Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:46:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524537.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_SRR10524537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524537.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:46:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,560,161
Mapped reads	1,431,009 / 91.72%
Unmapped reads	129,152 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,870 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	63,115 / 4.05%
Duplication rate	3.36%
Clipped reads	1,435,390 / 92%

2.2. ACGT Content

Number/percentage of A's	21,360,491 / 25.48%
Number/percentage of C's	17,323,887 / 20.66%
Number/percentage of T's	25,310,190 / 30.19%
Number/percentage of G's	19,837,471 / 23.66%
Number/percentage of N's	1,217 / 0%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.259

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

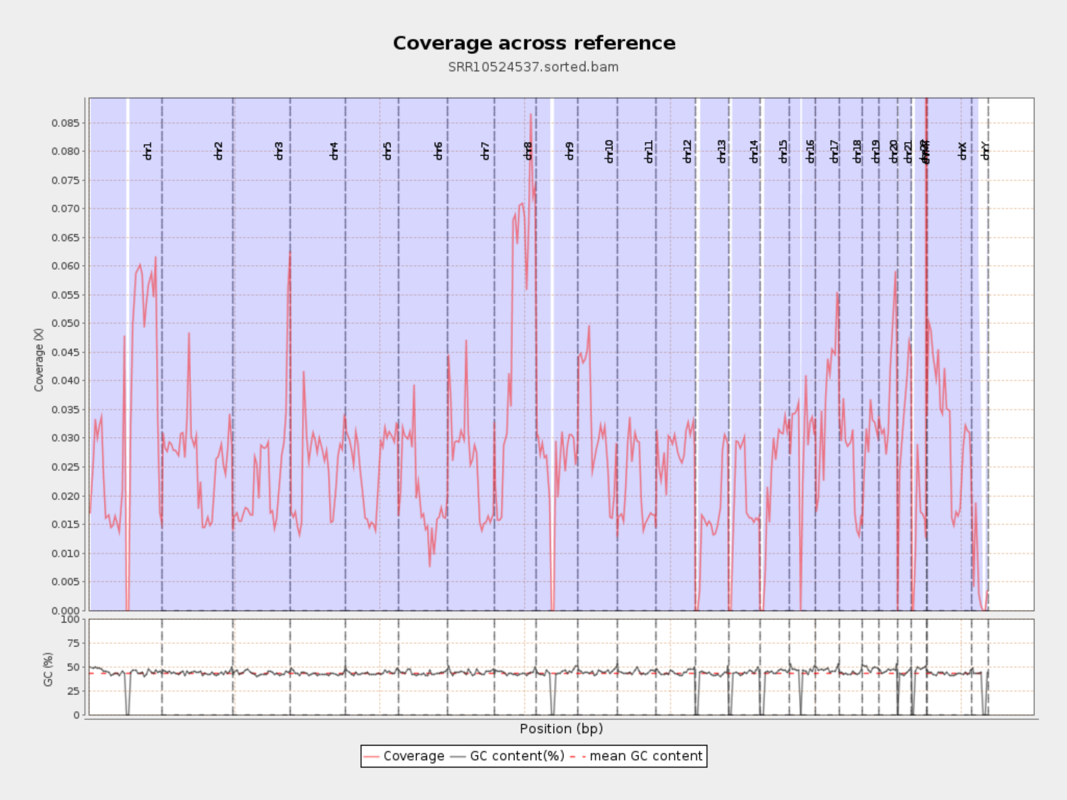
General error rate	0.52%
Mismatches	426,771
Insertions	4,617
Mapped reads with at least one insertion	0.32%
Deletions	15,752
Mapped reads with at least one deletion	1.09%
Homopolymer indels	45.71%

