Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525041.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_SRR10525041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525041.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:33:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,048,767
Mapped reads	962,102 / 91.74%
Unmapped reads	86,665 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,869 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	27,939 / 2.66%
Duplication rate	2.18%
Clipped reads	963,161 / 91.84%

2.2. ACGT Content

Number/percentage of A's	13,791,007 / 24.68%
Number/percentage of C's	10,895,247 / 19.5%
Number/percentage of T's	17,477,210 / 31.28%
Number/percentage of G's	13,710,127 / 24.54%
Number/percentage of N's	602 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.184

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

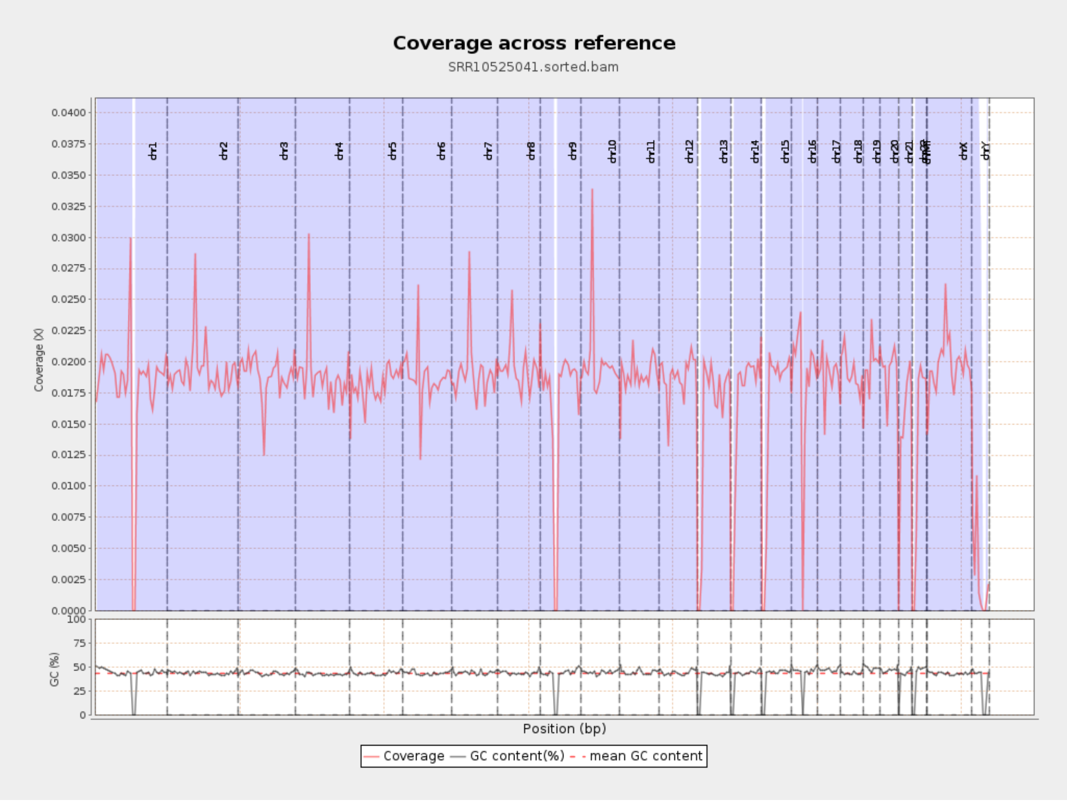
General error rate	0.51%
Mismatches	277,765
Insertions	4,279
Mapped reads with at least one insertion	0.44%
Deletions	10,815
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.31%

2.6. Chromosome stats

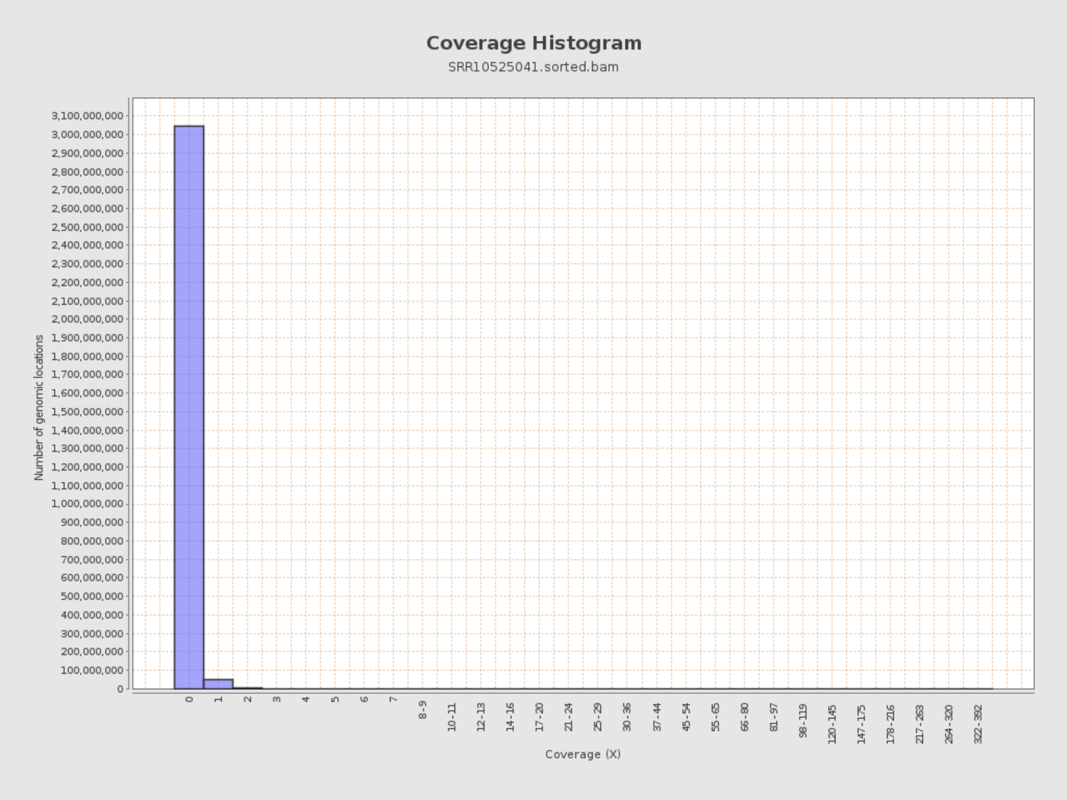
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4481251	0.018	0.3093
chr2	243199373	4690041	0.0193	0.2019
chr3	198022430	3738527	0.0189	0.1463
chr4	191154276	3623257	0.019	0.1581
chr5	180915260	3309785	0.0183	0.1435
chr6	171115067	3206092	0.0187	0.1678
chr7	159138663	3049451	0.0192	0.2079

chr8	146364022	2856218	0.0195	0.1989
chr9	141213431	2338410	0.0166	0.1572
chr10	135534747	2720545	0.0201	0.1942
chr11	135006516	2575056	0.0191	0.1767
chr12	133851895	2511814	0.0188	0.1461
chr13	115169878	1757754	0.0153	0.132
chr14	107349540	1717062	0.016	0.1362
chr15	102531392	1615605	0.0158	0.1347
chr16	90354753	1642381	0.0182	0.1487
chr17	81195210	1534535	0.0189	0.1561
chr18	78077248	1495814	0.0192	0.2516
chr19	59128983	1165409	0.0197	0.2117
chr20	63025520	1209013	0.0192	0.1496
chr21	48129895	727708	0.0151	0.144
chr22	51304566	669146	0.013	0.1212
chrMT	16571	234	0.0141	0.118
chrX	155270560	3083002	0.0199	0.1596
chrY	59373566	173843	0.0029	0.099

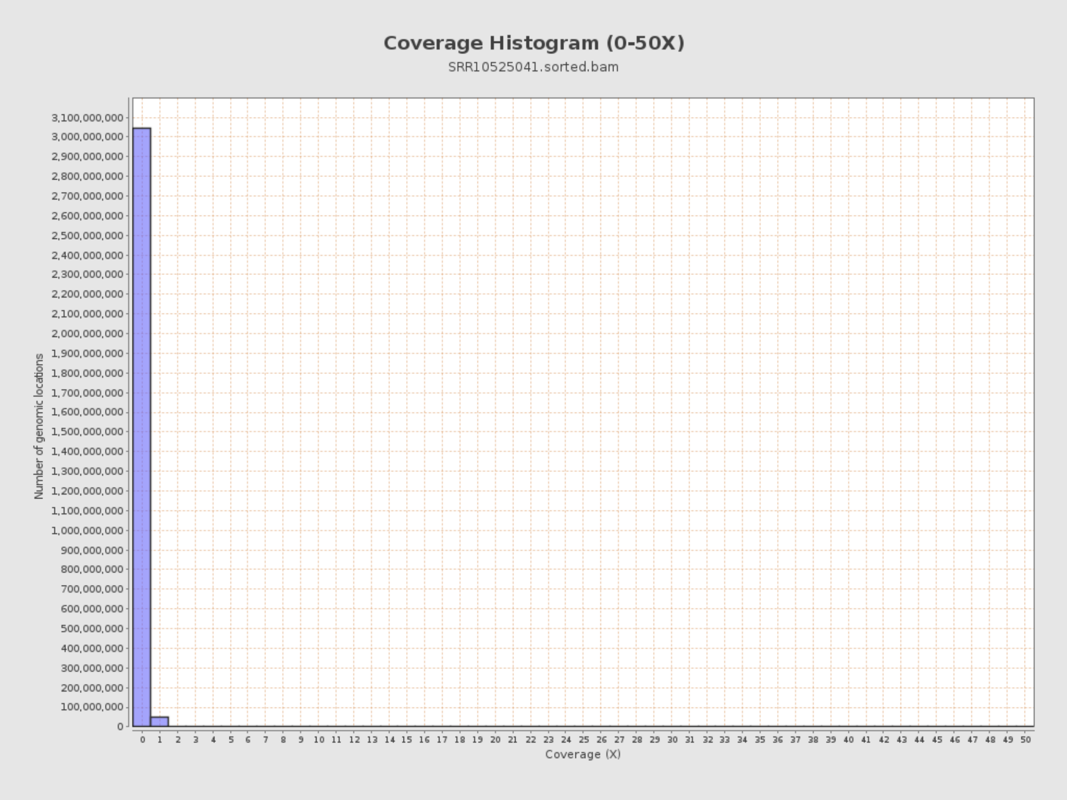
3. Results : Coverage across reference



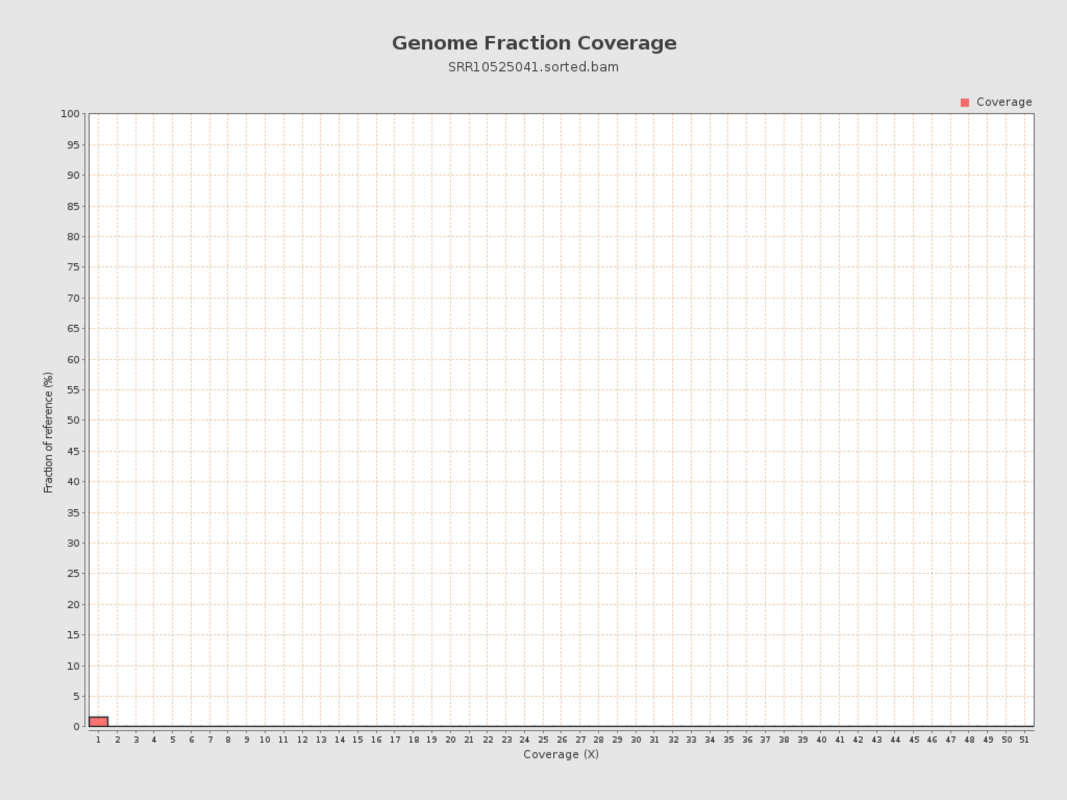
4. Results : Coverage Histogram



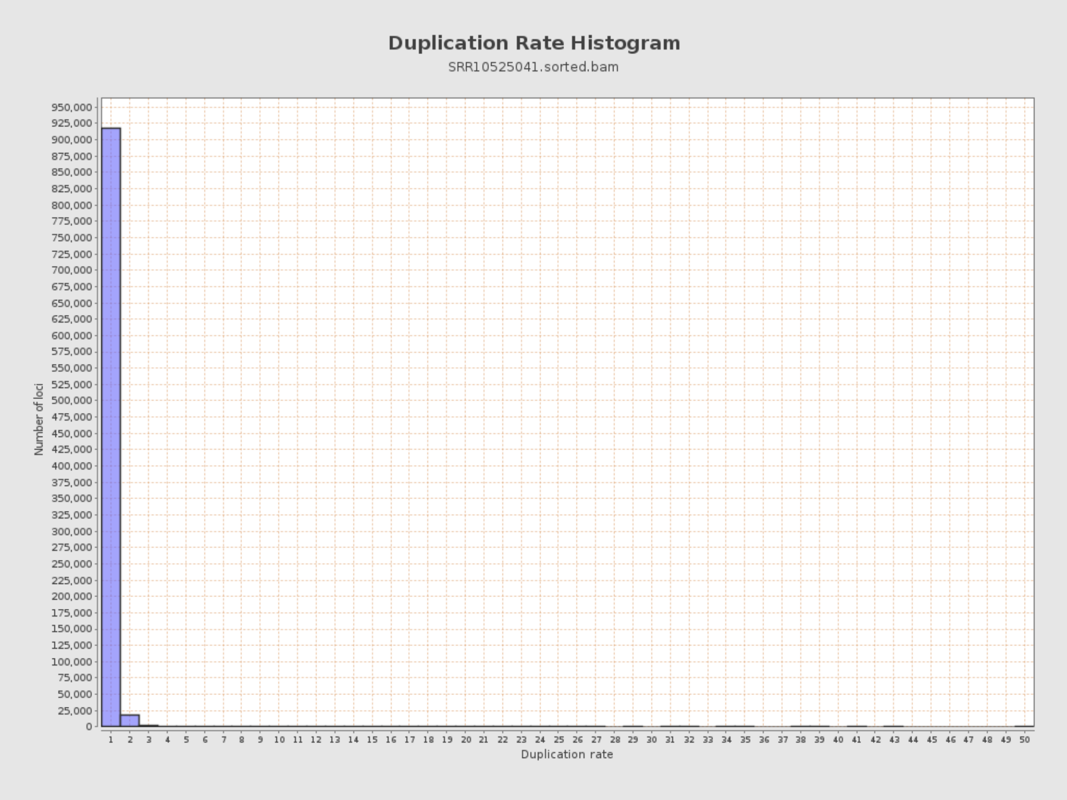
5. Results : Coverage Histogram (0-50X)



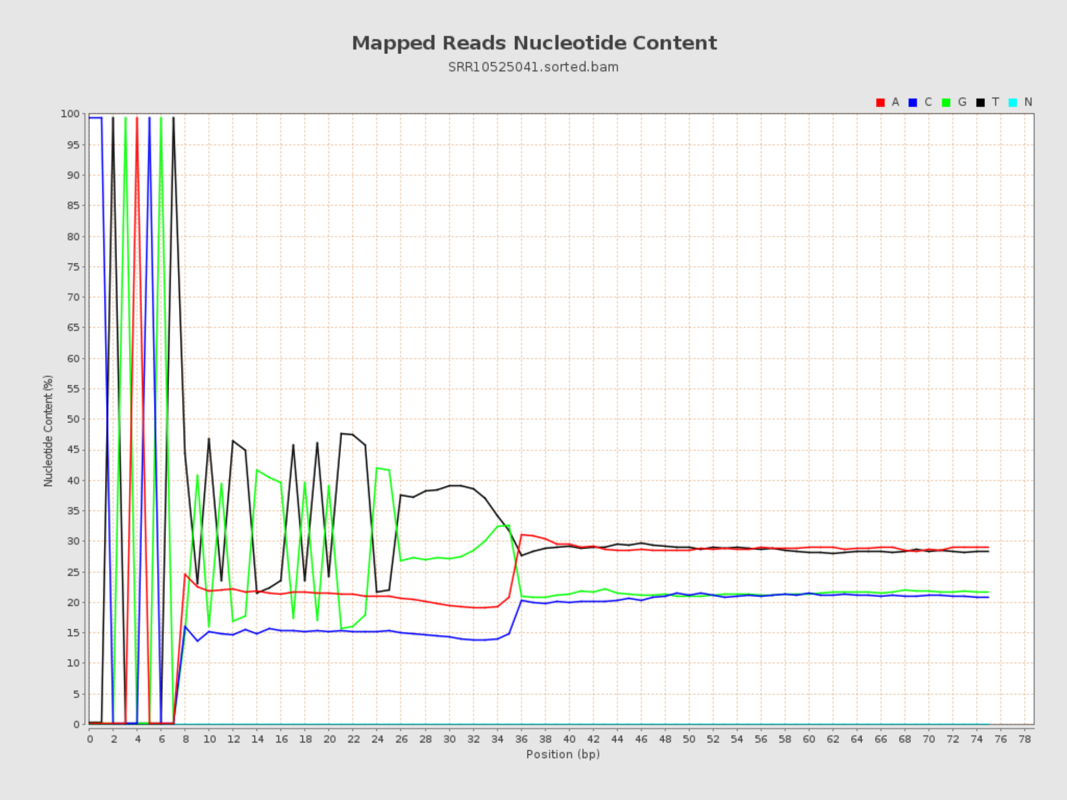
6. Results : Genome Fraction Coverage



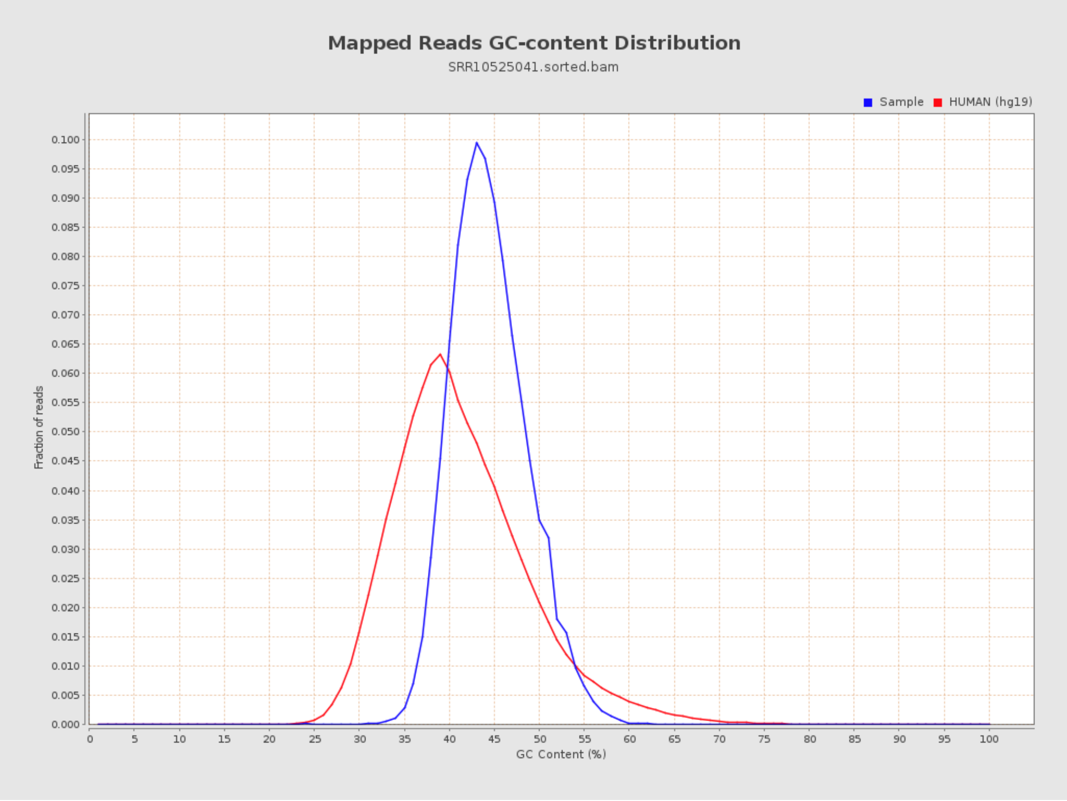
7. Results : Duplication Rate Histogram



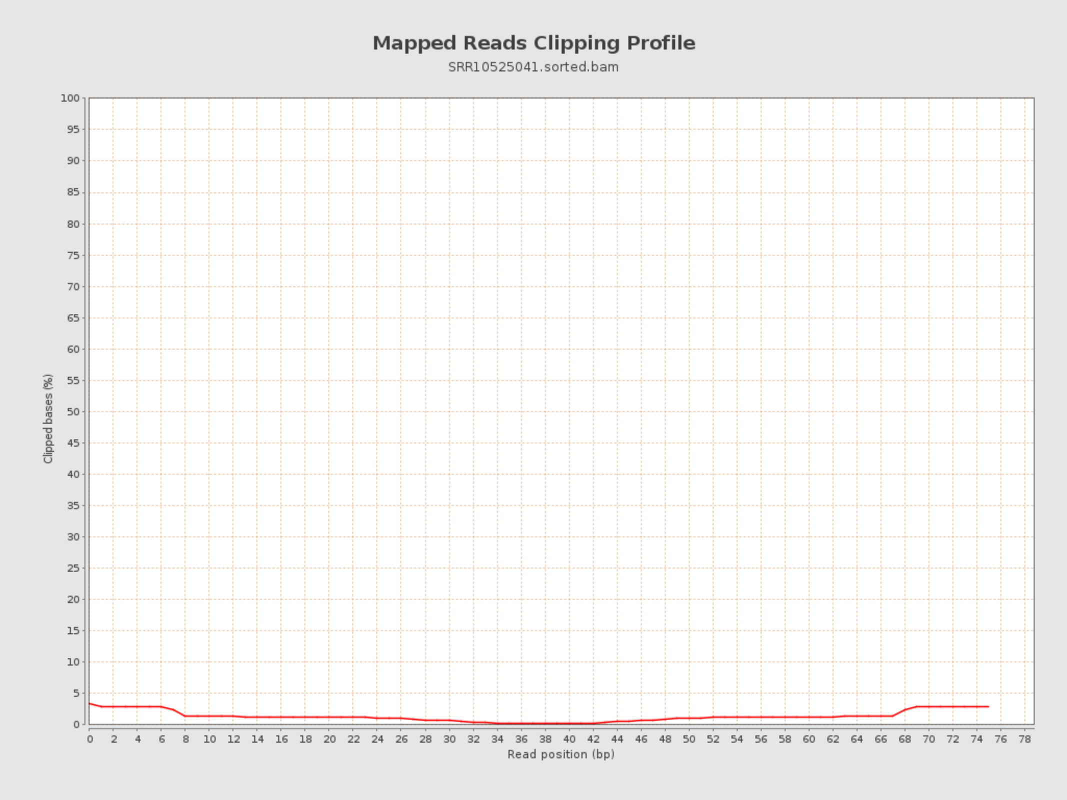
8. Results : Mapped Reads Nucleotide Content



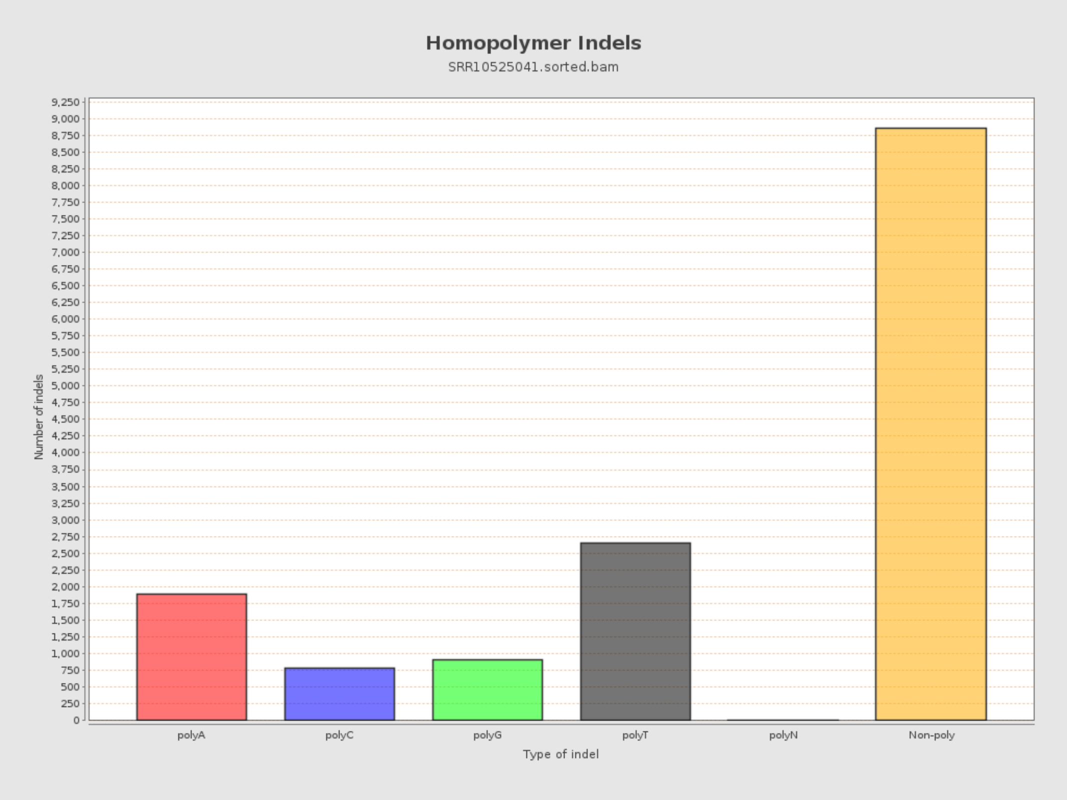
9. Results : Mapped Reads GC-content Distribution



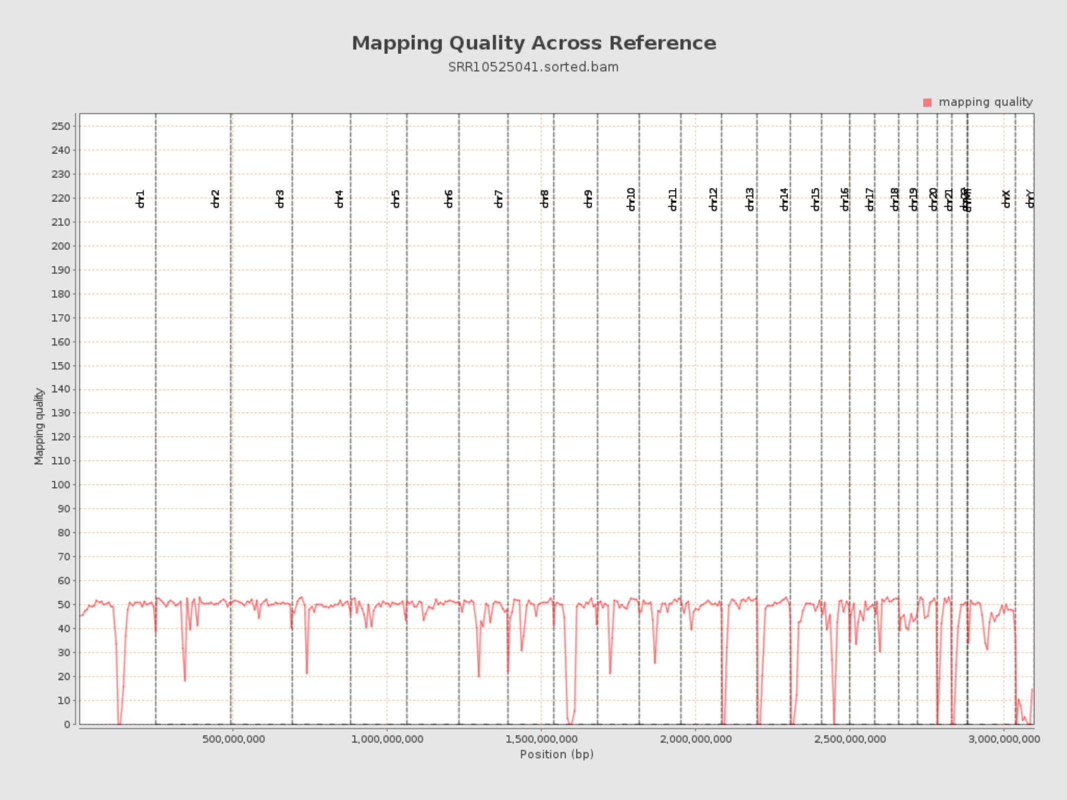
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram