Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 06:59:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524935.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_SRR10524935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 06:59:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,518,867
Mapped reads	2,329,822 / 92.49%
Unmapped reads	189,045 / 7.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,922 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	154,340 / 6.13%
Duplication rate	5.04%
Clipped reads	2,338,198 / 92.83%

2.2. ACGT Content

Number/percentage of A's	32,479,006 / 23.92%
Number/percentage of C's	26,561,983 / 19.56%
Number/percentage of T's	42,474,664 / 31.28%
Number/percentage of G's	34,283,355 / 25.25%
Number/percentage of N's	1,037 / 0%
GC Percentage	44.81%

2.3. Coverage

Mean	0.0439

Standard Deviation	0.3836

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

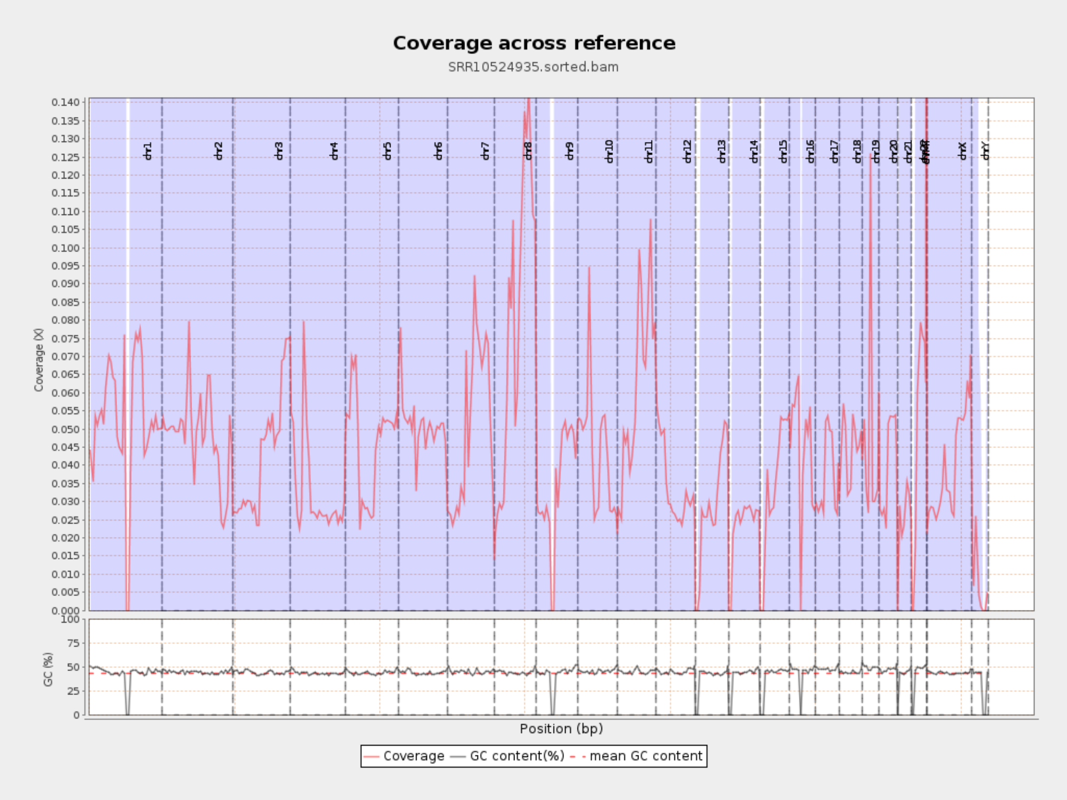
General error rate	0.51%
Mismatches	671,729
Insertions	7,616
Mapped reads with at least one insertion	0.33%
Deletions	25,486
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.4%

2.6. Chromosome stats

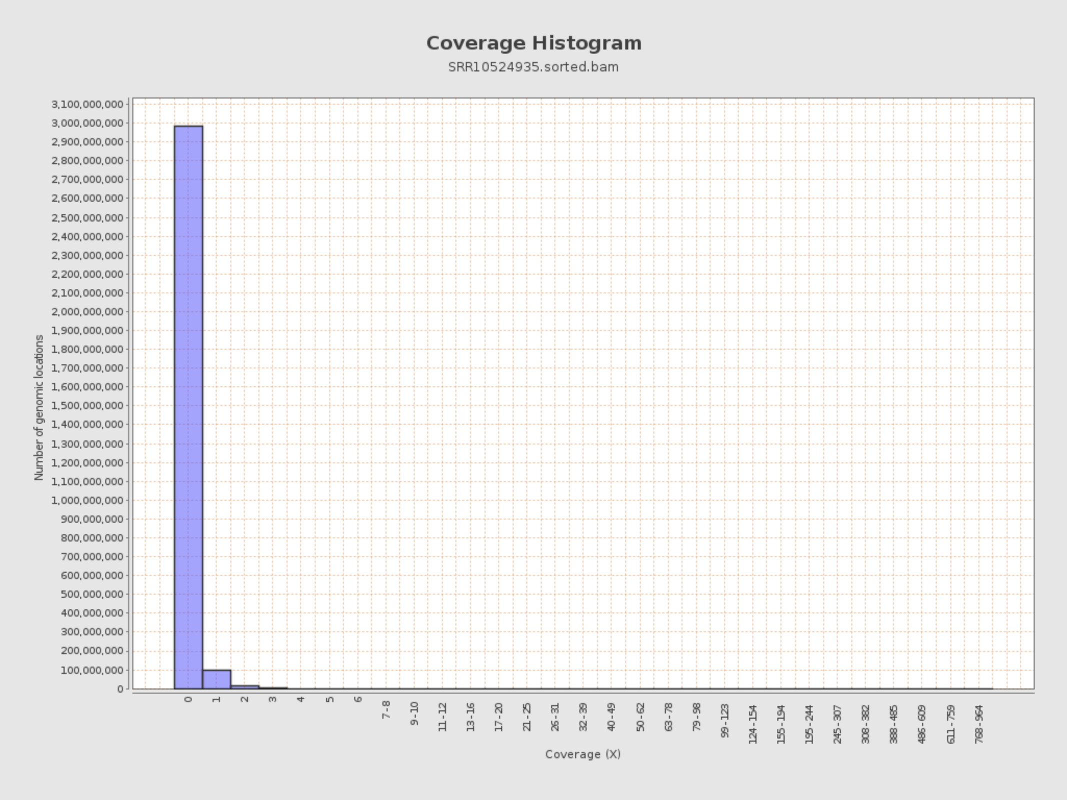
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13107254	0.0526	0.7379
chr2	243199373	11801573	0.0485	0.4616
chr3	198022430	8437458	0.0426	0.2422
chr4	191154276	6176074	0.0323	0.2755
chr5	180915260	8361856	0.0462	0.2488
chr6	171115067	8788705	0.0514	0.2871
chr7	159138663	8193028	0.0515	0.4797

chr8	146364022	11870222	0.0811	0.4857
chr9	141213431	4777241	0.0338	0.2981
chr10	135534747	5959287	0.044	0.4266
chr11	135006516	8385476	0.0621	0.353
chr12	133851895	4519447	0.0338	0.2234
chr13	115169878	3298038	0.0286	0.2009
chr14	107349540	2483925	0.0231	0.1887
chr15	102531392	3500127	0.0341	0.2155
chr16	90354753	4037418	0.0447	0.2674
chr17	81195210	3047101	0.0375	0.2361
chr18	78077248	3541557	0.0454	0.5168
chr19	59128983	2817327	0.0476	0.5026
chr20	63025520	2537365	0.0403	0.2465
chr21	48129895	1210681	0.0252	0.234
chr22	51304566	2500363	0.0487	0.2589
chrMT	16571	7347	0.4434	0.8074
chrX	155270560	6091351	0.0392	0.2649
chrY	59373566	392752	0.0066	0.2327

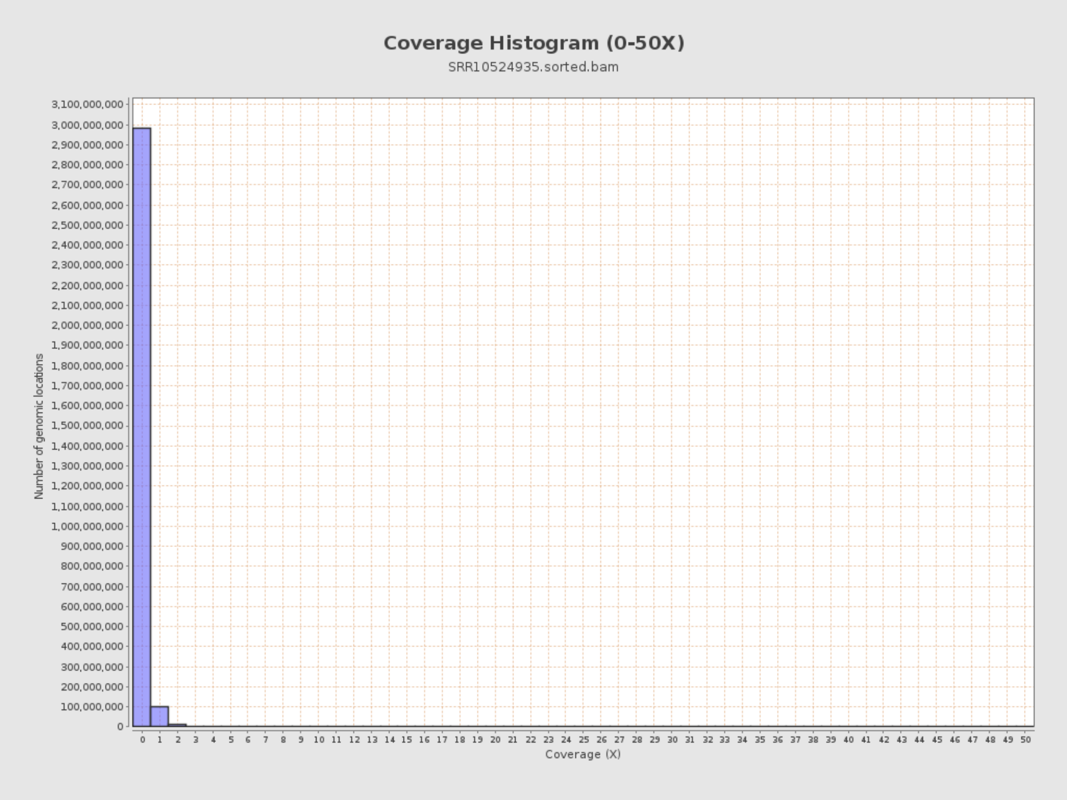
3. Results : Coverage across reference



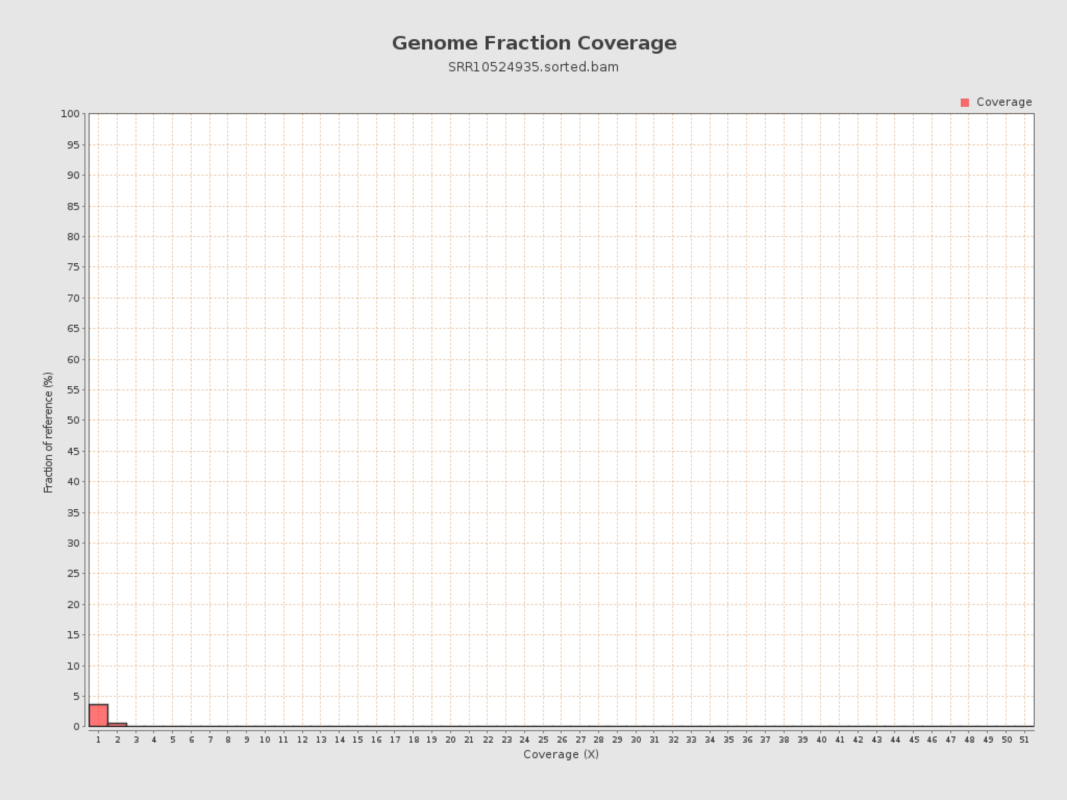
4. Results : Coverage Histogram



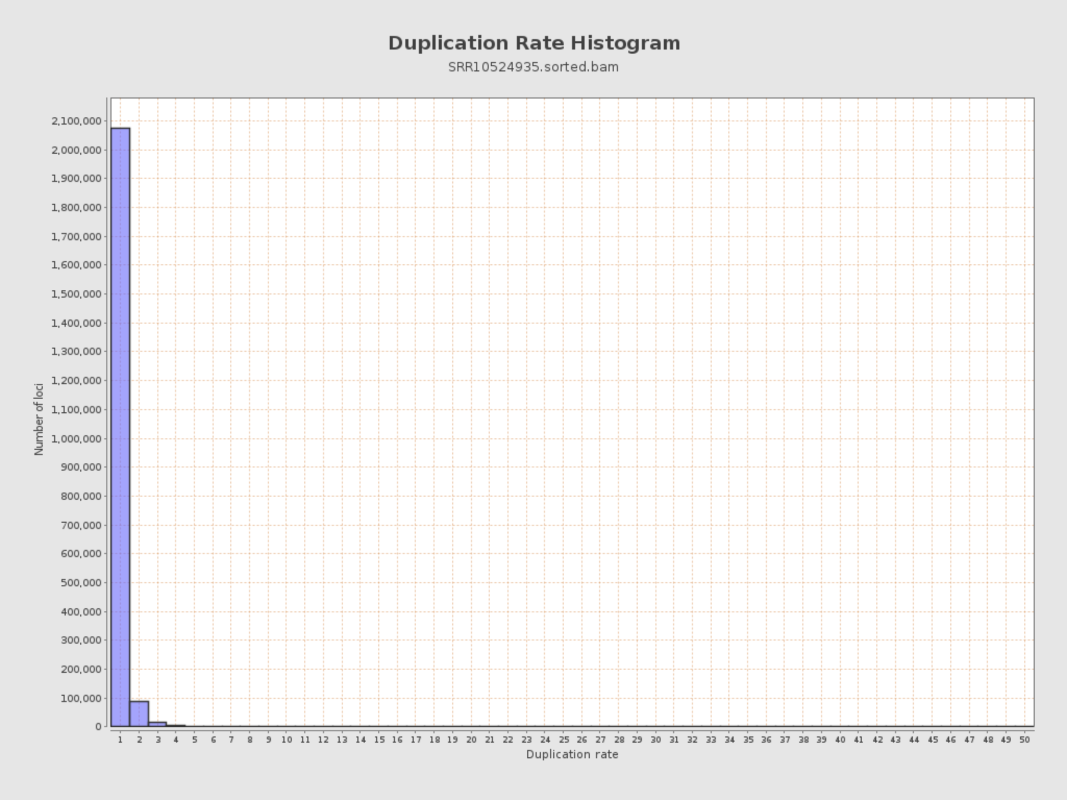
5. Results : Coverage Histogram (0-50X)



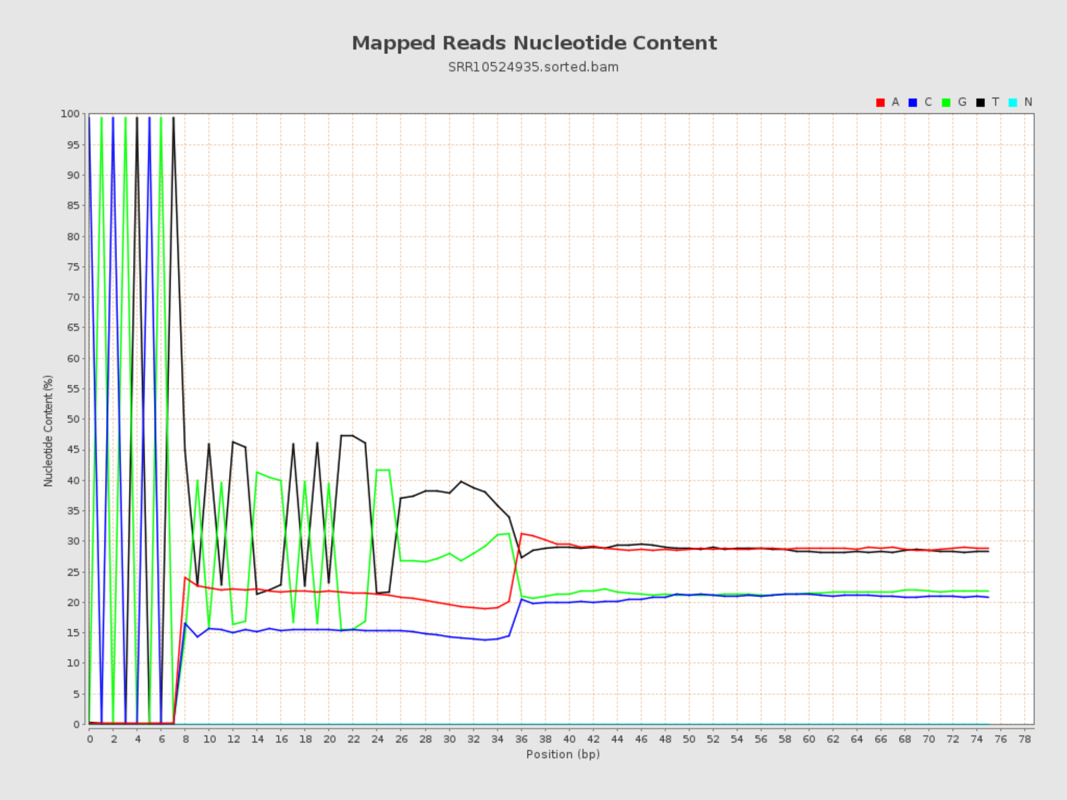
6. Results : Genome Fraction Coverage



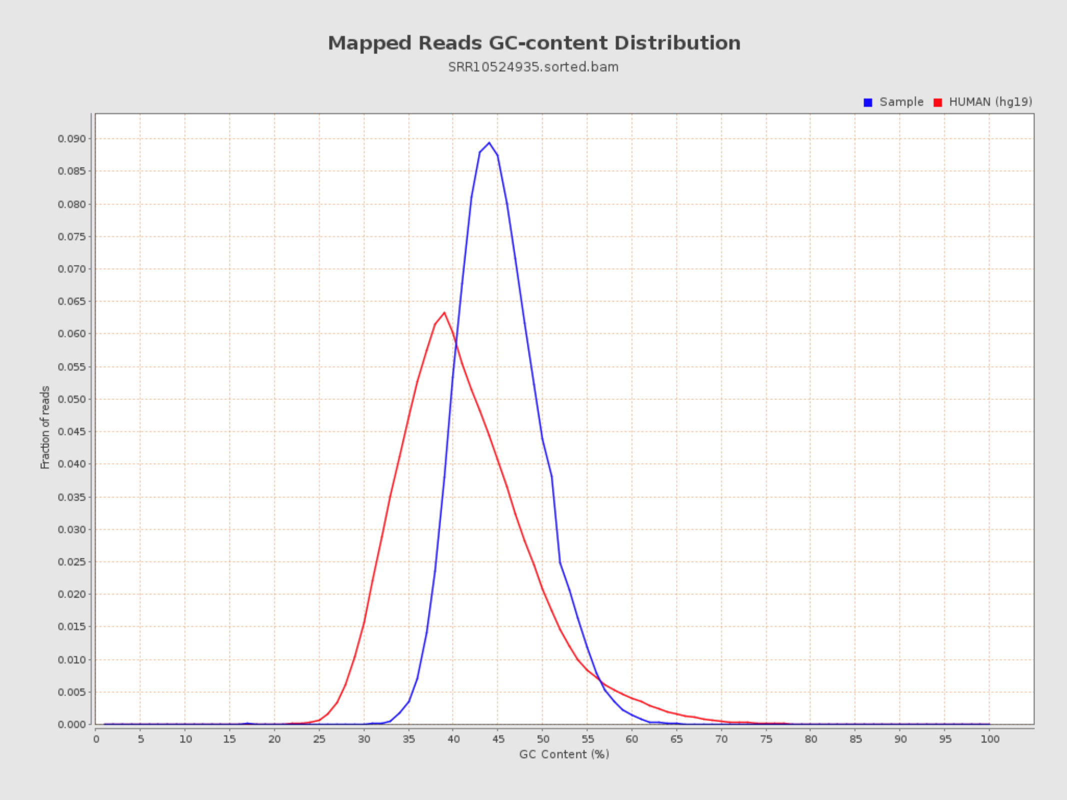
7. Results : Duplication Rate Histogram



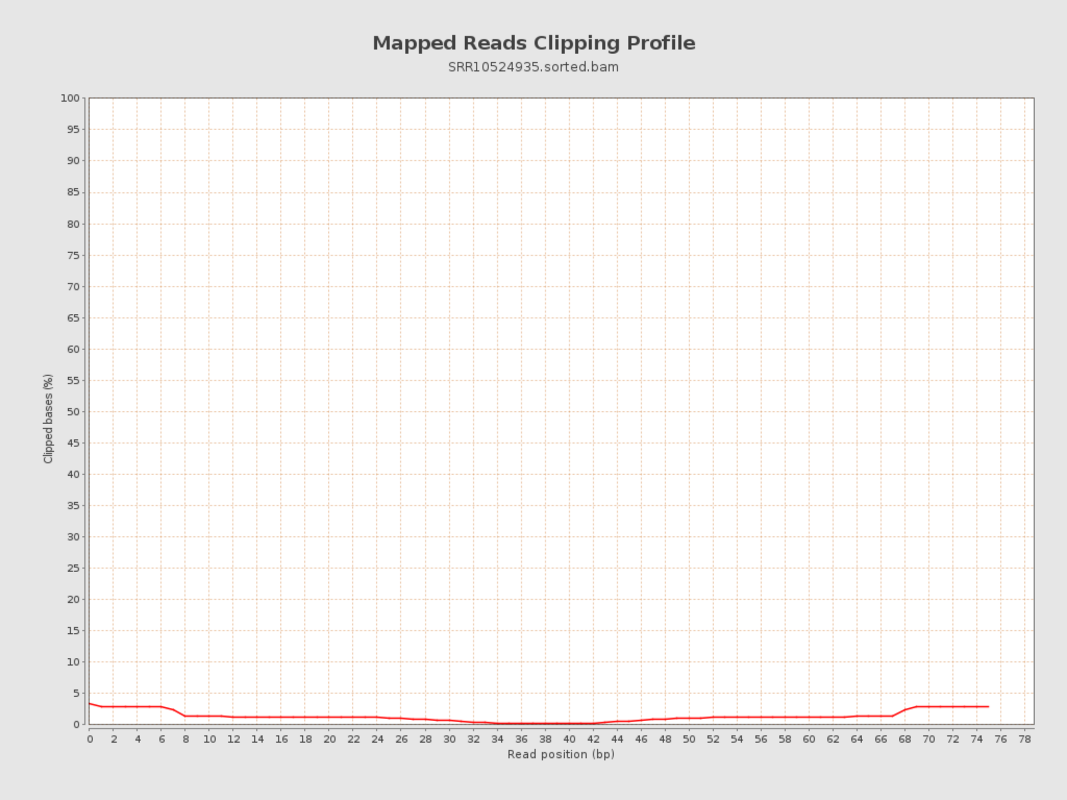
8. Results : Mapped Reads Nucleotide Content



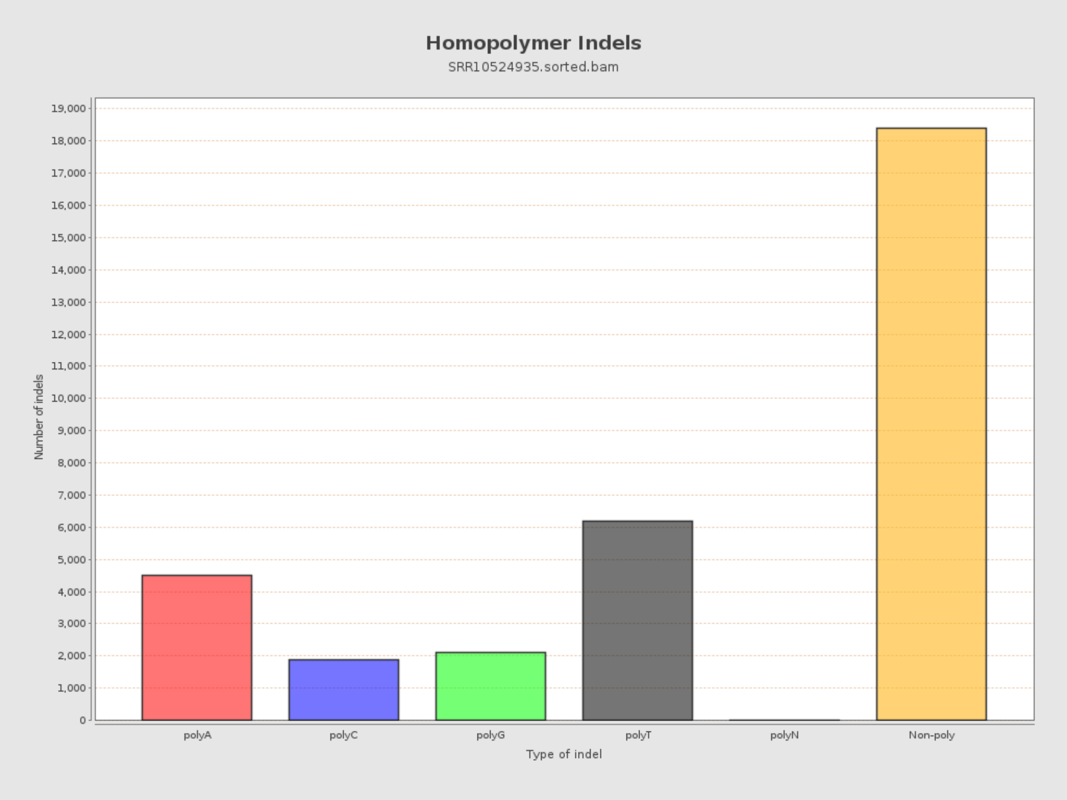
9. Results : Mapped Reads GC-content Distribution



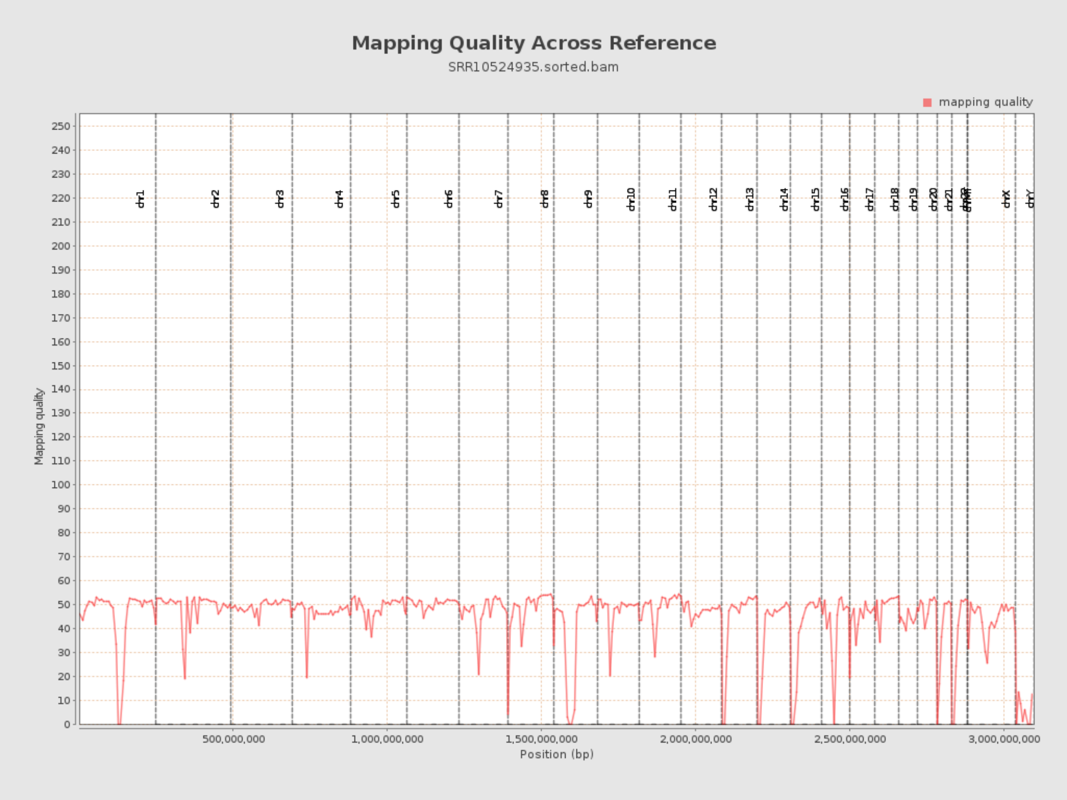
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram