Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:30:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524577.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_SRR10524577 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524577.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:30:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524577.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,333,597
Mapped reads	2,144,463 / 91.9%
Unmapped reads	189,134 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,076 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	80,115 / 3.43%
Duplication rate	2.72%
Clipped reads	2,150,272 / 92.14%

2.2. ACGT Content

Number/percentage of A's	31,821,334 / 25.48%
Number/percentage of C's	23,747,126 / 19.02%
Number/percentage of T's	39,473,567 / 31.61%
Number/percentage of G's	29,826,447 / 23.89%
Number/percentage of N's	3,893 / 0%
GC Percentage	42.9%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.3401

2.4. Mapping Quality

Mean Mapping Quality	45.64

2.5. Mismatches and indels

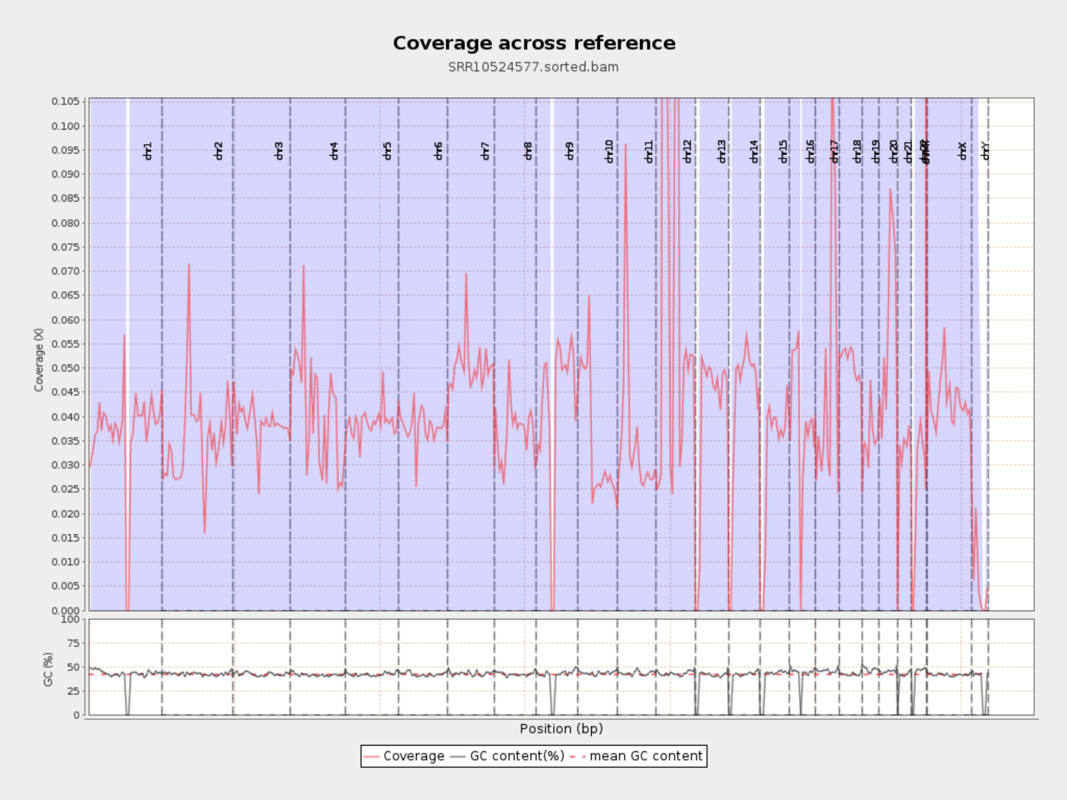
General error rate	0.49%
Mismatches	598,678
Insertions	6,823
Mapped reads with at least one insertion	0.32%
Deletions	19,586
Mapped reads with at least one deletion	0.91%
Homopolymer indels	43.08%

2.6. Chromosome stats

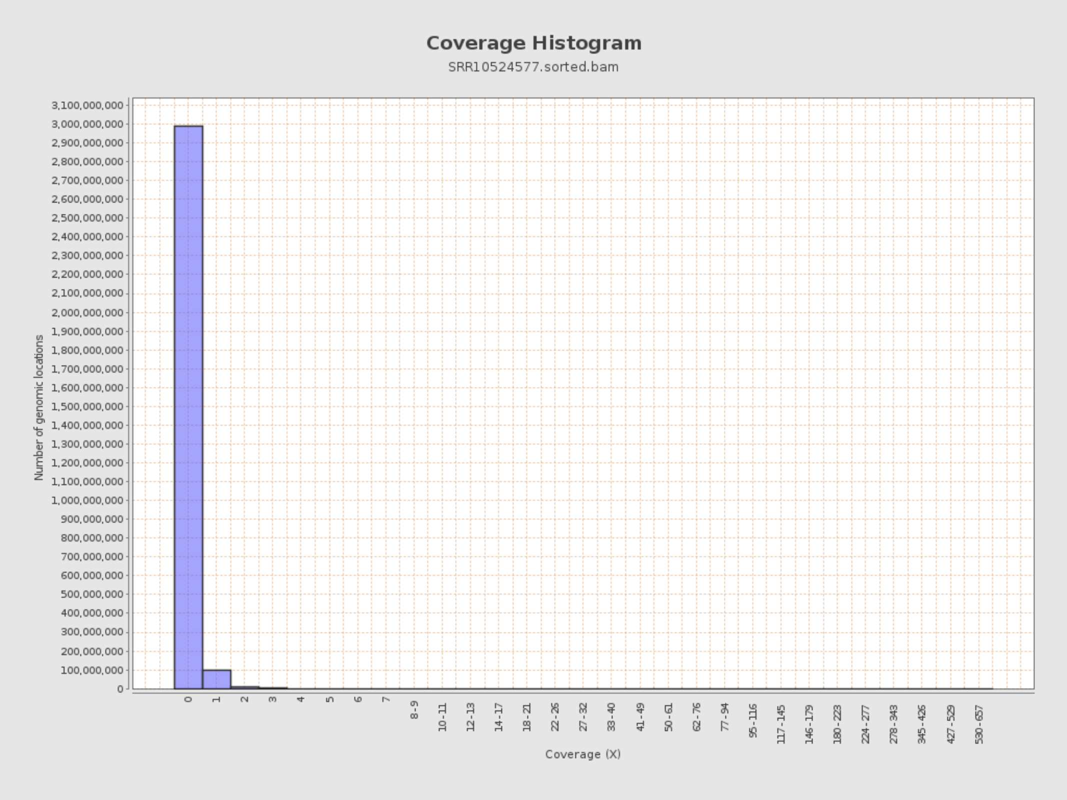
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9132884	0.0366	0.5613
chr2	243199373	8678853	0.0357	0.367
chr3	198022430	7694508	0.0389	0.2172
chr4	191154276	7892095	0.0413	0.2617
chr5	180915260	7000421	0.0387	0.2196
chr6	171115067	6512975	0.0381	0.239
chr7	159138663	8065092	0.0507	0.4692

chr8	146364022	5449696	0.0372	0.3579
chr9	141213431	5984051	0.0424	0.3473
chr10	135534747	4741022	0.035	0.362
chr11	135006516	4912340	0.0364	0.2844
chr12	133851895	9427473	0.0704	0.3417
chr13	115169878	4616274	0.0401	0.2202
chr14	107349540	4504991	0.042	0.243
chr15	102531392	3240266	0.0316	0.197
chr16	90354753	3546506	0.0393	0.2392
chr17	81195210	3816541	0.047	0.2505
chr18	78077248	4011959	0.0514	0.6394
chr19	59128983	2113286	0.0357	0.4183
chr20	63025520	3737384	0.0593	0.2795
chr21	48129895	1492632	0.031	0.2306
chr22	51304566	1236995	0.0241	0.1698
chrMT	16571	18964	1.1444	1.3407
chrX	155270560	6721898	0.0433	0.2743
chrY	59373566	355992	0.006	0.1515

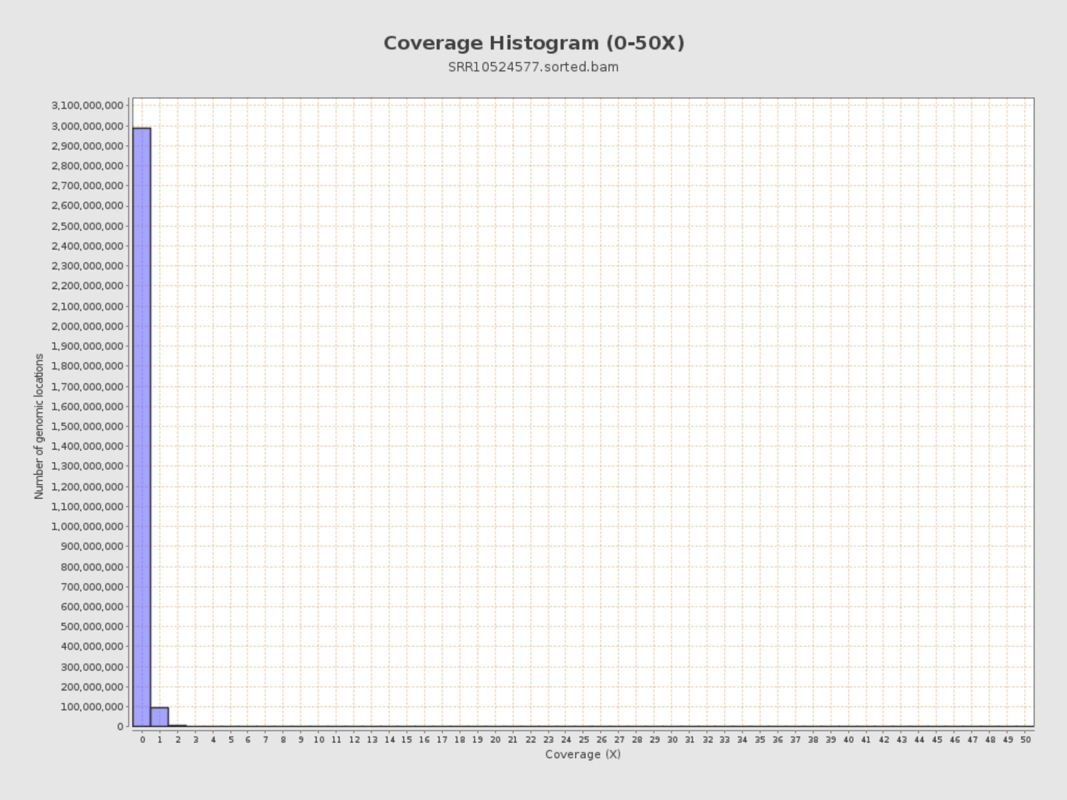
3. Results : Coverage across reference



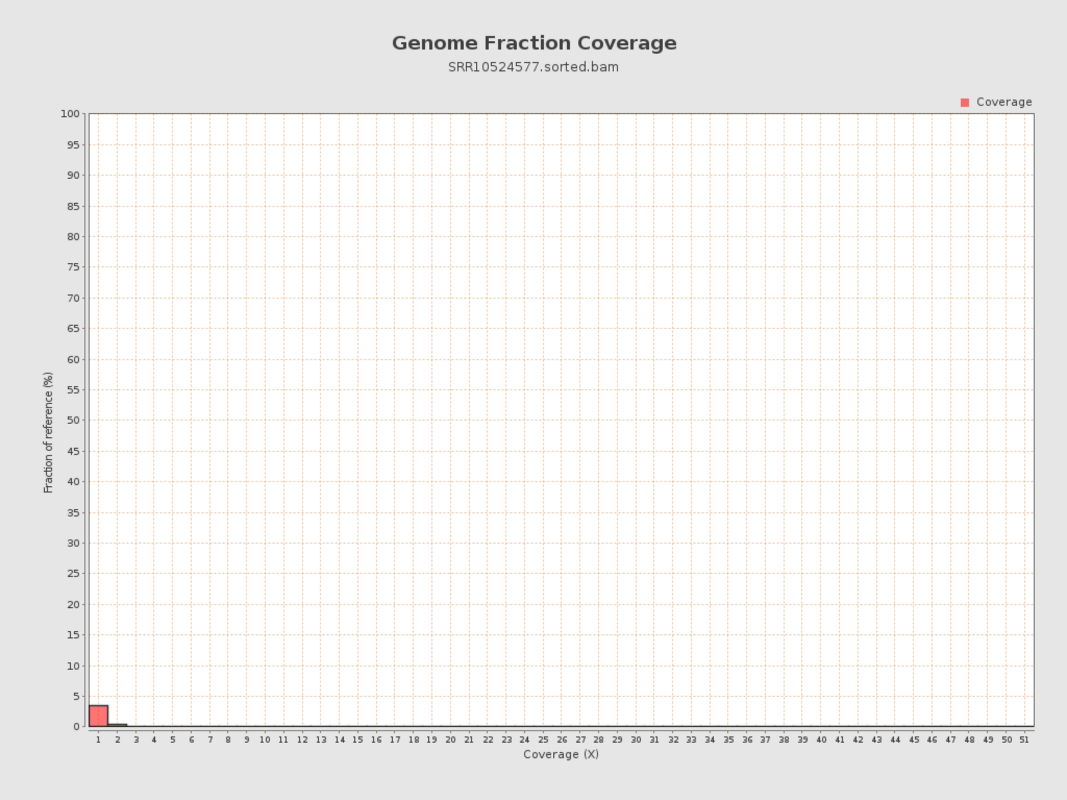
4. Results : Coverage Histogram



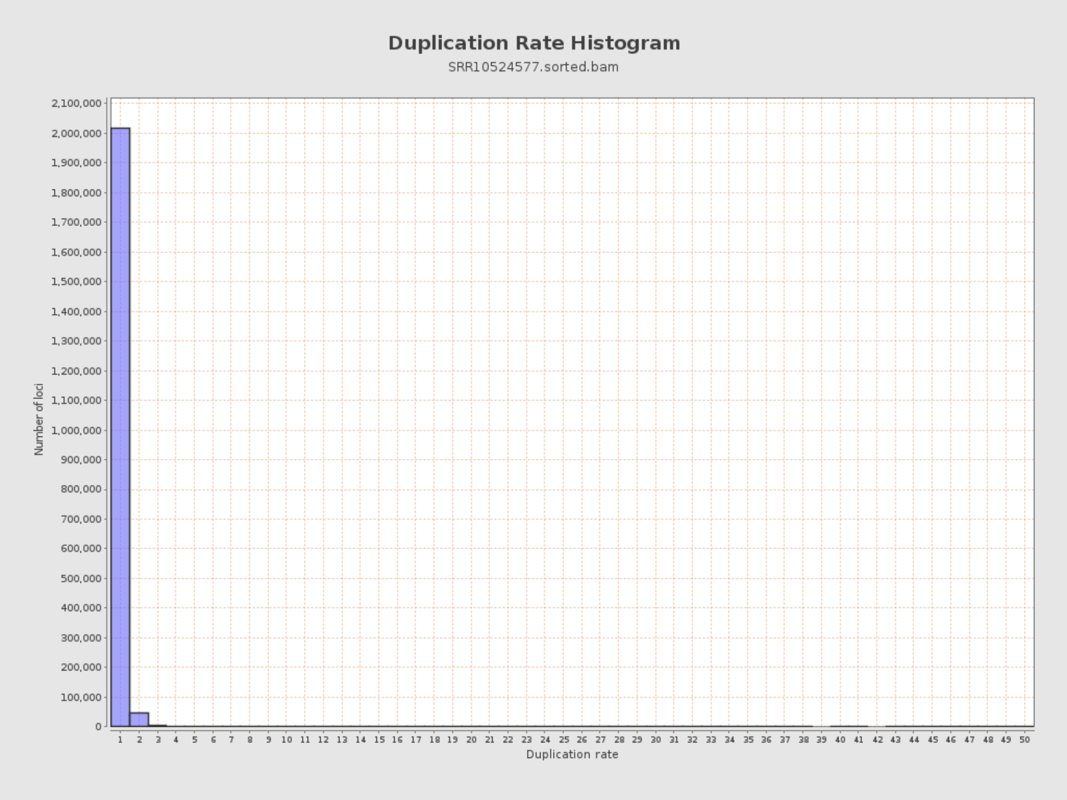
5. Results : Coverage Histogram (0-50X)



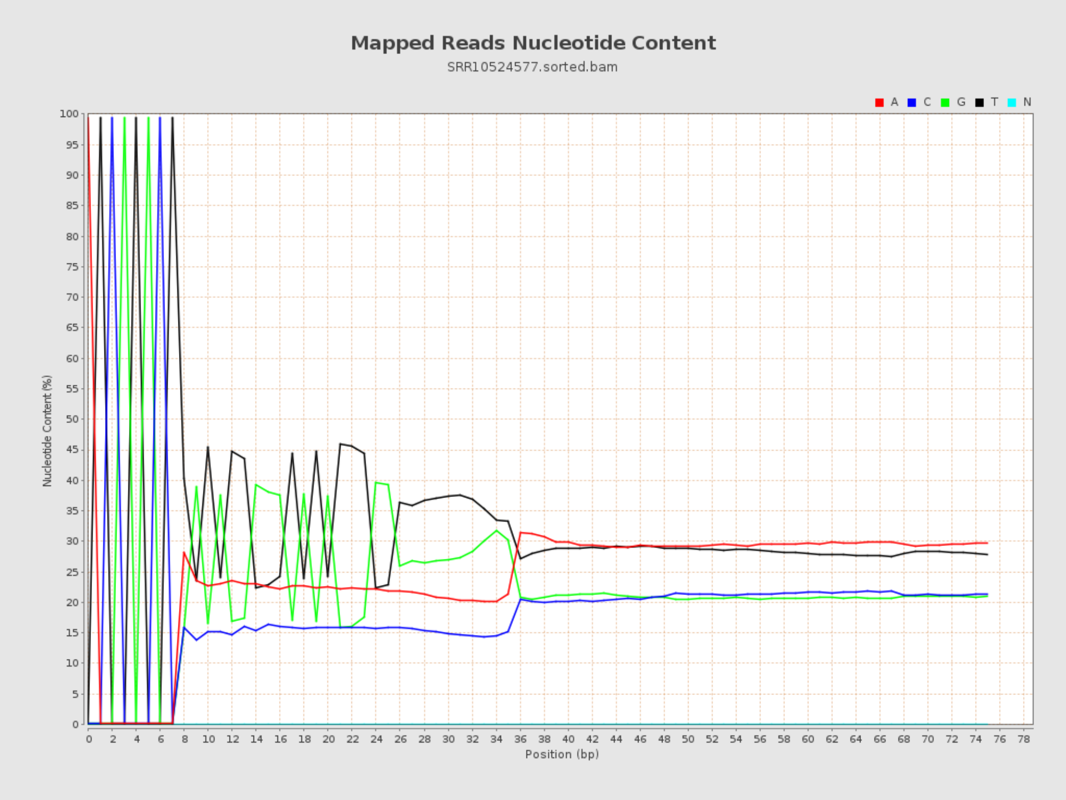
6. Results : Genome Fraction Coverage



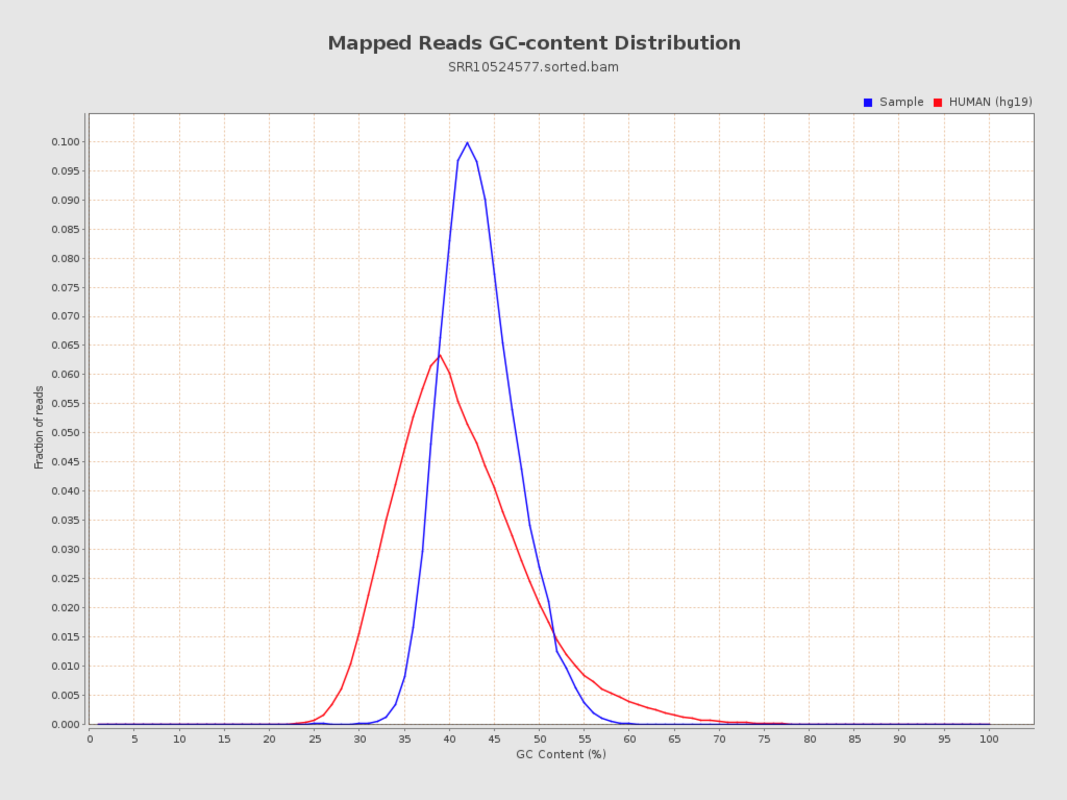
7. Results : Duplication Rate Histogram



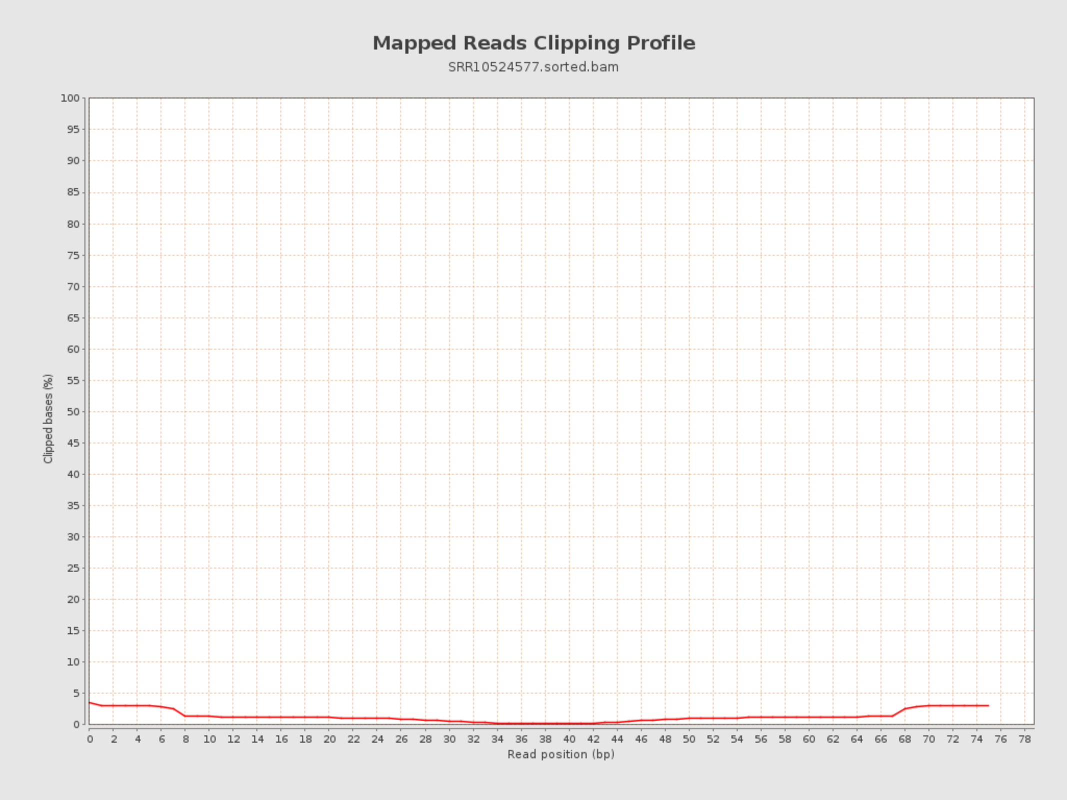
8. Results : Mapped Reads Nucleotide Content



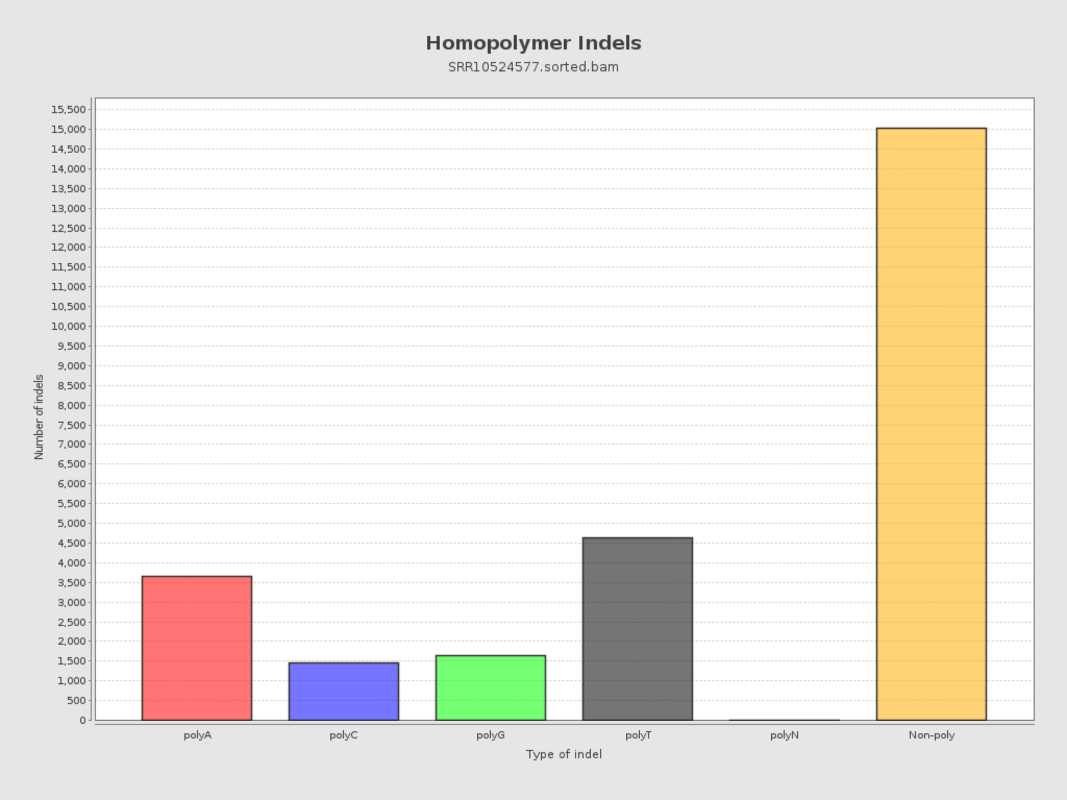
9. Results : Mapped Reads GC-content Distribution



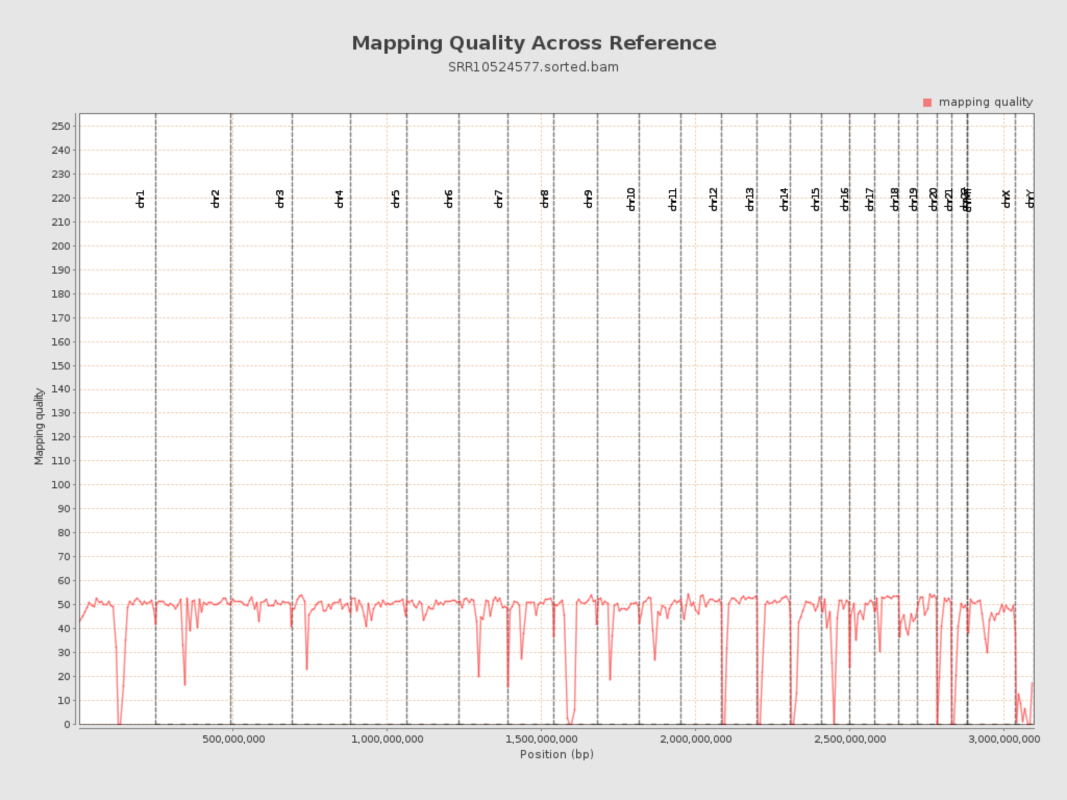
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram