Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:39:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524605.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_SRR10524605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:39:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,333,580
Mapped reads	1,231,850 / 92.37%
Unmapped reads	101,730 / 7.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,454 / 0.18%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	52,432 / 3.93%
Duplication rate	3.33%
Clipped reads	1,231,708 / 92.36%

2.2. ACGT Content

Number/percentage of A's	18,063,000 / 25.4%
Number/percentage of C's	12,939,139 / 18.19%
Number/percentage of T's	23,194,813 / 32.61%
Number/percentage of G's	16,926,730 / 23.8%
Number/percentage of N's	456 / 0%
GC Percentage	41.99%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2216

2.4. Mapping Quality

Mean Mapping Quality	45.21

2.5. Mismatches and indels

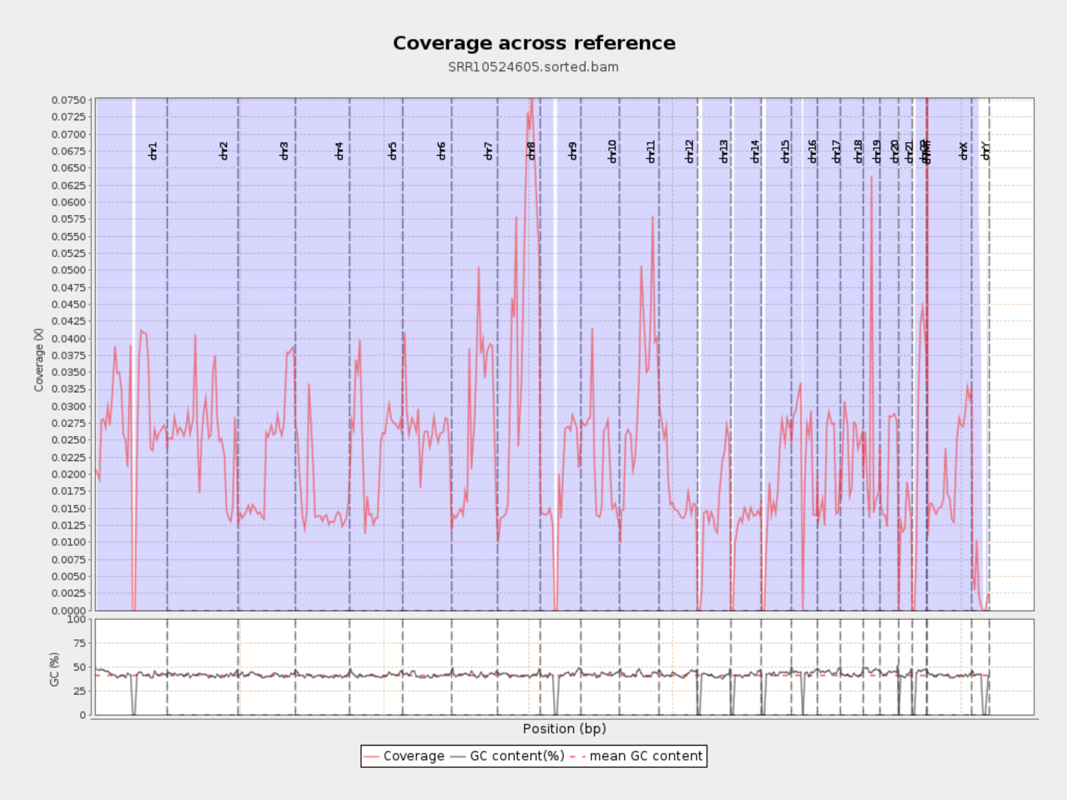
General error rate	0.49%
Mismatches	337,103
Insertions	4,831
Mapped reads with at least one insertion	0.39%
Deletions	12,982
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.34%

2.6. Chromosome stats

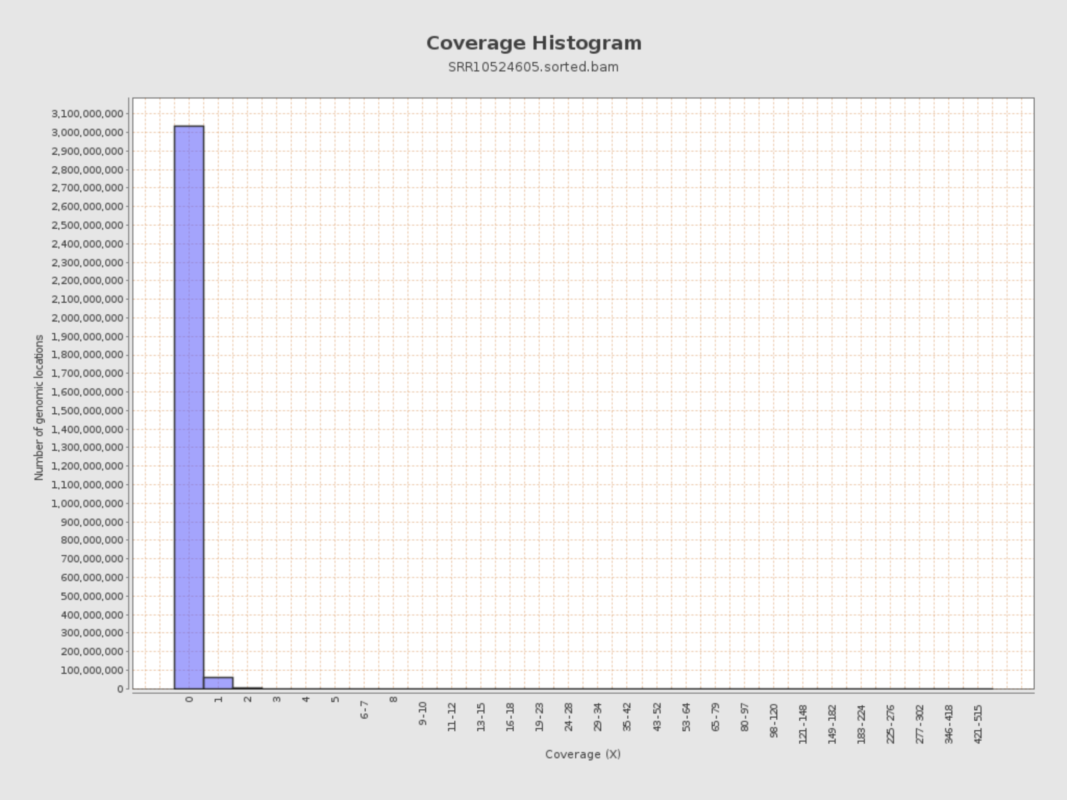
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6909103	0.0277	0.3728
chr2	243199373	6257209	0.0257	0.2678
chr3	198022430	4472926	0.0226	0.1663
chr4	191154276	3154962	0.0165	0.1567
chr5	180915260	4423002	0.0244	0.1719
chr6	171115067	4589964	0.0268	0.1919
chr7	159138663	4308510	0.0271	0.2814

chr8	146364022	6229576	0.0426	0.2899
chr9	141213431	2542455	0.018	0.1927
chr10	135534747	3068503	0.0226	0.2177
chr11	135006516	4371756	0.0324	0.2301
chr12	133851895	2397860	0.0179	0.1501
chr13	115169878	1682952	0.0146	0.1341
chr14	107349540	1284128	0.012	0.1235
chr15	102531392	1799655	0.0176	0.1539
chr16	90354753	2076103	0.023	0.1724
chr17	81195210	1604289	0.0198	0.1561
chr18	78077248	1877524	0.024	0.2975
chr19	59128983	1421174	0.024	0.2606
chr20	63025520	1353325	0.0215	0.1646
chr21	48129895	611284	0.0127	0.1355
chr22	51304566	1351780	0.0263	0.1781
chrMT	16571	6751	0.4074	0.771
chrX	155270560	3179490	0.0205	0.1764
chrY	59373566	171776	0.0029	0.0883

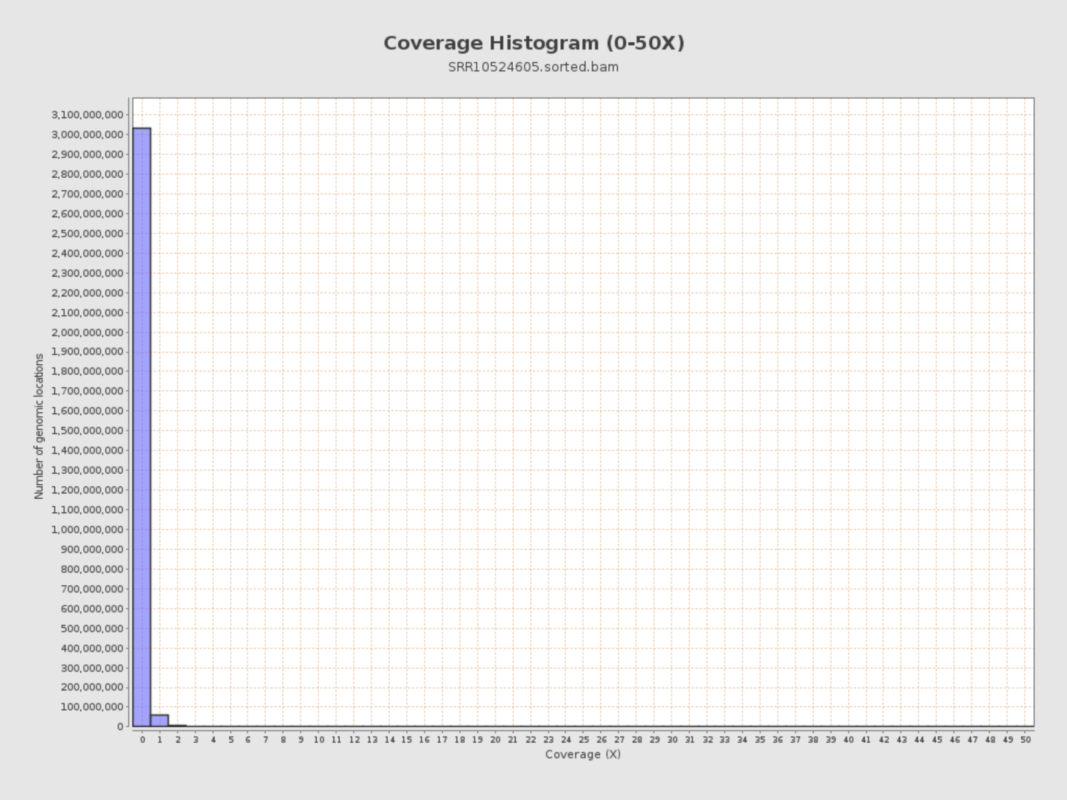
3. Results : Coverage across reference



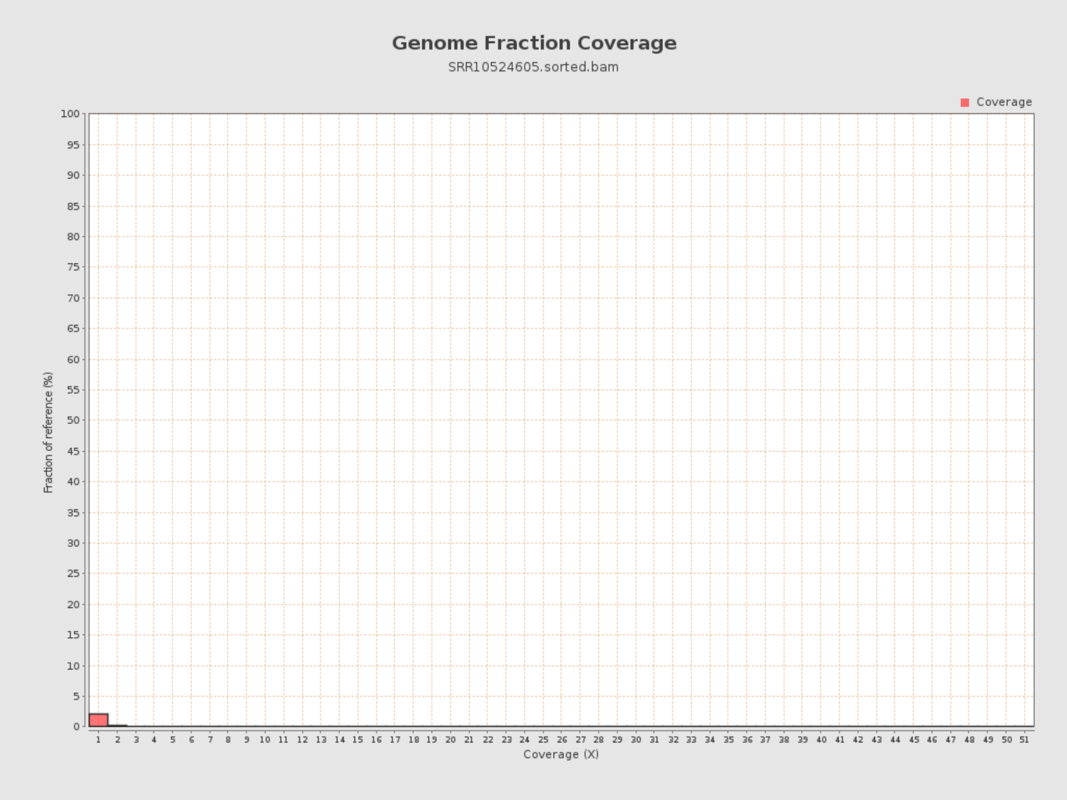
4. Results : Coverage Histogram



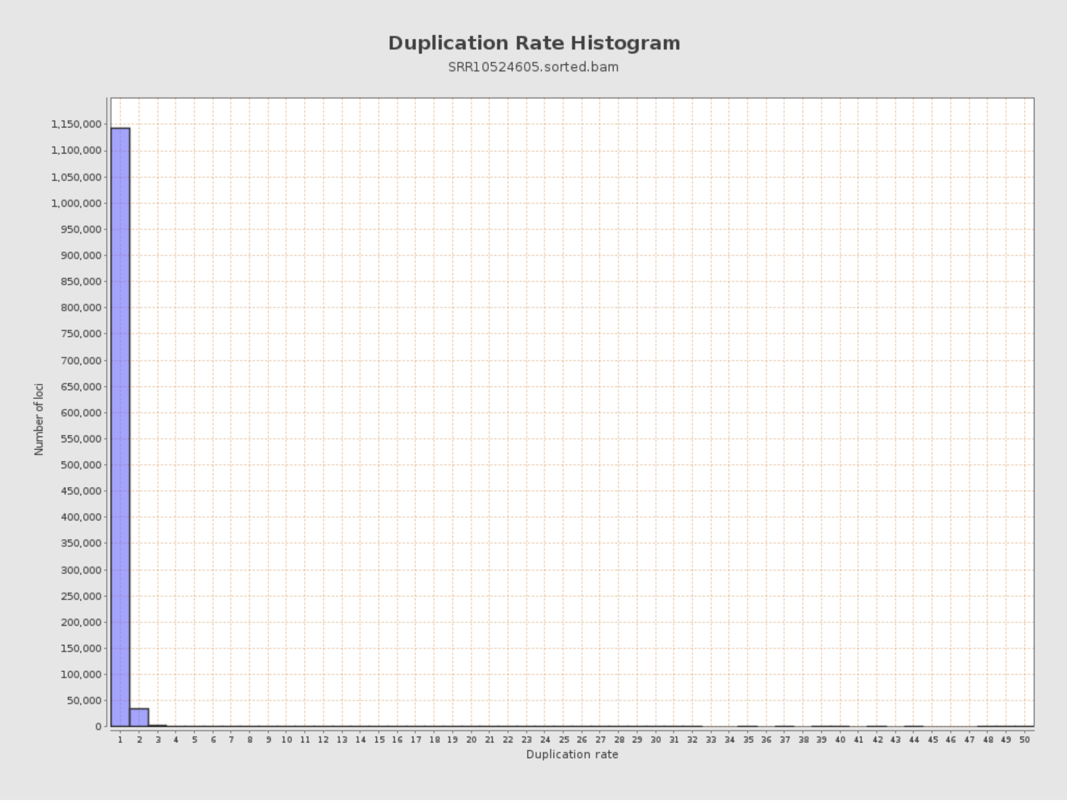
5. Results : Coverage Histogram (0-50X)



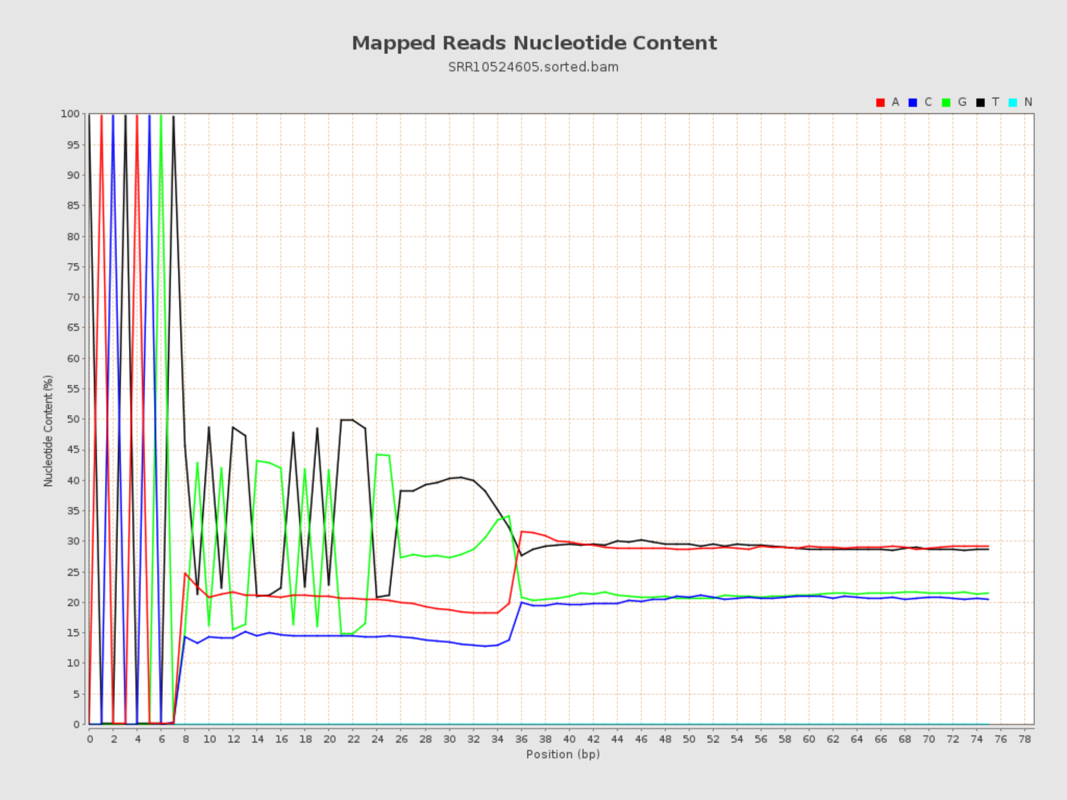
6. Results : Genome Fraction Coverage



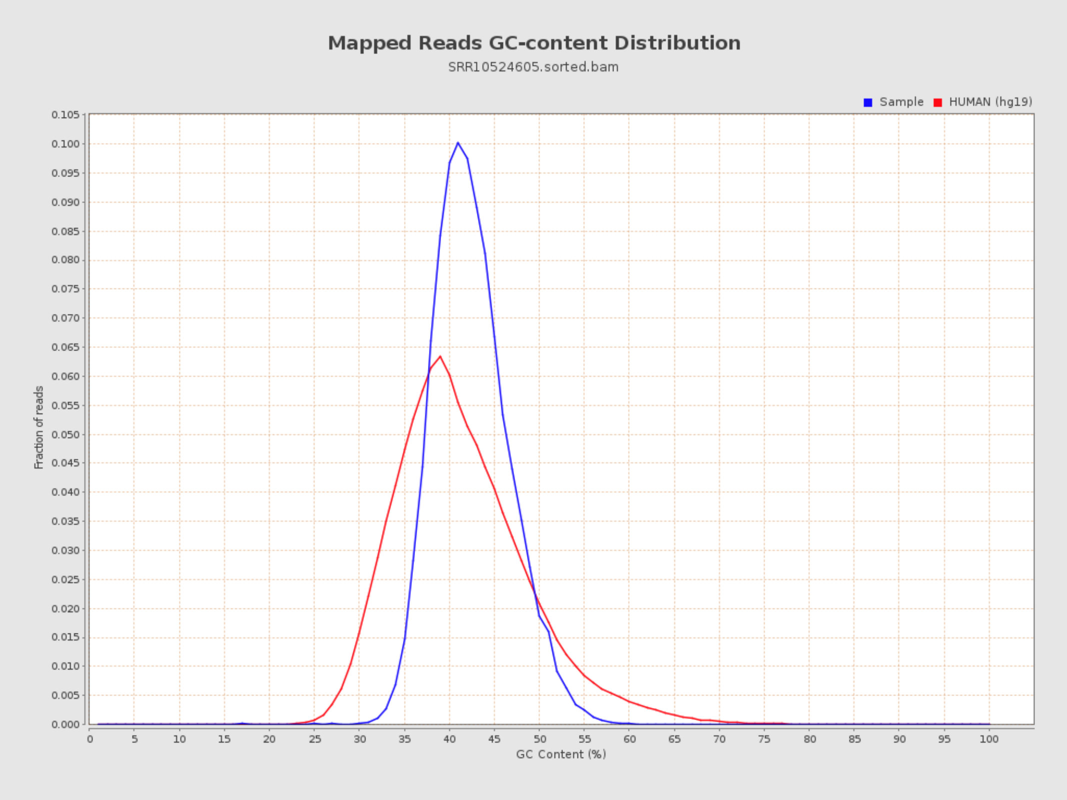
7. Results : Duplication Rate Histogram



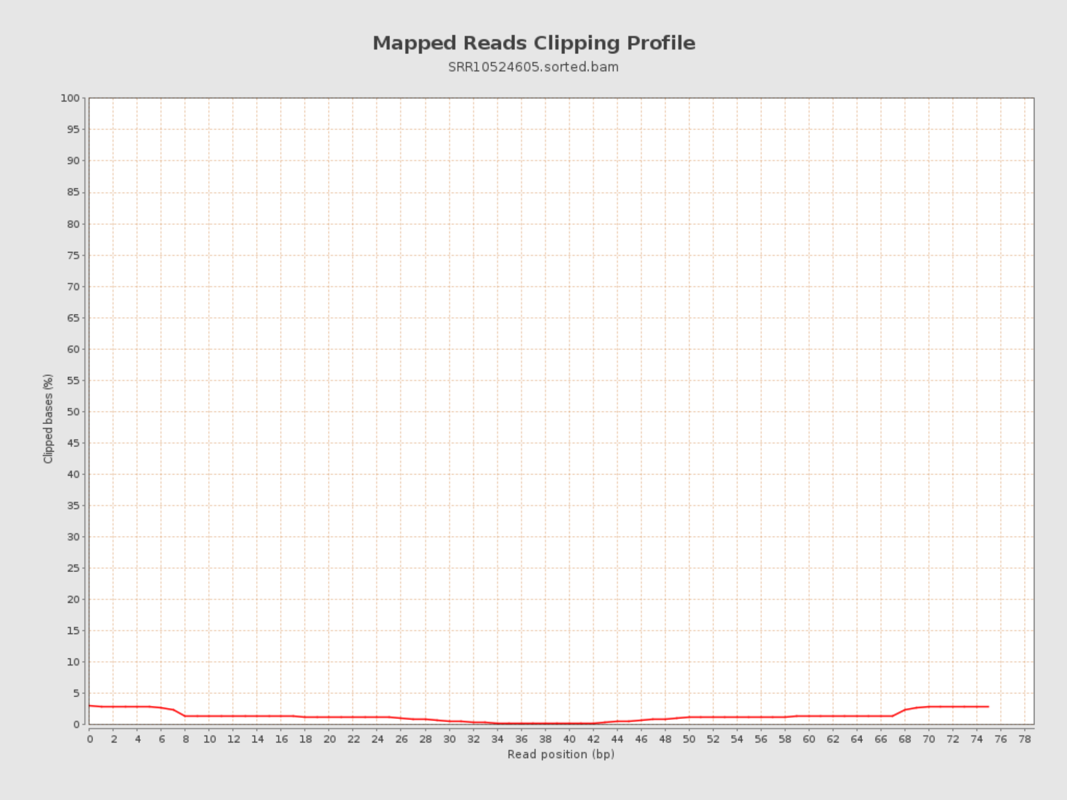
8. Results : Mapped Reads Nucleotide Content



