

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:37:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525078.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_SRR10525078 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525078.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:37:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525078.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,784,892
Mapped reads	4,303,642 / 89.94%
Unmapped reads	481,250 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,217 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	295,586 / 6.18%
Duplication rate	5.2%
Clipped reads	4,312,579 / 90.13%

2.2. ACGT Content

Number/percentage of A's	65,348,231 / 26.25%
Number/percentage of C's	47,248,212 / 18.98%
Number/percentage of T's	78,713,300 / 31.62%
Number/percentage of G's	57,619,311 / 23.15%
Number/percentage of N's	7,419 / 0%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0804

Standard Deviation	0.6355
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2.4. Mapping Quality

Mean Mapping Quality	45.7
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2.5. Mismatches and indels

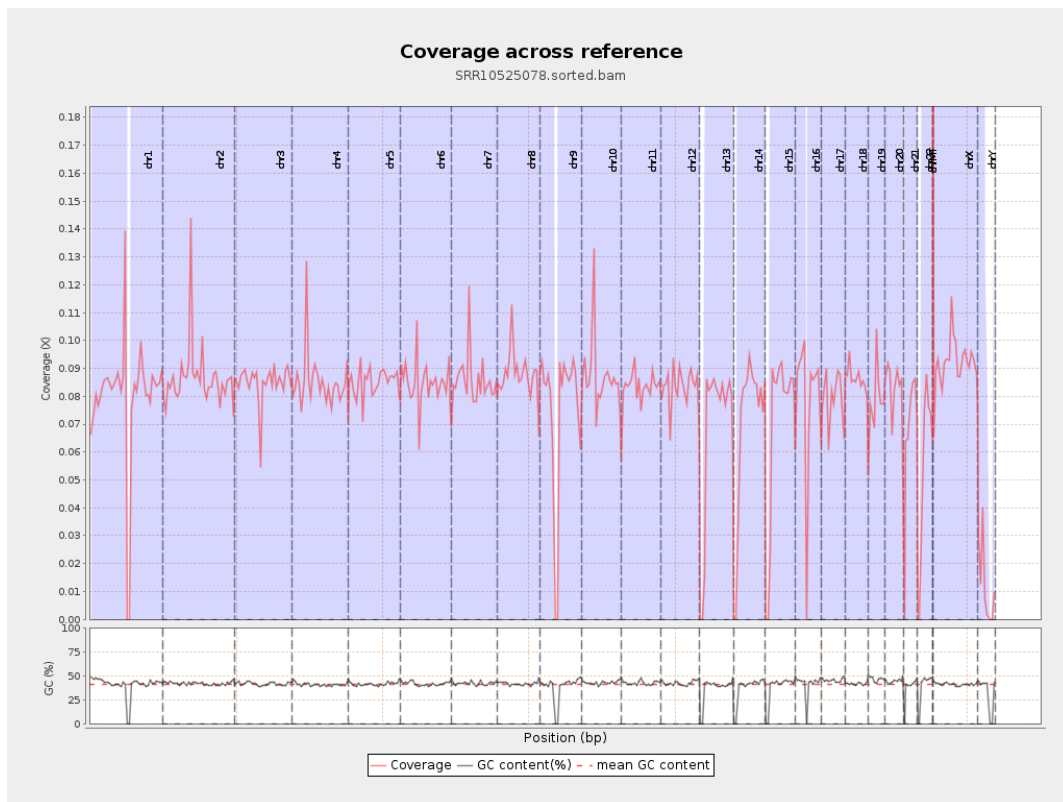
General error rate	0.5%
Mismatches	1,205,195
Insertions	16,011
Mapped reads with at least one insertion	0.37%
Deletions	38,892
Mapped reads with at least one deletion	0.9%
Homopolymer indels	41.29%

2.6. Chromosome stats

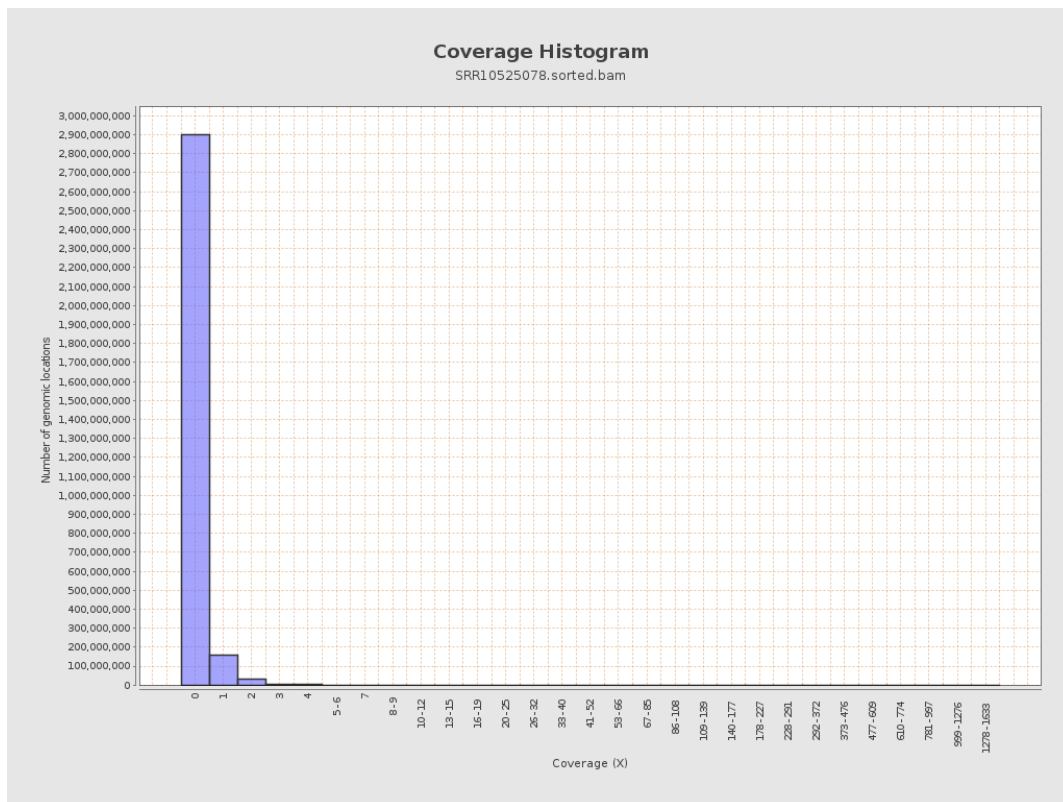
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19908288	0.0799	1.3152
chr2	243199373	21055490	0.0866	0.6655
chr3	198022430	16817730	0.0849	0.3592
chr4	191154276	16303116	0.0853	0.4269
chr5	180915260	15380058	0.085	0.3684
chr6	171115067	14533643	0.0849	0.4239
chr7	159138663	13624725	0.0856	0.6785

chr8	146364022	12846093	0.0878	0.8064
chr9	141213431	10557510	0.0748	0.5955
chr10	135534747	11780872	0.0869	0.5875
chr11	135006516	11265240	0.0834	0.5746
chr12	133851895	11194935	0.0836	0.3791
chr13	115169878	7901947	0.0686	0.3238
chr14	107349540	7512374	0.07	0.3913
chr15	102531392	7075396	0.069	0.3263
chr16	90354753	7005053	0.0775	0.3873
chr17	81195210	6484379	0.0799	0.4013
chr18	78077248	6744329	0.0864	1.0917
chr19	59128983	4678629	0.0791	0.9024
chr20	63025520	5234700	0.0831	0.3801
chr21	48129895	3293339	0.0684	0.3905
chr22	51304566	2773620	0.0541	0.2849
chrMT	16571	10041	0.6059	0.8933
chrX	155270560	14310928	0.0922	0.4678
chrY	59373566	708547	0.0119	0.2719

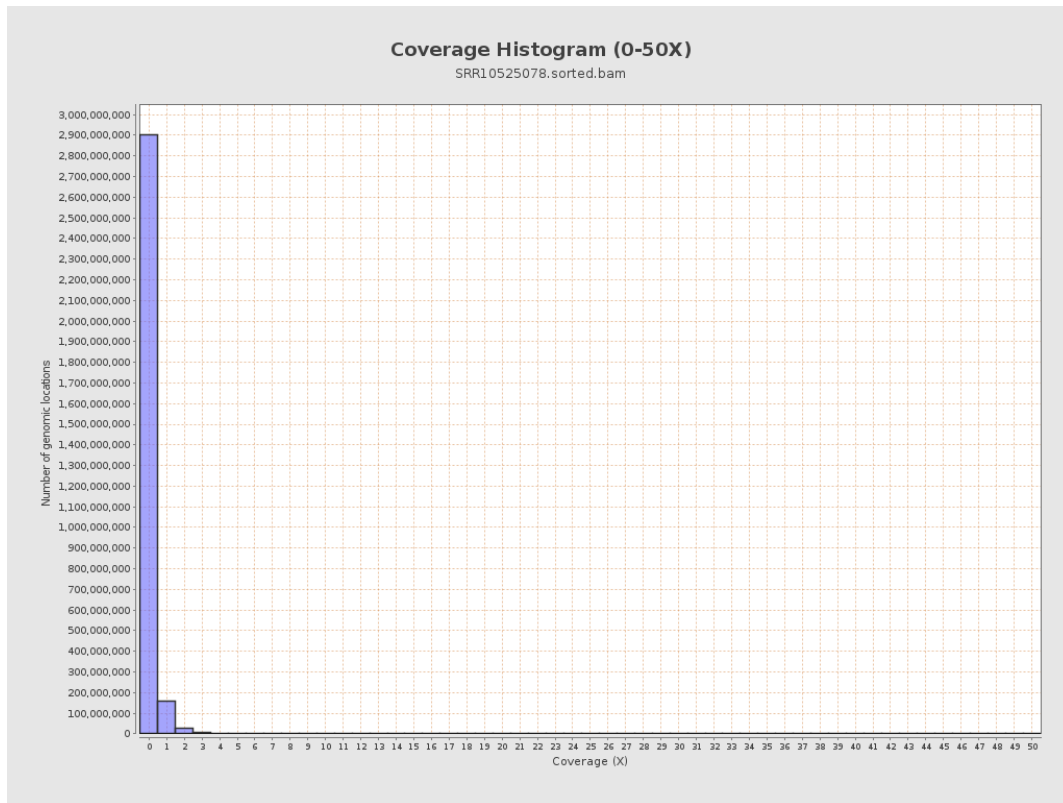
3. Results : Coverage across reference



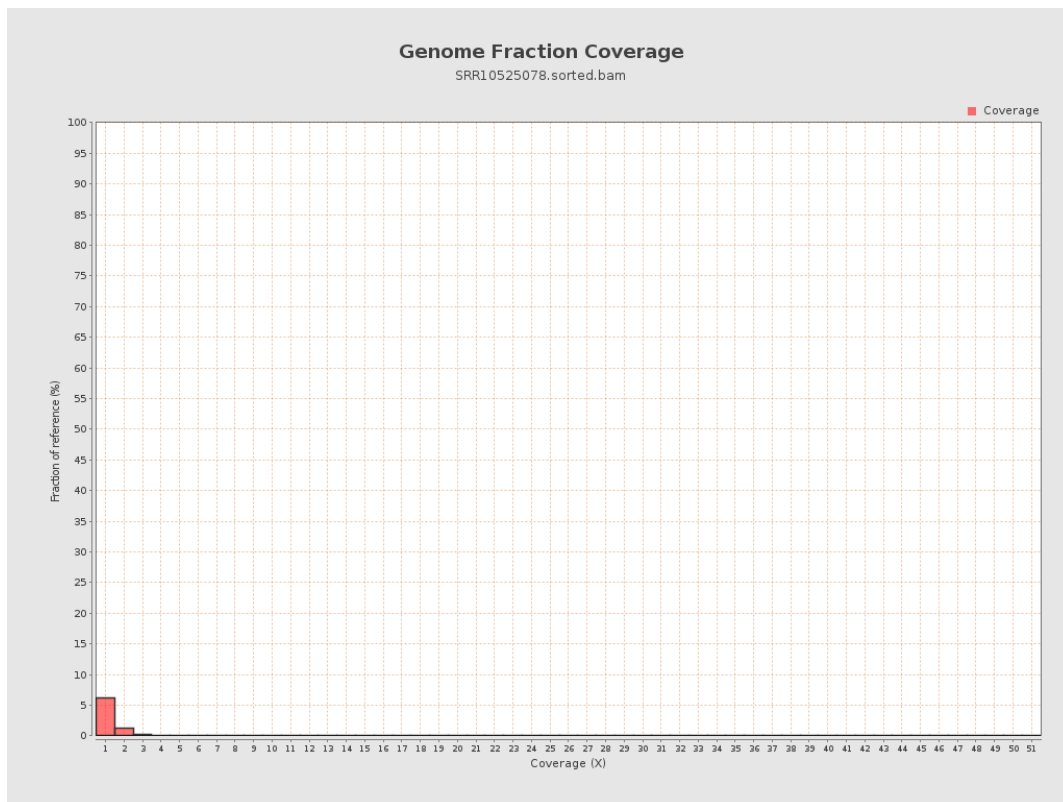
4. Results : Coverage Histogram



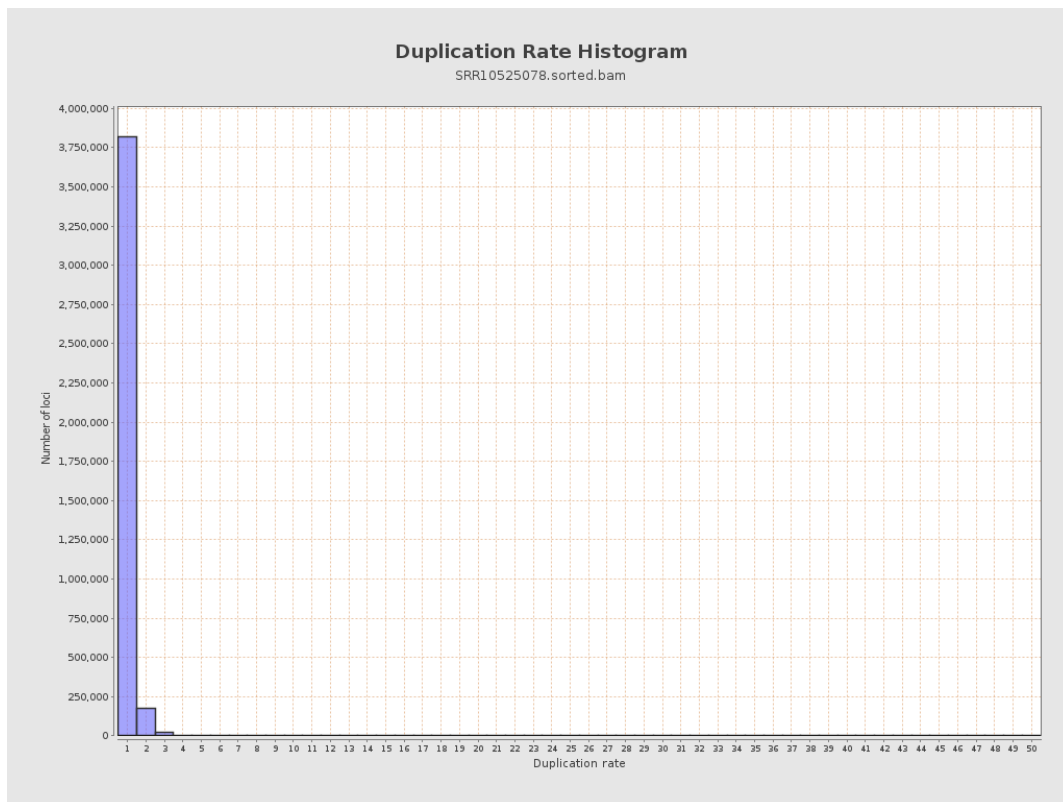
5. Results : Coverage Histogram (0-50X)



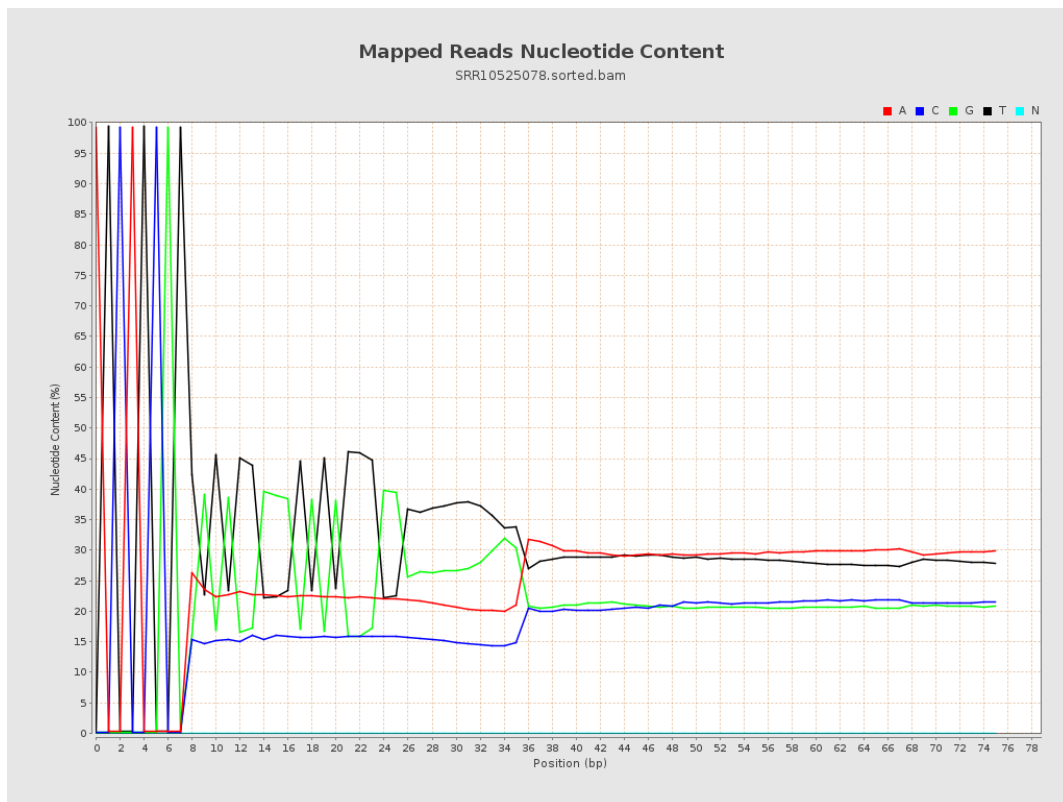
6. Results : Genome Fraction Coverage



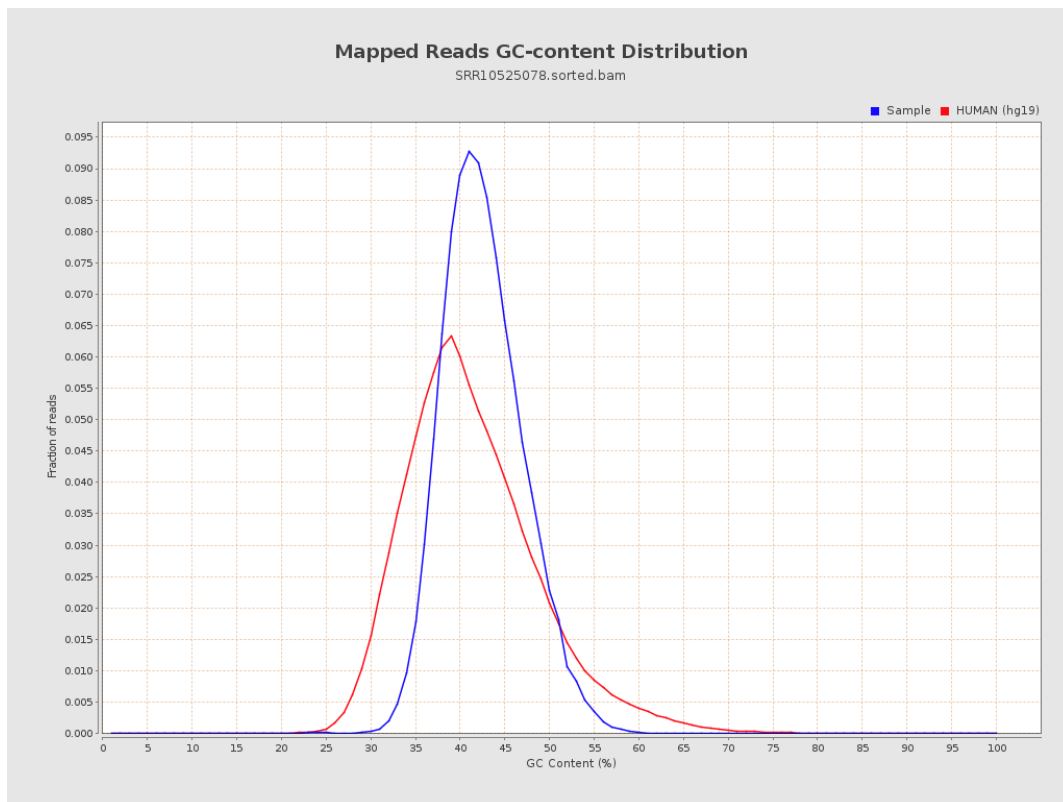
7. Results : Duplication Rate Histogram



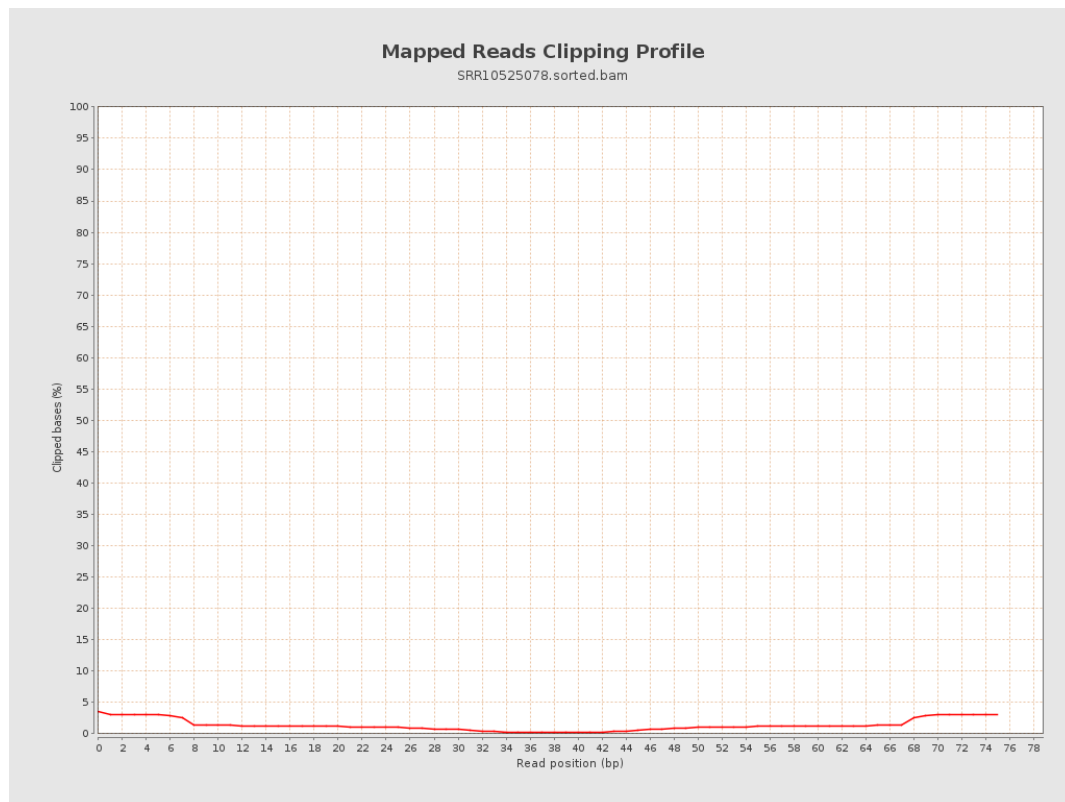
8. Results : Mapped Reads Nucleotide Content



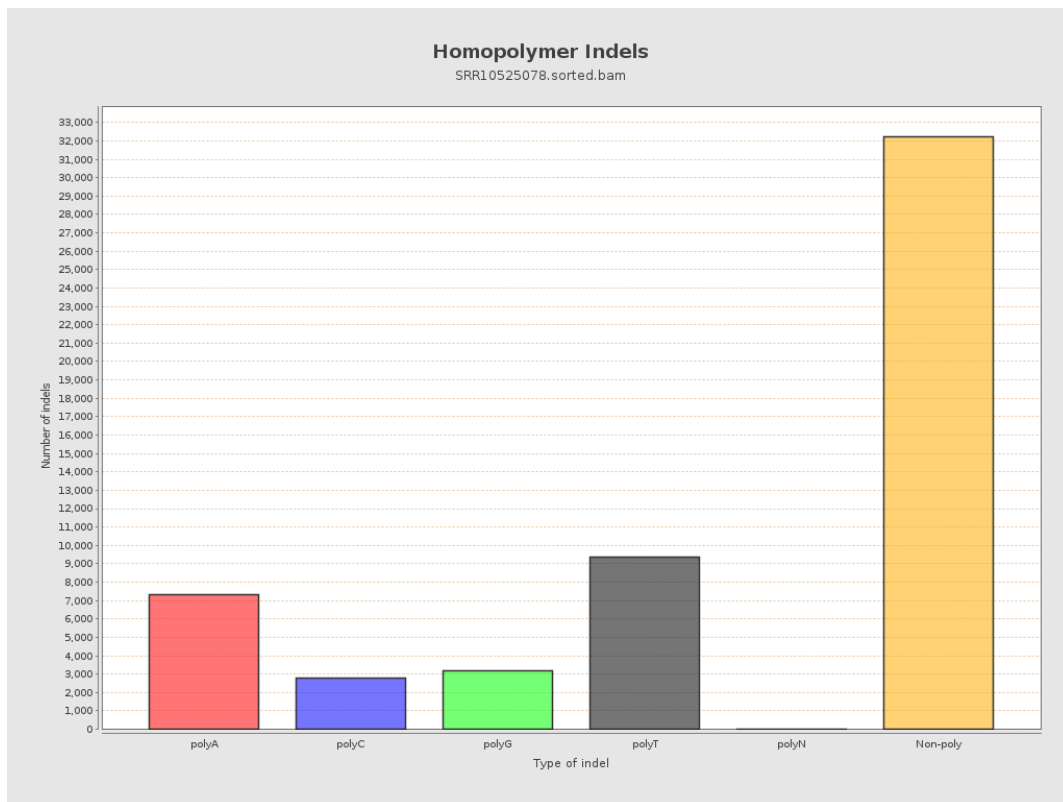
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

