Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:49:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524867.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_SRR10524867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524867.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:49:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,536,274
Mapped reads	1,392,747 / 90.66%
Unmapped reads	143,527 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,724 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	38,265 / 2.49%
Duplication rate	1.85%
Clipped reads	1,398,996 / 91.06%

2.2. ACGT Content

Number/percentage of A's	21,078,340 / 26.1%
Number/percentage of C's	14,816,102 / 18.35%
Number/percentage of T's	25,923,914 / 32.1%
Number/percentage of G's	18,934,351 / 23.44%
Number/percentage of N's	10,823 / 0.01%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2603

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

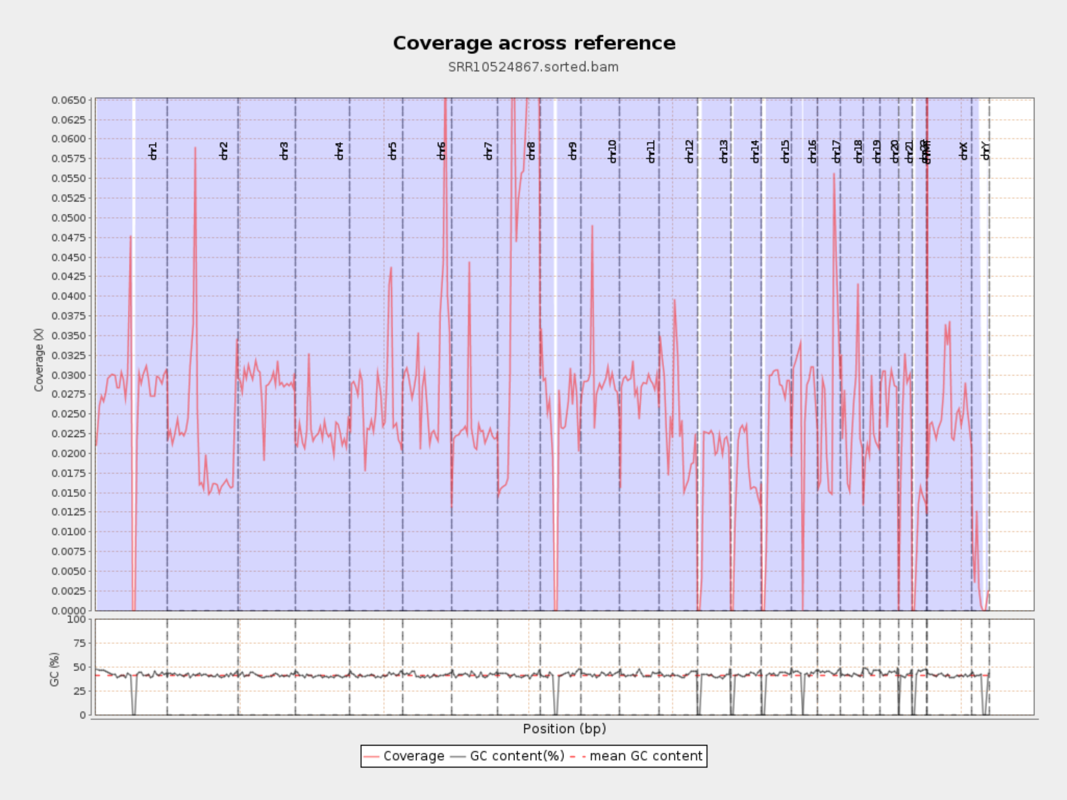
General error rate	0.51%
Mismatches	398,737
Insertions	5,302
Mapped reads with at least one insertion	0.38%
Deletions	14,952
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.65%

2.6. Chromosome stats

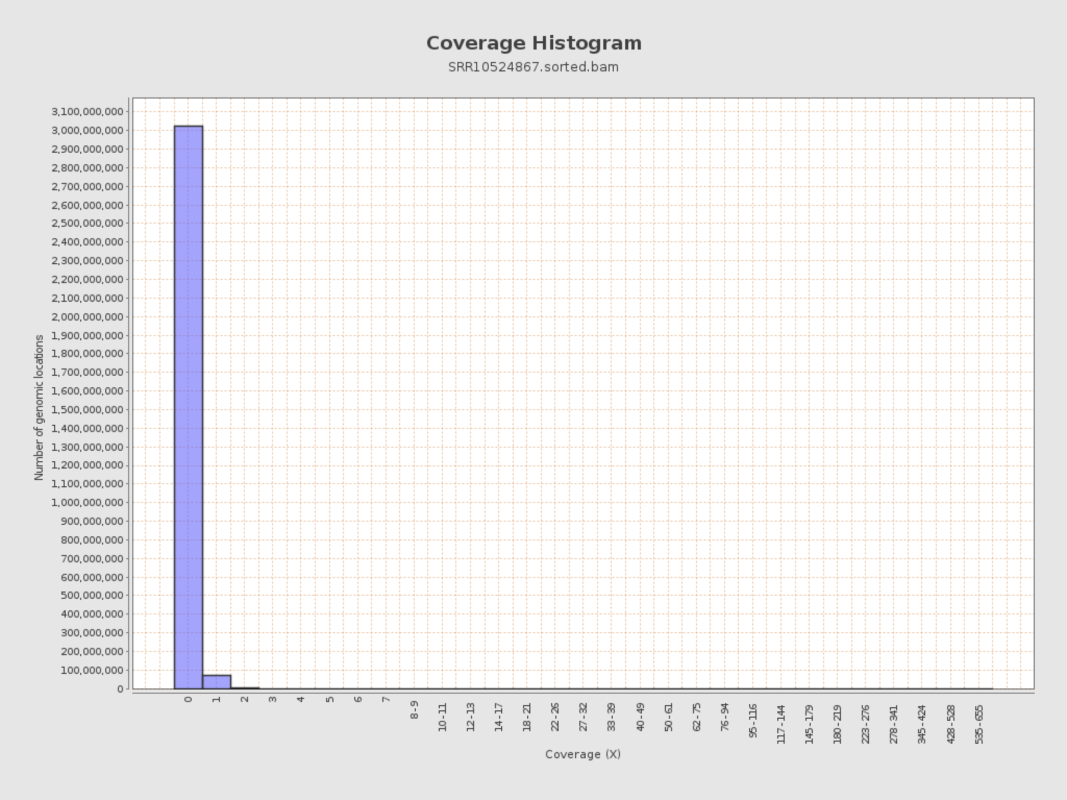
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6797522	0.0273	0.4944
chr2	243199373	5258156	0.0216	0.2815
chr3	198022430	5750576	0.029	0.1823
chr4	191154276	4345058	0.0227	0.1754
chr5	180915260	4859690	0.0269	0.1755
chr6	171115067	5276559	0.0308	0.2036
chr7	159138663	3708957	0.0233	0.3453

chr8	146364022	8604519	0.0588	0.3388
chr9	141213431	3353127	0.0237	0.2182
chr10	135534747	4014938	0.0296	0.2555
chr11	135006516	3858616	0.0286	0.2336
chr12	133851895	3199898	0.0239	0.1678
chr13	115169878	2076993	0.018	0.1429
chr14	107349540	1712593	0.016	0.146
chr15	102531392	2420416	0.0236	0.1641
chr16	90354753	2412516	0.0267	0.186
chr17	81195210	2256122	0.0278	0.1961
chr18	78077248	1943000	0.0249	0.3859
chr19	59128983	1288747	0.0218	0.3195
chr20	63025520	1769915	0.0281	0.1816
chr21	48129895	1157550	0.0241	0.1737
chr22	51304566	519251	0.0101	0.1061
chrMT	16571	2832	0.1709	0.435
chrX	155270560	3984833	0.0257	0.1915
chrY	59373566	214724	0.0036	0.094

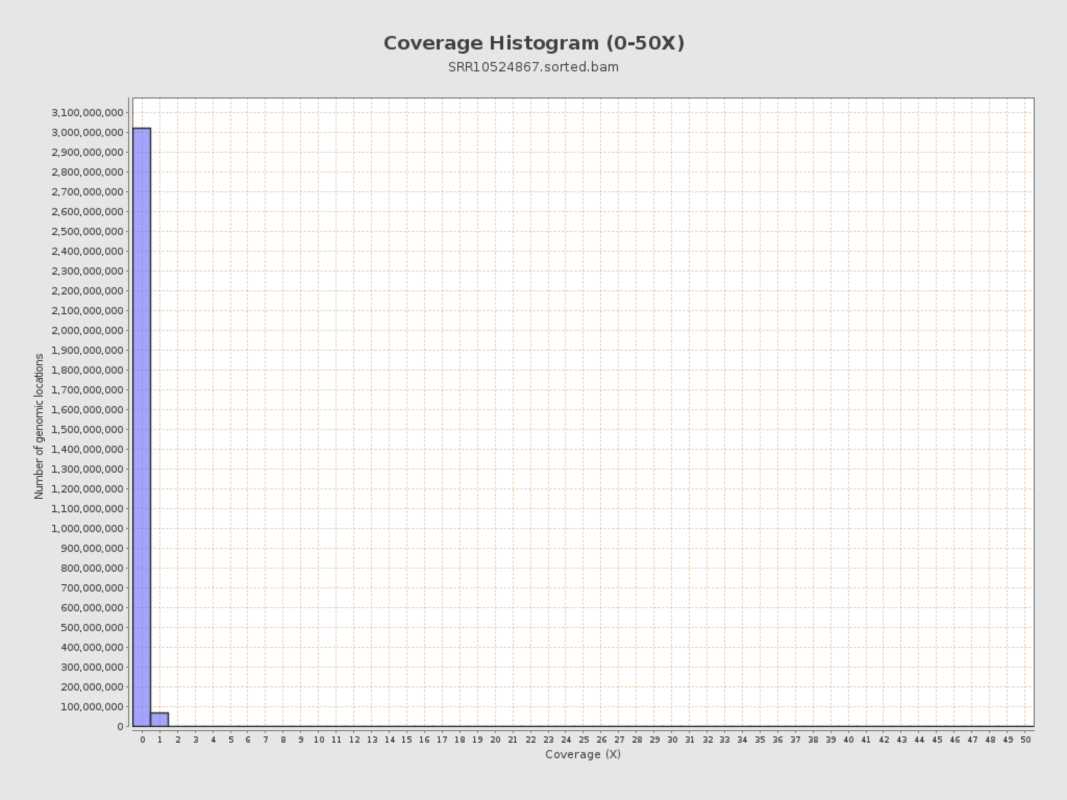
3. Results : Coverage across reference



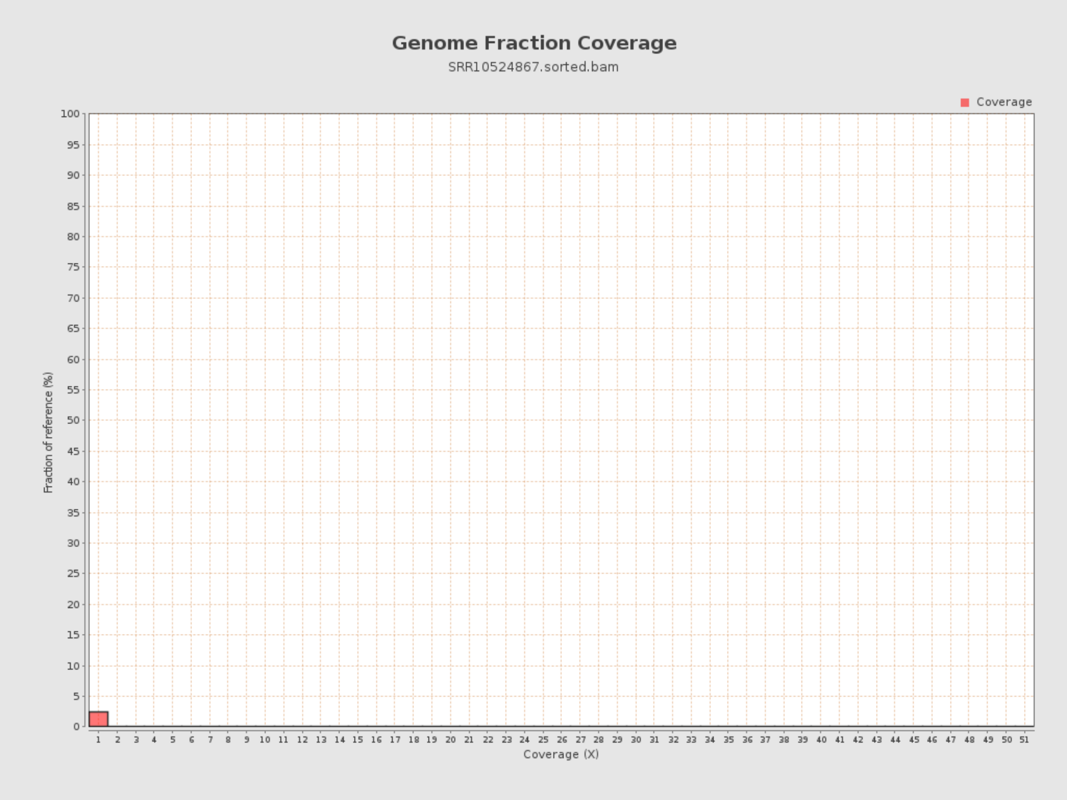
4. Results : Coverage Histogram



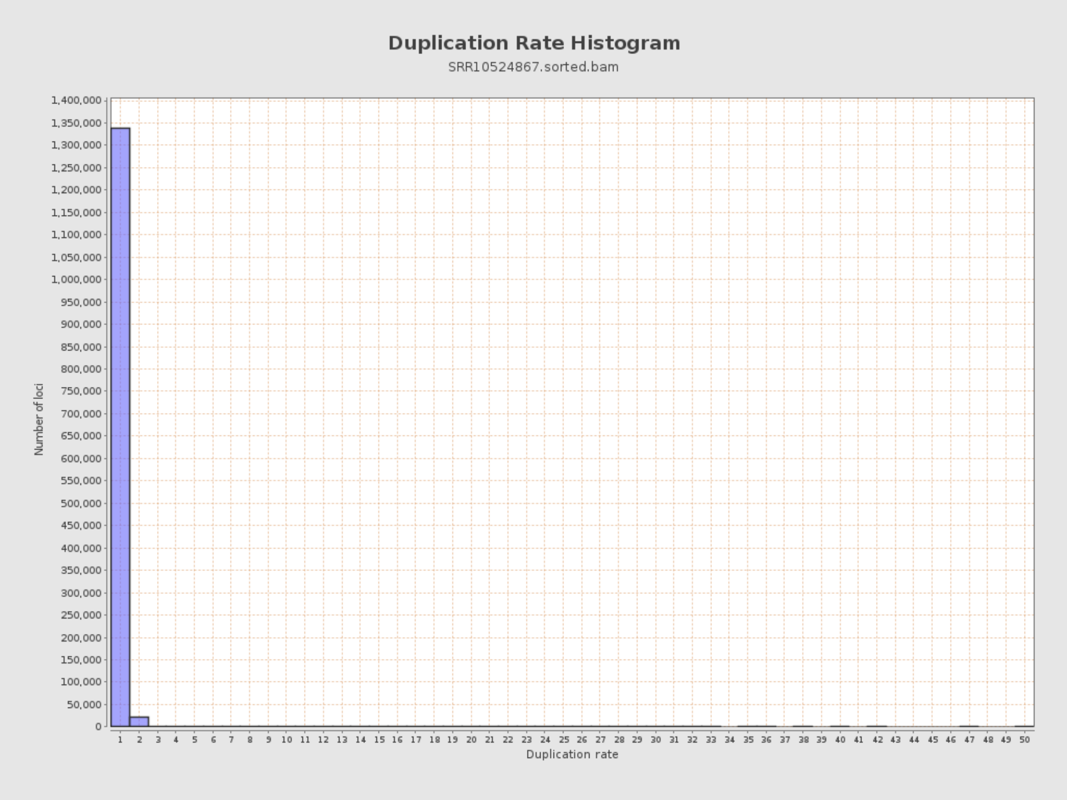
5. Results : Coverage Histogram (0-50X)



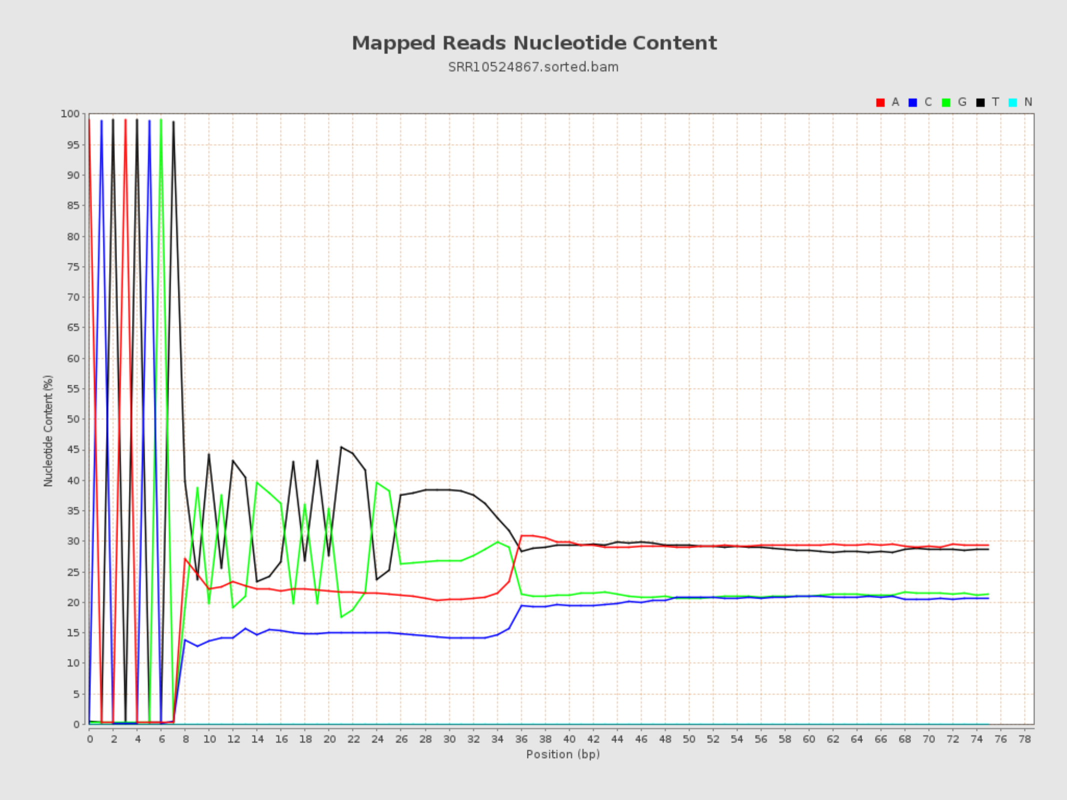
6. Results : Genome Fraction Coverage



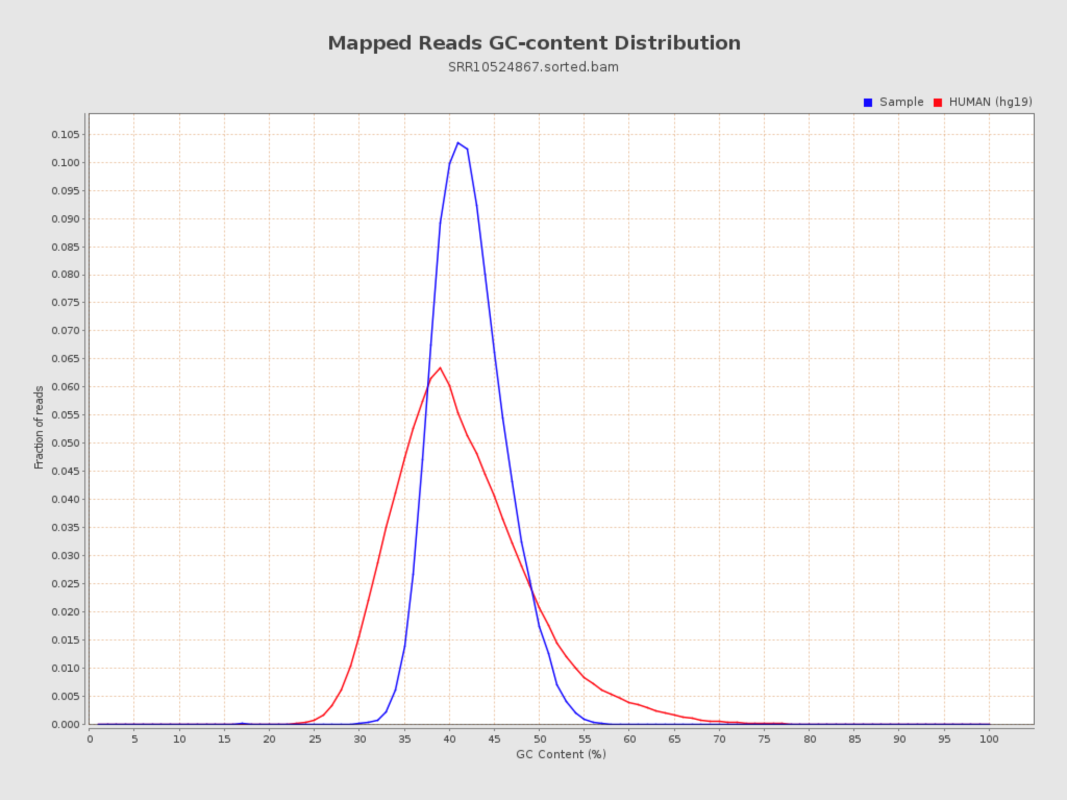
7. Results : Duplication Rate Histogram



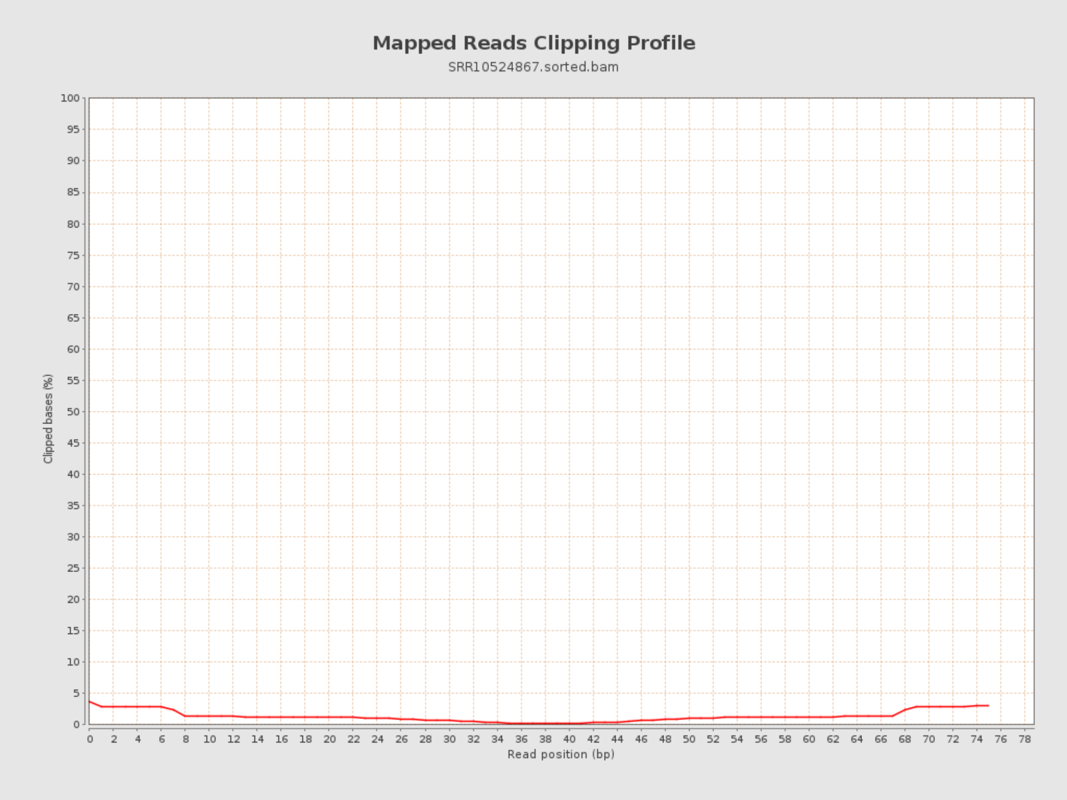
8. Results : Mapped Reads Nucleotide Content



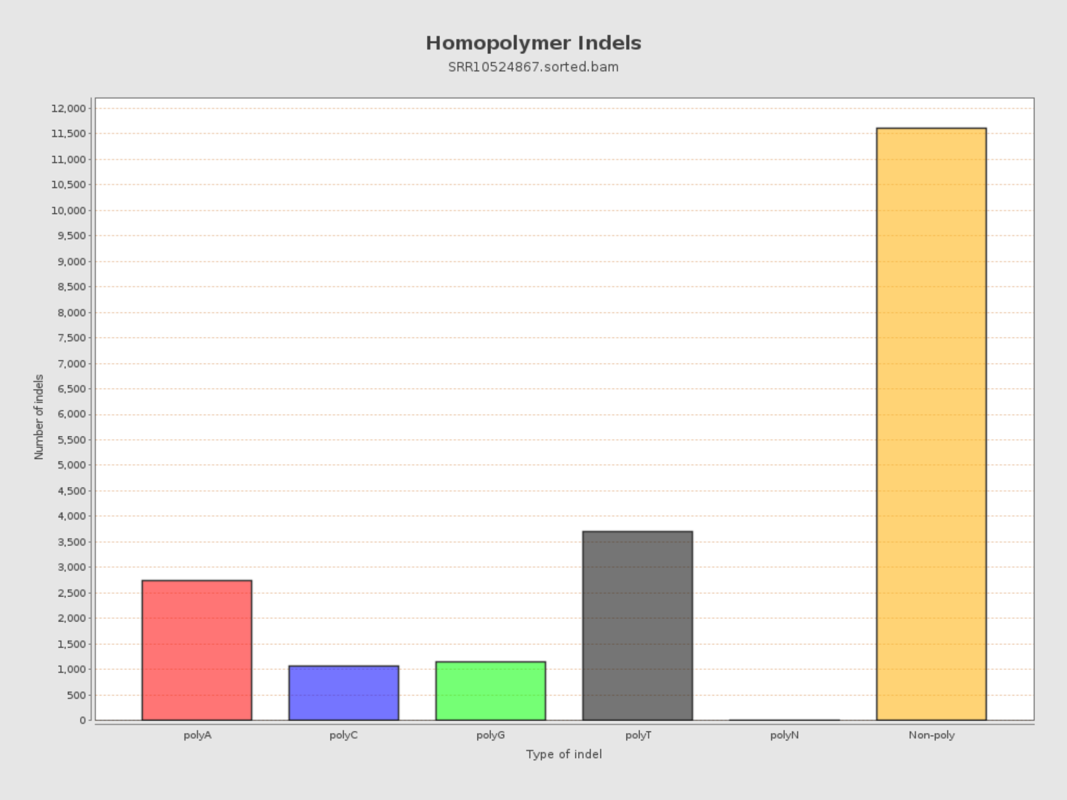
9. Results : Mapped Reads GC-content Distribution



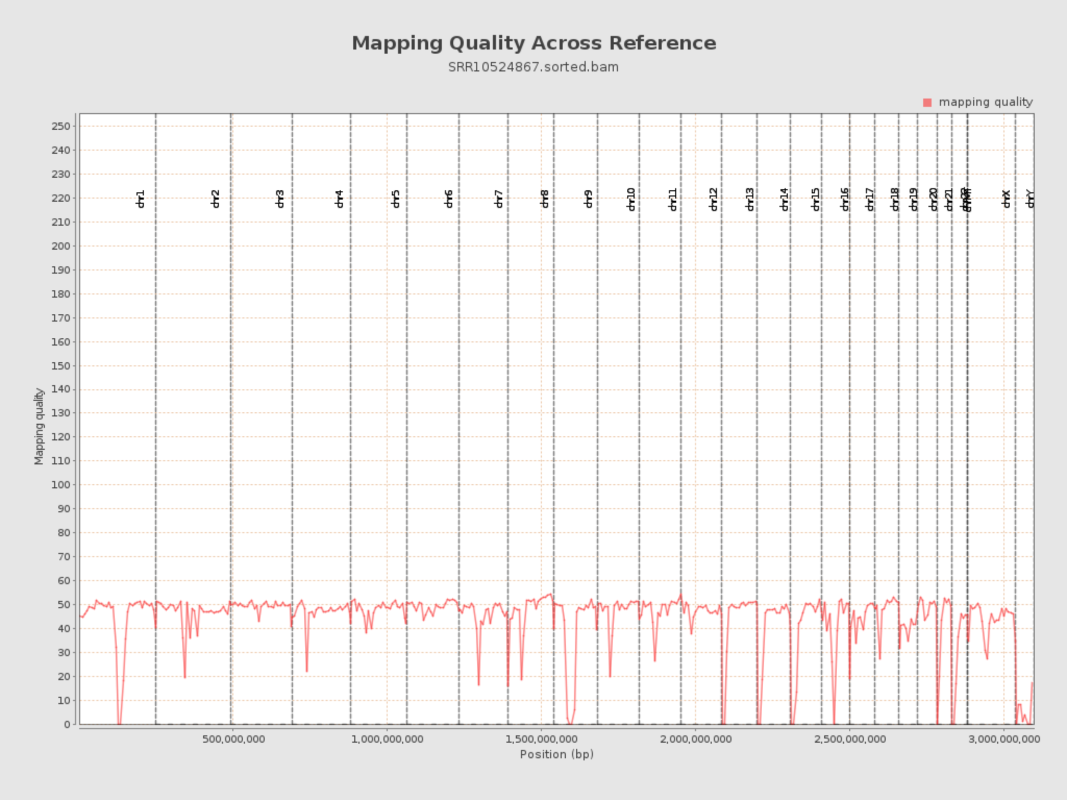
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram