Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524797.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_SRR10524797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:59:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,330,669
Mapped reads	1,205,485 / 90.59%
Unmapped reads	125,184 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,314 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	41,437 / 3.11%
Duplication rate	2.62%
Clipped reads	1,206,419 / 90.66%

2.2. ACGT Content

Number/percentage of A's	17,015,718 / 24.77%
Number/percentage of C's	12,641,678 / 18.4%
Number/percentage of T's	22,356,858 / 32.54%
Number/percentage of G's	16,673,789 / 24.27%
Number/percentage of N's	8,037 / 0.01%
GC Percentage	42.67%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.2099

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

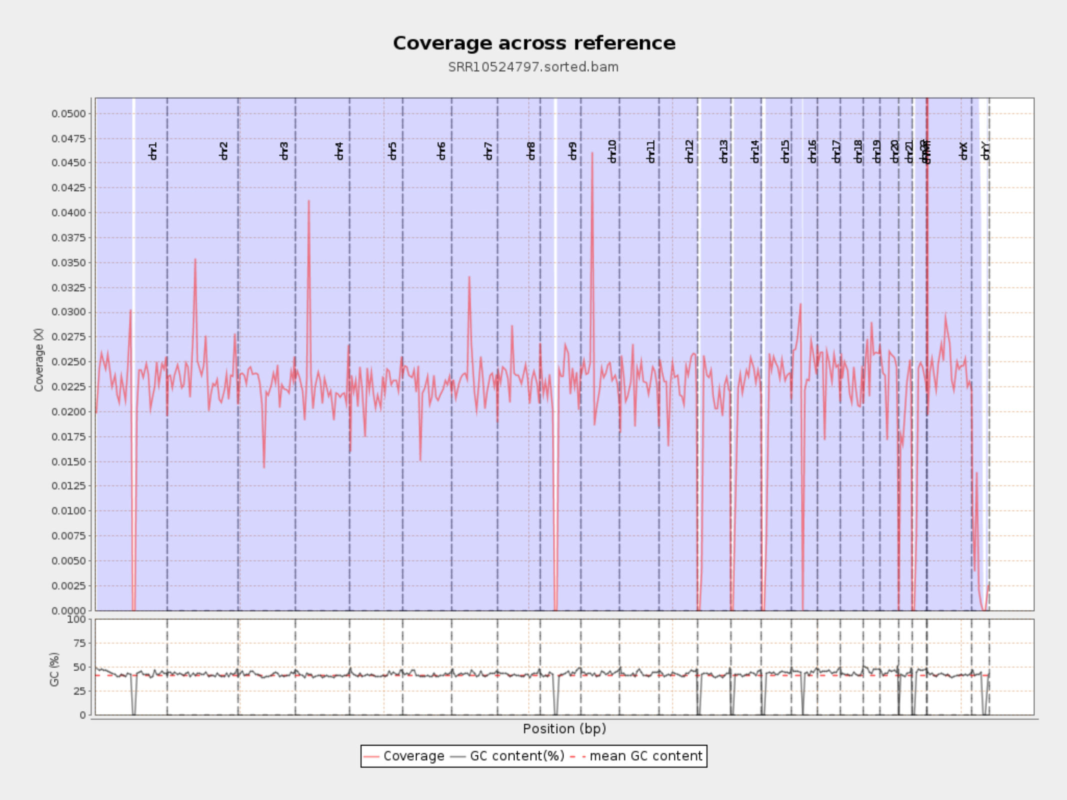
General error rate	0.53%
Mismatches	353,940
Insertions	4,675
Mapped reads with at least one insertion	0.39%
Deletions	13,616
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.12%

2.6. Chromosome stats

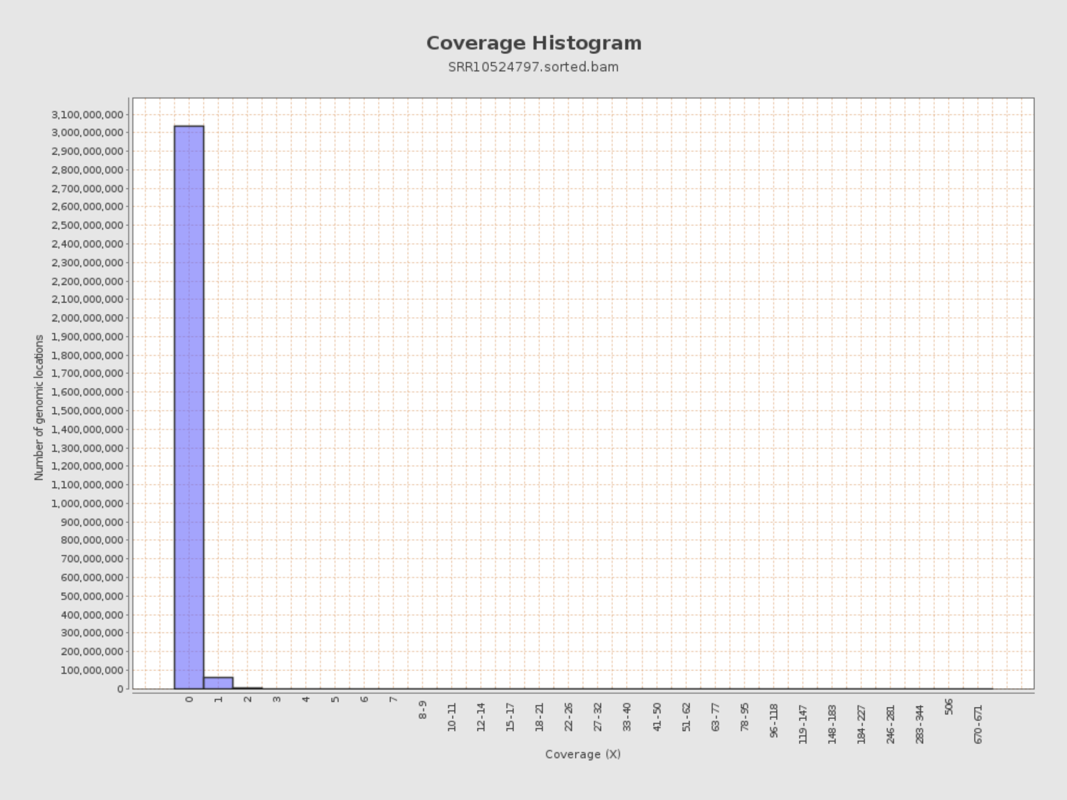
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5503097	0.0221	0.2855
chr2	243199373	5814220	0.0239	0.3306
chr3	198022430	4485918	0.0227	0.1647
chr4	191154276	4401721	0.023	0.184
chr5	180915260	4077107	0.0225	0.1622
chr6	171115067	3846672	0.0225	0.174
chr7	159138663	3751309	0.0236	0.2431

chr8	146364022	3438310	0.0235	0.1887
chr9	141213431	2924738	0.0207	0.1806
chr10	135534747	3327824	0.0246	0.242
chr11	135006516	3121031	0.0231	0.1894
chr12	133851895	3113235	0.0233	0.1671
chr13	115169878	2159026	0.0187	0.1482
chr14	107349540	2096487	0.0195	0.1541
chr15	102531392	2012146	0.0196	0.1549
chr16	90354753	2094495	0.0232	0.179
chr17	81195210	1960624	0.0241	0.1729
chr18	78077248	1782997	0.0228	0.2737
chr19	59128983	1512254	0.0256	0.2368
chr20	63025520	1489775	0.0236	0.1699
chr21	48129895	902149	0.0187	0.1645
chr22	51304566	851136	0.0166	0.1399
chrMT	16571	8297	0.5007	0.804
chrX	155270560	3812883	0.0246	0.1803
chrY	59373566	230321	0.0039	0.1127

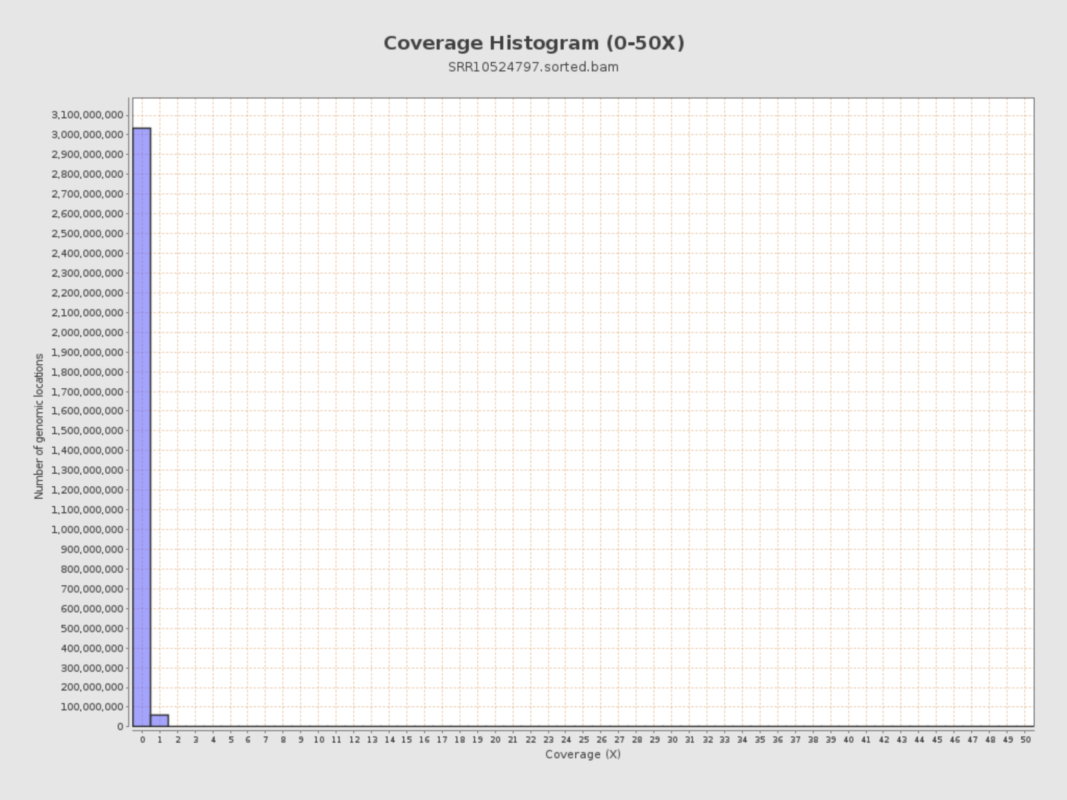
3. Results : Coverage across reference



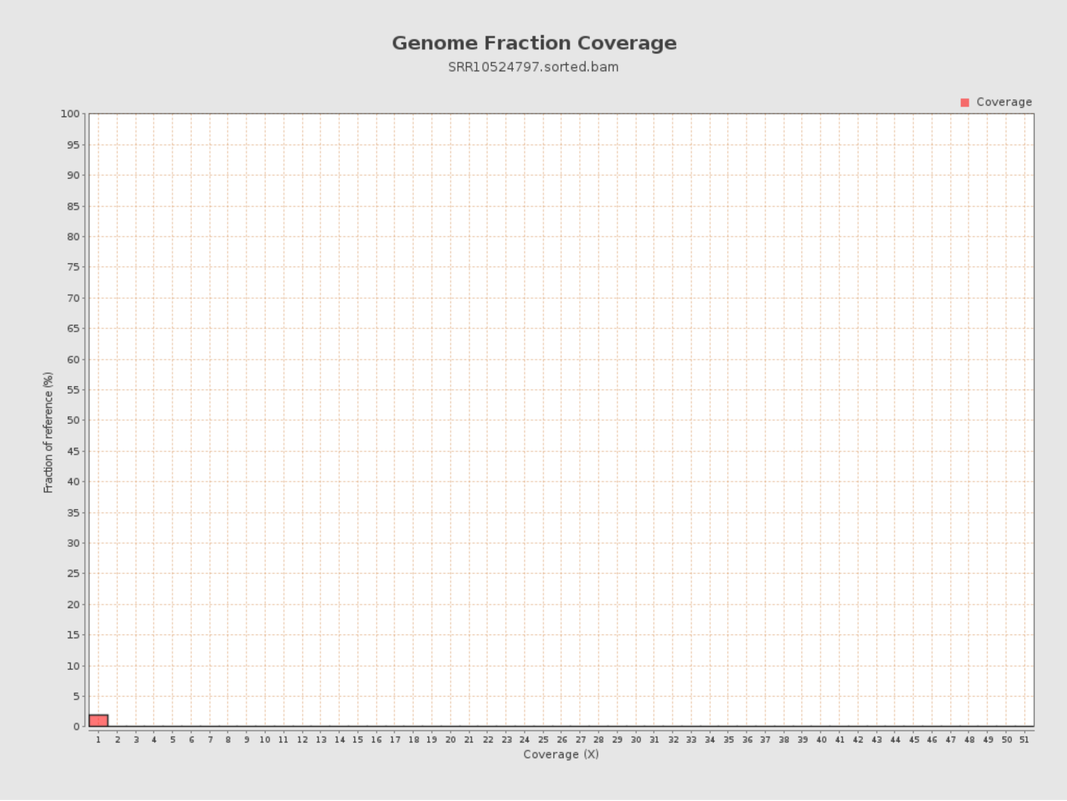
4. Results : Coverage Histogram



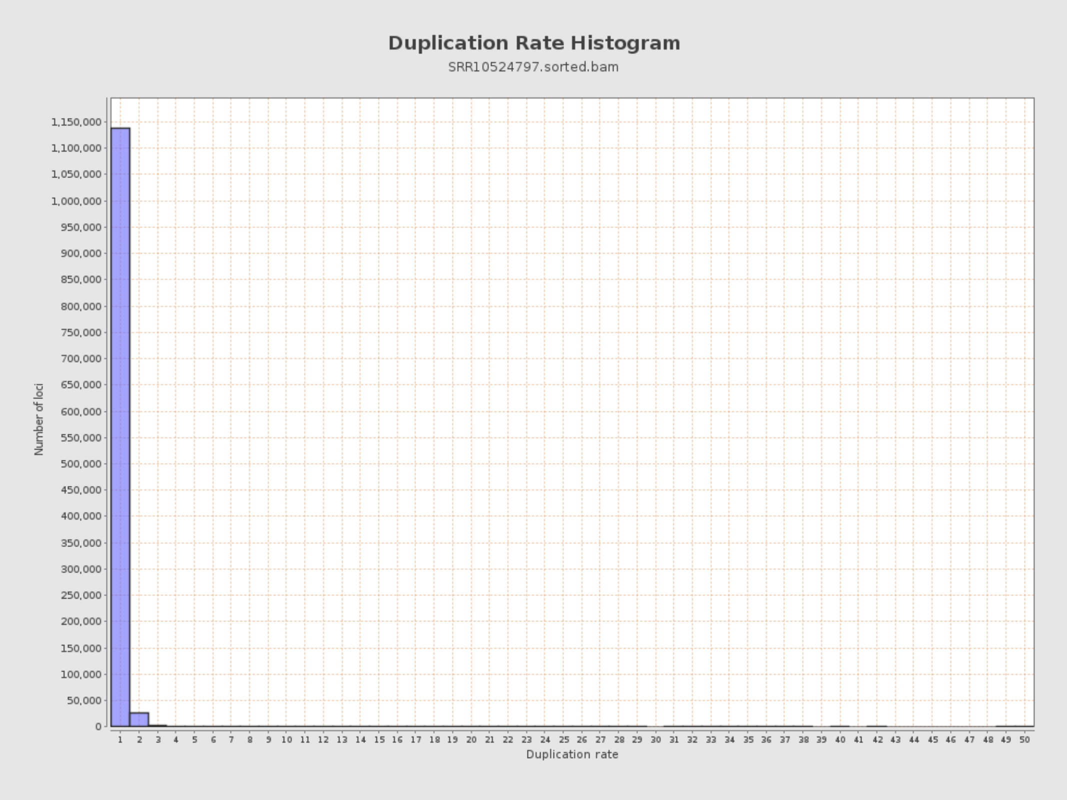
5. Results : Coverage Histogram (0-50X)



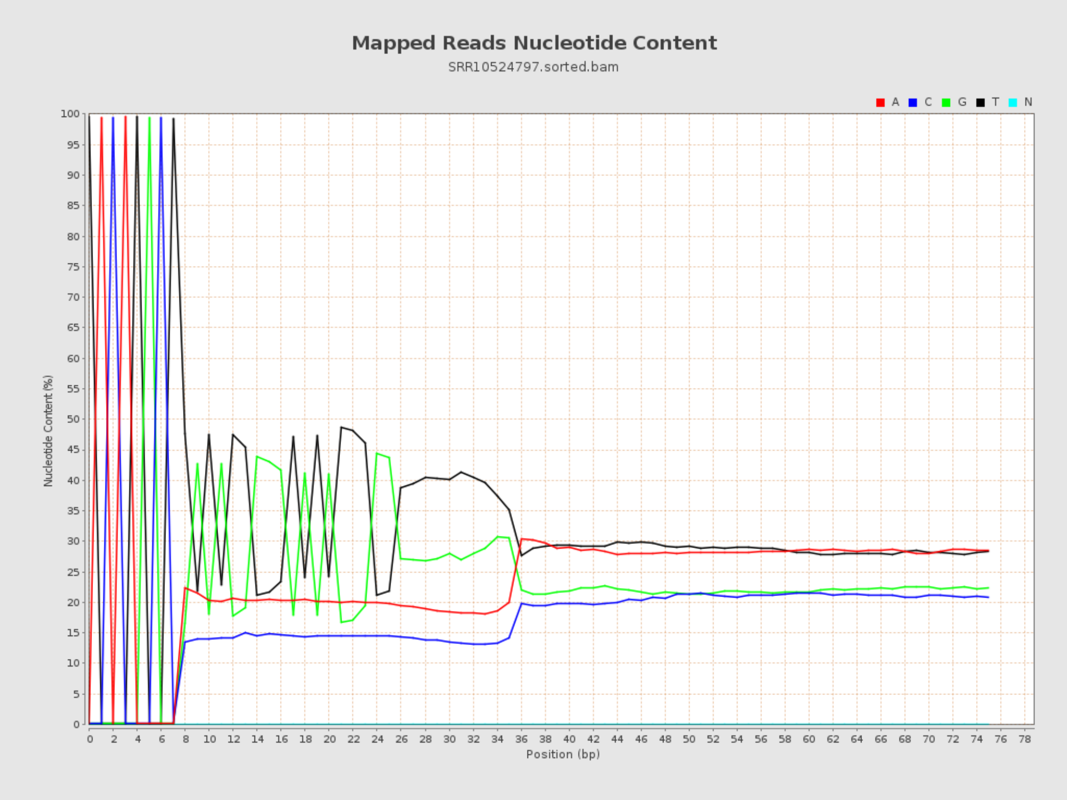
6. Results : Genome Fraction Coverage



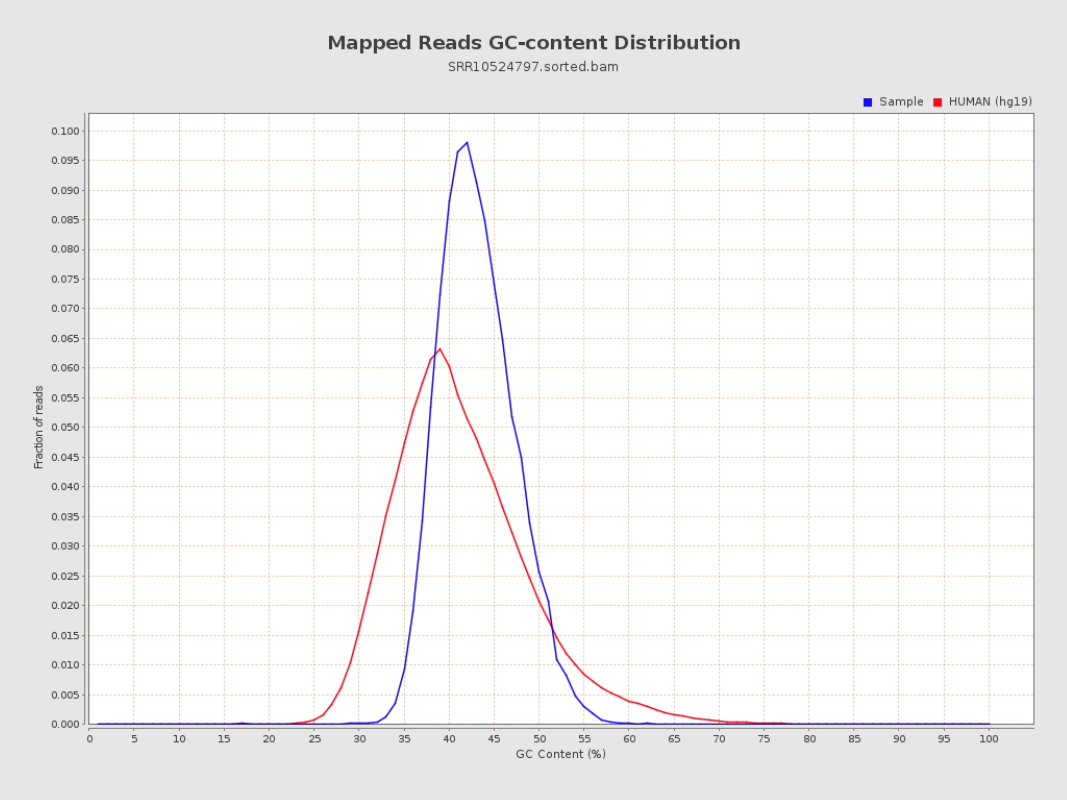
7. Results : Duplication Rate Histogram



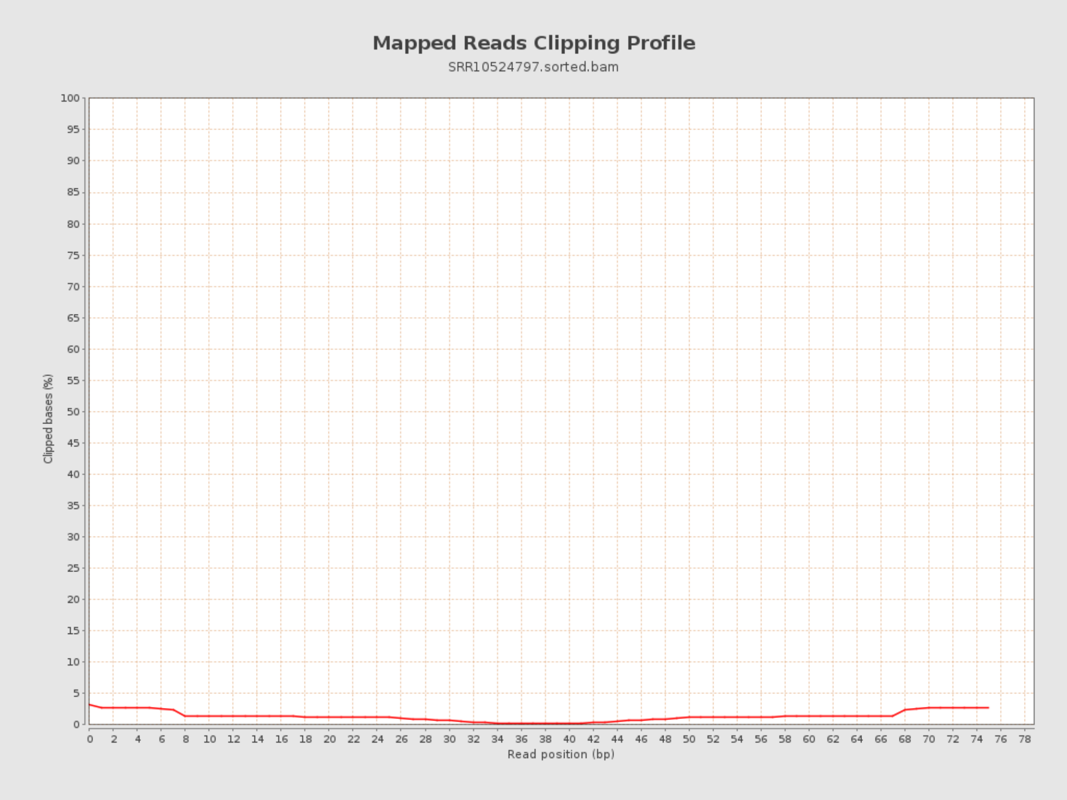
8. Results : Mapped Reads Nucleotide Content



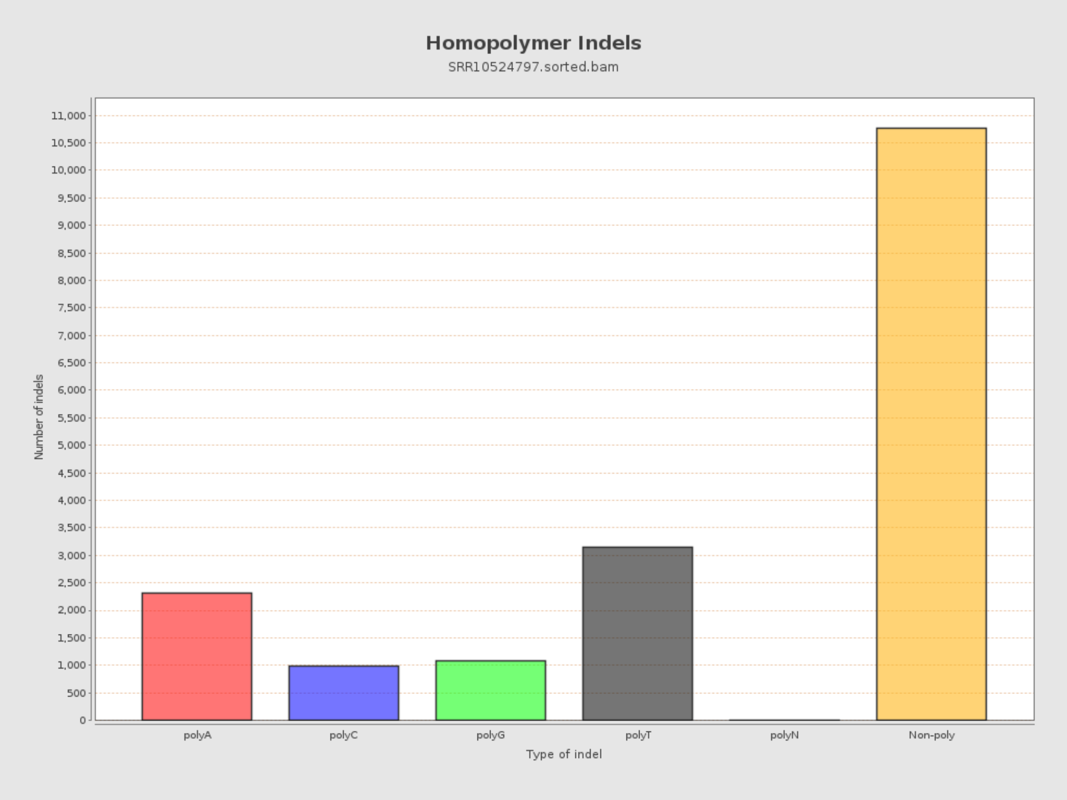
9. Results : Mapped Reads GC-content Distribution



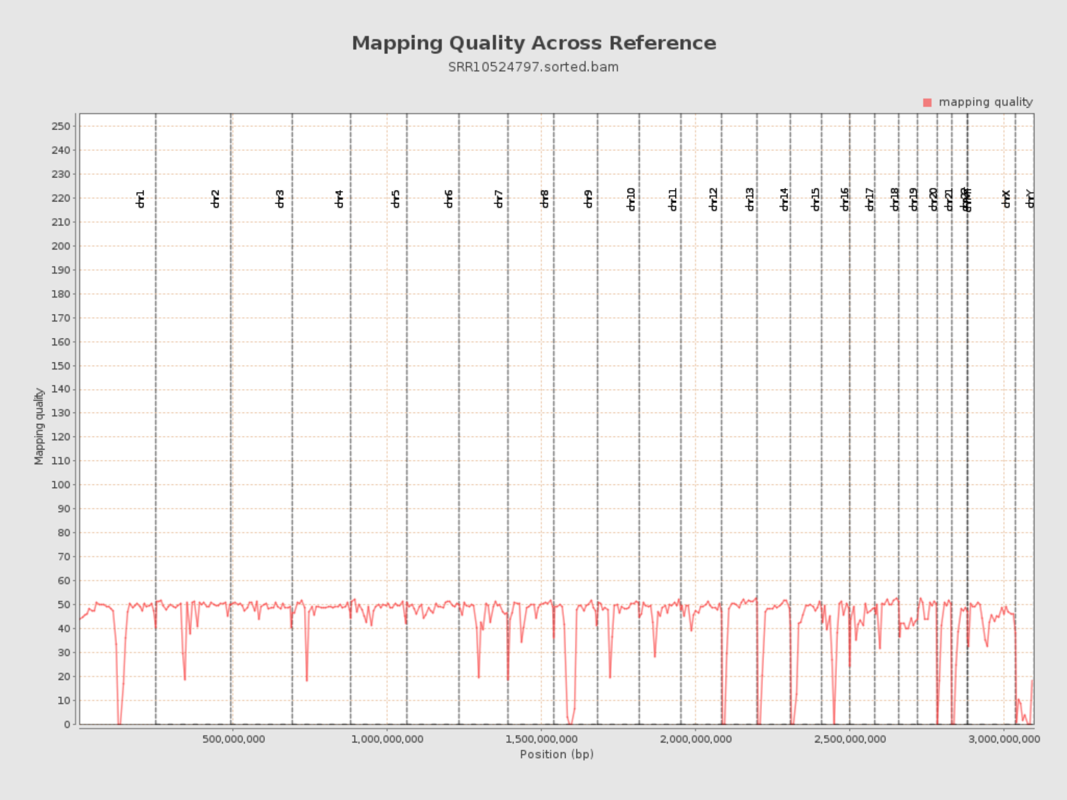
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram