Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:36:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524837.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_SRR10524837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,111,111
Mapped reads	1,955,509 / 92.63%
Unmapped reads	155,602 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,158 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	66,754 / 3.16%
Duplication rate	2.24%
Clipped reads	1,964,408 / 93.05%

2.2. ACGT Content

Number/percentage of A's	28,841,241 / 25.08%
Number/percentage of C's	19,896,364 / 17.3%
Number/percentage of T's	38,421,589 / 33.41%
Number/percentage of G's	27,819,461 / 24.19%
Number/percentage of N's	15,483 / 0.01%
GC Percentage	41.49%

2.3. Coverage

Mean	0.0372

Standard Deviation	0.3798

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

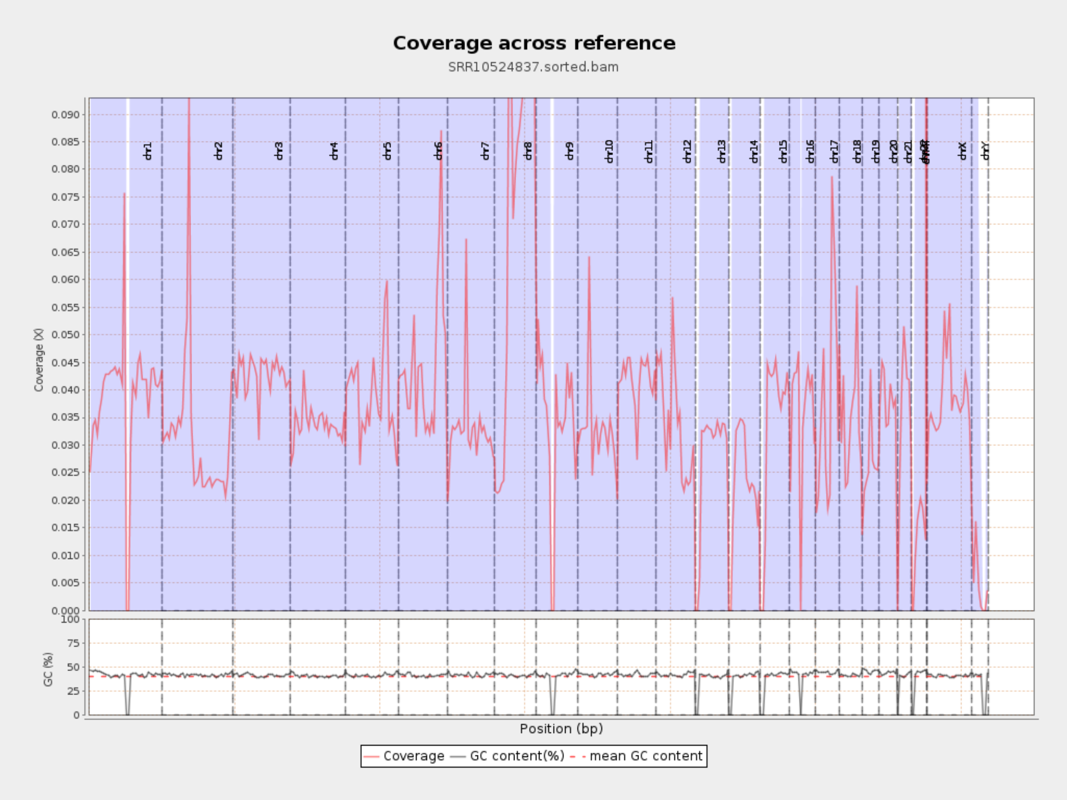
General error rate	0.49%
Mismatches	551,397
Insertions	7,848
Mapped reads with at least one insertion	0.4%
Deletions	21,433
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.99%

2.6. Chromosome stats

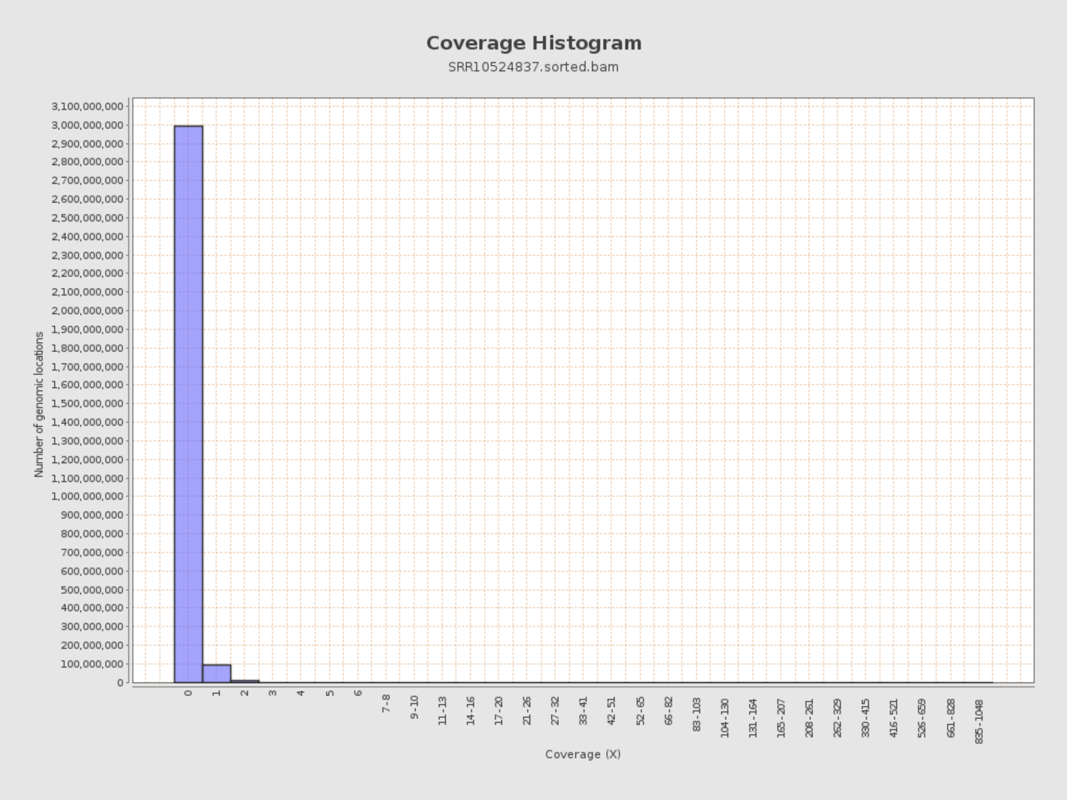
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9628867	0.0386	0.8226
chr2	243199373	7639326	0.0314	0.35
chr3	198022430	8485080	0.0428	0.2248
chr4	191154276	6455401	0.0338	0.2183
chr5	180915260	7101042	0.0393	0.2166
chr6	171115067	7580459	0.0443	0.2594
chr7	159138663	5320198	0.0334	0.5302

chr8	146364022	12769665	0.0872	0.5028
chr9	141213431	4785262	0.0339	0.2993
chr10	135534747	4509330	0.0333	0.3219
chr11	135006516	5601047	0.0415	0.3163
chr12	133851895	4518405	0.0338	0.2075
chr13	115169878	3127623	0.0272	0.1795
chr14	107349540	2442028	0.0227	0.1809
chr15	102531392	3429142	0.0334	0.1993
chr16	90354753	3252207	0.036	0.2309
chr17	81195210	3017643	0.0372	0.2439
chr18	78077248	2805814	0.0359	0.5931
chr19	59128983	1586184	0.0268	0.5097
chr20	63025520	2378109	0.0377	0.2132
chr21	48129895	1690736	0.0351	0.2204
chr22	51304566	646353	0.0126	0.1212
chrMT	16571	14345	0.8657	1.1055
chrX	155270560	5958759	0.0384	0.255
chrY	59373566	284477	0.0048	0.1205

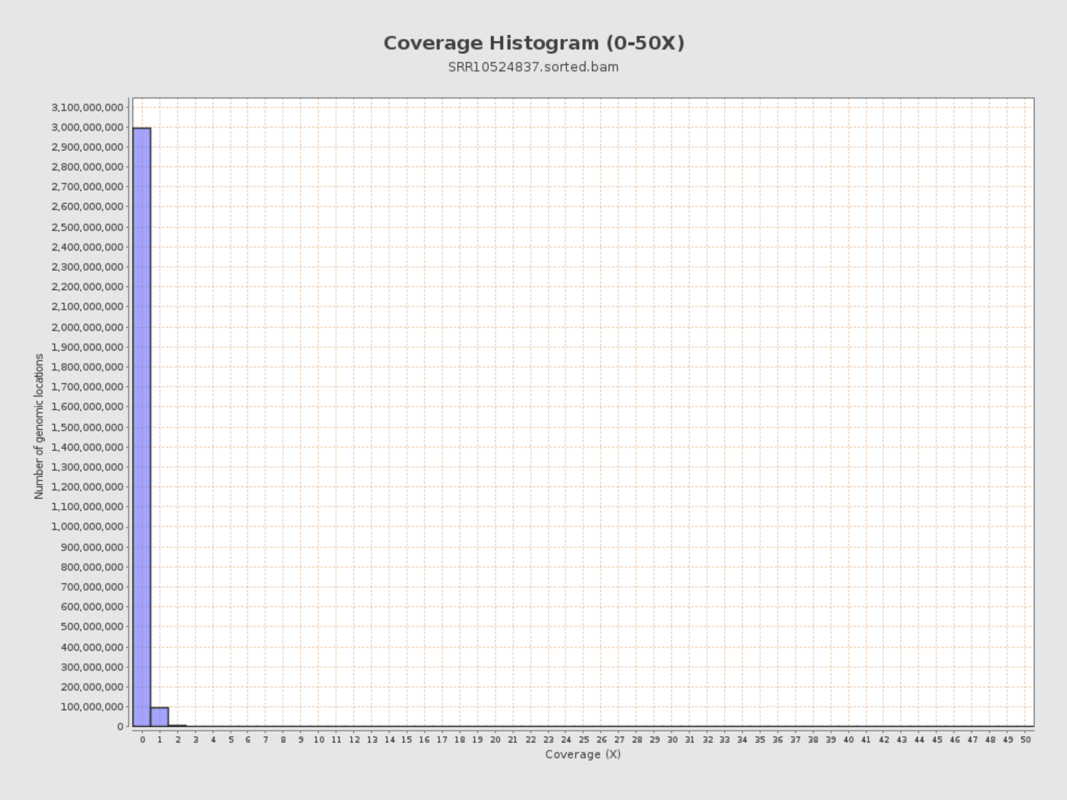
3. Results : Coverage across reference



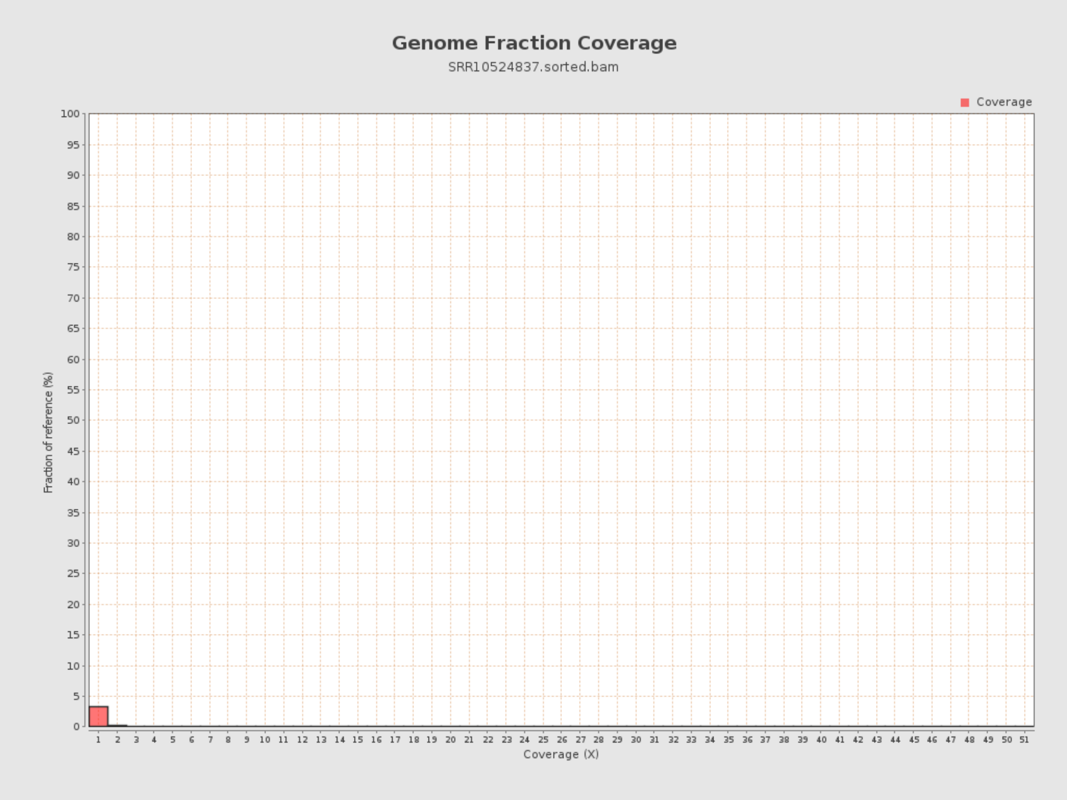
4. Results : Coverage Histogram



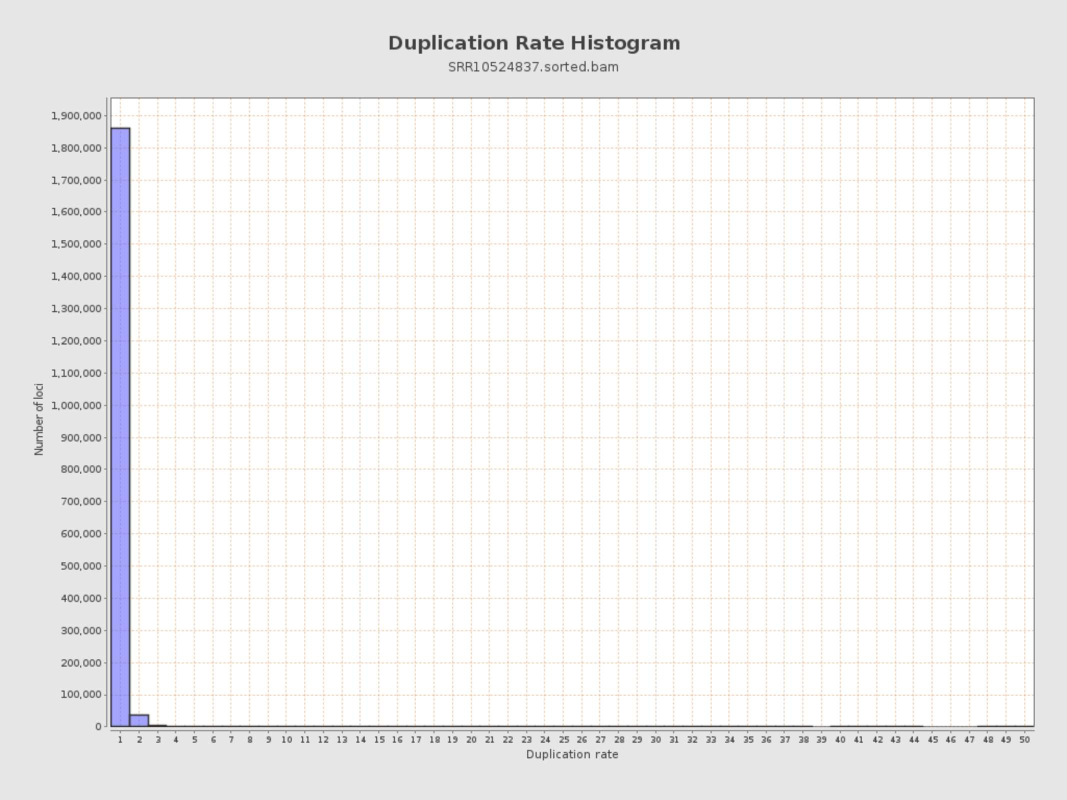
5. Results : Coverage Histogram (0-50X)



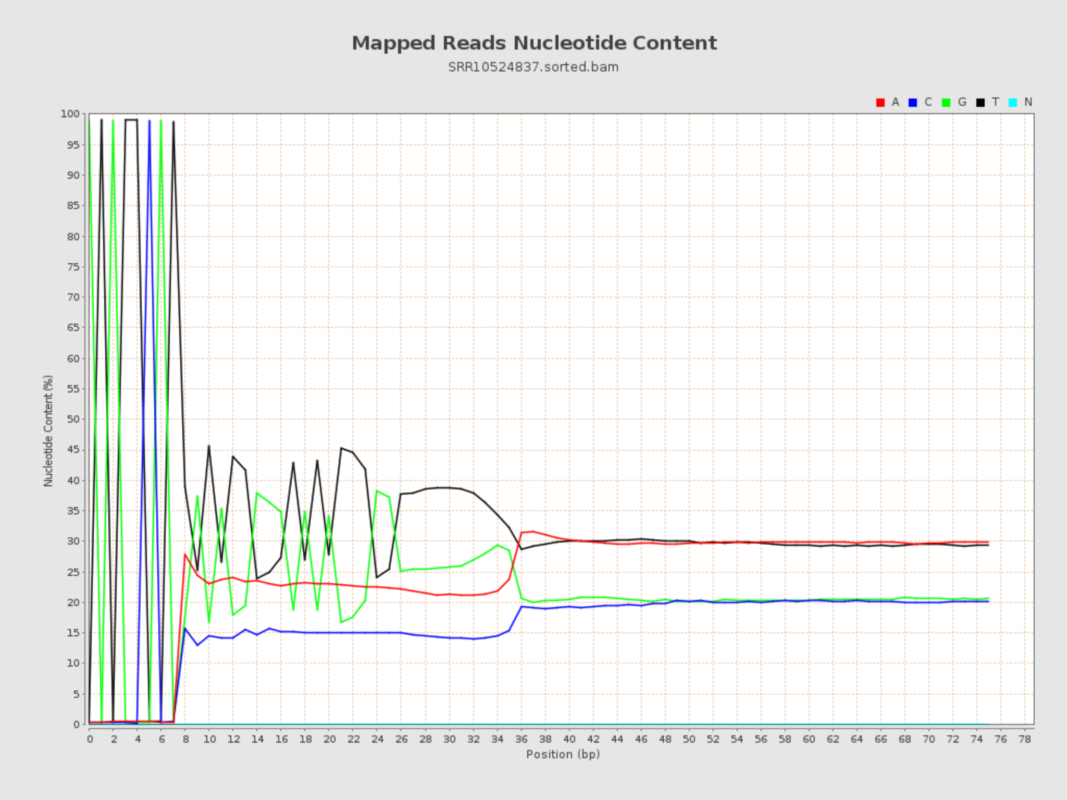
6. Results : Genome Fraction Coverage



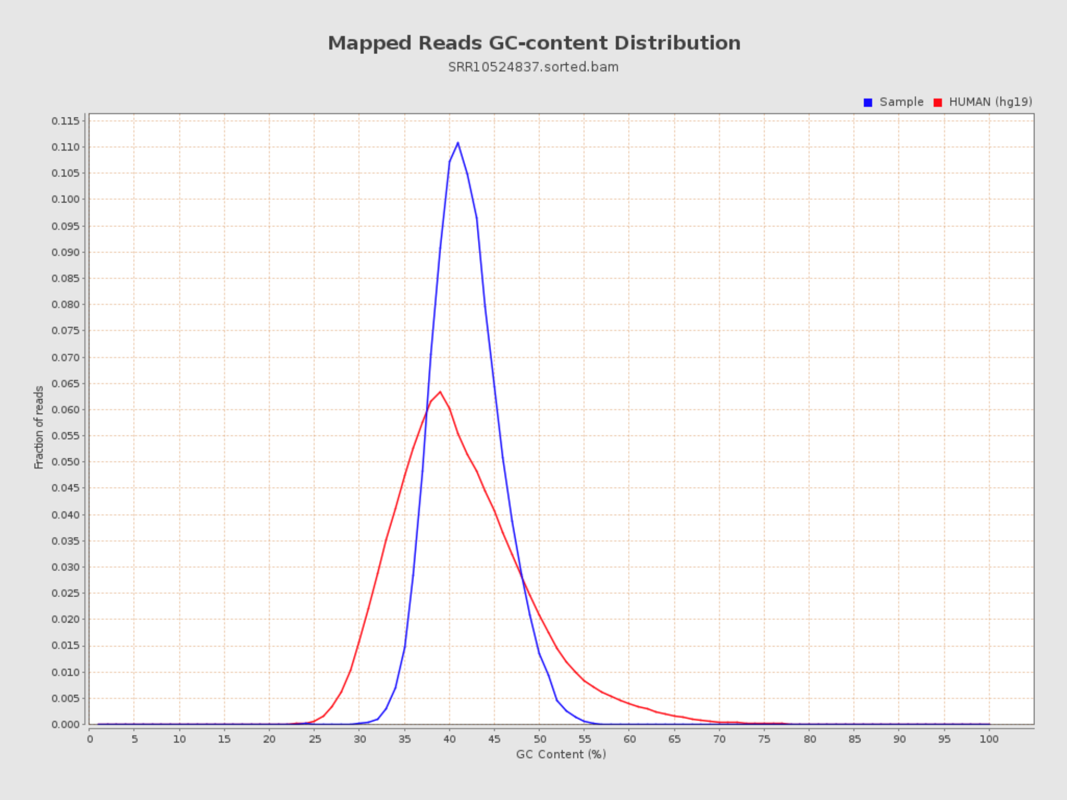
7. Results : Duplication Rate Histogram



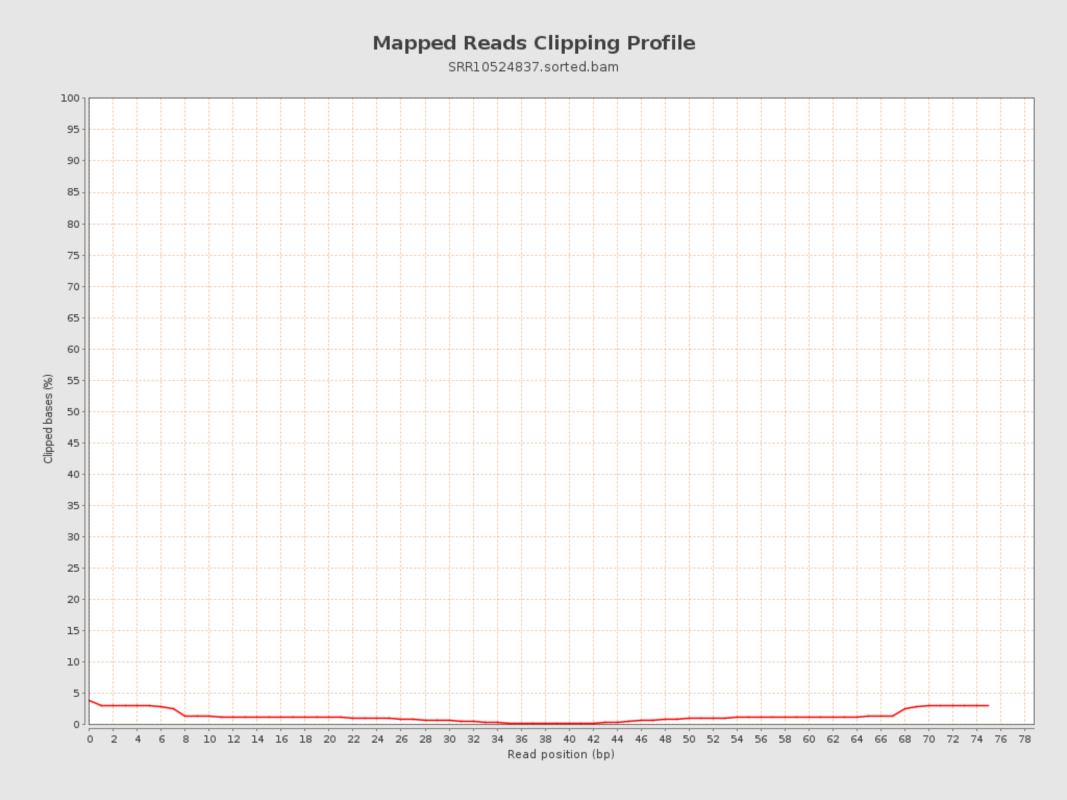
8. Results : Mapped Reads Nucleotide Content



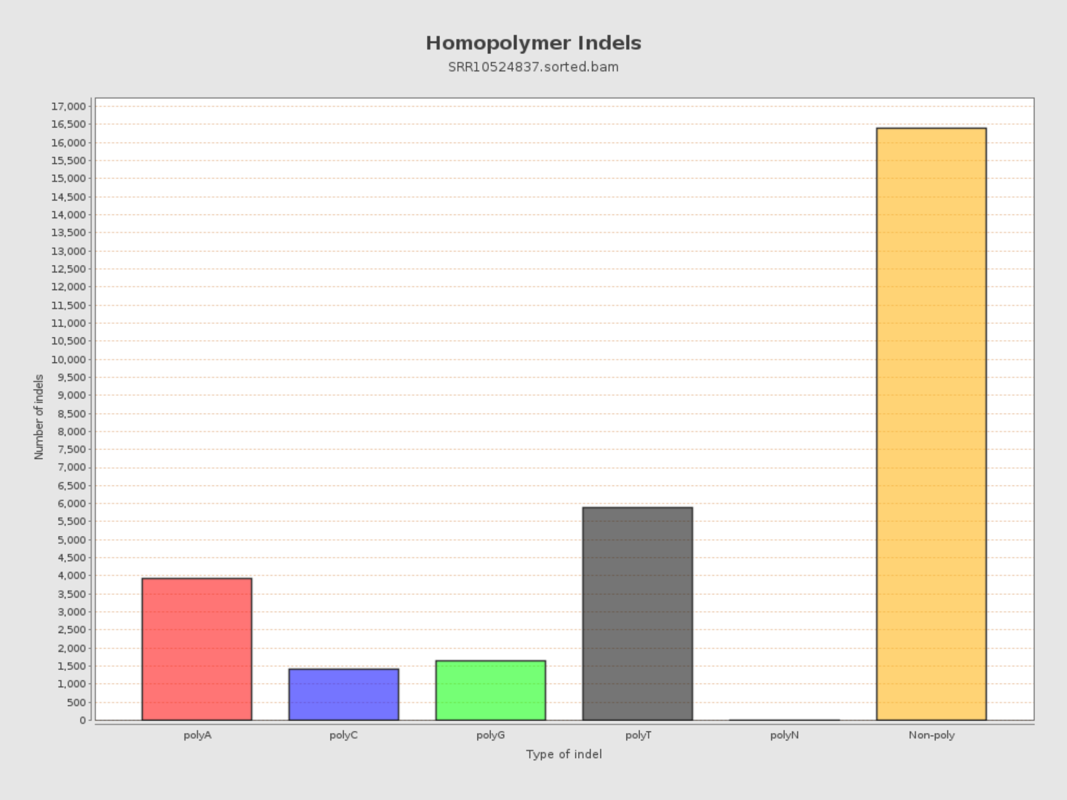
9. Results : Mapped Reads GC-content Distribution



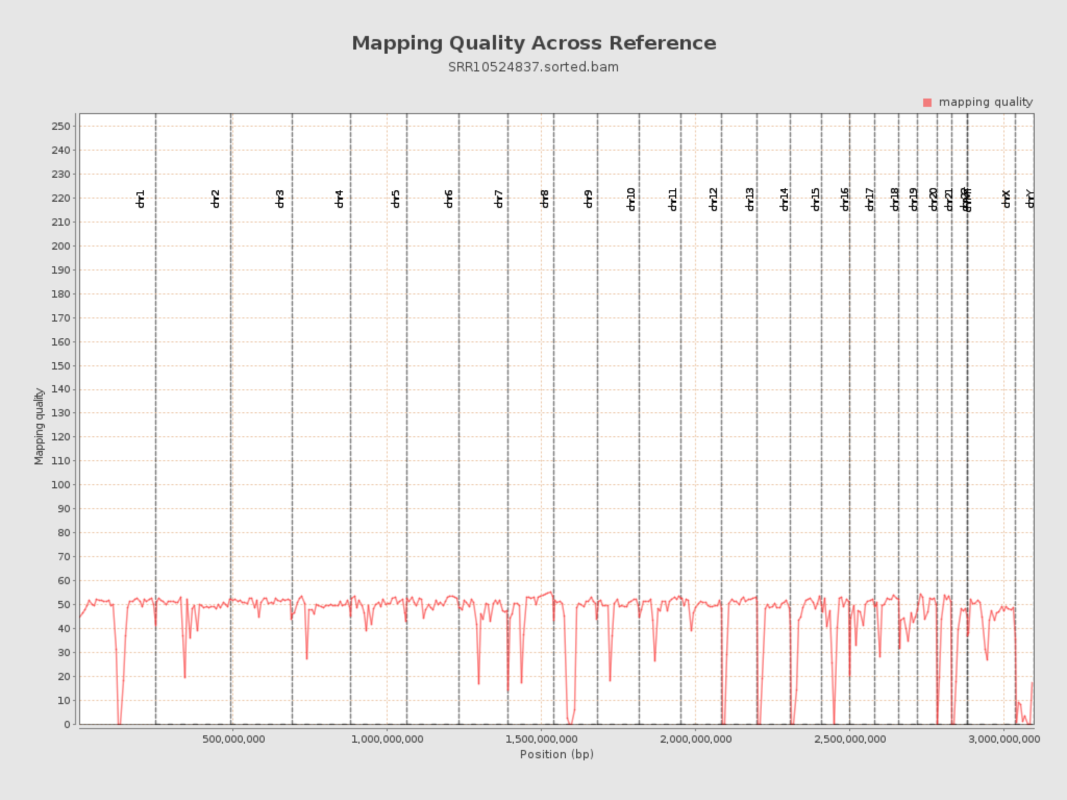
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram