Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:20:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525274.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_SRR10525274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525274.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:20:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,183,405
Mapped reads	1,075,871 / 90.91%
Unmapped reads	107,534 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,494 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,271 / 2.73%
Duplication rate	2.18%
Clipped reads	1,077,962 / 91.09%

2.2. ACGT Content

Number/percentage of A's	16,013,733 / 25.71%
Number/percentage of C's	11,819,045 / 18.98%
Number/percentage of T's	19,948,185 / 32.03%
Number/percentage of G's	14,503,729 / 23.29%
Number/percentage of N's	1,218 / 0%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2172

2.4. Mapping Quality

Mean Mapping Quality	45.08

2.5. Mismatches and indels

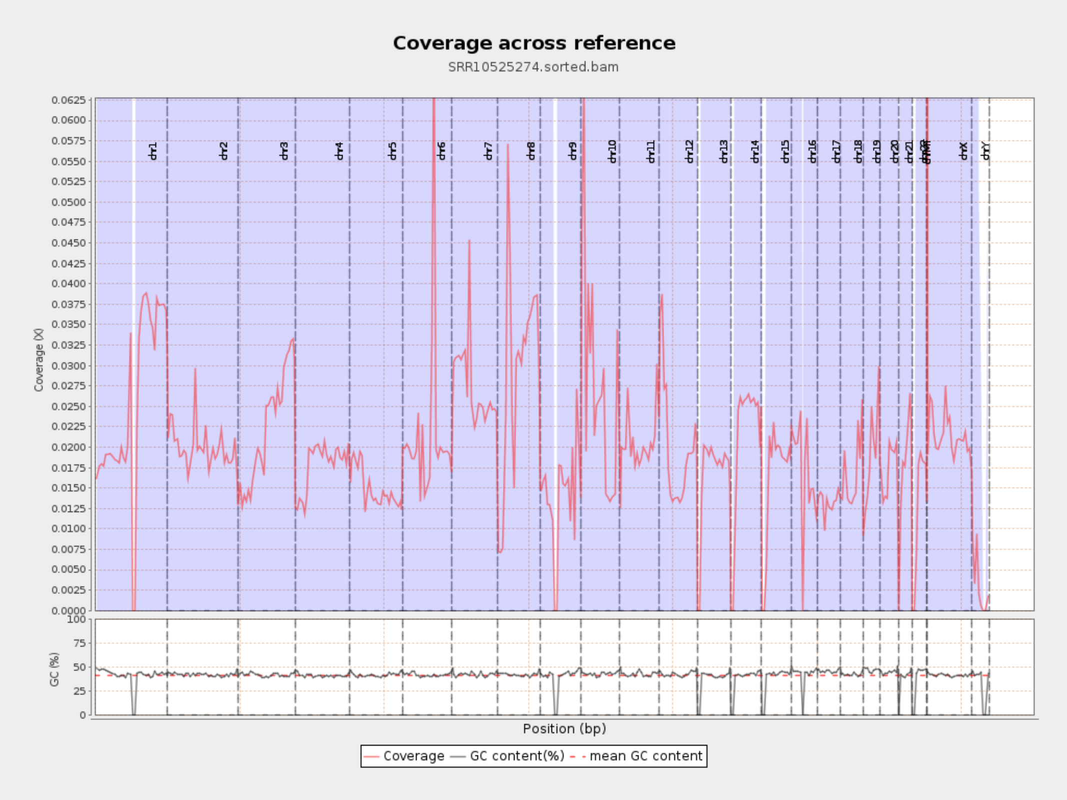
General error rate	0.52%
Mismatches	315,857
Insertions	4,395
Mapped reads with at least one insertion	0.41%
Deletions	13,444
Mapped reads with at least one deletion	1.24%
Homopolymer indels	43.6%

2.6. Chromosome stats

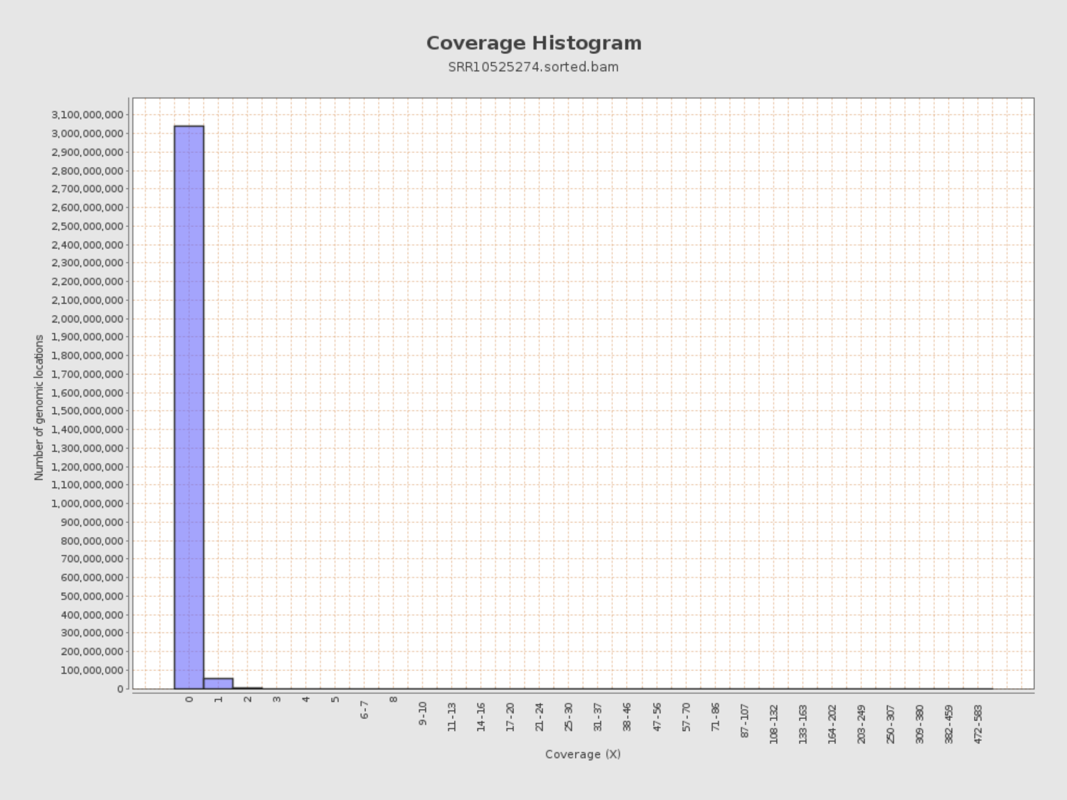
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6309216	0.0253	0.3852
chr2	243199373	4855742	0.02	0.2773
chr3	198022430	4394317	0.0222	0.1581
chr4	191154276	3408184	0.0178	0.1458
chr5	180915260	2711115	0.015	0.1302
chr6	171115067	3753422	0.0219	0.1702
chr7	159138663	4380060	0.0275	0.3529

chr8	146364022	4300296	0.0294	0.2335
chr9	141213431	1994297	0.0141	0.1516
chr10	135534747	3735706	0.0276	0.2224
chr11	135006516	2756134	0.0204	0.1805
chr12	133851895	2692834	0.0201	0.1509
chr13	115169878	1895360	0.0165	0.1366
chr14	107349540	2236807	0.0208	0.1543
chr15	102531392	1630154	0.0159	0.137
chr16	90354753	1529289	0.0169	0.1464
chr17	81195210	1081664	0.0133	0.1253
chr18	78077248	1283956	0.0164	0.2657
chr19	59128983	1126000	0.019	0.2526
chr20	63025520	1079799	0.0171	0.1388
chr21	48129895	856026	0.0178	0.1471
chr22	51304566	647843	0.0126	0.1184
chrMT	16571	124611	7.5198	5.0202
chrX	155270560	3347827	0.0216	0.1628
chrY	59373566	176713	0.003	0.0866

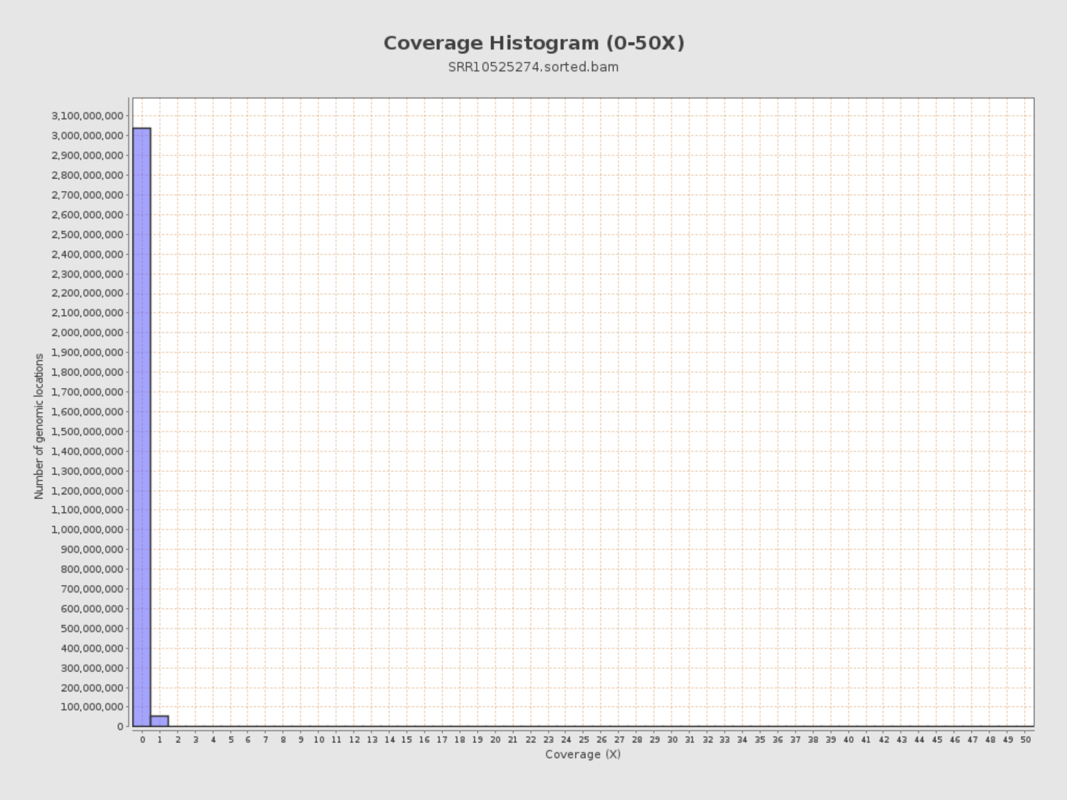
3. Results : Coverage across reference



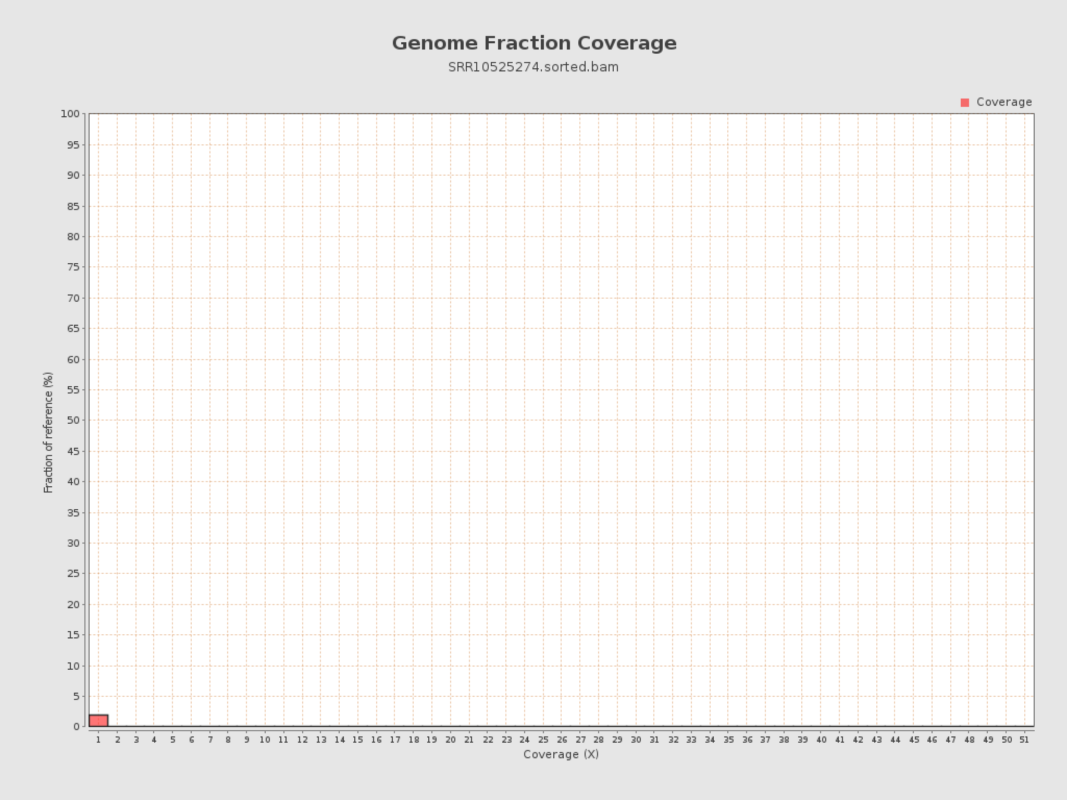
4. Results : Coverage Histogram



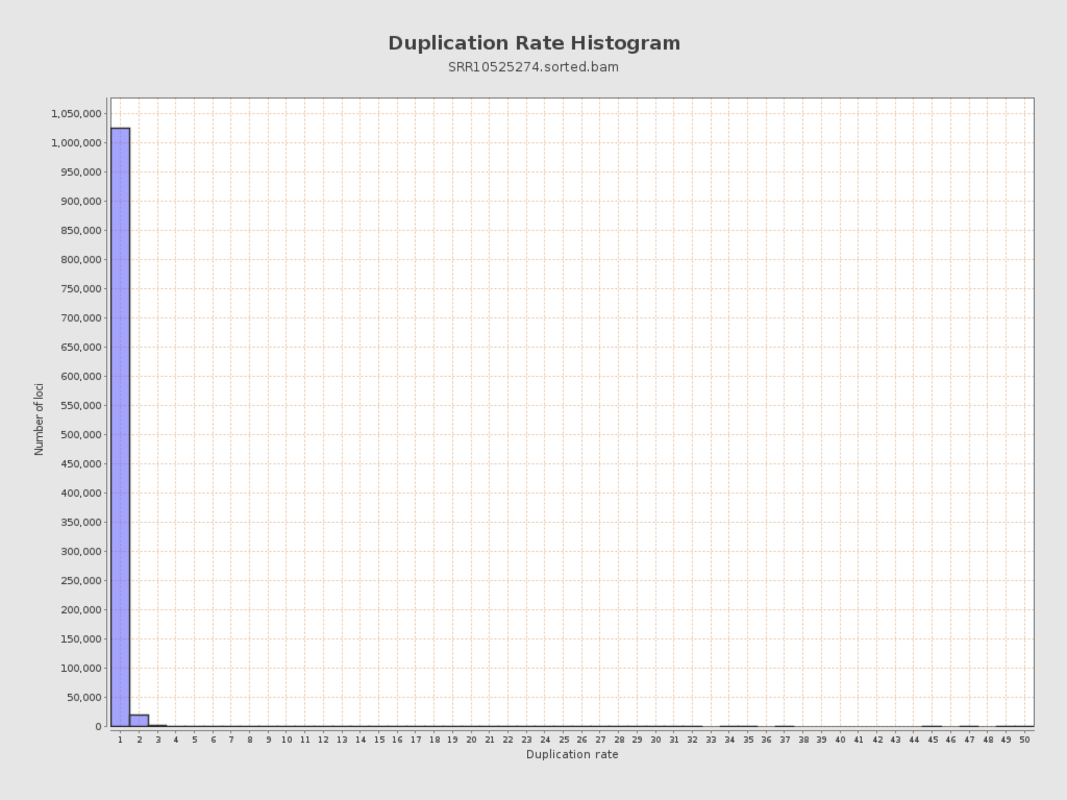
5. Results : Coverage Histogram (0-50X)



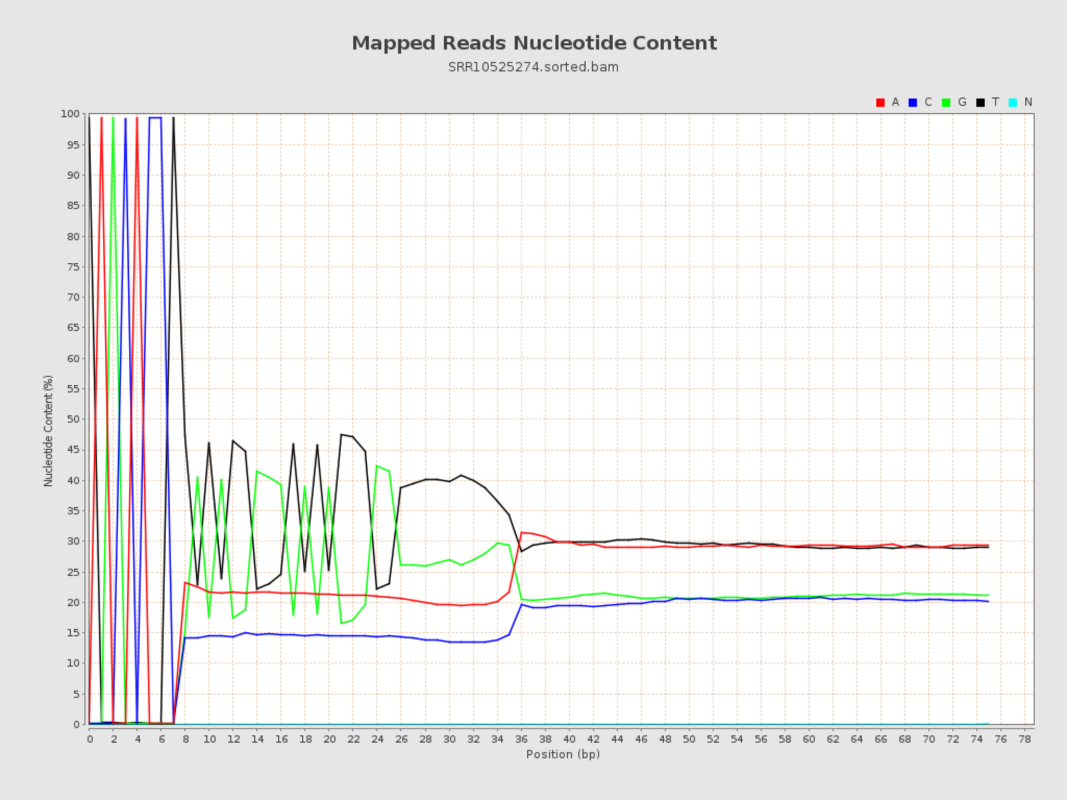
6. Results : Genome Fraction Coverage



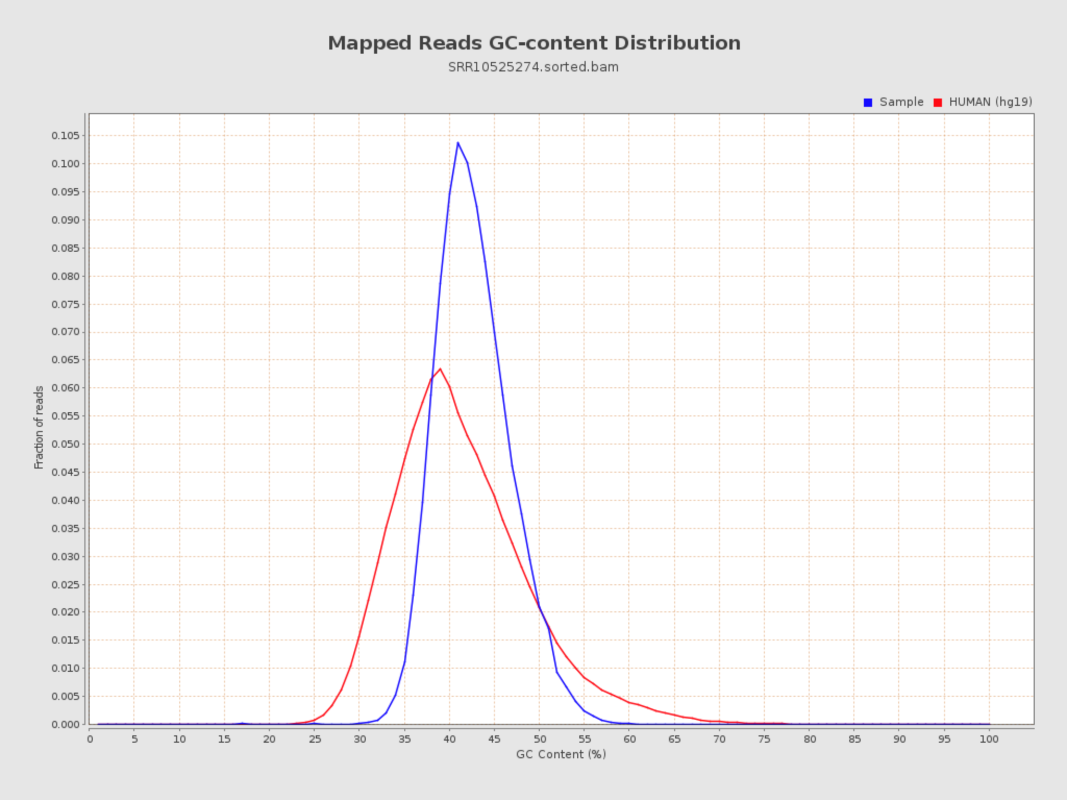
7. Results : Duplication Rate Histogram



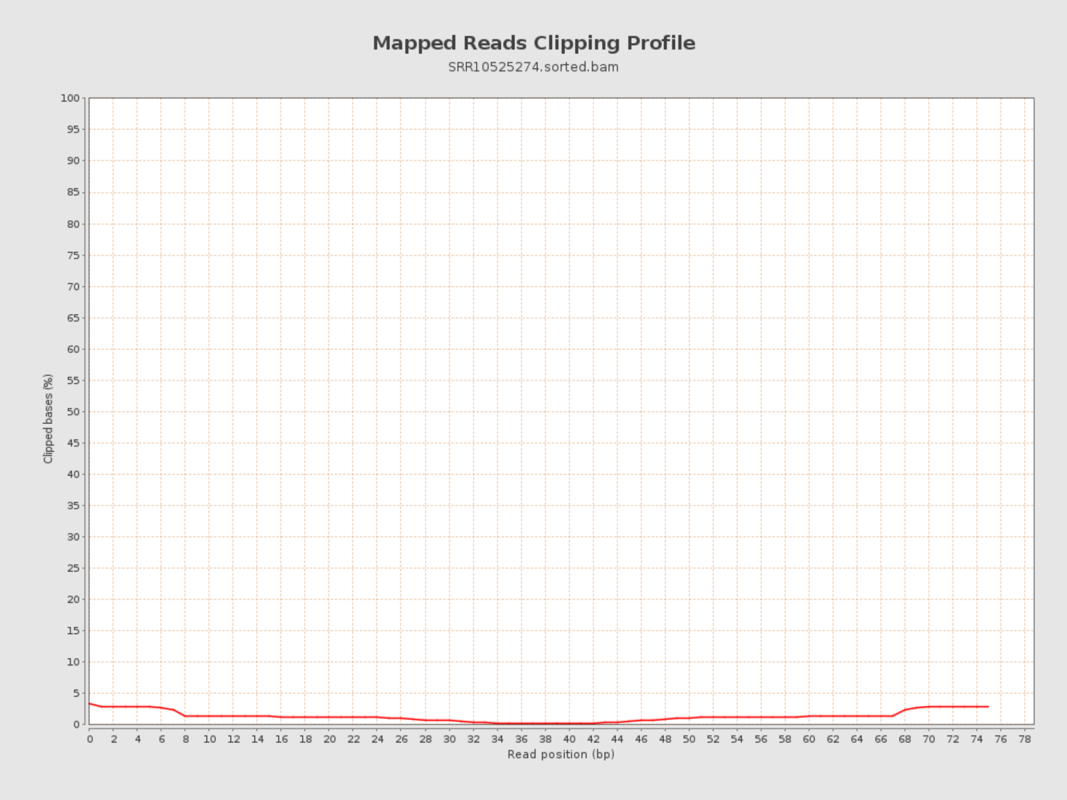
8. Results : Mapped Reads Nucleotide Content



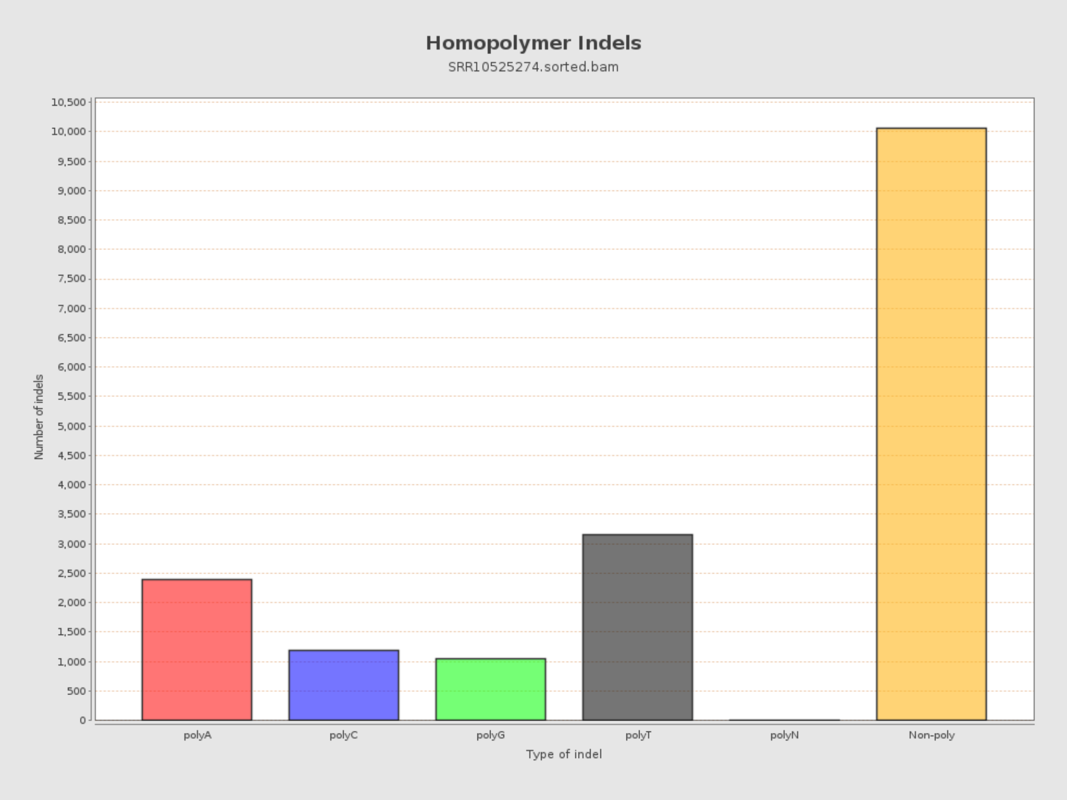
9. Results : Mapped Reads GC-content Distribution



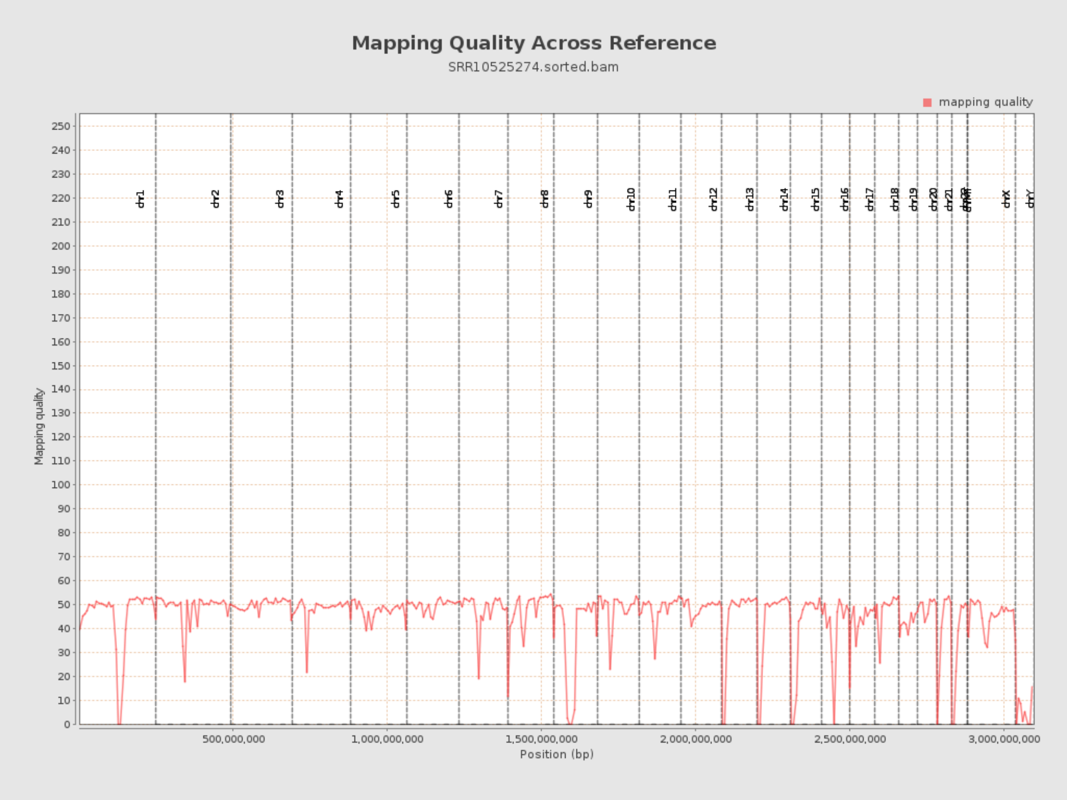
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram