Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:37:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524689.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_SRR10524689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524689.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:37:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,043,369
Mapped reads	1,862,990 / 91.17%
Unmapped reads	180,379 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,353 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	75,833 / 3.71%
Duplication rate	2.98%
Clipped reads	1,865,533 / 91.3%

2.2. ACGT Content

Number/percentage of A's	27,135,399 / 25.47%
Number/percentage of C's	18,991,671 / 17.83%
Number/percentage of T's	35,281,227 / 33.12%
Number/percentage of G's	25,128,389 / 23.59%
Number/percentage of N's	2,013 / 0%
GC Percentage	41.41%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.3324

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

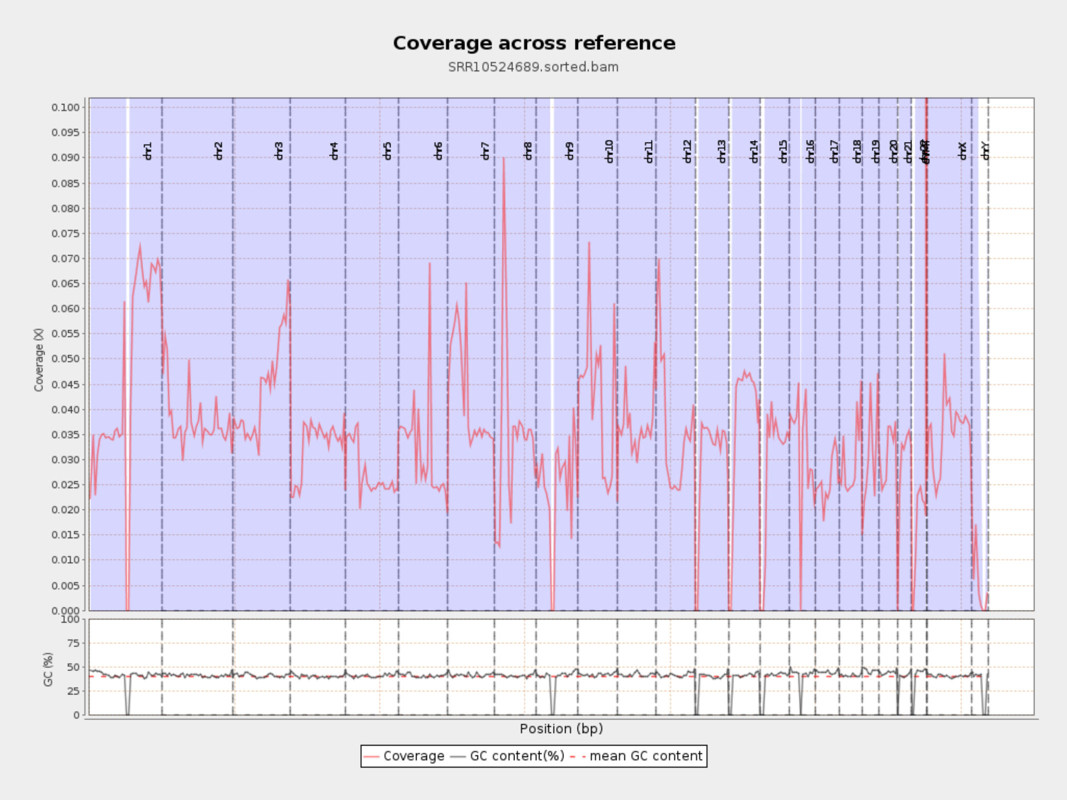
General error rate	0.52%
Mismatches	543,845
Insertions	8,024
Mapped reads with at least one insertion	0.43%
Deletions	22,443
Mapped reads with at least one deletion	1.2%
Homopolymer indels	42.91%

2.6. Chromosome stats

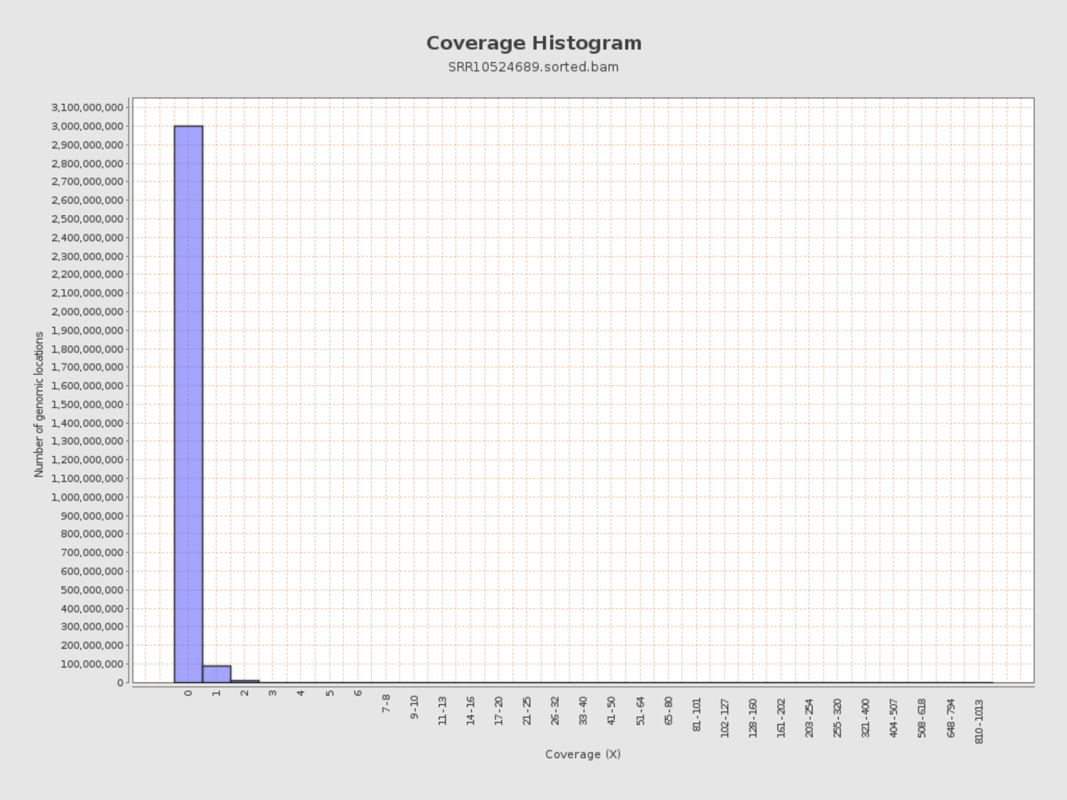
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11469199	0.046	0.6249
chr2	243199373	9234591	0.038	0.458
chr3	198022430	8658347	0.0437	0.2305
chr4	191154276	6256819	0.0327	0.209
chr5	180915260	4945386	0.0273	0.1818
chr6	171115067	5476871	0.032	0.2343
chr7	159138663	6856937	0.0431	0.5062

chr8	146364022	5027158	0.0343	0.3214
chr9	141213431	3468600	0.0246	0.2284
chr10	135534747	5800701	0.0428	0.3483
chr11	135006516	4957708	0.0367	0.271
chr12	133851895	4832894	0.0361	0.2118
chr13	115169878	3465057	0.0301	0.1936
chr14	107349540	4006048	0.0373	0.2184
chr15	102531392	2942536	0.0287	0.1919
chr16	90354753	2837260	0.0314	0.2173
chr17	81195210	2093714	0.0258	0.1831
chr18	78077248	2322814	0.0298	0.4617
chr19	59128983	1846159	0.0312	0.4316
chr20	63025520	1942028	0.0308	0.1959
chr21	48129895	1398419	0.0291	0.1981
chr22	51304566	813126	0.0158	0.1372
chrMT	16571	100025	6.0361	3.8514
chrX	155270560	5512750	0.0355	0.2322
chrY	59373566	309283	0.0052	0.1458

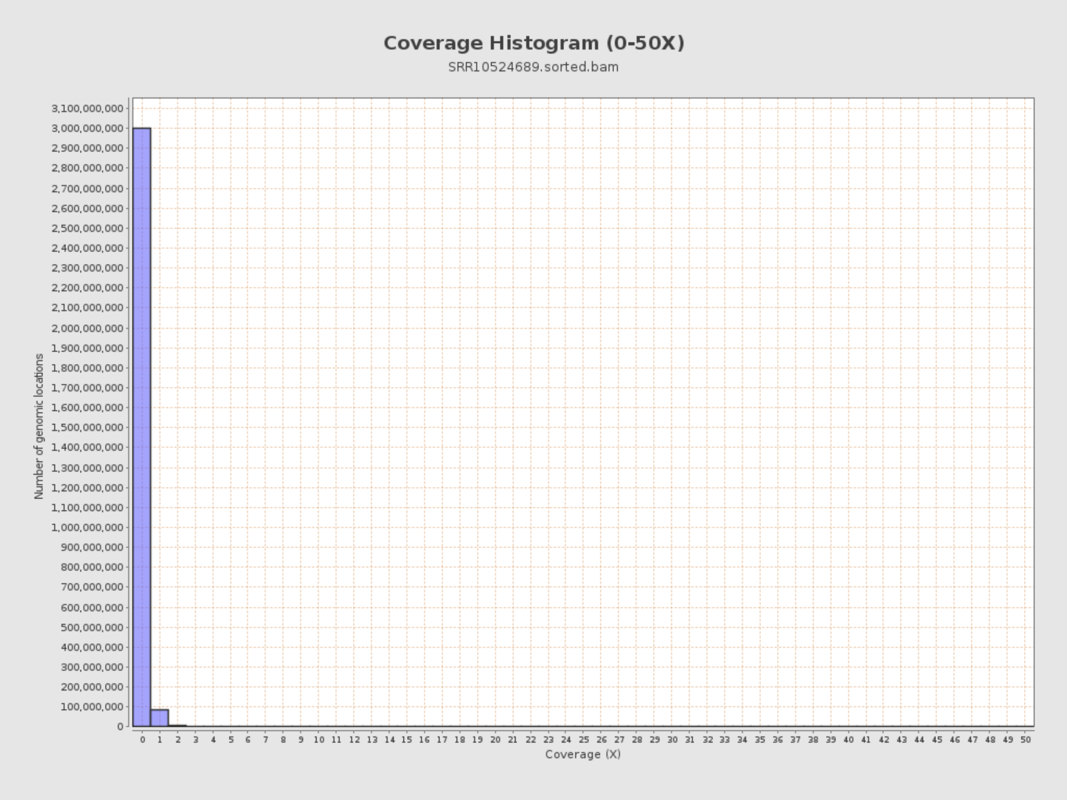
3. Results : Coverage across reference



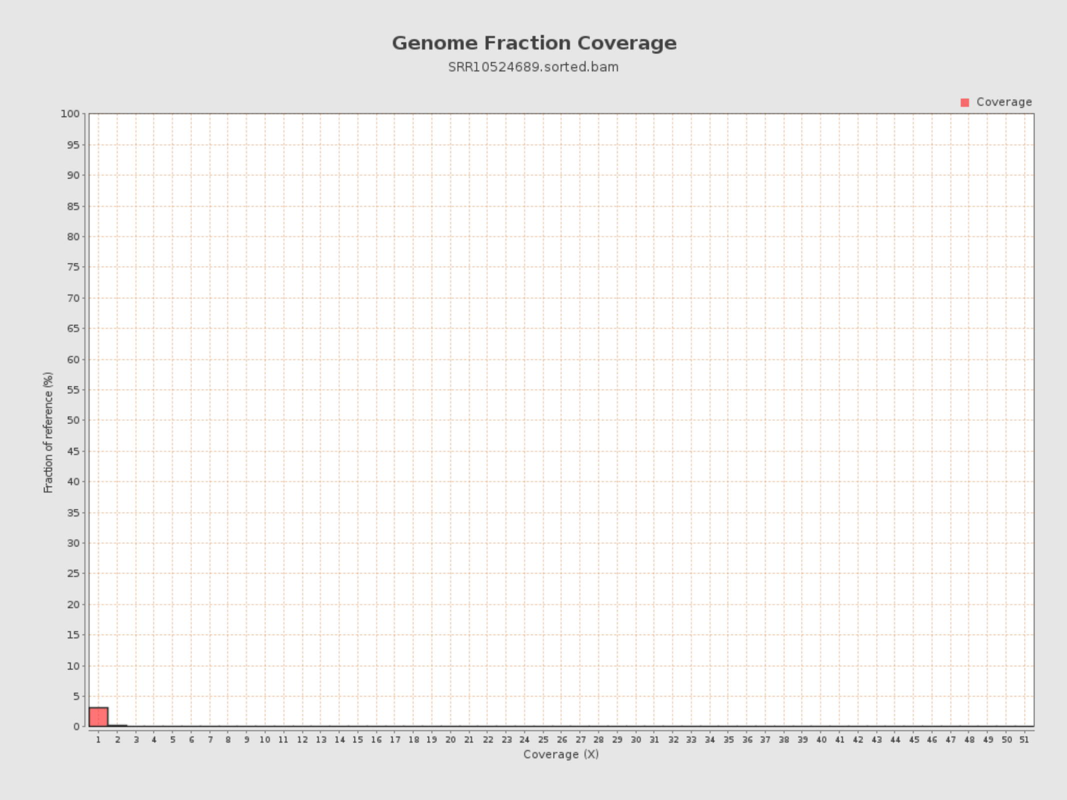
4. Results : Coverage Histogram



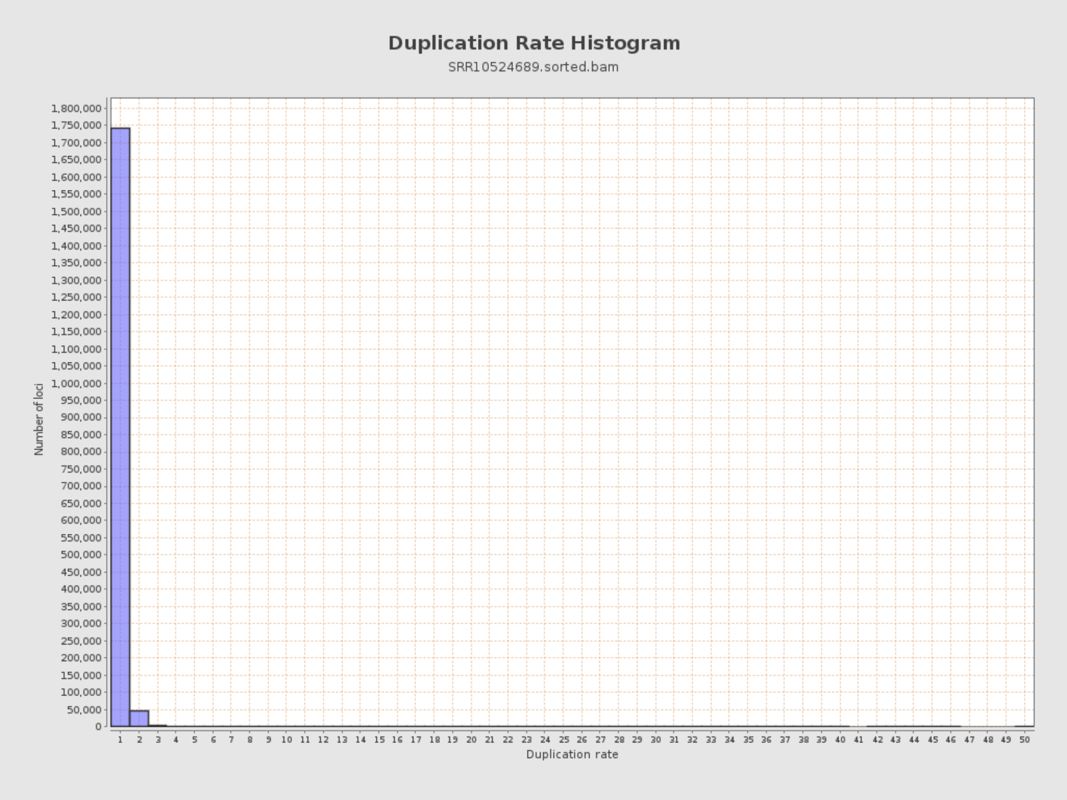
5. Results : Coverage Histogram (0-50X)



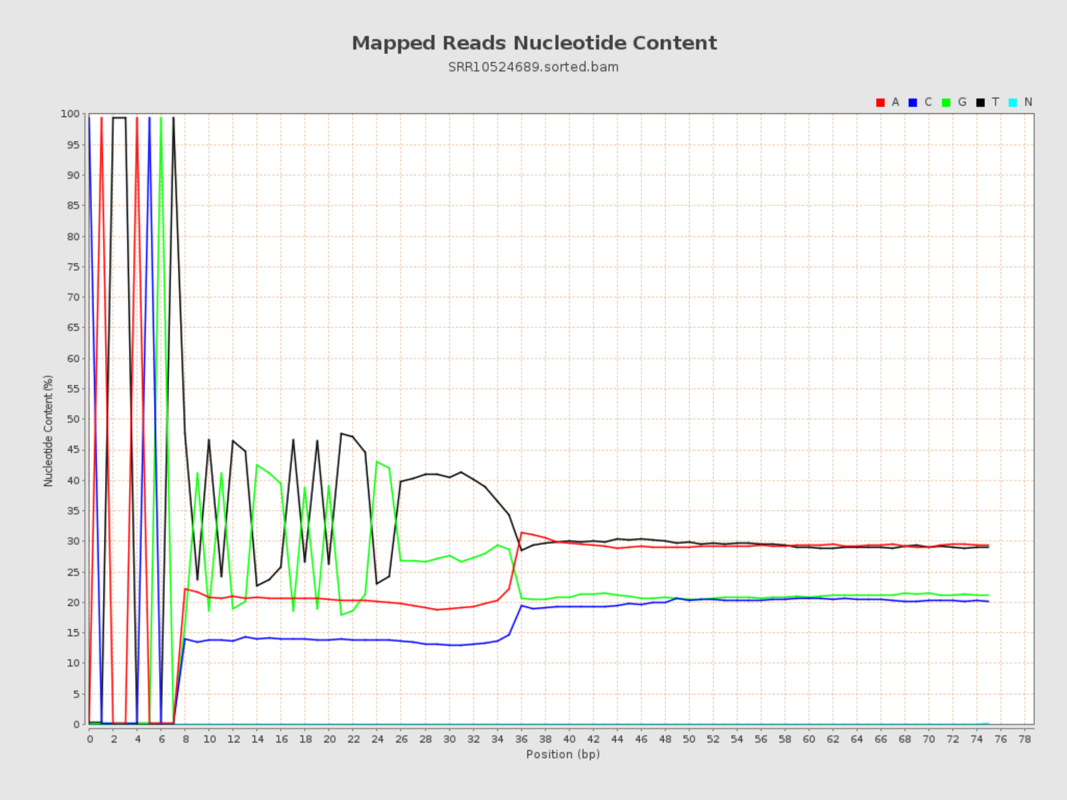
6. Results : Genome Fraction Coverage



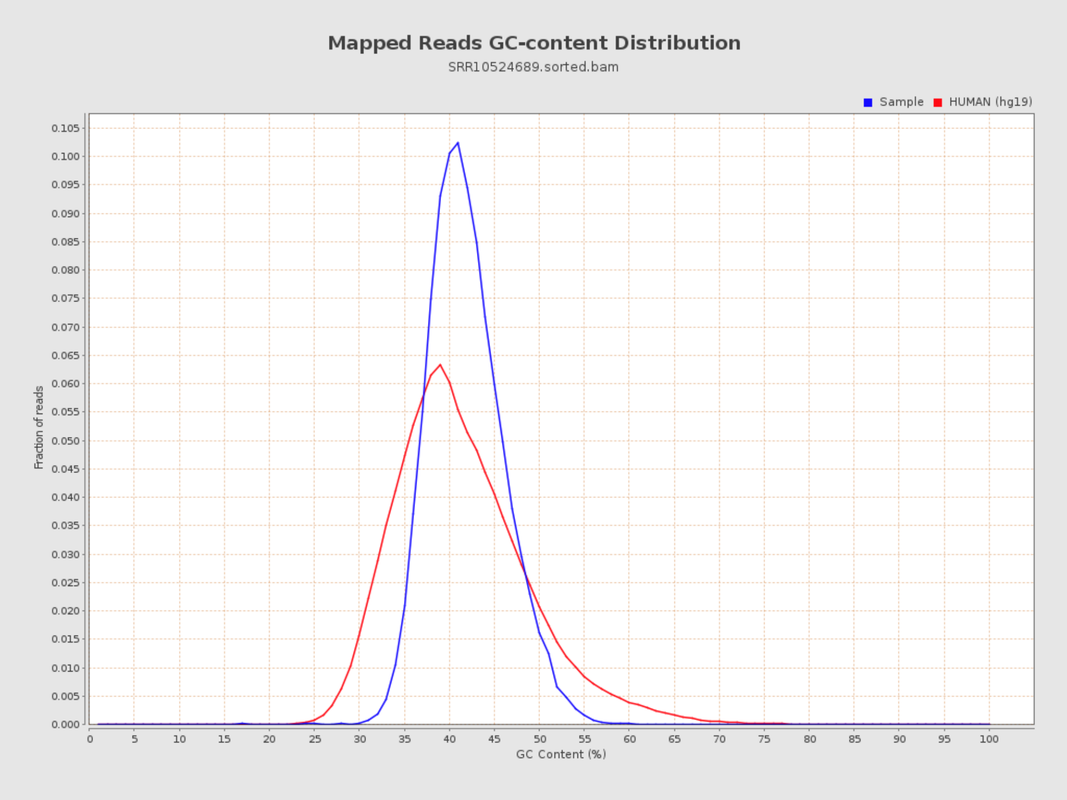
7. Results : Duplication Rate Histogram



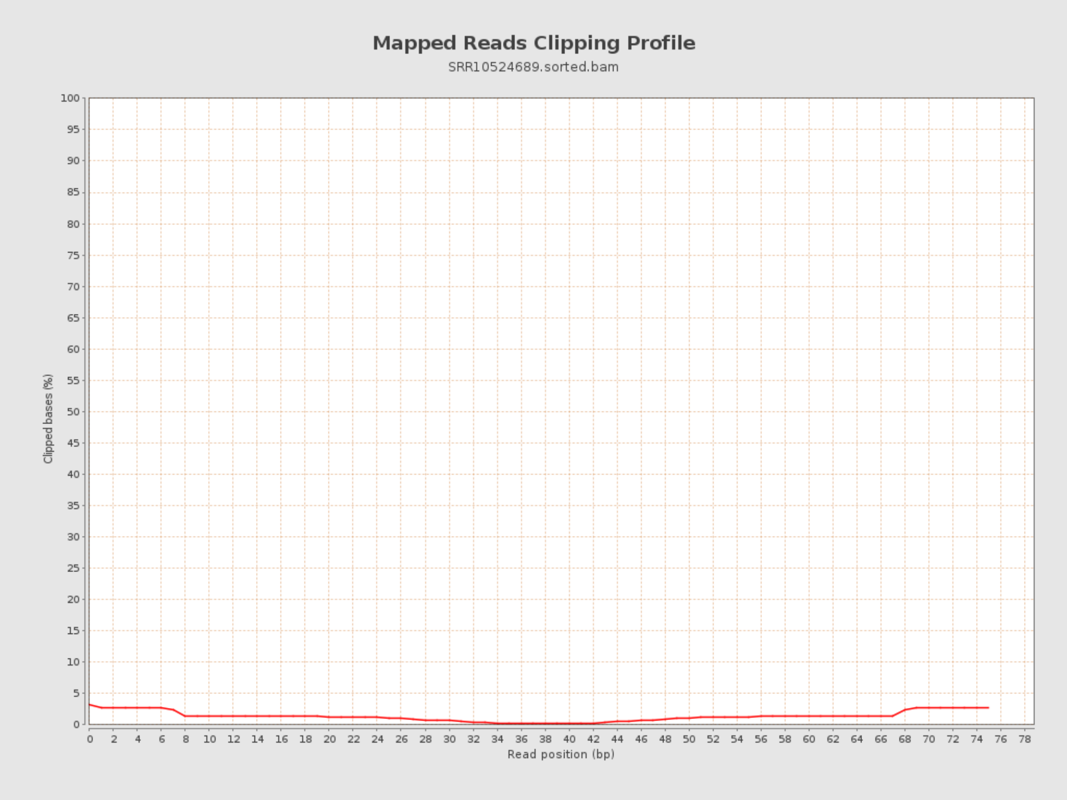
8. Results : Mapped Reads Nucleotide Content



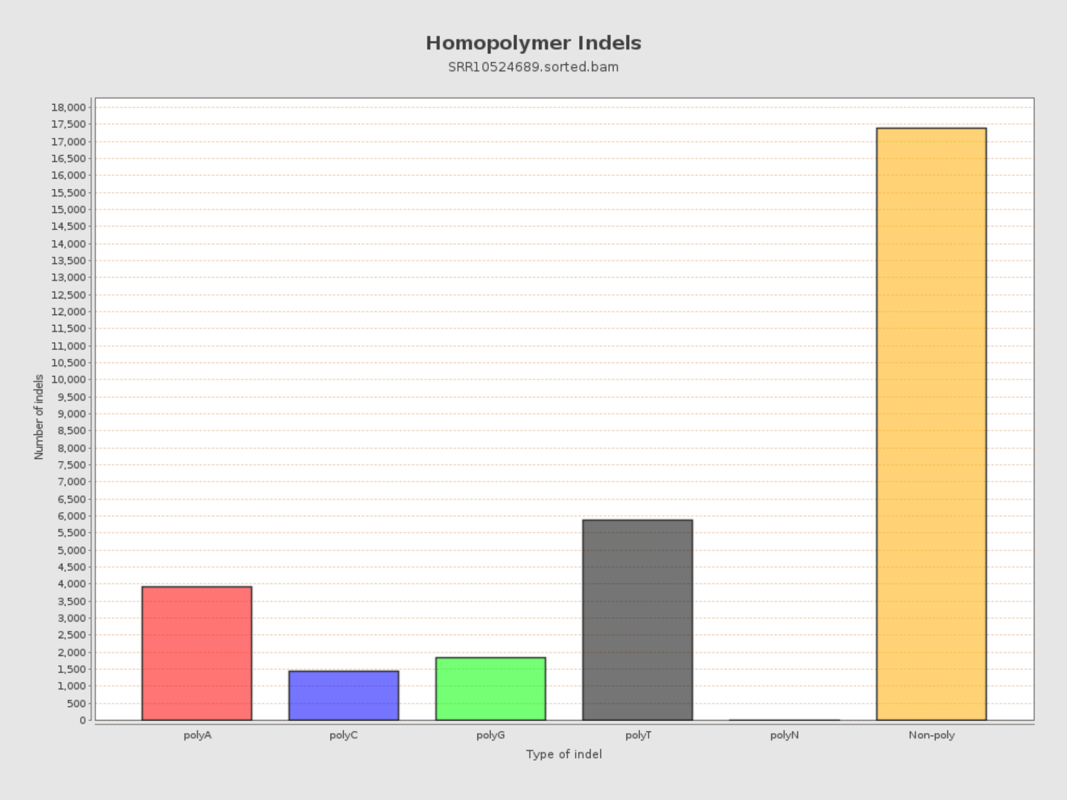
9. Results : Mapped Reads GC-content Distribution



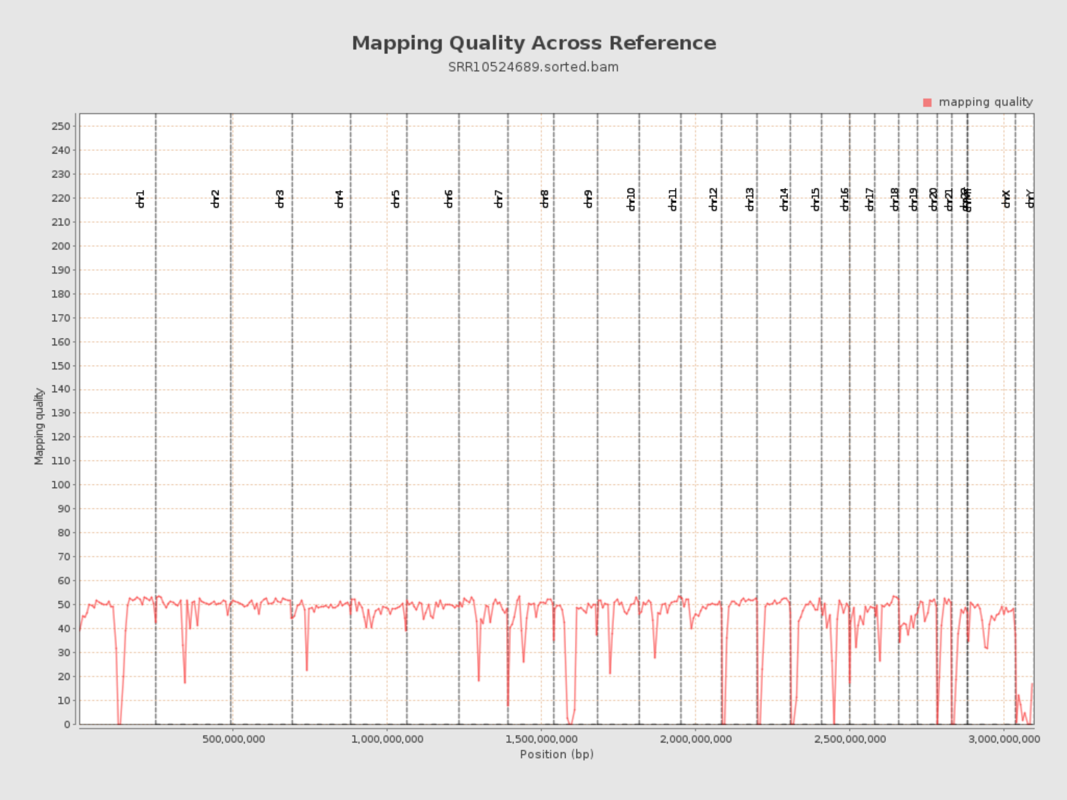
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram