Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 19:03:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524747.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_SRR10524747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 19:03:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,271,289
Mapped reads	1,169,137 / 91.96%
Unmapped reads	102,152 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,822 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	43,564 / 3.43%
Duplication rate	2.89%
Clipped reads	1,170,382 / 92.06%

2.2. ACGT Content

Number/percentage of A's	15,758,261 / 23.37%
Number/percentage of C's	12,574,558 / 18.65%
Number/percentage of T's	21,748,867 / 32.25%
Number/percentage of G's	17,346,106 / 25.72%
Number/percentage of N's	7,768 / 0.01%
GC Percentage	44.37%

2.3. Coverage

Mean	0.0218

Standard Deviation	0.2051

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

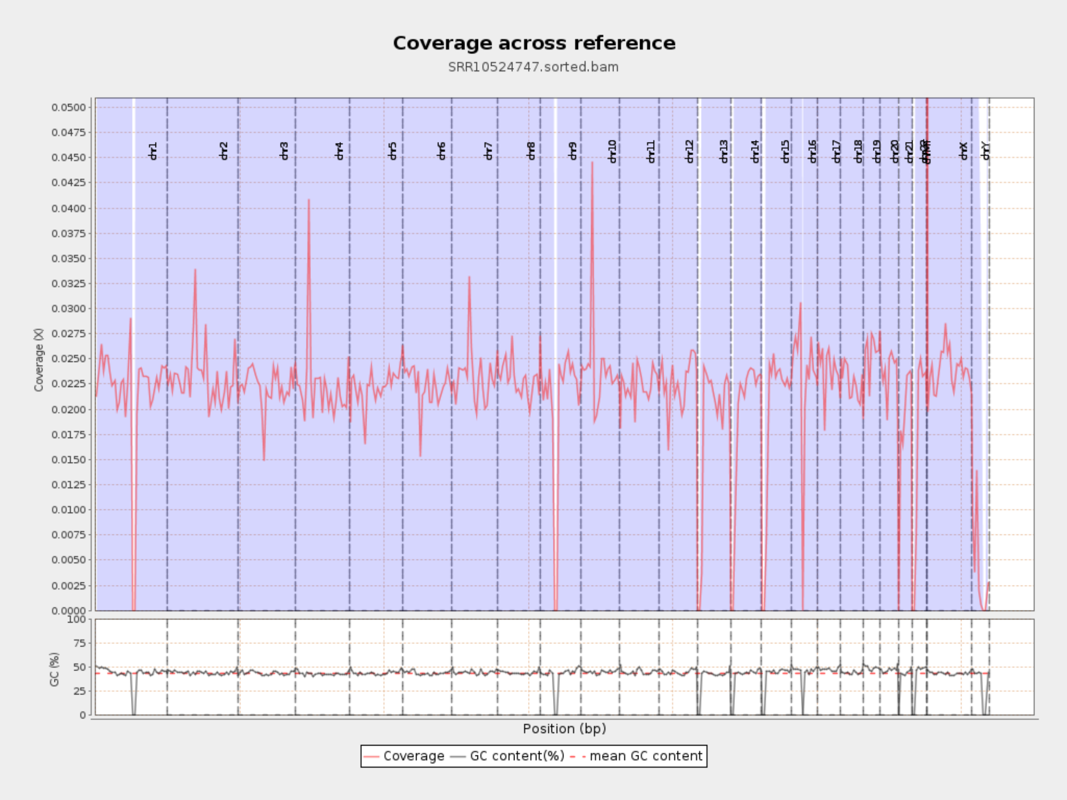
General error rate	0.52%
Mismatches	342,329
Insertions	4,823
Mapped reads with at least one insertion	0.41%
Deletions	13,708
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.62%

2.6. Chromosome stats

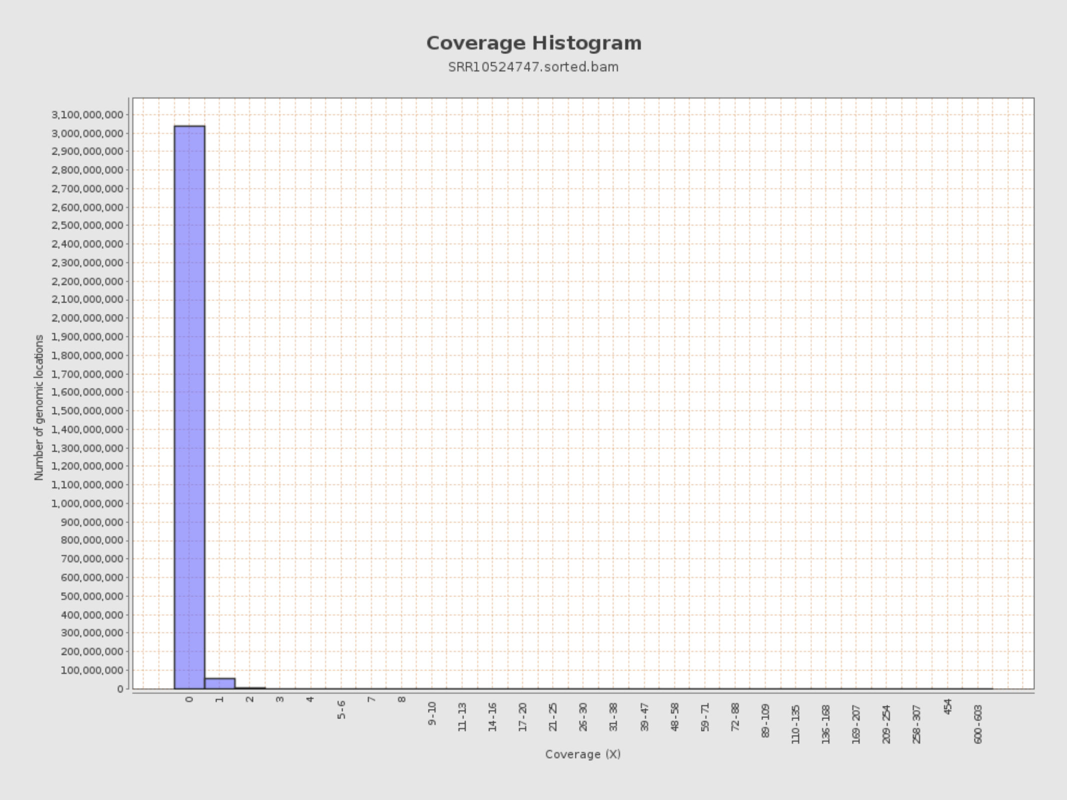
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5384013	0.0216	0.2721
chr2	243199373	5645474	0.0232	0.3087
chr3	198022430	4393843	0.0222	0.1646
chr4	191154276	4292046	0.0225	0.1824
chr5	180915260	4039024	0.0223	0.1626
chr6	171115067	3834204	0.0224	0.1765
chr7	159138663	3714063	0.0233	0.2349

chr8	146364022	3352622	0.0229	0.1986
chr9	141213431	2890767	0.0205	0.1788
chr10	135534747	3301165	0.0244	0.2346
chr11	135006516	3040881	0.0225	0.1878
chr12	133851895	3032649	0.0227	0.1655
chr13	115169878	2098014	0.0182	0.1472
chr14	107349540	2030892	0.0189	0.1543
chr15	102531392	1937743	0.0189	0.1508
chr16	90354753	2065256	0.0229	0.1773
chr17	81195210	1942313	0.0239	0.1746
chr18	78077248	1766126	0.0226	0.2783
chr19	59128983	1508623	0.0255	0.2308
chr20	63025520	1487248	0.0236	0.1738
chr21	48129895	901205	0.0187	0.1624
chr22	51304566	846040	0.0165	0.1409
chrMT	16571	13592	0.8202	1.0855
chrX	155270560	3712442	0.0239	0.1777
chrY	59373566	227444	0.0038	0.1126

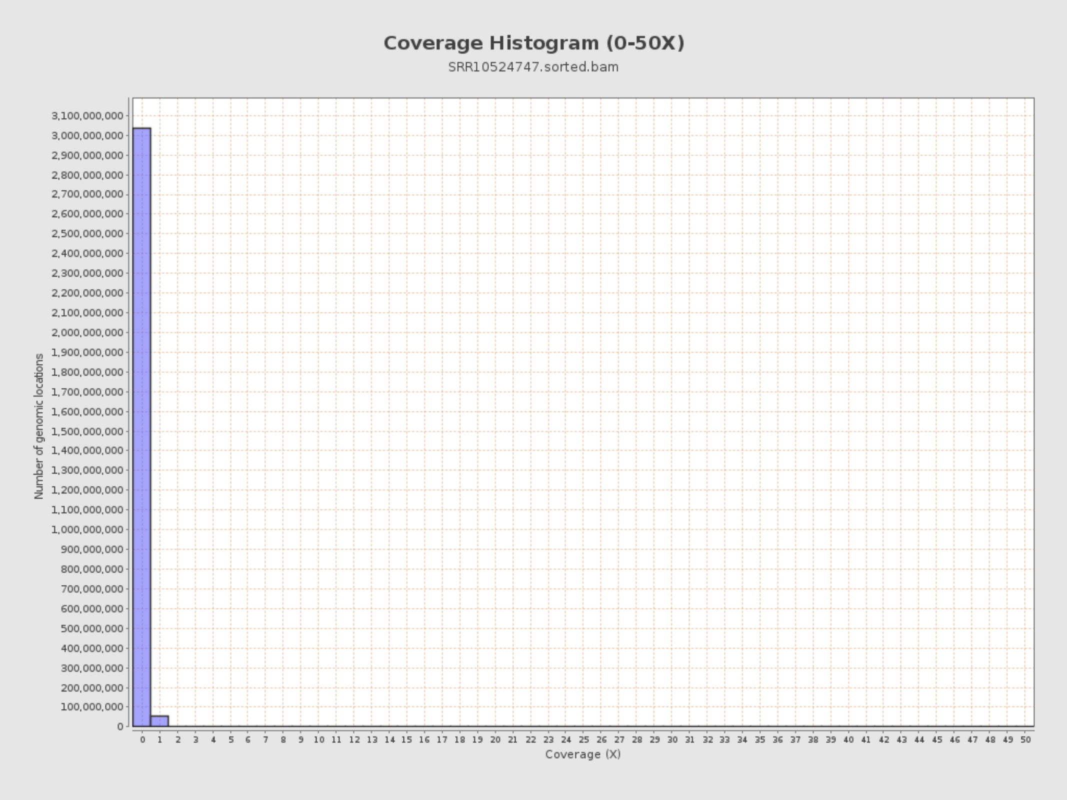
3. Results : Coverage across reference



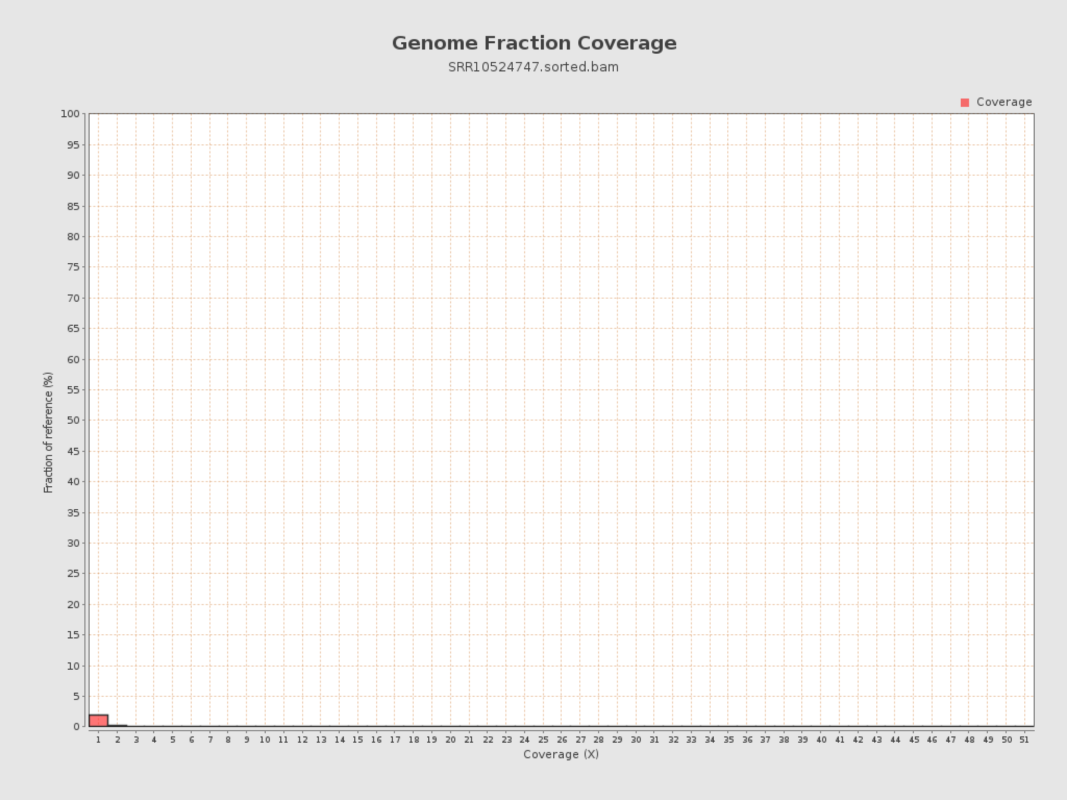
4. Results : Coverage Histogram



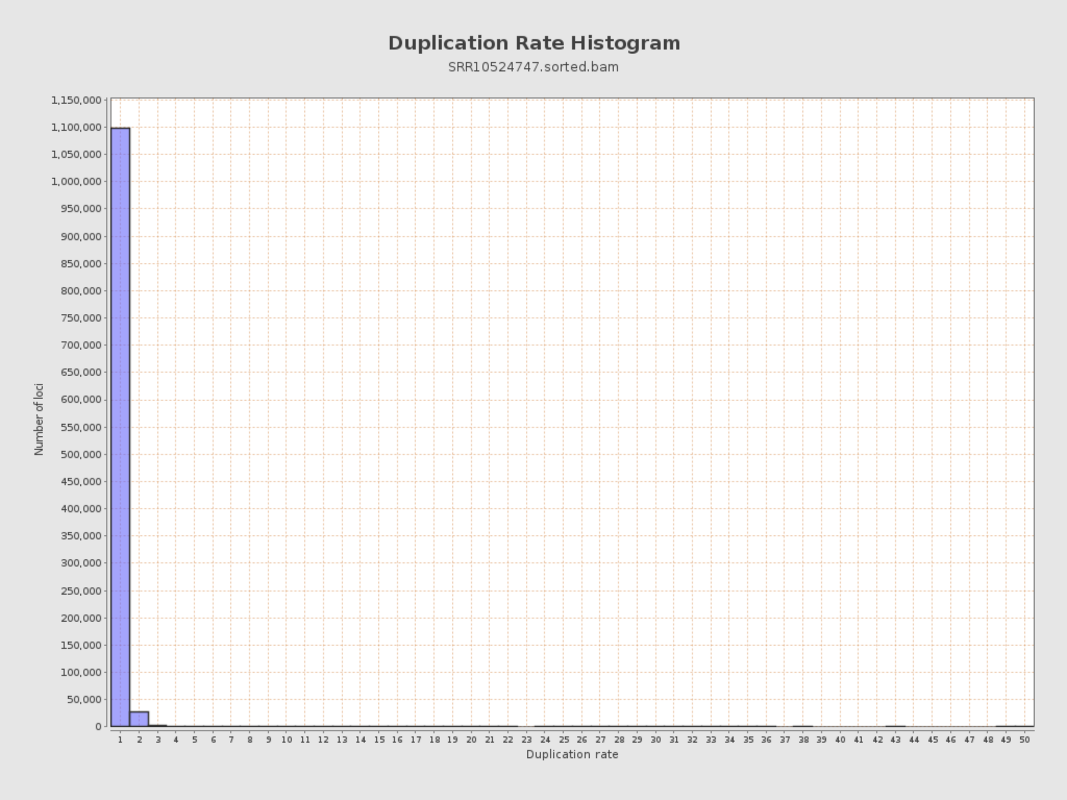
5. Results : Coverage Histogram (0-50X)



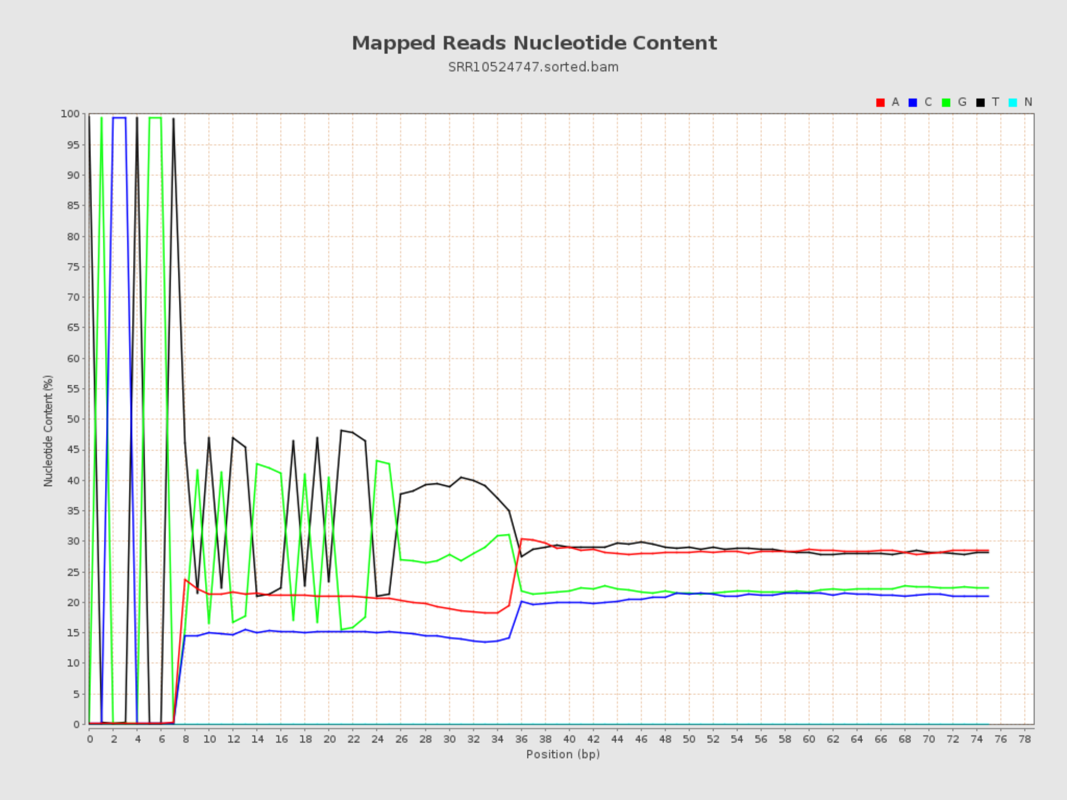
6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



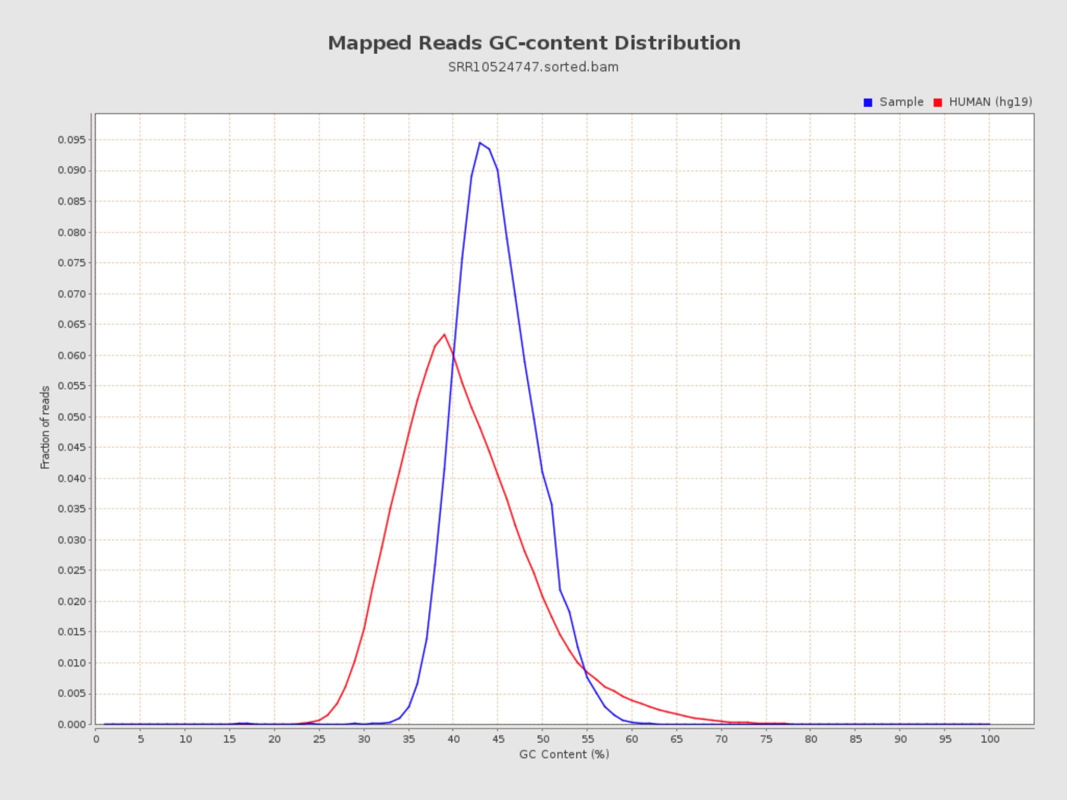
8. Results : Mapped Reads Nucleotide Content



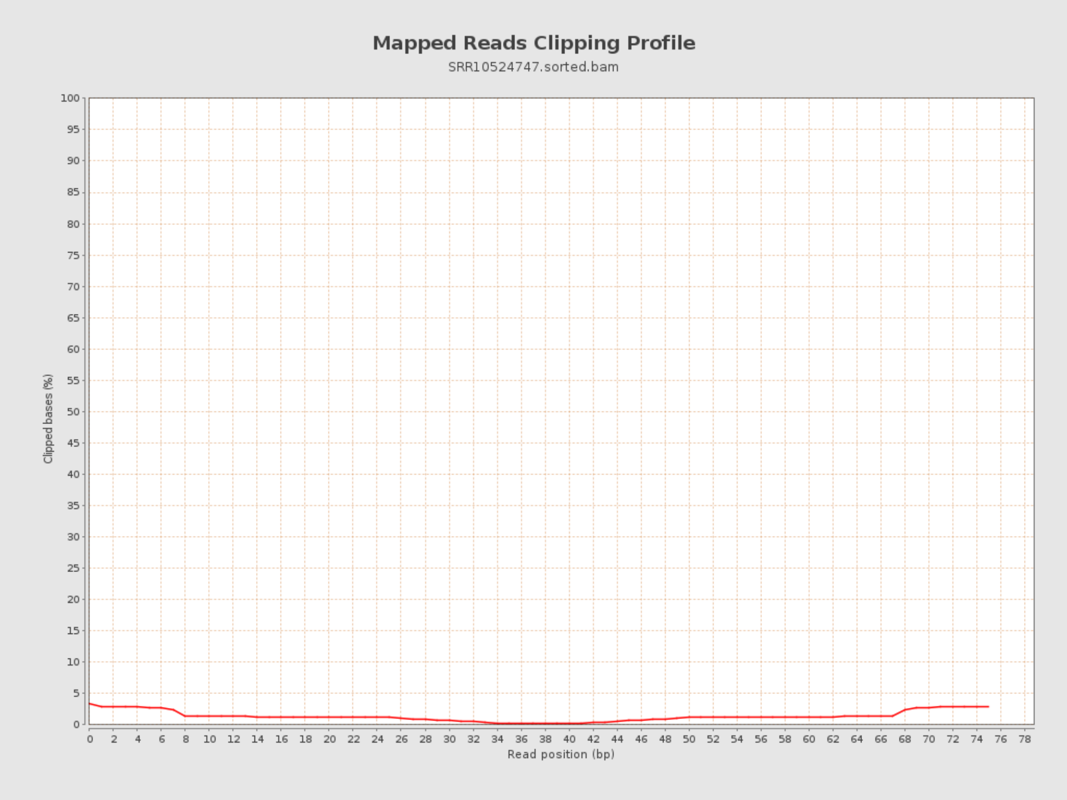
Mapped Reads Nucleotide Content

SRR10524747.sorted.bam

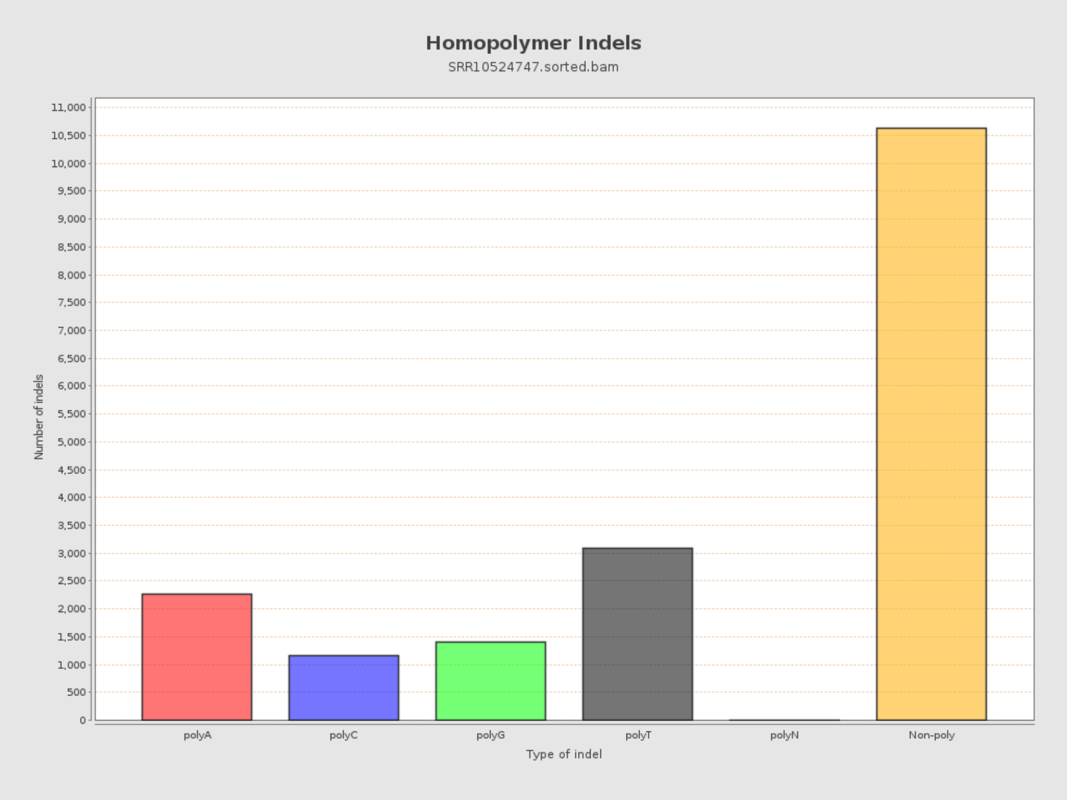
9. Results : Mapped Reads GC-content Distribution



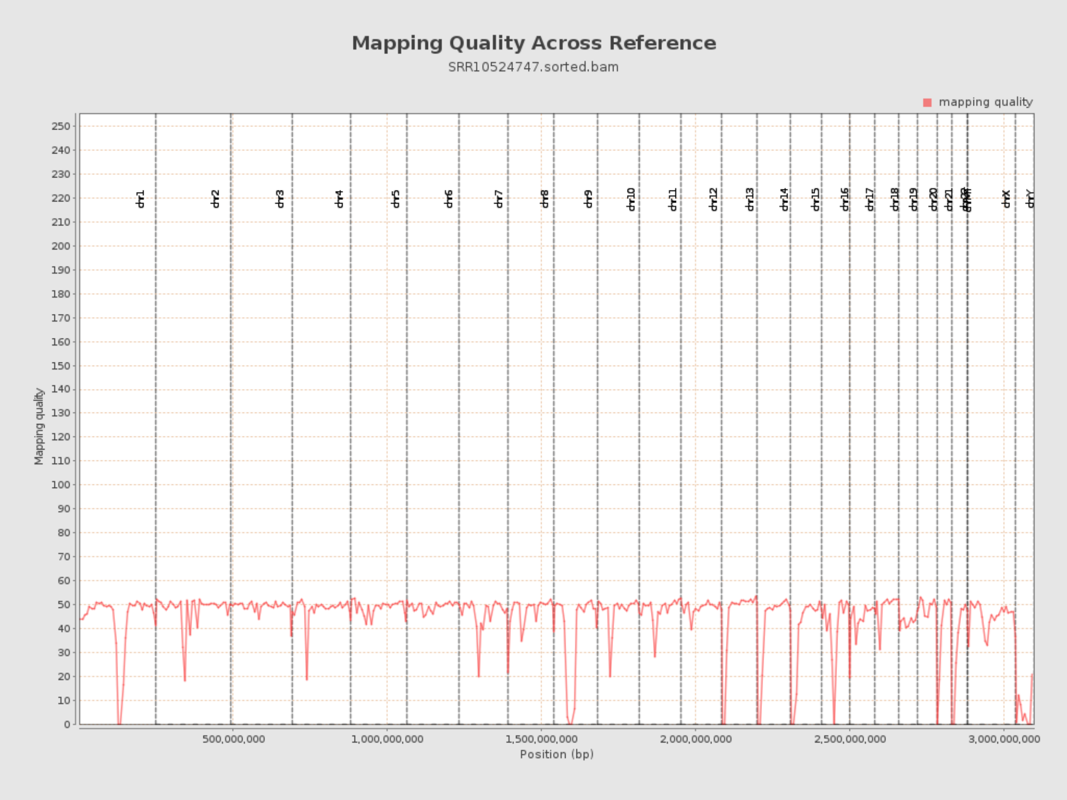
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram