

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:56:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525052.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_SRR10525052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:56:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	641,334
Mapped reads	578,380 / 90.18%
Unmapped reads	62,954 / 9.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,697 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	22,405 / 3.49%
Duplication rate	3.24%
Clipped reads	578,510 / 90.2%

2.2. ACGT Content

Number/percentage of A's	8,872,422 / 26.15%
Number/percentage of C's	6,508,321 / 19.19%
Number/percentage of T's	10,780,960 / 31.78%
Number/percentage of G's	7,758,372 / 22.87%
Number/percentage of N's	3,274 / 0.01%
GC Percentage	42.06%

2.3. Coverage

Mean	0.011

Standard Deviation	0.138
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2.4. Mapping Quality

Mean Mapping Quality	46.46
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2.5. Mismatches and indels

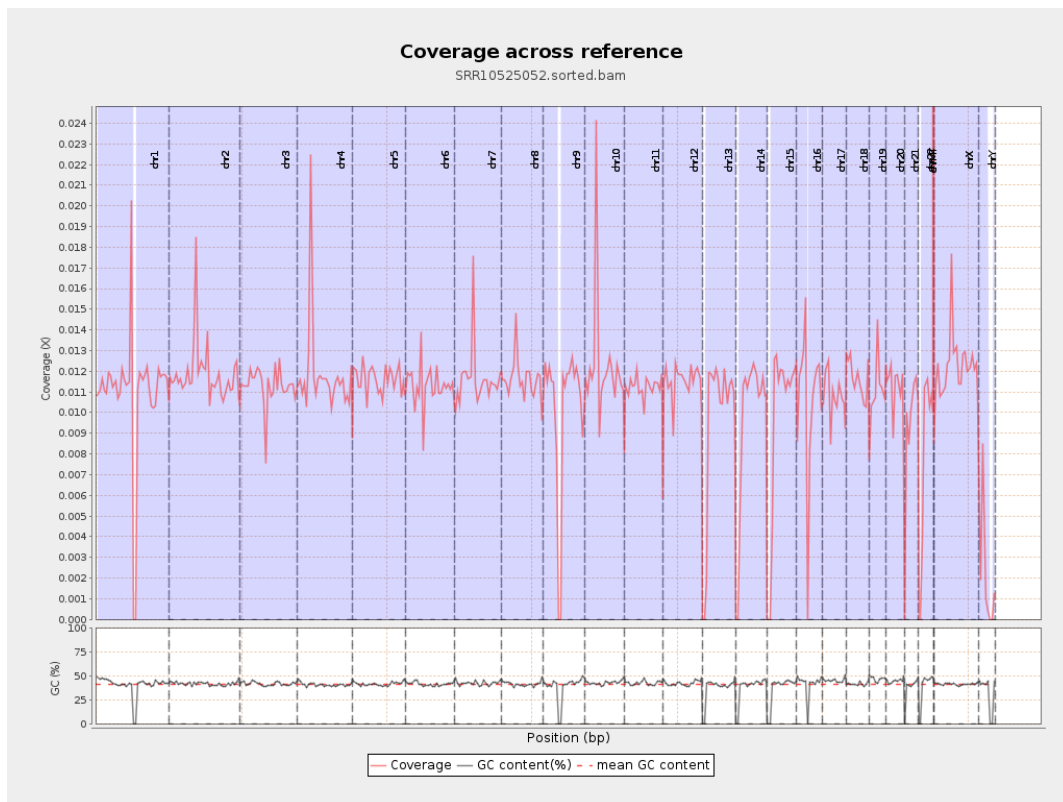
General error rate	0.51%
Mismatches	168,225
Insertions	2,707
Mapped reads with at least one insertion	0.47%
Deletions	7,256
Mapped reads with at least one deletion	1.25%
Homopolymer indels	41.74%

2.6. Chromosome stats

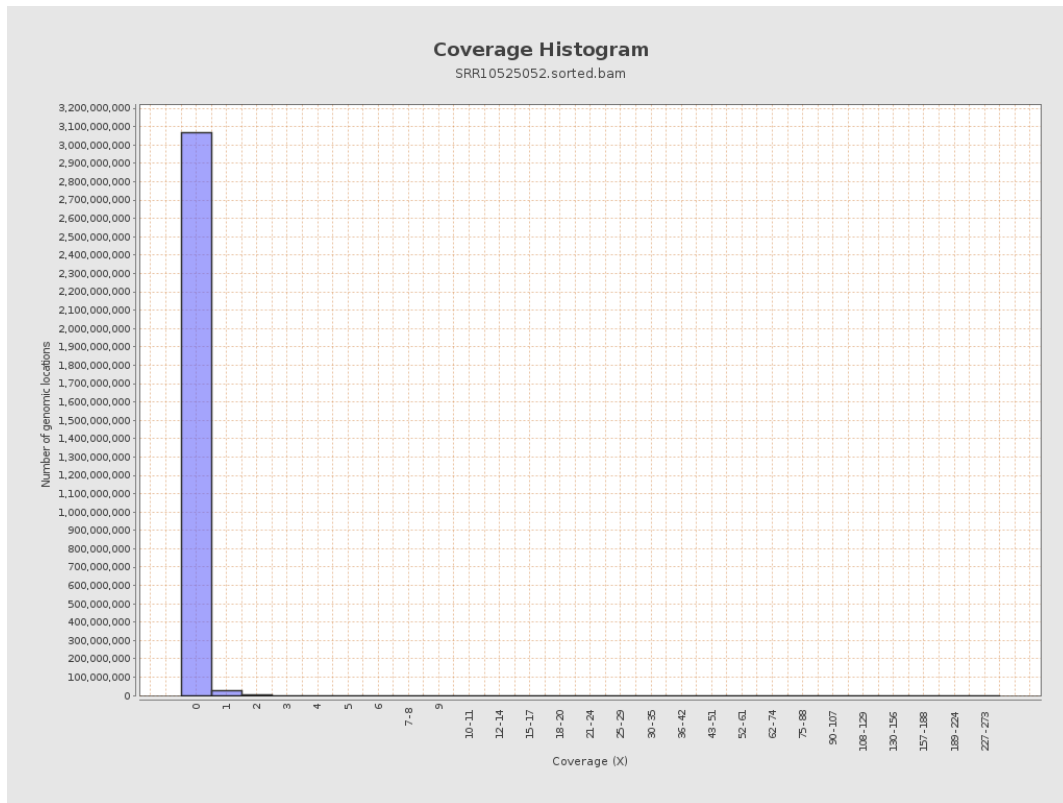
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2730200	0.011	0.2296
chr2	243199373	2891507	0.0119	0.1578
chr3	198022430	2235331	0.0113	0.1122
chr4	191154276	2251832	0.0118	0.1244
chr5	180915260	2099154	0.0116	0.1142
chr6	171115067	1930622	0.0113	0.1174
chr7	159138663	1850310	0.0116	0.1473

chr8	146364022	1696715	0.0116	0.1471
chr9	141213431	1429251	0.0101	0.1182
chr10	135534747	1661211	0.0123	0.1491
chr11	135006516	1510371	0.0112	0.1225
chr12	133851895	1545794	0.0115	0.1149
chr13	115169878	1090667	0.0095	0.1028
chr14	107349540	1029149	0.0096	0.1046
chr15	102531392	989155	0.0096	0.104
chr16	90354753	960708	0.0106	0.1125
chr17	81195210	869860	0.0107	0.1138
chr18	78077248	905405	0.0116	0.1629
chr19	59128983	662372	0.0112	0.1677
chr20	63025520	702187	0.0111	0.1136
chr21	48129895	452160	0.0094	0.1098
chr22	51304566	389785	0.0076	0.0928
chrMT	16571	26505	1.5995	1.4753
chrX	155270560	1900325	0.0122	0.1241
chrY	59373566	124297	0.0021	0.0876

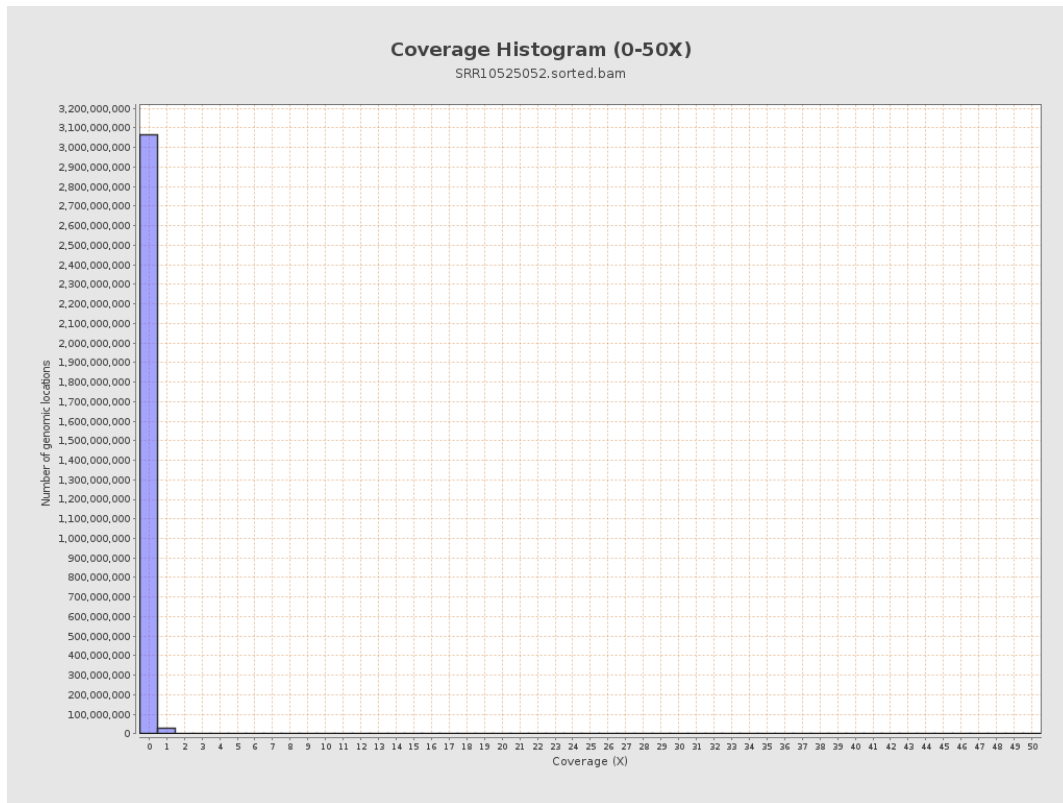
3. Results : Coverage across reference



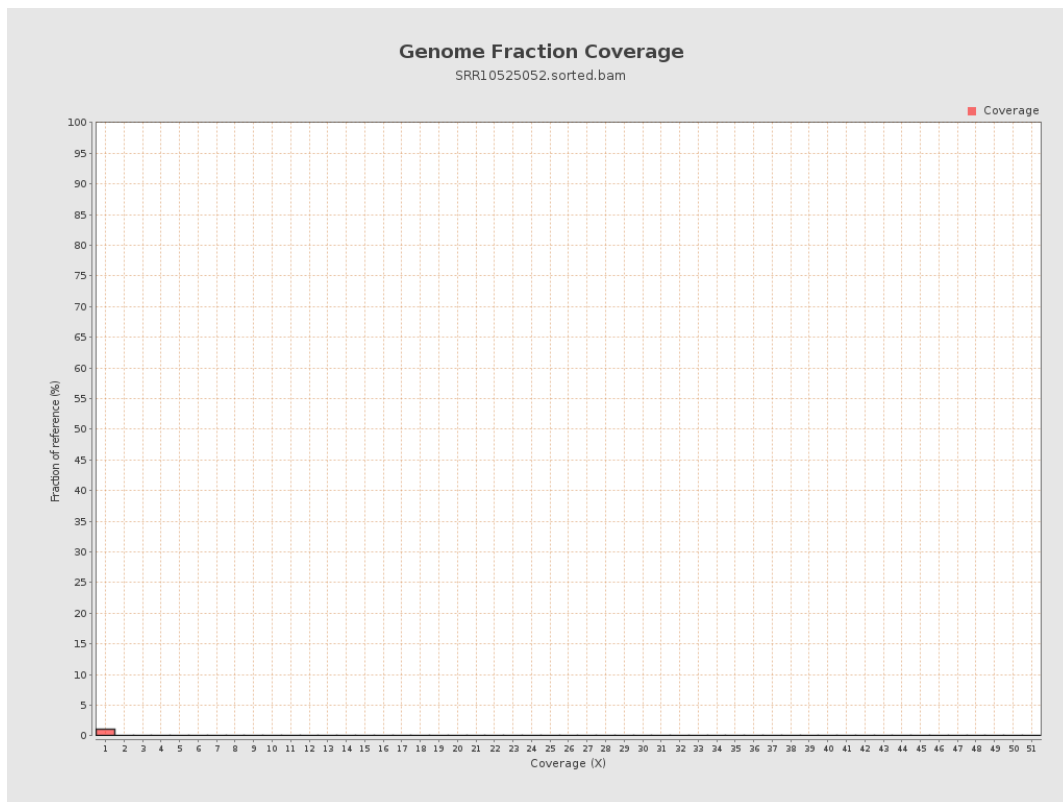
4. Results : Coverage Histogram



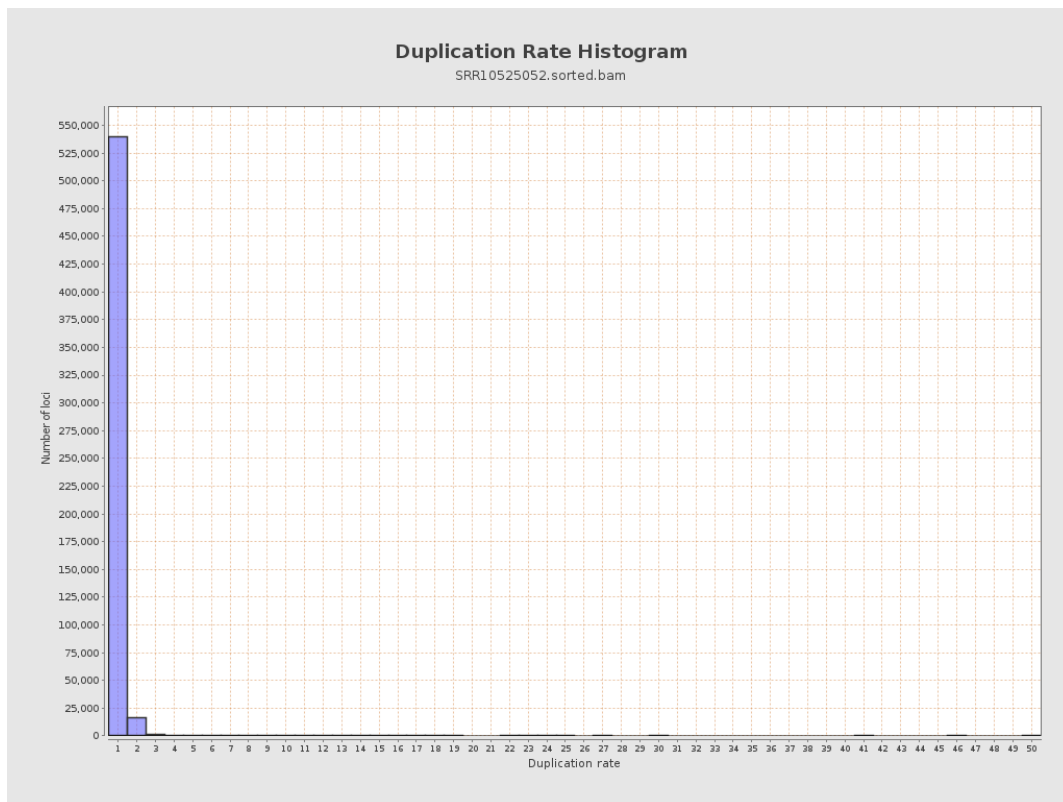
5. Results : Coverage Histogram (0-50X)



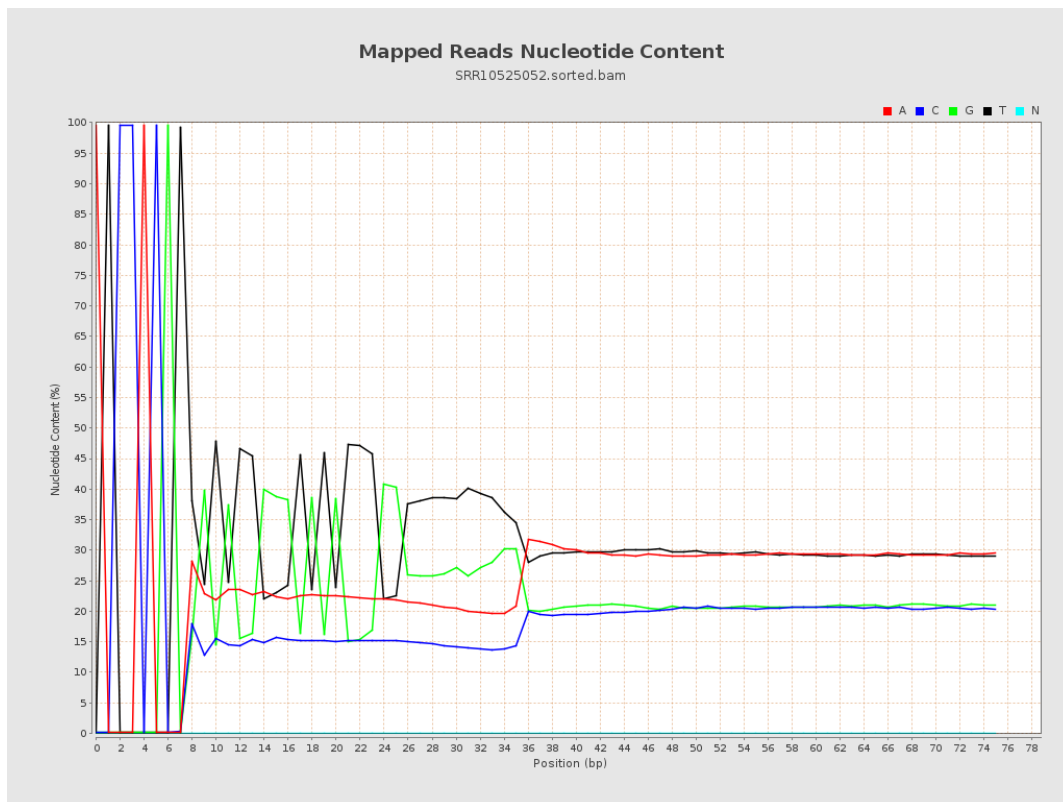
6. Results : Genome Fraction Coverage



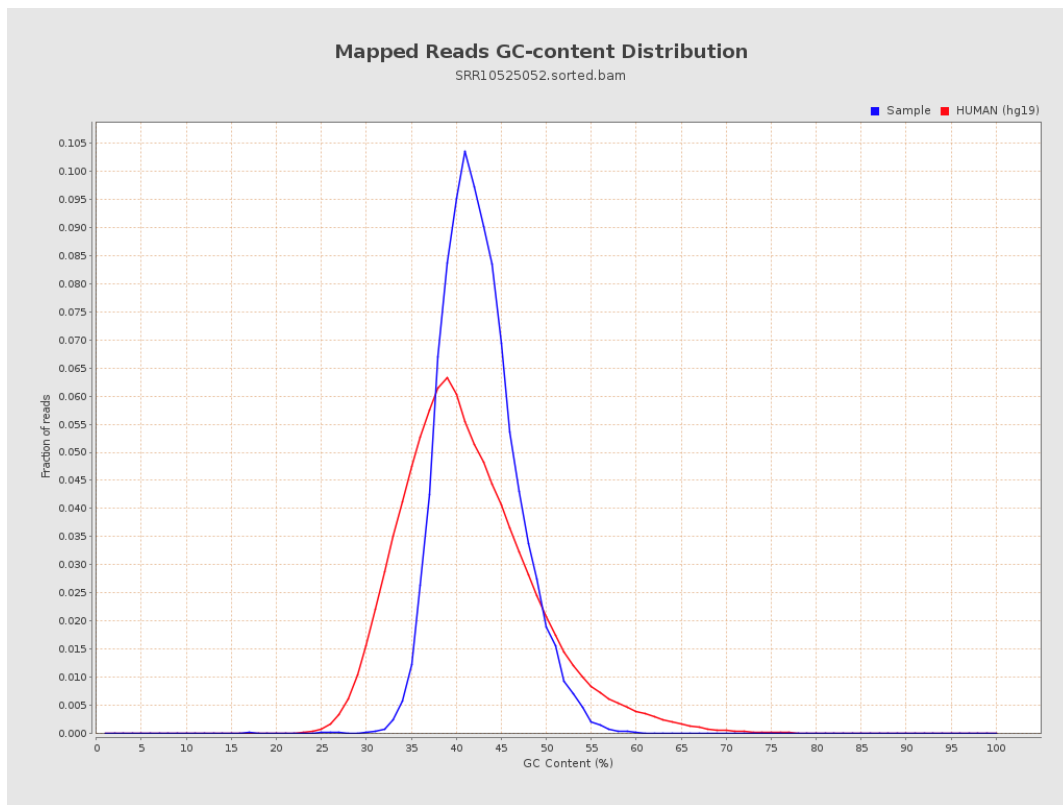
7. Results : Duplication Rate Histogram



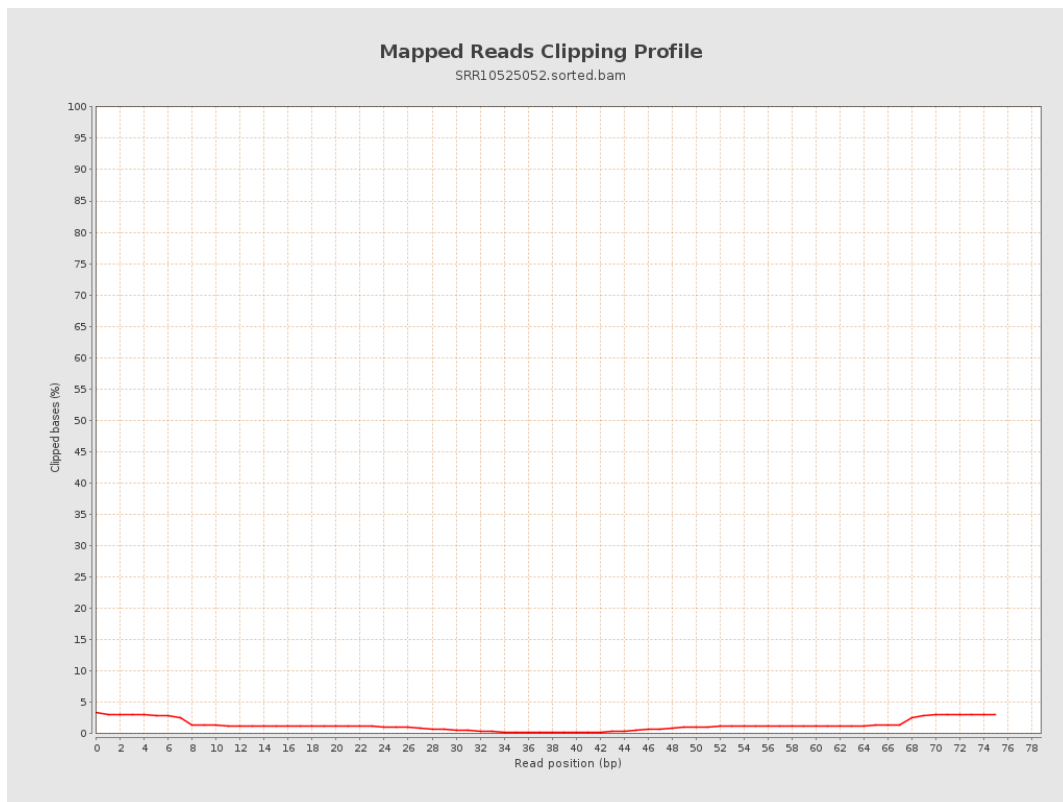
8. Results : Mapped Reads Nucleotide Content



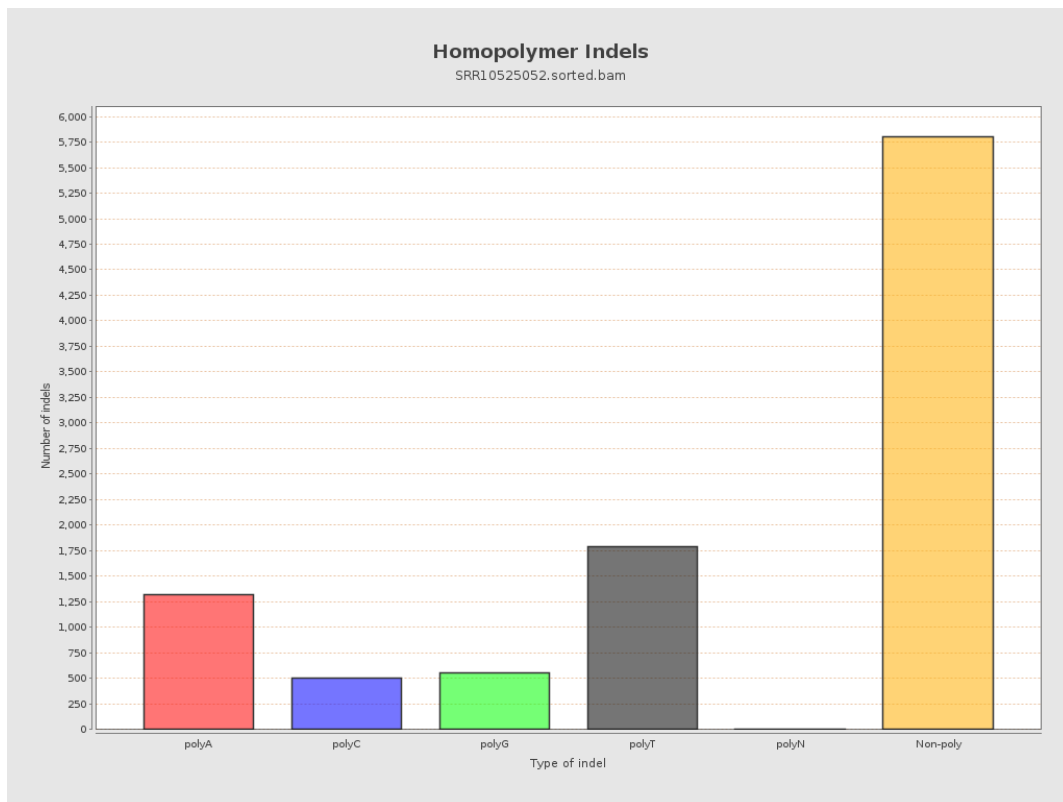
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

