Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:05:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525252.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_SRR10525252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525252.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:05:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,329,426
Mapped reads	1,213,945 / 91.31%
Unmapped reads	115,481 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,142 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	38,621 / 2.91%
Duplication rate	2.32%
Clipped reads	1,216,315 / 91.49%

2.2. ACGT Content

Number/percentage of A's	17,852,579 / 25.55%
Number/percentage of C's	13,177,425 / 18.86%
Number/percentage of T's	22,439,913 / 32.11%
Number/percentage of G's	16,413,548 / 23.49%
Number/percentage of N's	1,423 / 0%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2353

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

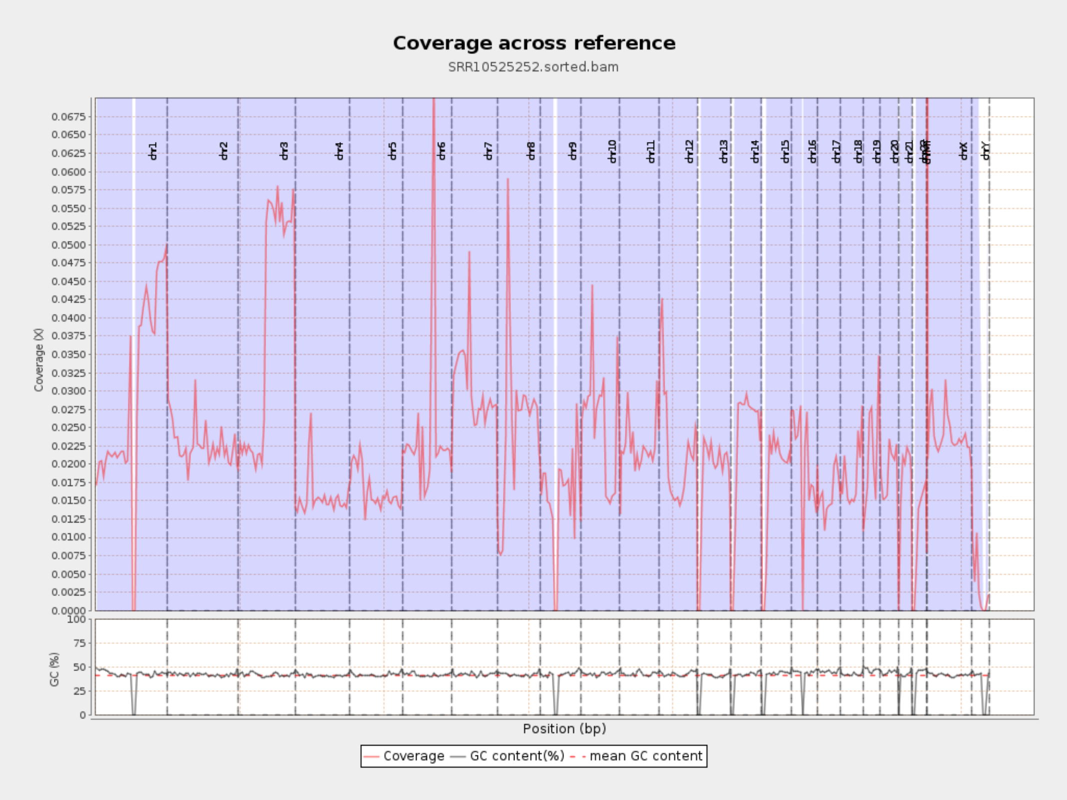
General error rate	0.52%
Mismatches	352,710
Insertions	4,505
Mapped reads with at least one insertion	0.37%
Deletions	14,264
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.75%

2.6. Chromosome stats

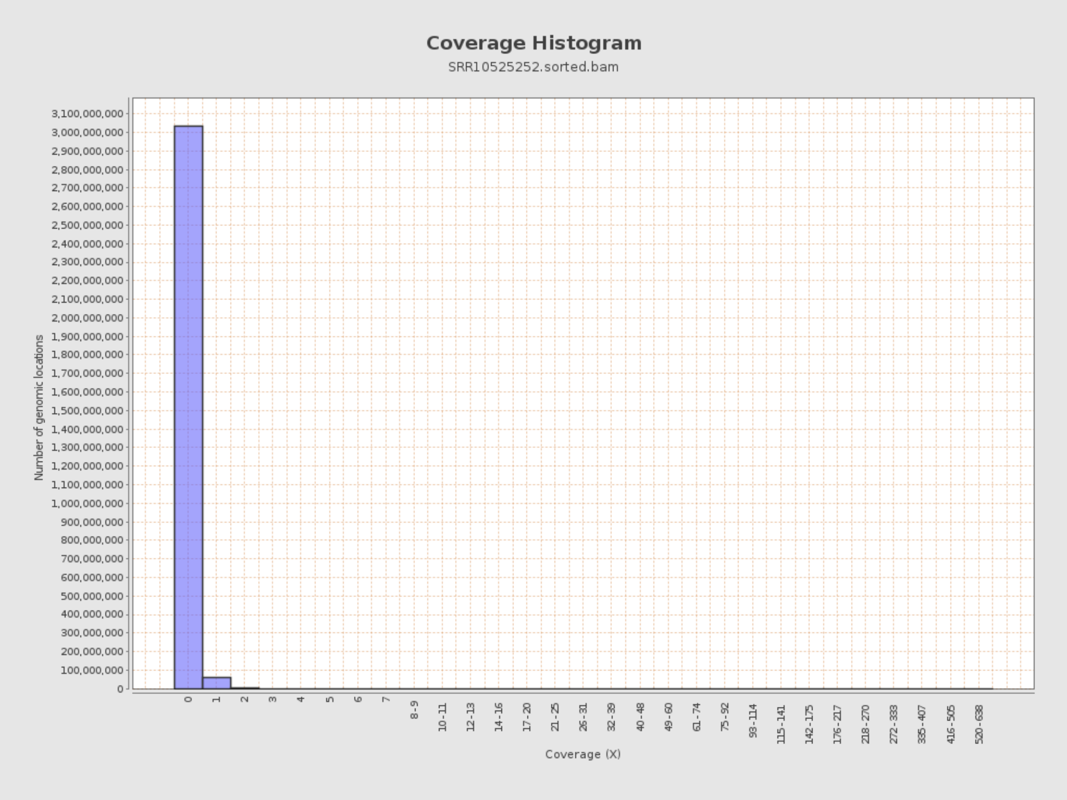
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7297680	0.0293	0.4112
chr2	243199373	5534469	0.0228	0.3033
chr3	198022430	7663364	0.0387	0.2115
chr4	191154276	2975672	0.0156	0.1388
chr5	180915260	3001400	0.0166	0.1379
chr6	171115067	4258568	0.0249	0.1836
chr7	159138663	4885992	0.0307	0.3973

chr8	146364022	3796177	0.0259	0.2377
chr9	141213431	2201118	0.0156	0.1616
chr10	135534747	3516262	0.0259	0.2378
chr11	135006516	3019078	0.0224	0.1912
chr12	133851895	2966447	0.0222	0.1612
chr13	115169878	2098238	0.0182	0.1457
chr14	107349540	2453483	0.0229	0.163
chr15	102531392	1799622	0.0176	0.1438
chr16	90354753	1802323	0.0199	0.162
chr17	81195210	1294880	0.0159	0.1376
chr18	78077248	1426371	0.0183	0.2951
chr19	59128983	1283072	0.0217	0.2766
chr20	63025520	1189770	0.0189	0.1489
chr21	48129895	860464	0.0179	0.148
chr22	51304566	548100	0.0107	0.1098
chrMT	16571	75144	4.5347	3.0735
chrX	155270560	3758490	0.0242	0.1778
chrY	59373566	201434	0.0034	0.1039

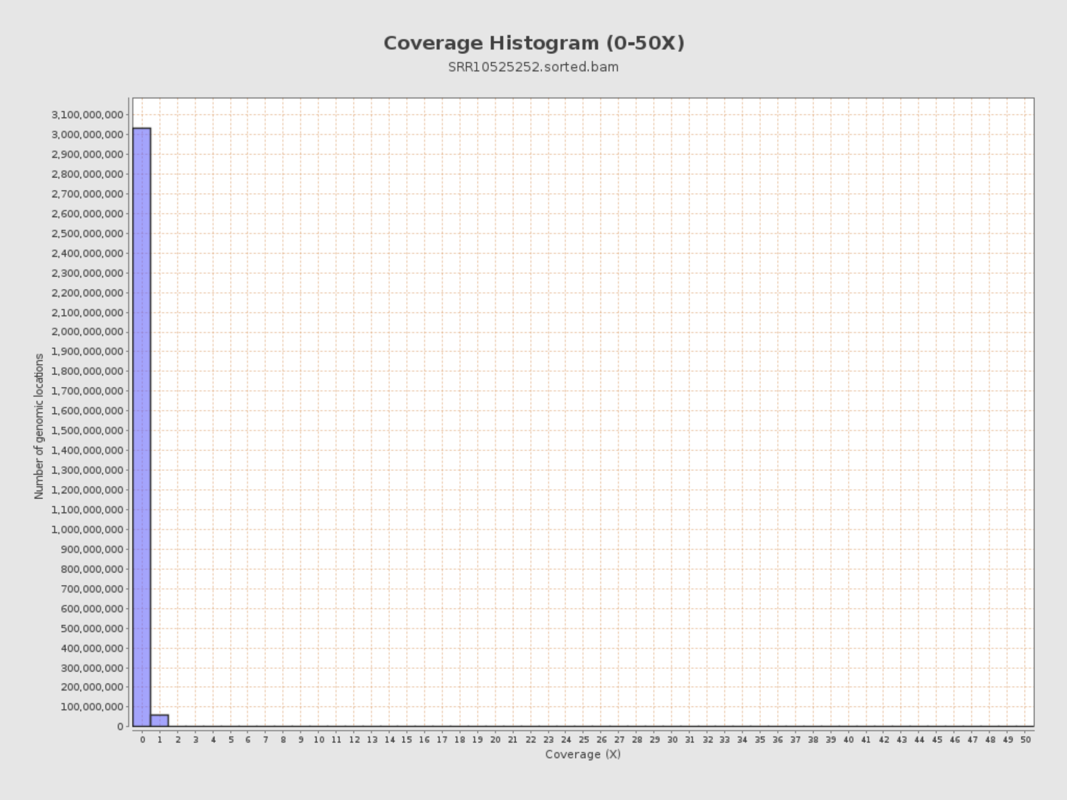
3. Results : Coverage across reference



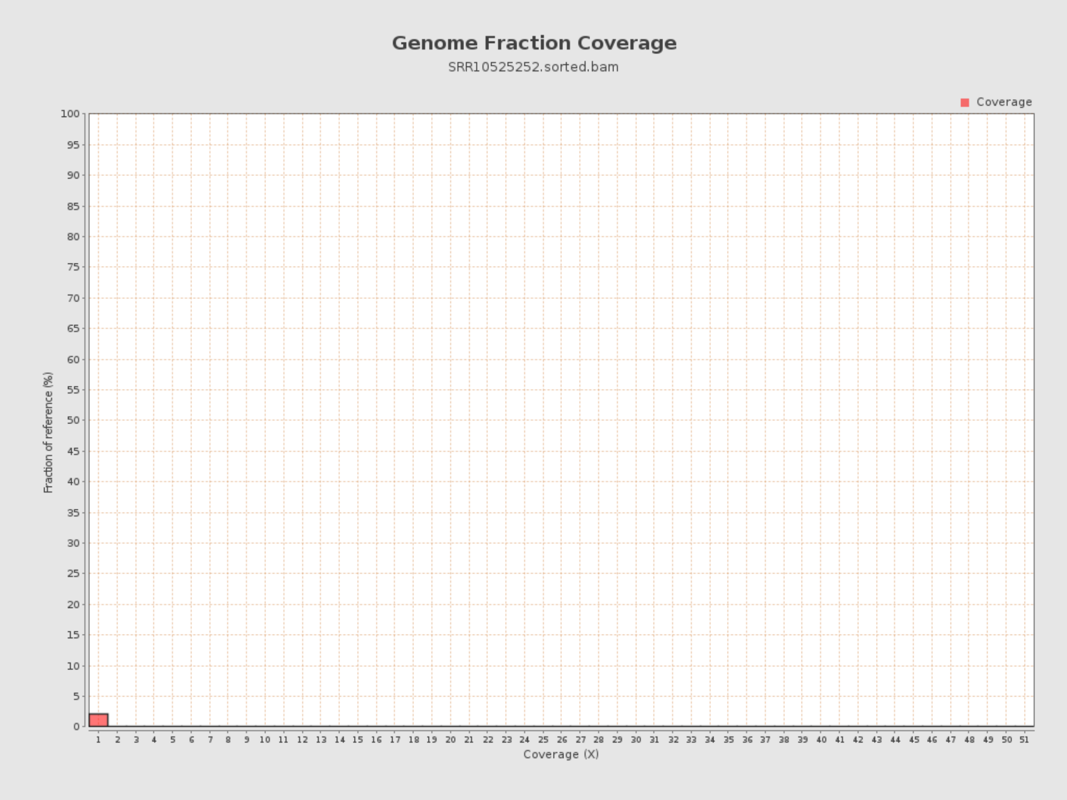
4. Results : Coverage Histogram



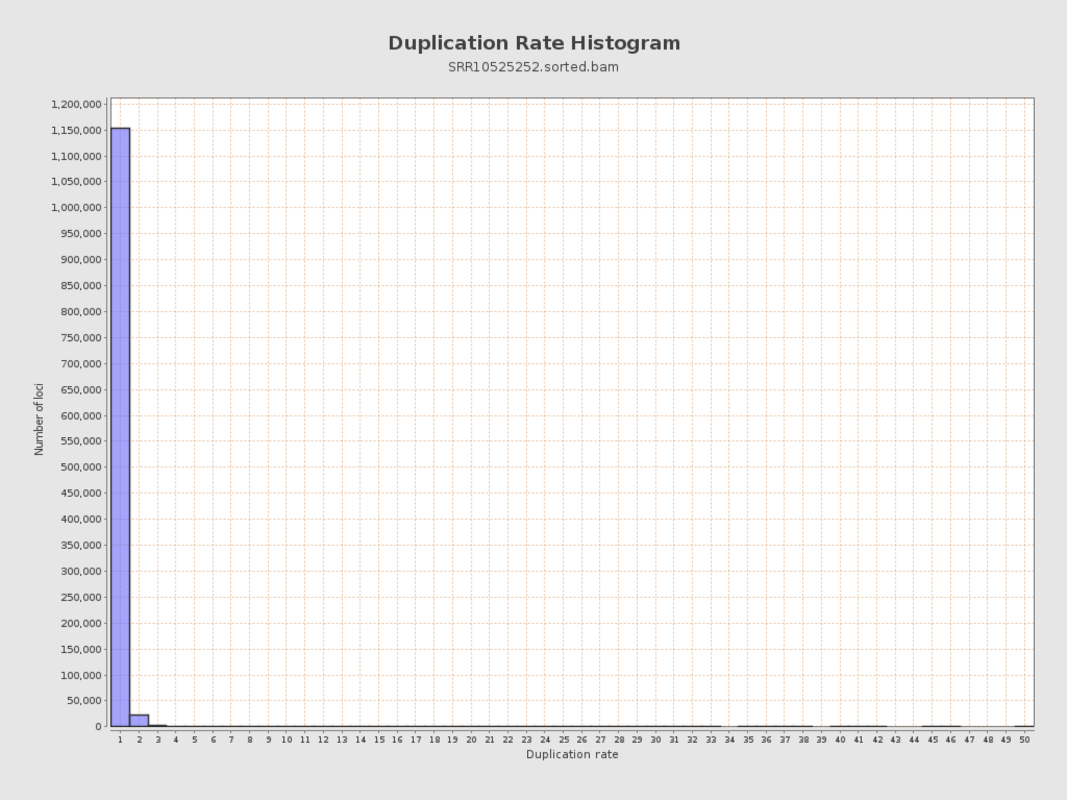
5. Results : Coverage Histogram (0-50X)



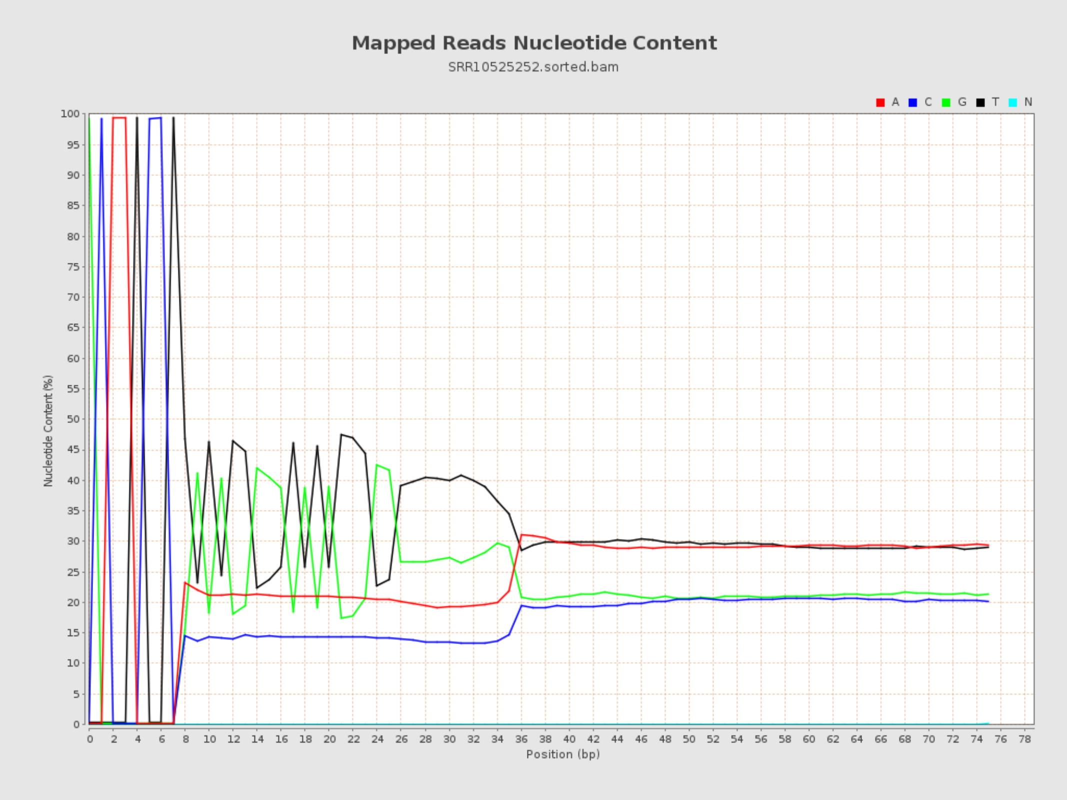
6. Results : Genome Fraction Coverage



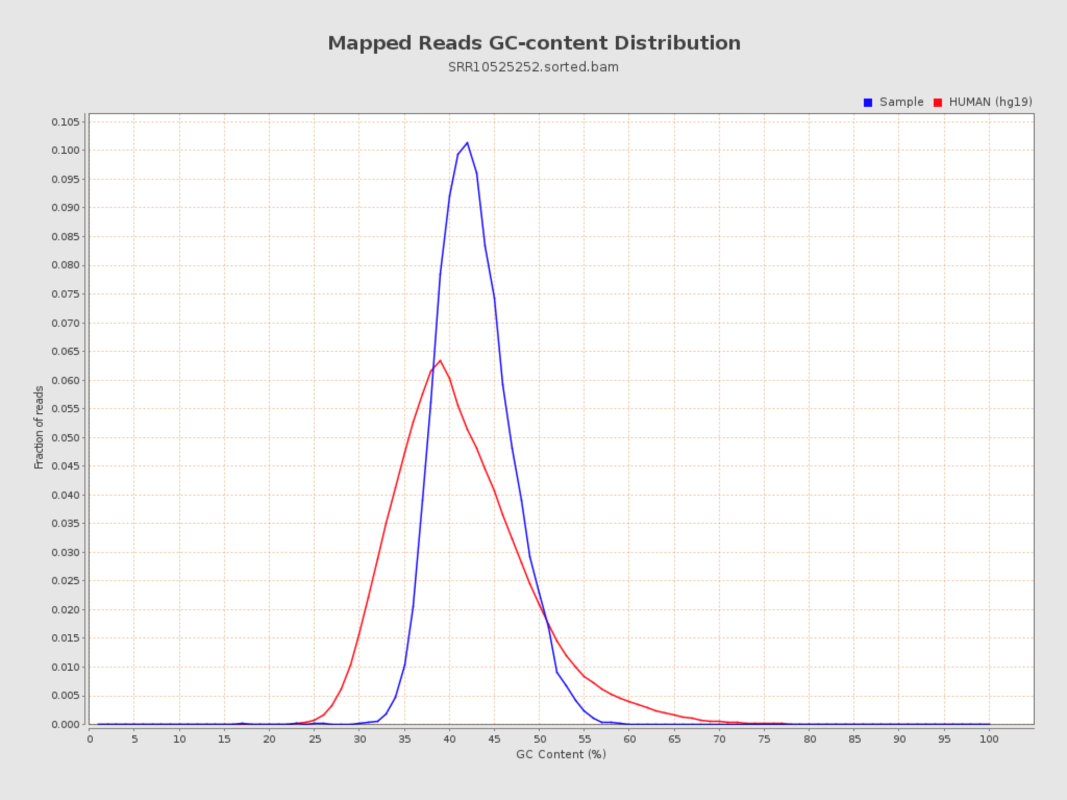
7. Results : Duplication Rate Histogram



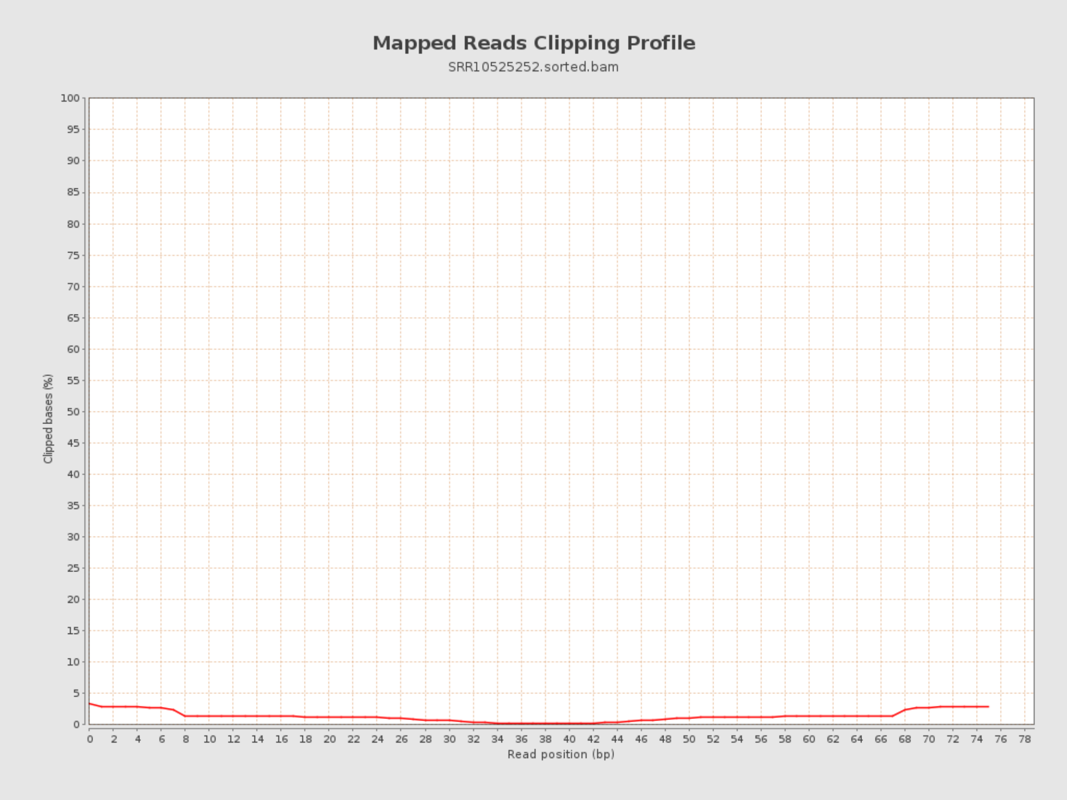
8. Results : Mapped Reads Nucleotide Content



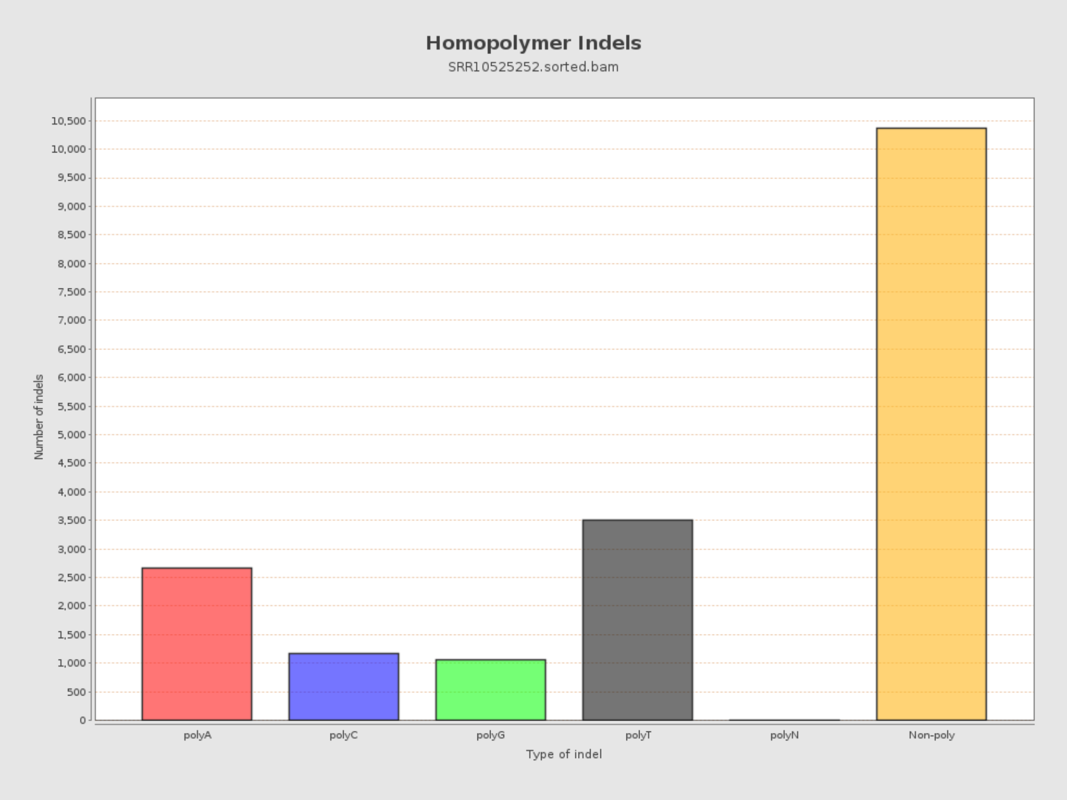
9. Results : Mapped Reads GC-content Distribution



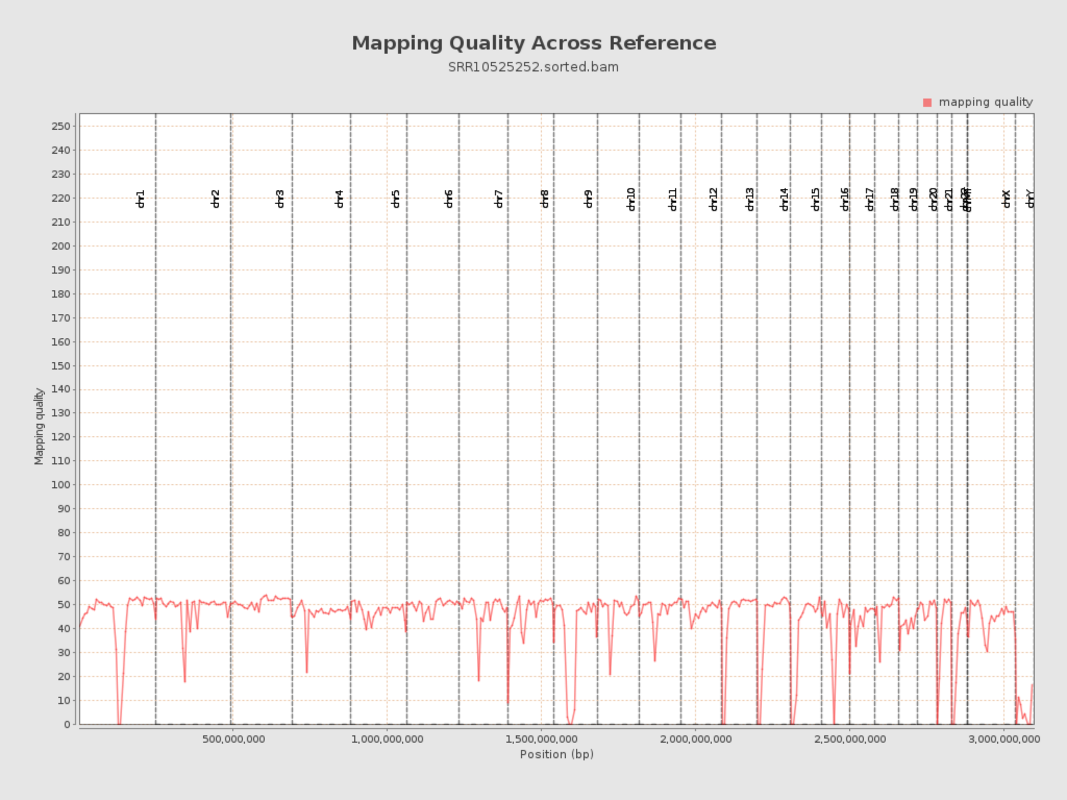
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram