Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:58:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525085.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_SRR10525085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:58:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,390,080
Mapped reads	1,289,001 / 92.73%
Unmapped reads	101,079 / 7.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,233 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	104,571 / 7.52%
Duplication rate	6.41%
Clipped reads	1,293,920 / 93.08%

2.2. ACGT Content

Number/percentage of A's	18,582,085 / 24.38%
Number/percentage of C's	15,055,289 / 19.75%
Number/percentage of T's	23,593,551 / 30.95%
Number/percentage of G's	18,988,981 / 24.91%
Number/percentage of N's	7,725 / 0.01%
GC Percentage	44.66%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2671

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

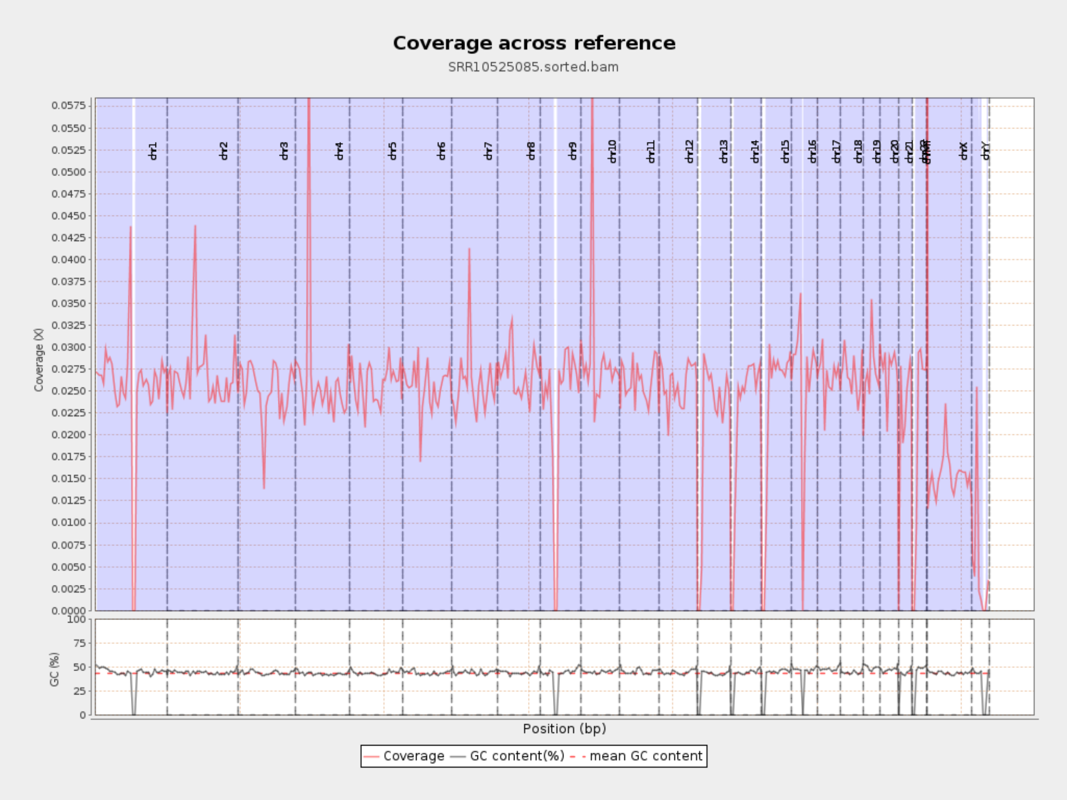
General error rate	0.5%
Mismatches	368,943
Insertions	4,964
Mapped reads with at least one insertion	0.38%
Deletions	14,443
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.71%

2.6. Chromosome stats

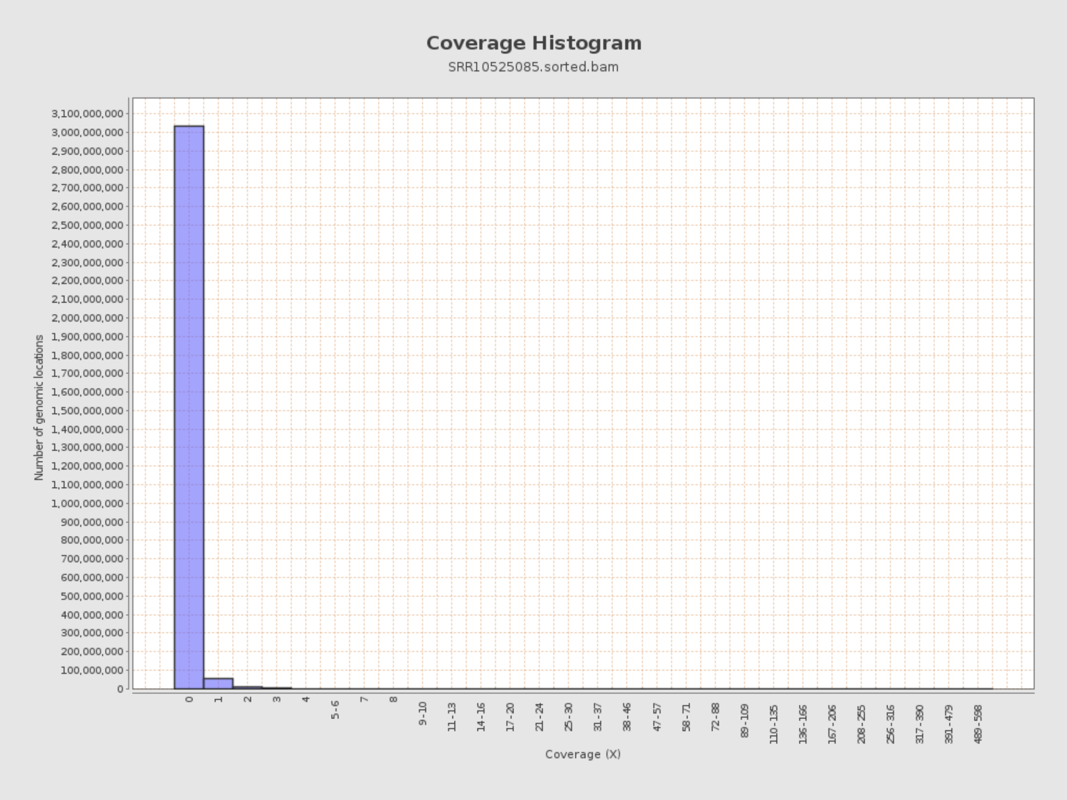
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6275946	0.0252	0.4668
chr2	243199373	6574040	0.027	0.3144
chr3	198022430	4976551	0.0251	0.1834
chr4	191154276	5120407	0.0268	0.2625
chr5	180915260	4707720	0.026	0.1883
chr6	171115067	4365721	0.0255	0.1989
chr7	159138663	4132198	0.026	0.2844

chr8	146364022	3961194	0.0271	0.3321
chr9	141213431	3300780	0.0234	0.2146
chr10	135534747	3935374	0.029	0.3427
chr11	135006516	3549645	0.0263	0.2172
chr12	133851895	3455161	0.0258	0.1919
chr13	115169878	2428206	0.0211	0.1693
chr14	107349540	2361906	0.022	0.1762
chr15	102531392	2334979	0.0228	0.1738
chr16	90354753	2321833	0.0257	0.1998
chr17	81195210	2165379	0.0267	0.2034
chr18	78077248	2087985	0.0267	0.3447
chr19	59128983	1628390	0.0275	0.3318
chr20	63025520	1729435	0.0274	0.2045
chr21	48129895	1076039	0.0224	0.2404
chr22	51304566	1013214	0.0197	0.1656
chrMT	16571	30085	1.8155	1.7477
chrX	155270560	2408751	0.0155	0.1573
chrY	59373566	310603	0.0052	0.2436

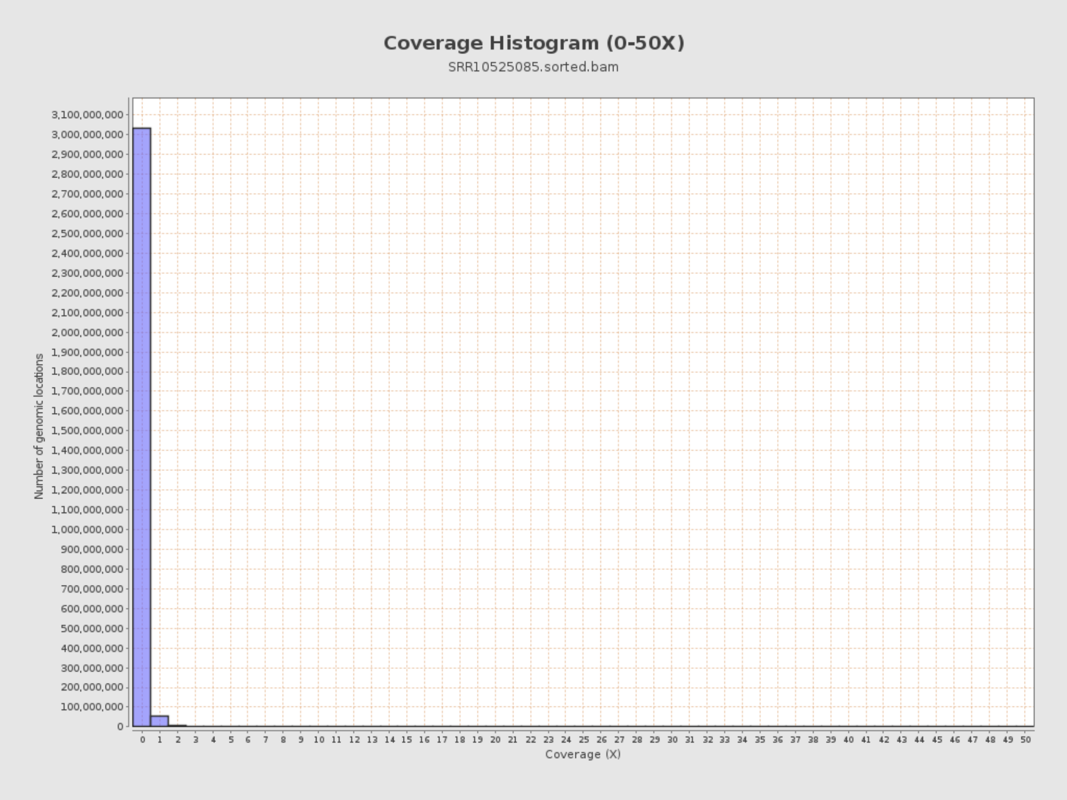
3. Results : Coverage across reference



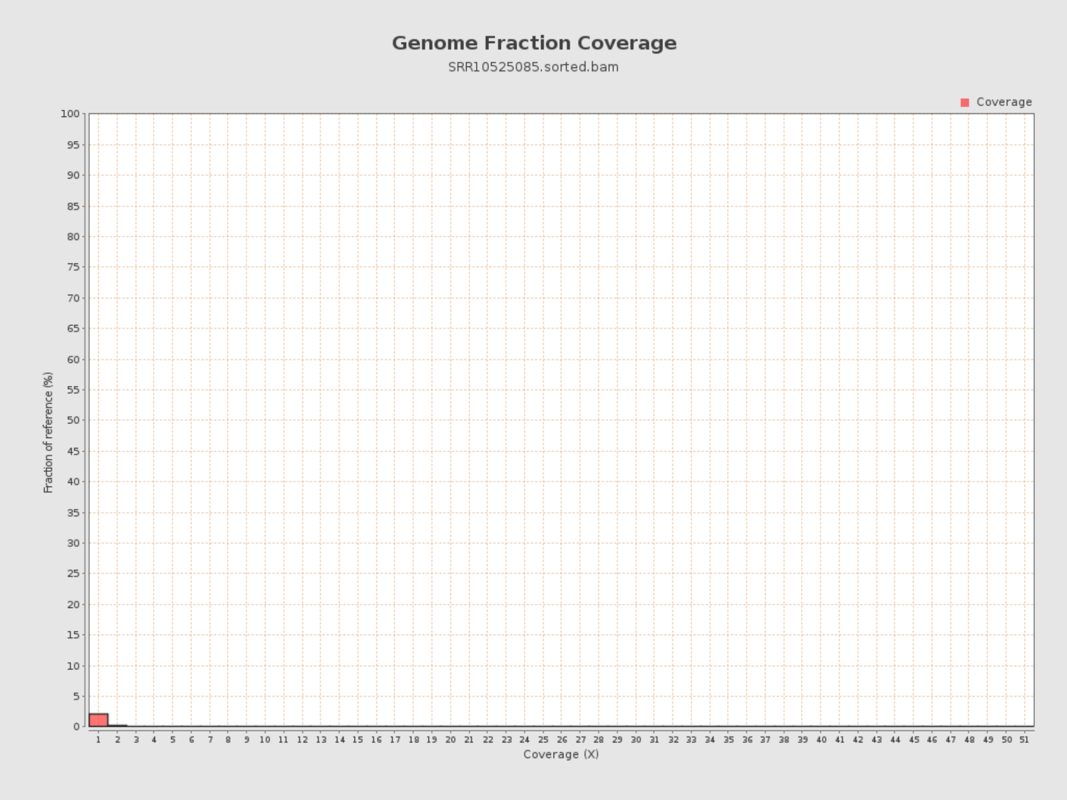
4. Results : Coverage Histogram



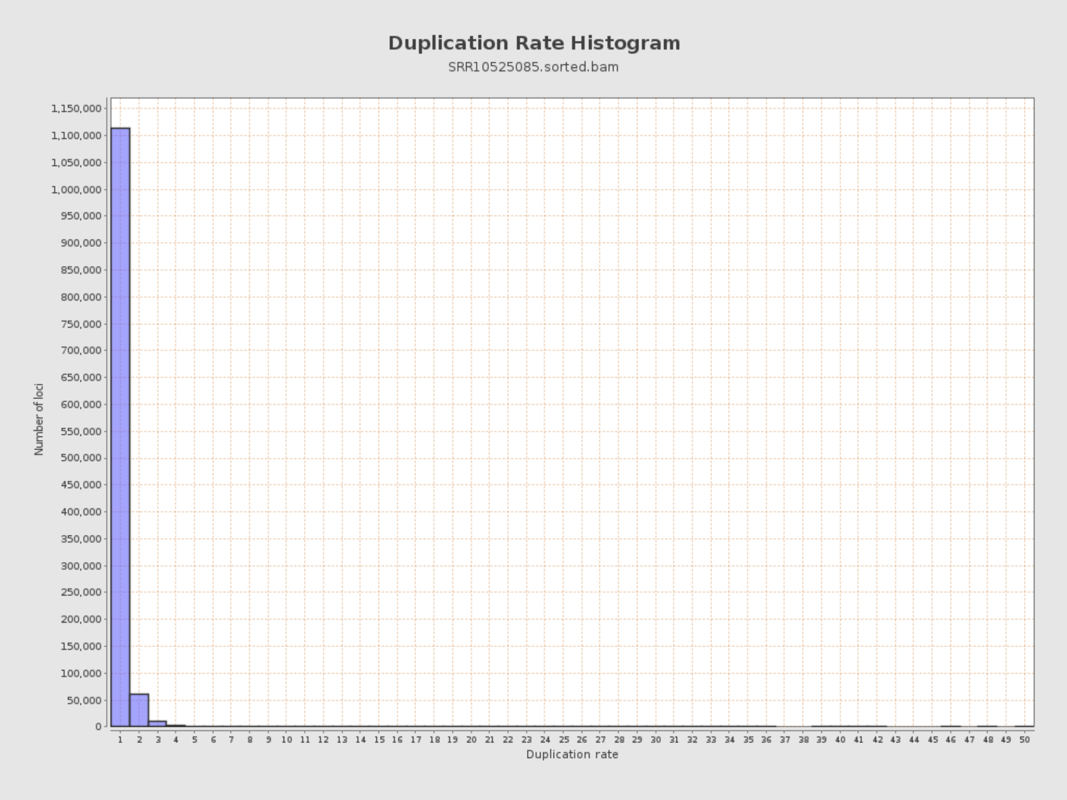
5. Results : Coverage Histogram (0-50X)



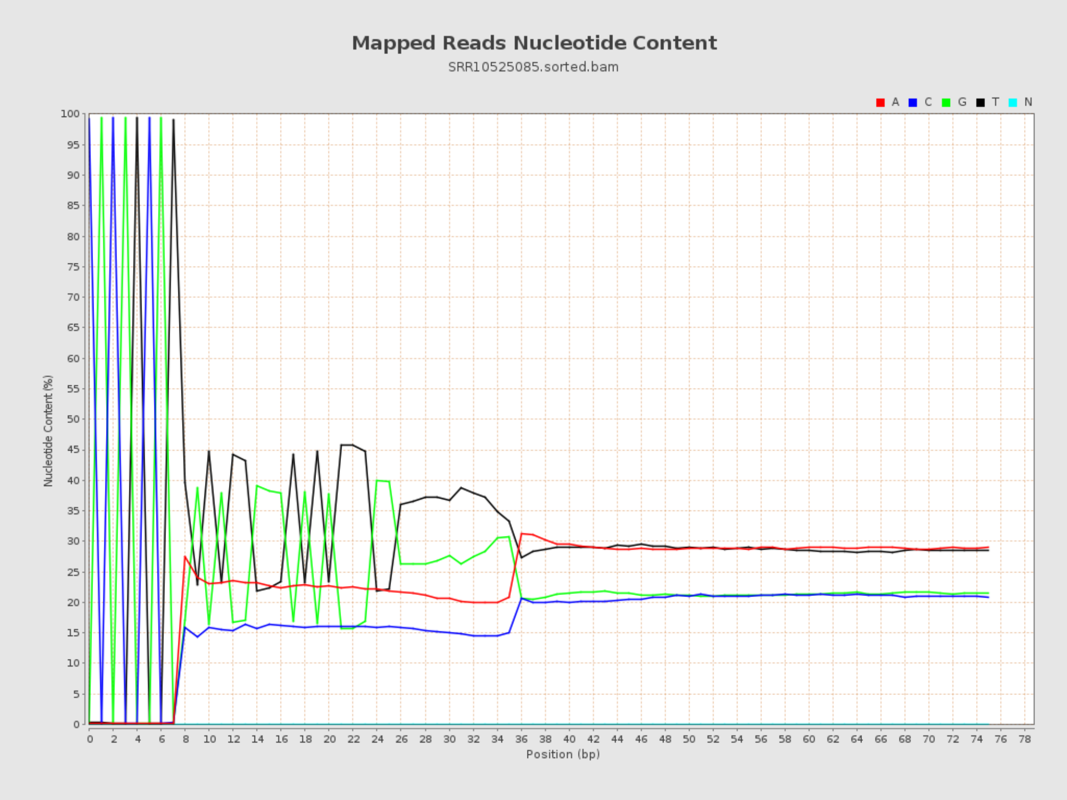
6. Results : Genome Fraction Coverage



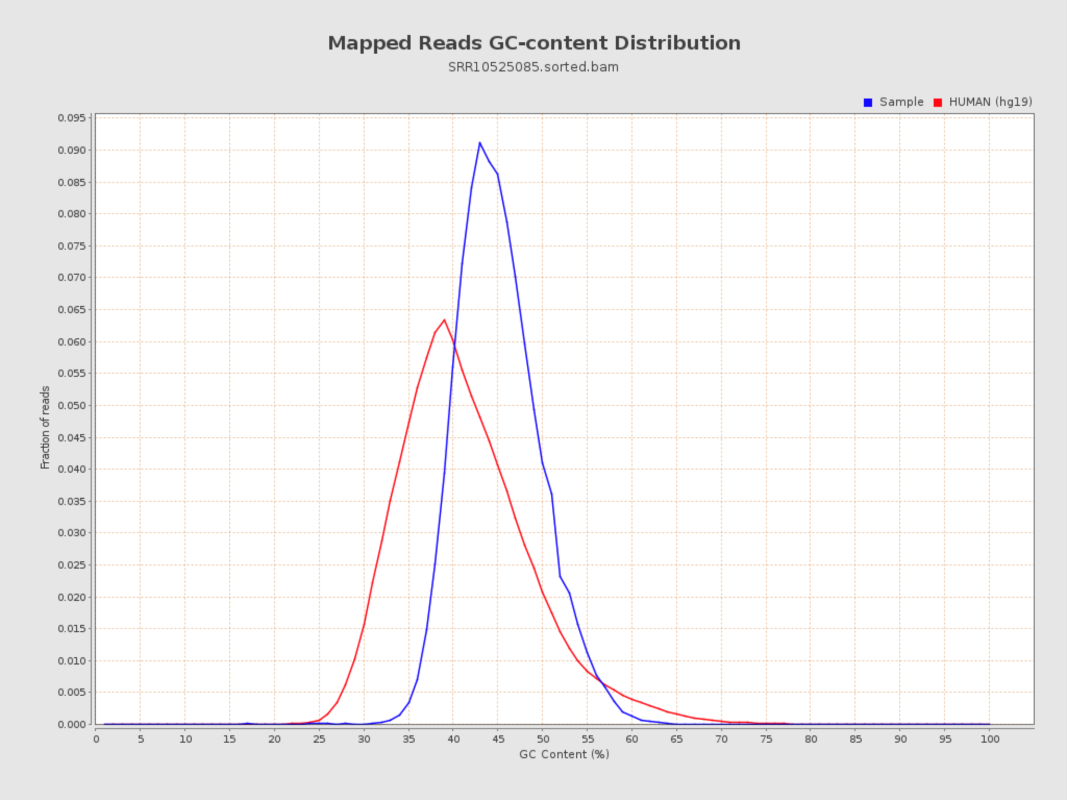
7. Results : Duplication Rate Histogram



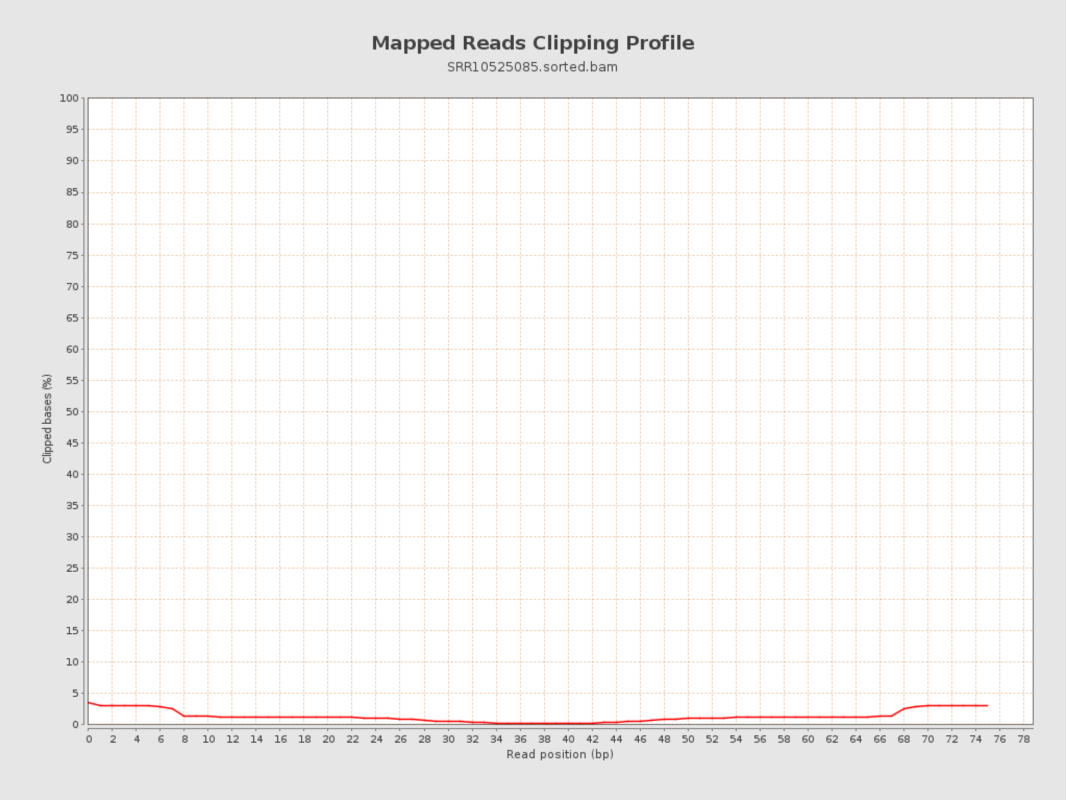
8. Results : Mapped Reads Nucleotide Content



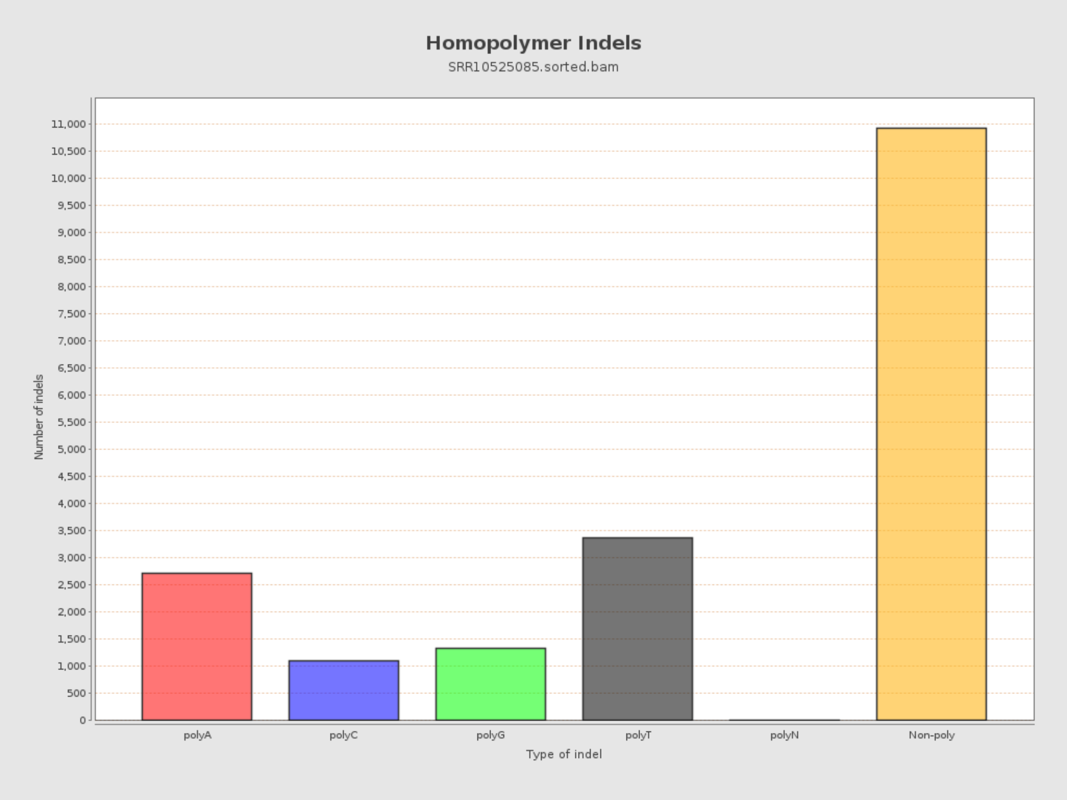
9. Results : Mapped Reads GC-content Distribution



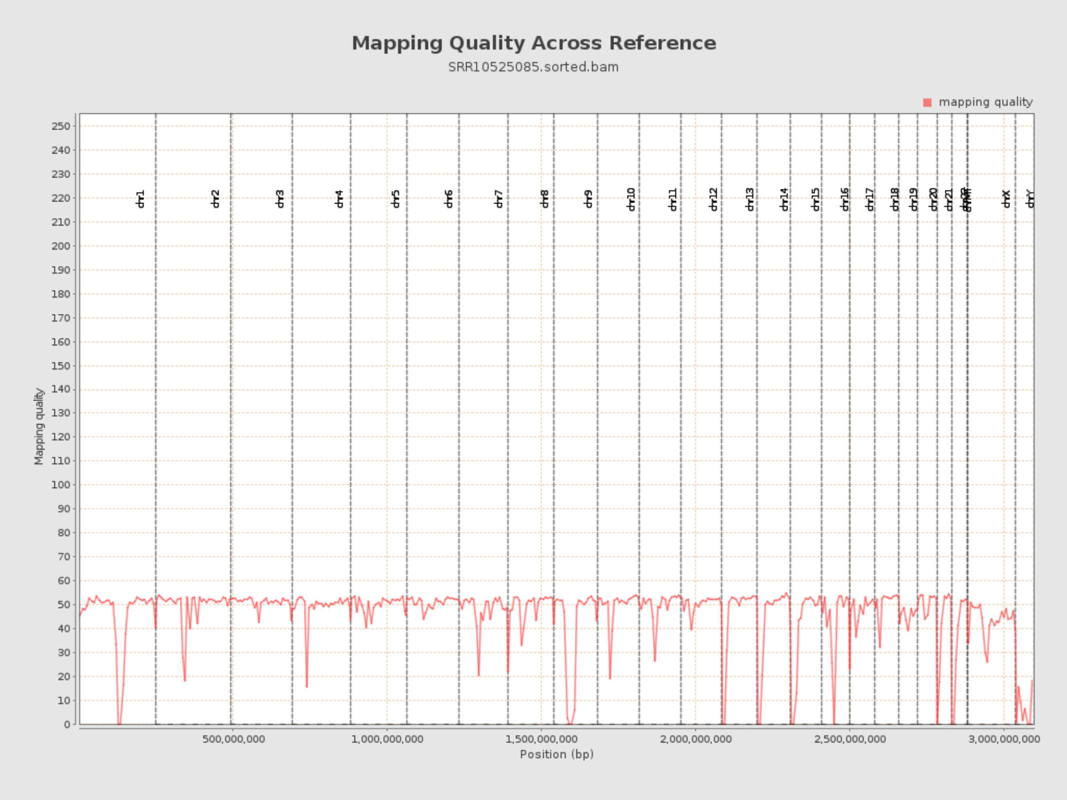
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram