

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:47:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008705.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_SRR6008705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:47:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,621,895
Mapped reads	579,715 / 35.74%
Unmapped reads	1,042,180 / 64.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,288 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	13,506 / 0.83%
Duplication rate	1.78%
Clipped reads	257,283 / 15.86%

2.2. ACGT Content

Number/percentage of A's	10,489,982 / 27.33%
Number/percentage of C's	7,213,223 / 18.79%
Number/percentage of T's	11,929,616 / 31.08%
Number/percentage of G's	8,694,611 / 22.65%
Number/percentage of N's	61,253 / 0.16%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1463
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.48
----------------------	-------

2.5. Mismatches and indels

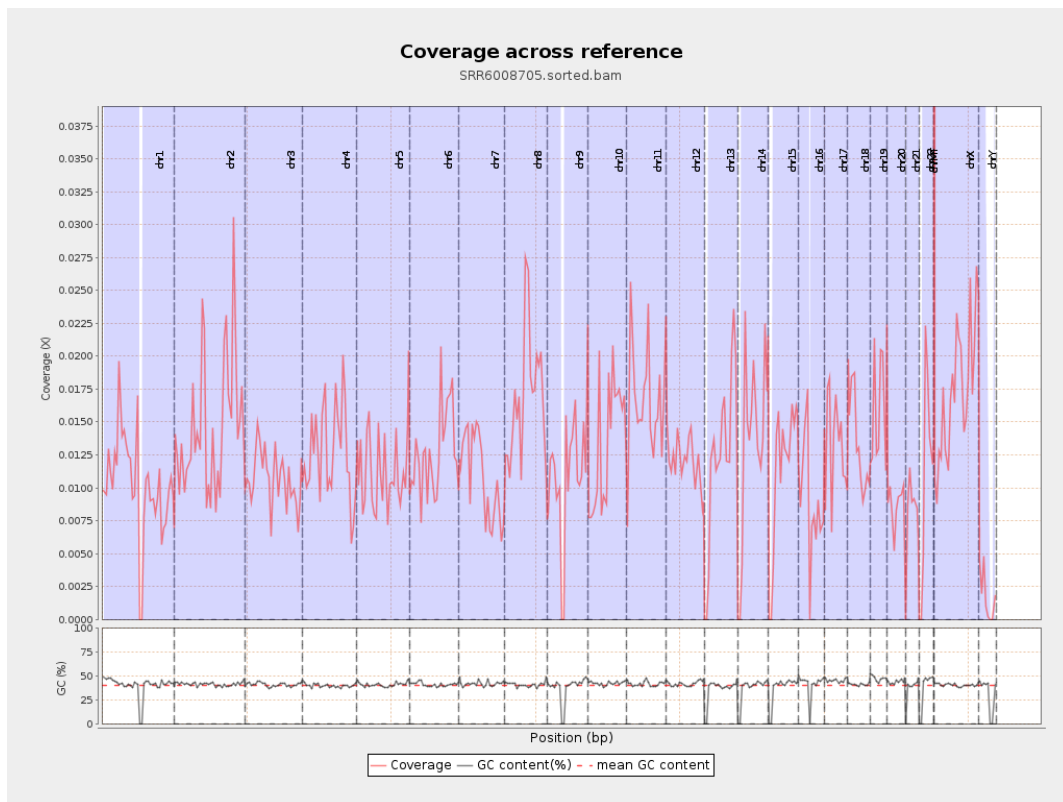
General error rate	0.85%
Mismatches	319,940
Insertions	2,799
Mapped reads with at least one insertion	0.48%
Deletions	10,438
Mapped reads with at least one deletion	1.78%
Homopolymer indels	45.59%

2.6. Chromosome stats

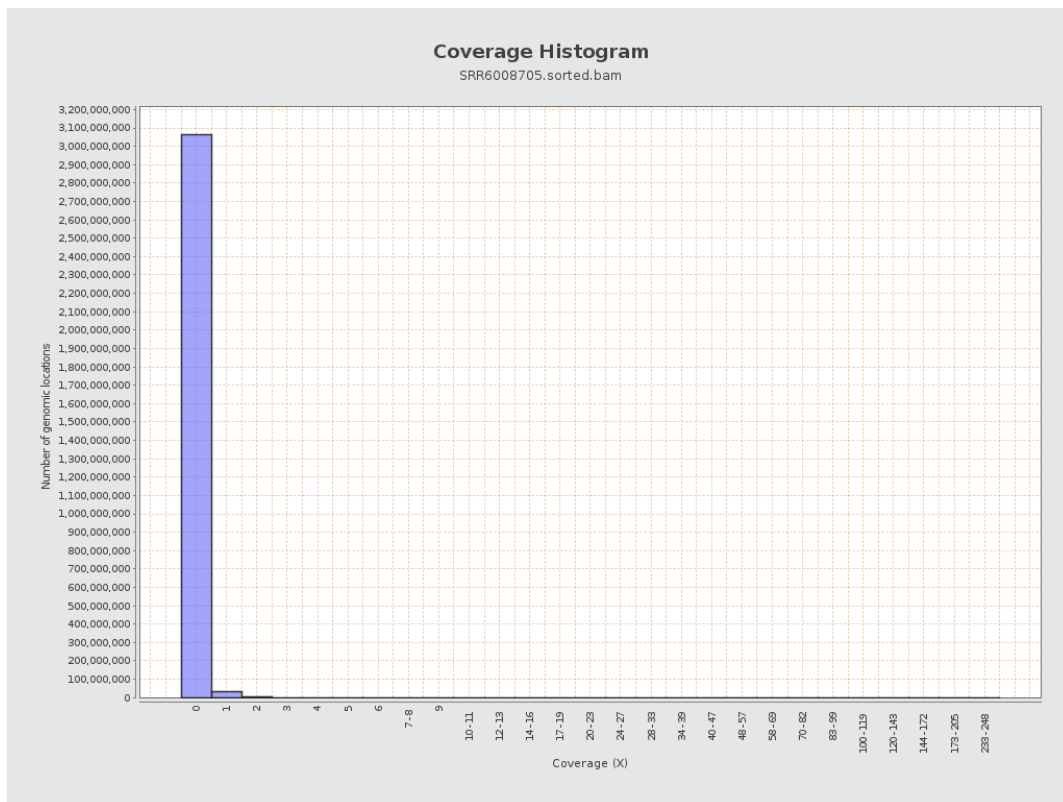
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2534139	0.0102	0.183
chr2	243199373	3591574	0.0148	0.1792
chr3	198022430	2109998	0.0107	0.112
chr4	191154276	2406174	0.0126	0.1252
chr5	180915260	2005010	0.0111	0.114
chr6	171115067	2158265	0.0126	0.1286
chr7	159138663	1709413	0.0107	0.1471

chr8	146364022	2462593	0.0168	0.2046
chr9	141213431	1502996	0.0106	0.1303
chr10	135534747	1808967	0.0133	0.1501
chr11	135006516	2251399	0.0167	0.1549
chr12	133851895	1617528	0.0121	0.125
chr13	115169878	1458353	0.0127	0.1214
chr14	107349540	1461583	0.0136	0.1387
chr15	102531392	1160257	0.0113	0.1149
chr16	90354753	807497	0.0089	0.1289
chr17	81195210	1063974	0.0131	0.129
chr18	78077248	1041193	0.0133	0.2055
chr19	59128983	943150	0.016	0.1657
chr20	63025520	536360	0.0085	0.1004
chr21	48129895	392637	0.0082	0.145
chr22	51304566	584285	0.0114	0.1145
chrMT	16571	13903	0.839	1.0303
chrX	155270560	2687590	0.0173	0.1533
chrY	59373566	98082	0.0017	0.0532

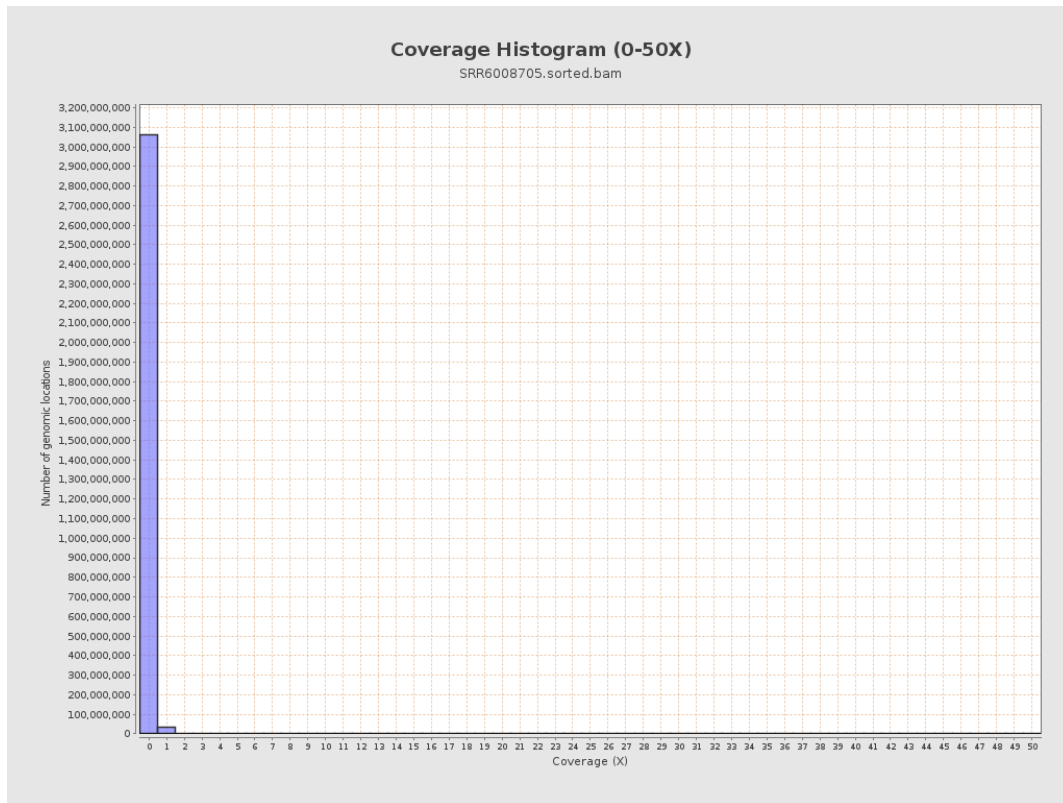
3. Results : Coverage across reference



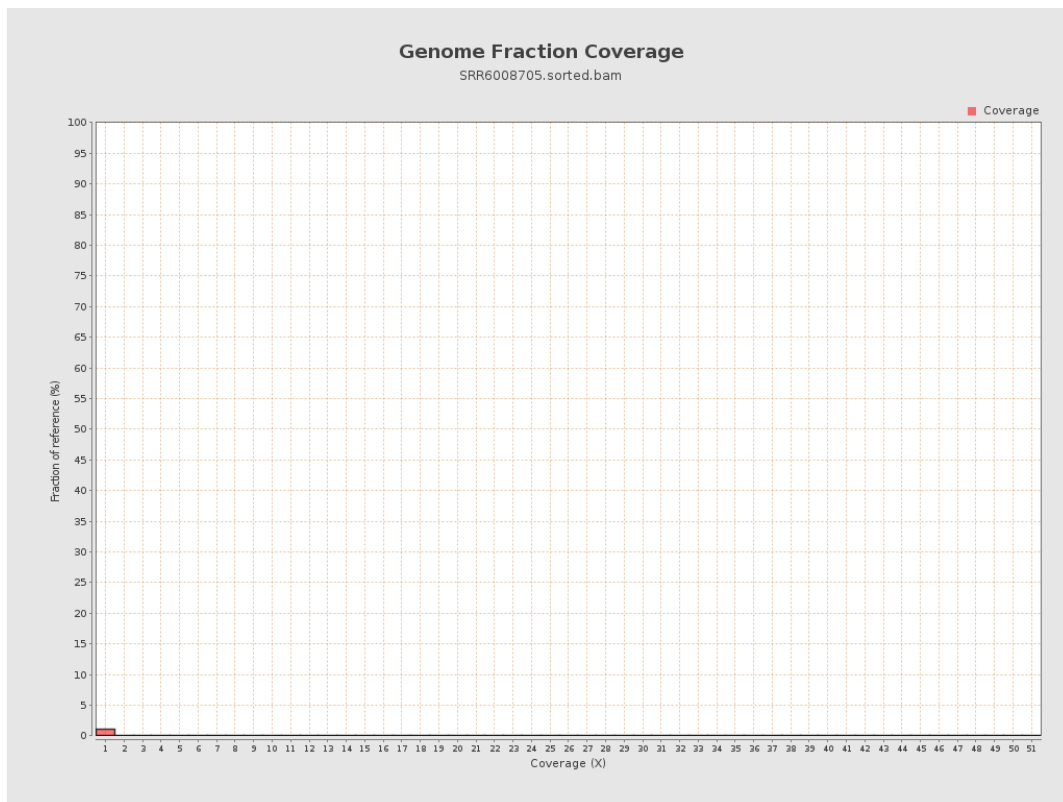
4. Results : Coverage Histogram



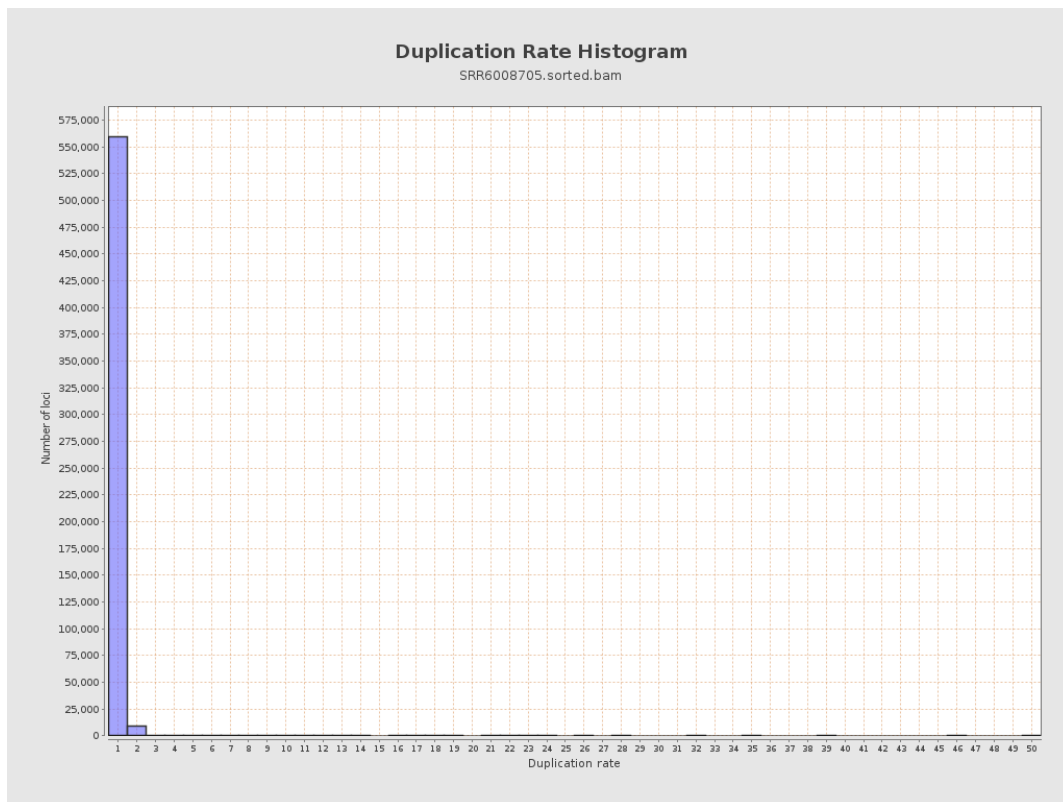
5. Results : Coverage Histogram (0-50X)



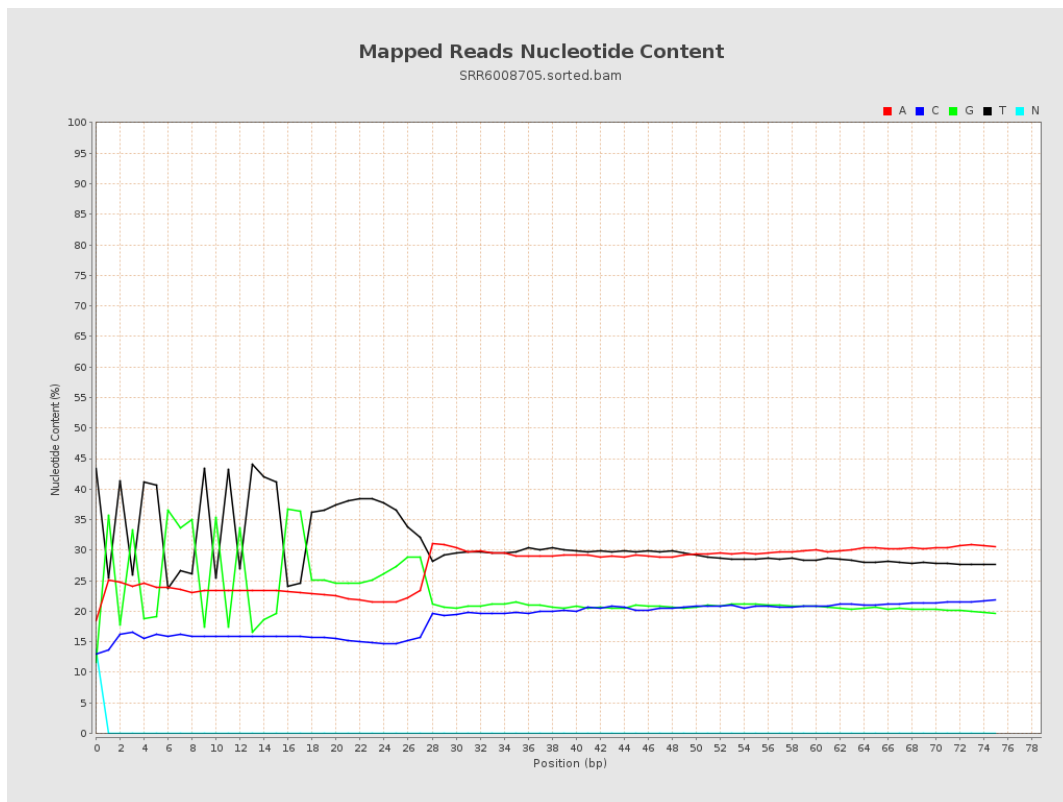
6. Results : Genome Fraction Coverage



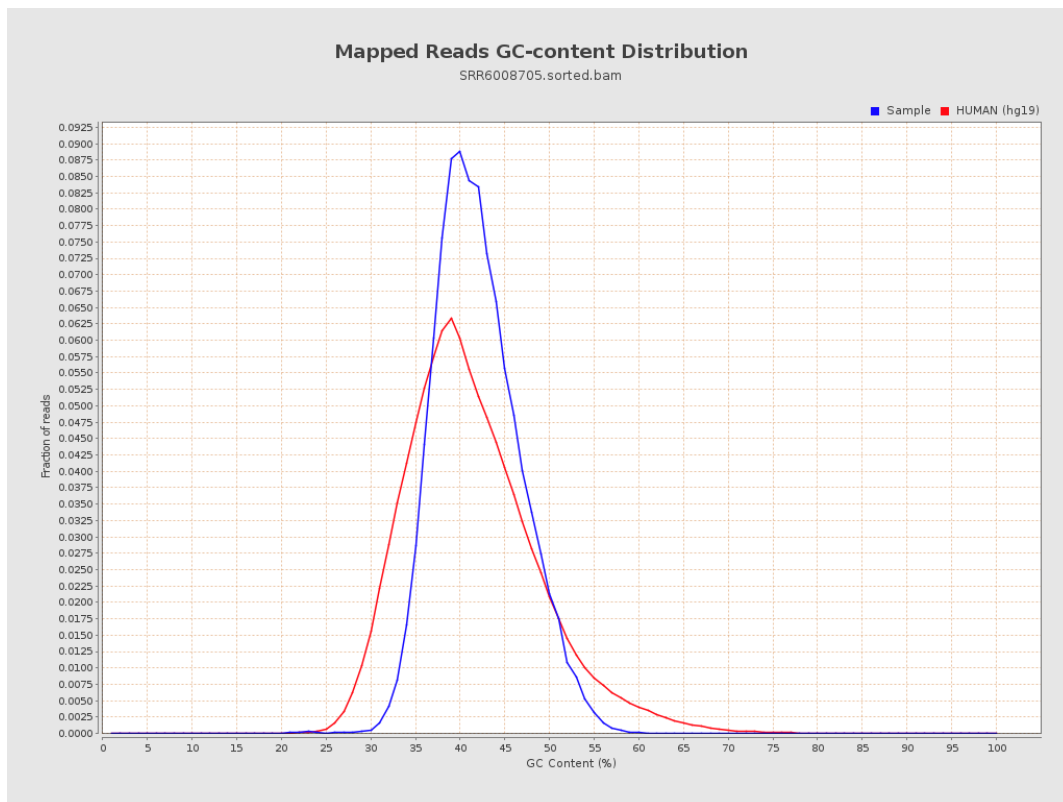
7. Results : Duplication Rate Histogram



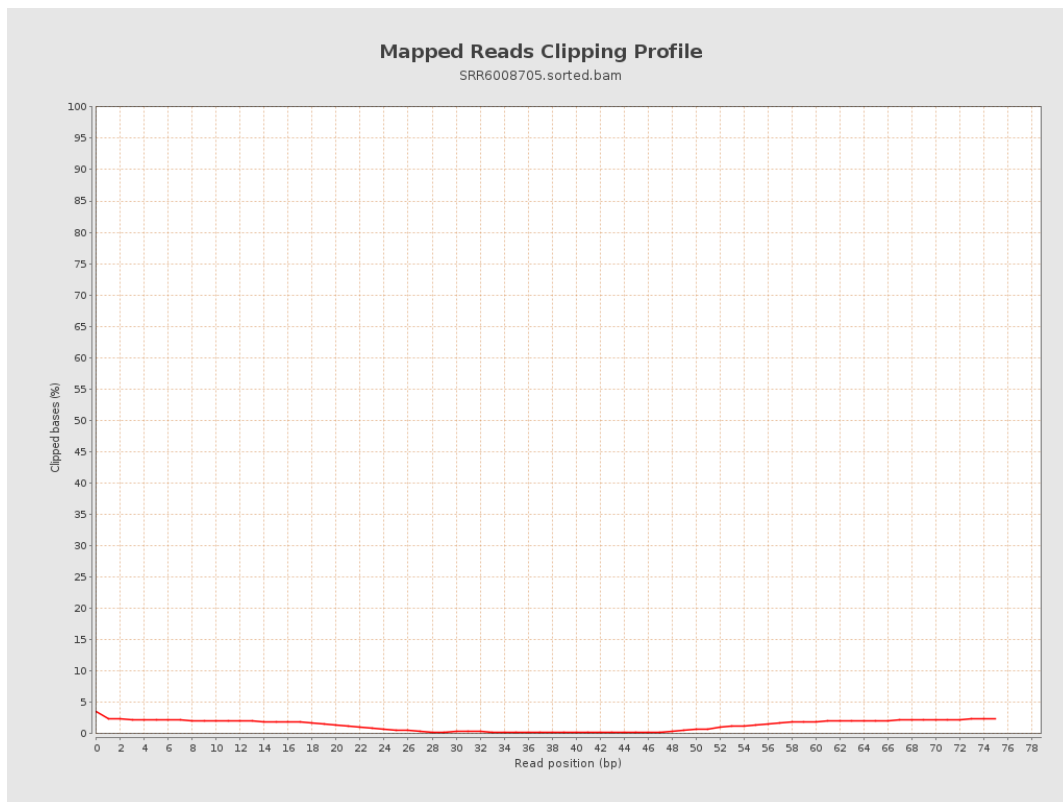
8. Results : Mapped Reads Nucleotide Content



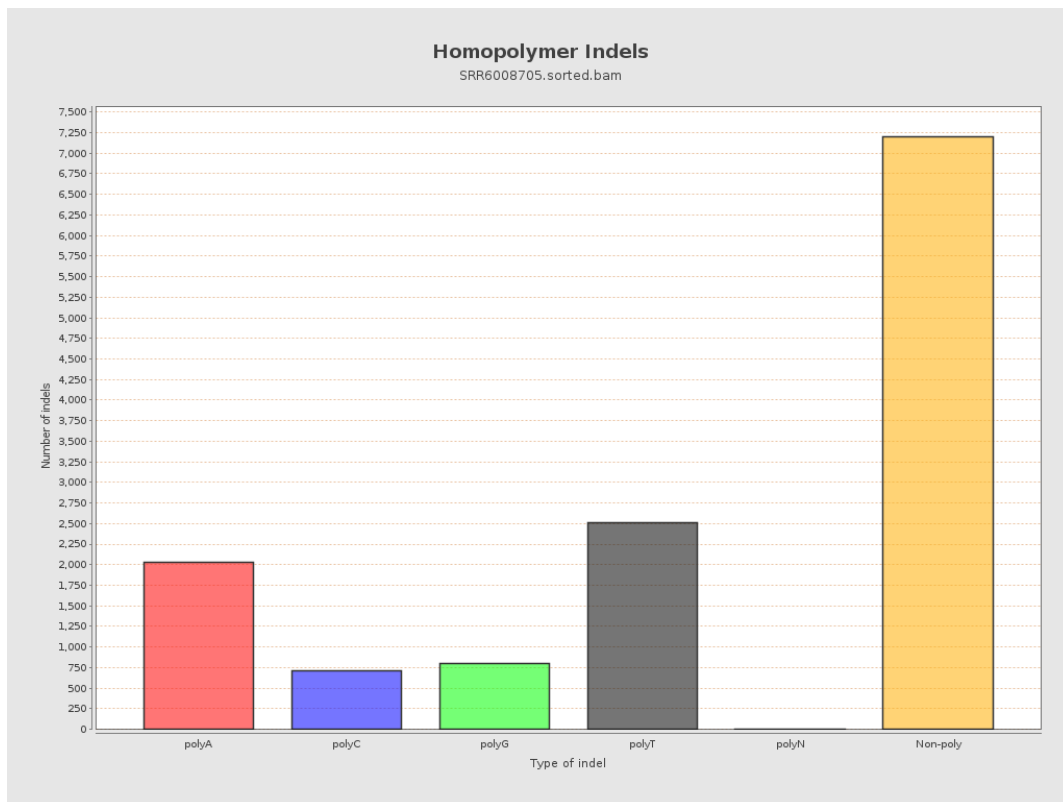
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

