Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:34:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524862.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_SRR10524862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:34:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,199,913
Mapped reads	2,021,003 / 91.87%
Unmapped reads	178,910 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,852 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	69,544 / 3.16%
Duplication rate	2.32%
Clipped reads	2,025,865 / 92.09%

2.2. ACGT Content

Number/percentage of A's	31,043,171 / 26.33%
Number/percentage of C's	22,416,768 / 19.01%
Number/percentage of T's	37,384,747 / 31.7%
Number/percentage of G's	27,060,470 / 22.95%
Number/percentage of N's	15,014 / 0.01%
GC Percentage	41.96%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.362

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

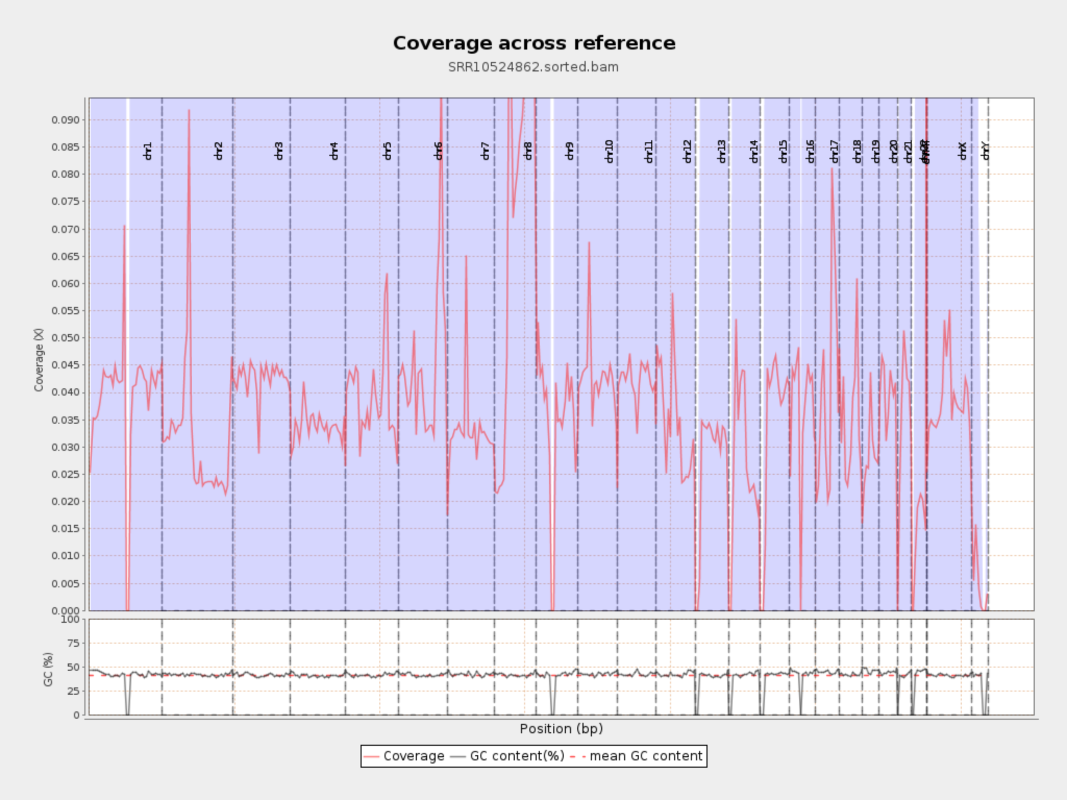
General error rate	0.49%
Mismatches	565,717
Insertions	8,541
Mapped reads with at least one insertion	0.42%
Deletions	21,978
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.97%

2.6. Chromosome stats

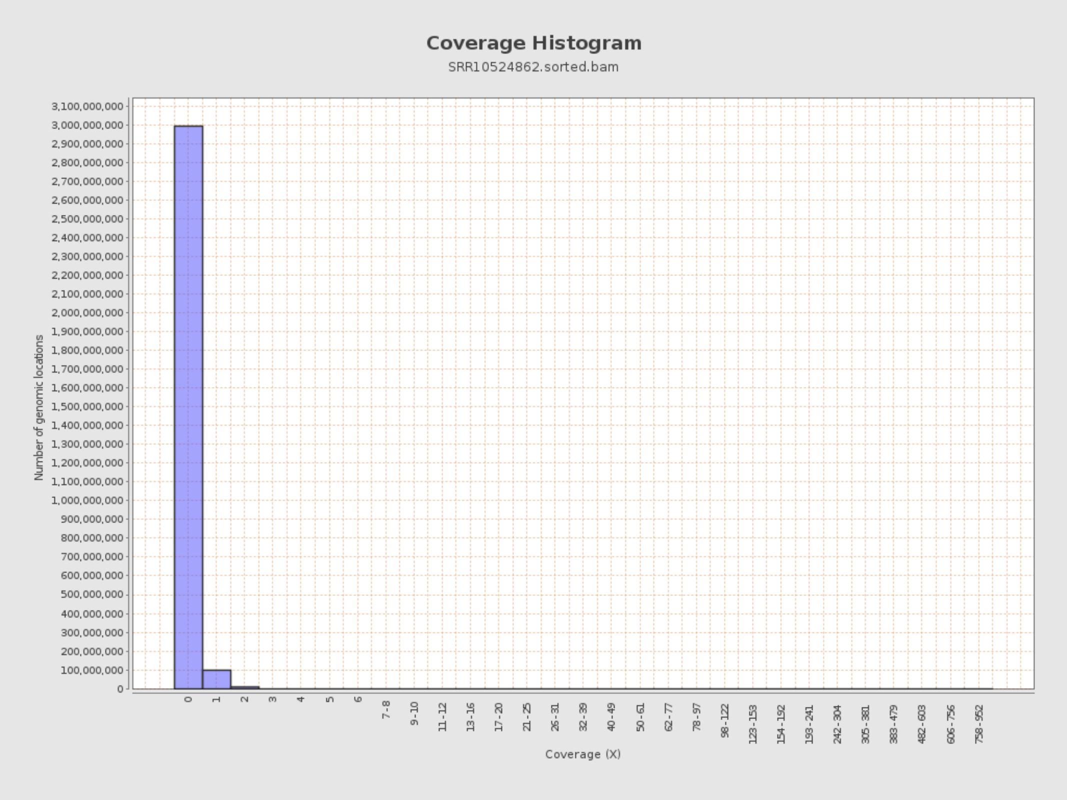
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9745740	0.0391	0.7089
chr2	243199373	7668666	0.0315	0.3778
chr3	198022430	8443468	0.0426	0.2245
chr4	191154276	6451093	0.0337	0.217
chr5	180915260	7130101	0.0394	0.2191
chr6	171115067	7728163	0.0452	0.2631
chr7	159138663	5336368	0.0335	0.5159

chr8	146364022	12704451	0.0868	0.4776
chr9	141213431	4880703	0.0346	0.3084
chr10	135534747	5846091	0.0431	0.3289
chr11	135006516	5658640	0.0419	0.3309
chr12	133851895	4650144	0.0347	0.2076
chr13	115169878	3122043	0.0271	0.1793
chr14	107349540	2883868	0.0269	0.1966
chr15	102531392	3467818	0.0338	0.2014
chr16	90354753	3350582	0.0371	0.2343
chr17	81195210	3238772	0.0399	0.251
chr18	78077248	2798281	0.0358	0.6191
chr19	59128983	1704185	0.0288	0.4623
chr20	63025520	2491514	0.0395	0.2201
chr21	48129895	1688079	0.0351	0.2217
chr22	51304566	709373	0.0138	0.1266
chrMT	16571	4440	0.2679	0.5268
chrX	155270560	5967380	0.0384	0.2493
chrY	59373566	284688	0.0048	0.1142

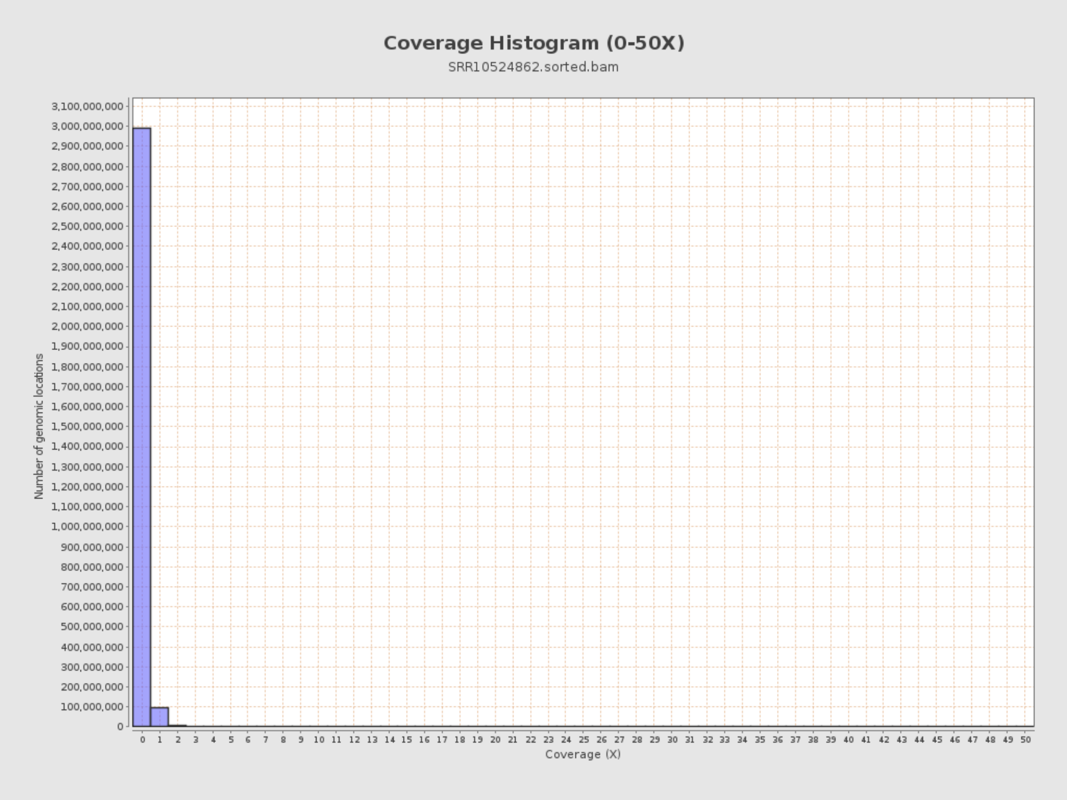
3. Results : Coverage across reference



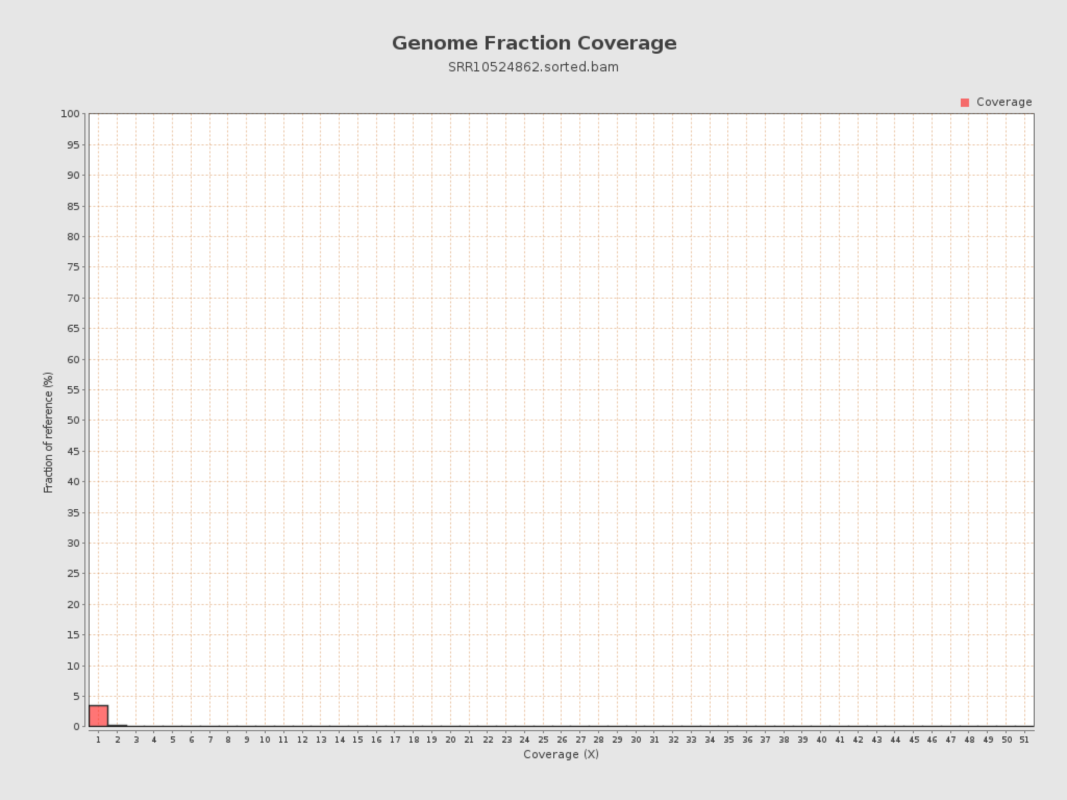
4. Results : Coverage Histogram



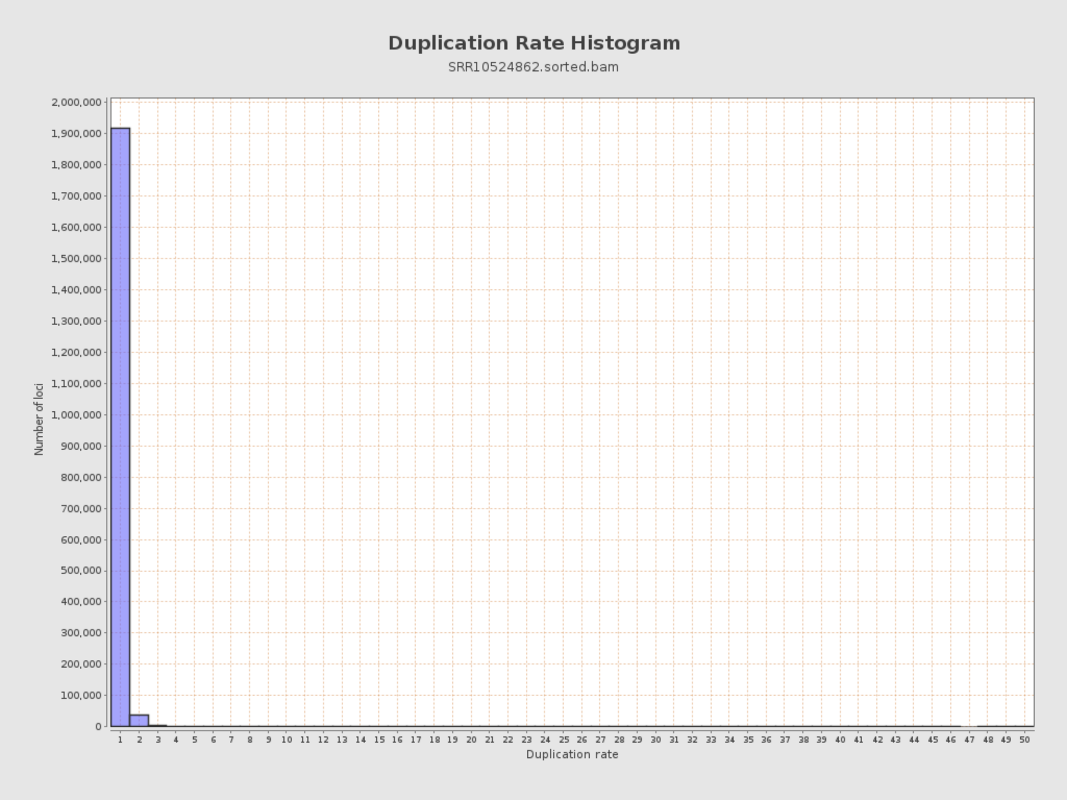
5. Results : Coverage Histogram (0-50X)



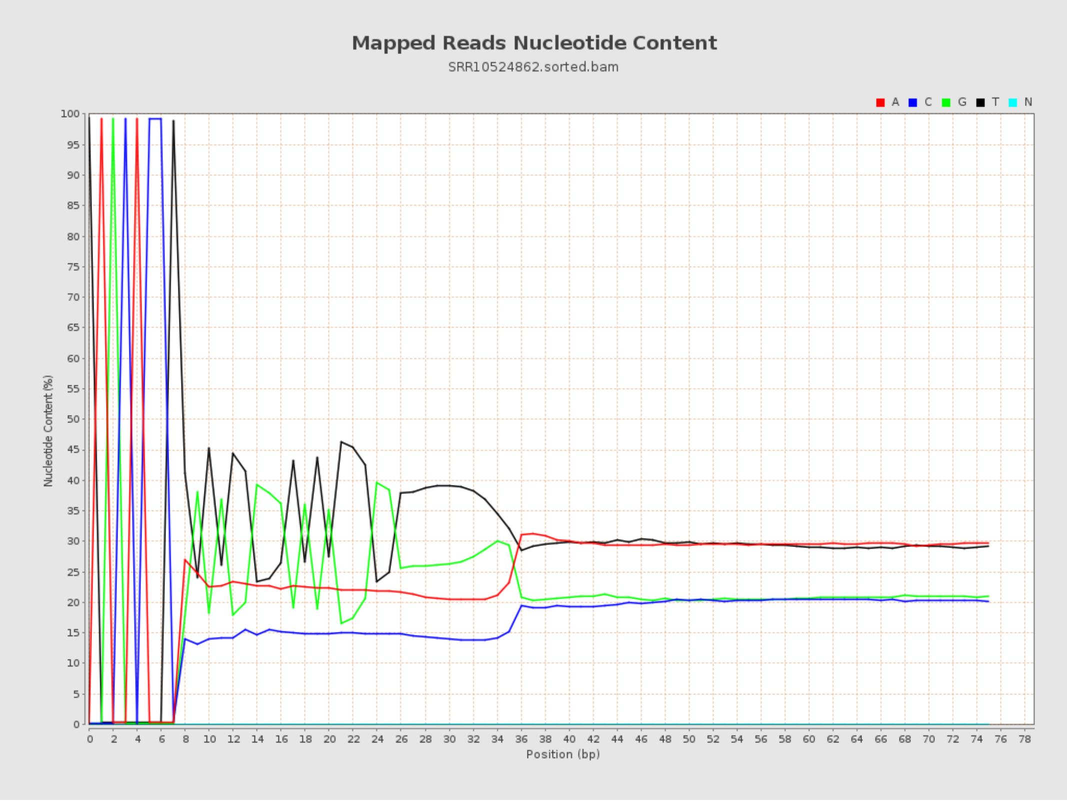
6. Results : Genome Fraction Coverage



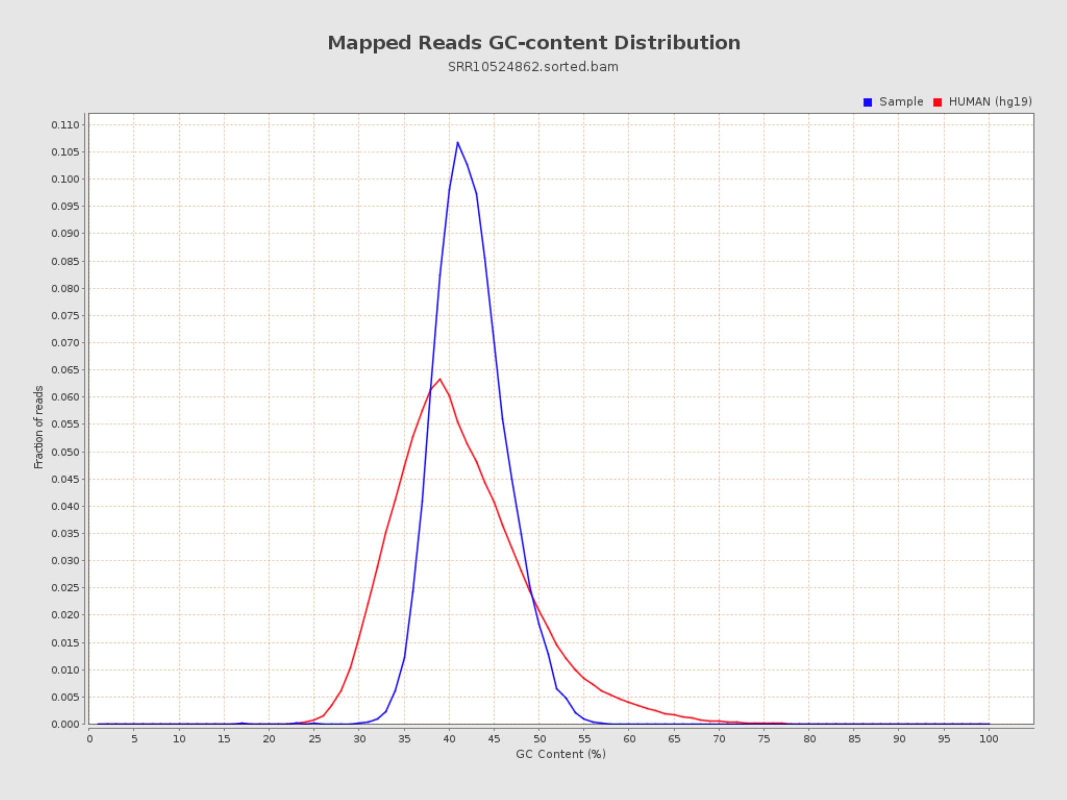
7. Results : Duplication Rate Histogram



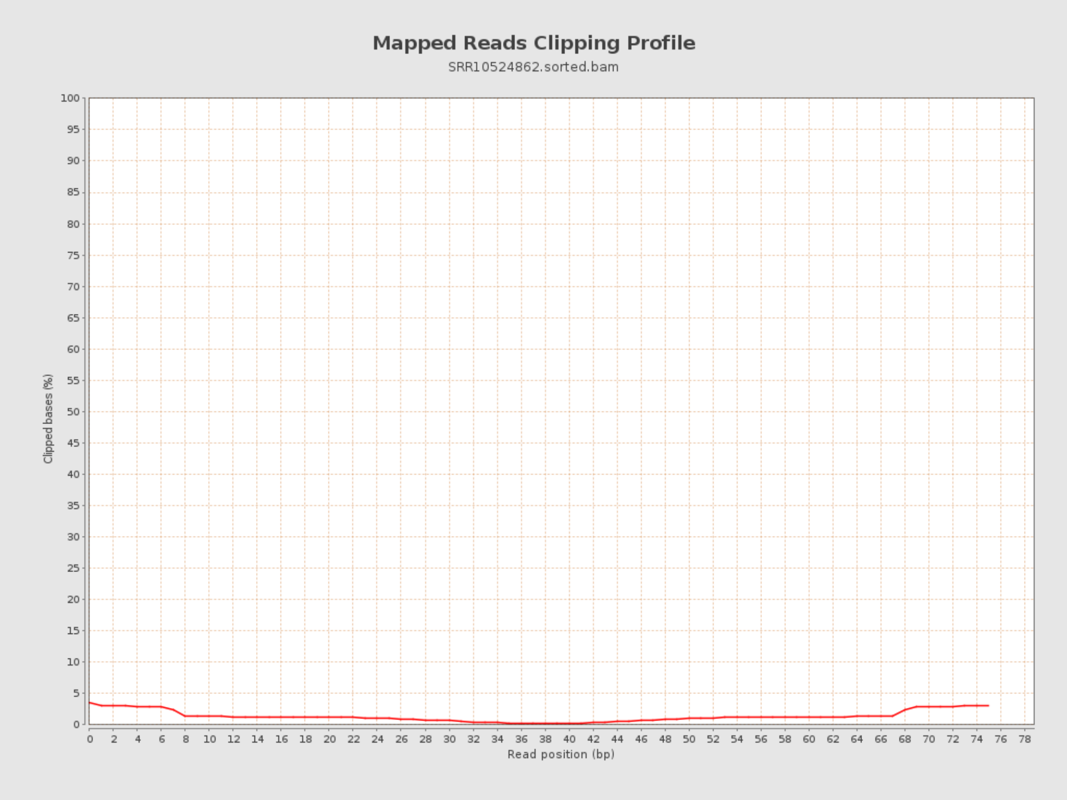
8. Results : Mapped Reads Nucleotide Content



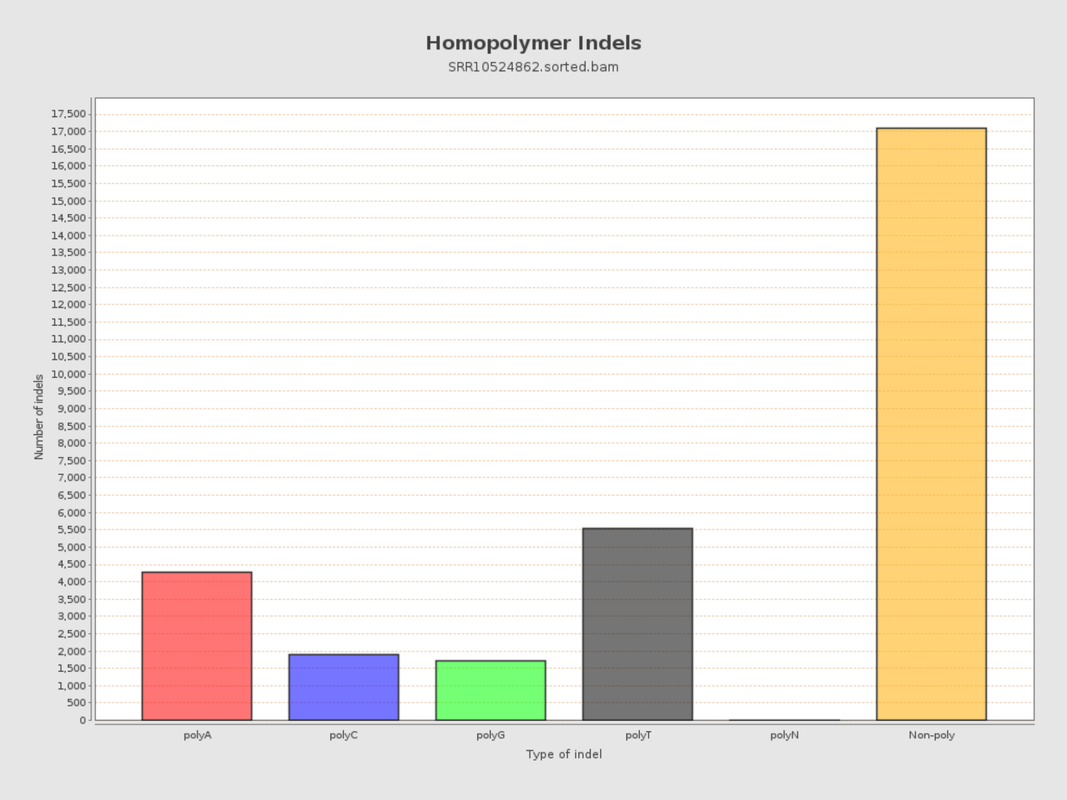
9. Results : Mapped Reads GC-content Distribution



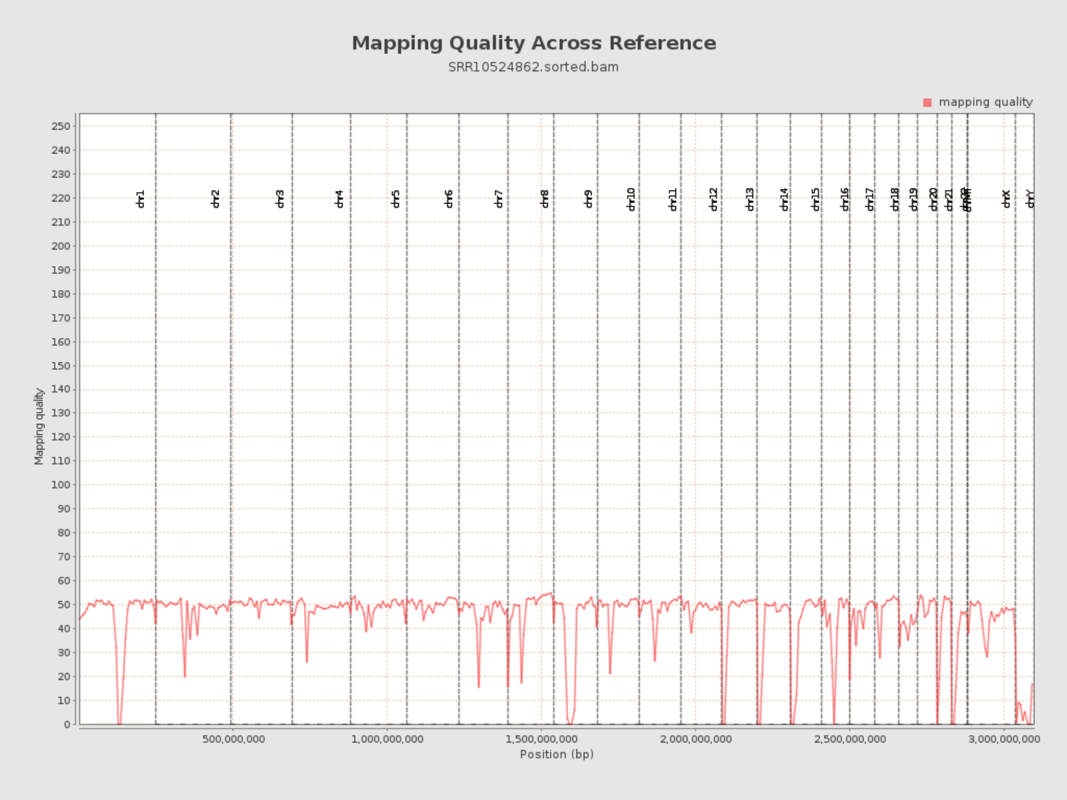
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram