

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:43:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524763.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_SRR10524763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:43:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,223,122
Mapped reads	1,116,908 / 91.32%
Unmapped reads	106,214 / 8.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,830 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	36,622 / 2.99%
Duplication rate	2.51%
Clipped reads	1,118,450 / 91.44%

2.2. ACGT Content

Number/percentage of A's	15,788,225 / 24.48%
Number/percentage of C's	11,457,044 / 17.76%
Number/percentage of T's	20,282,387 / 31.45%
Number/percentage of G's	16,960,934 / 26.3%
Number/percentage of N's	8,403 / 0.01%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0208

Standard Deviation	0.1991
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.93
----------------------	-------

2.5. Mismatches and indels

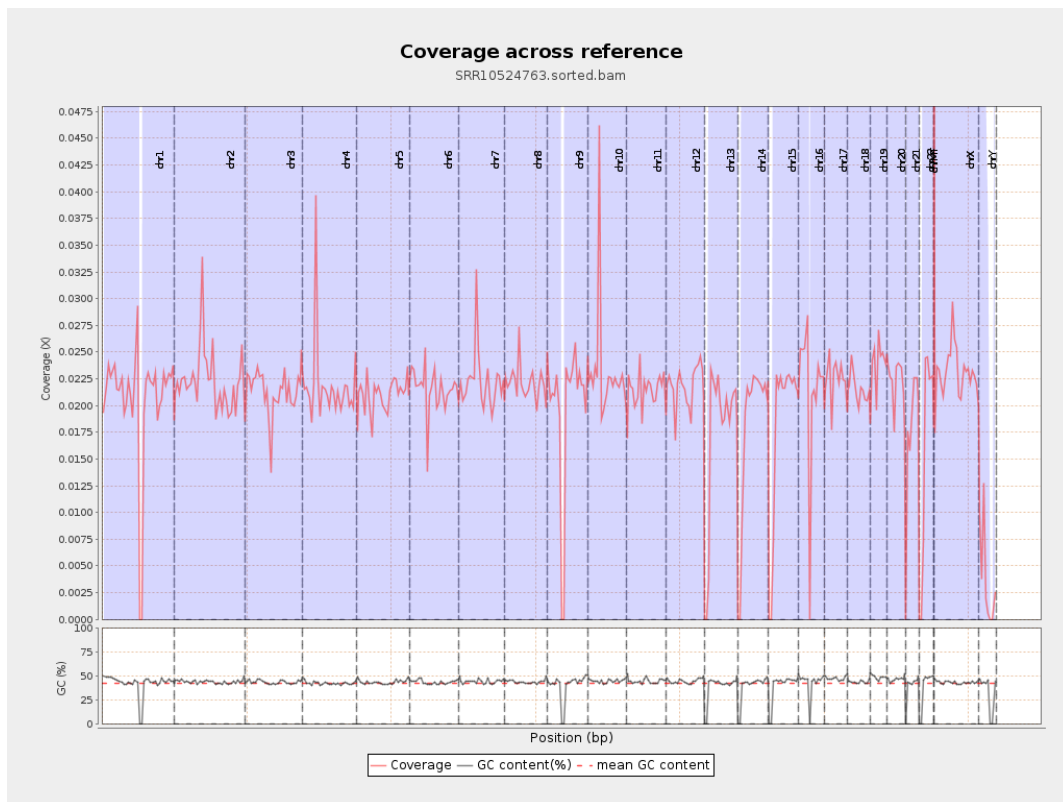
General error rate	0.53%
Mismatches	329,989
Insertions	4,459
Mapped reads with at least one insertion	0.4%
Deletions	13,215
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.98%

2.6. Chromosome stats

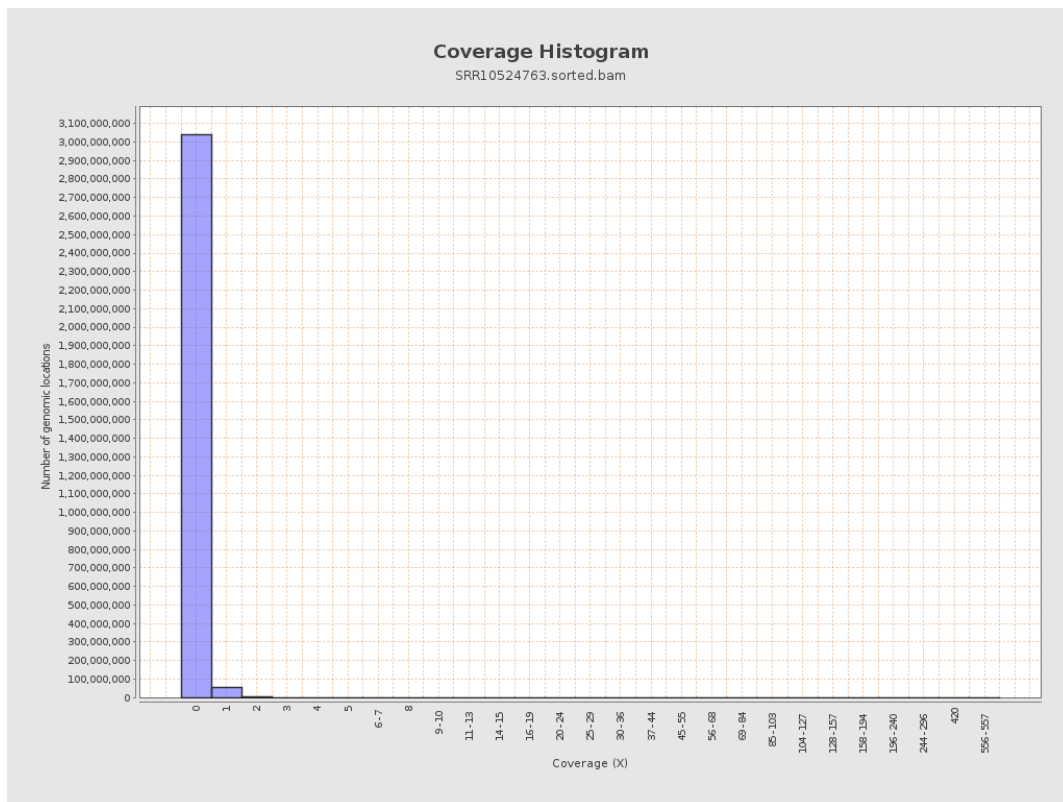
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5133459	0.0206	0.2694
chr2	243199373	5430137	0.0223	0.2917
chr3	198022430	4212681	0.0213	0.159
chr4	191154276	4175065	0.0218	0.1778
chr5	180915260	3832599	0.0212	0.1575
chr6	171115067	3681618	0.0215	0.1704
chr7	159138663	3548330	0.0223	0.2347

chr8	146364022	3233604	0.0221	0.1882
chr9	141213431	2778269	0.0197	0.1778
chr10	135534747	3147608	0.0232	0.2356
chr11	135006516	2914612	0.0216	0.1831
chr12	133851895	2918622	0.0218	0.1611
chr13	115169878	1994351	0.0173	0.1421
chr14	107349540	1931102	0.018	0.1463
chr15	102531392	1839643	0.0179	0.1449
chr16	90354753	1936466	0.0214	0.1727
chr17	81195210	1823307	0.0225	0.167
chr18	78077248	1680871	0.0215	0.2604
chr19	59128983	1418357	0.024	0.2266
chr20	63025520	1391526	0.0221	0.1643
chr21	48129895	858474	0.0178	0.1599
chr22	51304566	822323	0.016	0.1371
chrMT	16571	1412	0.0852	0.3167
chrX	155270560	3595917	0.0232	0.1746
chrY	59373566	218012	0.0037	0.1103

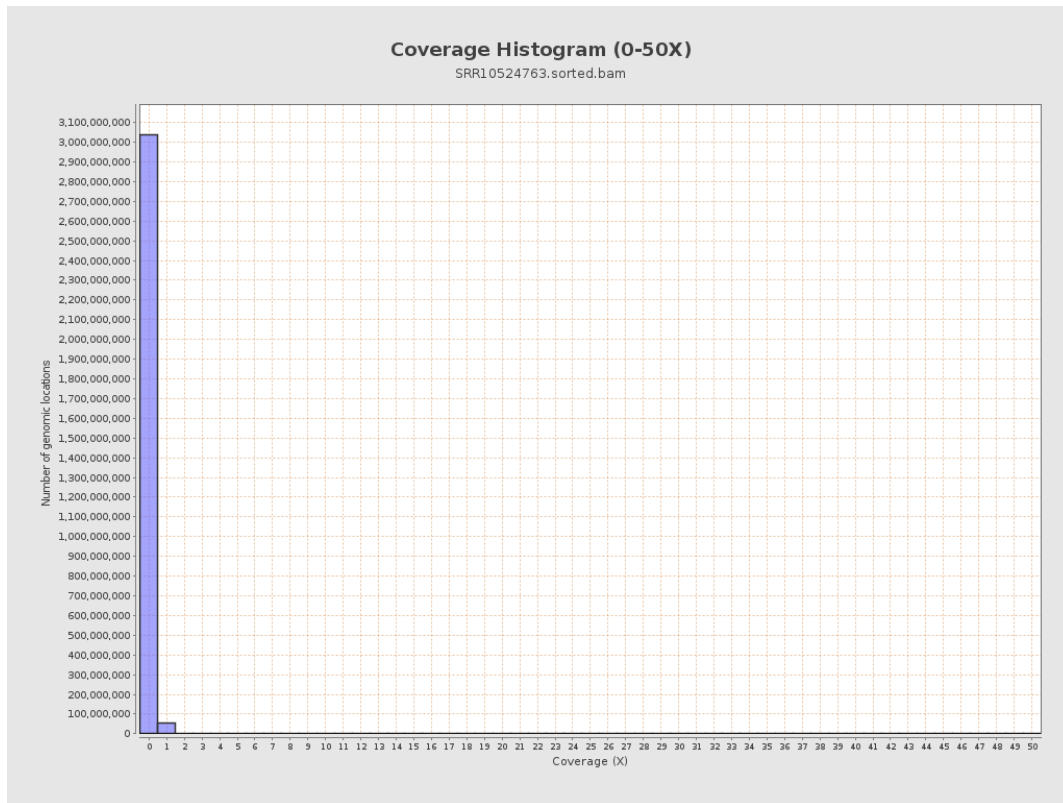
3. Results : Coverage across reference



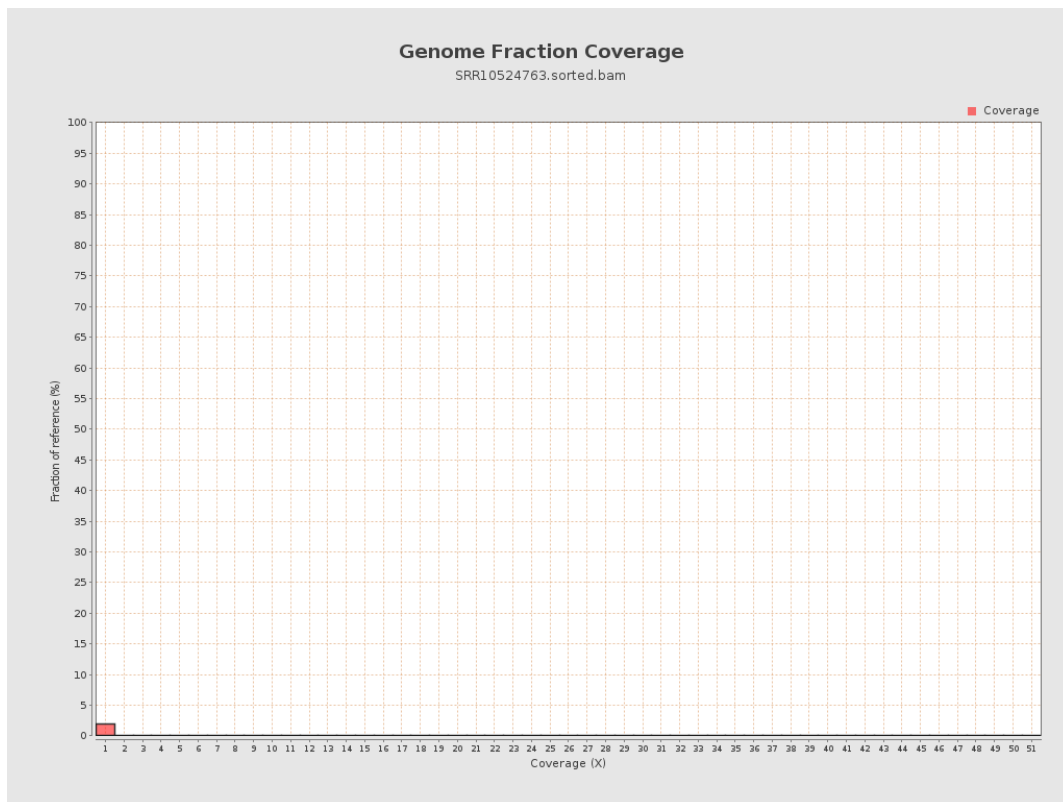
4. Results : Coverage Histogram



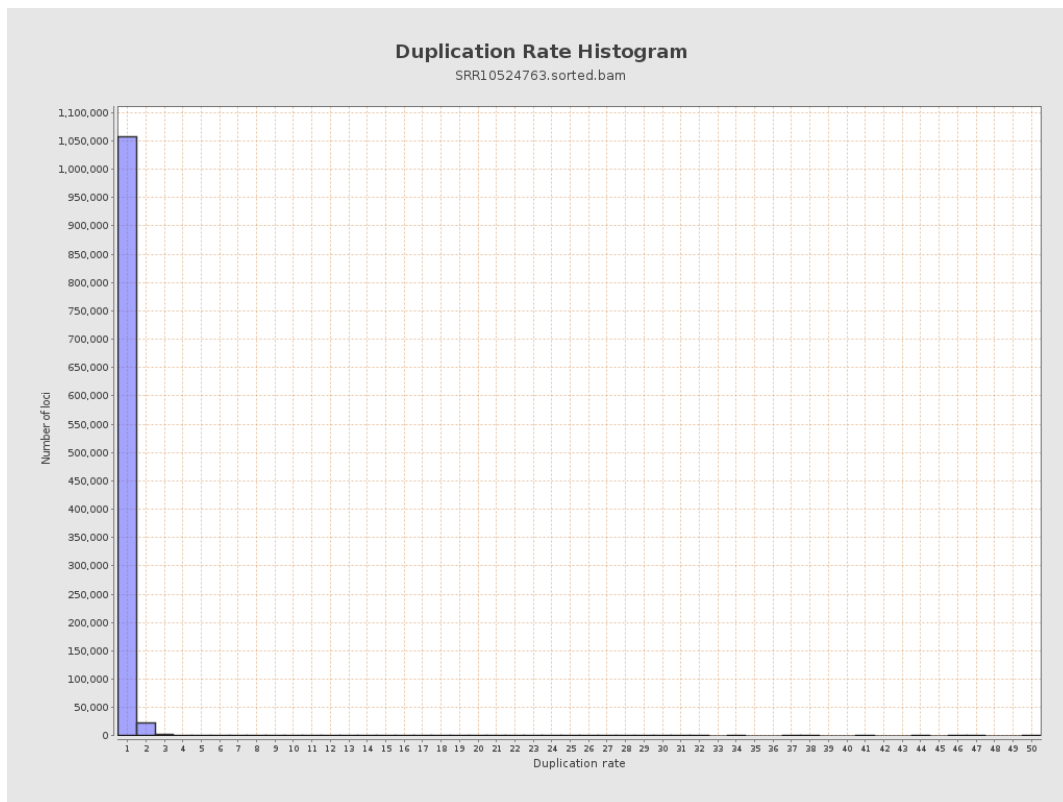
5. Results : Coverage Histogram (0-50X)



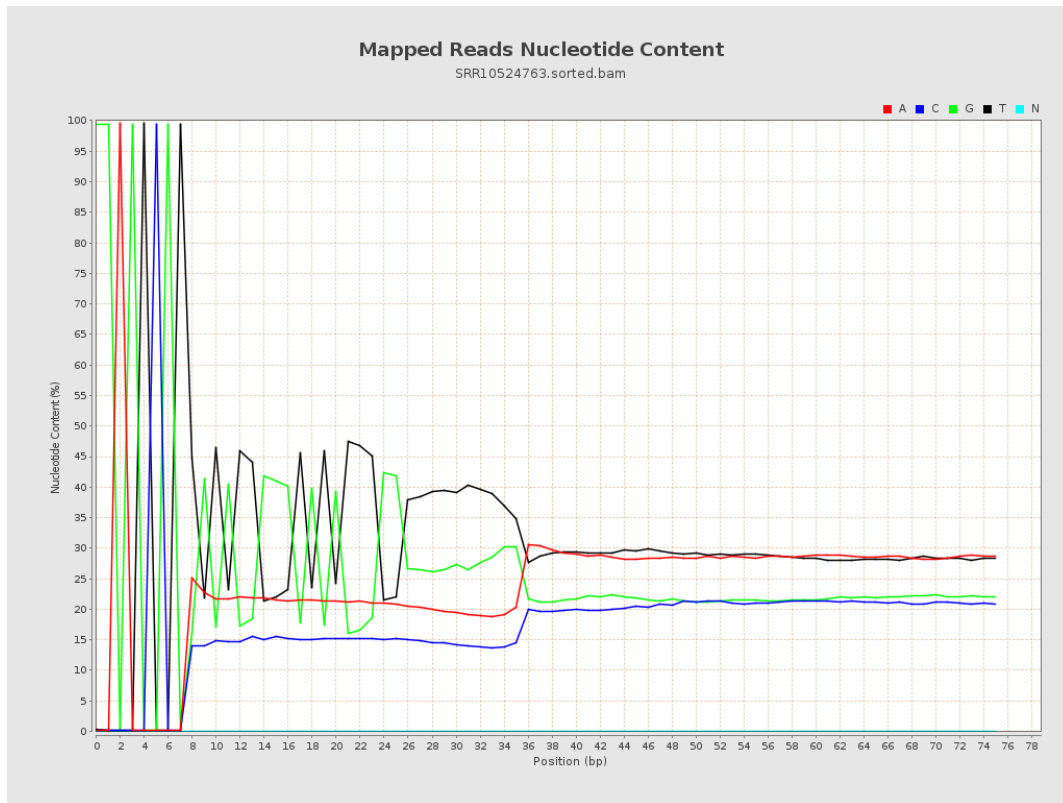
6. Results : Genome Fraction Coverage



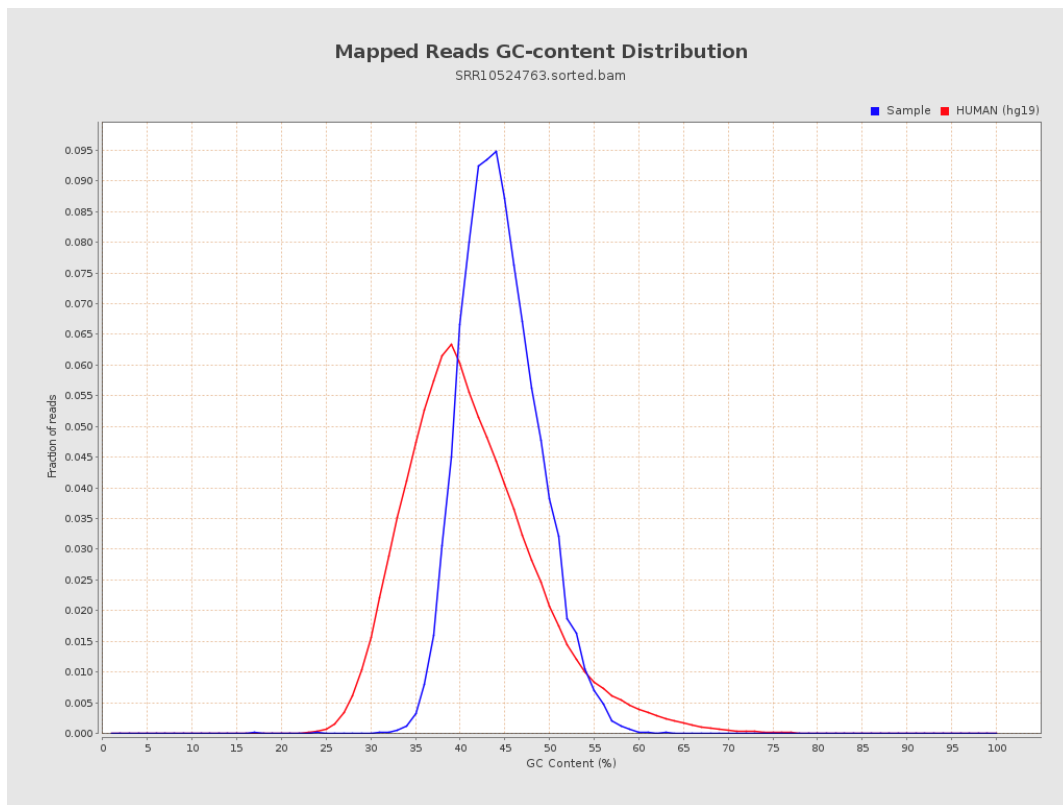
7. Results : Duplication Rate Histogram



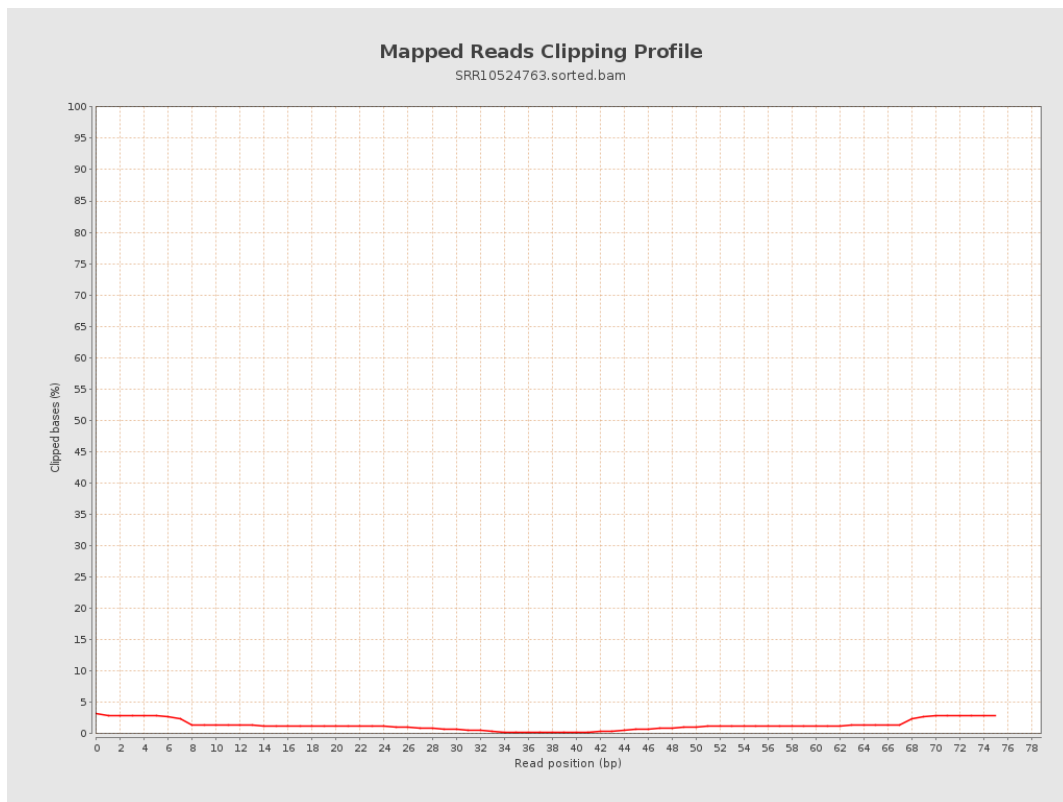
8. Results : Mapped Reads Nucleotide Content



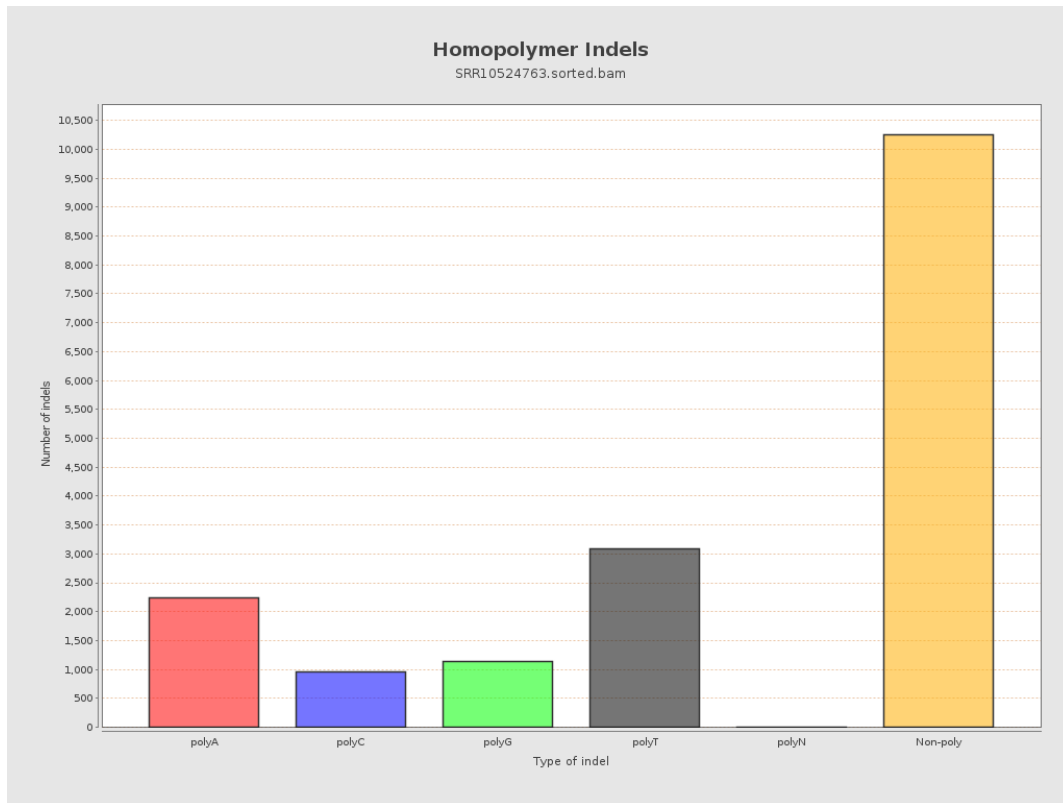
9. Results : Mapped Reads GC-content Distribution



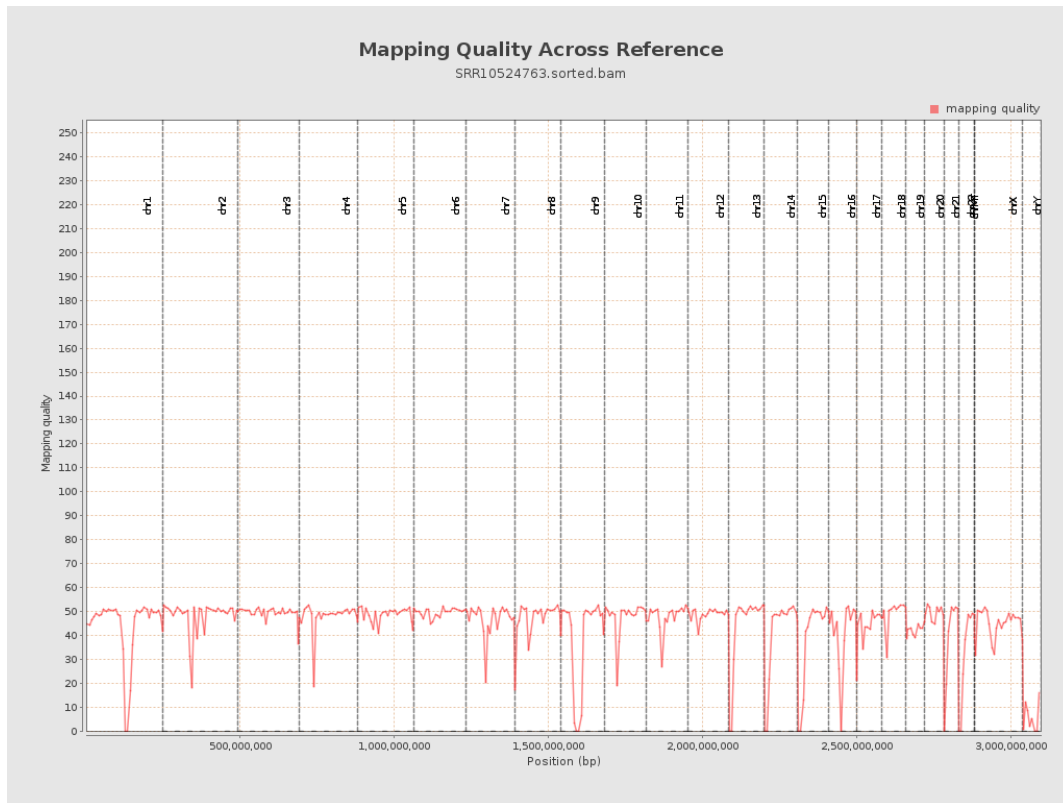
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

