Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:21:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525075.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_SRR10525075 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525075.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:21:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525075.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	987,954
Mapped reads	897,742 / 90.87%
Unmapped reads	90,212 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,090 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	39,537 / 4%
Duplication rate	3.59%
Clipped reads	898,376 / 90.93%

2.2. ACGT Content

Number/percentage of A's	13,481,802 / 25.7%
Number/percentage of C's	10,212,953 / 19.47%
Number/percentage of T's	16,470,562 / 31.4%
Number/percentage of G's	12,282,188 / 23.42%
Number/percentage of N's	5,577 / 0.01%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1843

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

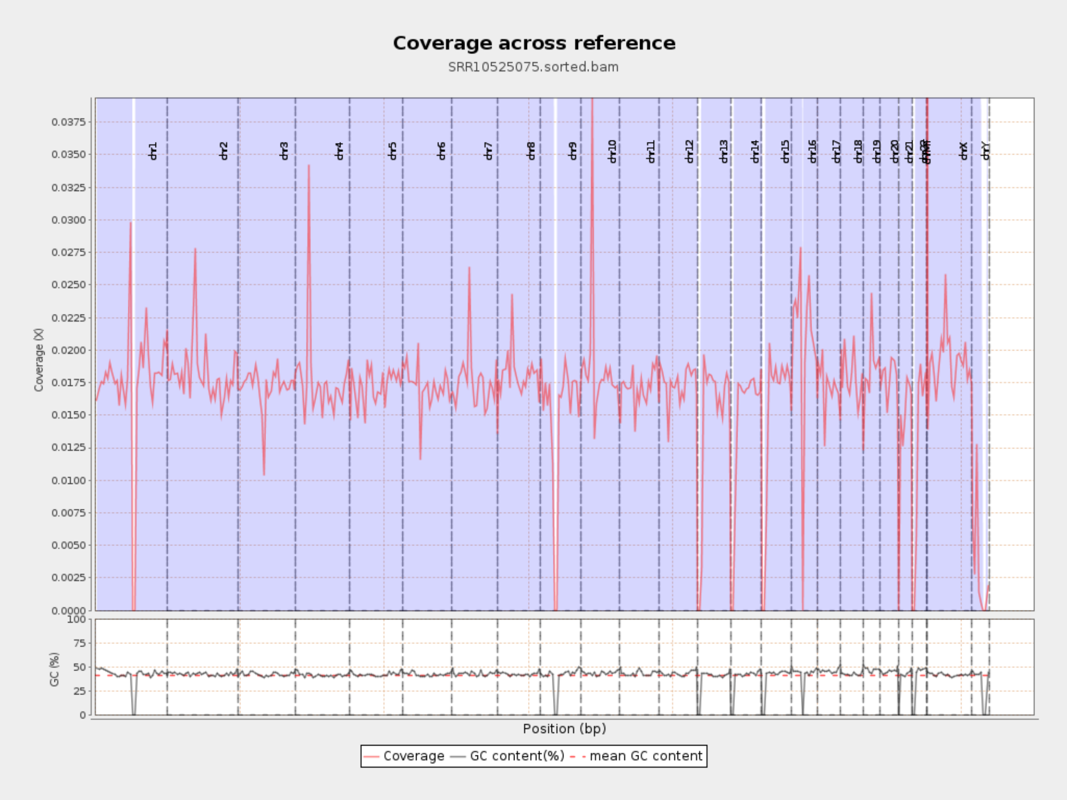
General error rate	0.49%
Mismatches	248,718
Insertions	3,901
Mapped reads with at least one insertion	0.43%
Deletions	9,978
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.38%

2.6. Chromosome stats

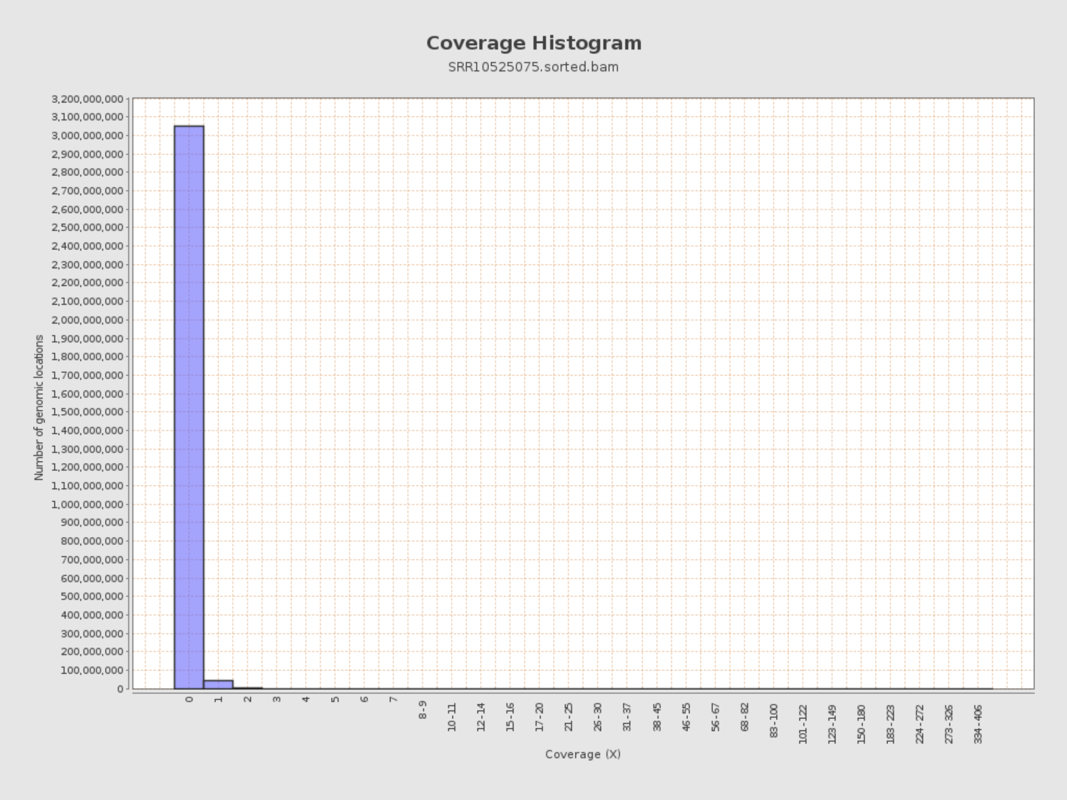
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4335521	0.0174	0.3152
chr2	243199373	4437191	0.0182	0.2238
chr3	198022430	3399151	0.0172	0.1418
chr4	191154276	3387075	0.0177	0.1612
chr5	180915260	3132979	0.0173	0.1426
chr6	171115067	2944764	0.0172	0.1485
chr7	159138663	2815947	0.0177	0.1971

chr8	146364022	2669205	0.0182	0.1796
chr9	141213431	2097129	0.0149	0.1513
chr10	135534747	2545862	0.0188	0.2101
chr11	135006516	2323842	0.0172	0.1548
chr12	133851895	2332371	0.0174	0.1464
chr13	115169878	1664780	0.0145	0.1311
chr14	107349540	1531245	0.0143	0.1302
chr15	102531392	1522153	0.0148	0.1315
chr16	90354753	1837086	0.0203	0.1644
chr17	81195210	1394649	0.0172	0.1469
chr18	78077248	1400189	0.0179	0.24
chr19	59128983	1109027	0.0188	0.2389
chr20	63025520	1123737	0.0178	0.1478
chr21	48129895	681448	0.0142	0.1418
chr22	51304566	624494	0.0122	0.1202
chrMT	16571	9861	0.5951	0.8543
chrX	155270560	2962985	0.0191	0.1587
chrY	59373566	186777	0.0031	0.121

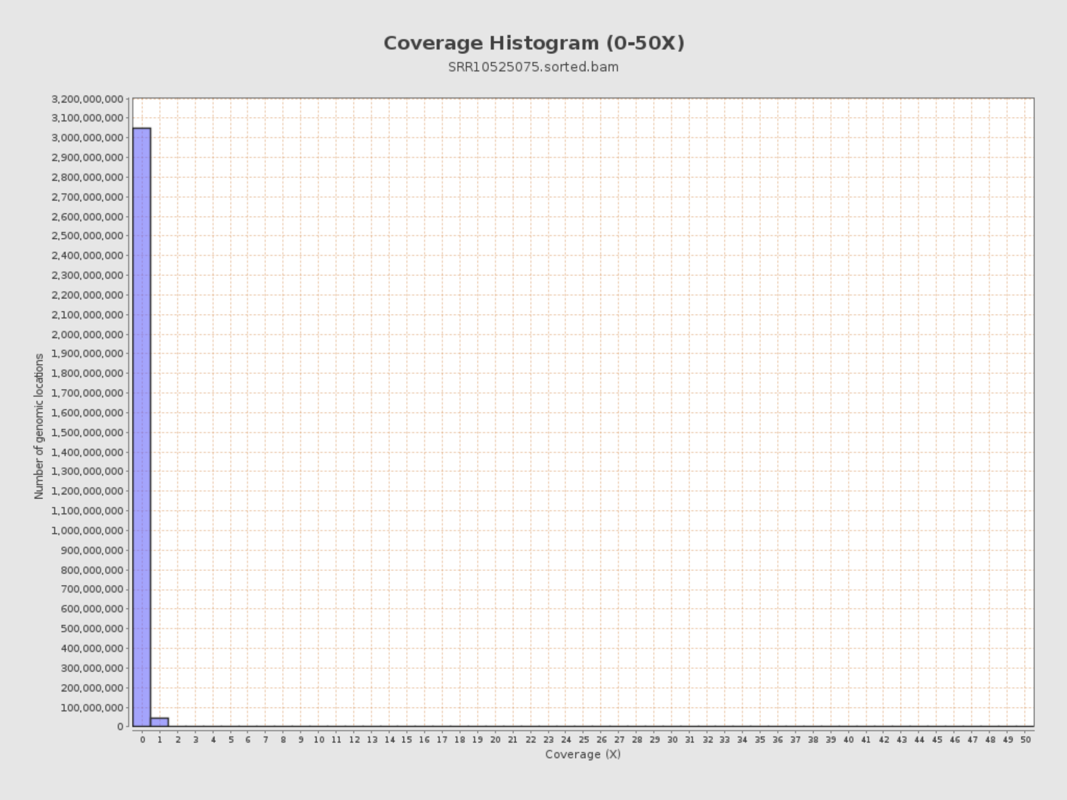
3. Results : Coverage across reference



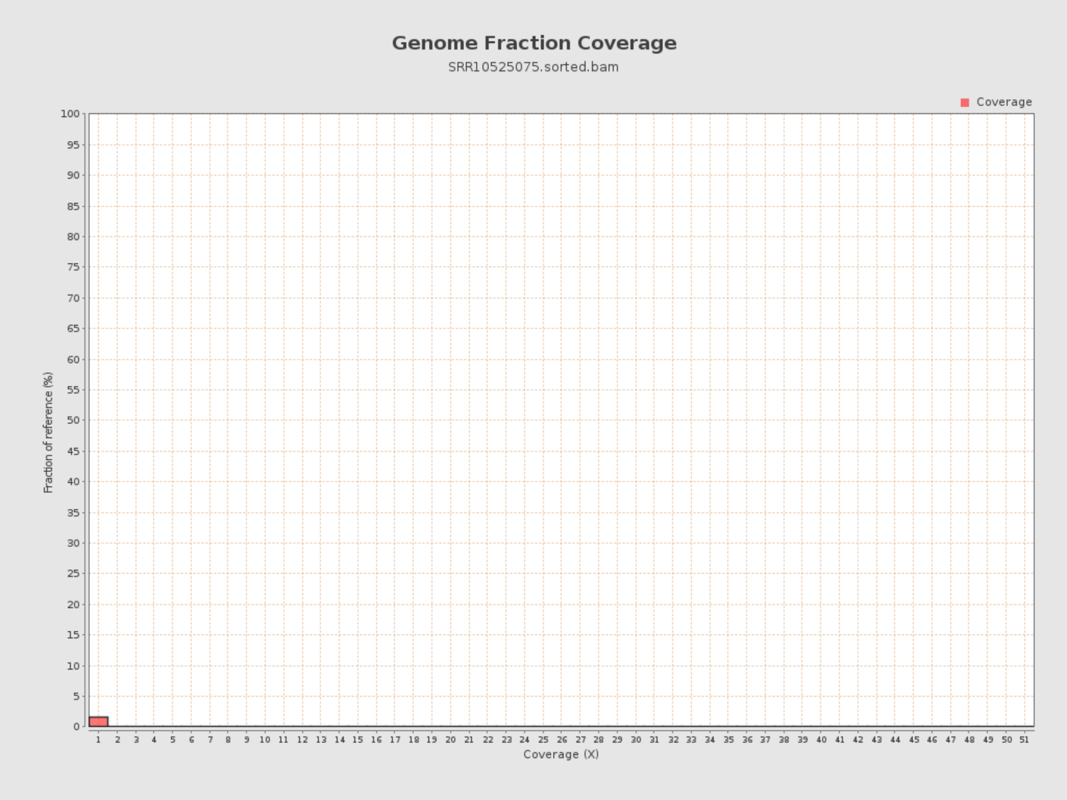
4. Results : Coverage Histogram



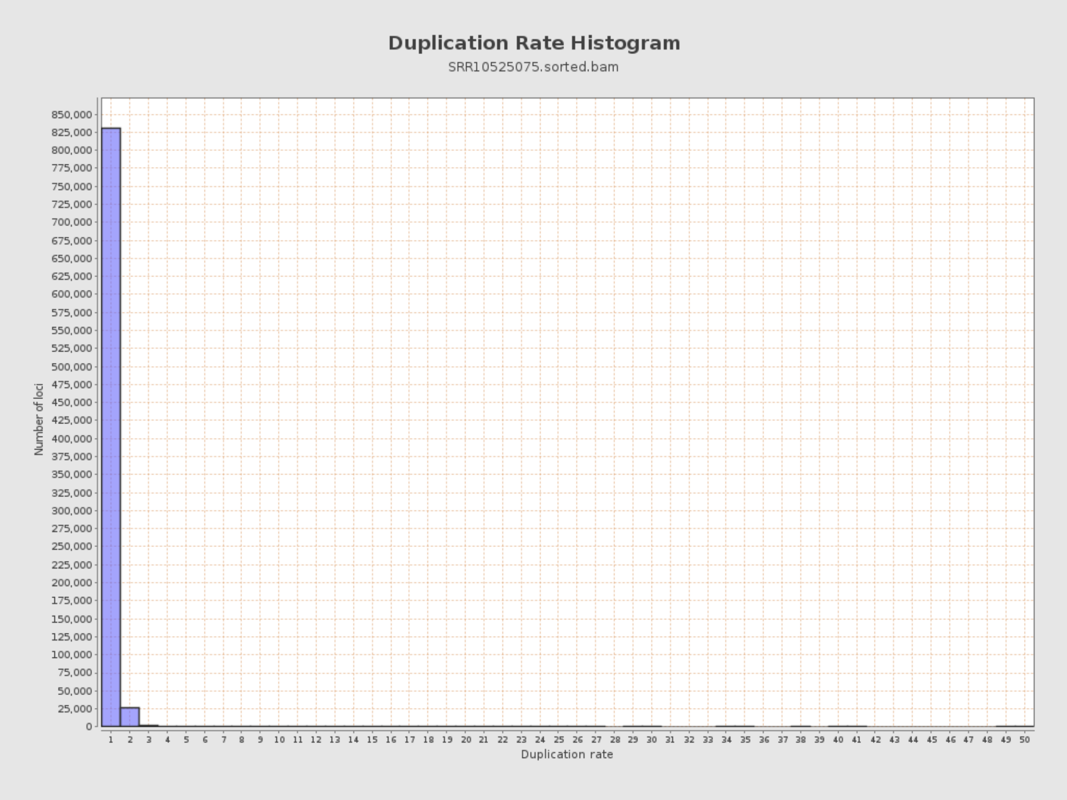
5. Results : Coverage Histogram (0-50X)



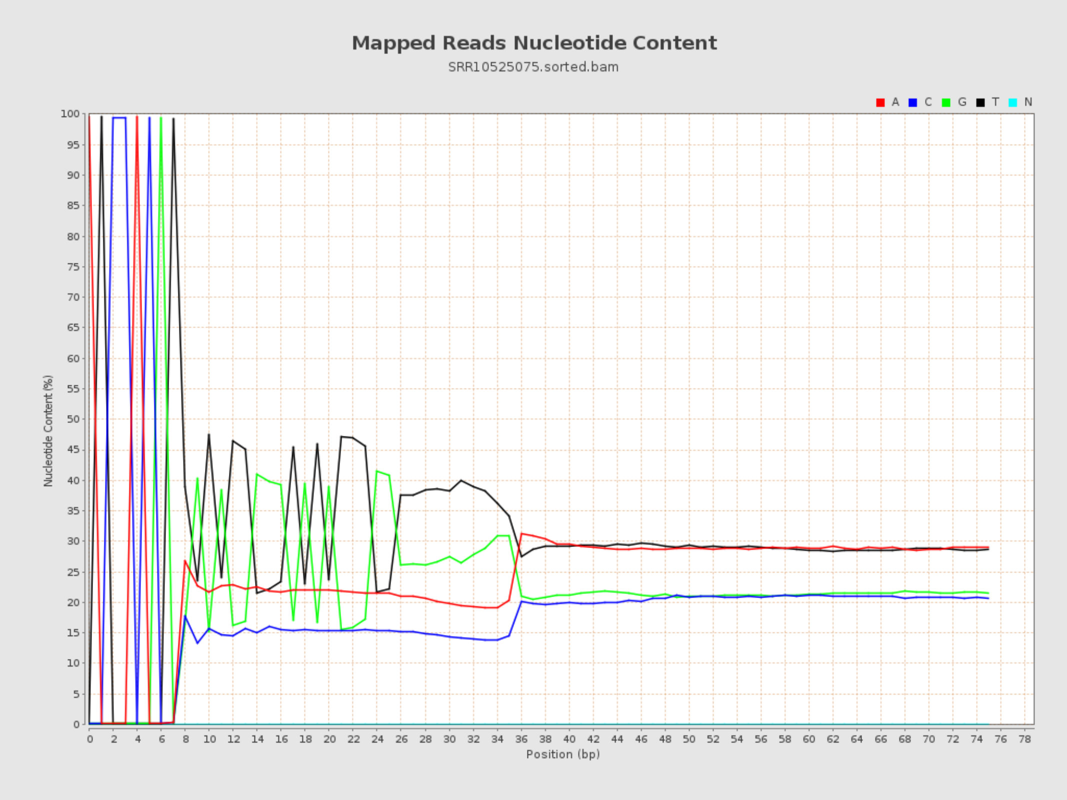
6. Results : Genome Fraction Coverage



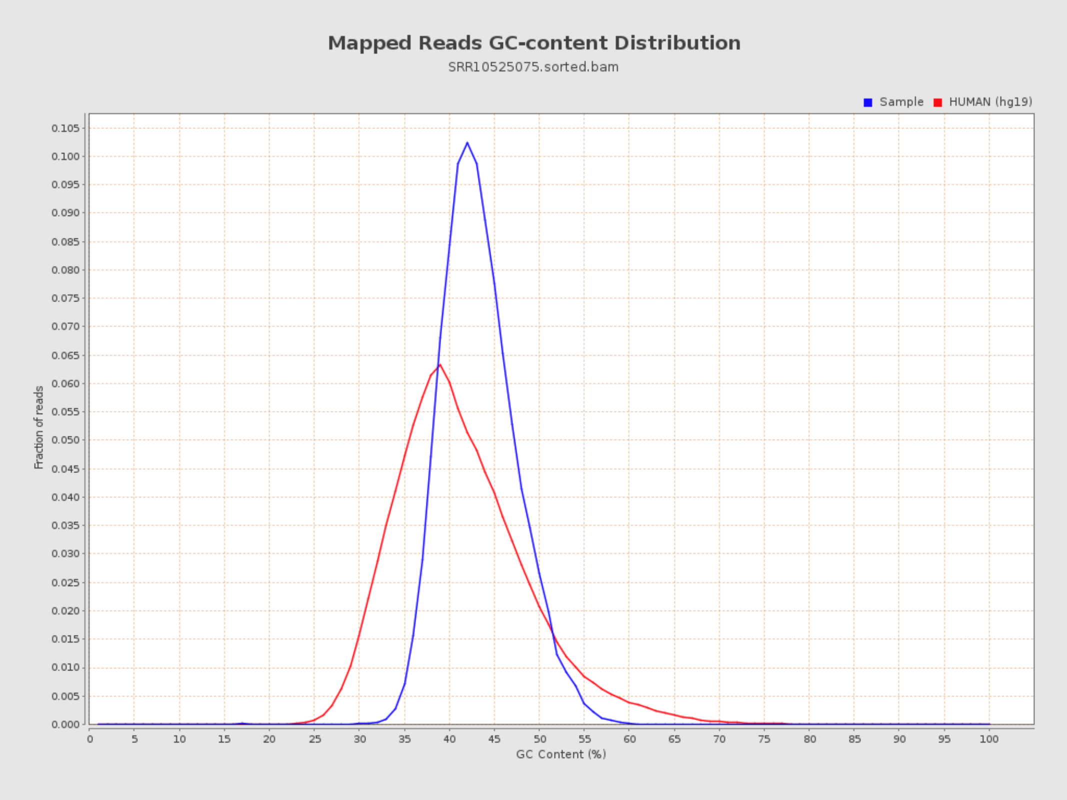
7. Results : Duplication Rate Histogram



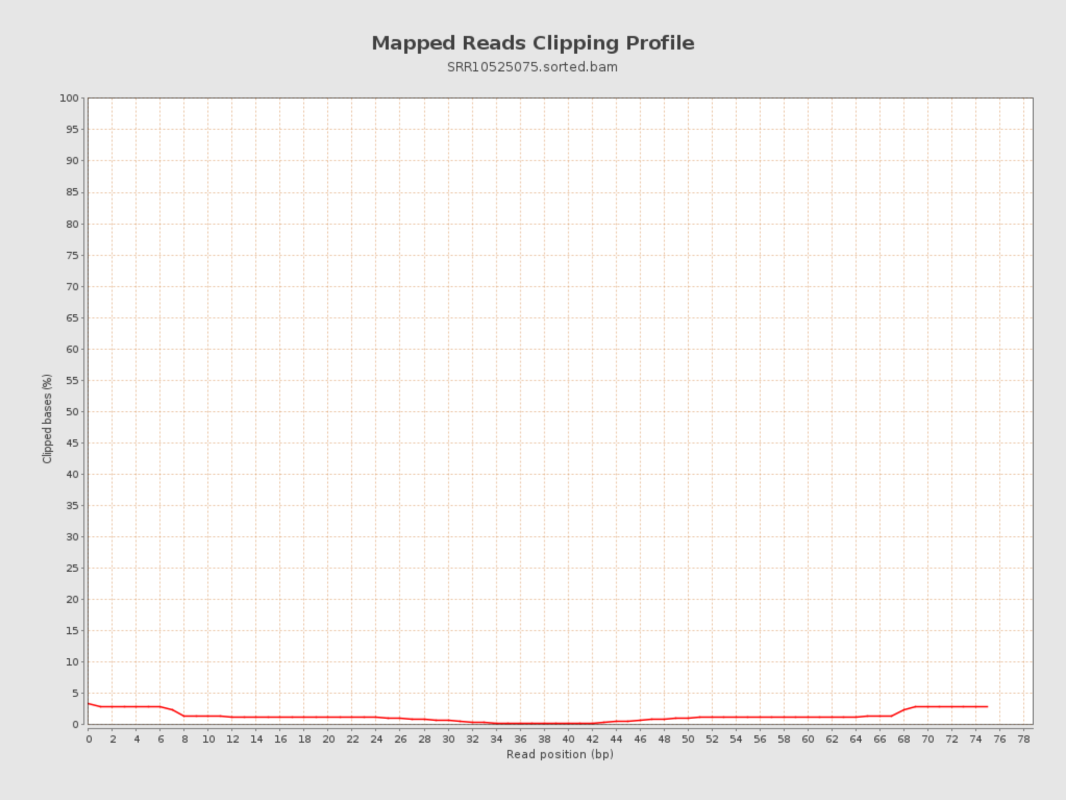
8. Results : Mapped Reads Nucleotide Content



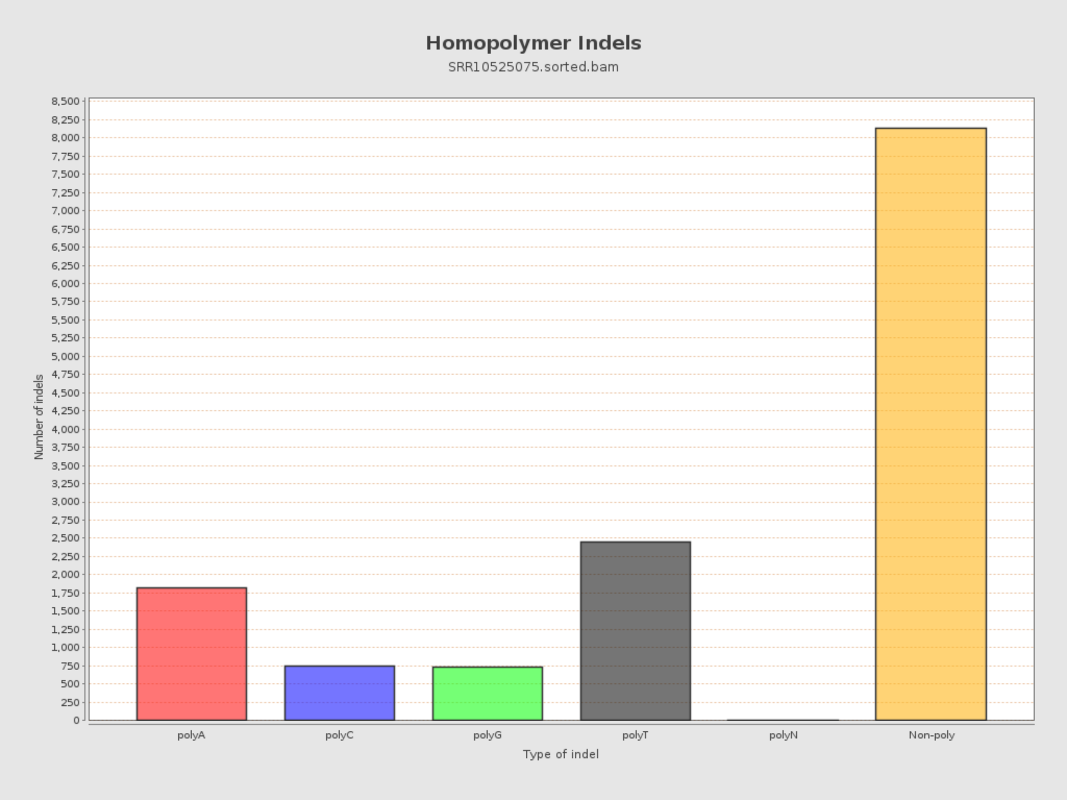
9. Results : Mapped Reads GC-content Distribution



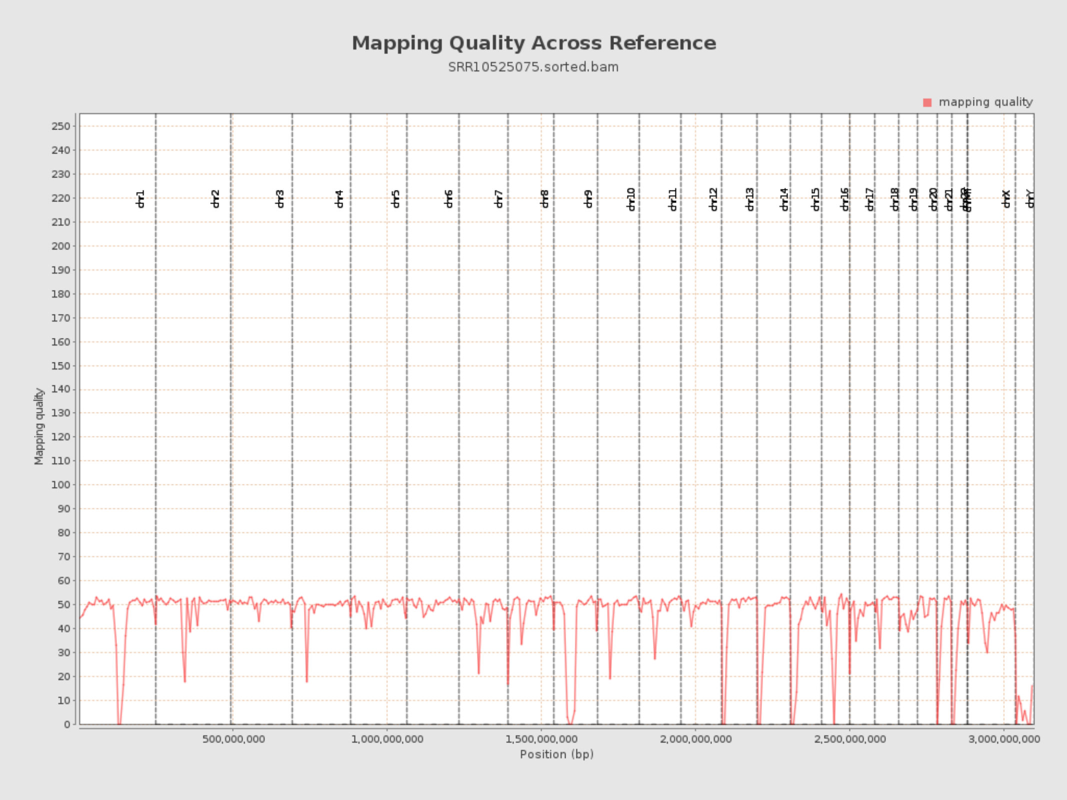
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram