Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:14:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524855.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_SRR10524855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524855.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:14:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,661,613
Mapped reads	1,520,588 / 91.51%
Unmapped reads	141,025 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,957 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	52,449 / 3.16%
Duplication rate	2.47%
Clipped reads	1,525,750 / 91.82%

2.2. ACGT Content

Number/percentage of A's	21,424,044 / 24.29%
Number/percentage of C's	15,261,415 / 17.3%
Number/percentage of T's	29,561,764 / 33.52%
Number/percentage of G's	21,949,418 / 24.89%
Number/percentage of N's	1,866 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2864

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

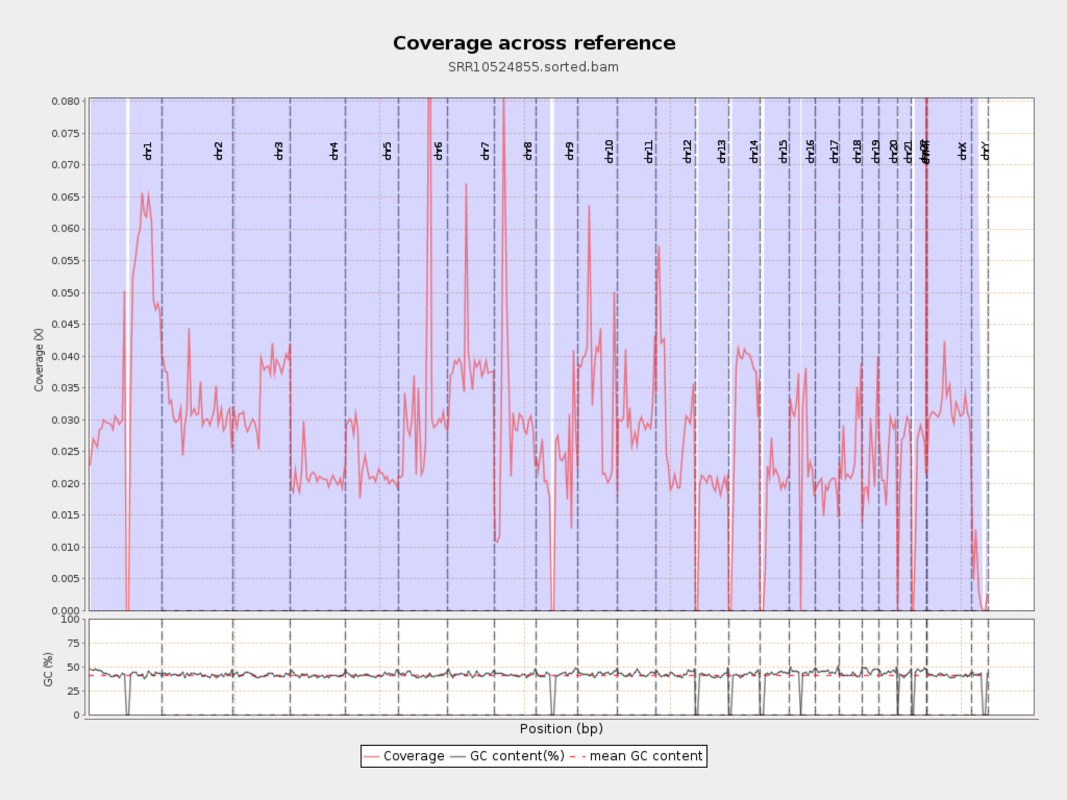
General error rate	0.52%
Mismatches	449,231
Insertions	5,177
Mapped reads with at least one insertion	0.34%
Deletions	18,998
Mapped reads with at least one deletion	1.24%
Homopolymer indels	45.71%

2.6. Chromosome stats

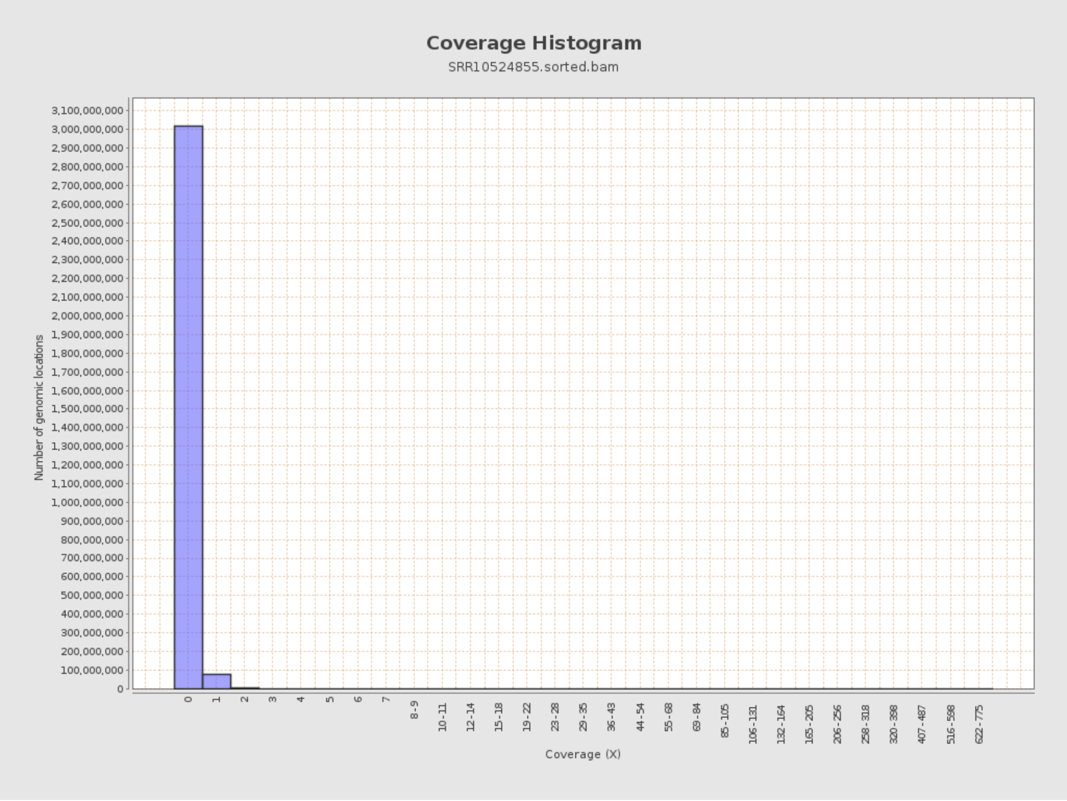
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9698584	0.0389	0.5105
chr2	243199373	7708942	0.0317	0.3718
chr3	198022430	6789743	0.0343	0.2019
chr4	191154276	3995073	0.0209	0.1662
chr5	180915260	4180828	0.0231	0.1635
chr6	171115067	5656363	0.0331	0.2228
chr7	159138663	6228871	0.0391	0.5107

chr8	146364022	4412145	0.0301	0.2404
chr9	141213431	3051195	0.0216	0.2028
chr10	135534747	4880876	0.036	0.3188
chr11	135006516	4122533	0.0305	0.2469
chr12	133851895	4044900	0.0302	0.1886
chr13	115169878	2065044	0.0179	0.1472
chr14	107349540	3443927	0.0321	0.1962
chr15	102531392	1772930	0.0173	0.1455
chr16	90354753	2385991	0.0264	0.199
chr17	81195210	1552268	0.0191	0.155
chr18	78077248	1997136	0.0256	0.3973
chr19	59128983	1419782	0.024	0.3511
chr20	63025520	1532391	0.0243	0.1698
chr21	48129895	1148665	0.0239	0.1756
chr22	51304566	971596	0.0189	0.1473
chrMT	16571	4985	0.3008	0.5501
chrX	155270560	4921465	0.0317	0.2103
chrY	59373566	242975	0.0041	0.113

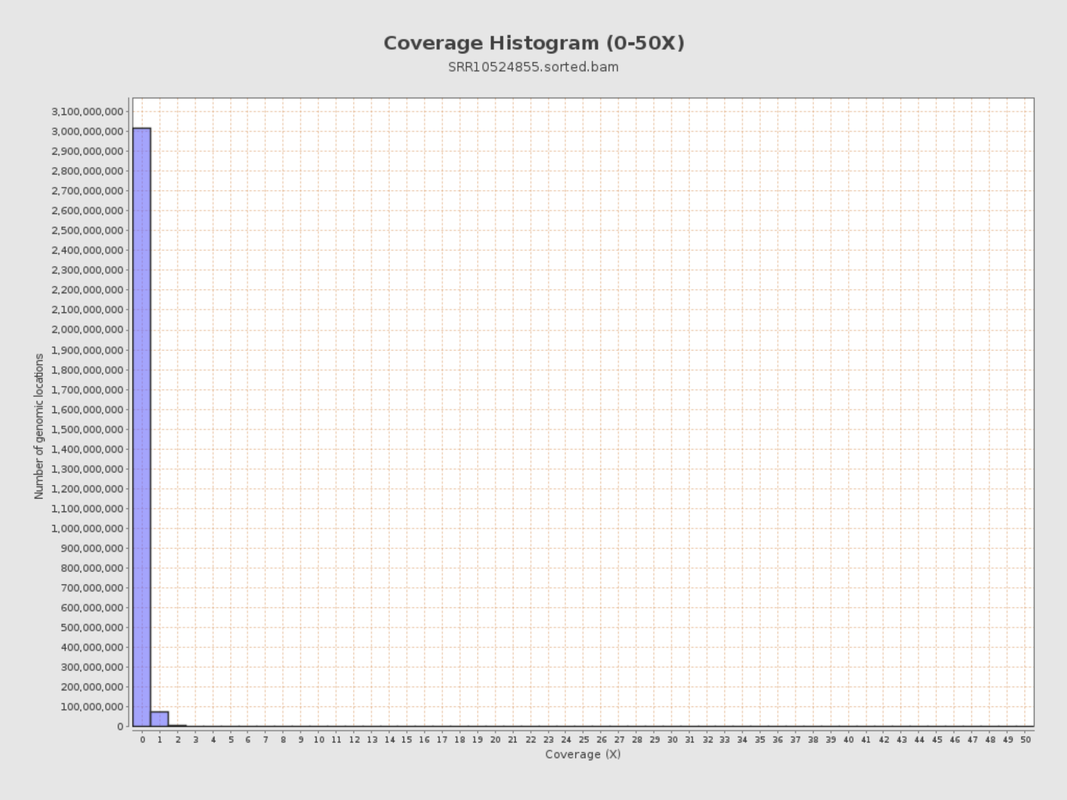
3. Results : Coverage across reference



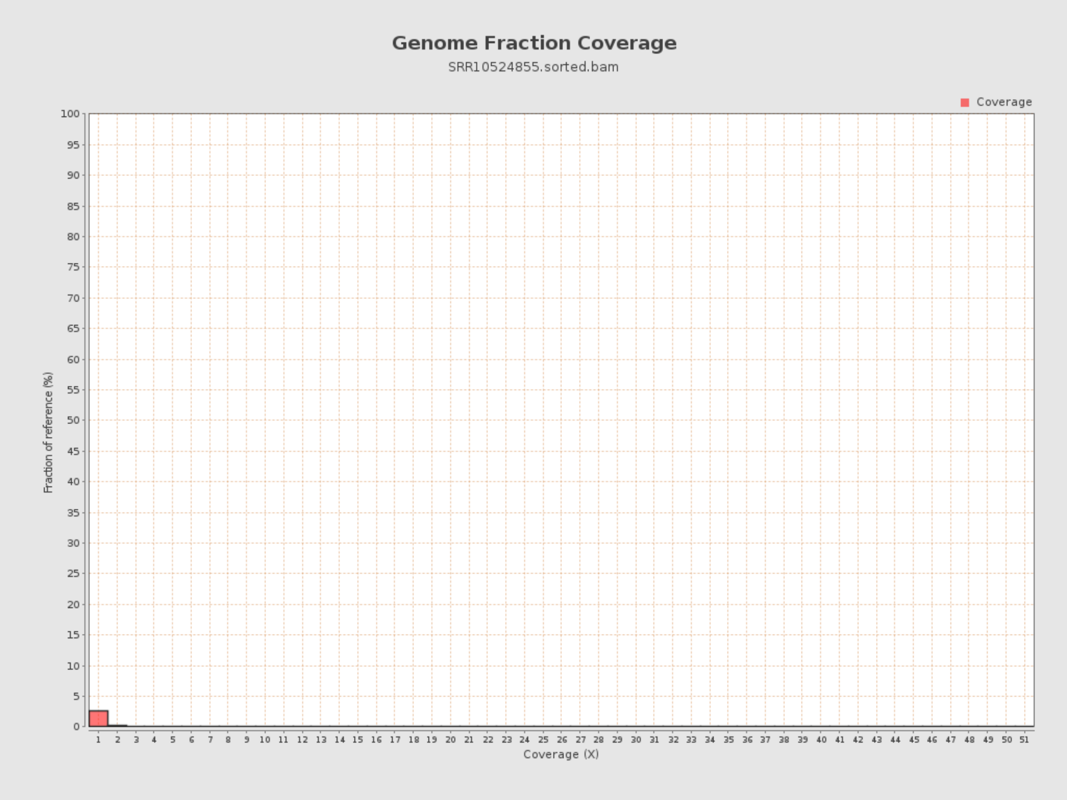
4. Results : Coverage Histogram



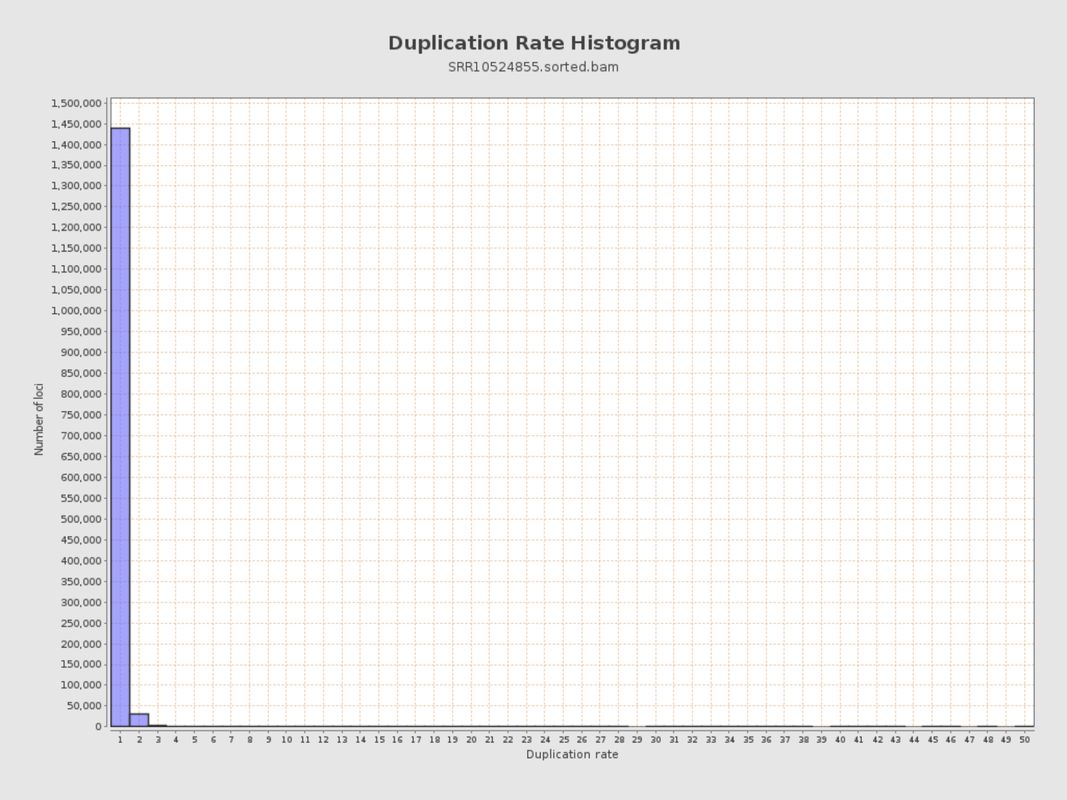
5. Results : Coverage Histogram (0-50X)



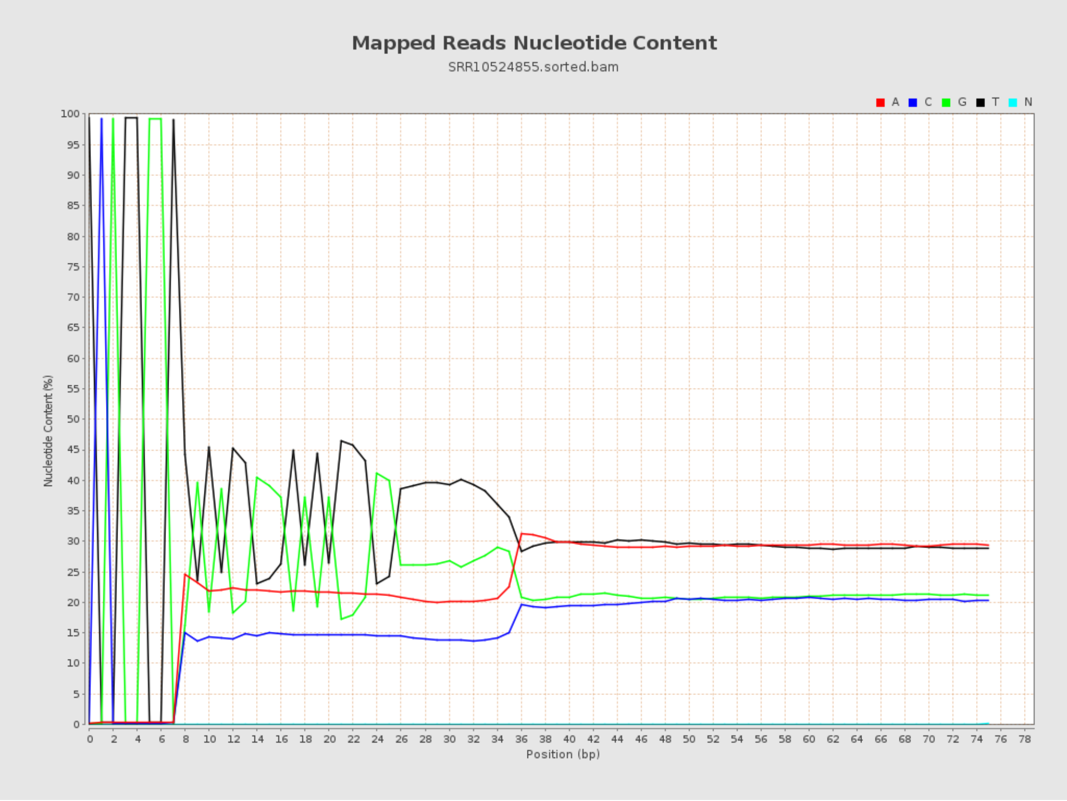
6. Results : Genome Fraction Coverage



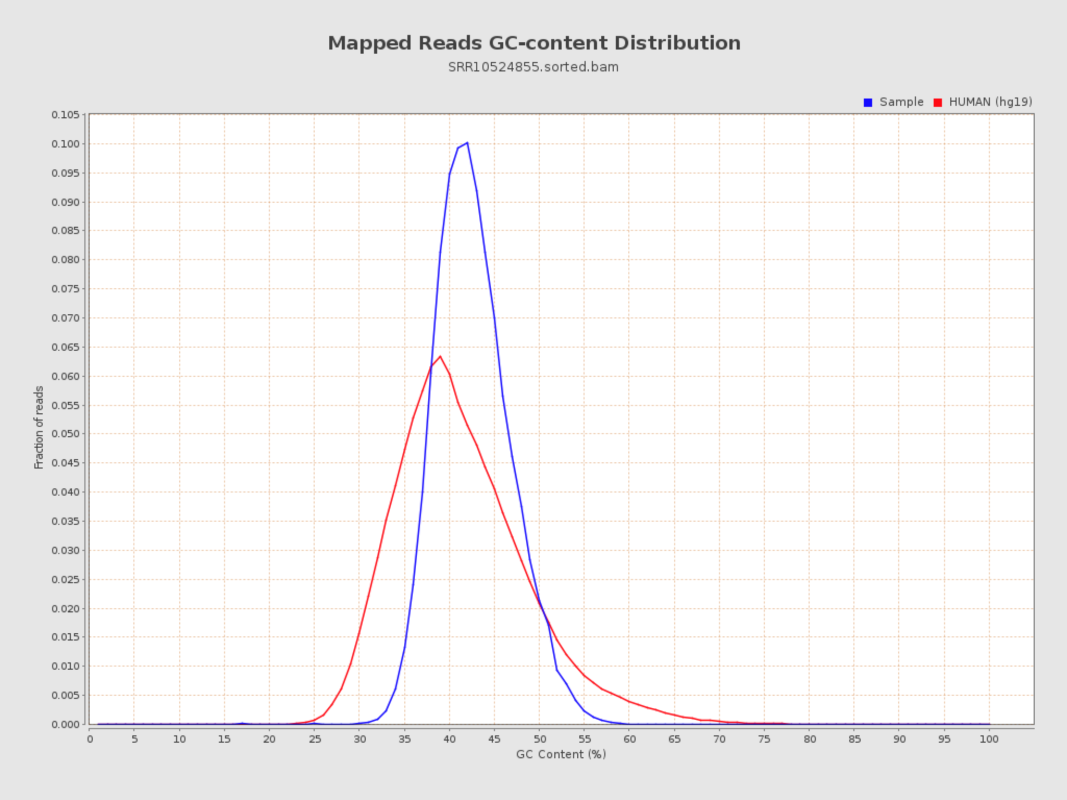
7. Results : Duplication Rate Histogram



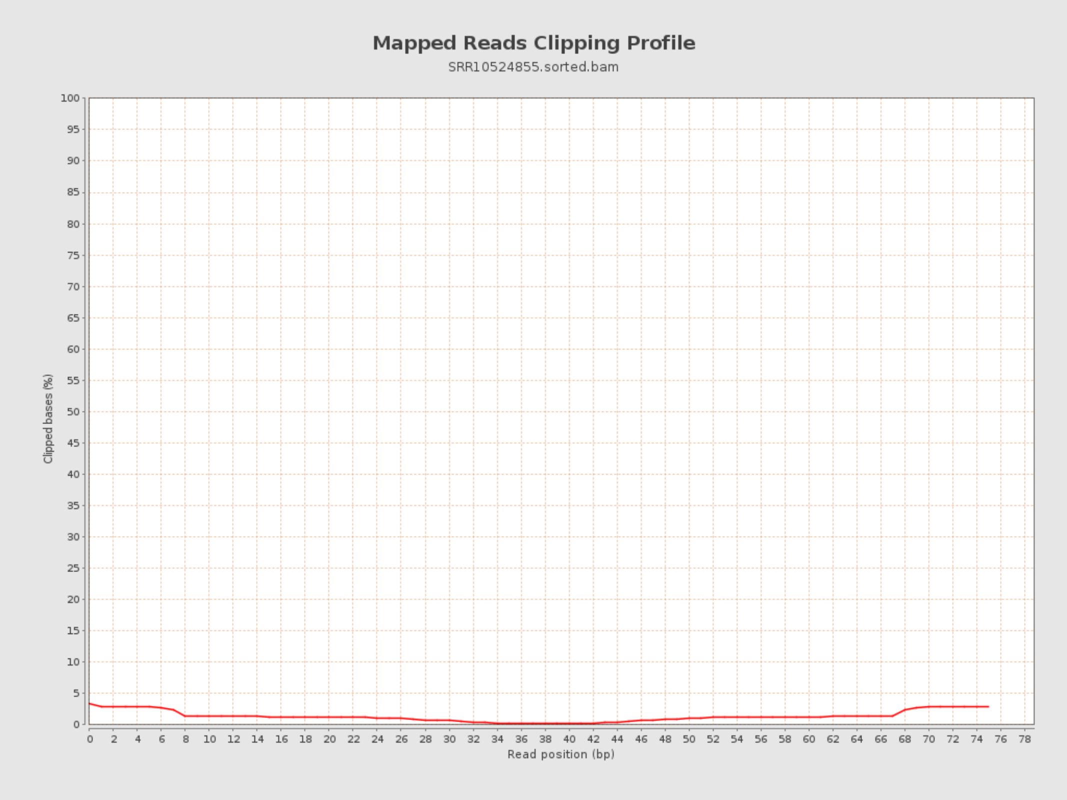
8. Results : Mapped Reads Nucleotide Content



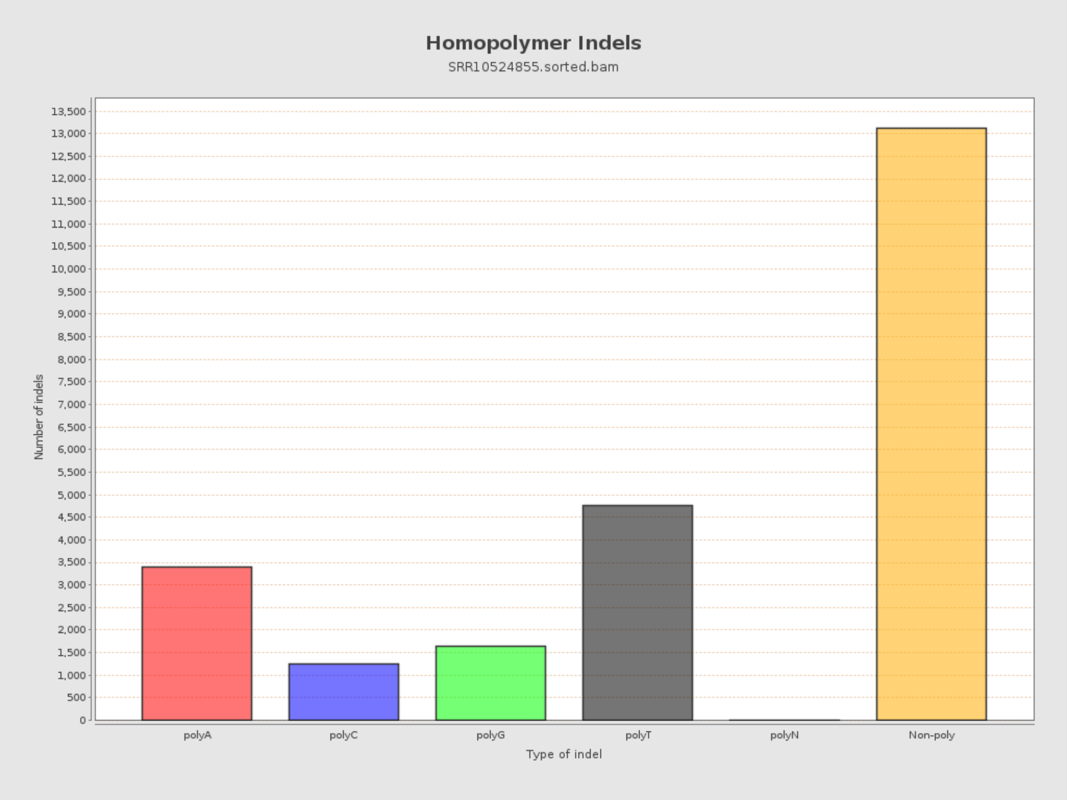
9. Results : Mapped Reads GC-content Distribution



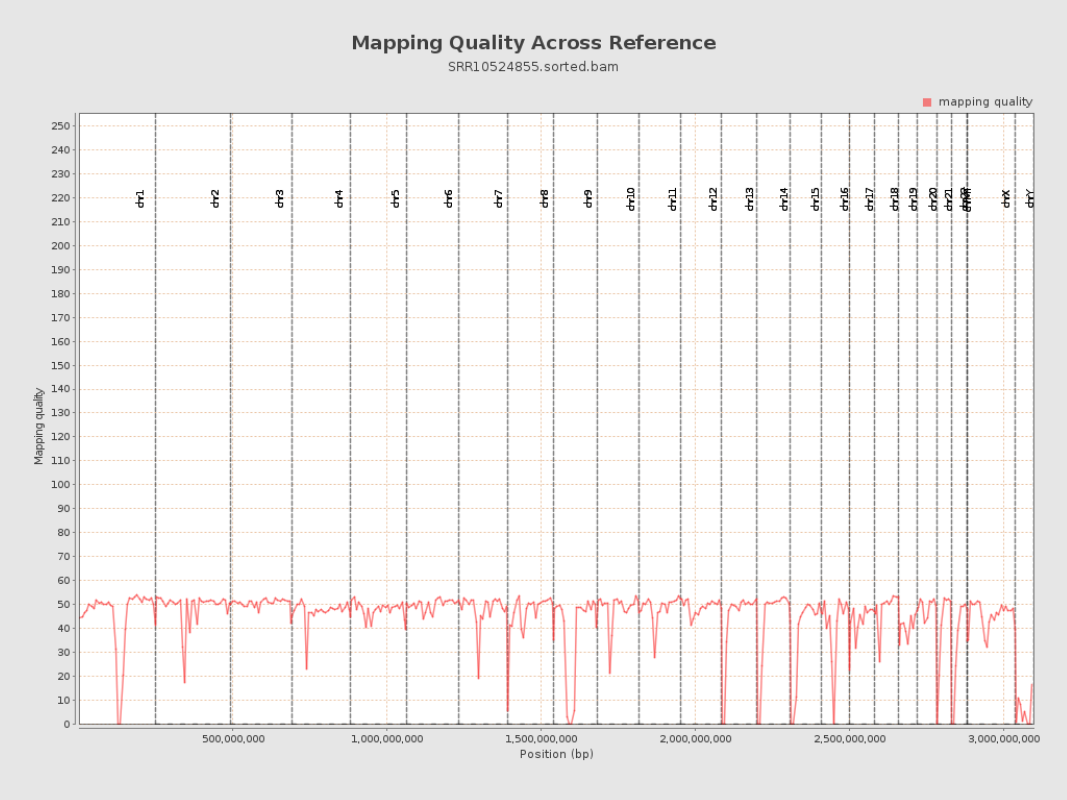
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram