

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:35:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080985.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_SRR3080985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:35:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,200,422
Mapped reads	3,526,410 / 83.95%
Unmapped reads	674,012 / 16.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,173 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	256,266 / 6.1%
Duplication rate	5.61%
Clipped reads	1,386,662 / 33.01%

2.2. ACGT Content

Number/percentage of A's	67,526,161 / 28.34%
Number/percentage of C's	41,932,297 / 17.6%
Number/percentage of T's	77,850,944 / 32.67%
Number/percentage of G's	50,501,529 / 21.19%
Number/percentage of N's	485,663 / 0.2%
GC Percentage	38.79%

2.3. Coverage

Mean	0.077

Standard Deviation	0.7175
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2.4. Mapping Quality

Mean Mapping Quality	47.27
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2.5. Mismatches and indels

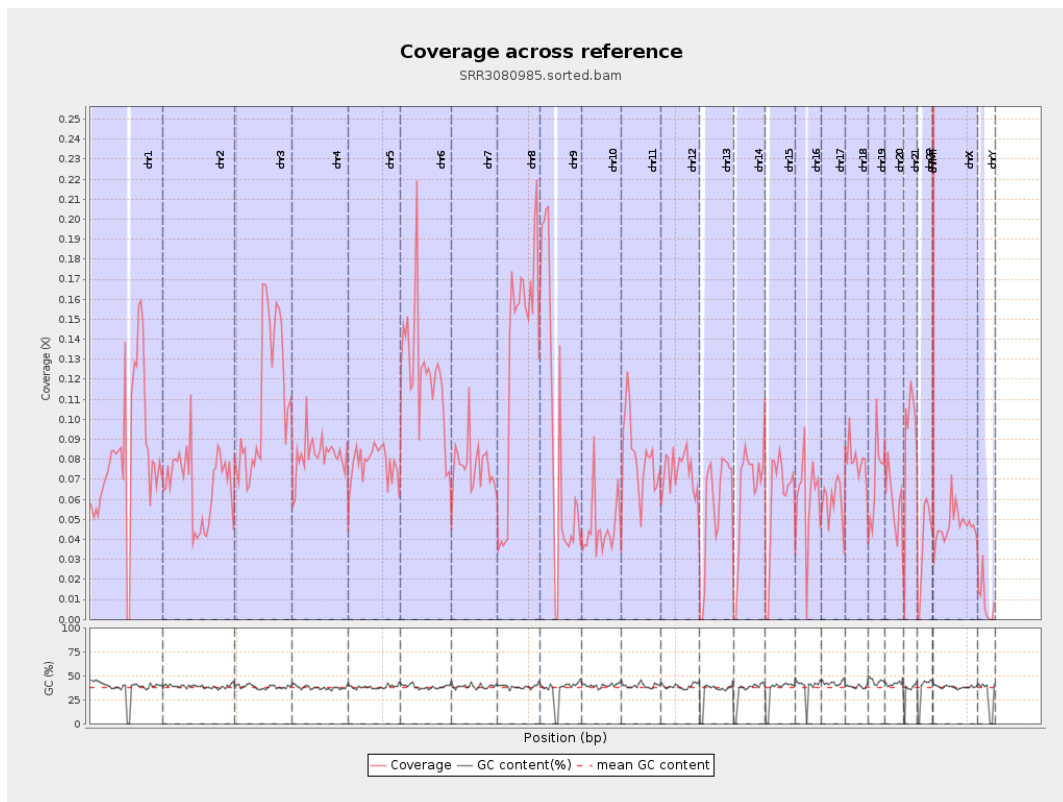
General error rate	1%
Mismatches	2,339,558
Insertions	18,468
Mapped reads with at least one insertion	0.52%
Deletions	48,760
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.9%

2.6. Chromosome stats

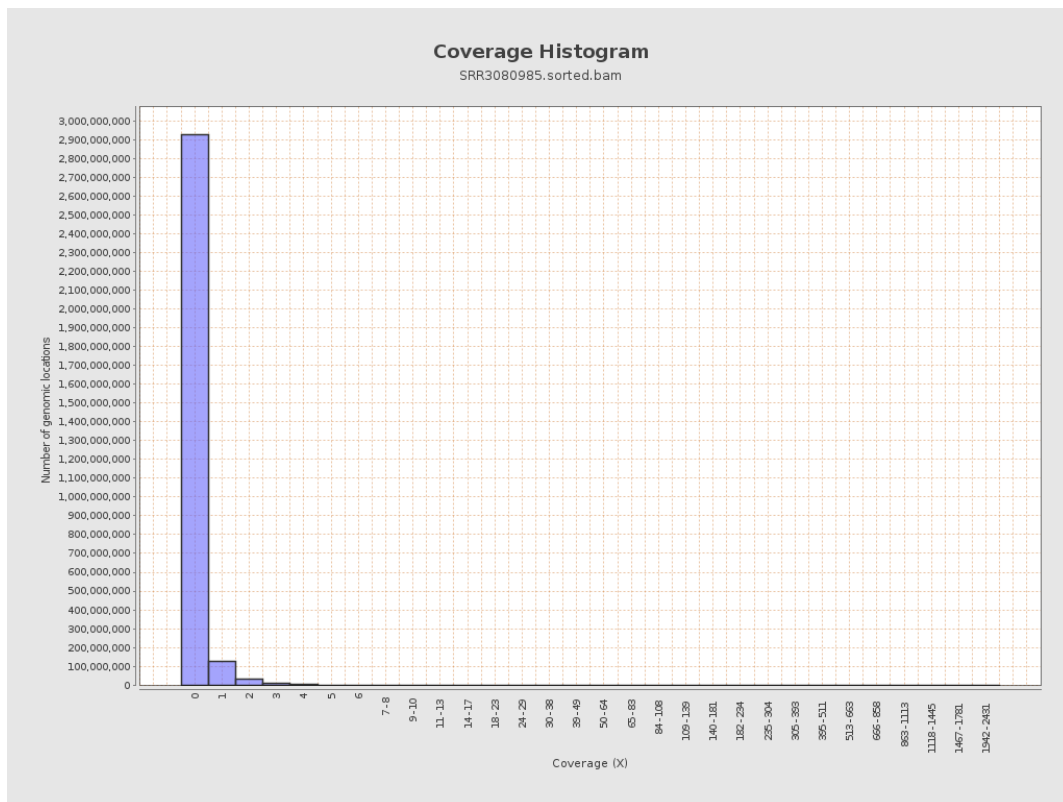
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20429434	0.082	1.2343
chr2	243199373	16393613	0.0674	0.591
chr3	198022430	21584746	0.109	0.4412
chr4	191154276	15736189	0.0823	0.4109
chr5	180915260	14079843	0.0778	0.3774
chr6	171115067	21138009	0.1235	0.7547
chr7	159138663	12190928	0.0766	0.7288

chr8	146364022	19181894	0.1311	1.5562
chr9	141213431	12487208	0.0884	0.8389
chr10	135534747	6177515	0.0456	0.5009
chr11	135006516	10956161	0.0812	0.5007
chr12	133851895	9796461	0.0732	0.3996
chr13	115169878	6566484	0.057	0.3122
chr14	107349540	6779347	0.0632	0.4164
chr15	102531392	6085507	0.0594	0.3208
chr16	90354753	5364709	0.0594	0.4143
chr17	81195210	4827795	0.0595	0.3389
chr18	78077248	6229847	0.0798	1.3905
chr19	59128983	4178851	0.0707	0.8604
chr20	63025520	3752668	0.0595	0.3579
chr21	48129895	4528237	0.0941	0.4997
chr22	51304566	1977109	0.0385	0.2564
chrMT	16571	105874	6.3891	4.3702
chrX	155270560	7299527	0.047	0.3469
chrY	59373566	534616	0.009	0.2045

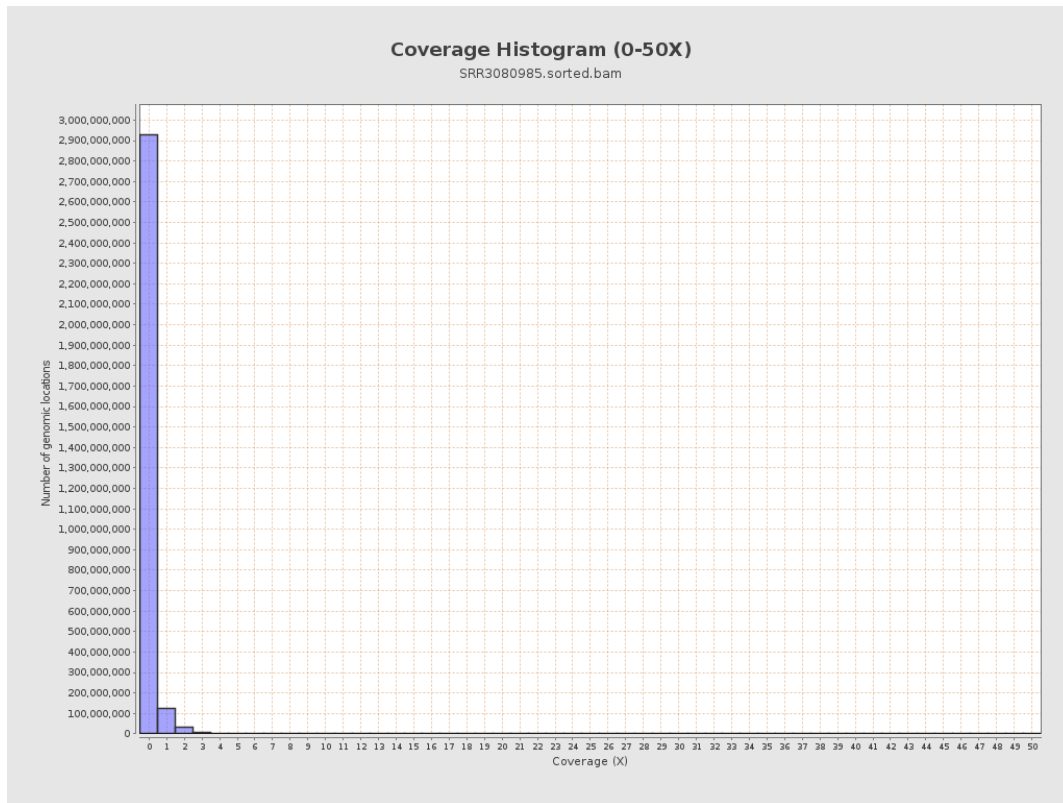
3. Results : Coverage across reference



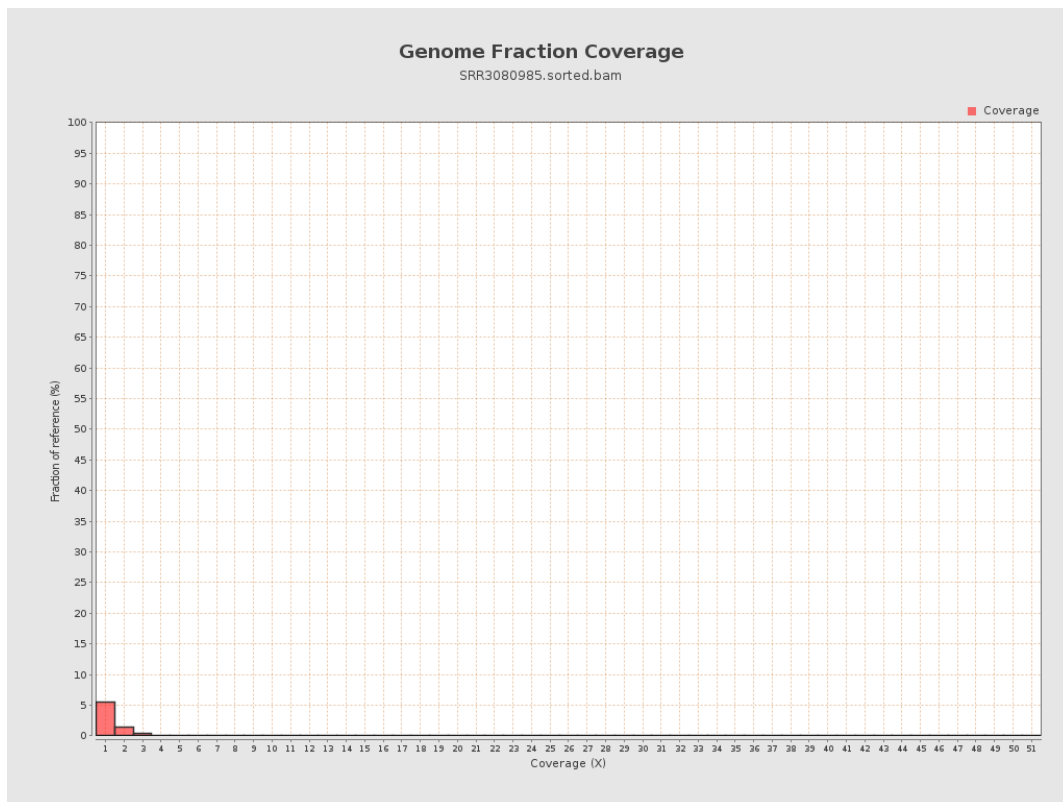
4. Results : Coverage Histogram



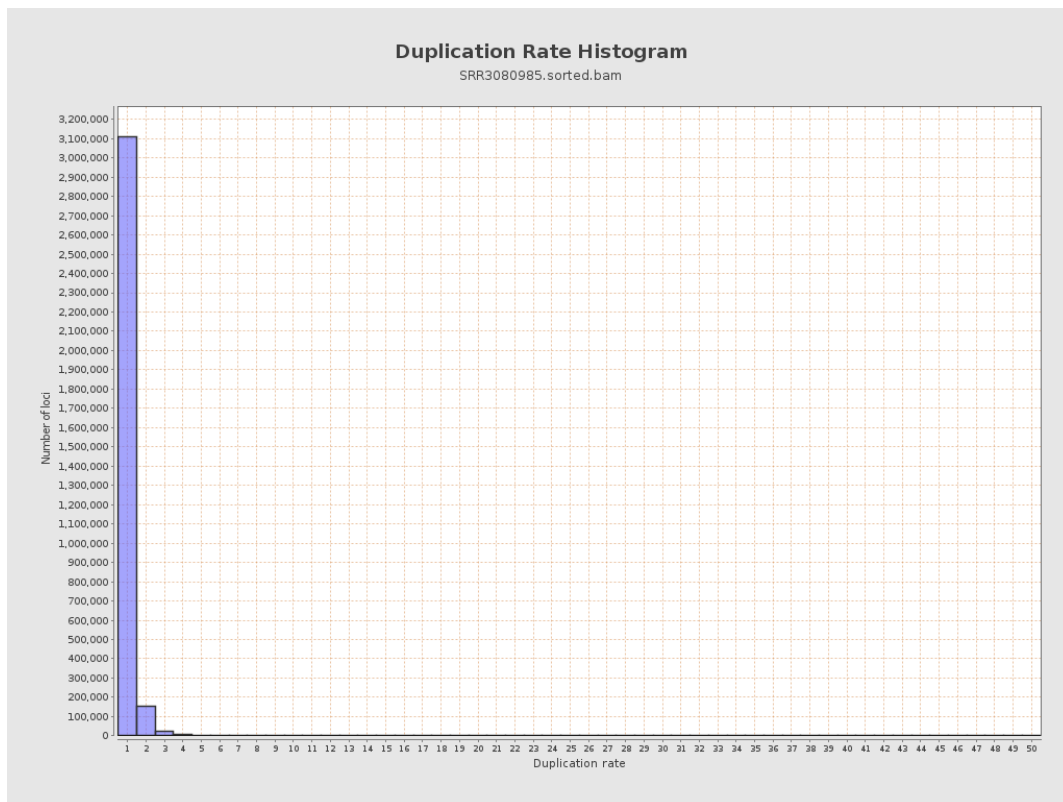
5. Results : Coverage Histogram (0-50X)



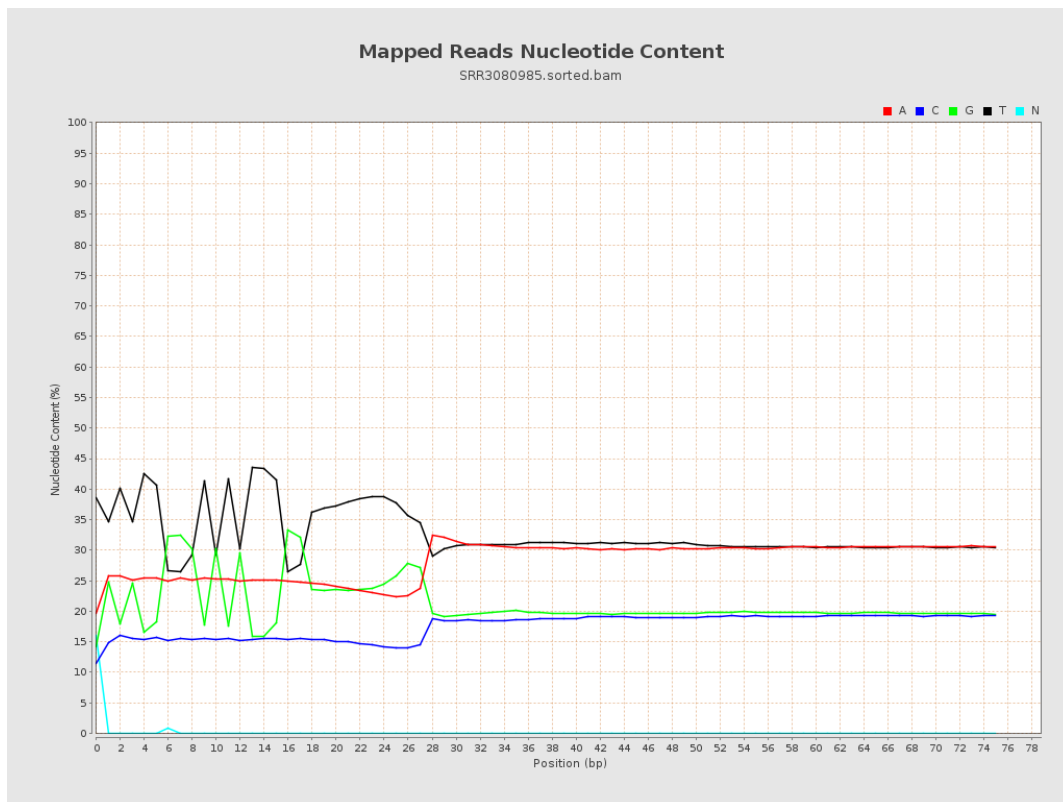
6. Results : Genome Fraction Coverage



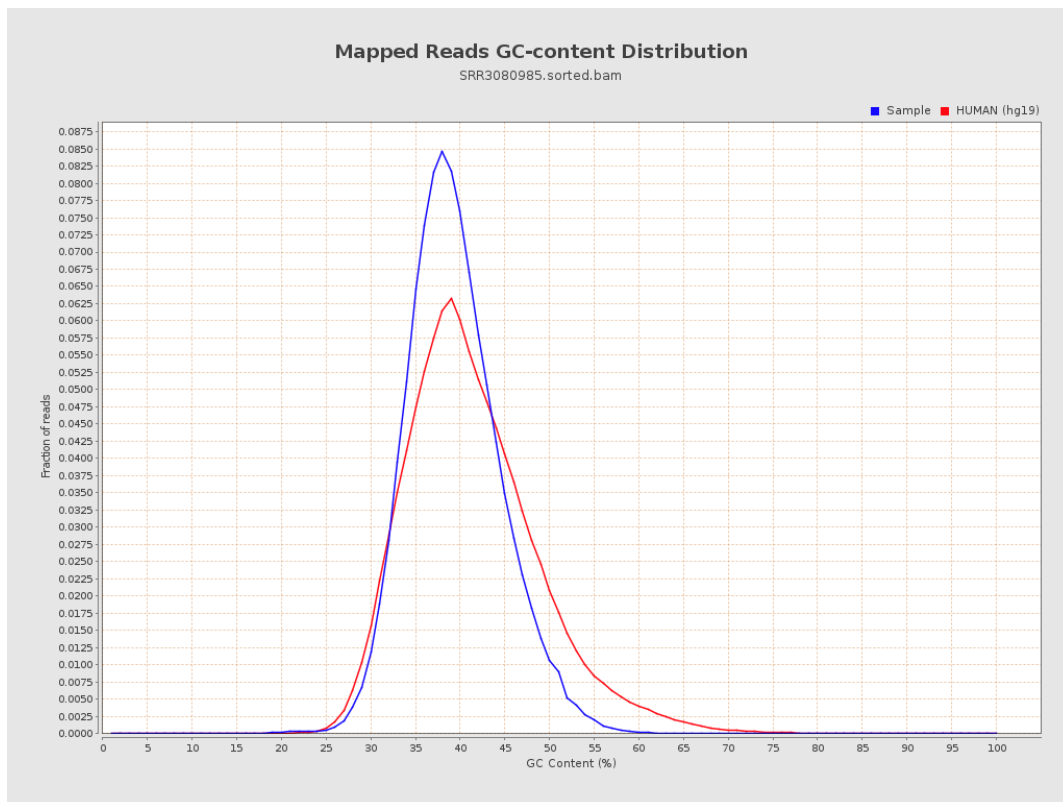
7. Results : Duplication Rate Histogram



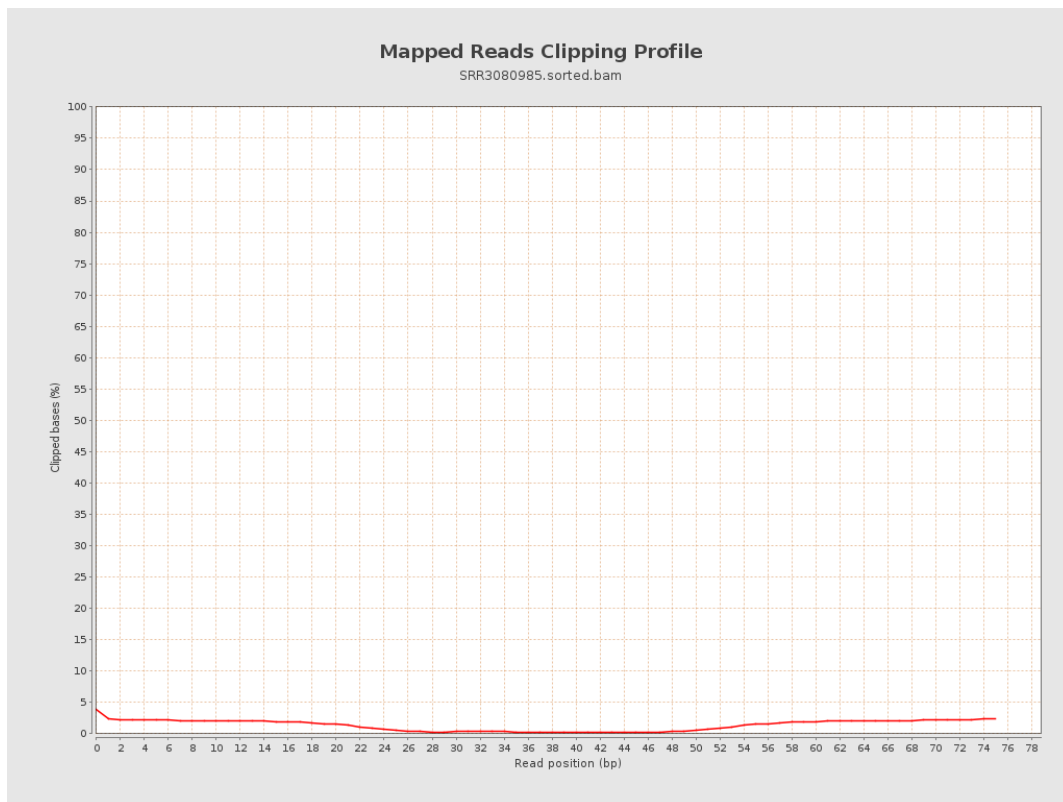
8. Results : Mapped Reads Nucleotide Content



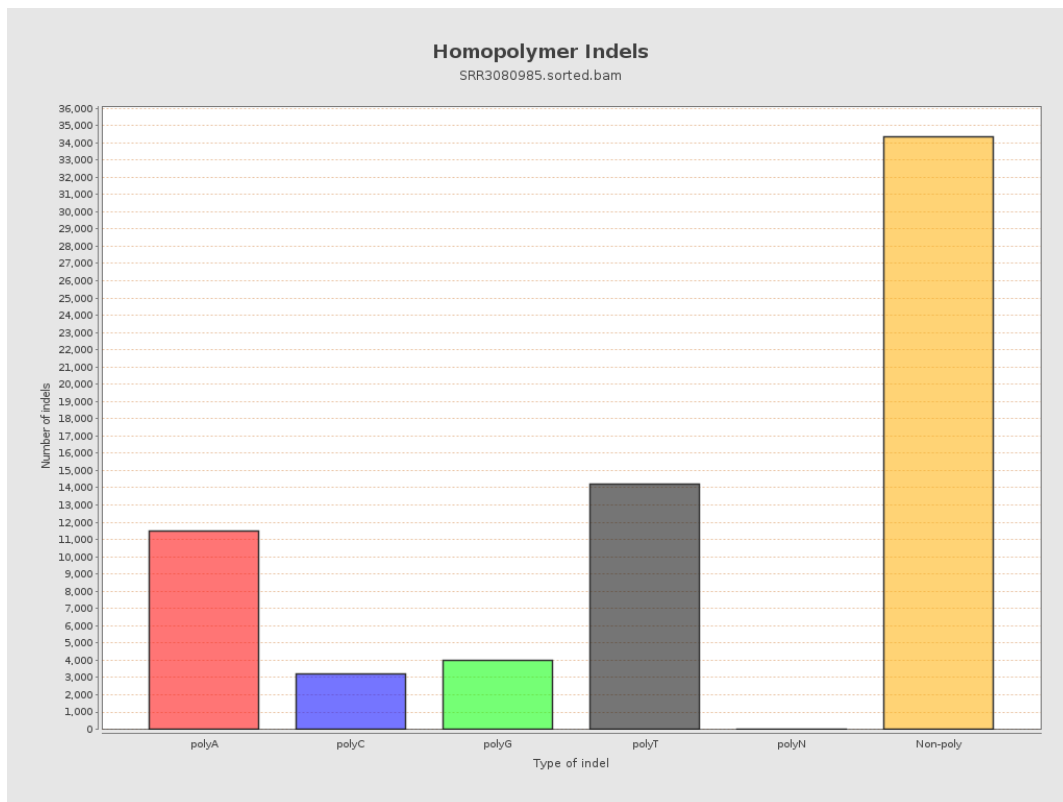
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

