

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 18:26:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238502.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_SRR6238502 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238502.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 18:26:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238502.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,755,890
Mapped reads	2,343,650 / 85.04%
Unmapped reads	412,240 / 14.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,072 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	865,939 / 31.42%
Duplication rate	20.4%
Clipped reads	1,587,134 / 57.59%

2.2. ACGT Content

Number/percentage of A's	35,909,214 / 25.27%
Number/percentage of C's	24,397,204 / 17.17%
Number/percentage of T's	48,943,544 / 34.44%
Number/percentage of G's	32,860,259 / 23.12%
Number/percentage of N's	3,357 / 0%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0459

Standard Deviation	1.117
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2.4. Mapping Quality

Mean Mapping Quality	42.59
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2.5. Mismatches and indels

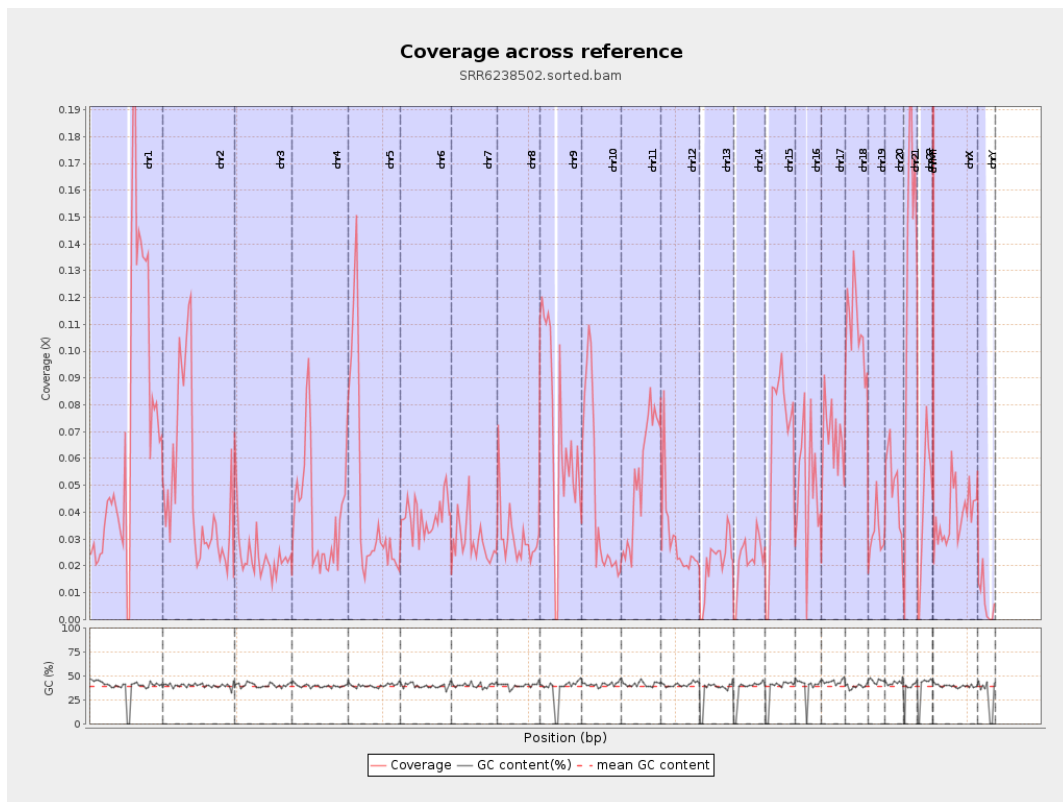
General error rate	0.68%
Mismatches	953,965
Insertions	10,195
Mapped reads with at least one insertion	0.43%
Deletions	47,573
Mapped reads with at least one deletion	2.01%
Homopolymer indels	38.78%

2.6. Chromosome stats

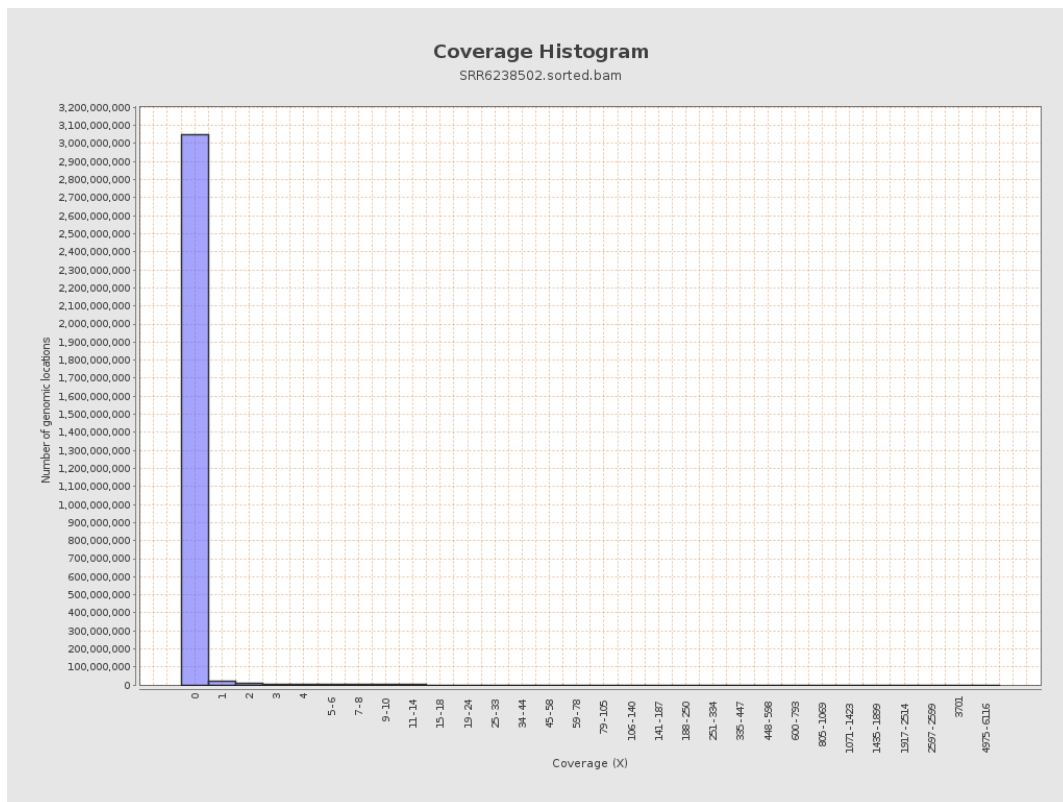
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17137308	0.0688	0.9206
chr2	243199373	11761919	0.0484	2.7172
chr3	198022430	4771272	0.0241	0.4214
chr4	191154276	7675001	0.0402	0.5165
chr5	180915260	7823406	0.0432	0.5519
chr6	171115067	6551331	0.0383	1.0539
chr7	159138663	4667570	0.0293	0.5964

chr8	146364022	4462417	0.0305	0.9526
chr9	141213431	9761280	0.0691	0.8756
chr10	135534747	6011131	0.0444	0.5715
chr11	135006516	7211470	0.0534	0.6422
chr12	133851895	3866216	0.0289	0.4854
chr13	115169878	2458305	0.0213	0.6856
chr14	107349540	2407908	0.0224	0.5047
chr15	102531392	6823054	0.0665	0.9891
chr16	90354753	4445015	0.0492	0.6827
chr17	81195210	5525833	0.0681	0.6811
chr18	78077248	8508195	0.109	2.9294
chr19	59128983	1909973	0.0323	0.629
chr20	63025520	3134327	0.0497	0.6157
chr21	48129895	6433266	0.1337	0.983
chr22	51304566	2249575	0.0438	0.525
chrMT	16571	109743	6.6226	7.5043
chrX	155270560	6059918	0.039	0.549
chrY	59373566	426627	0.0072	0.3045

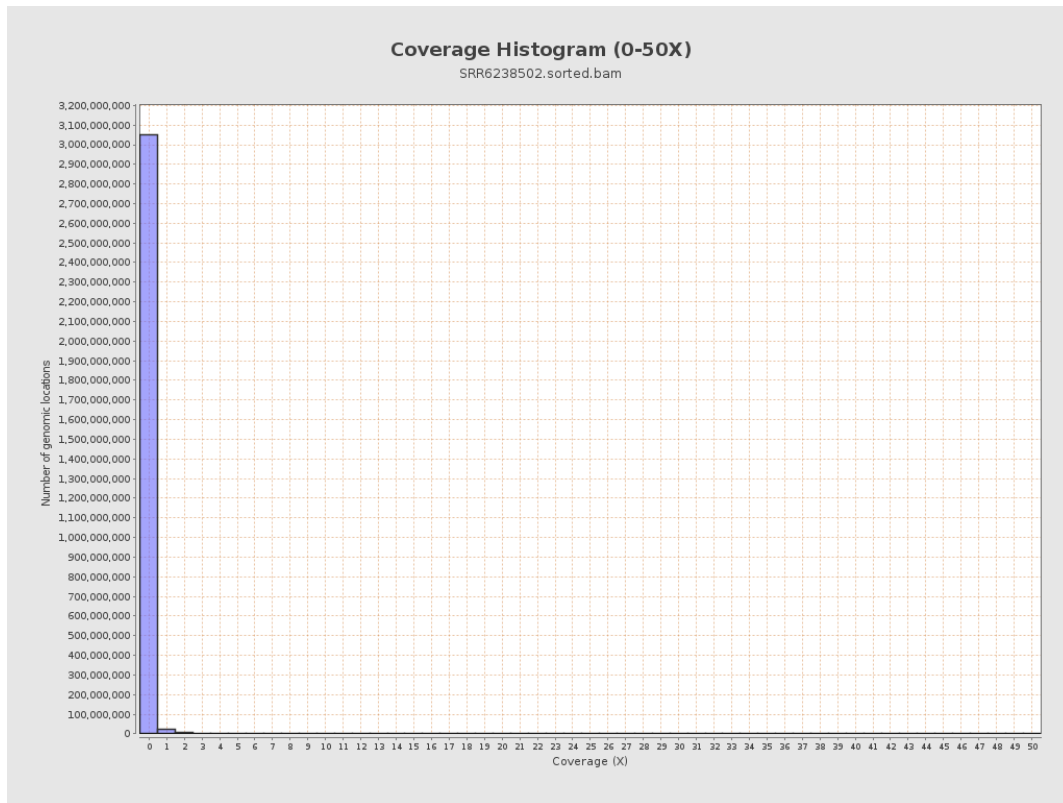
3. Results : Coverage across reference



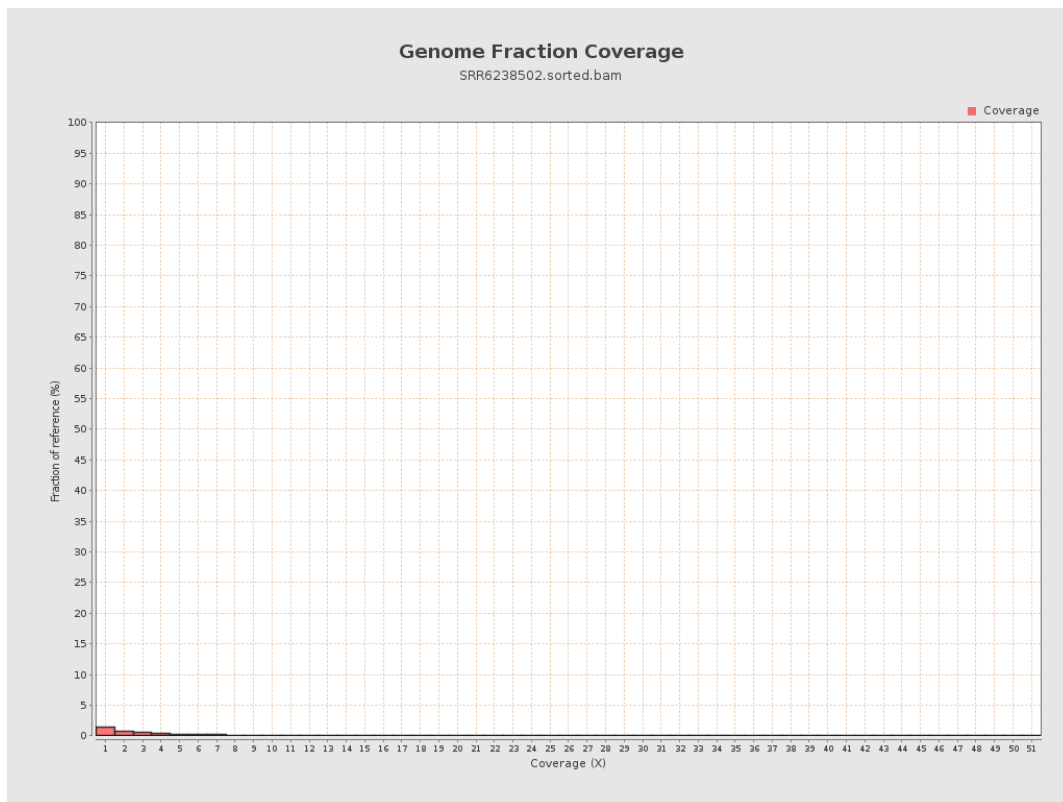
4. Results : Coverage Histogram



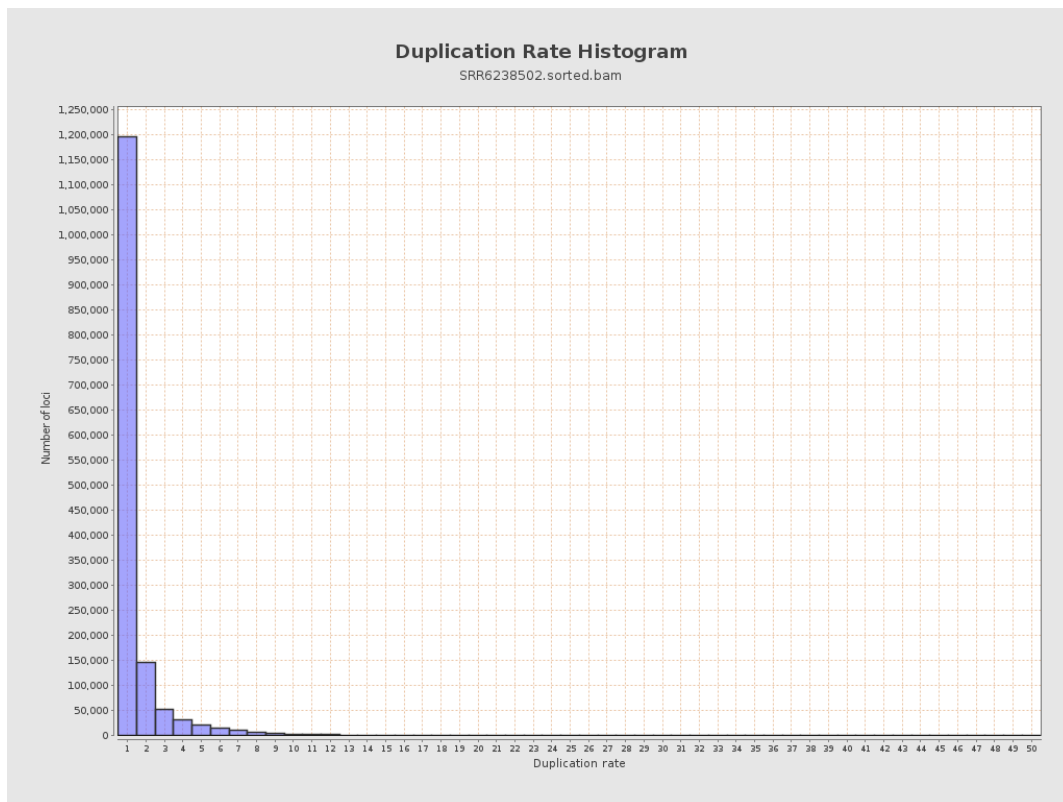
5. Results : Coverage Histogram (0-50X)



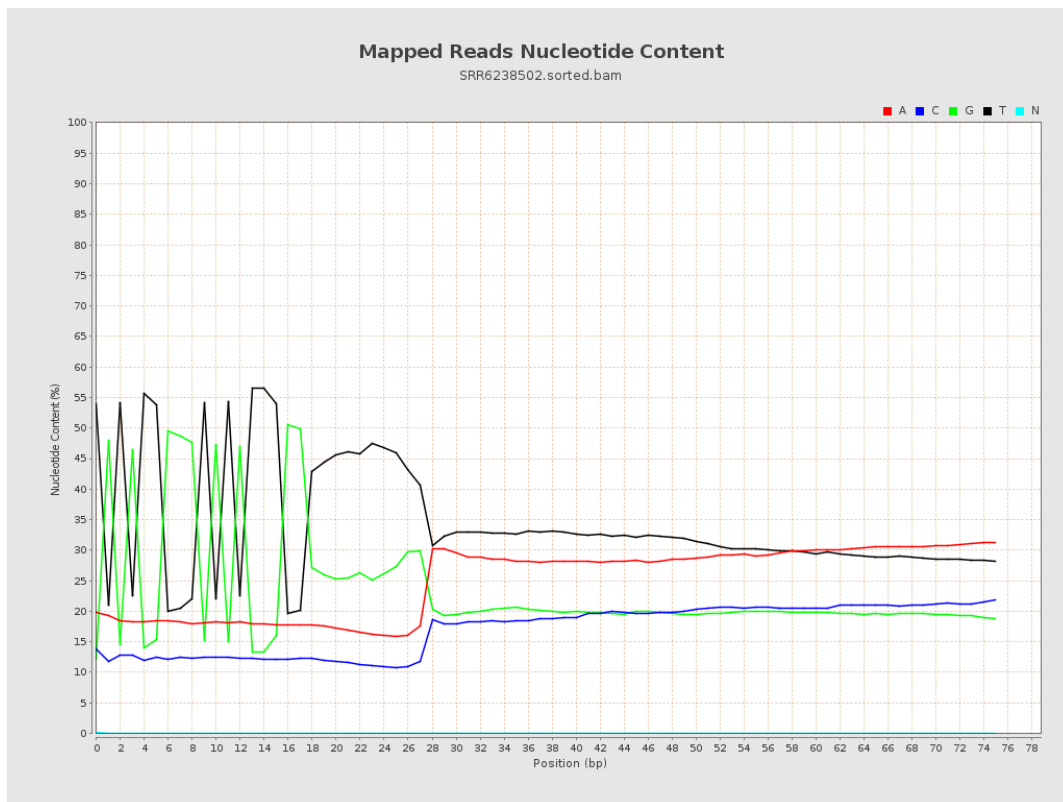
6. Results : Genome Fraction Coverage



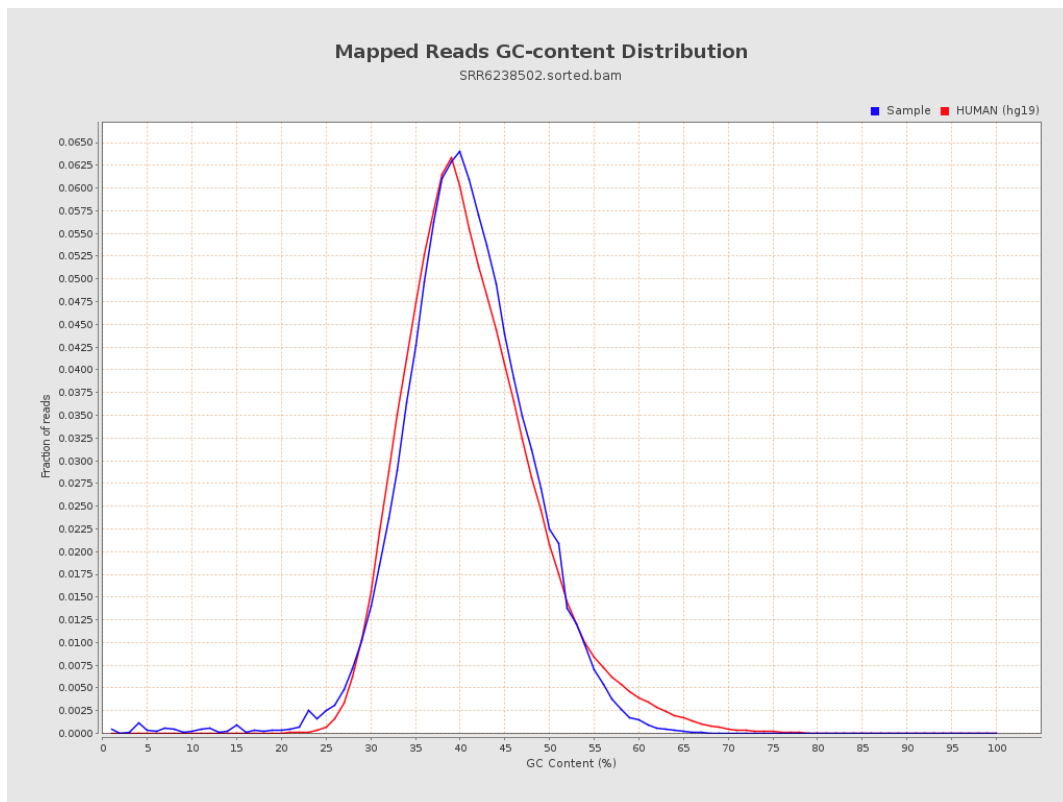
7. Results : Duplication Rate Histogram



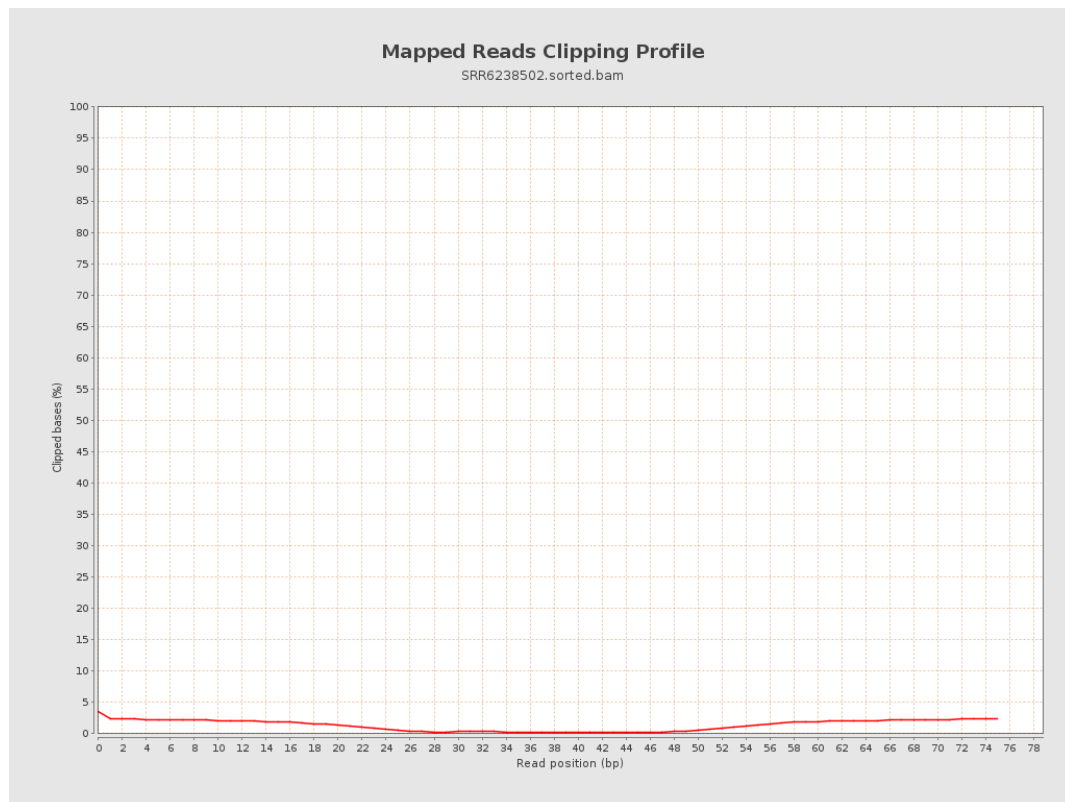
8. Results : Mapped Reads Nucleotide Content



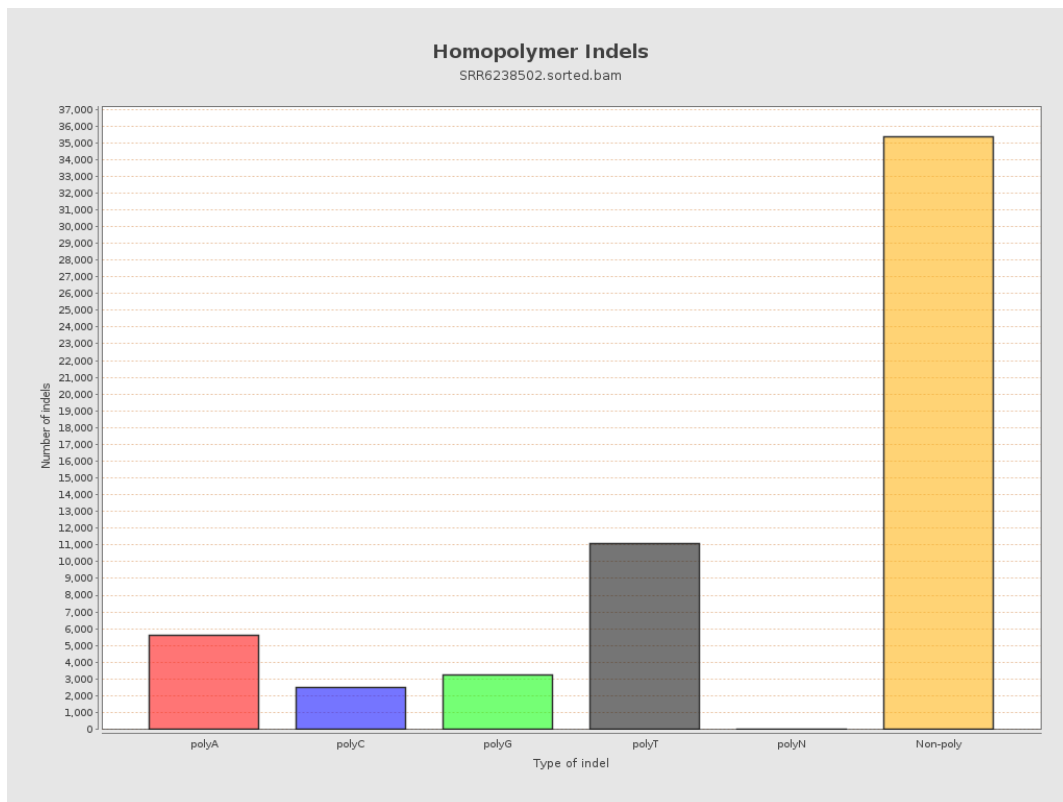
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