2.6. Chromosome stats

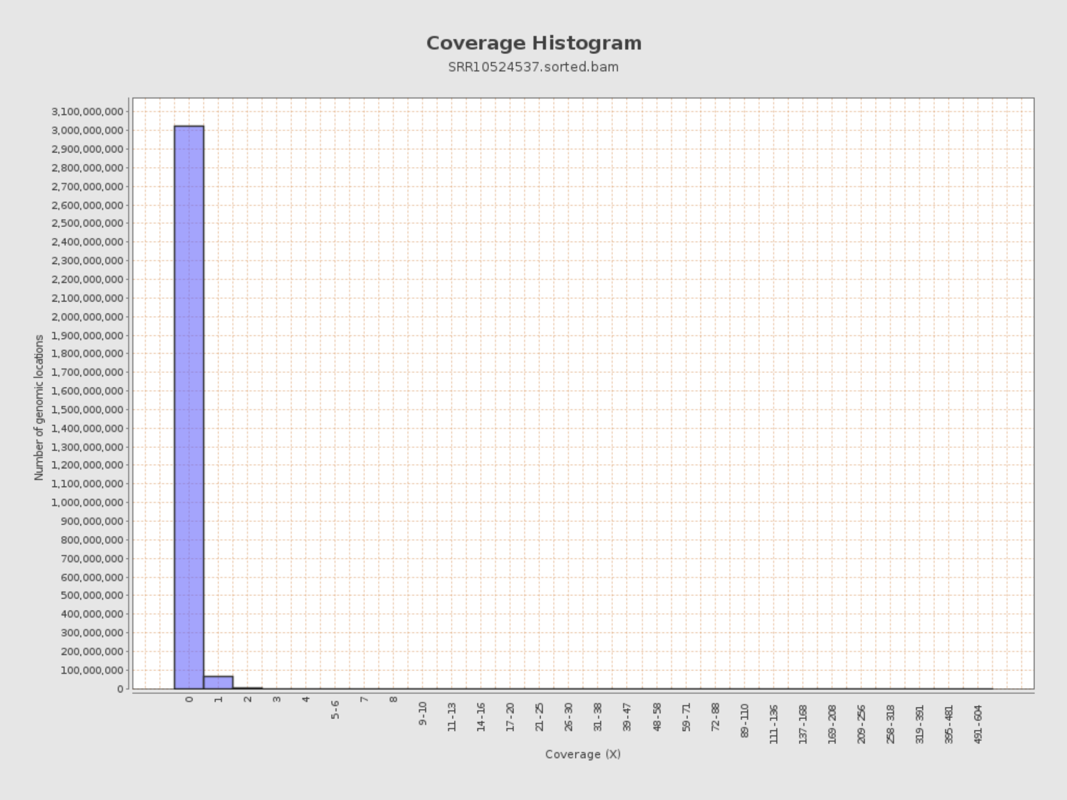
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8351258	0.0335	0.4638
chr2	243199373	6419038	0.0264	0.2851
chr3	198022430	4563952	0.023	0.1676
chr4	191154276	4707709	0.0246	0.2
chr5	180915260	4569577	0.0253	0.1747
chr6	171115067	3481963	0.0203	0.1942
chr7	159138663	4138042	0.026	0.3179

chr8	146364022	7463787	0.051	0.298
chr9	141213431	3429685	0.0243	0.226
chr10	135534747	4367031	0.0322	0.2612
chr11	135006516	2855696	0.0212	0.2277
chr12	133851895	3788201	0.0283	0.1864
chr13	115169878	1828663	0.0159	0.1387
chr14	107349540	1990692	0.0185	0.1535
chr15	102531392	2291355	0.0223	0.1666
chr16	90354753	2691150	0.0298	0.1997
chr17	81195210	3021082	0.0372	0.2239
chr18	78077248	1974942	0.0253	0.4419
chr19	59128983	1790022	0.0303	0.3073
chr20	63025520	2460657	0.039	0.2224
chr21	48129895	1574403	0.0327	0.2197
chr22	51304566	709421	0.0138	0.129
chrMT	16571	56667	3.4196	2.6975
chrX	155270560	5034483	0.0324	0.2181
chrY	59373566	300238	0.0051	0.1639

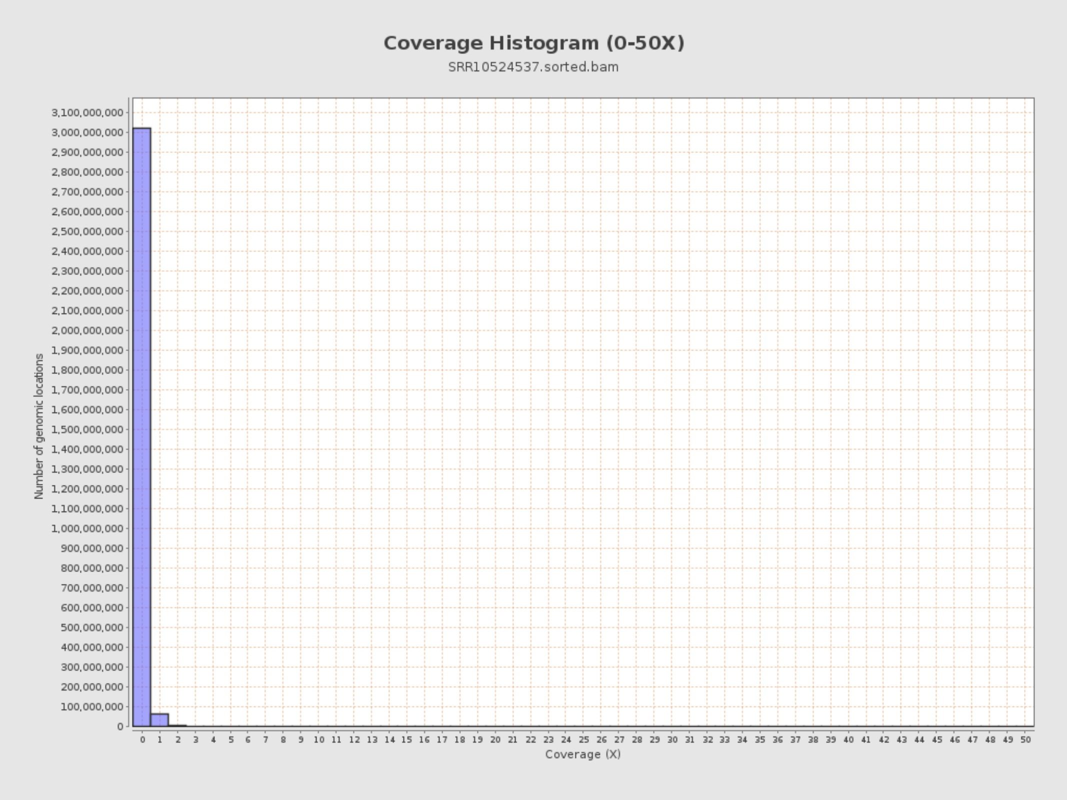
3. Results : Coverage across reference



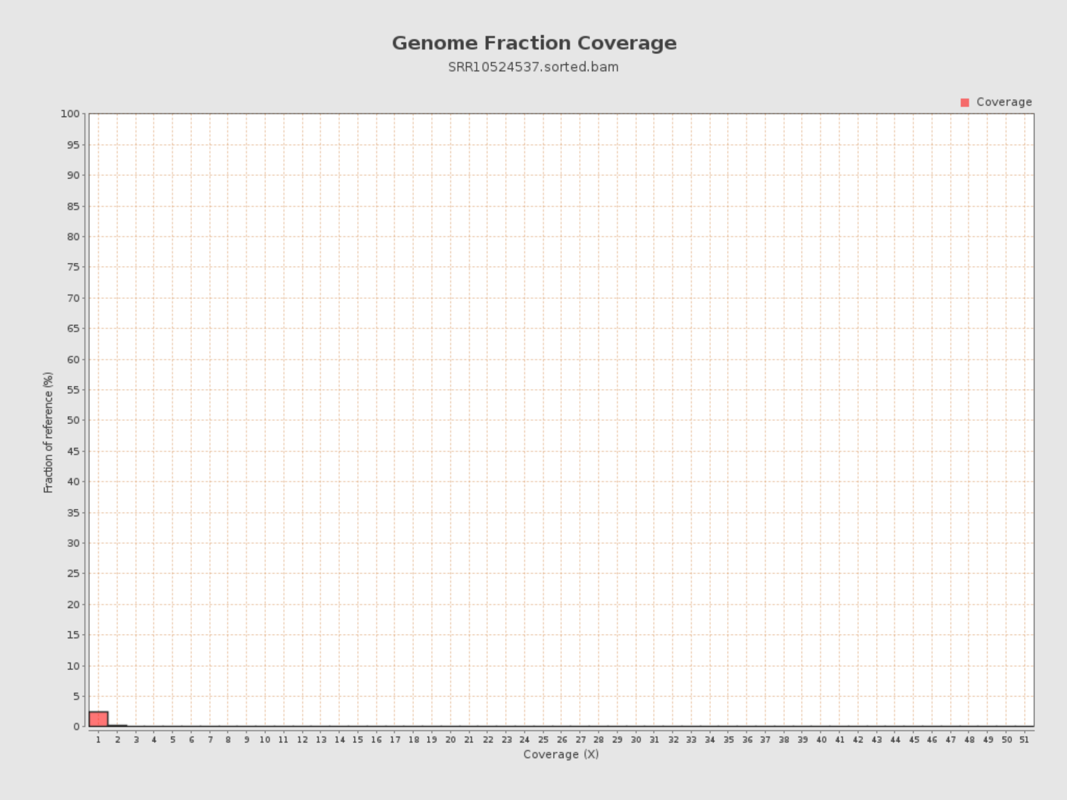
4. Results : Coverage Histogram



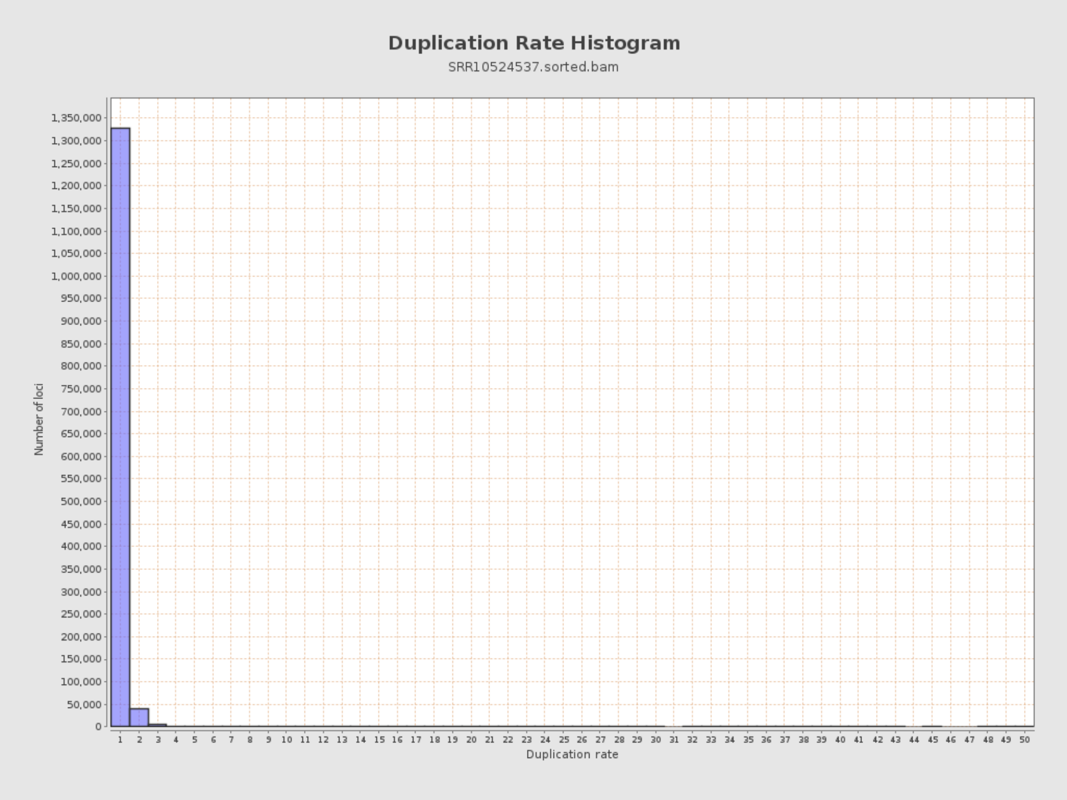
5. Results : Coverage Histogram (0-50X)



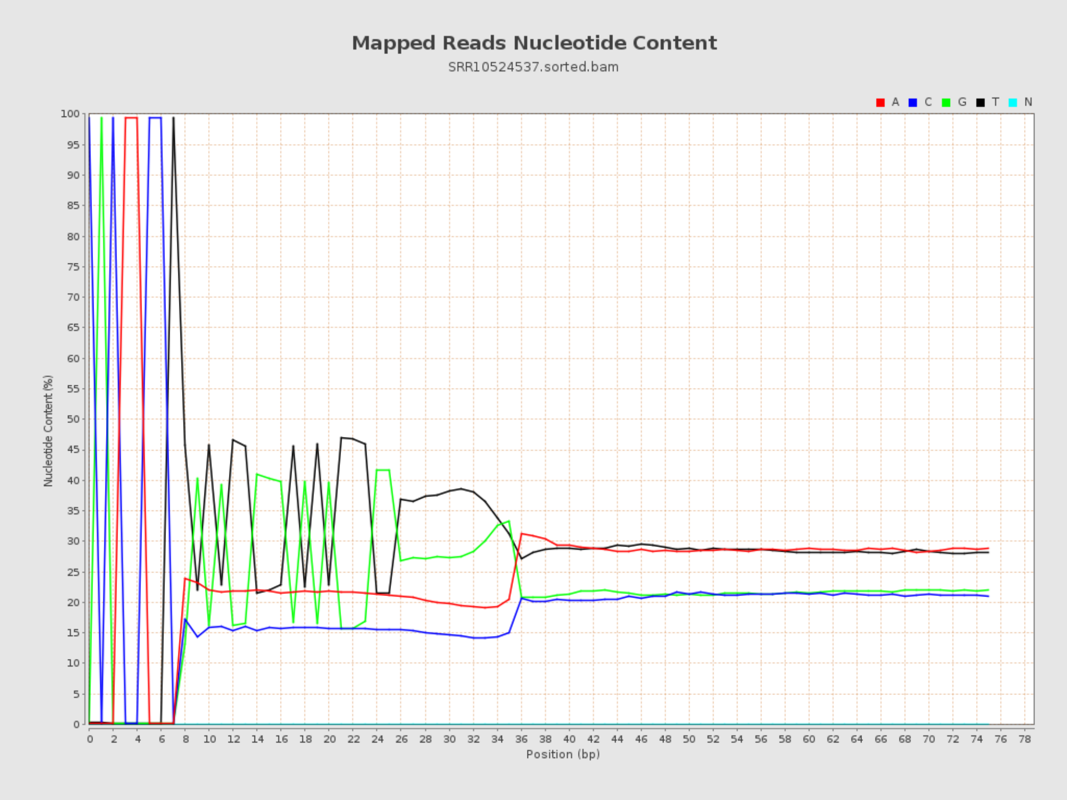
6. Results : Genome Fraction Coverage



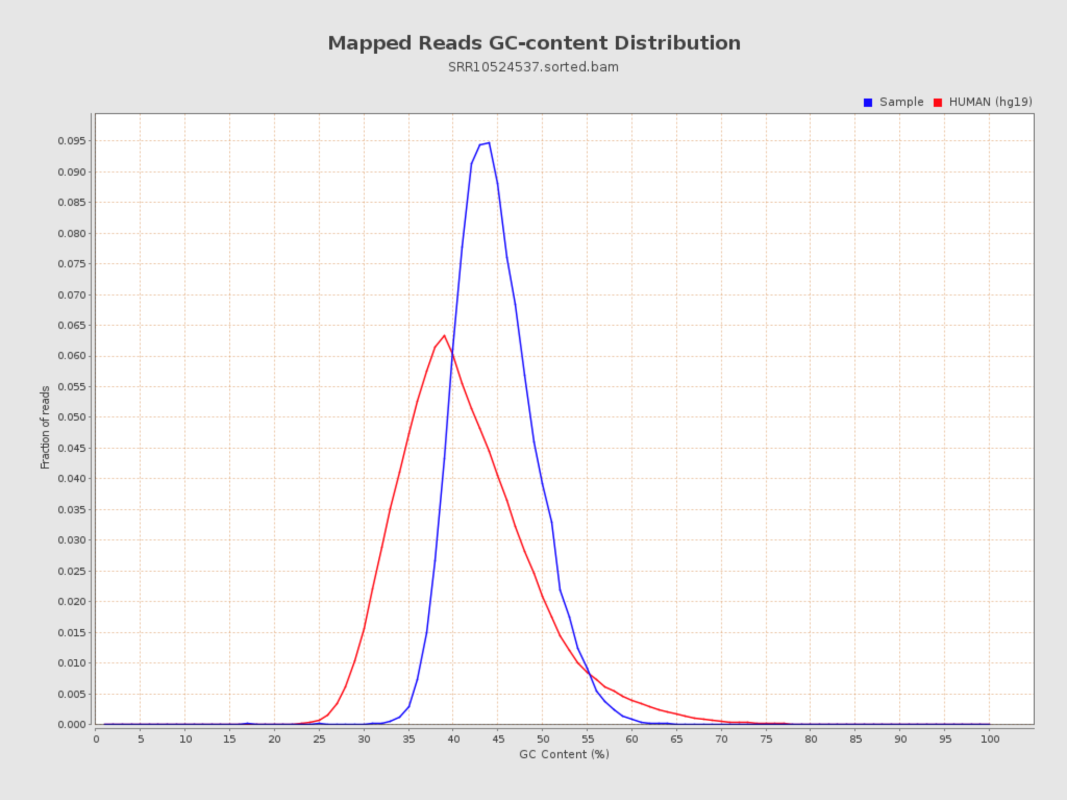
7. Results : Duplication Rate Histogram



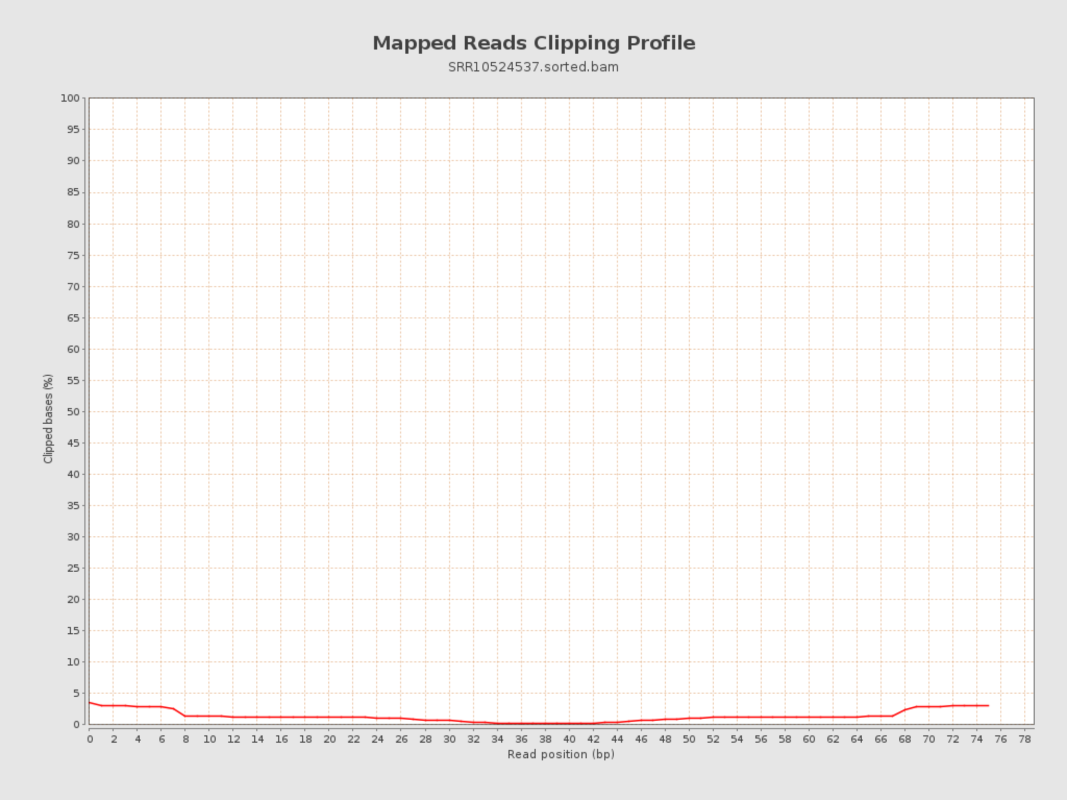
8. Results : Mapped Reads Nucleotide Content



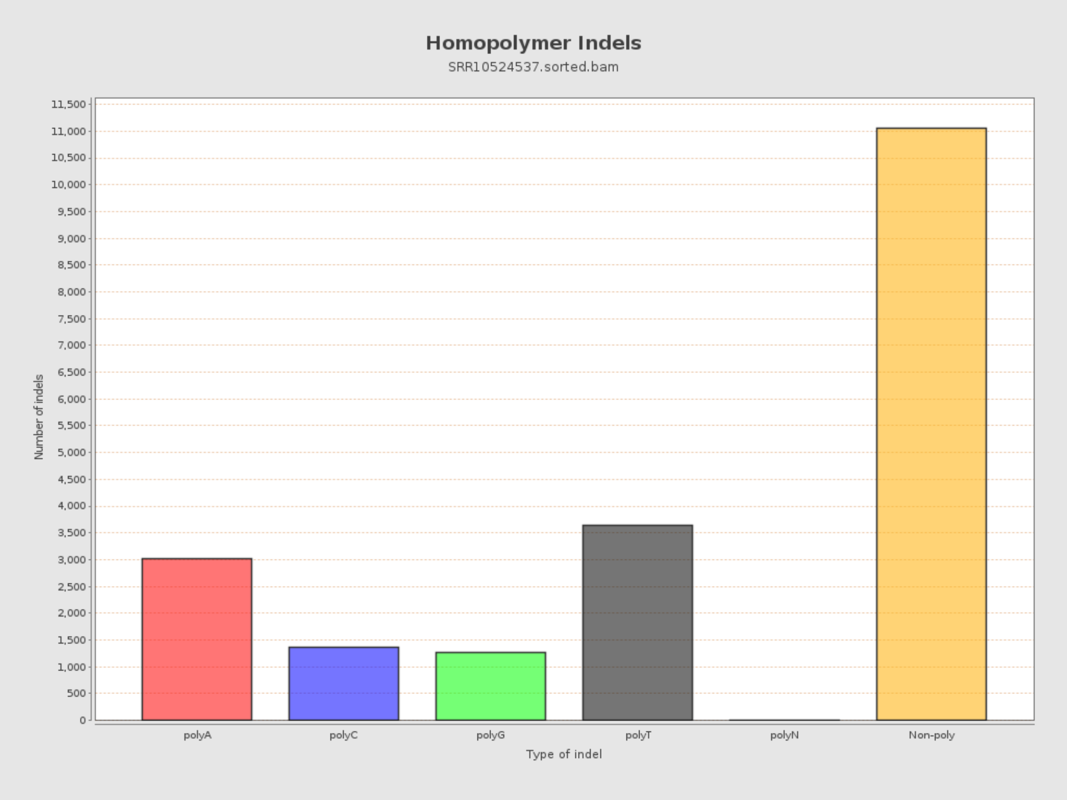
9. Results : Mapped Reads GC-content Distribution



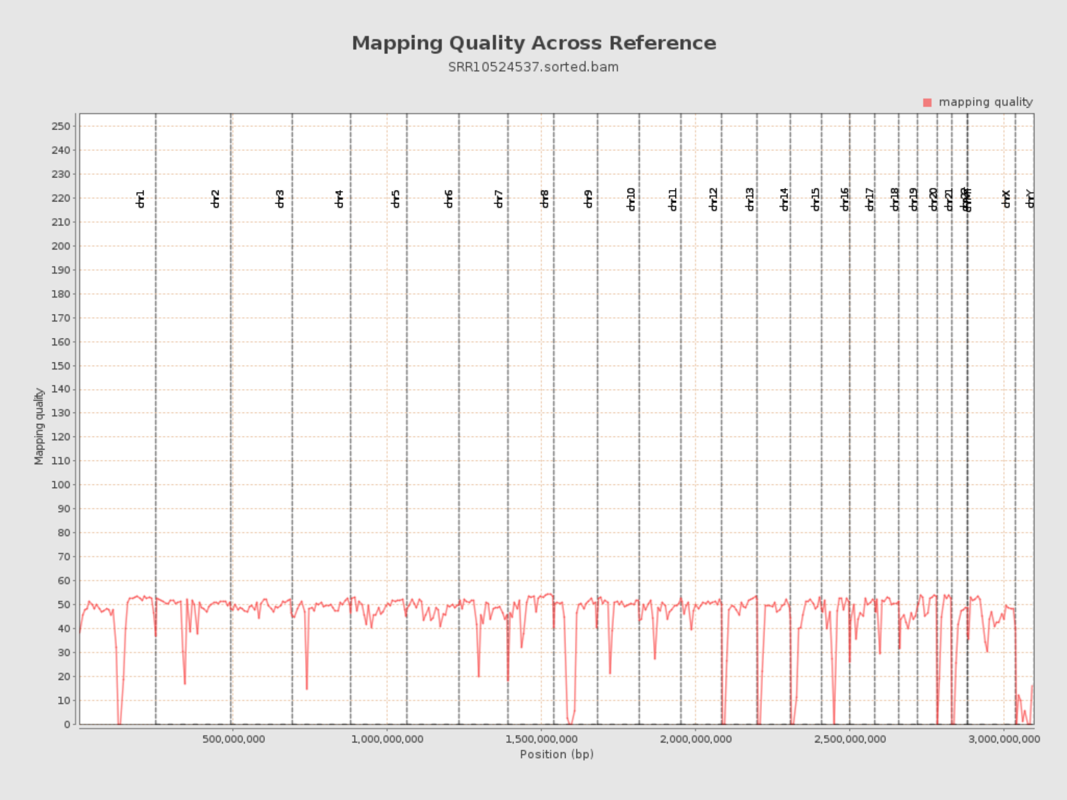
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram