Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:20:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524754.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_SRR10524754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:20:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,893,748
Mapped reads	1,708,846 / 90.24%
Unmapped reads	184,902 / 9.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,012 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	67,639 / 3.57%
Duplication rate	3%
Clipped reads	1,710,667 / 90.33%

2.2. ACGT Content

Number/percentage of A's	23,730,590 / 24.52%
Number/percentage of C's	17,713,827 / 18.3%
Number/percentage of T's	31,468,016 / 32.51%
Number/percentage of G's	23,864,649 / 24.66%
Number/percentage of N's	11,417 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2686

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Mismatches and indels

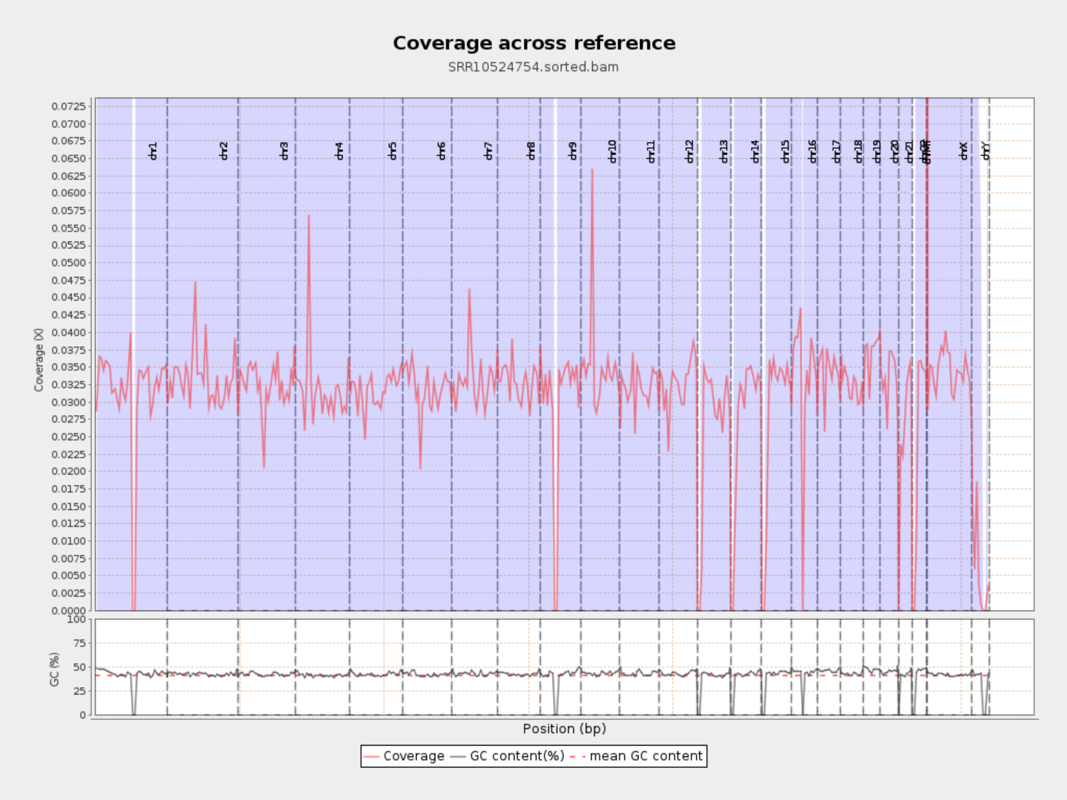
General error rate	0.53%
Mismatches	495,463
Insertions	7,097
Mapped reads with at least one insertion	0.41%
Deletions	18,535
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.25%

2.6. Chromosome stats

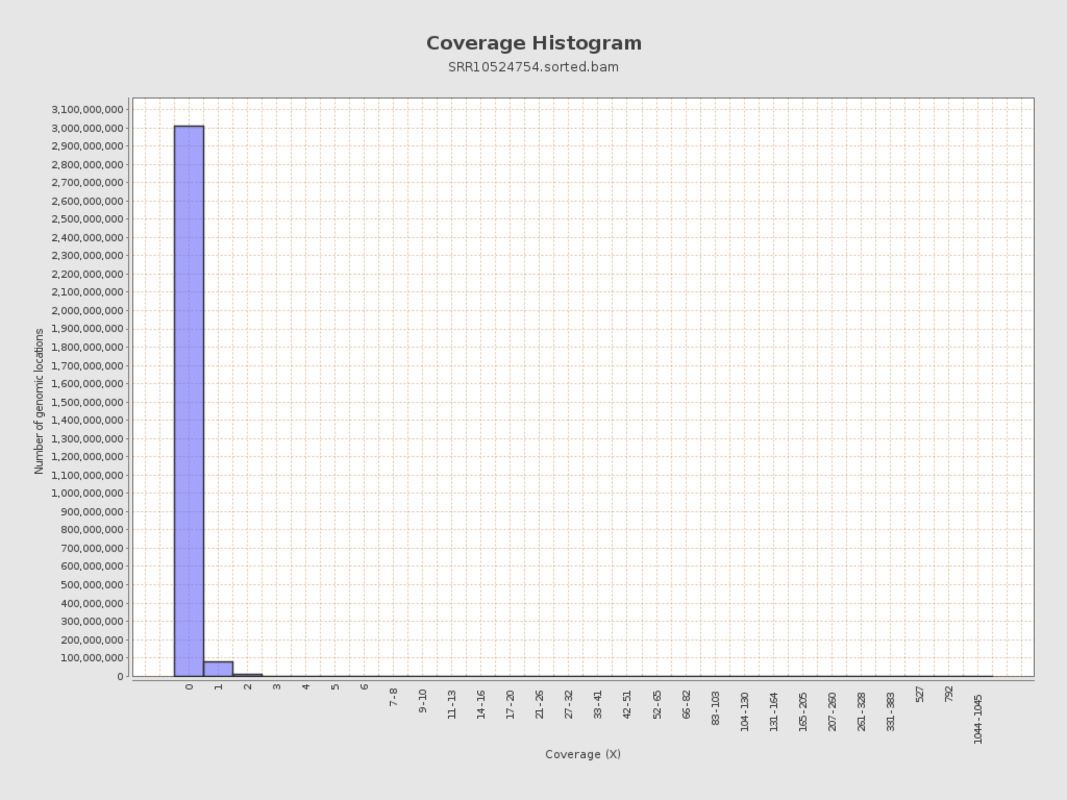
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7741960	0.0311	0.3286
chr2	243199373	8129629	0.0334	0.4778
chr3	198022430	6402464	0.0323	0.2033
chr4	191154276	6106603	0.0319	0.2301
chr5	180915260	5753605	0.0318	0.1985
chr6	171115067	5450805	0.0319	0.2206
chr7	159138663	5273514	0.0331	0.3027

chr8	146364022	4803724	0.0328	0.2311
chr9	141213431	4164038	0.0295	0.2352
chr10	135534747	4781028	0.0353	0.3163
chr11	135006516	4357128	0.0323	0.2394
chr12	133851895	4370845	0.0327	0.2039
chr13	115169878	2976006	0.0258	0.1789
chr14	107349540	2911044	0.0271	0.1892
chr15	102531392	2826330	0.0276	0.1877
chr16	90354753	2974842	0.0329	0.223
chr17	81195210	2804602	0.0345	0.2175
chr18	78077248	2525261	0.0323	0.3542
chr19	59128983	2184950	0.037	0.2924
chr20	63025520	2101905	0.0334	0.2131
chr21	48129895	1262542	0.0262	0.2035
chr22	51304566	1226120	0.0239	0.1729
chrMT	16571	21214	1.2802	1.3633
chrX	155270560	5343008	0.0344	0.2264
chrY	59373566	325553	0.0055	0.149

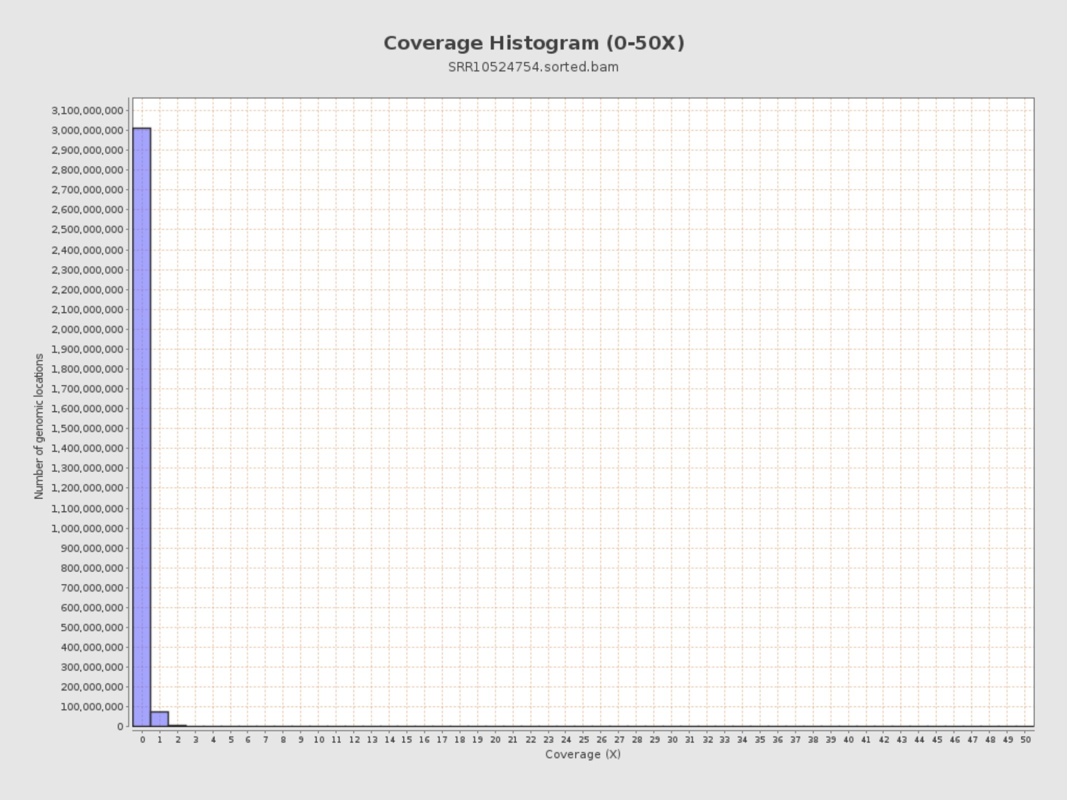
3. Results : Coverage across reference



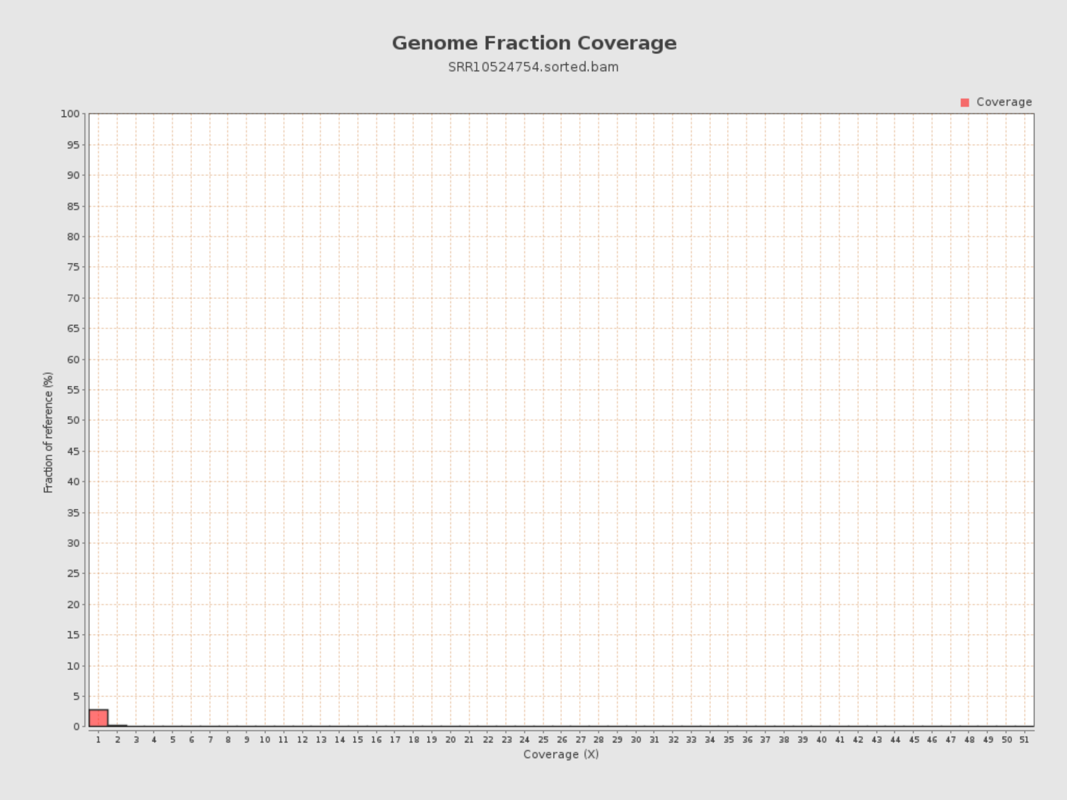
4. Results : Coverage Histogram



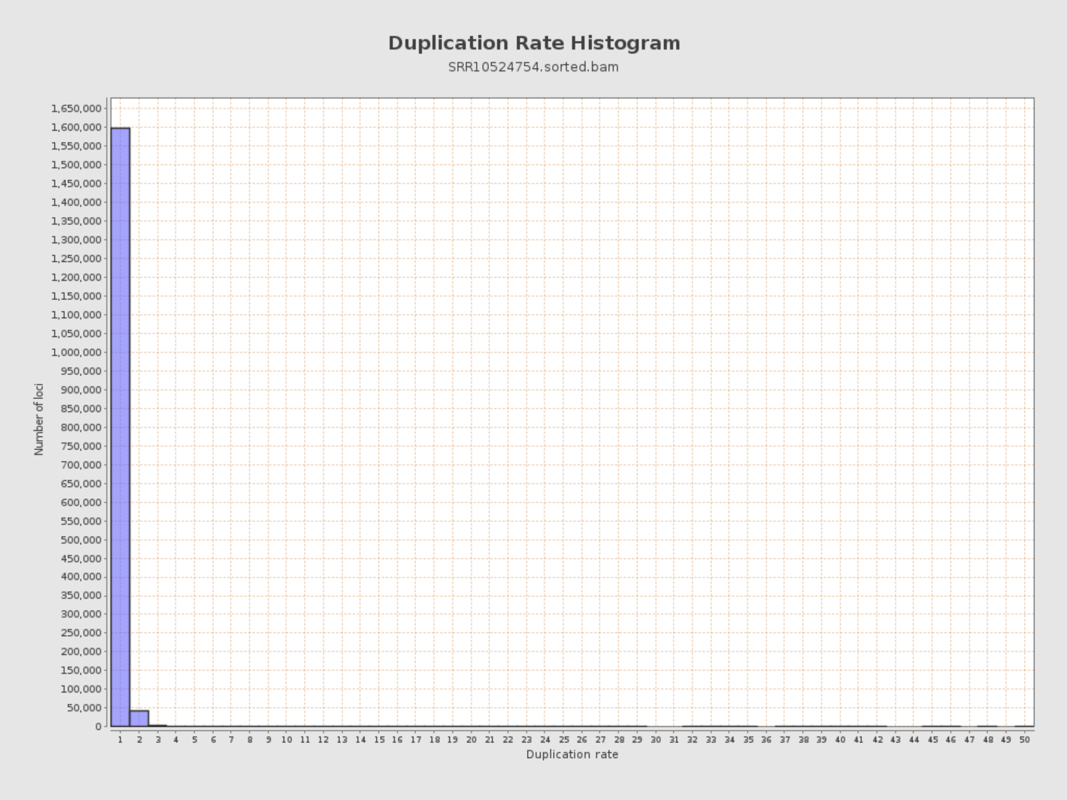
5. Results : Coverage Histogram (0-50X)



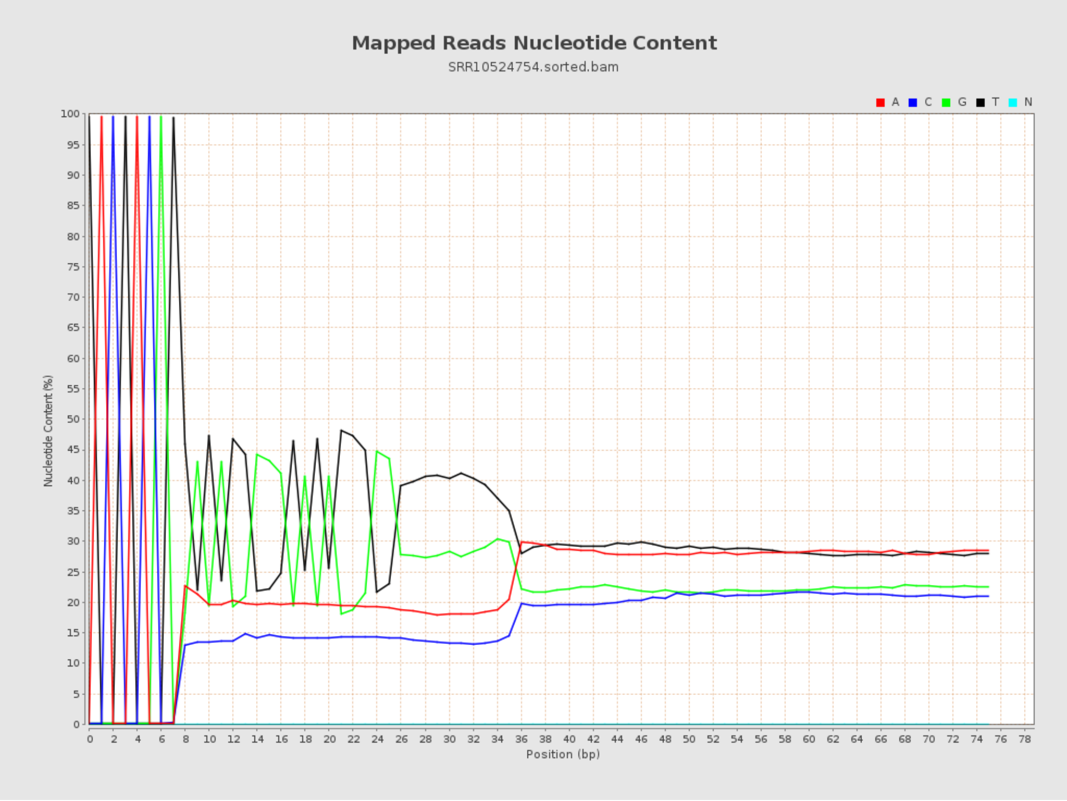
6. Results : Genome Fraction Coverage



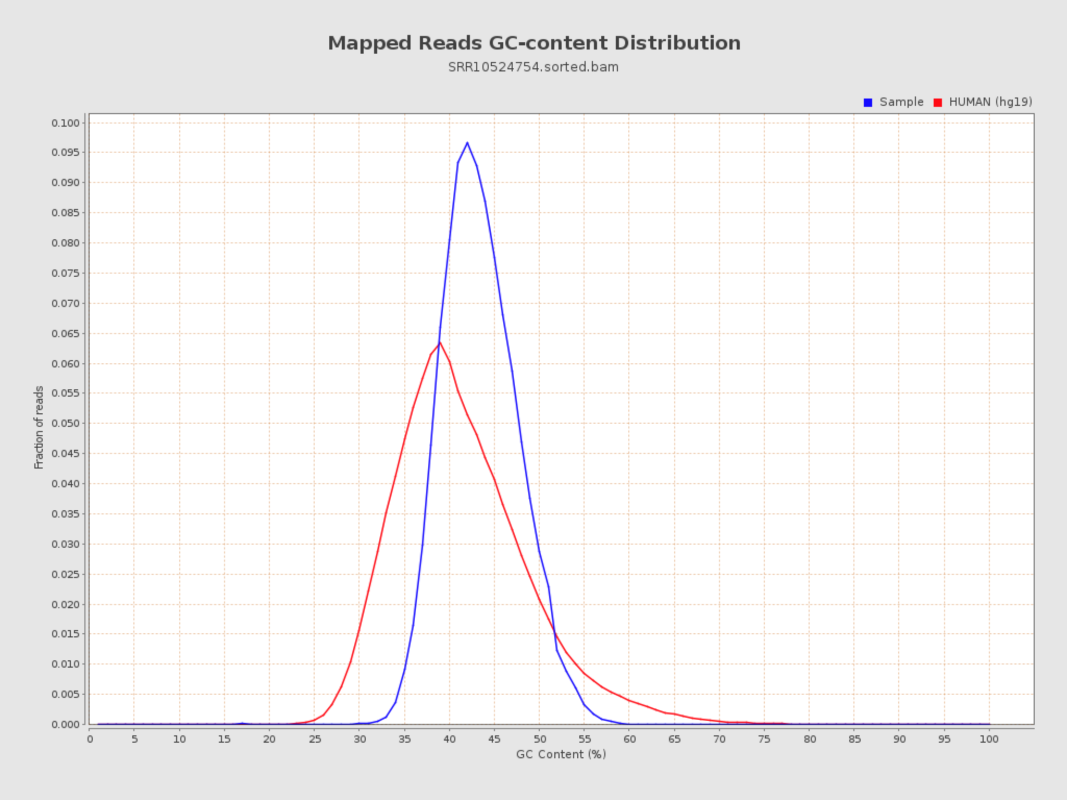
7. Results : Duplication Rate Histogram



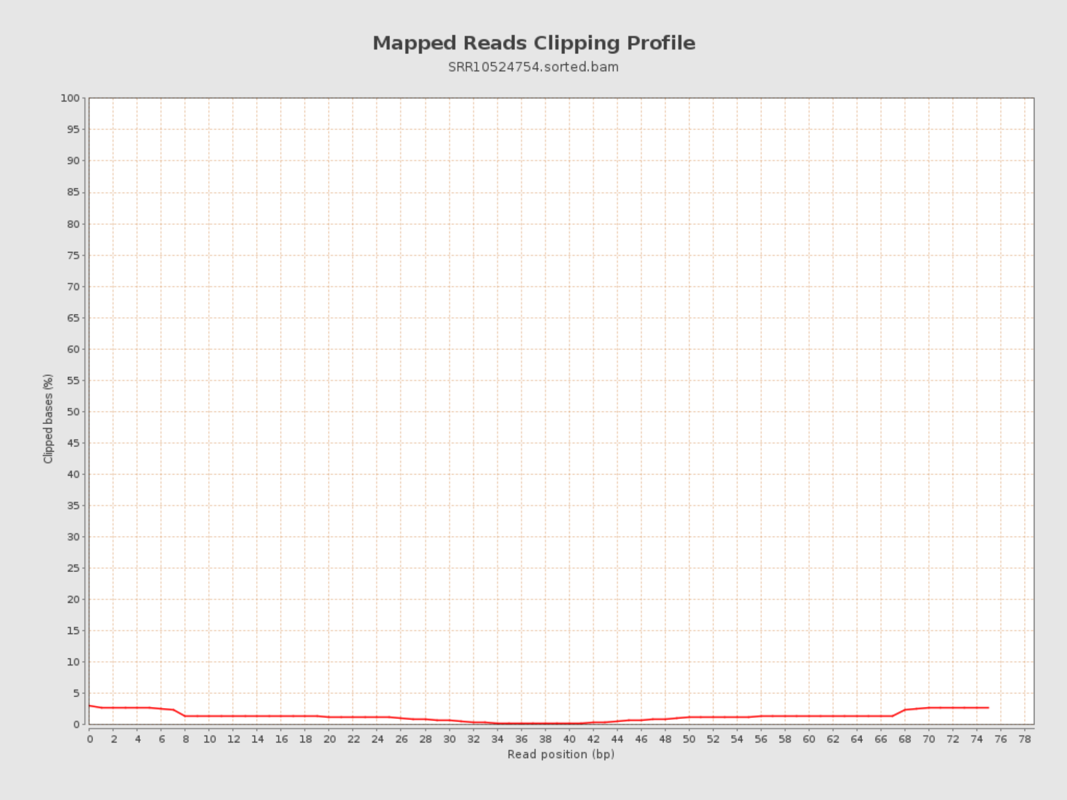
8. Results : Mapped Reads Nucleotide Content



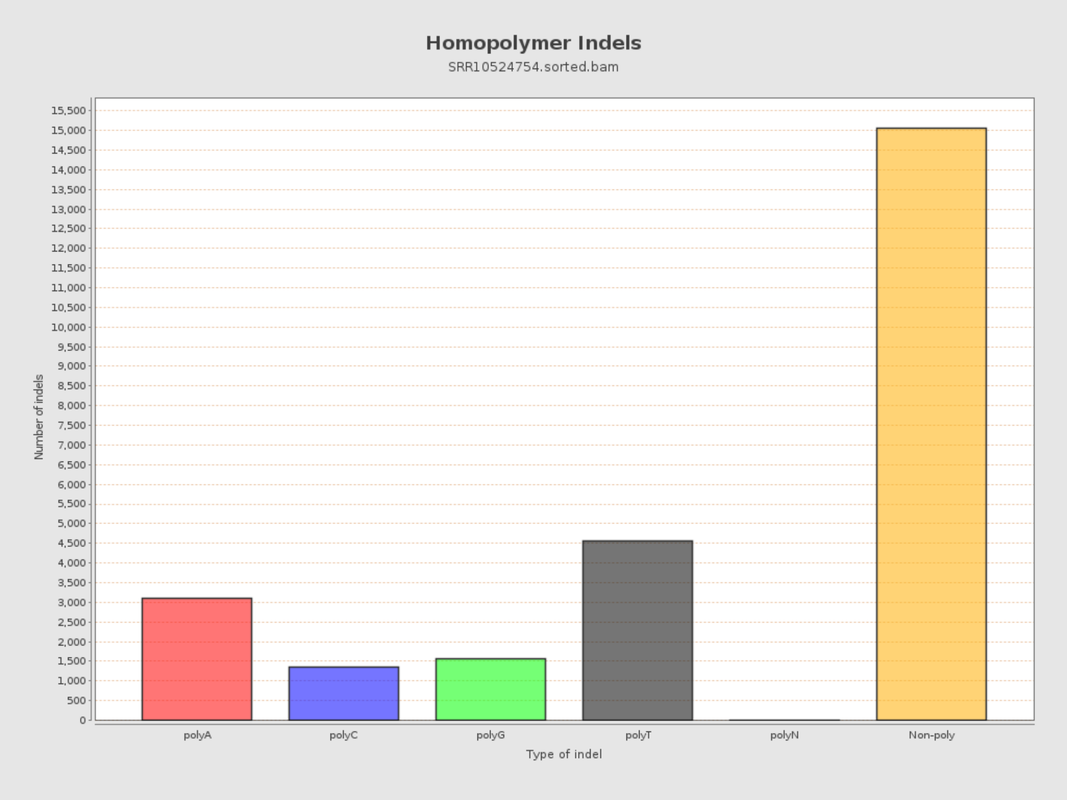
9. Results : Mapped Reads GC-content Distribution



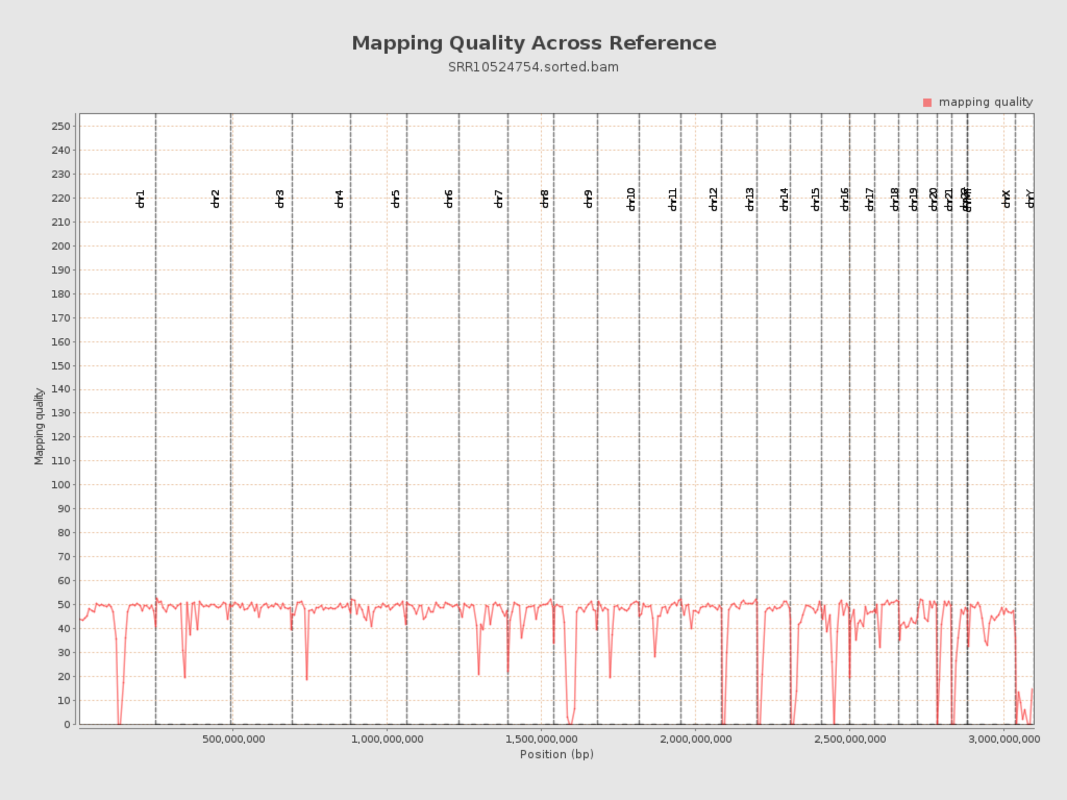
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram