Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 00:57:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524876.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_SRR10524876 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524876.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 00:57:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524876.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,026,831
Mapped reads	1,856,584 / 91.6%
Unmapped reads	170,247 / 8.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,046 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	64,332 / 3.17%
Duplication rate	2.39%
Clipped reads	1,861,038 / 91.82%

2.2. ACGT Content

Number/percentage of A's	28,370,029 / 26.29%
Number/percentage of C's	19,431,952 / 18.01%
Number/percentage of T's	35,313,542 / 32.72%
Number/percentage of G's	24,788,159 / 22.97%
Number/percentage of N's	14,388 / 0.01%
GC Percentage	40.98%

2.3. Coverage

Mean	0.0349

Standard Deviation	0.3368

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

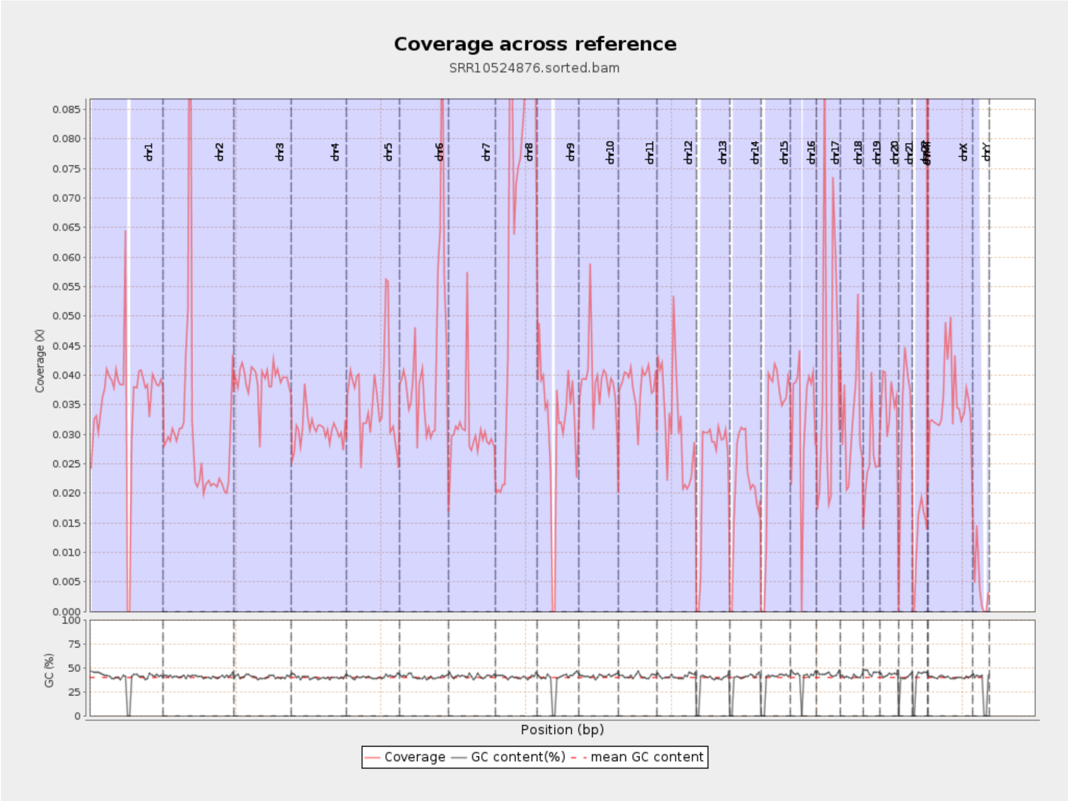
General error rate	0.5%
Mismatches	521,422
Insertions	7,933
Mapped reads with at least one insertion	0.42%
Deletions	20,560
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.51%

2.6. Chromosome stats

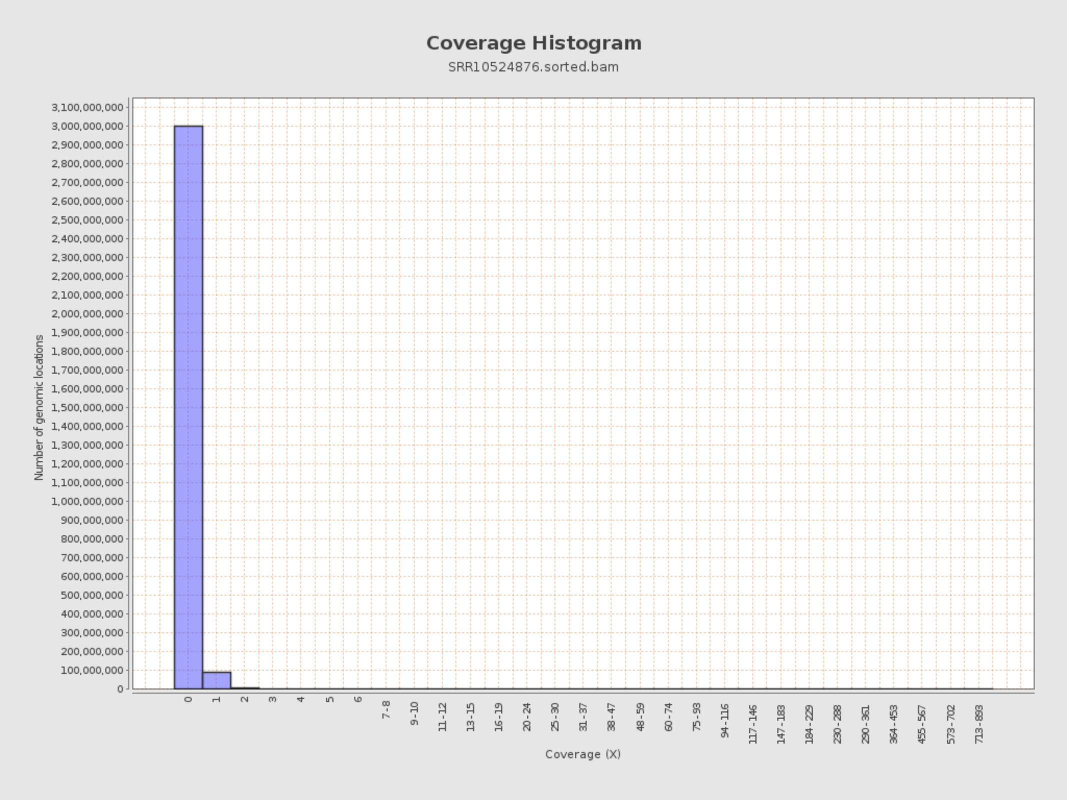
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8869010	0.0356	0.6686
chr2	243199373	7380276	0.0303	0.3852
chr3	198022430	7772895	0.0393	0.213
chr4	191154276	5866710	0.0307	0.2047
chr5	180915260	6526845	0.0361	0.2079
chr6	171115067	7220840	0.0422	0.25
chr7	159138663	4877984	0.0307	0.4329

chr8	146364022	11587011	0.0792	0.4607
chr9	141213431	4388360	0.0311	0.2754
chr10	135534747	5301590	0.0391	0.2956
chr11	135006516	5142619	0.0381	0.3013
chr12	133851895	4217912	0.0315	0.1971
chr13	115169878	2819720	0.0245	0.1687
chr14	107349540	2257333	0.021	0.1704
chr15	102531392	3172723	0.0309	0.1907
chr16	90354753	3009700	0.0333	0.2144
chr17	81195210	3279916	0.0404	0.2468
chr18	78077248	2560047	0.0328	0.5161
chr19	59128983	1531267	0.0259	0.4456
chr20	63025520	2217566	0.0352	0.2044
chr21	48129895	1532817	0.0318	0.2081
chr22	51304566	627065	0.0122	0.1218
chrMT	16571	24634	1.4866	1.4487
chrX	155270560	5505484	0.0355	0.2373
chrY	59373566	259418	0.0044	0.1155

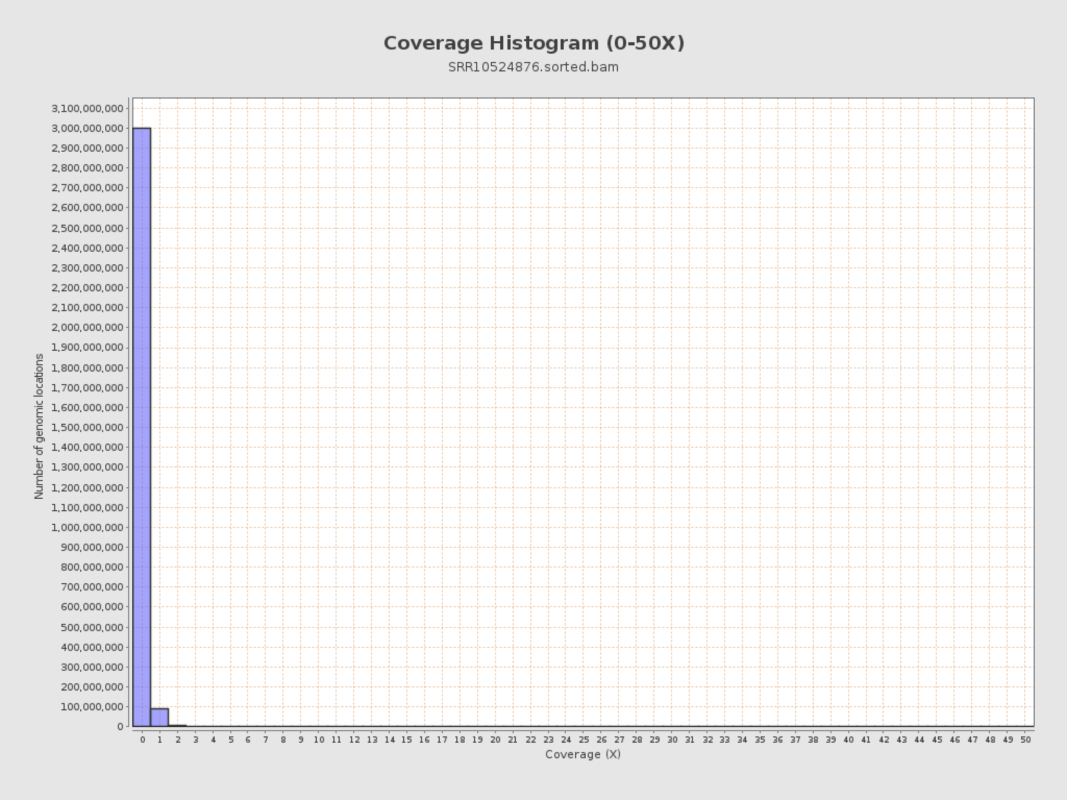
3. Results : Coverage across reference



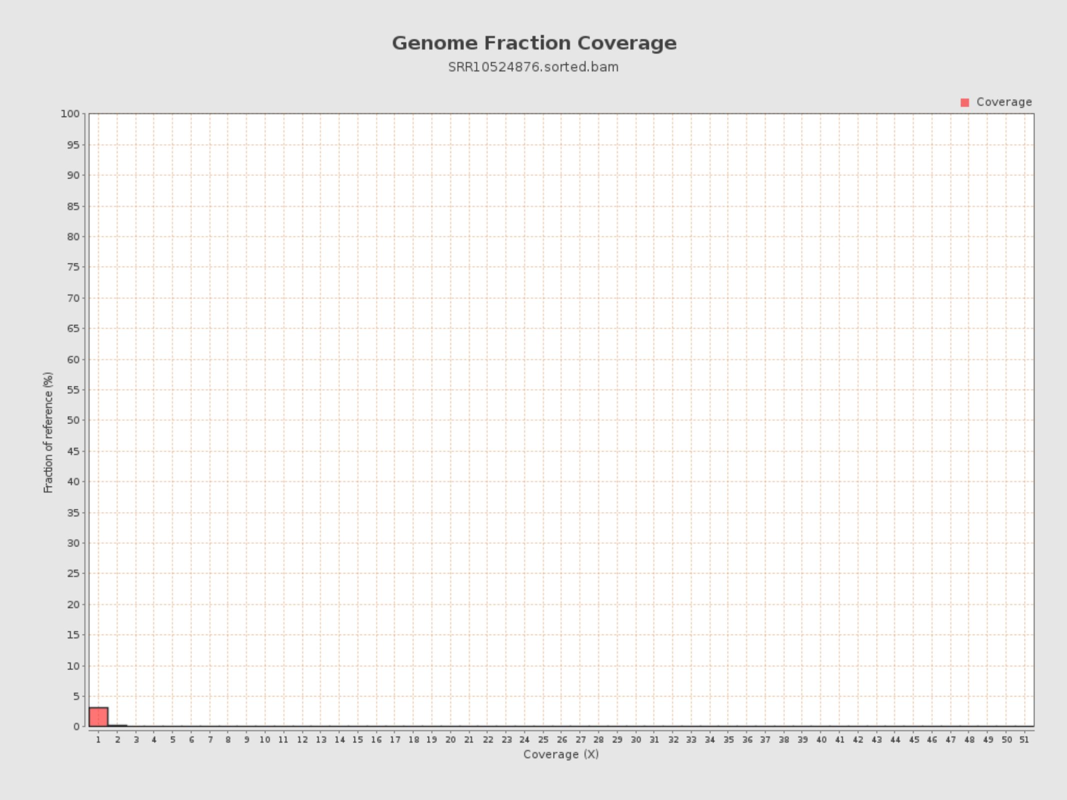
4. Results : Coverage Histogram



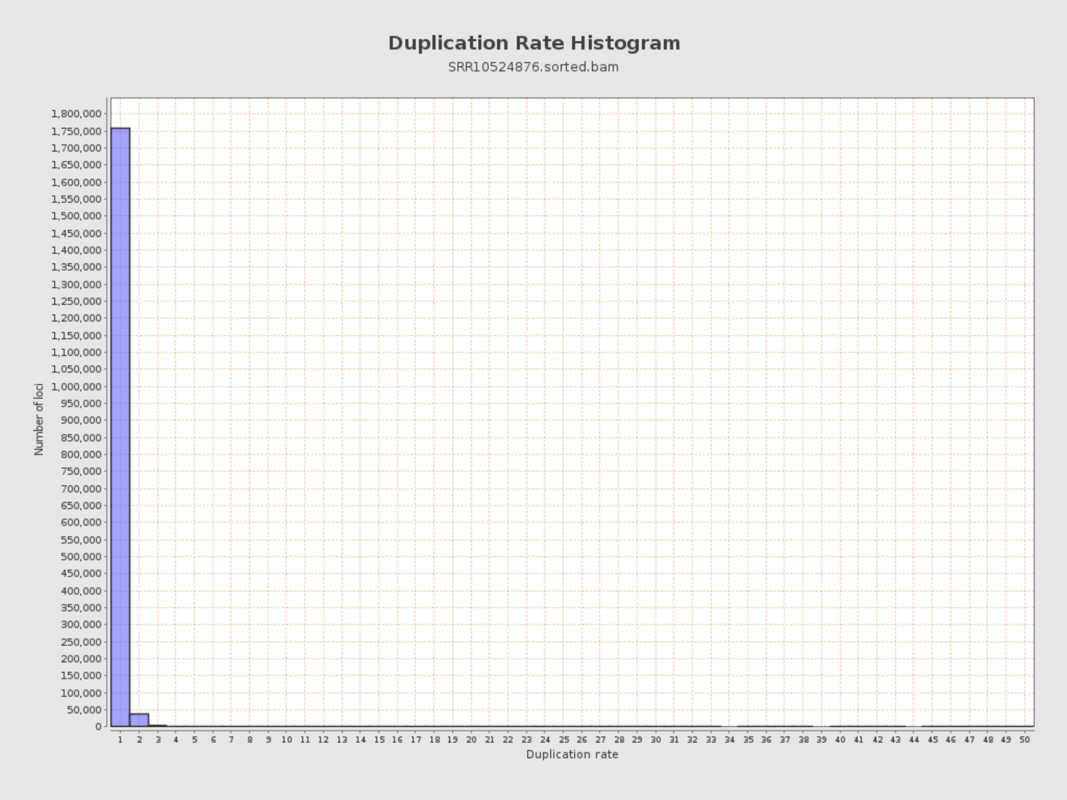
5. Results : Coverage Histogram (0-50X)



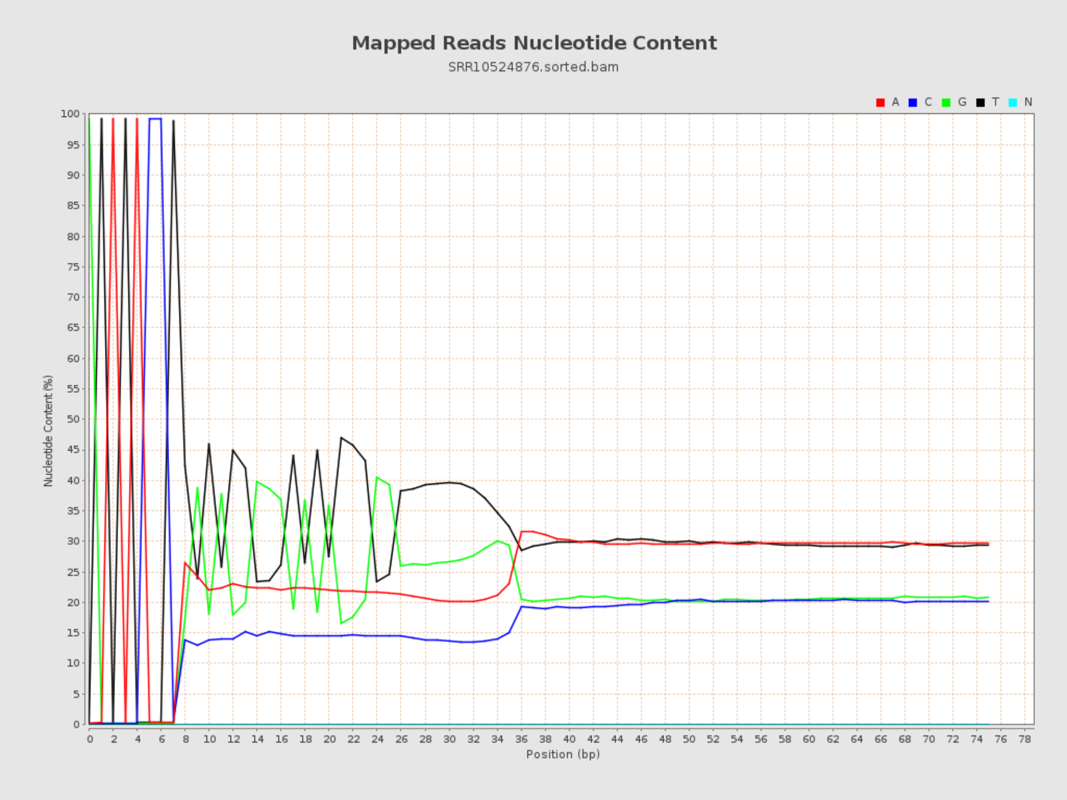
6. Results : Genome Fraction Coverage



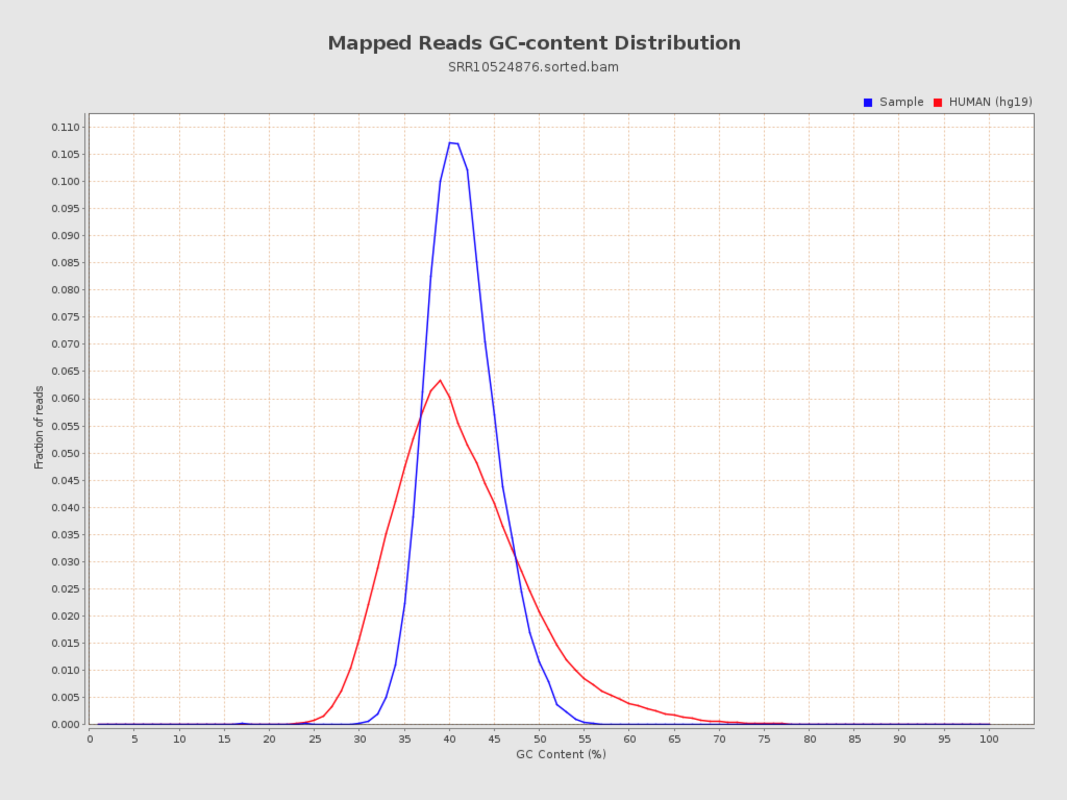
7. Results : Duplication Rate Histogram



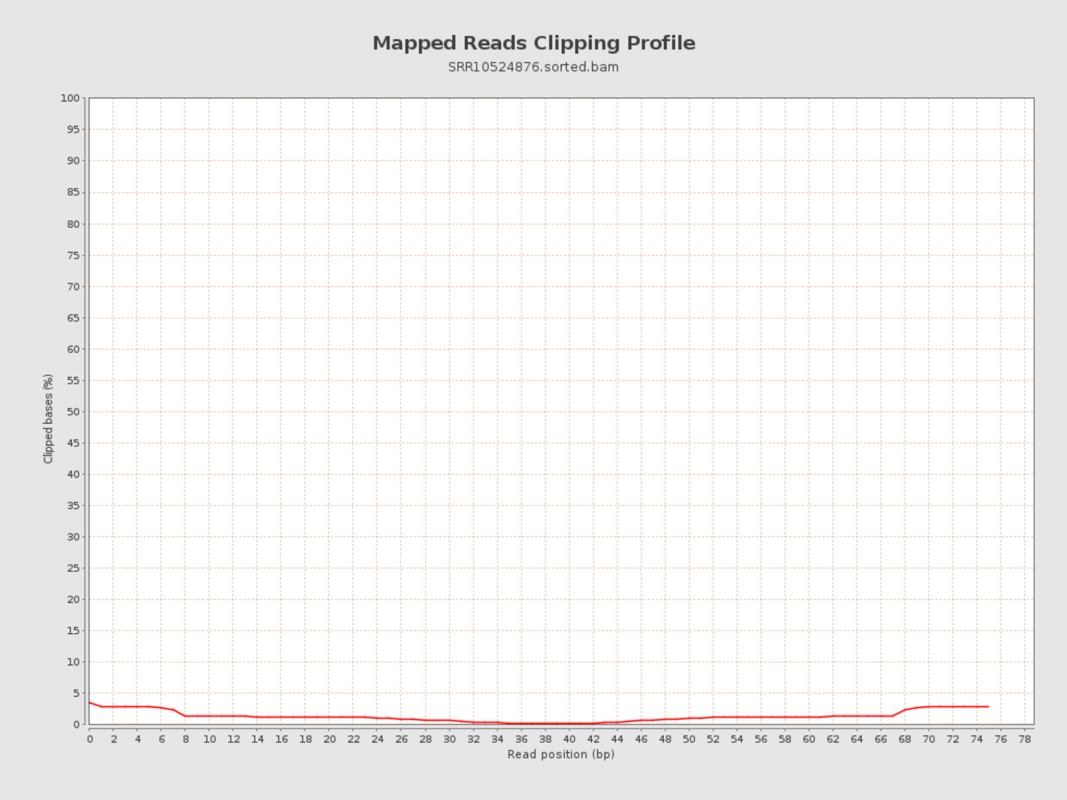
8. Results : Mapped Reads Nucleotide Content



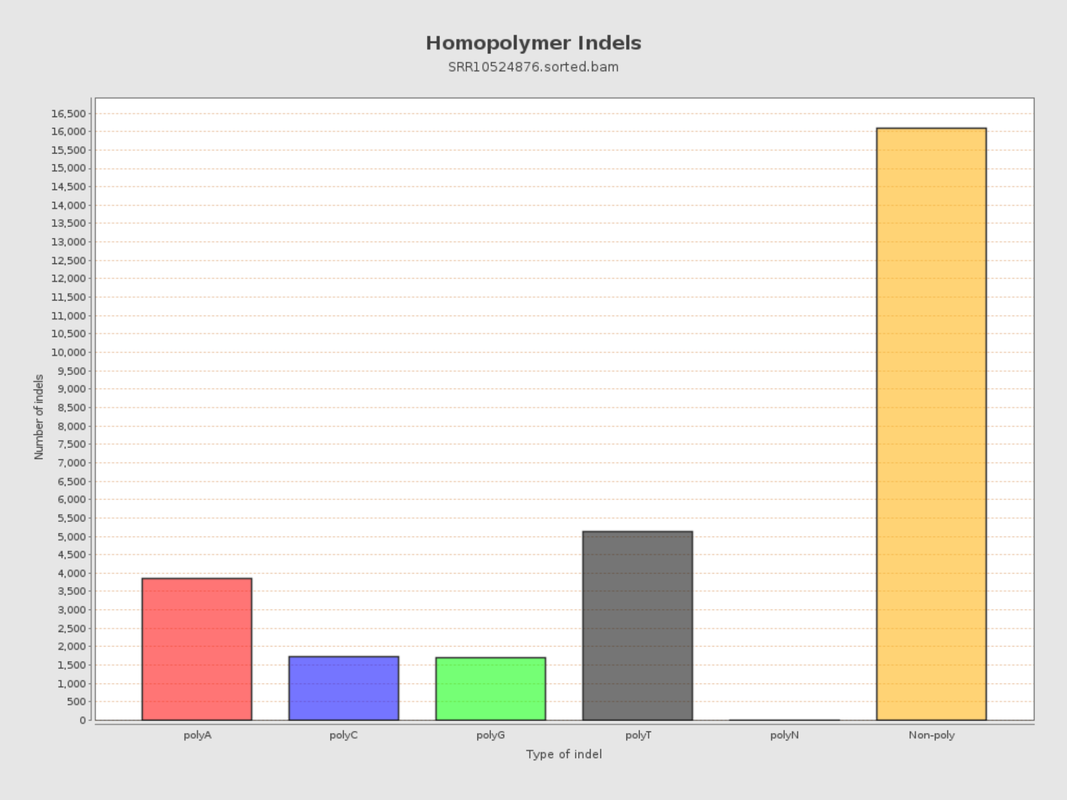
9. Results : Mapped Reads GC-content Distribution



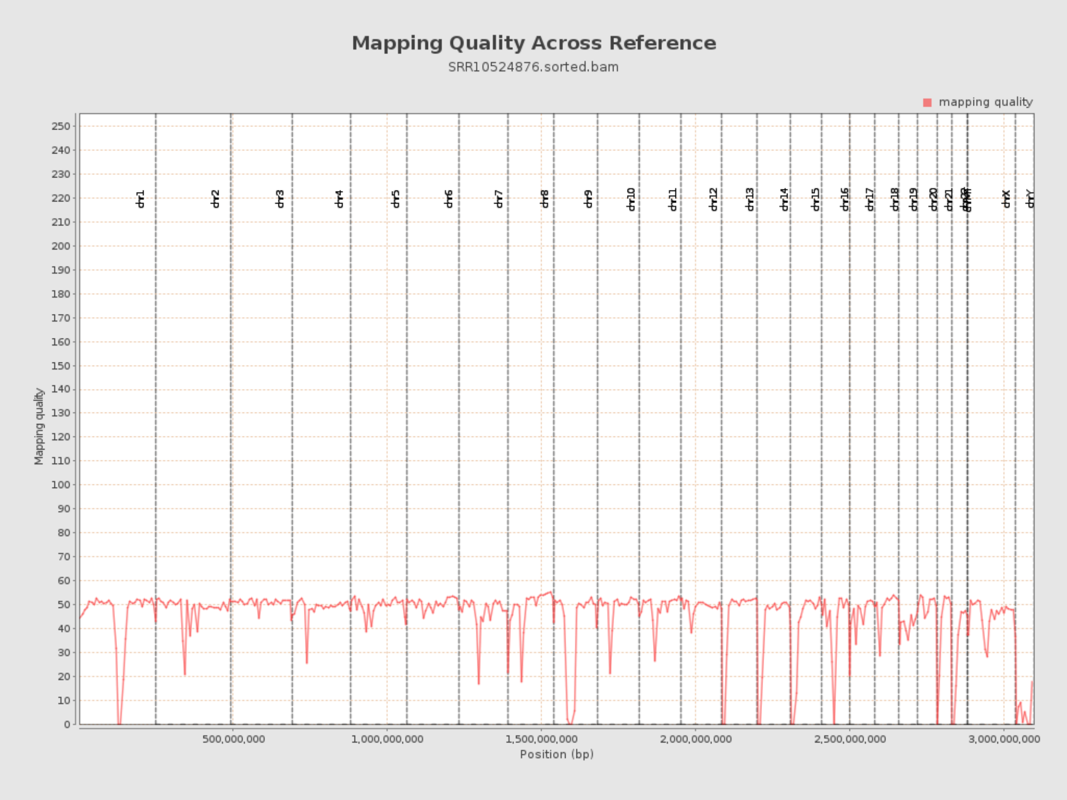
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram