Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 16:43:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525079.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_SRR10525079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 16:43:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,296,028
Mapped reads	1,076,513 / 83.06%
Unmapped reads	219,515 / 16.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,636 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	54,413 / 4.2%
Duplication rate	4.09%
Clipped reads	1,076,908 / 83.09%

2.2. ACGT Content

Number/percentage of A's	16,112,090 / 25.65%
Number/percentage of C's	11,749,680 / 18.71%
Number/percentage of T's	20,217,354 / 32.19%
Number/percentage of G's	14,725,291 / 23.44%
Number/percentage of N's	6,788 / 0.01%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0203

Standard Deviation	0.2124

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

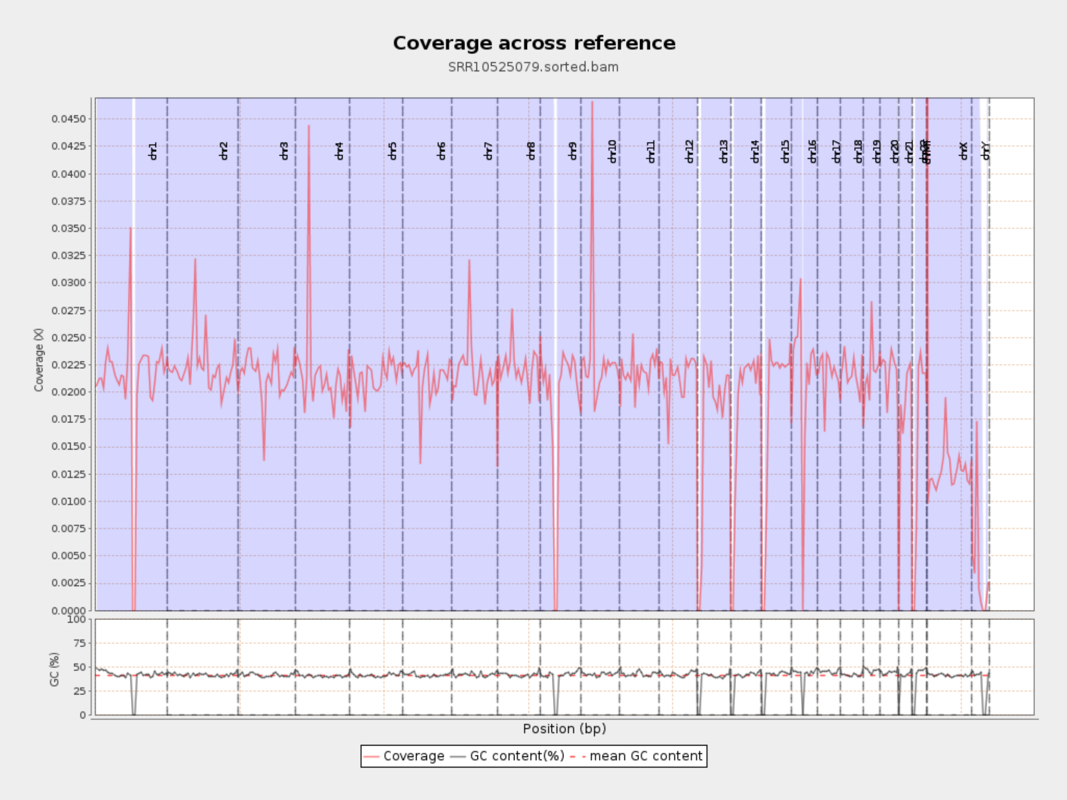
General error rate	0.5%
Mismatches	308,163
Insertions	4,458
Mapped reads with at least one insertion	0.41%
Deletions	13,014
Mapped reads with at least one deletion	1.2%
Homopolymer indels	41.33%

2.6. Chromosome stats

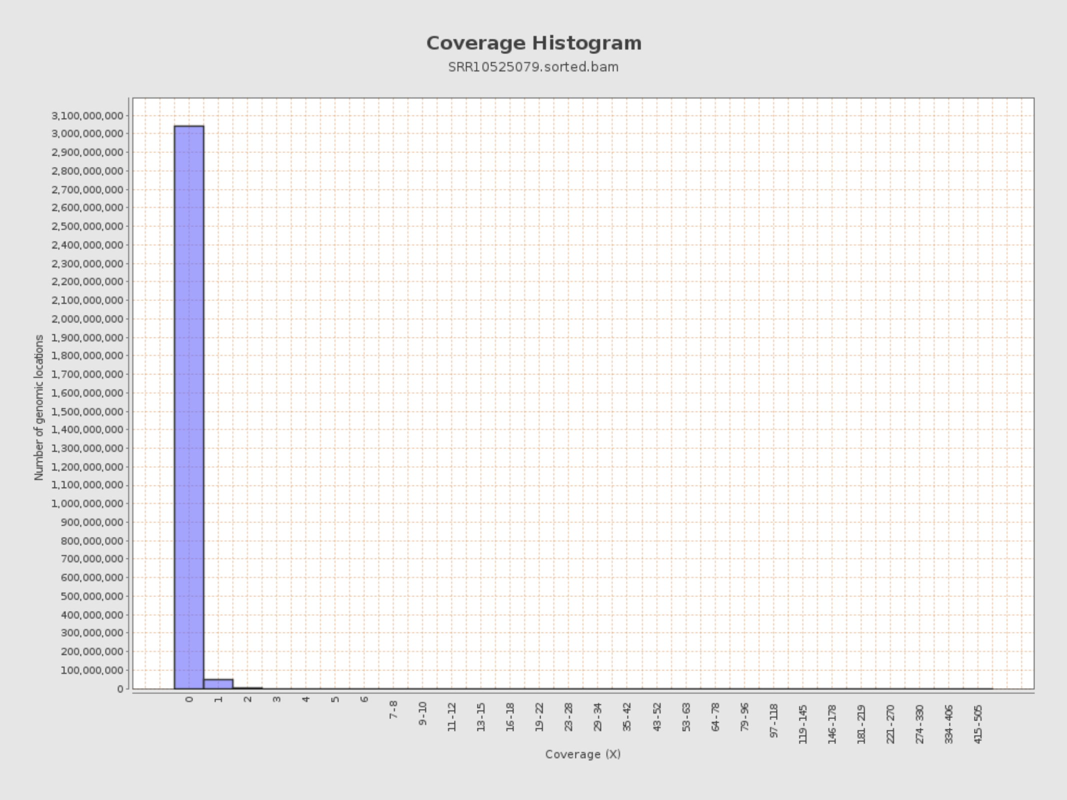
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5207240	0.0209	0.3724
chr2	243199373	5443618	0.0224	0.2622
chr3	198022430	4253174	0.0215	0.1605
chr4	191154276	4178216	0.0219	0.1875
chr5	180915260	3907804	0.0216	0.1609
chr6	171115067	3654864	0.0214	0.1686
chr7	159138663	3507584	0.022	0.235

chr8	146364022	3256594	0.0222	0.2176
chr9	141213431	2688415	0.019	0.1798
chr10	135534747	3145430	0.0232	0.2456
chr11	135006516	2968245	0.022	0.1826
chr12	133851895	2874432	0.0215	0.1646
chr13	115169878	1985527	0.0172	0.1436
chr14	107349540	1949994	0.0182	0.1502
chr15	102531392	1898248	0.0185	0.1491
chr16	90354753	1894453	0.021	0.1692
chr17	81195210	1757563	0.0216	0.1663
chr18	78077248	1693949	0.0217	0.2722
chr19	59128983	1306181	0.0221	0.2638
chr20	63025520	1381148	0.0219	0.1659
chr21	48129895	862233	0.0179	0.1693
chr22	51304566	787831	0.0154	0.1366
chrMT	16571	6445	0.3889	0.7311
chrX	155270560	1996172	0.0129	0.1377
chrY	59373566	227111	0.0038	0.1606

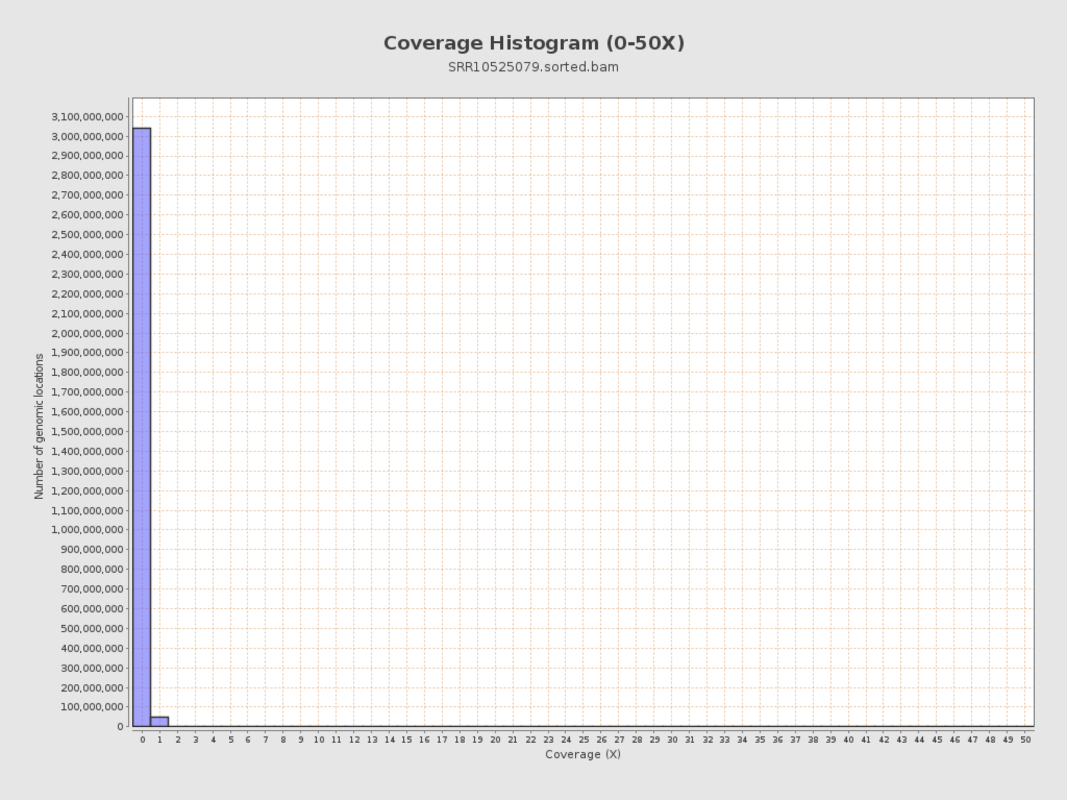
3. Results : Coverage across reference



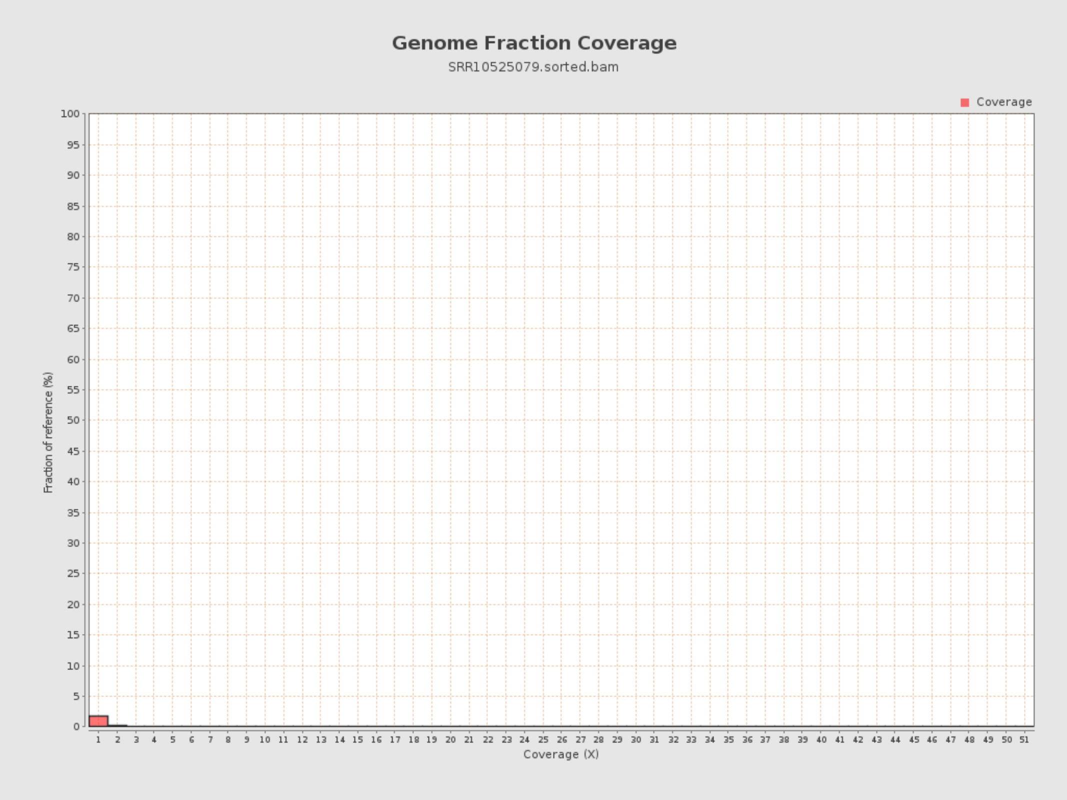
4. Results : Coverage Histogram



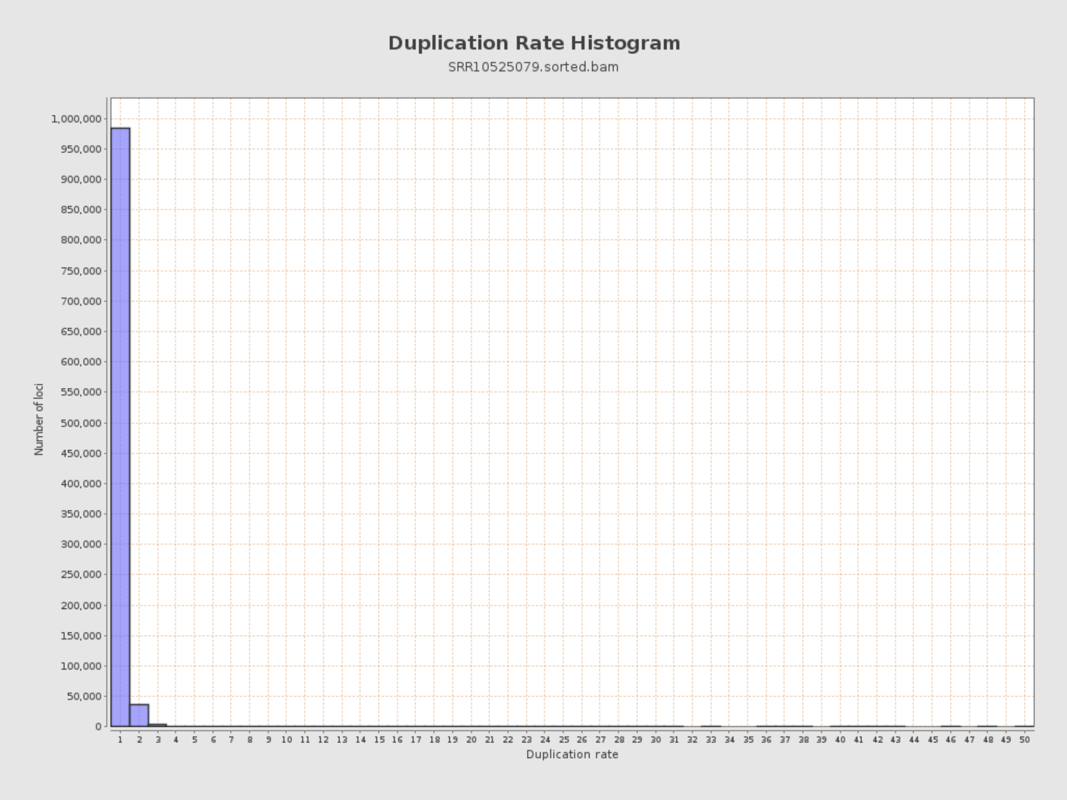
5. Results : Coverage Histogram (0-50X)



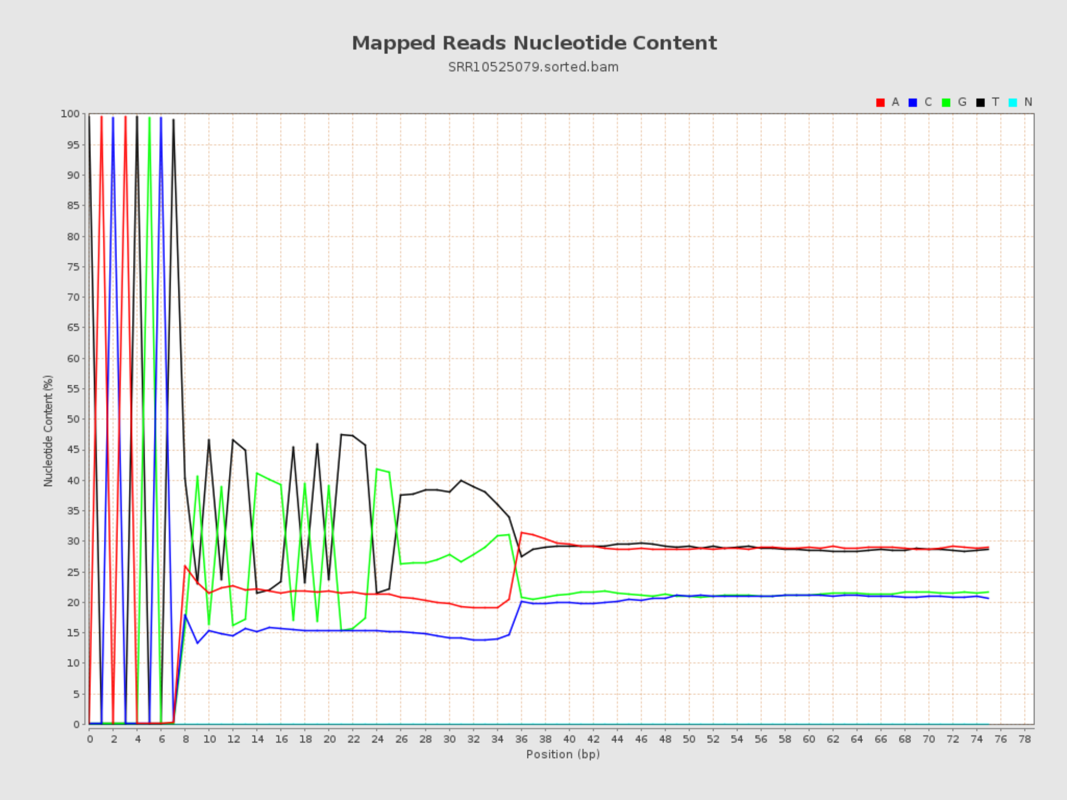
6. Results : Genome Fraction Coverage



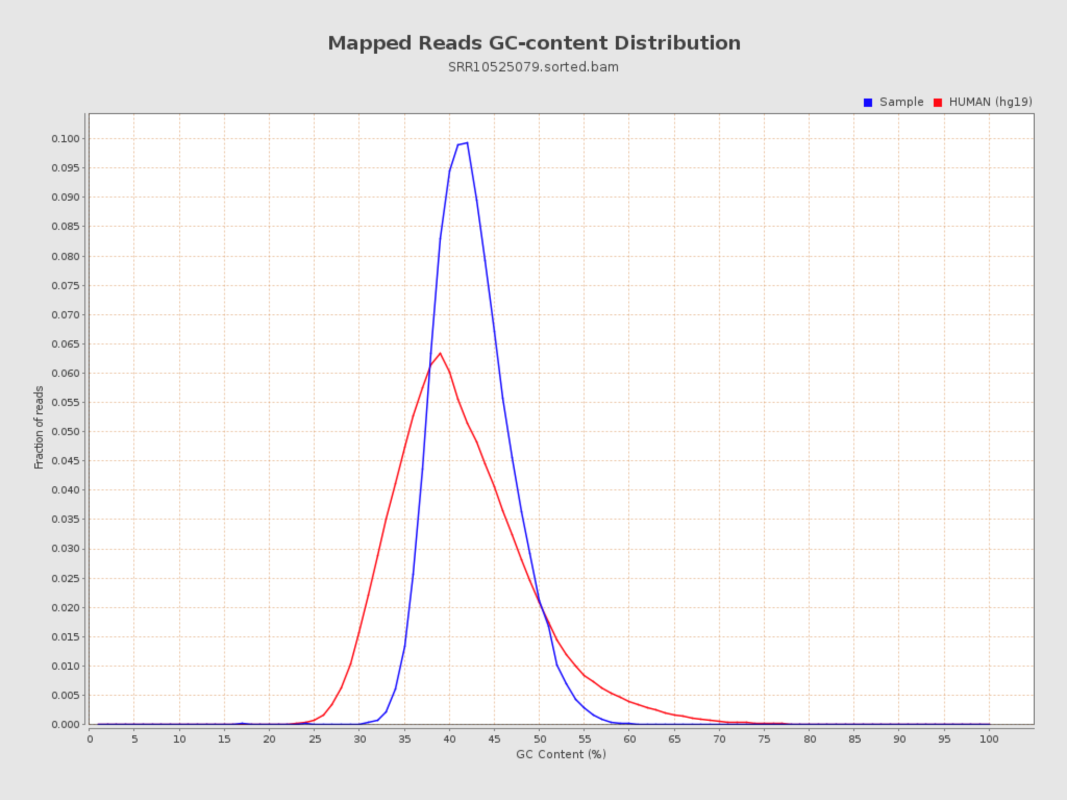
7. Results : Duplication Rate Histogram



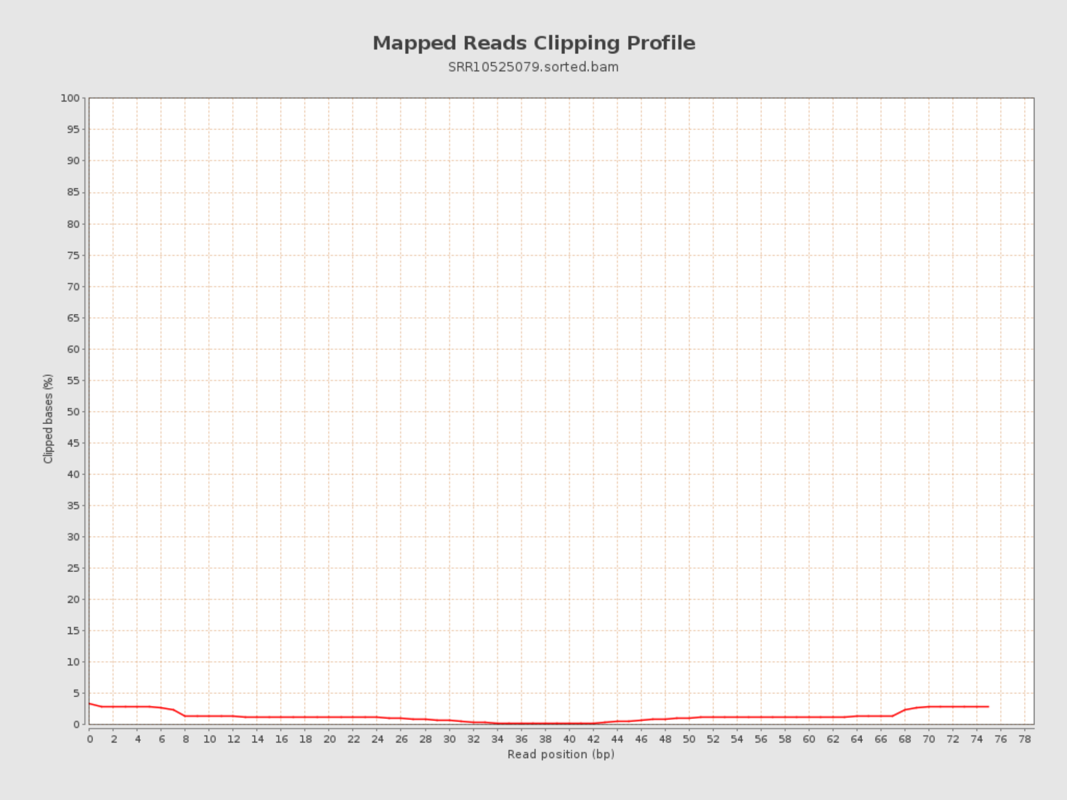
8. Results : Mapped Reads Nucleotide Content



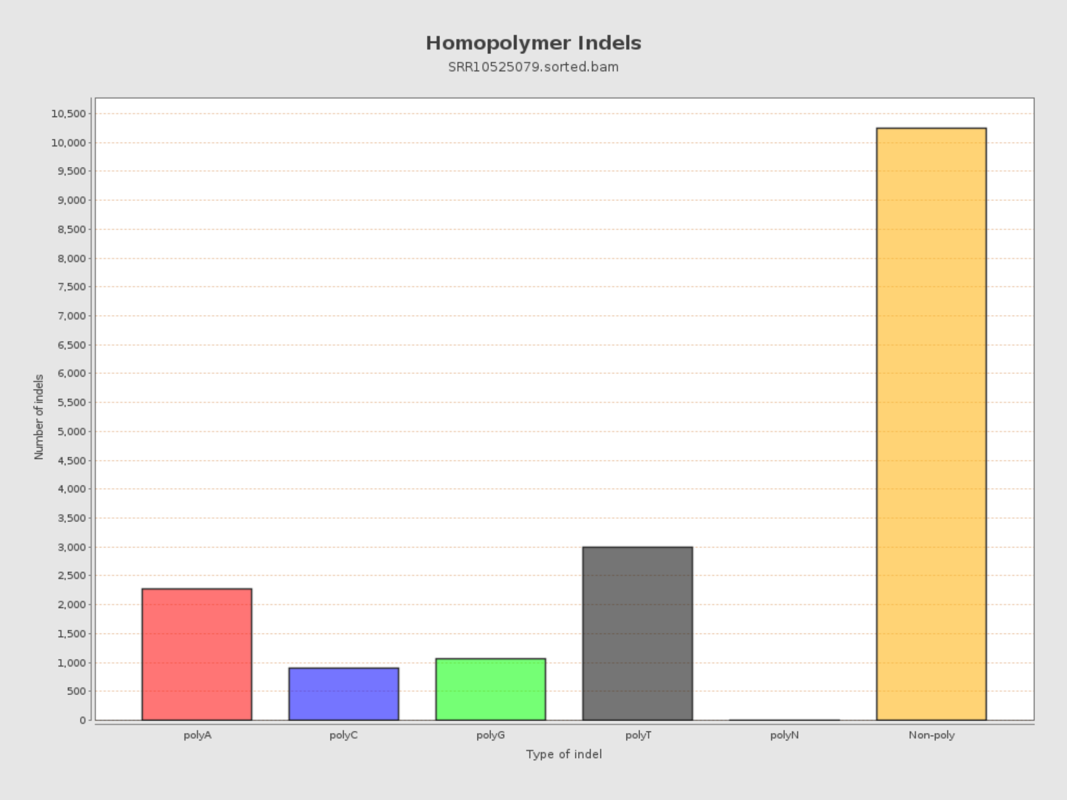
9. Results : Mapped Reads GC-content Distribution



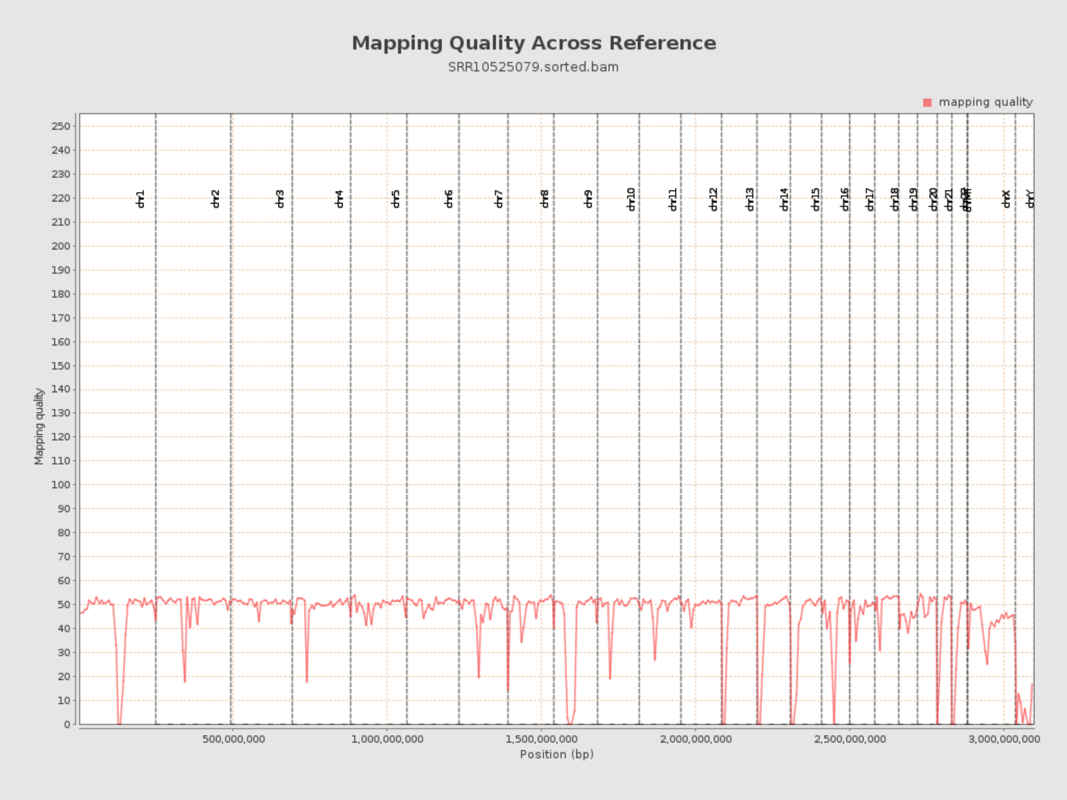
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram