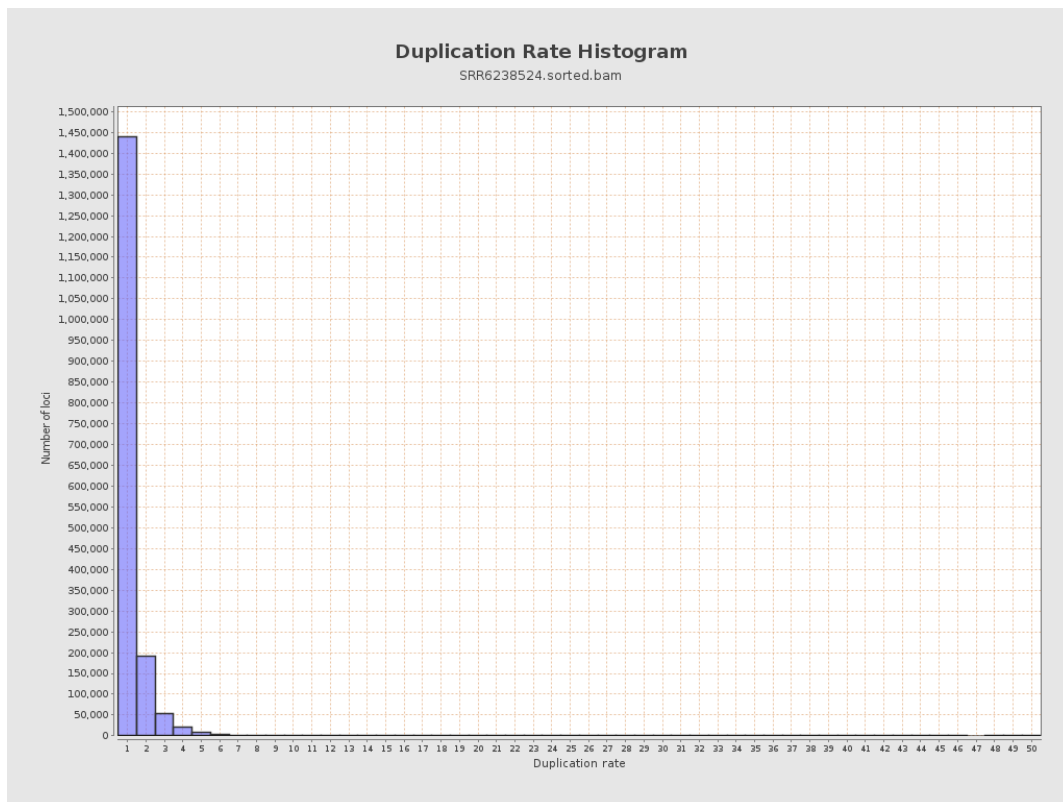
5. Results : Coverage Histogram (0-50X)



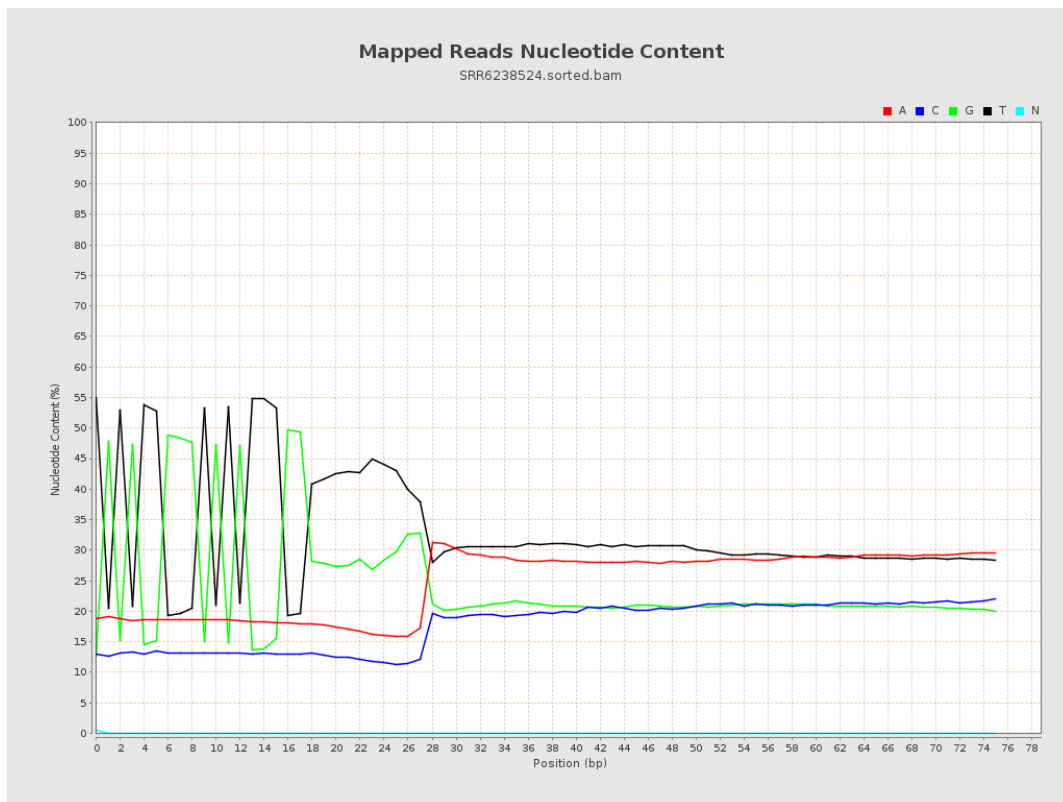
6. Results : Genome Fraction Coverage



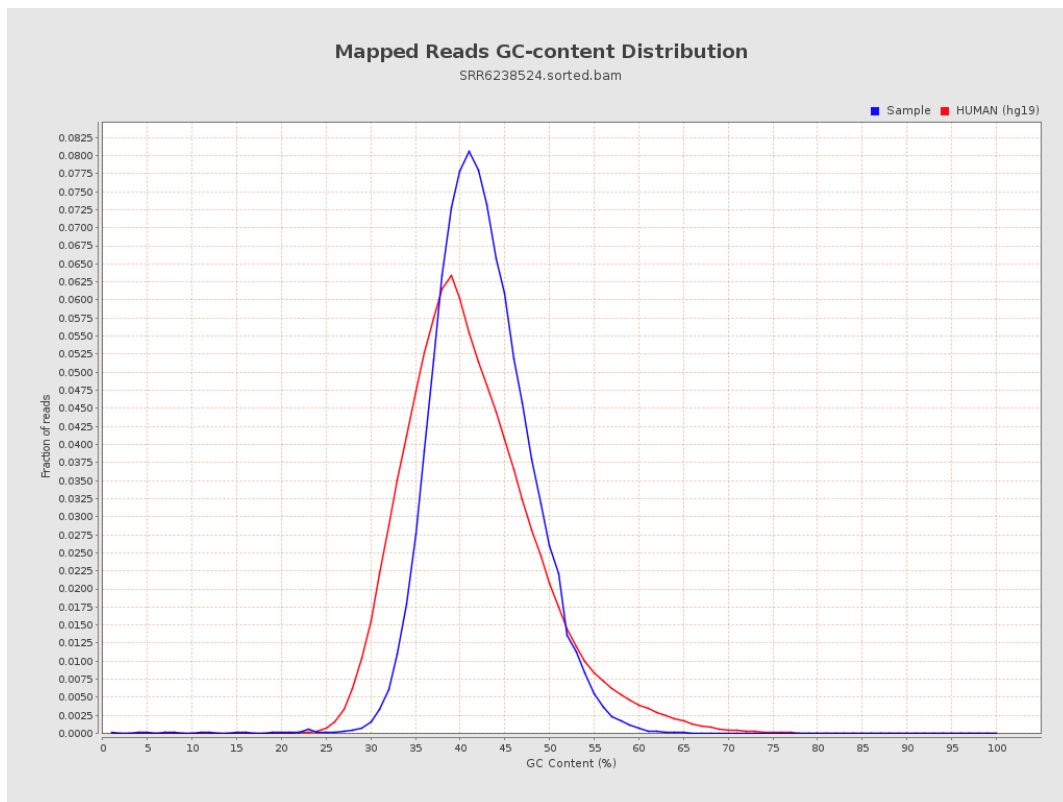
7. Results : Duplication Rate Histogram



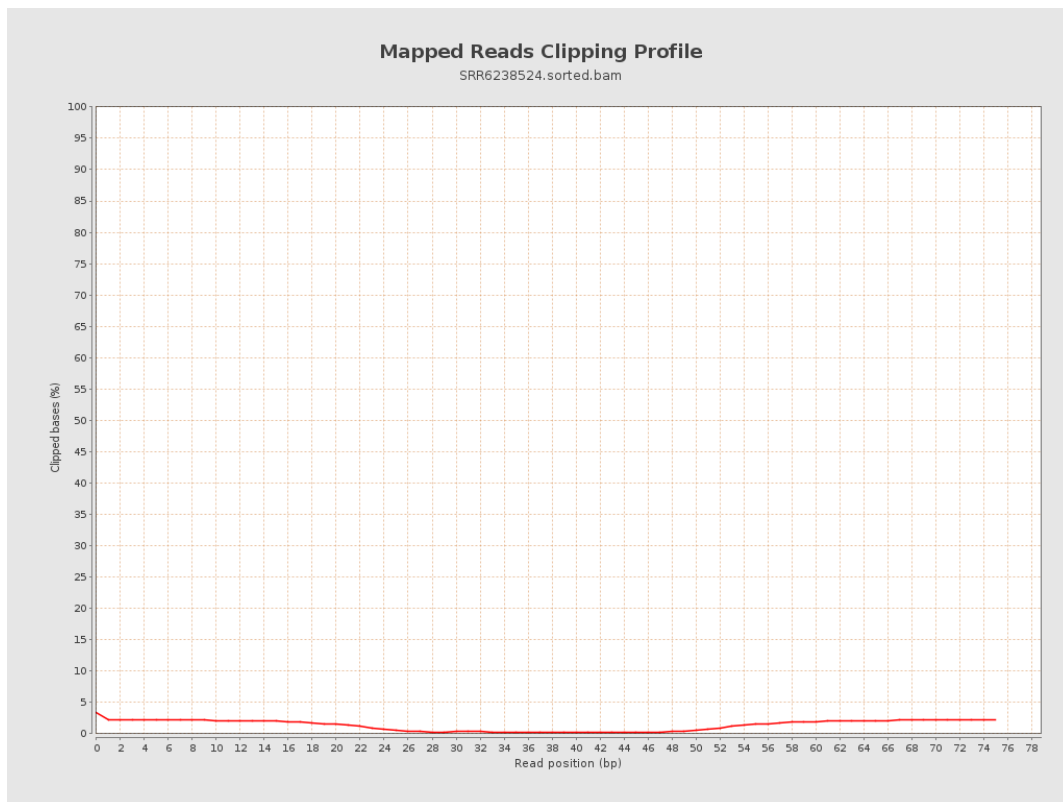
8. Results : Mapped Reads Nucleotide Content



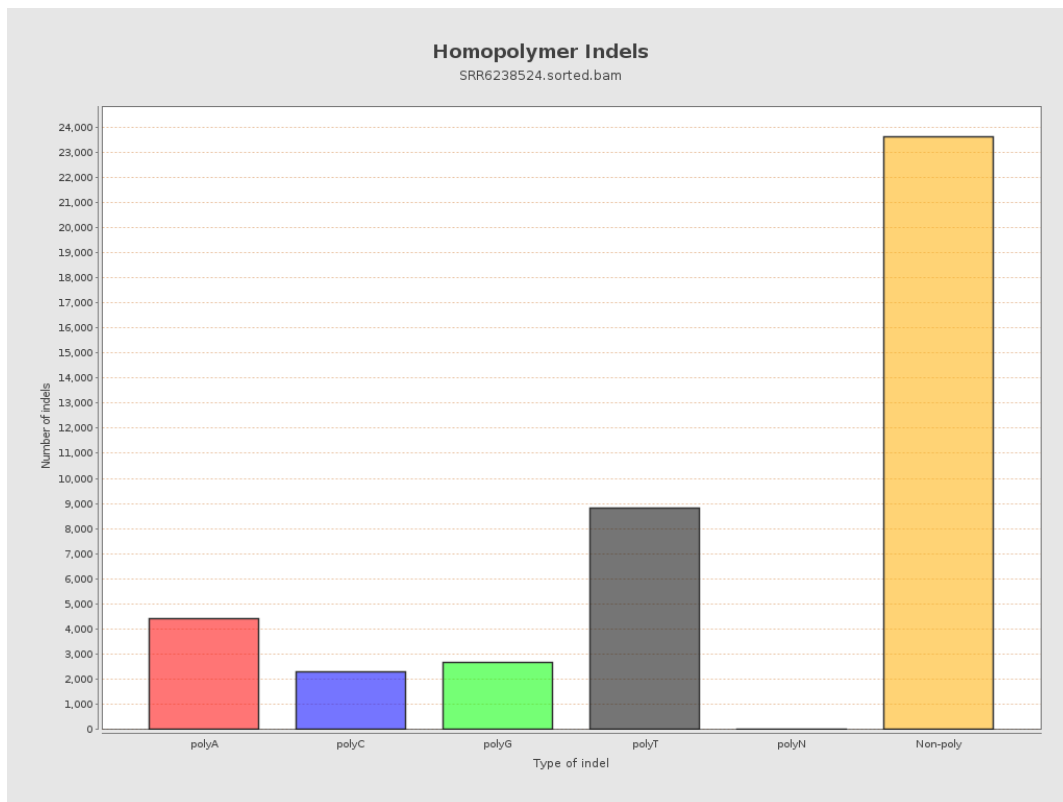
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

