

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:15:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238278.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_SRR6238278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238278.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:15:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	913,694
Mapped reads	766,085 / 83.84%
Unmapped reads	147,609 / 16.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,139 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	15,240 / 1.67%
Duplication rate	1.45%
Clipped reads	334,971 / 36.66%

2.2. ACGT Content

Number/percentage of A's	15,159,714 / 29.5%
Number/percentage of C's	9,325,176 / 18.15%
Number/percentage of T's	15,337,756 / 29.85%
Number/percentage of G's	11,548,875 / 22.47%
Number/percentage of N's	14,276 / 0.03%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0166

Standard Deviation	0.1827
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2.4. Mapping Quality

Mean Mapping Quality	45.29
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2.5. Mismatches and indels

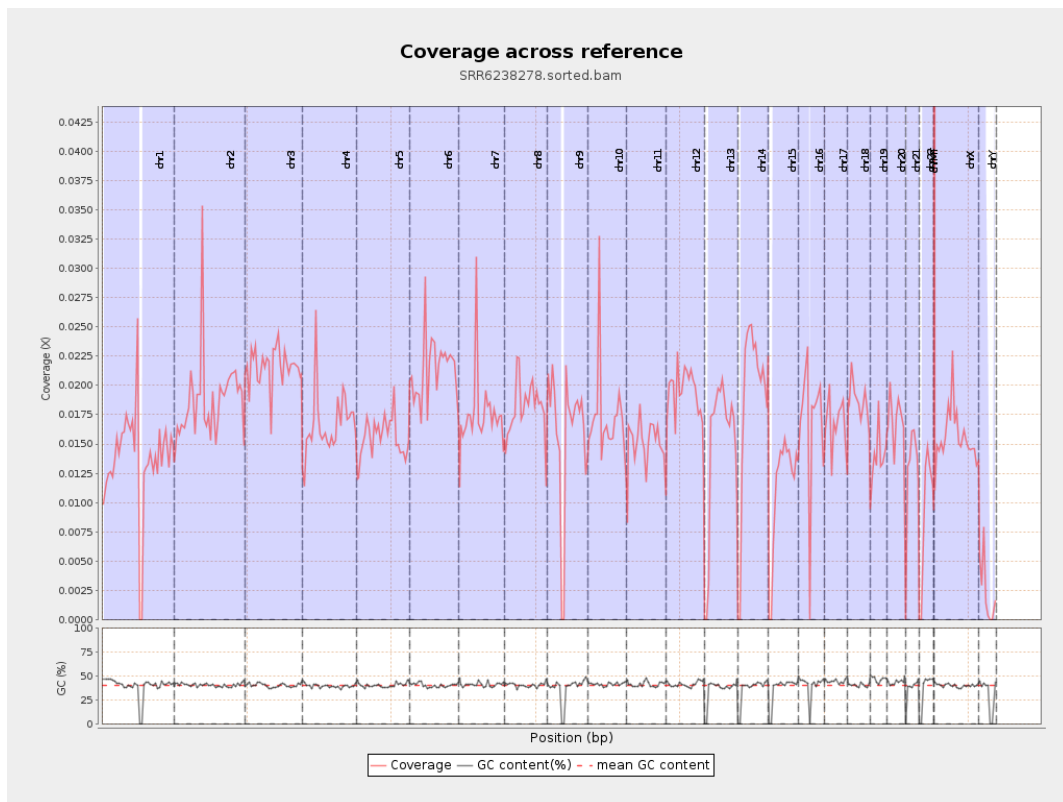
General error rate	1.01%
Mismatches	509,301
Insertions	4,515
Mapped reads with at least one insertion	0.58%
Deletions	15,623
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.86%

2.6. Chromosome stats

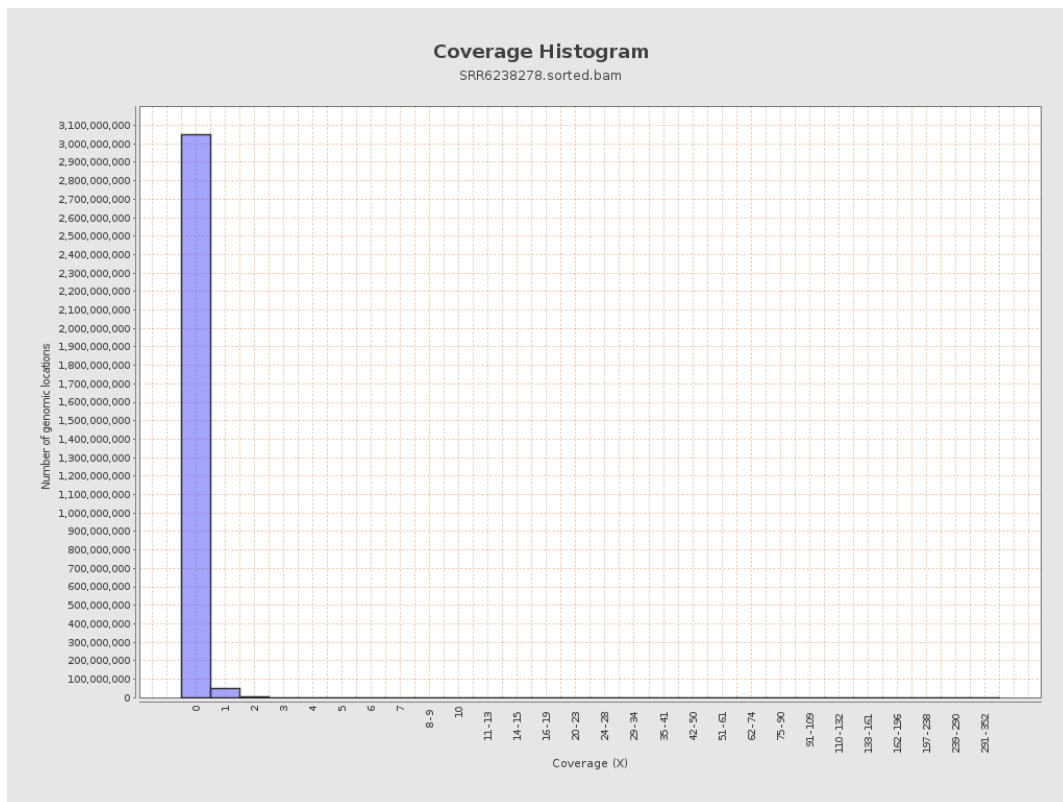
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3411910	0.0137	0.2747
chr2	243199373	4571942	0.0188	0.2007
chr3	198022430	4278727	0.0216	0.152
chr4	191154276	3188846	0.0167	0.1417
chr5	180915260	2824862	0.0156	0.1295
chr6	171115067	3652982	0.0213	0.175
chr7	159138663	2799182	0.0176	0.2308

chr8	146364022	2641834	0.018	0.2625
chr9	141213431	2259505	0.016	0.1699
chr10	135534747	2323457	0.0171	0.1947
chr11	135006516	2058843	0.0152	0.1475
chr12	133851895	2603721	0.0195	0.1458
chr13	115169878	1718586	0.0149	0.1258
chr14	107349540	2033263	0.0189	0.1519
chr15	102531392	1154495	0.0113	0.1101
chr16	90354753	1513608	0.0168	0.1485
chr17	81195210	1359125	0.0167	0.1472
chr18	78077248	1458717	0.0187	0.3019
chr19	59128983	830777	0.0141	0.195
chr20	63025520	1059190	0.0168	0.1376
chr21	48129895	623634	0.013	0.1302
chr22	51304566	476667	0.0093	0.0992
chrMT	16571	8344	0.5035	0.7482
chrX	155270560	2421569	0.0156	0.1373
chrY	59373566	138257	0.0023	0.0778

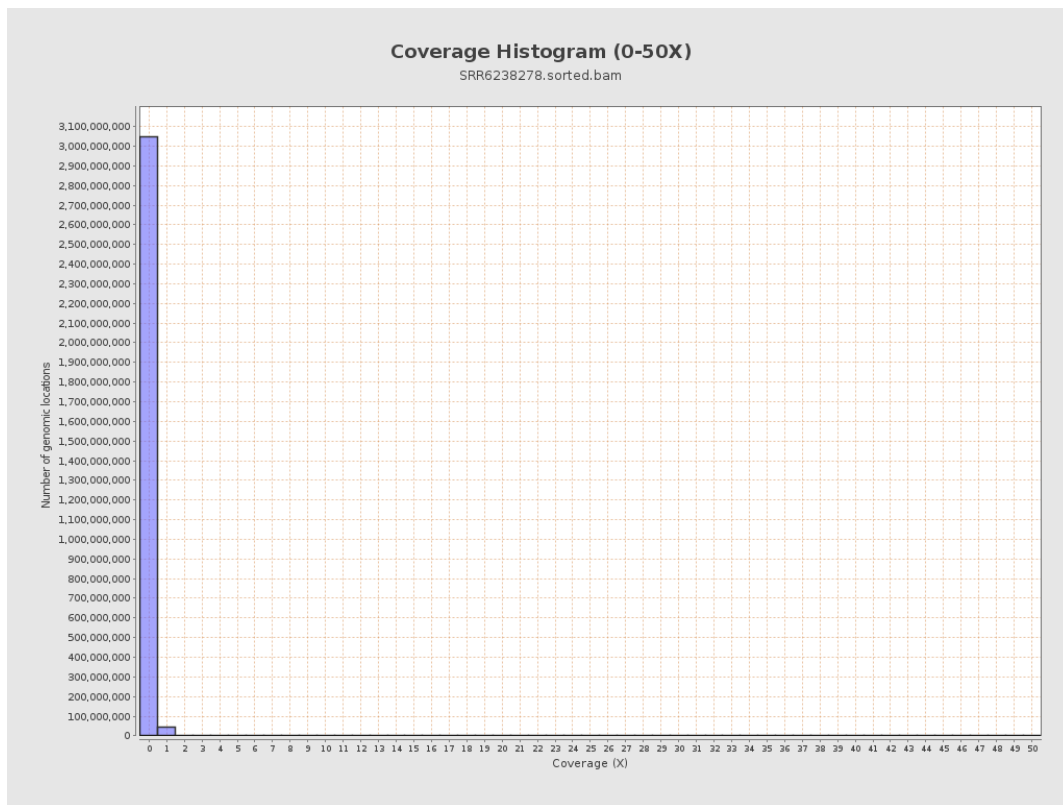
3. Results : Coverage across reference



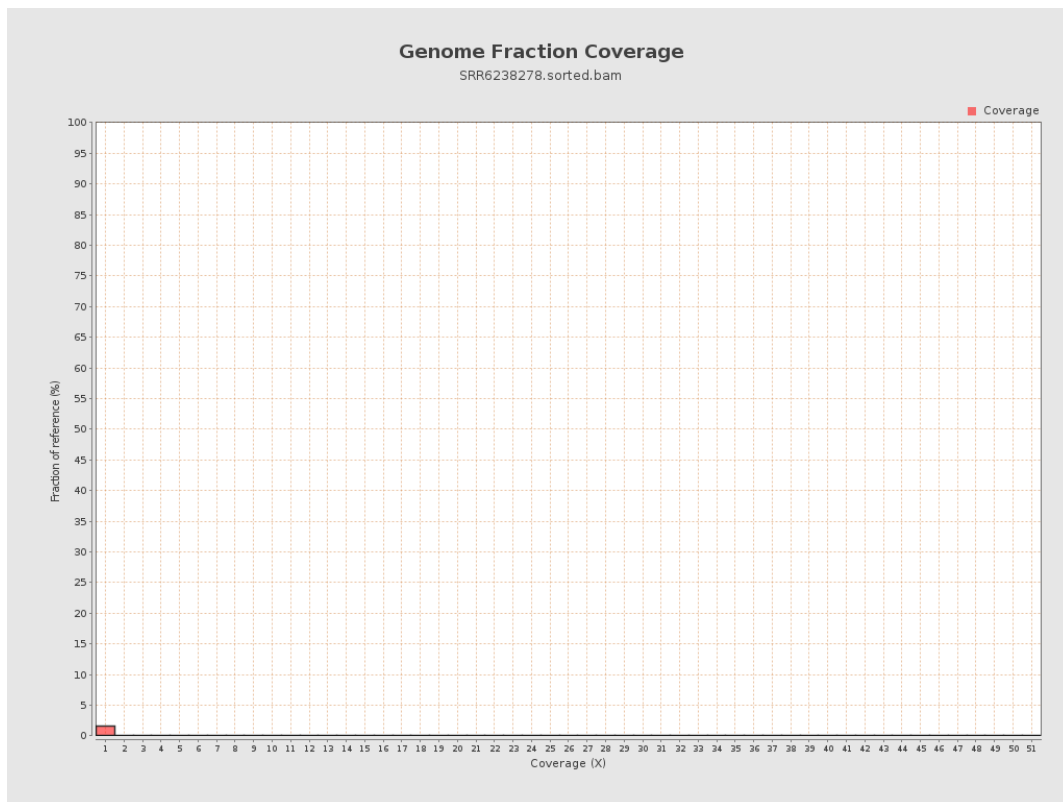
4. Results : Coverage Histogram



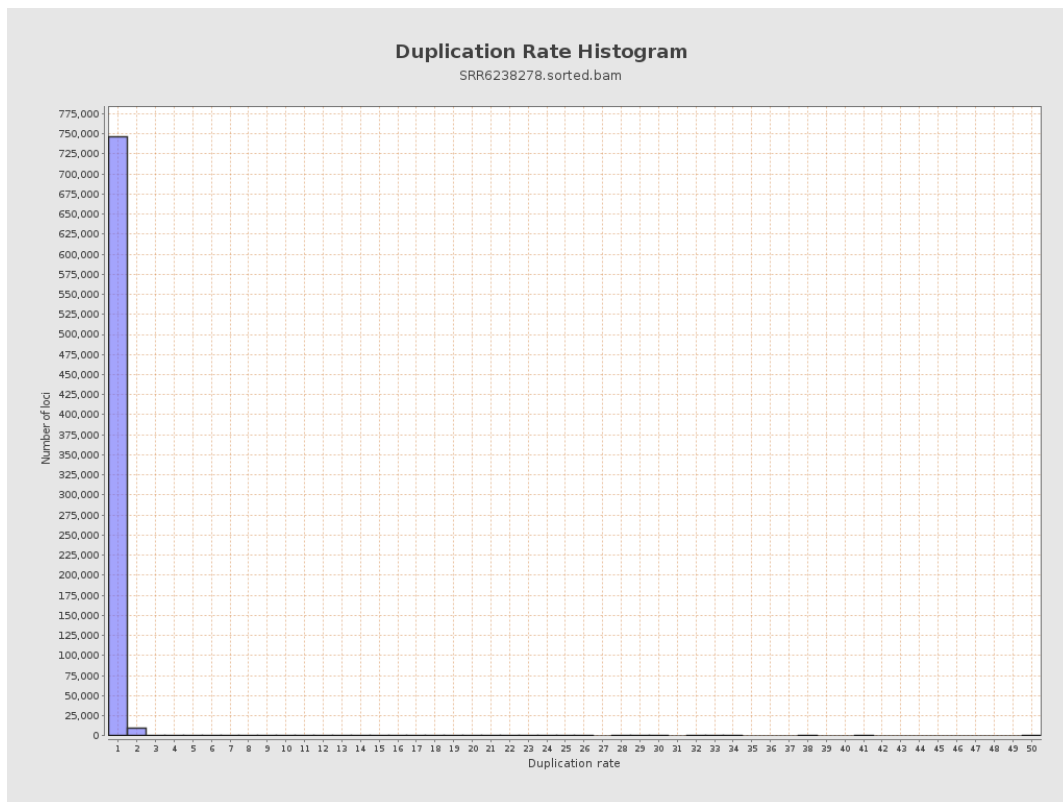
5. Results : Coverage Histogram (0-50X)



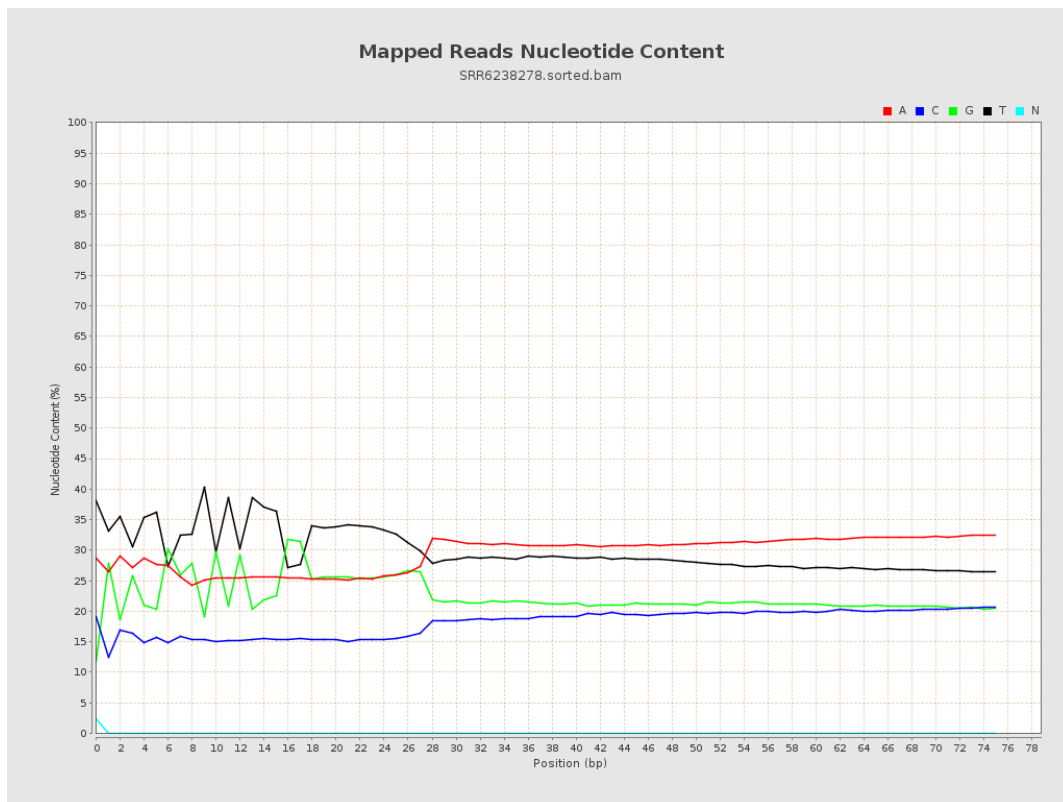
6. Results : Genome Fraction Coverage



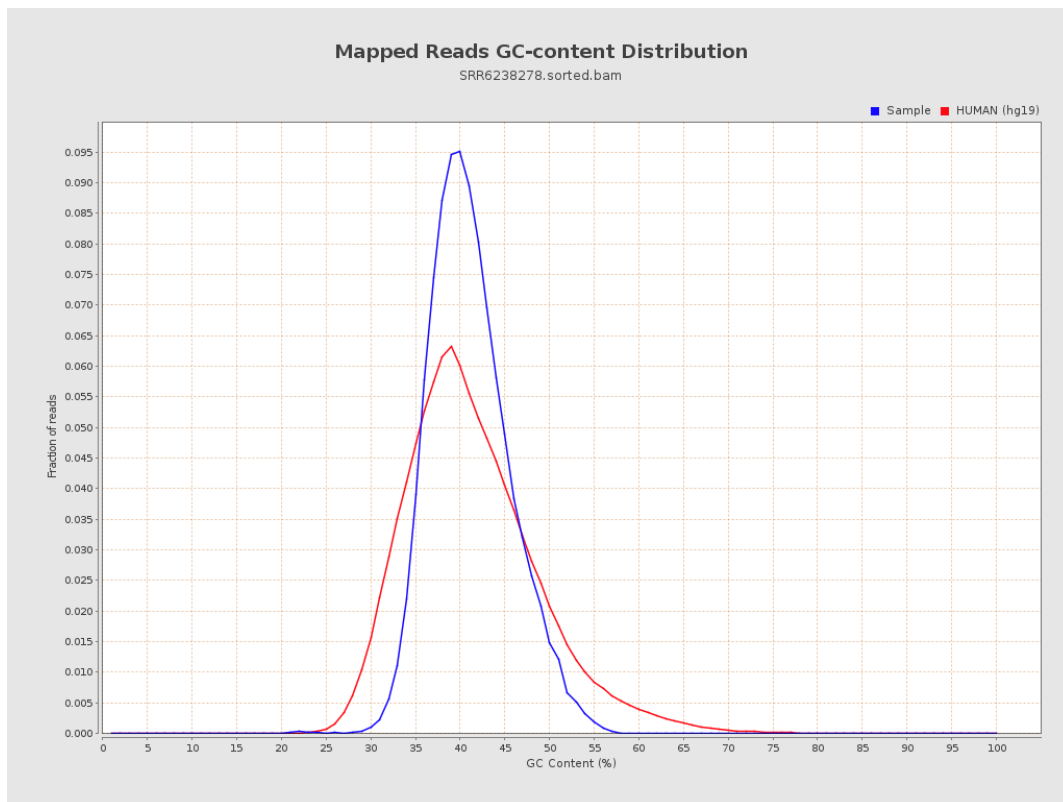
7. Results : Duplication Rate Histogram



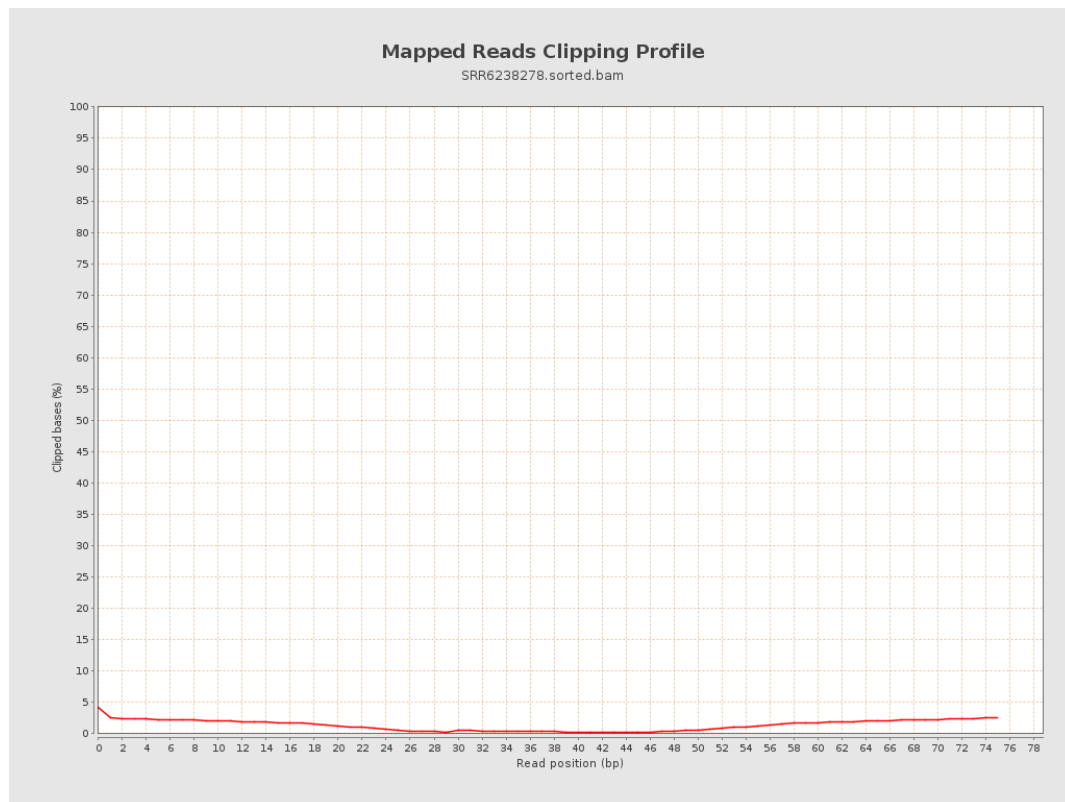
8. Results : Mapped Reads Nucleotide Content



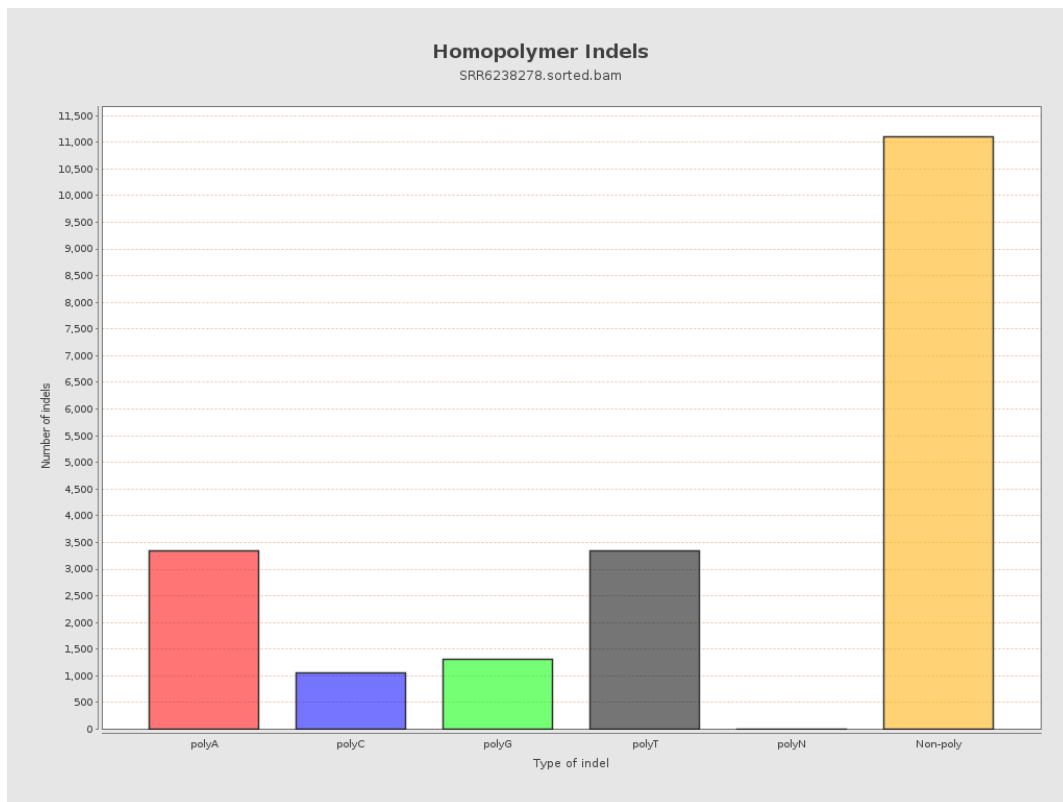
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

