

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:23:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082905.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_SRR3082905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082905.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:23:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,501,993
Mapped reads	2,198,671 / 87.88%
Unmapped reads	303,322 / 12.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,837 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	147,251 / 5.89%
Duplication rate	5.64%
Clipped reads	1,047,067 / 41.85%

2.2. ACGT Content

Number/percentage of A's	39,247,153 / 27.05%
Number/percentage of C's	27,103,891 / 18.68%
Number/percentage of T's	45,776,423 / 31.55%
Number/percentage of G's	32,963,751 / 22.72%
Number/percentage of N's	7,129 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.3677
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.85
----------------------	-------

2.5. Mismatches and indels

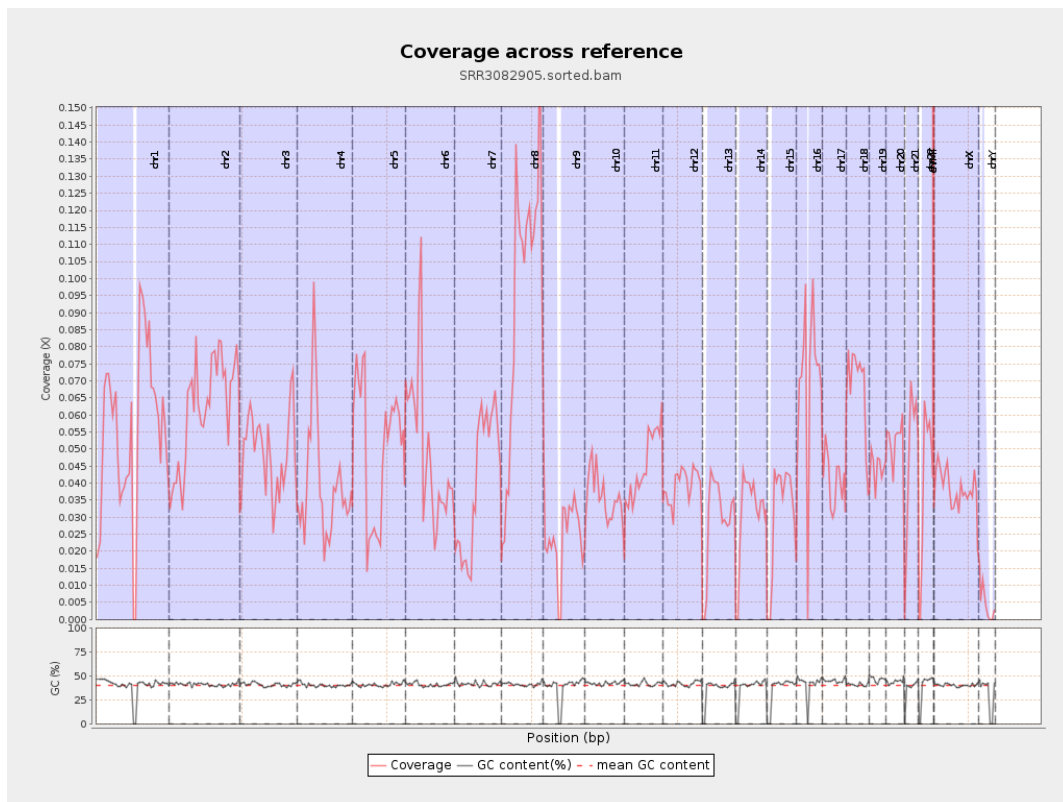
General error rate	0.75%
Mismatches	1,068,645
Insertions	11,710
Mapped reads with at least one insertion	0.53%
Deletions	33,071
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.43%

2.6. Chromosome stats

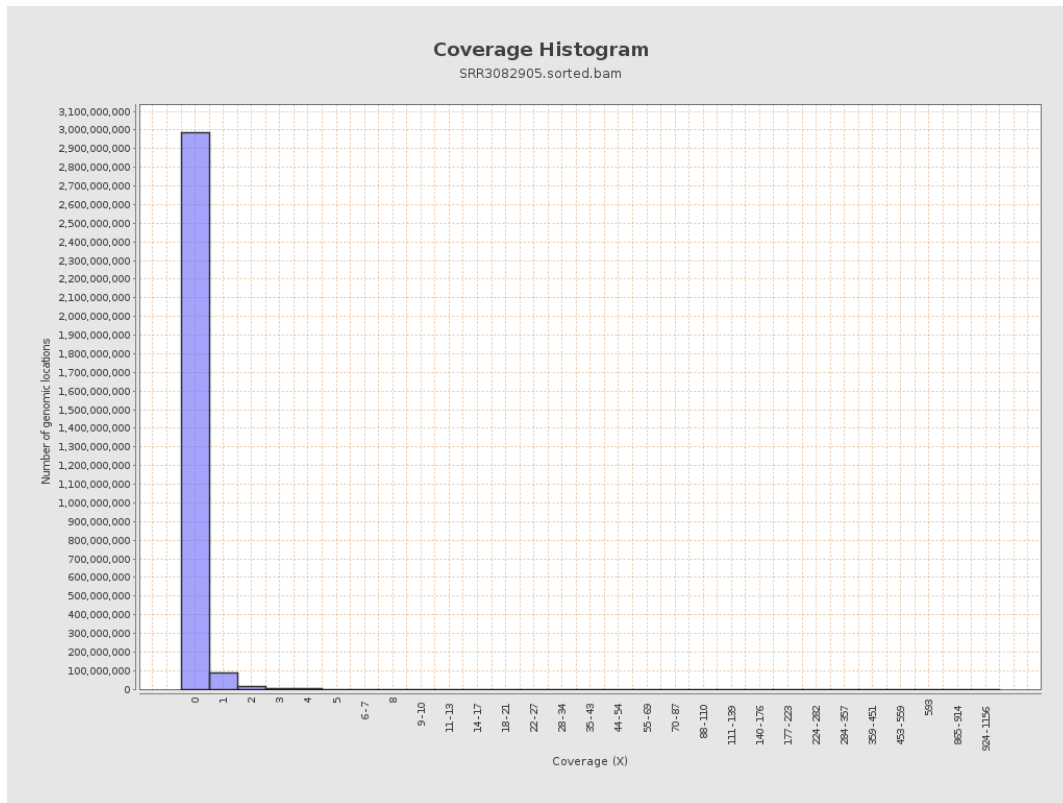
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13825921	0.0555	0.5708
chr2	243199373	15094017	0.0621	0.6054
chr3	198022430	9709773	0.049	0.2791
chr4	191154276	7569229	0.0396	0.2552
chr5	180915260	9091014	0.0503	0.2834
chr6	171115067	8406952	0.0491	0.3617
chr7	159138663	6459286	0.0406	0.2955

chr8	146364022	13938665	0.0952	0.478
chr9	141213431	3343358	0.0237	0.2585
chr10	135534747	4899261	0.0361	0.2879
chr11	135006516	6085821	0.0451	0.3025
chr12	133851895	5271964	0.0394	0.2525
chr13	115169878	3325084	0.0289	0.2162
chr14	107349540	3321426	0.0309	0.2325
chr15	102531392	3229157	0.0315	0.2282
chr16	90354753	6363699	0.0704	0.3473
chr17	81195210	3253868	0.0401	0.2627
chr18	78077248	5373404	0.0688	0.5442
chr19	59128983	2633423	0.0445	0.4604
chr20	63025520	3274736	0.052	0.2919
chr21	48129895	2284170	0.0475	0.2766
chr22	51304566	2021526	0.0394	0.2505
chrMT	16571	128102	7.7305	5.7516
chrX	155270560	5976652	0.0385	0.2618
chrY	59373566	272040	0.0046	0.0939

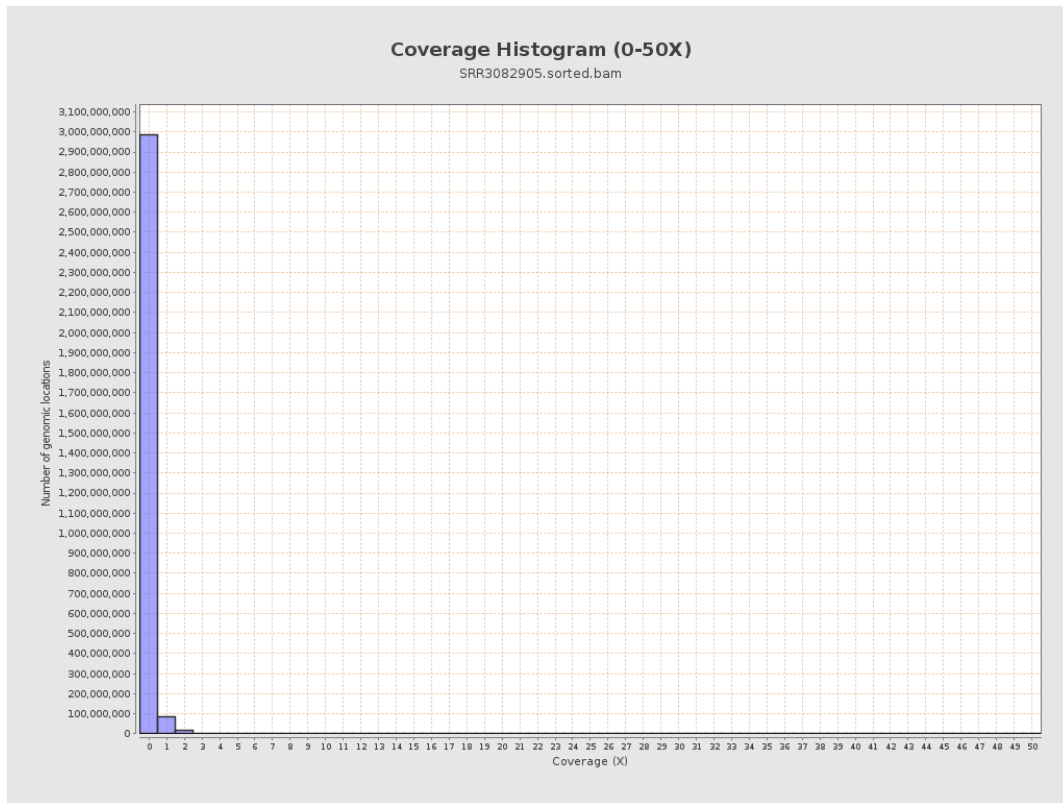
3. Results : Coverage across reference



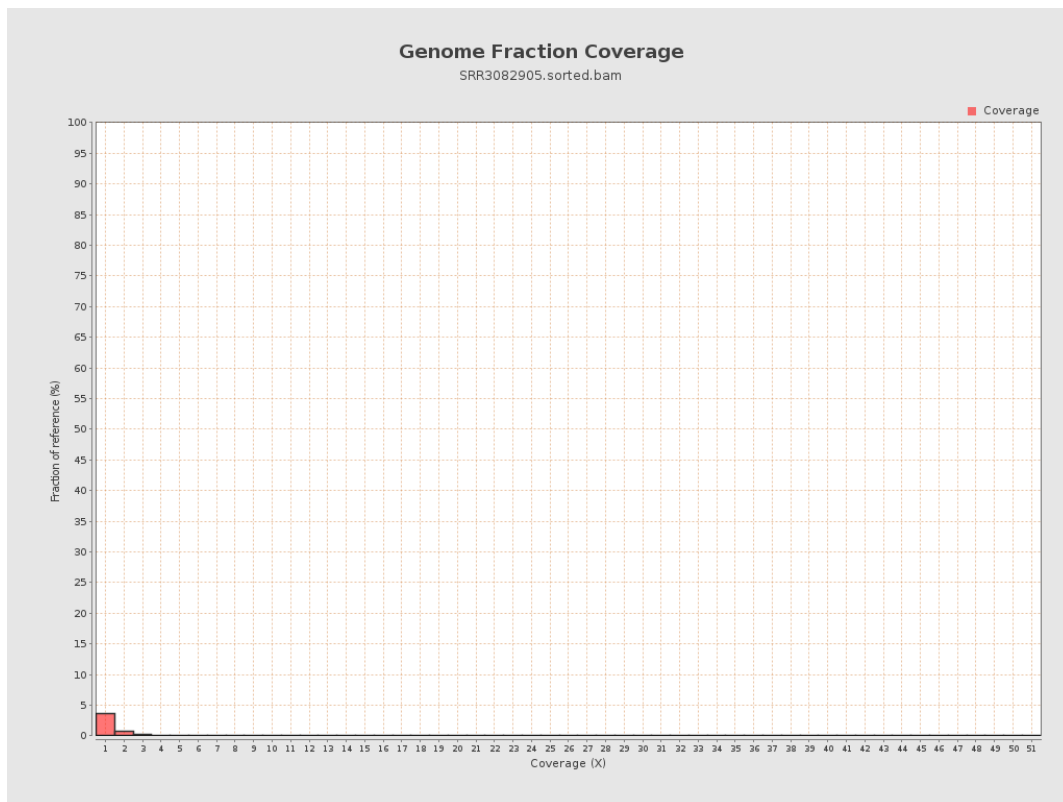
4. Results : Coverage Histogram



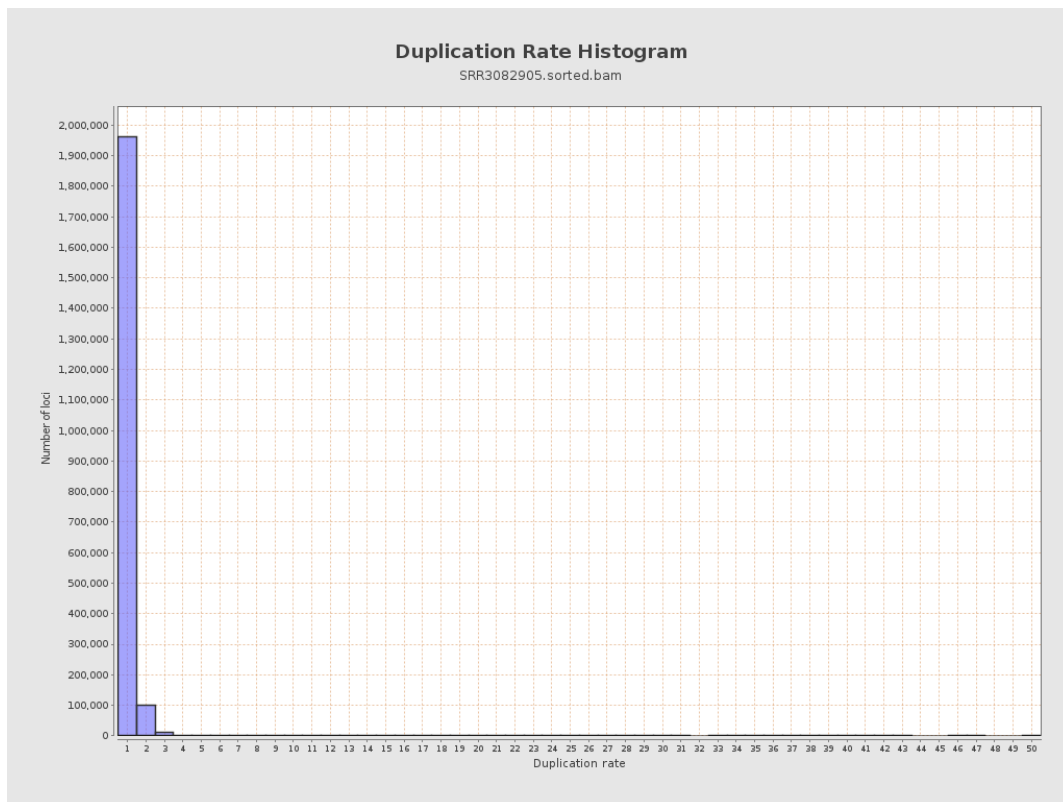
5. Results : Coverage Histogram (0-50X)



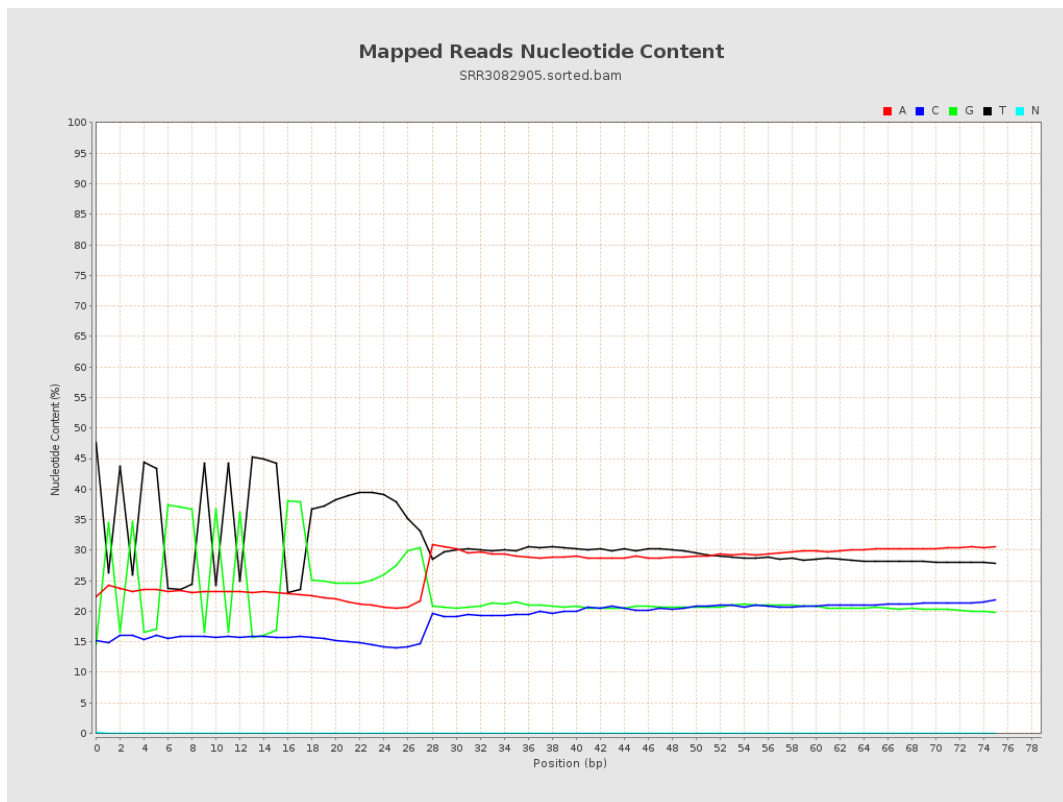
6. Results : Genome Fraction Coverage



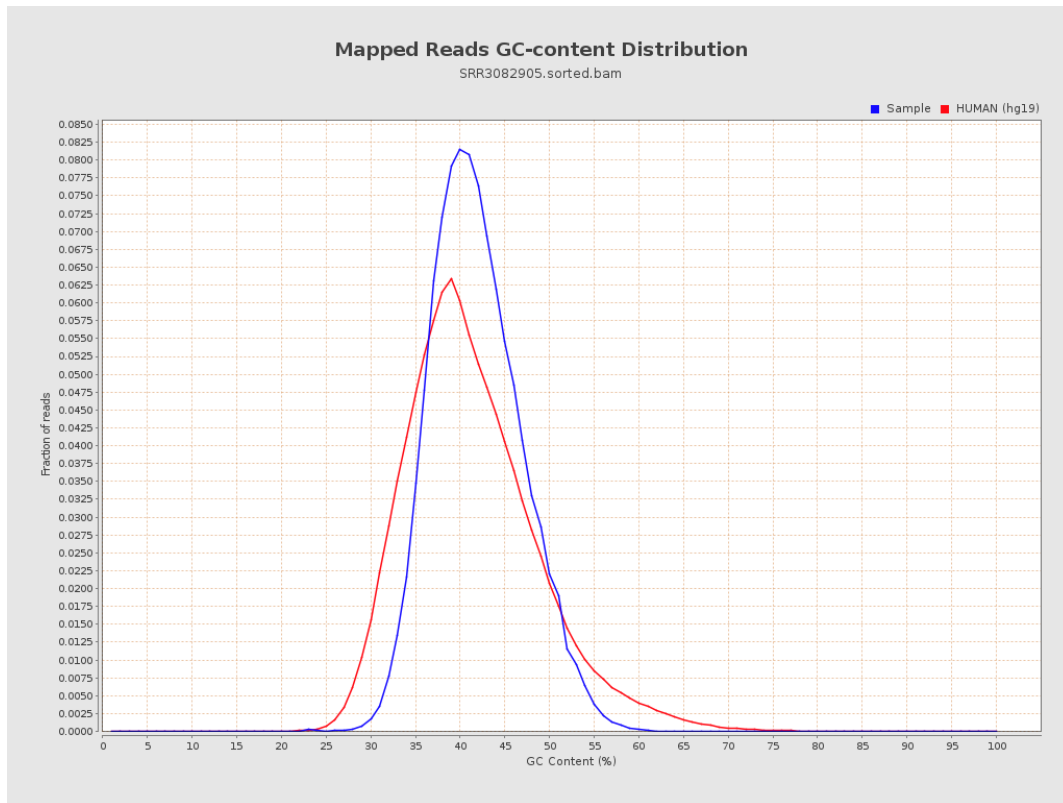
7. Results : Duplication Rate Histogram



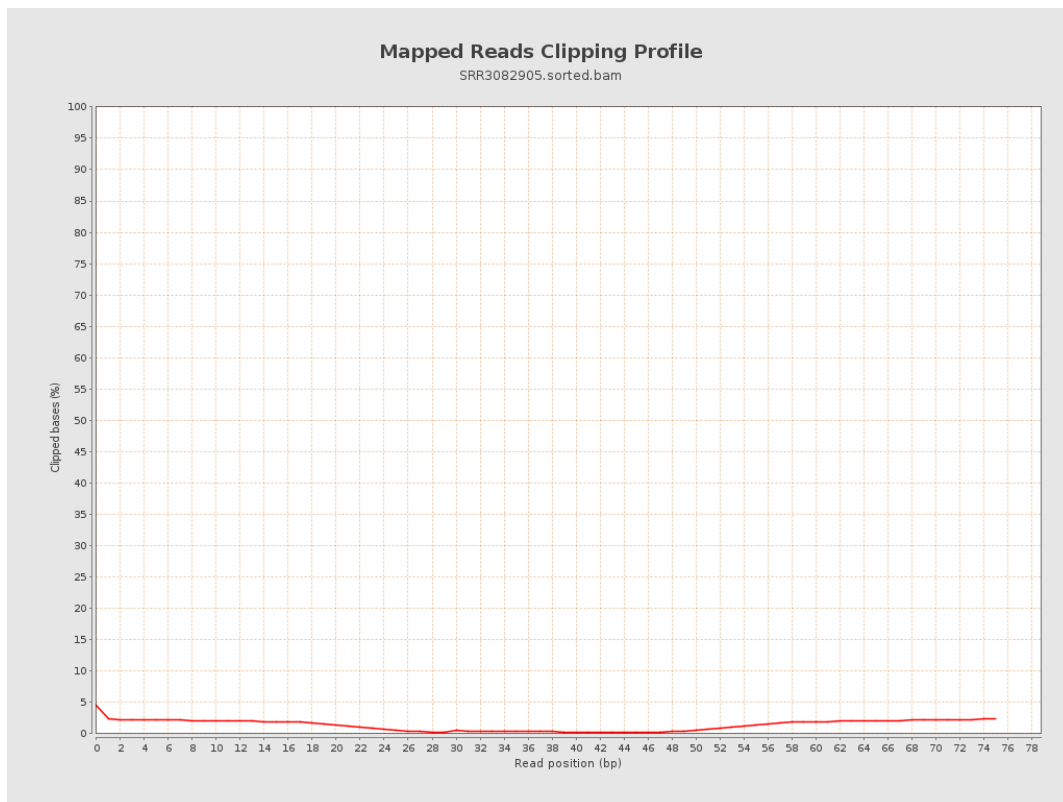
8. Results : Mapped Reads Nucleotide Content



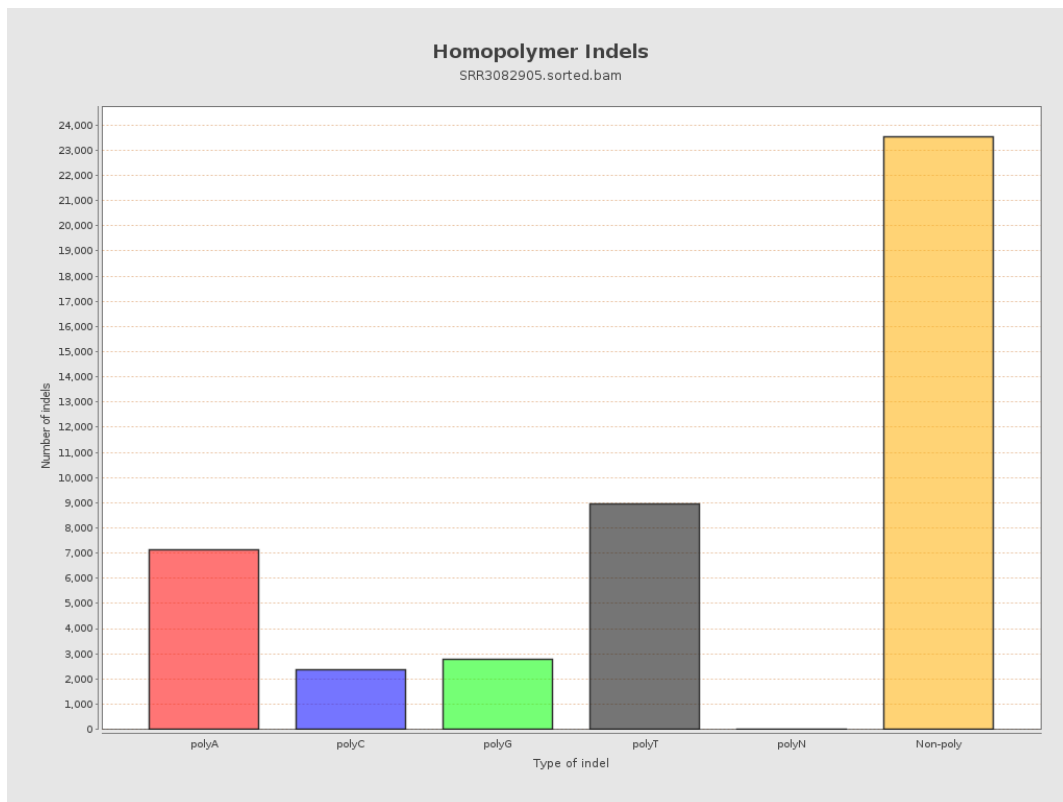
9. Results : Mapped Reads GC-content Distribution



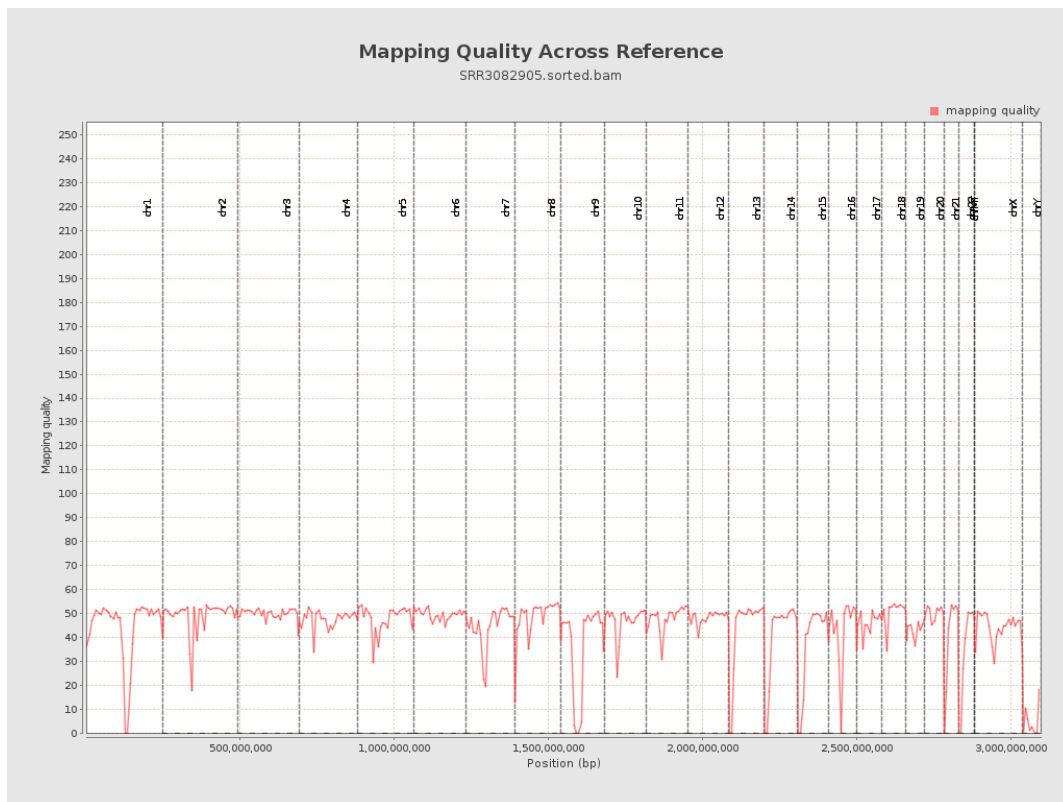
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

