

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:41:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251055.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_SRR10251055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:40:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,213,342
Mapped reads	4,006,851 / 95.1%
Unmapped reads	206,491 / 4.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,103 / 0.83%
Read min/max/mean length	30 / 80 / 80.3
Duplicated reads (estimated)	1,016,685 / 24.13%
Duplication rate	22.43%
Clipped reads	561,391 / 13.32%

2.2. ACGT Content

Number/percentage of A's	90,897,302 / 29.25%
Number/percentage of C's	61,924,723 / 19.92%
Number/percentage of T's	92,083,902 / 29.63%
Number/percentage of G's	65,901,517 / 21.2%
Number/percentage of N's	2,578 / 0%
GC Percentage	41.13%

2.3. Coverage

Mean	0.1005

Standard Deviation	1.093
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2.4. Mapping Quality

Mean Mapping Quality	48.1
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2.5. Mismatches and indels

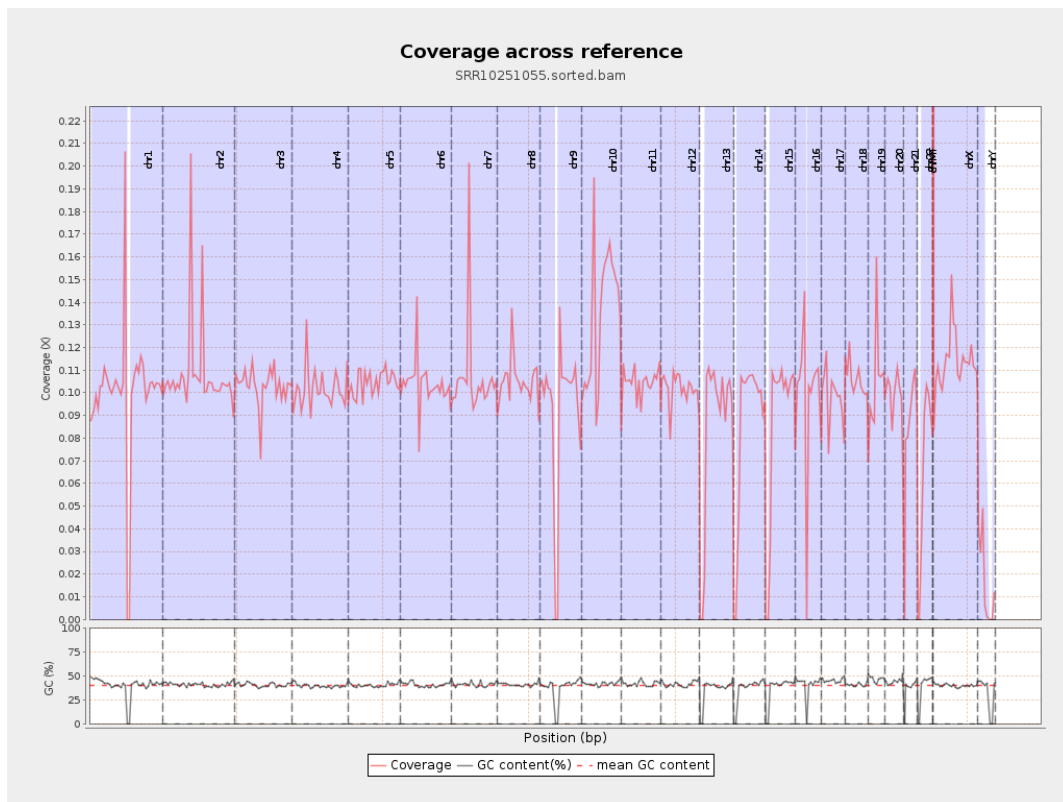
General error rate	0.62%
Mismatches	1,855,580
Insertions	37,526
Mapped reads with at least one insertion	0.92%
Deletions	109,701
Mapped reads with at least one deletion	2.69%
Homopolymer indels	44.95%

2.6. Chromosome stats

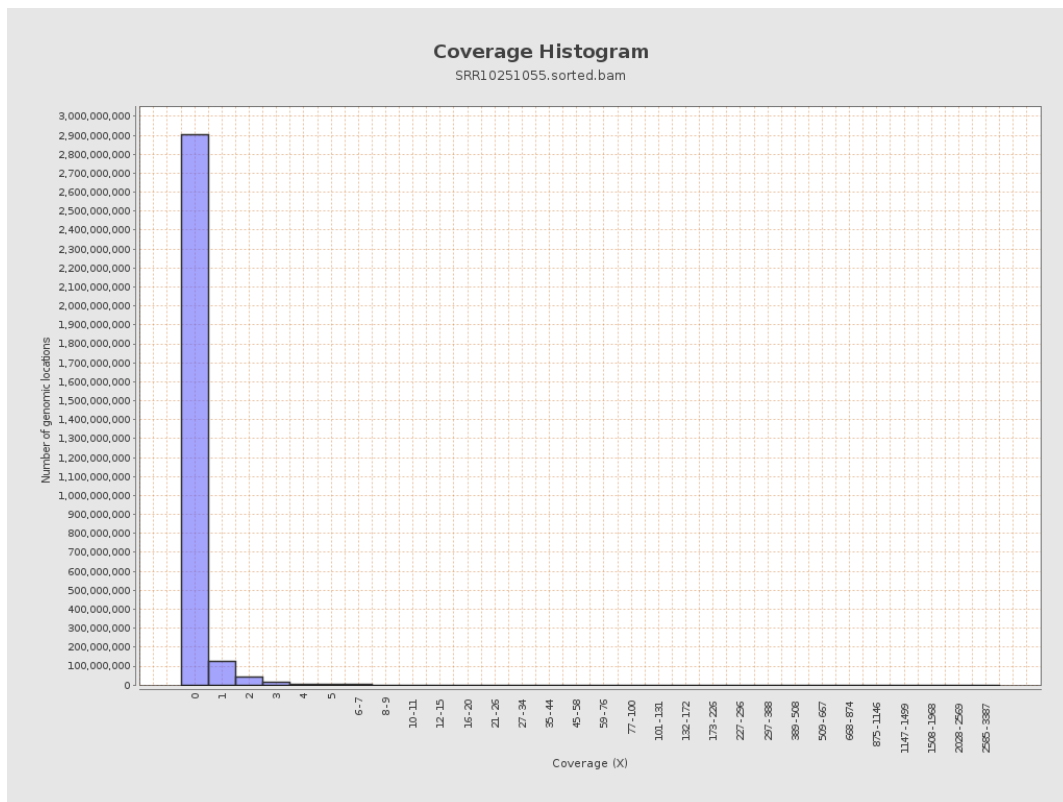
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24883706	0.0998	2.34
chr2	243199373	26351542	0.1084	1.2202
chr3	198022430	20409122	0.1031	0.4784
chr4	191154276	19488950	0.102	0.5431
chr5	180915260	18898044	0.1045	0.4935
chr6	171115067	17793704	0.104	0.6721
chr7	159138663	16979237	0.1067	1.6574

chr8	146364022	15375474	0.105	0.7356
chr9	141213431	13087579	0.0927	1.2409
chr10	135534747	18169680	0.1341	1.1519
chr11	135006516	14121925	0.1046	0.6665
chr12	133851895	13650222	0.102	0.4951
chr13	115169878	9781428	0.0849	0.4262
chr14	107349540	9285415	0.0865	0.7091
chr15	102531392	8723925	0.0851	0.4299
chr16	90354753	8791537	0.0973	0.7881
chr17	81195210	8030343	0.0989	0.6106
chr18	78077248	8276498	0.106	1.3563
chr19	59128983	6233199	0.1054	2.1714
chr20	63025520	6246934	0.0991	0.5151
chr21	48129895	4083889	0.0849	0.4865
chr22	51304566	3388594	0.066	0.3963
chrMT	16571	310926	18.7633	10.518
chrX	155270560	17684855	0.1139	0.5962
chrY	59373566	959988	0.0162	0.8164

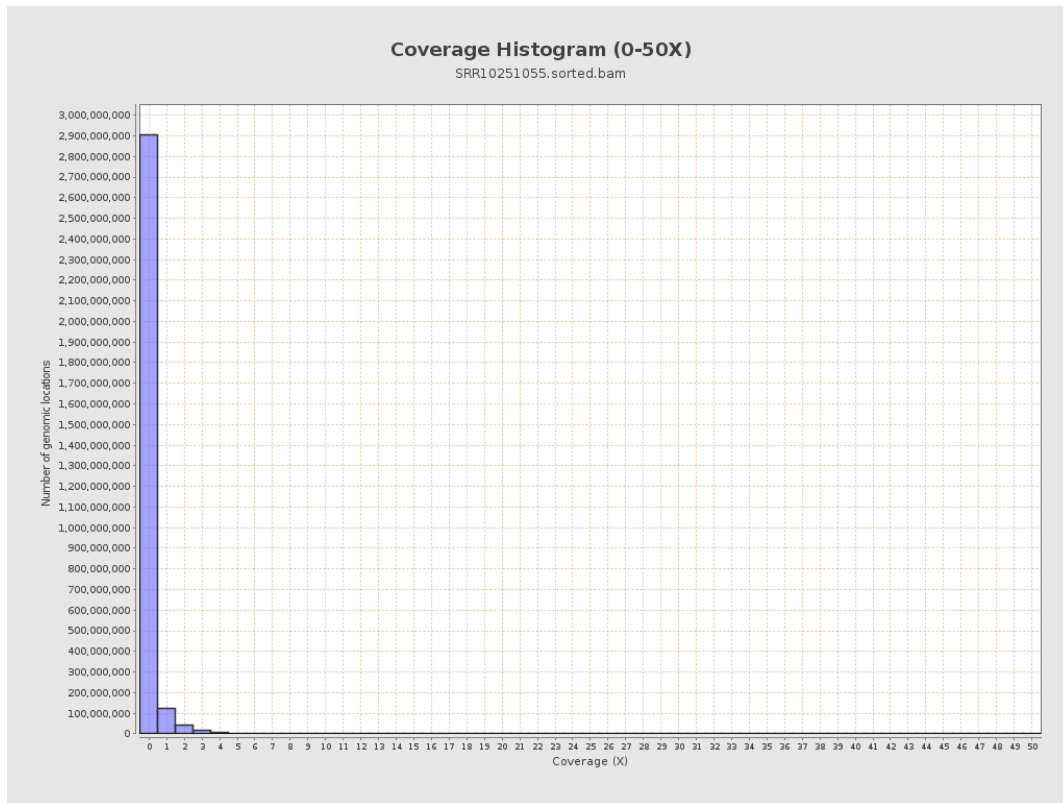
3. Results : Coverage across reference



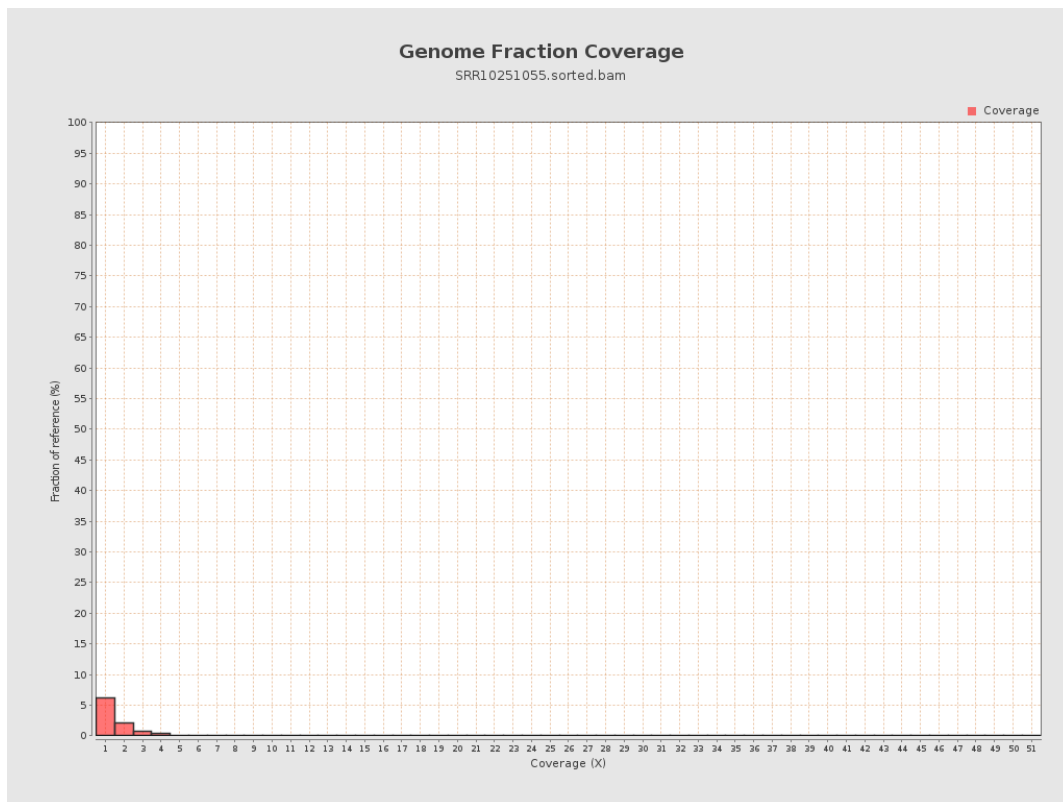
4. Results : Coverage Histogram



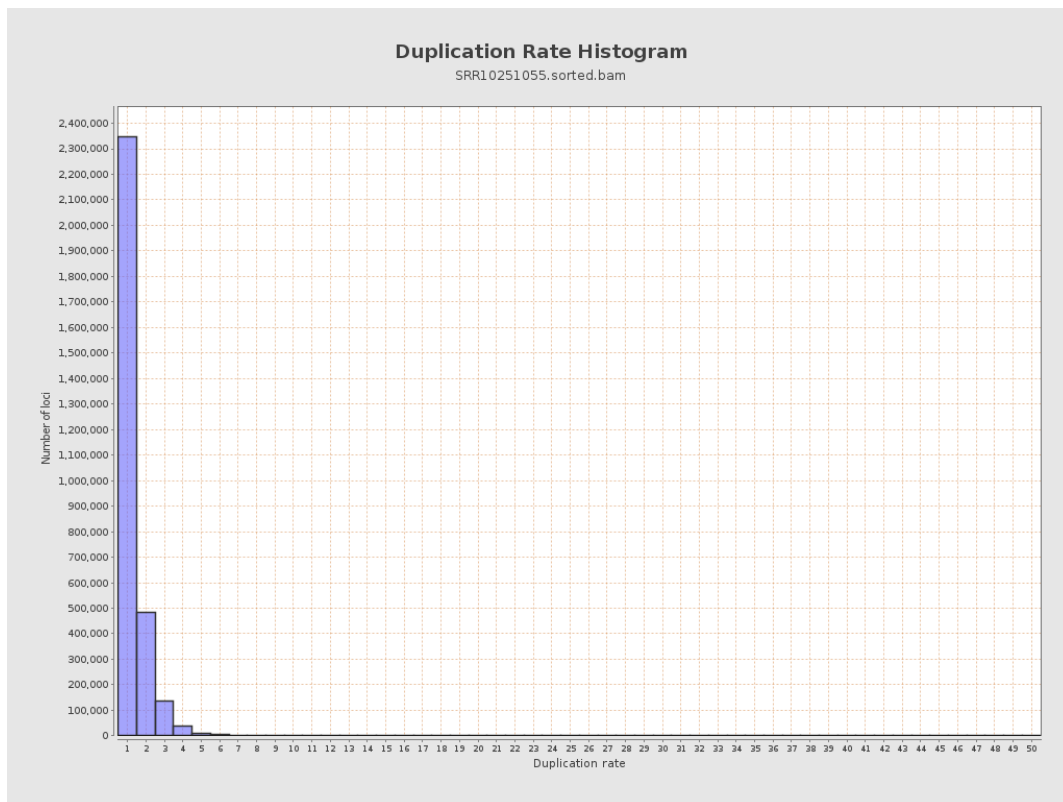
5. Results : Coverage Histogram (0-50X)



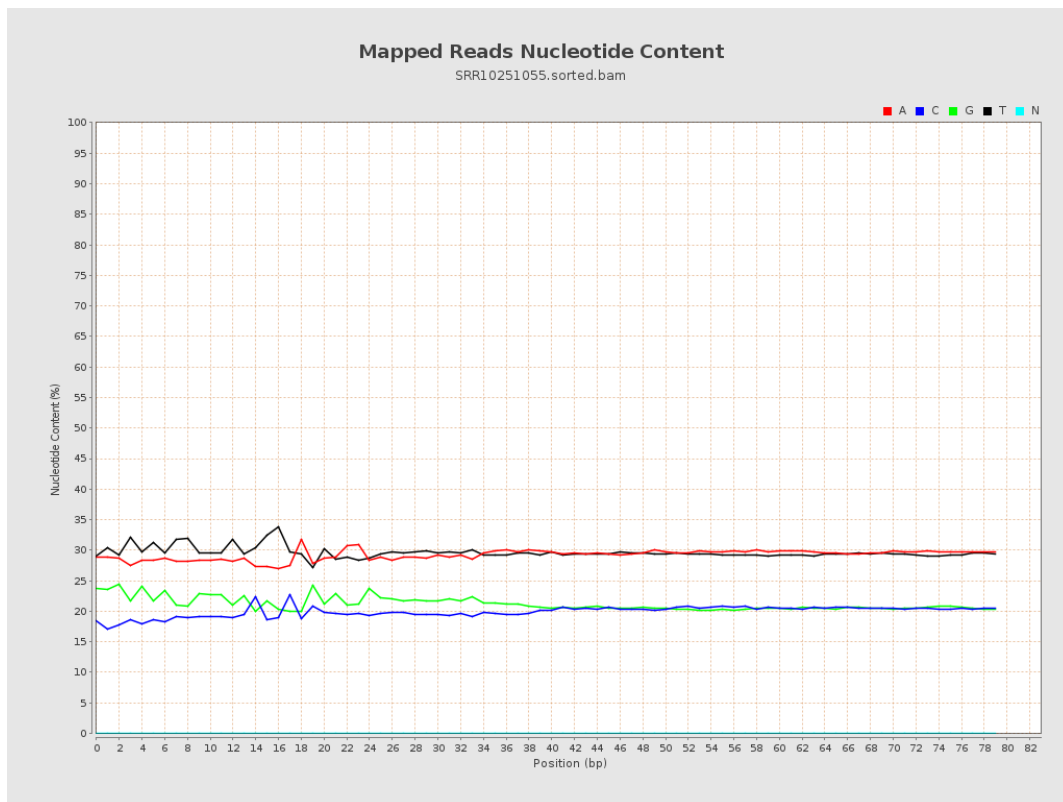
6. Results : Genome Fraction Coverage



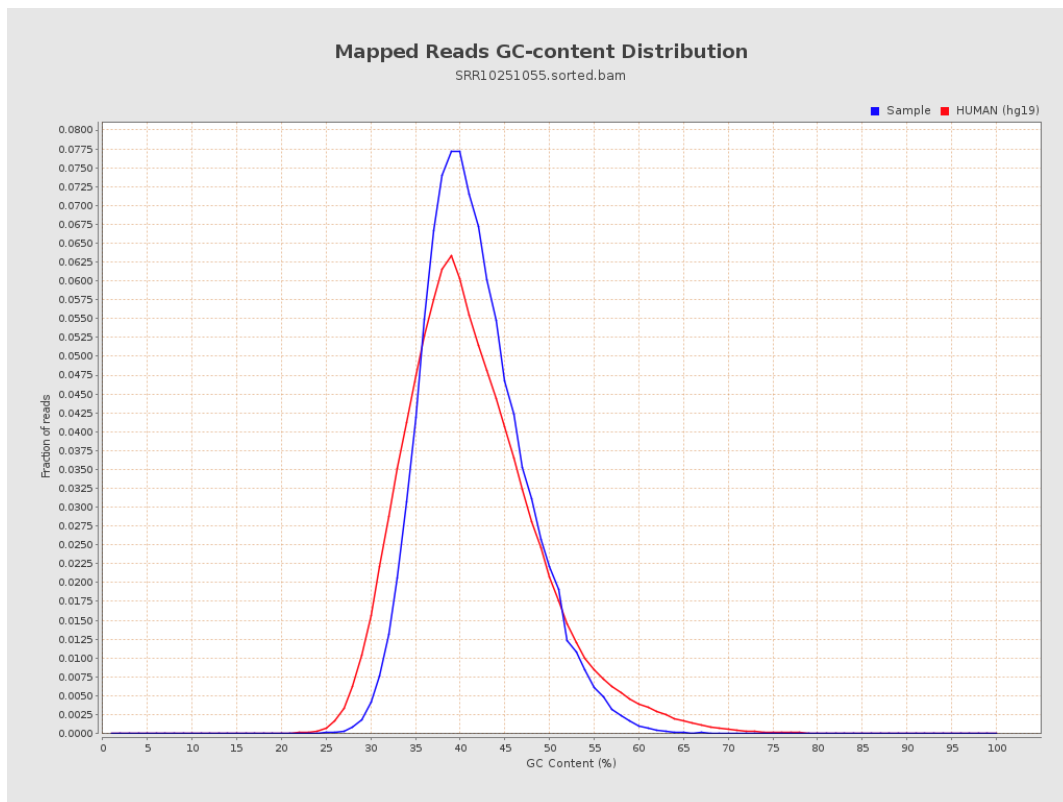
7. Results : Duplication Rate Histogram



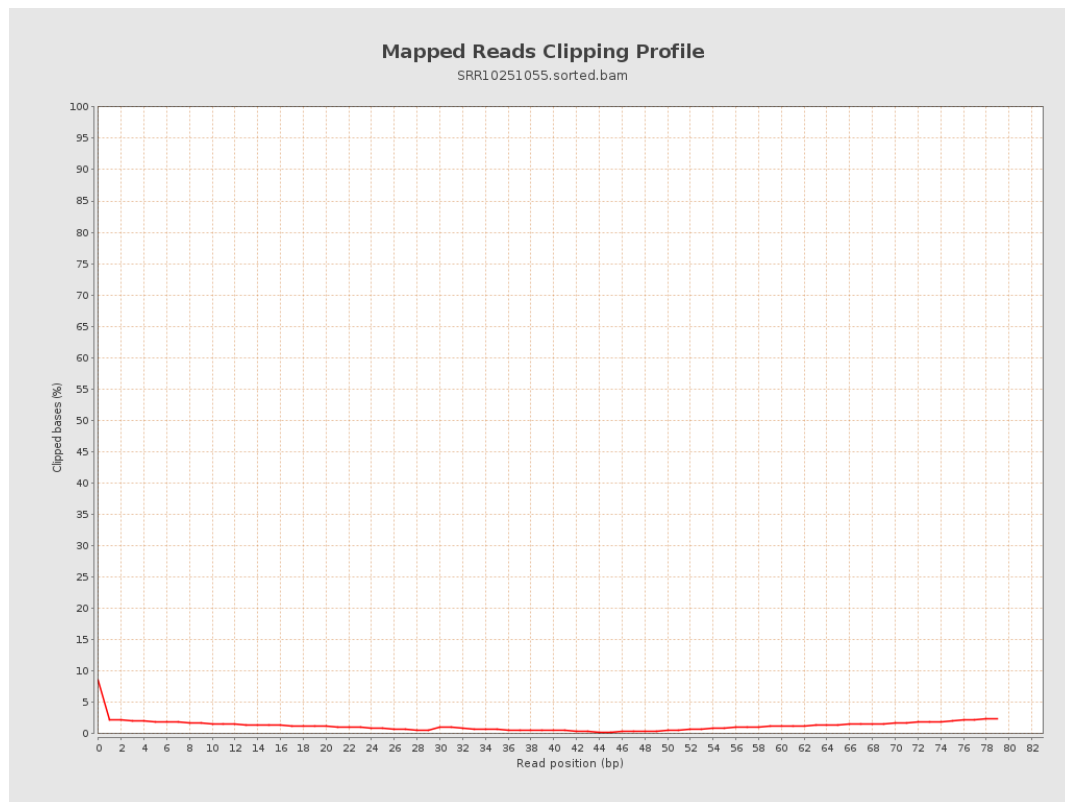
8. Results : Mapped Reads Nucleotide Content



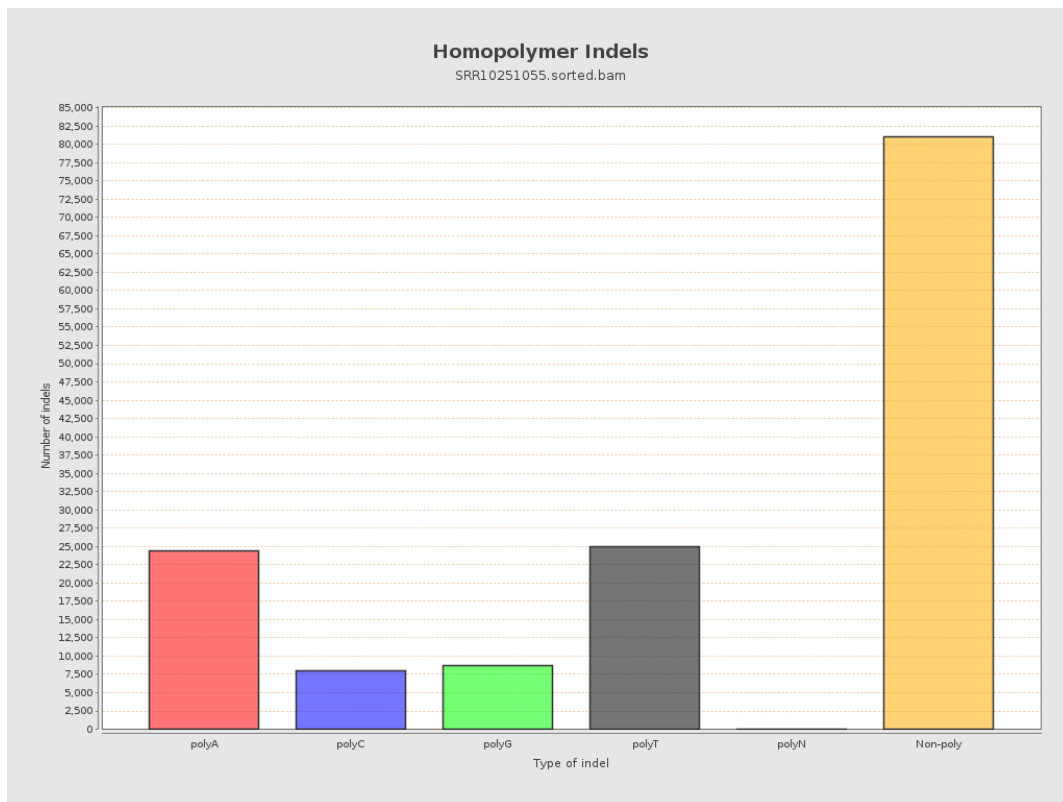
9. Results : Mapped Reads GC-content Distribution



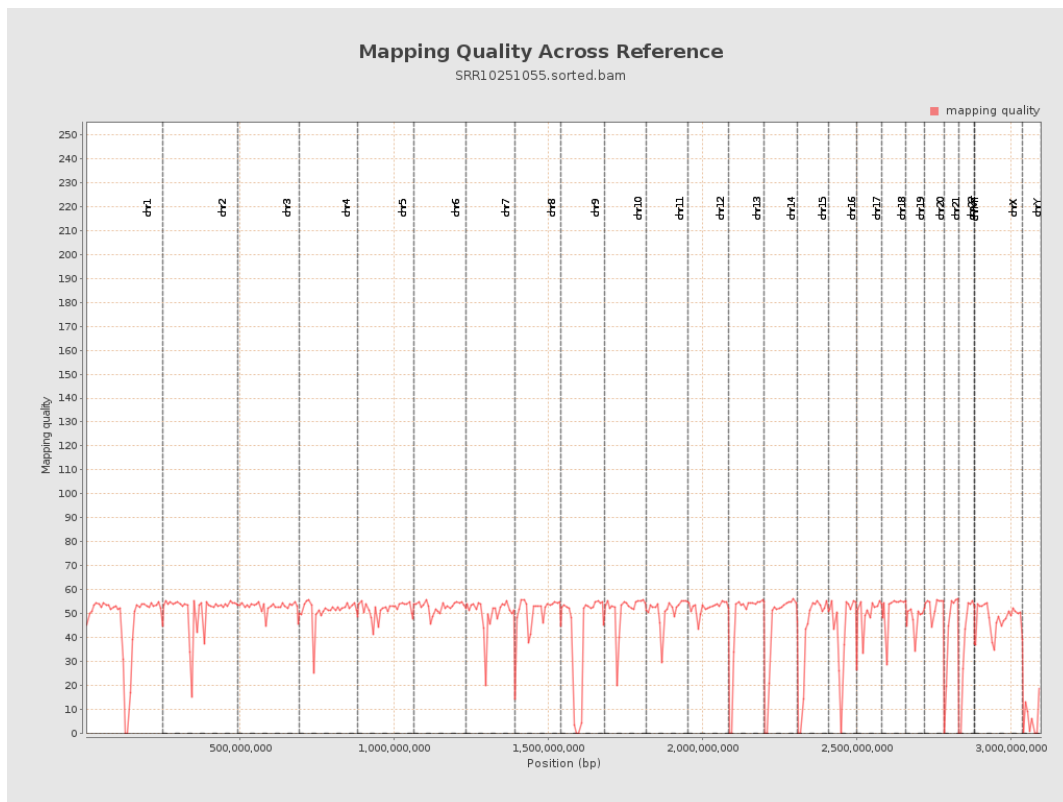
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

