Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:46:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525047.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_SRR10525047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:46:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,031,513
Mapped reads	882,013 / 85.51%
Unmapped reads	149,500 / 14.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,442 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	44,733 / 4.34%
Duplication rate	4.2%
Clipped reads	881,732 / 85.48%

2.2. ACGT Content

Number/percentage of A's	12,614,465 / 24.81%
Number/percentage of C's	10,052,123 / 19.77%
Number/percentage of T's	16,707,877 / 32.87%
Number/percentage of G's	11,456,604 / 22.54%
Number/percentage of N's	4,981 / 0.01%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1872

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

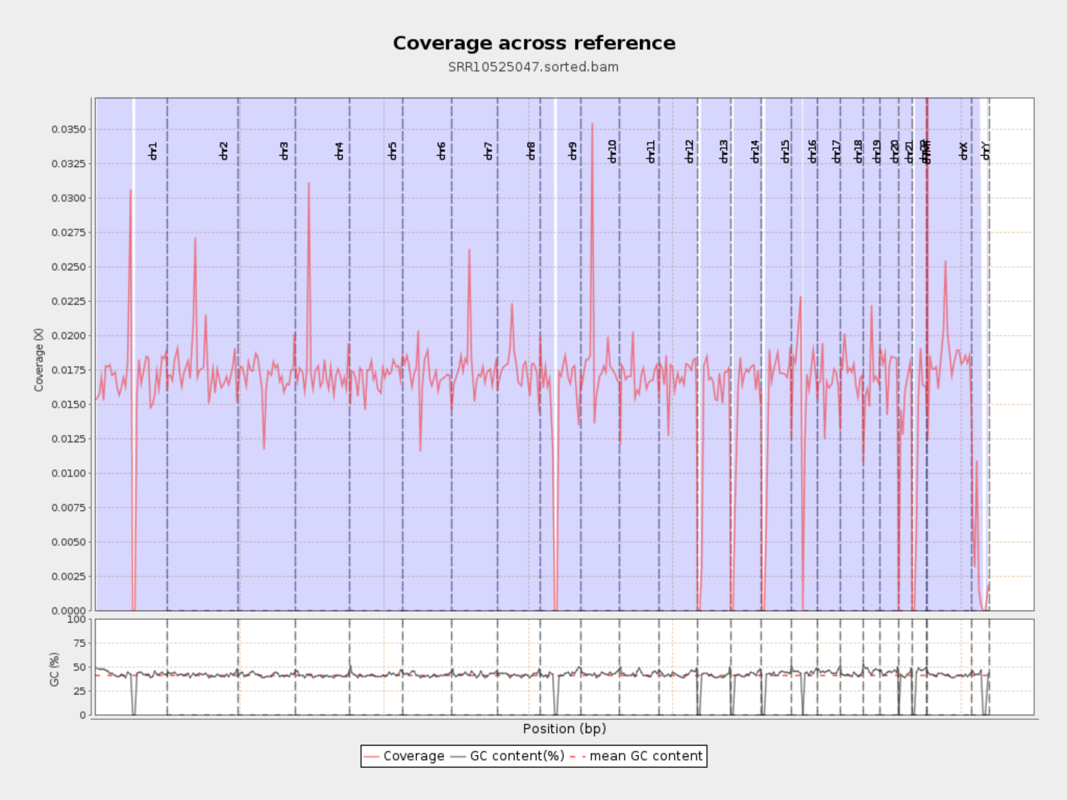
General error rate	0.51%
Mismatches	253,516
Insertions	3,491
Mapped reads with at least one insertion	0.39%
Deletions	10,659
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.62%

2.6. Chromosome stats

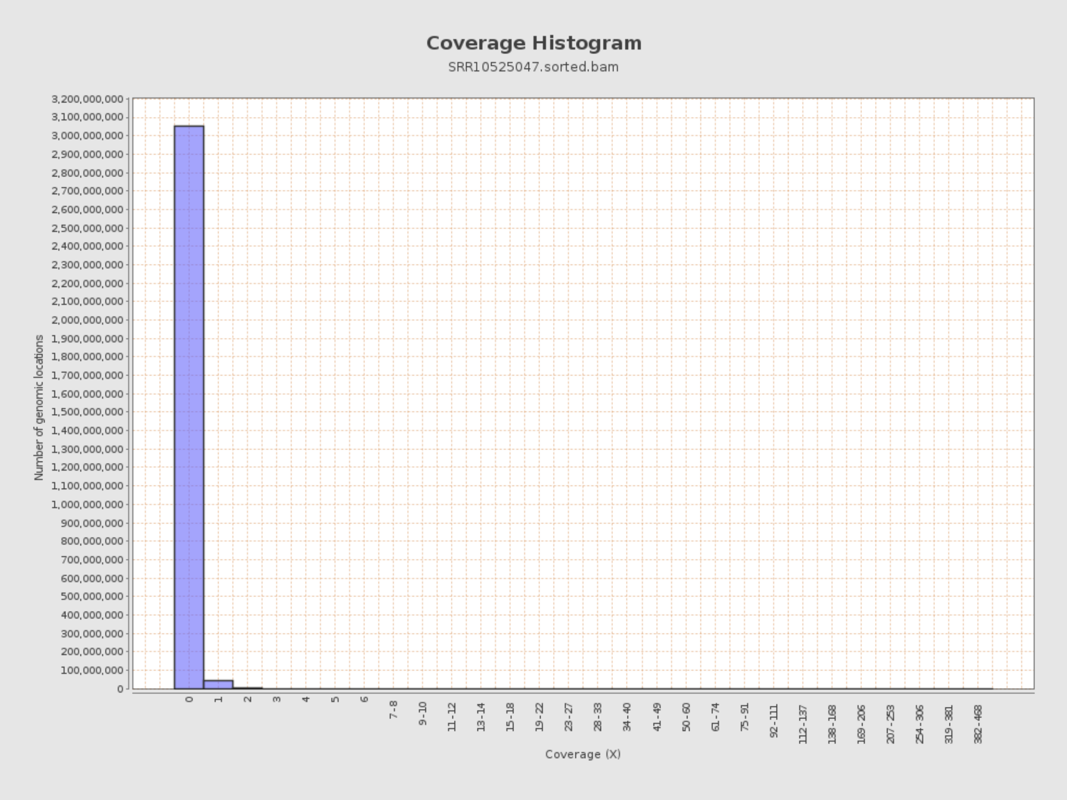
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4051689	0.0163	0.3306
chr2	243199373	4306998	0.0177	0.2295
chr3	198022430	3376528	0.0171	0.1413
chr4	191154276	3366098	0.0176	0.1559
chr5	180915260	3094054	0.0171	0.1426
chr6	171115067	2928514	0.0171	0.1509
chr7	159138663	2816930	0.0177	0.2051

chr8	146364022	2579201	0.0176	0.202
chr9	141213431	2093512	0.0148	0.1512
chr10	135534747	2481908	0.0183	0.2014
chr11	135006516	2289640	0.017	0.1607
chr12	133851895	2293335	0.0171	0.1452
chr13	115169878	1610704	0.014	0.1286
chr14	107349540	1528707	0.0142	0.1304
chr15	102531392	1471906	0.0144	0.1302
chr16	90354753	1443809	0.016	0.144
chr17	81195210	1331739	0.0164	0.1434
chr18	78077248	1360067	0.0174	0.2462
chr19	59128983	991845	0.0168	0.2328
chr20	63025520	1107841	0.0176	0.1473
chr21	48129895	687221	0.0143	0.1437
chr22	51304566	593921	0.0116	0.1173
chrMT	16571	20949	1.2642	1.3505
chrX	155270560	2852719	0.0184	0.158
chrY	59373566	173038	0.0029	0.1036

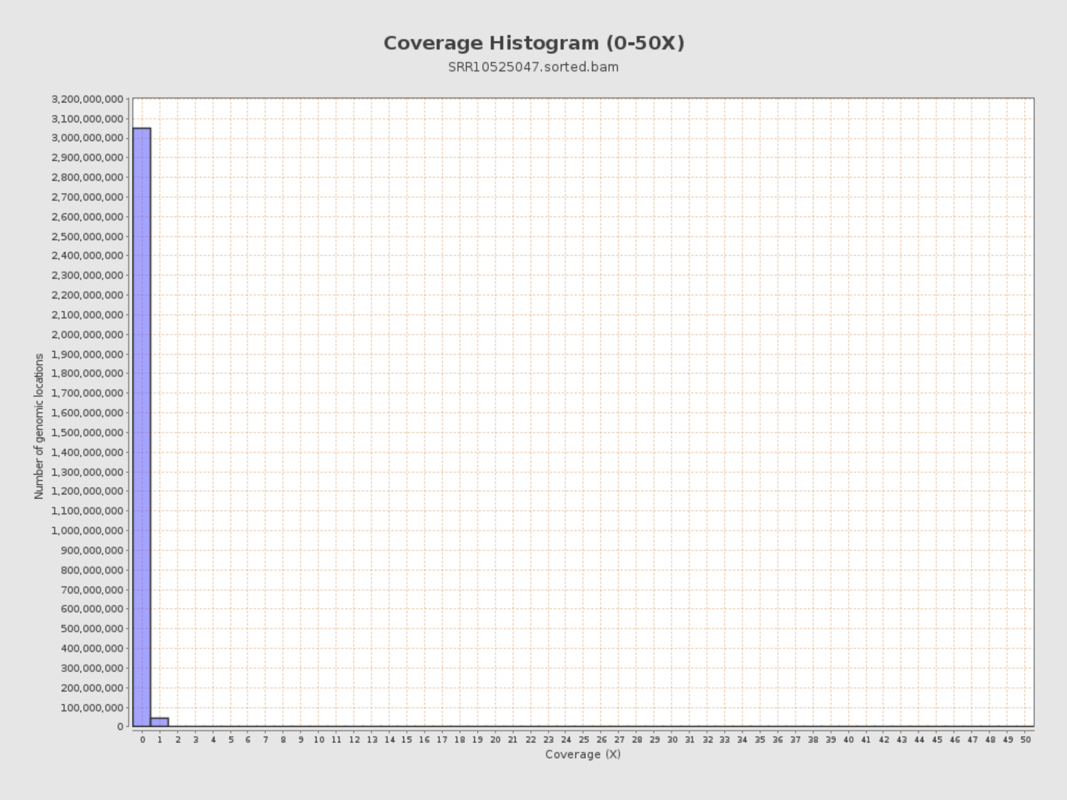
3. Results : Coverage across reference



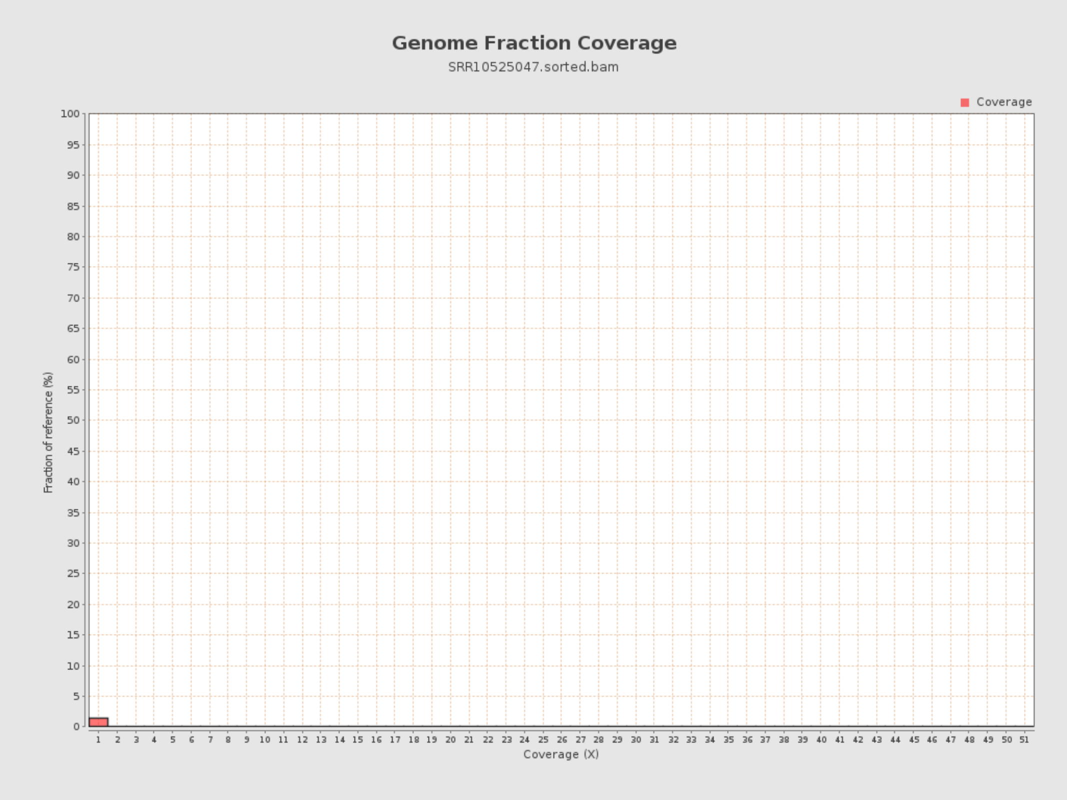
4. Results : Coverage Histogram



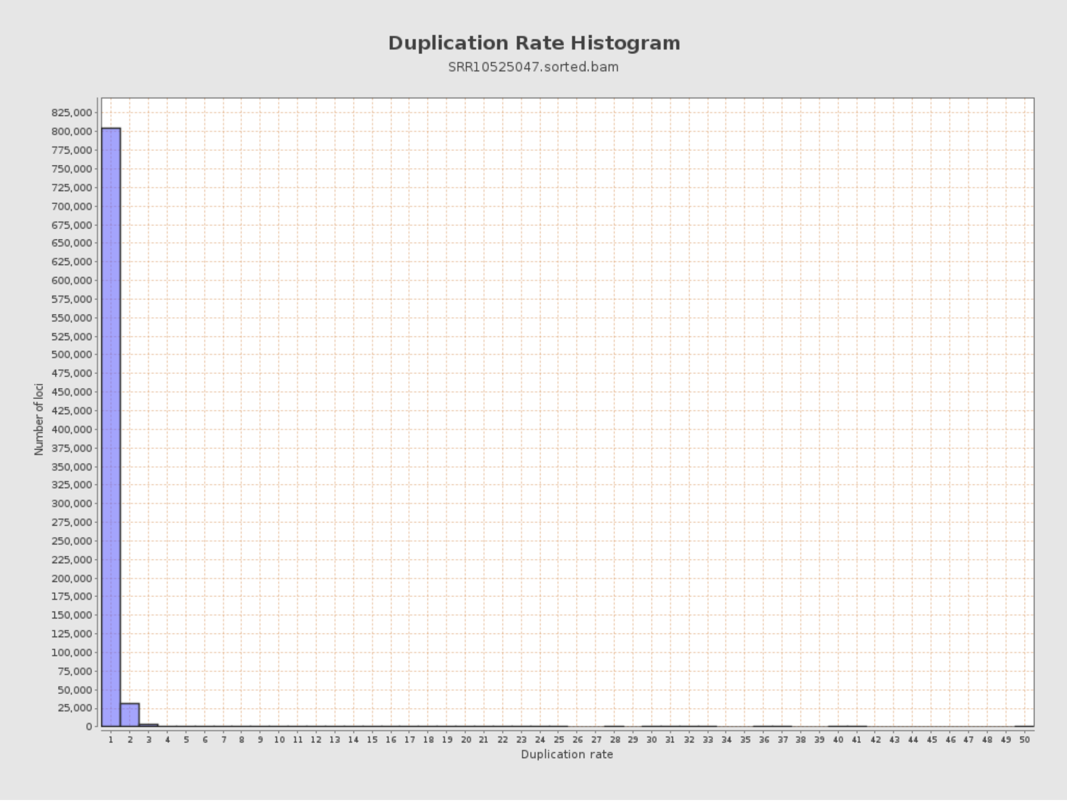
5. Results : Coverage Histogram (0-50X)



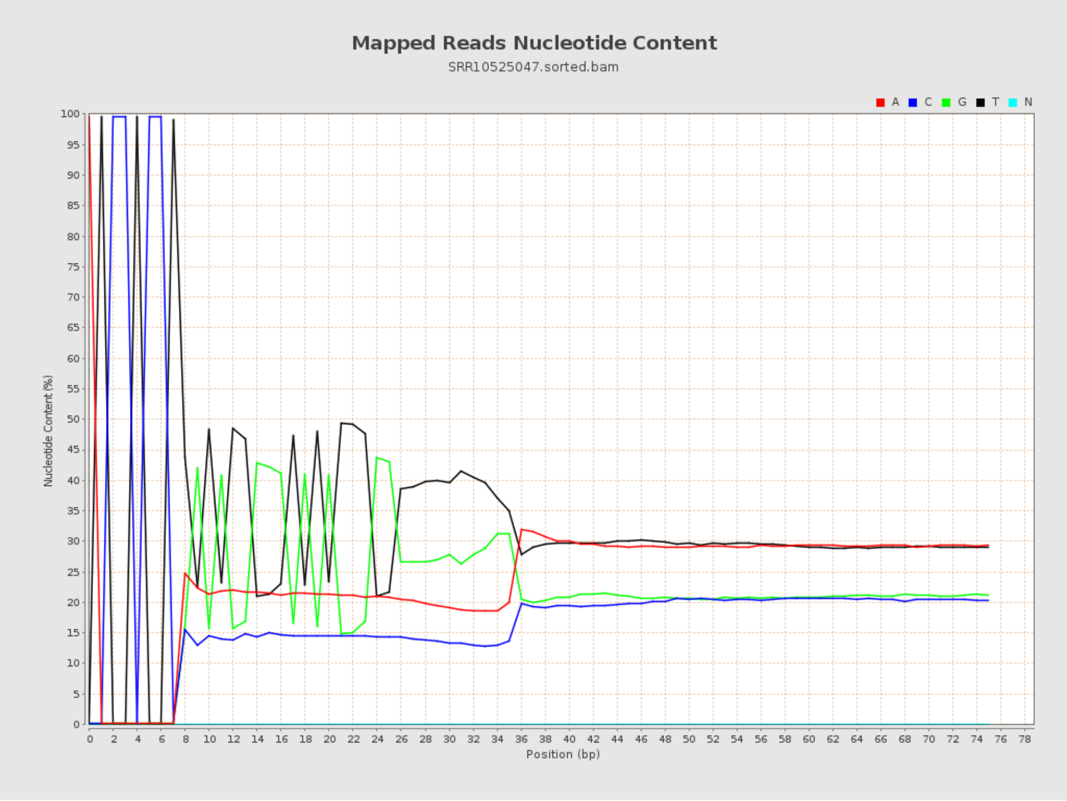
6. Results : Genome Fraction Coverage



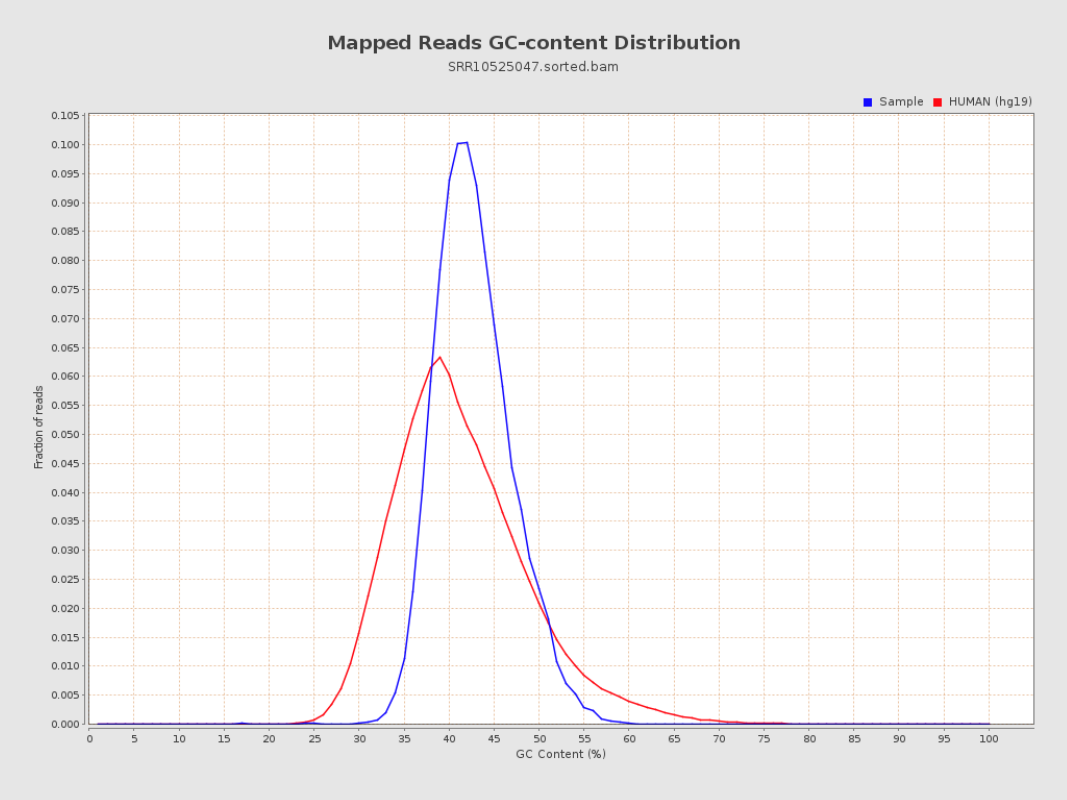
7. Results : Duplication Rate Histogram



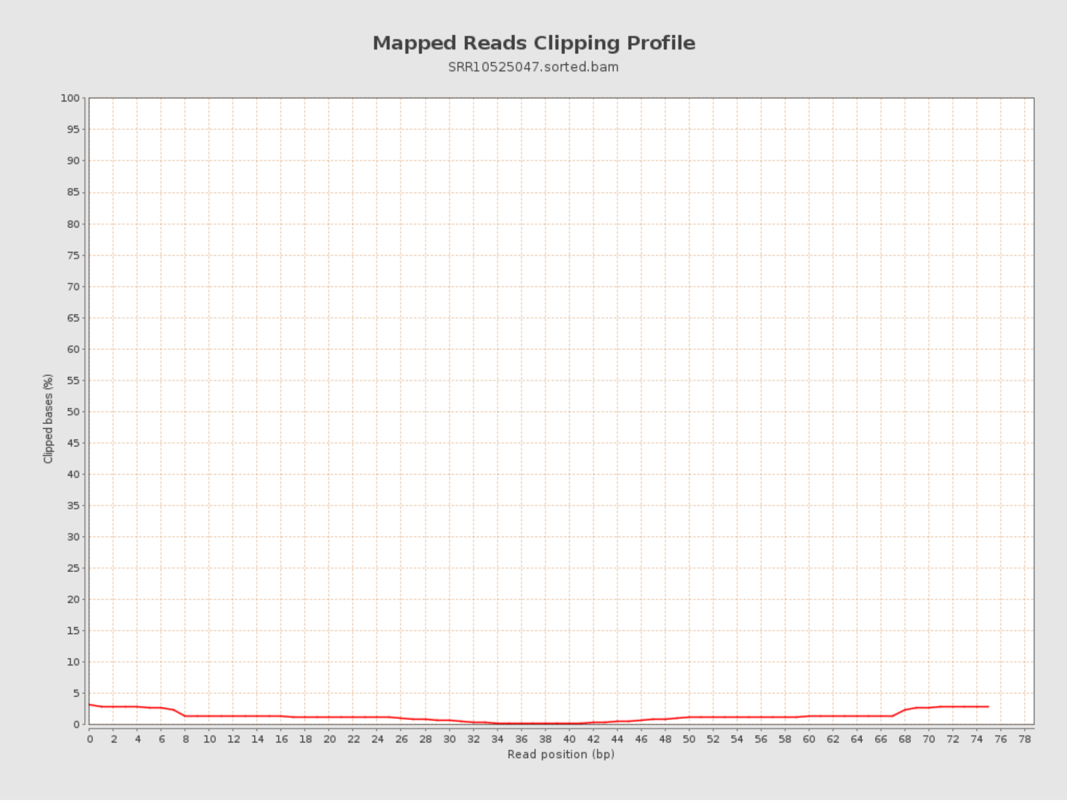
8. Results : Mapped Reads Nucleotide Content



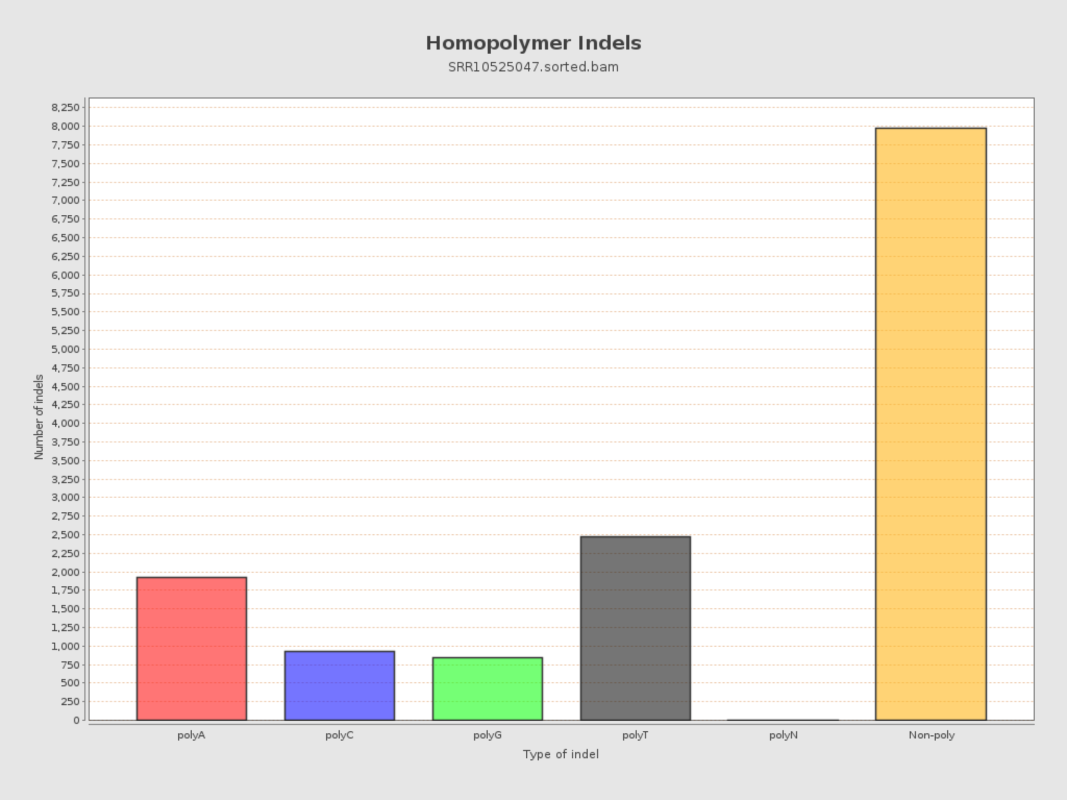
9. Results : Mapped Reads GC-content Distribution



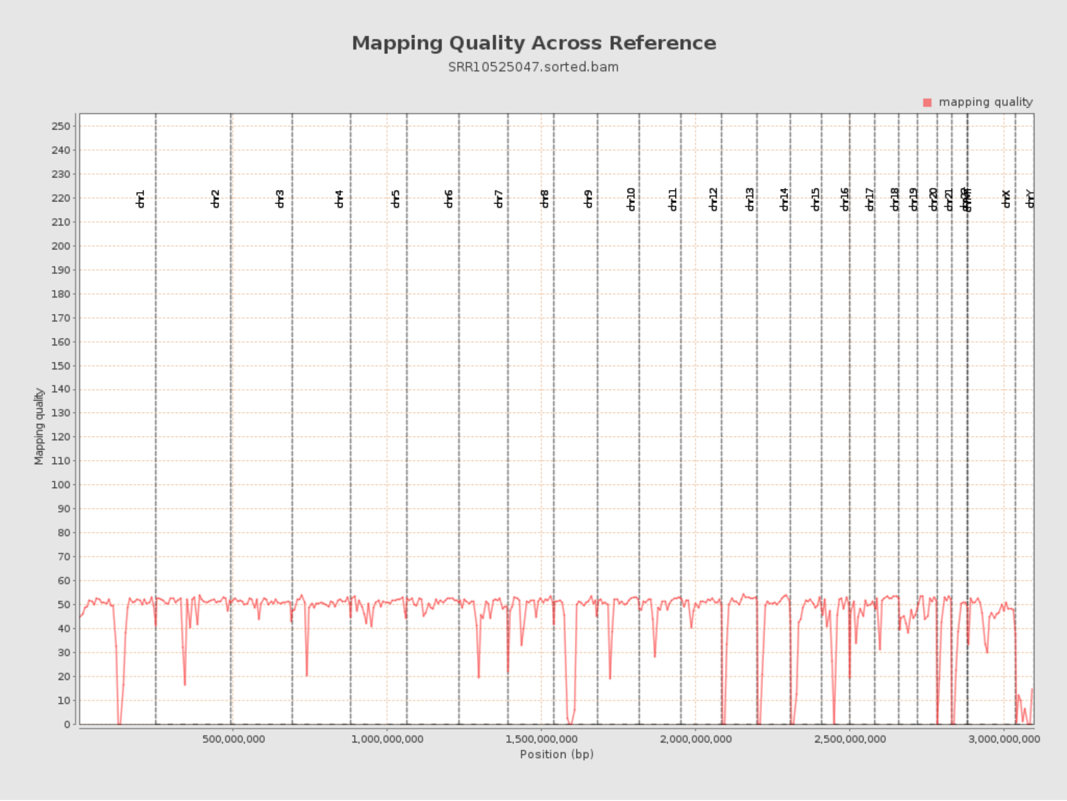
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram