Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:54:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524845.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_SRR10524845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:54:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	893,610
Mapped reads	817,474 / 91.48%
Unmapped reads	76,136 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,285 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	17,742 / 1.99%
Duplication rate	1.48%
Clipped reads	820,080 / 91.77%

2.2. ACGT Content

Number/percentage of A's	12,571,444 / 26.45%
Number/percentage of C's	8,583,732 / 18.06%
Number/percentage of T's	15,515,355 / 32.65%
Number/percentage of G's	10,850,069 / 22.83%
Number/percentage of N's	6,244 / 0.01%
GC Percentage	40.89%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1767

2.4. Mapping Quality

Mean Mapping Quality	45

2.5. Mismatches and indels

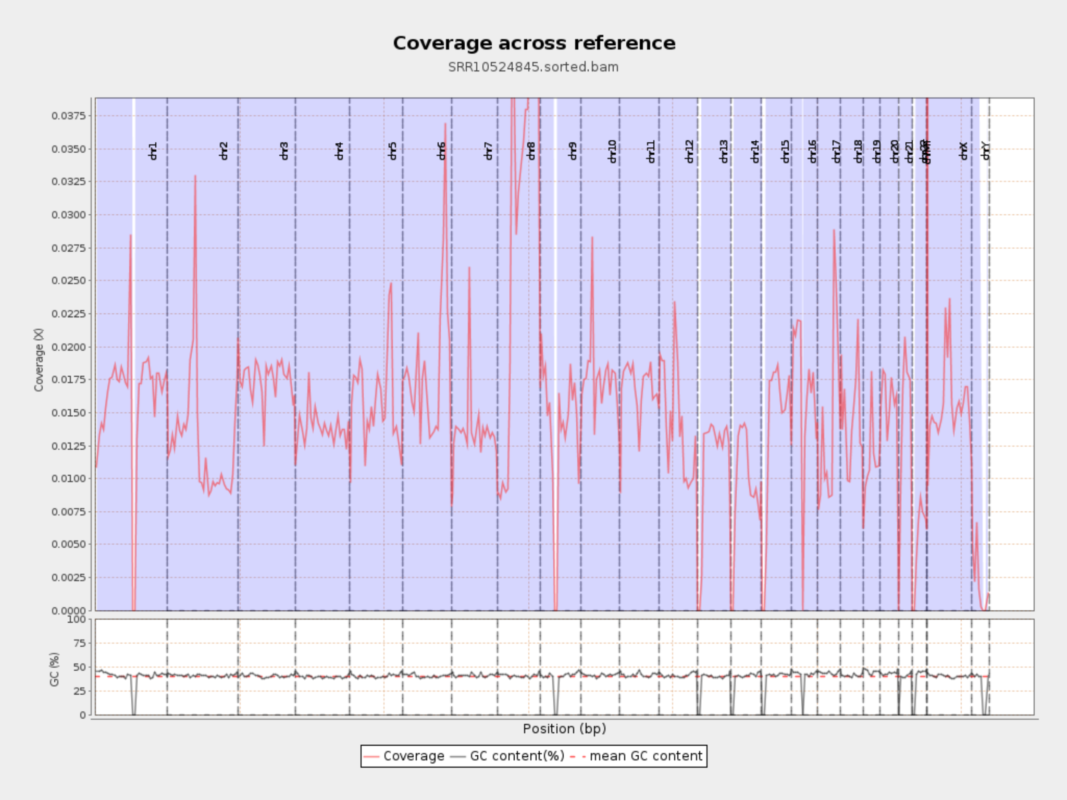
General error rate	0.5%
Mismatches	231,563
Insertions	3,856
Mapped reads with at least one insertion	0.47%
Deletions	9,177
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.46%

2.6. Chromosome stats

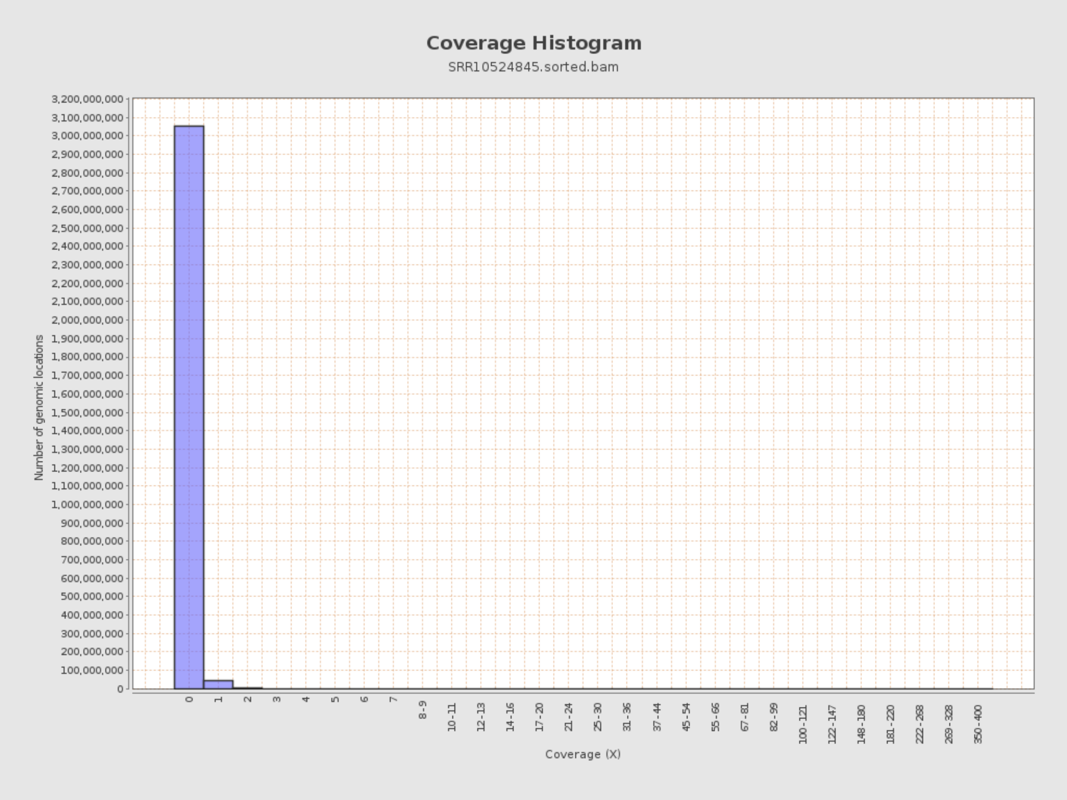
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4008296	0.0161	0.3202
chr2	243199373	3081928	0.0127	0.1758
chr3	198022430	3479993	0.0176	0.1376
chr4	191154276	2645707	0.0138	0.1269
chr5	180915260	2923236	0.0162	0.1322
chr6	171115067	3112030	0.0182	0.1482
chr7	159138663	2200821	0.0138	0.2162

chr8	146364022	4866675	0.0333	0.2444
chr9	141213431	1942725	0.0138	0.1529
chr10	135534747	2404234	0.0177	0.17
chr11	135006516	2282617	0.0169	0.1652
chr12	133851895	1890653	0.0141	0.1247
chr13	115169878	1277849	0.0111	0.1092
chr14	107349540	1000800	0.0093	0.1073
chr15	102531392	1403053	0.0137	0.123
chr16	90354753	1470565	0.0163	0.1376
chr17	81195210	1161275	0.0143	0.1325
chr18	78077248	1148393	0.0147	0.2564
chr19	59128983	678949	0.0115	0.2108
chr20	63025520	995872	0.0158	0.1309
chr21	48129895	700309	0.0146	0.1291
chr22	51304566	273414	0.0053	0.0753
chrMT	16571	18616	1.1234	1.2863
chrX	155270560	2453607	0.0158	0.142
chrY	59373566	119638	0.002	0.0605

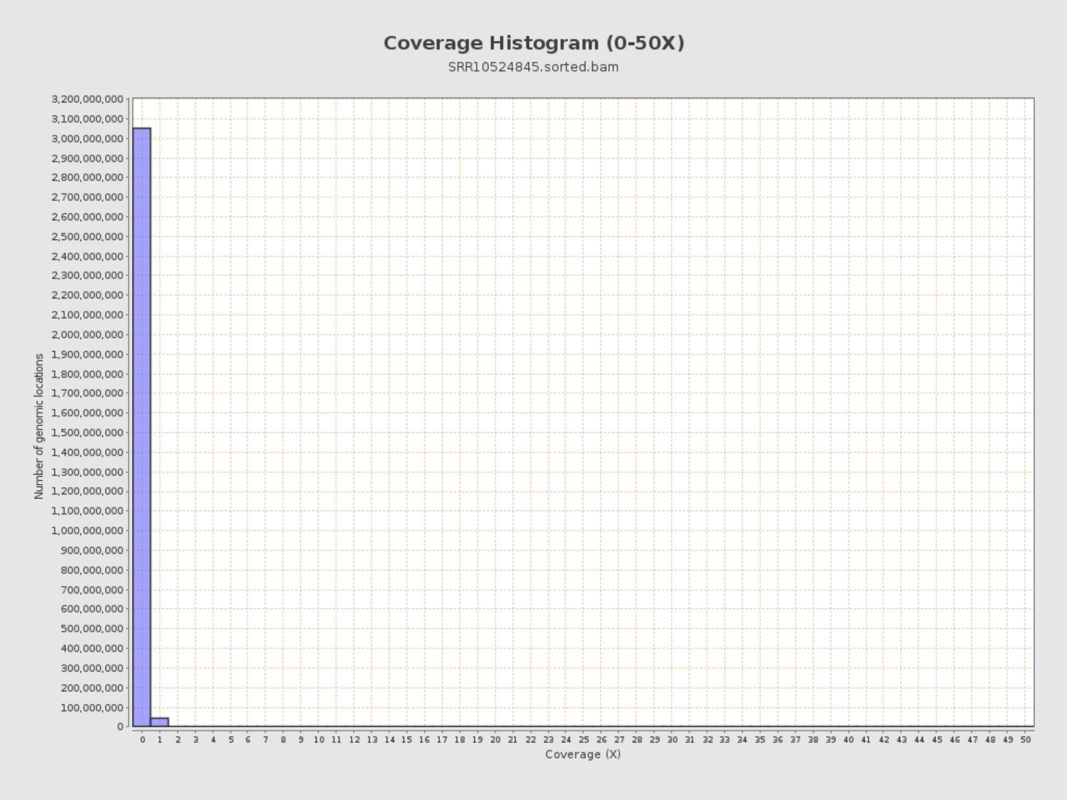
3. Results : Coverage across reference



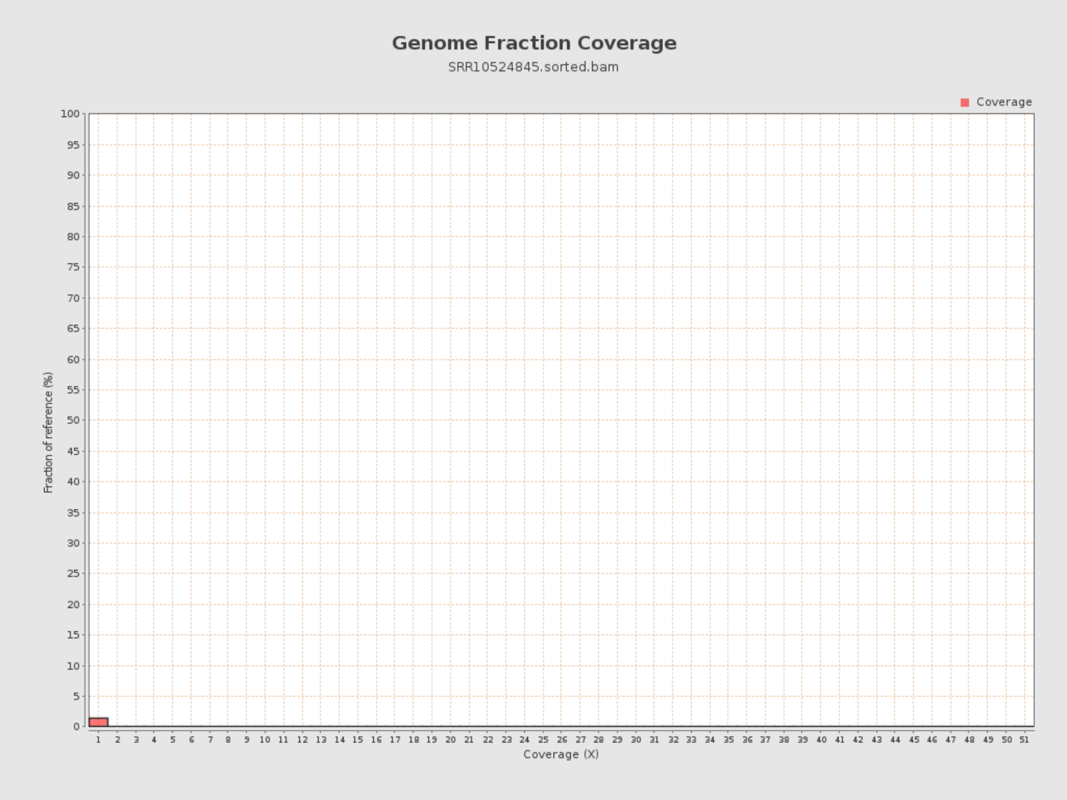
4. Results : Coverage Histogram



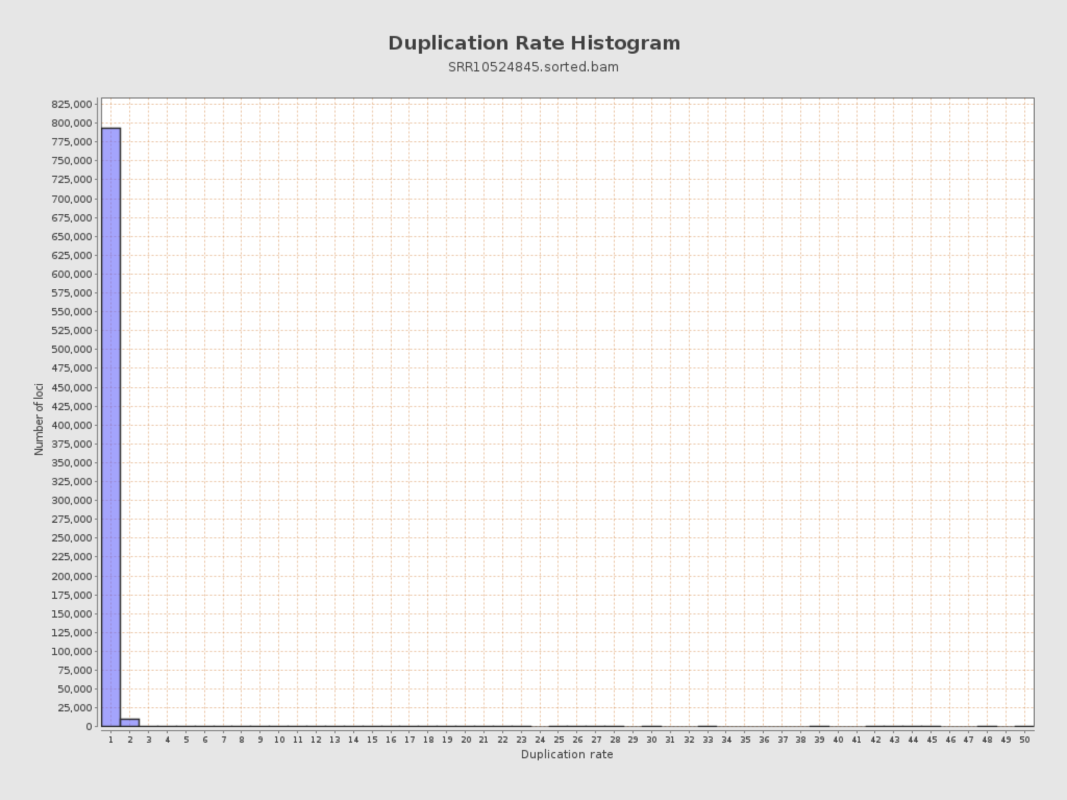
5. Results : Coverage Histogram (0-50X)



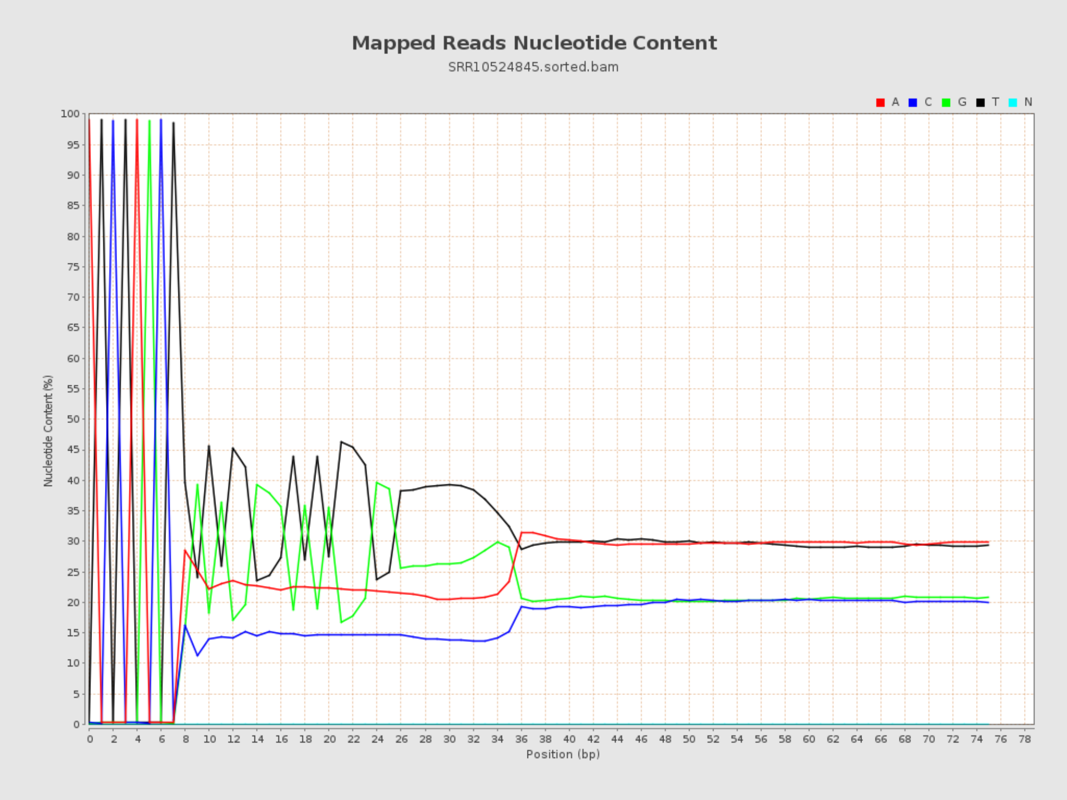
6. Results : Genome Fraction Coverage



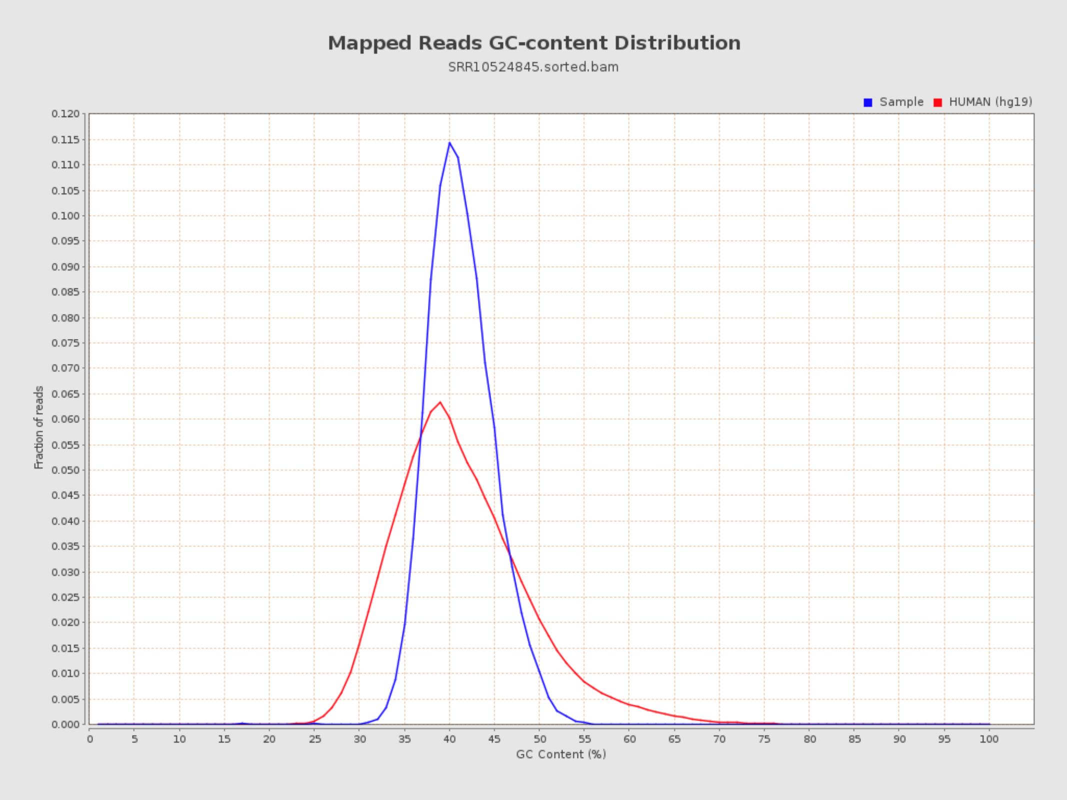
7. Results : Duplication Rate Histogram



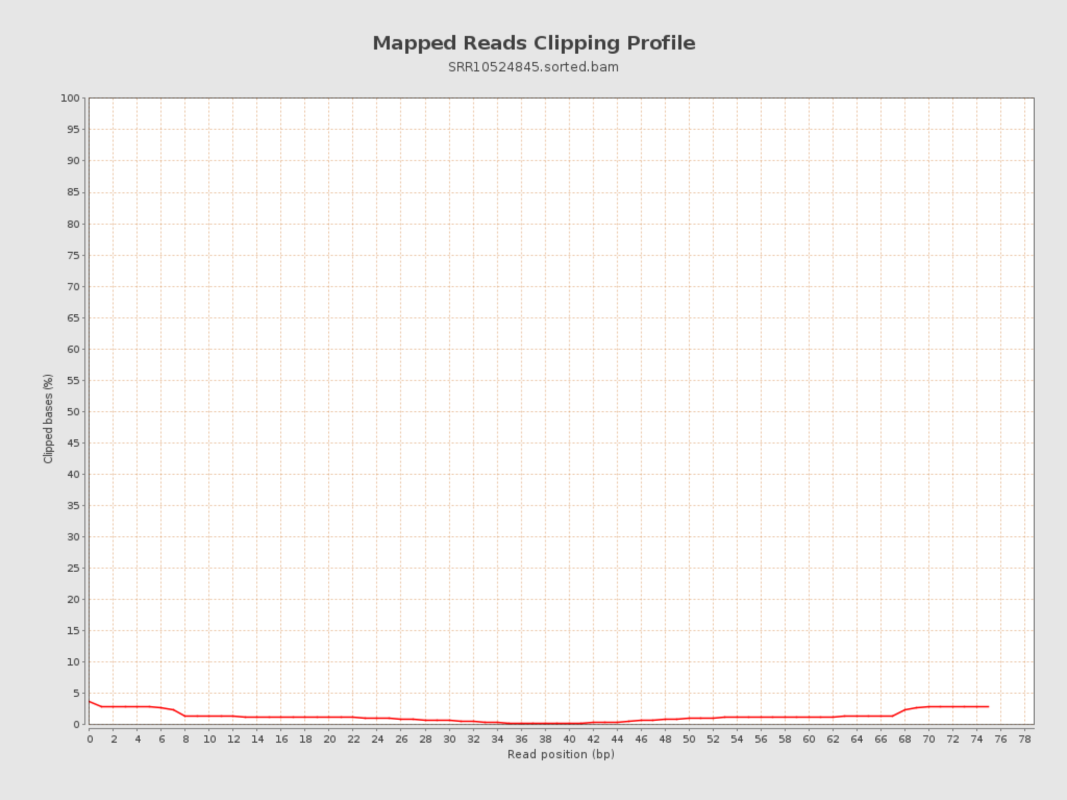
8. Results : Mapped Reads Nucleotide Content



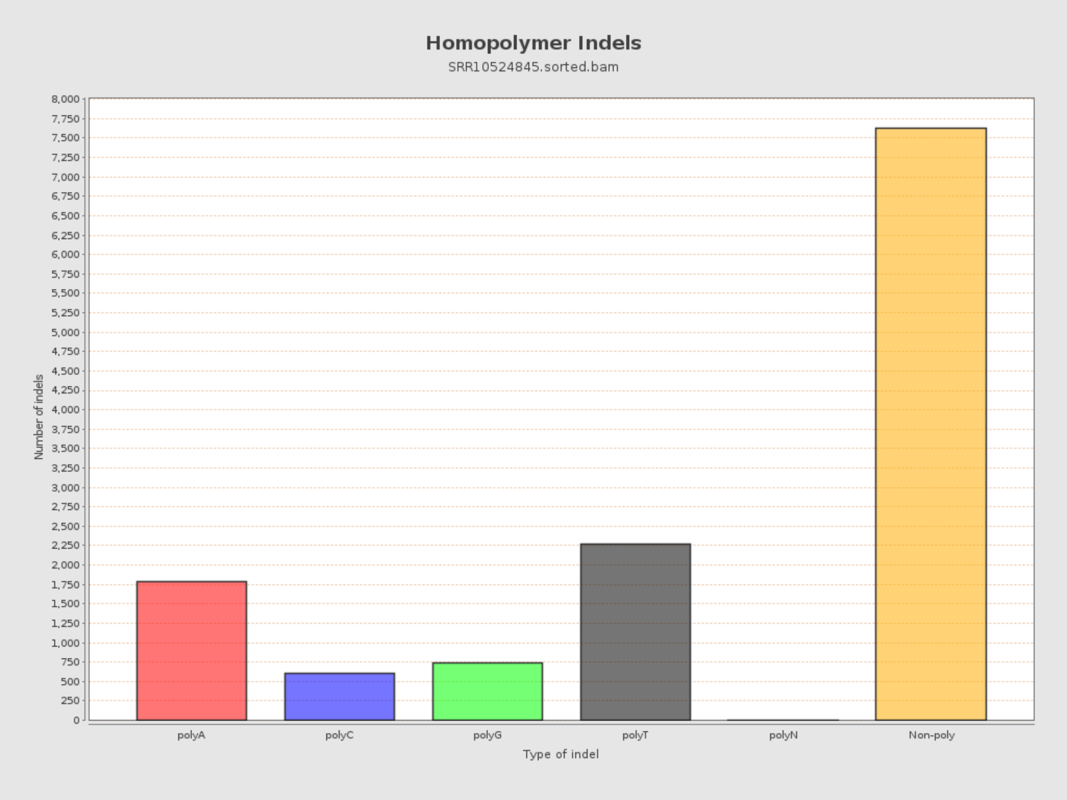
9. Results : Mapped Reads GC-content Distribution



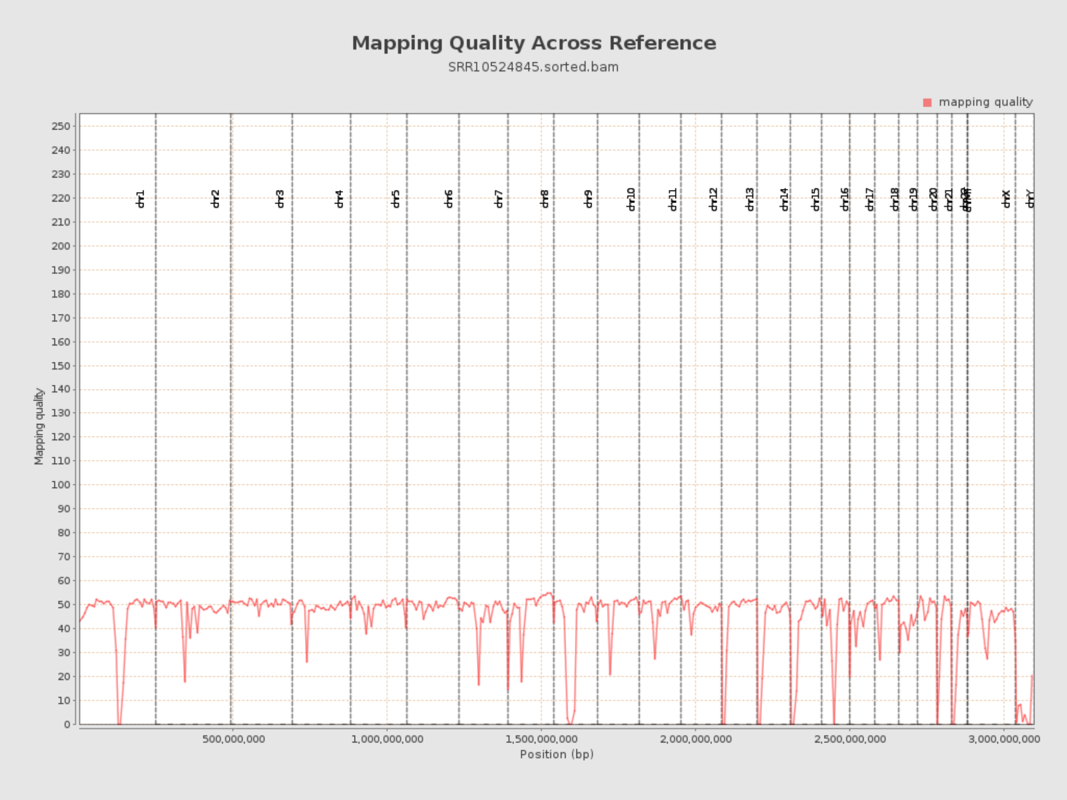
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram