

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:20:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238299.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_SRR6238299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:20:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,744,561
Mapped reads	1,541,577 / 88.36%
Unmapped reads	202,984 / 11.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,840 / 1.14%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	112,049 / 6.42%
Duplication rate	6.07%
Clipped reads	747,598 / 42.85%

2.2. ACGT Content

Number/percentage of A's	27,667,614 / 27.26%
Number/percentage of C's	18,578,137 / 18.3%
Number/percentage of T's	32,305,955 / 31.83%
Number/percentage of G's	22,861,433 / 22.52%
Number/percentage of N's	81,571 / 0.08%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.2981
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2.4. Mapping Quality

Mean Mapping Quality	44.62
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2.5. Mismatches and indels

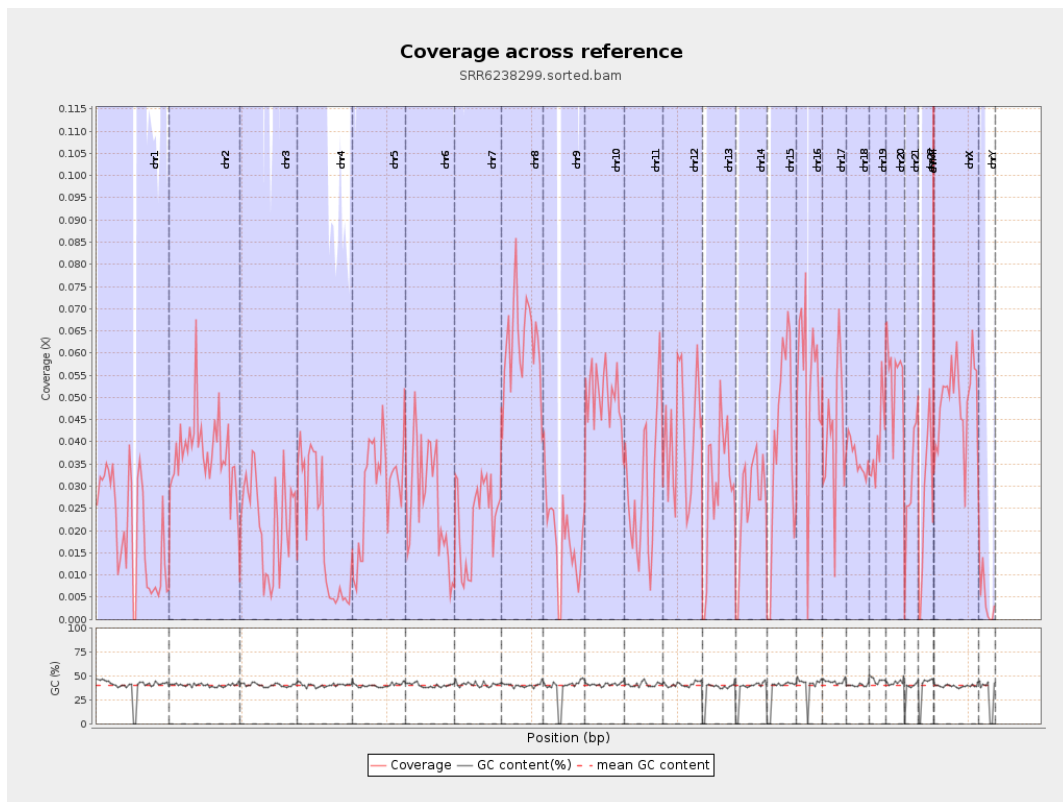
General error rate	0.82%
Mismatches	823,891
Insertions	7,172
Mapped reads with at least one insertion	0.46%
Deletions	27,372
Mapped reads with at least one deletion	1.75%
Homopolymer indels	46.91%

2.6. Chromosome stats

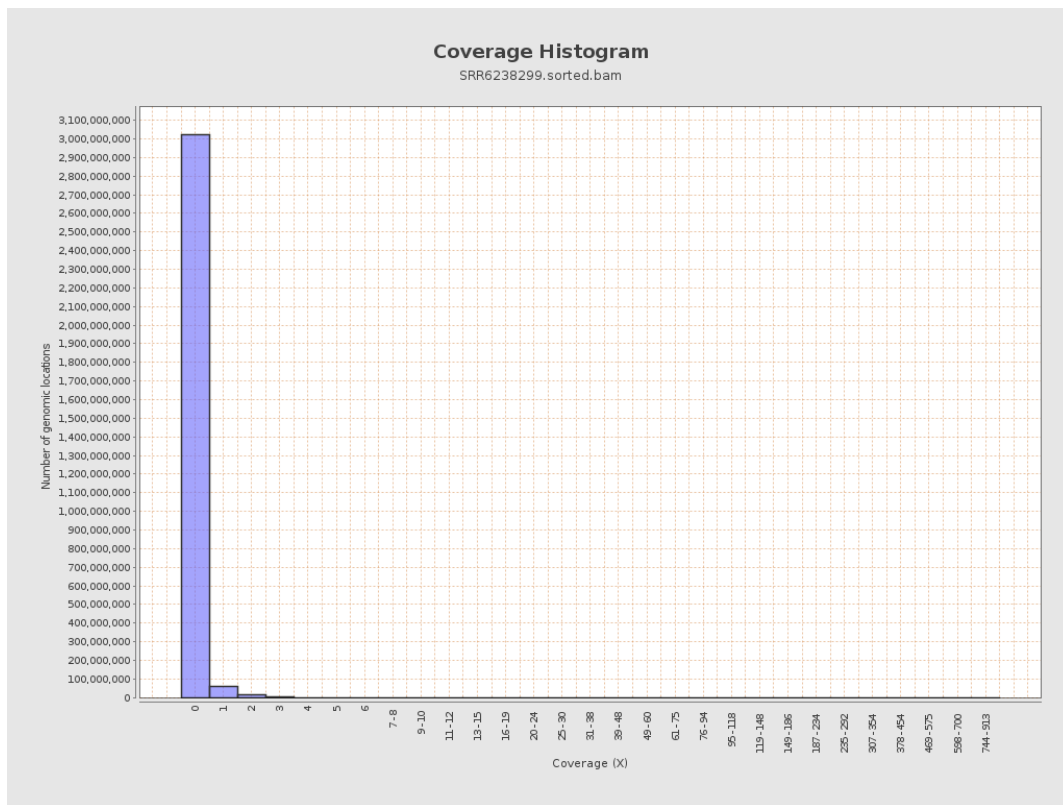
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4852773	0.0195	0.2875
chr2	243199373	9137229	0.0376	0.3829
chr3	198022430	4374987	0.0221	0.1895
chr4	191154276	3684649	0.0193	0.1862
chr5	180915260	5378659	0.0297	0.2222
chr6	171115067	4590995	0.0268	0.2443
chr7	159138663	3593404	0.0226	0.206

chr8	146364022	9091267	0.0621	0.6356
chr9	141213431	2468821	0.0175	0.2272
chr10	135534747	6847270	0.0505	0.3391
chr11	135006516	4043337	0.0299	0.2347
chr12	133851895	5498564	0.0411	0.2639
chr13	115169878	3425009	0.0297	0.2237
chr14	107349540	2813705	0.0262	0.214
chr15	102531392	4023045	0.0392	0.2583
chr16	90354753	4889256	0.0541	0.3059
chr17	81195210	3350616	0.0413	0.2721
chr18	78077248	2844396	0.0364	0.423
chr19	59128983	2368480	0.0401	0.3727
chr20	63025520	3459565	0.0549	0.3066
chr21	48129895	1521702	0.0316	0.2324
chr22	51304566	1357243	0.0265	0.2055
chrMT	16571	4242	0.256	0.5759
chrX	155270560	7659336	0.0493	0.2996
chrY	59373566	263707	0.0044	0.1323

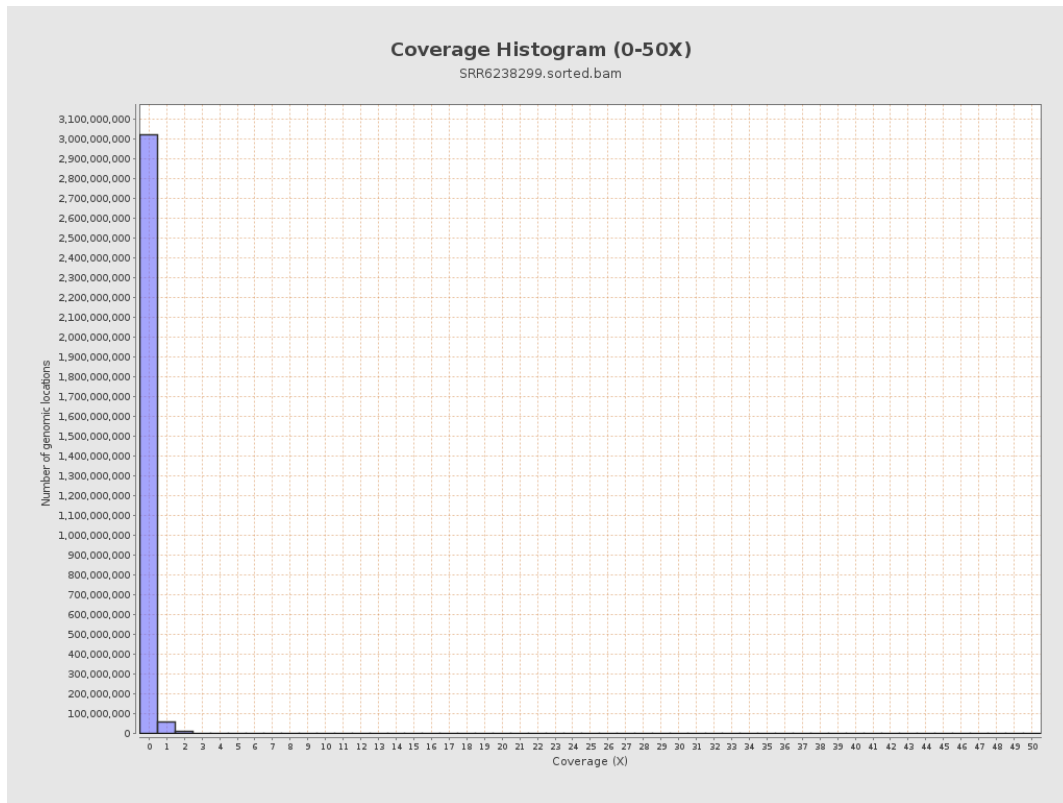
3. Results : Coverage across reference



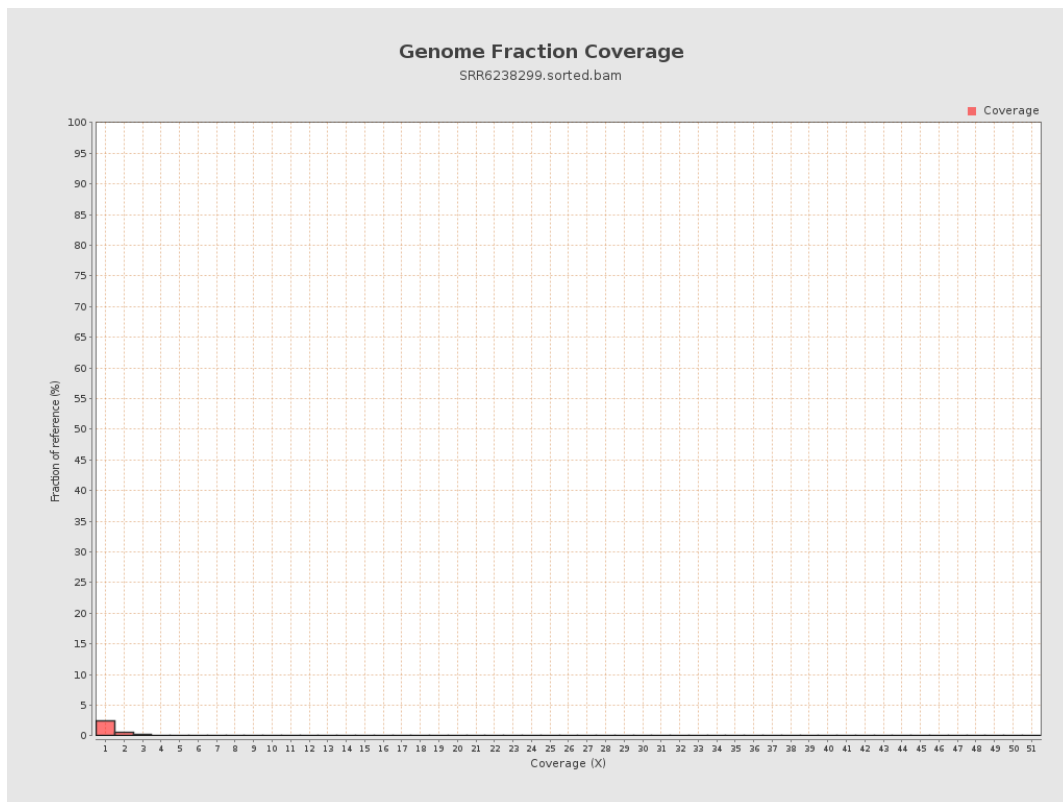
4. Results : Coverage Histogram



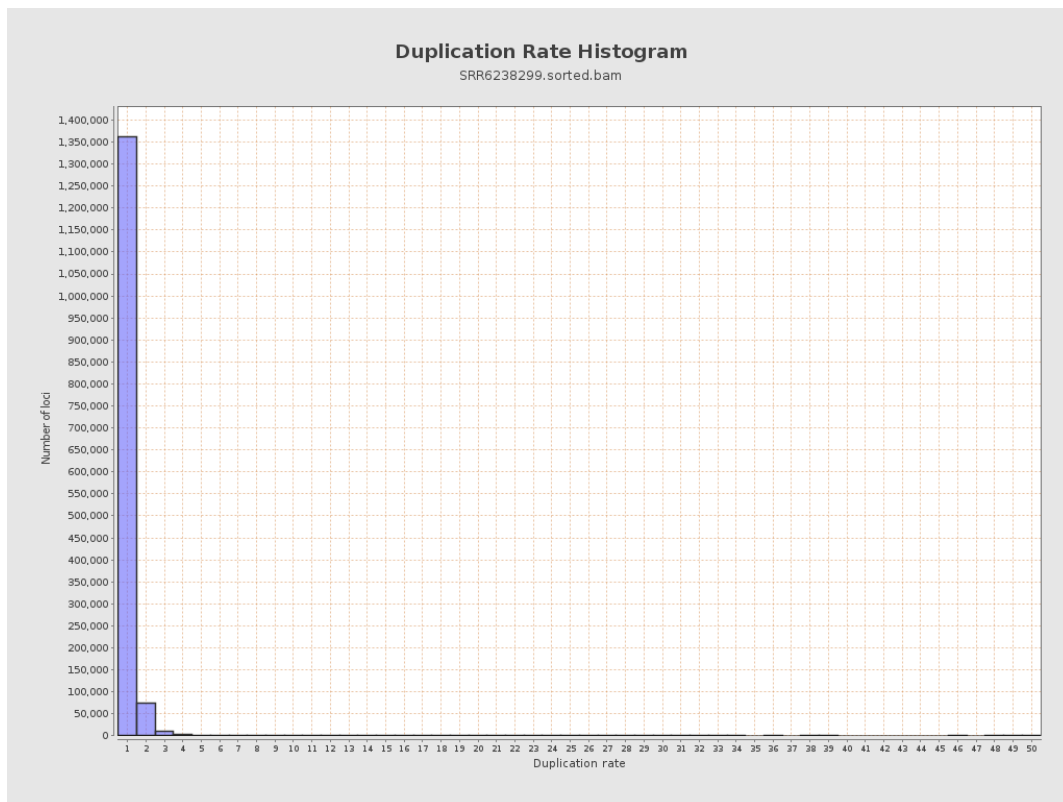
5. Results : Coverage Histogram (0-50X)



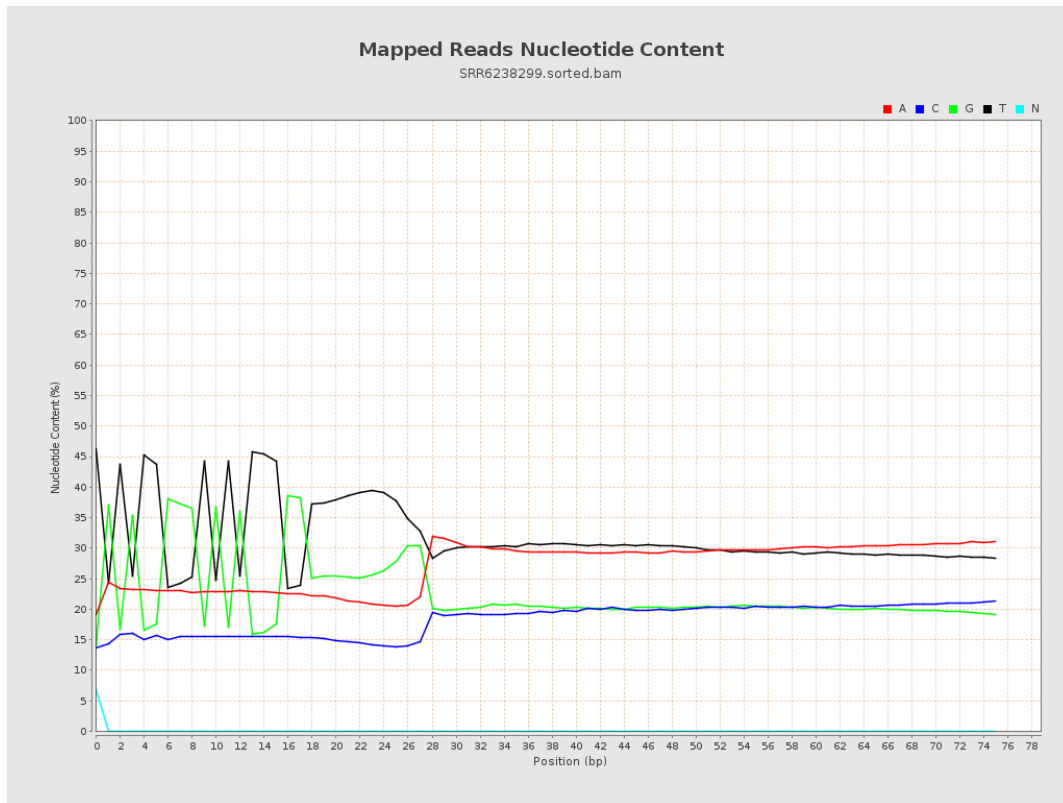
6. Results : Genome Fraction Coverage



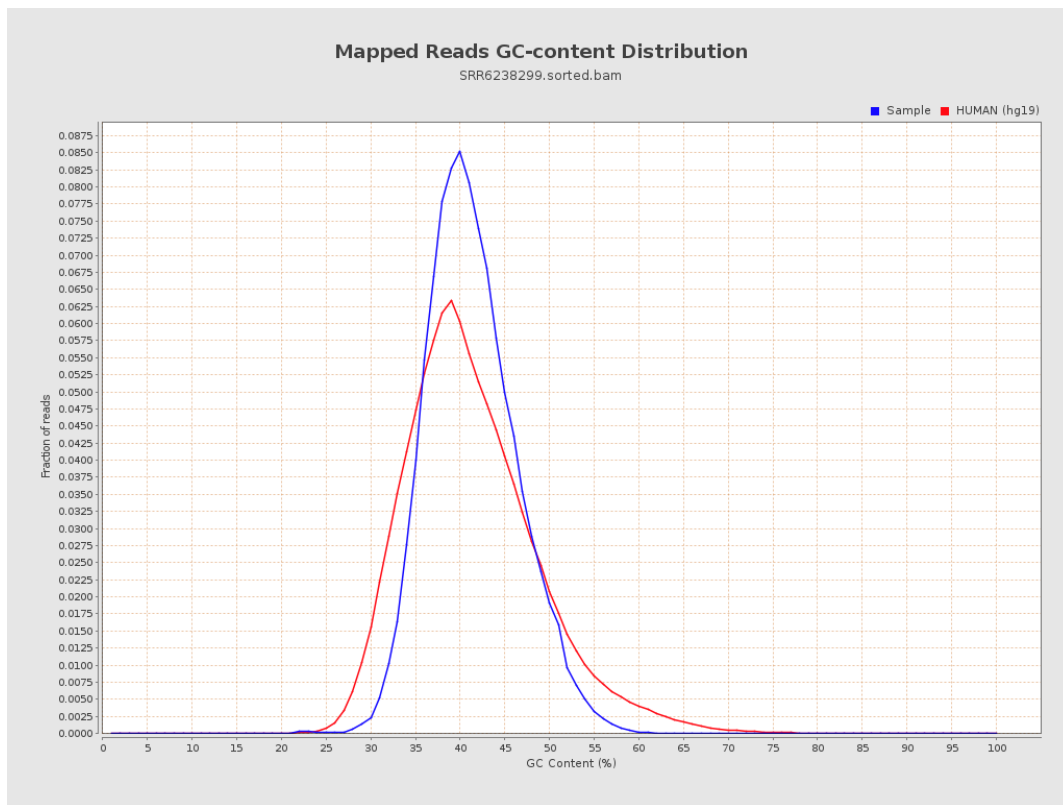
7. Results : Duplication Rate Histogram



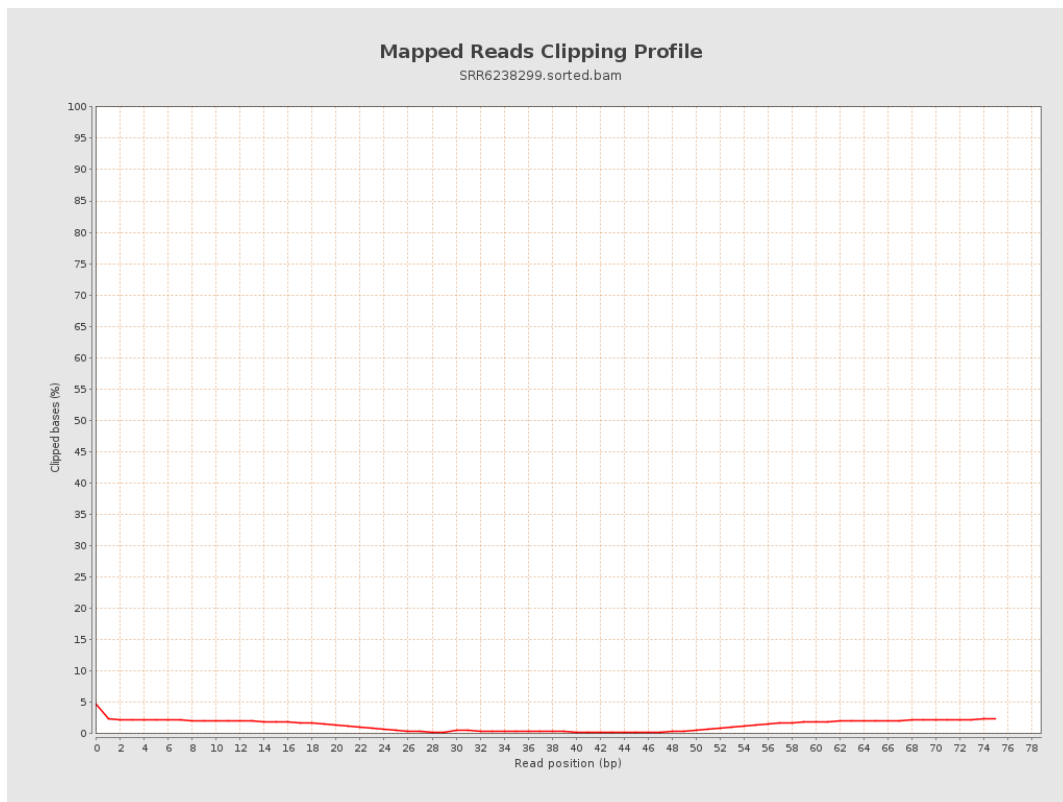
8. Results : Mapped Reads Nucleotide Content



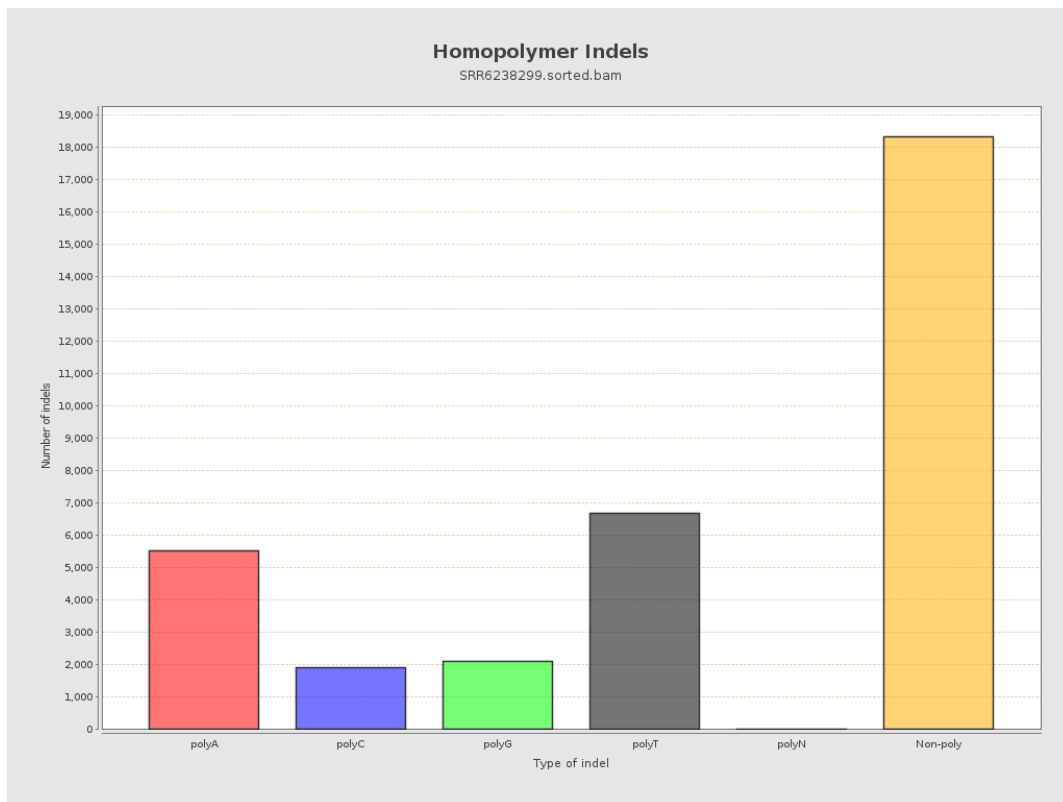
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