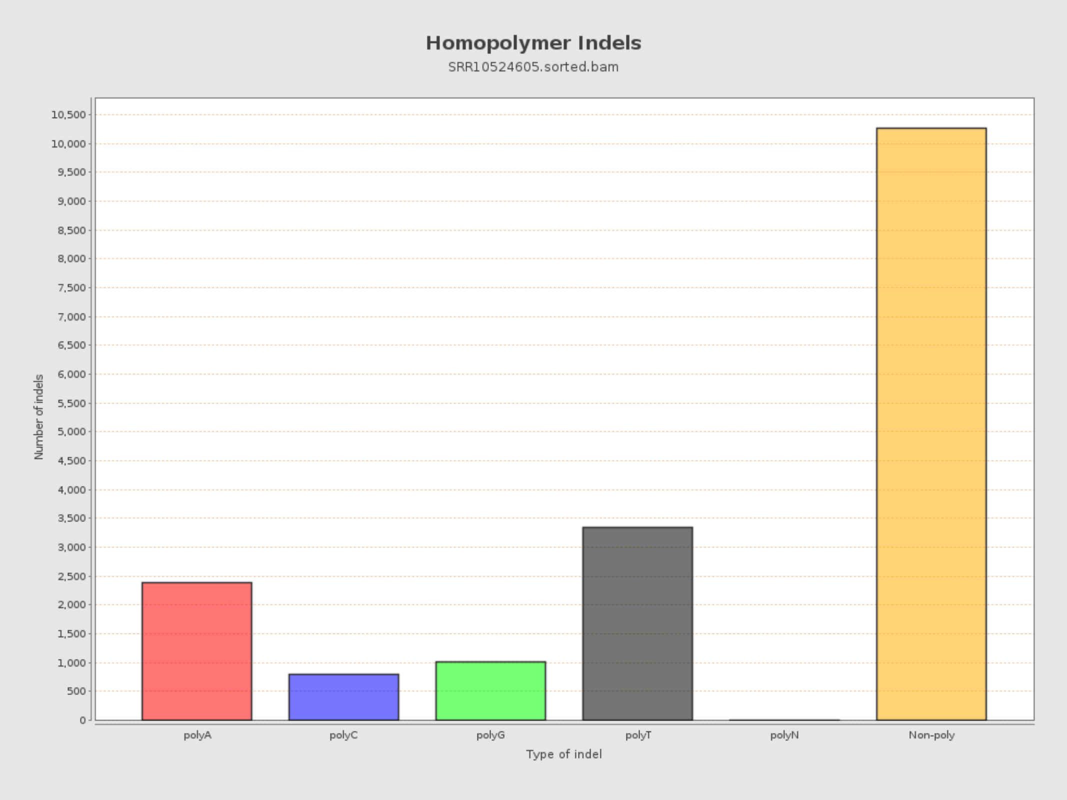
9. Results : Mapped Reads GC-content Distribution



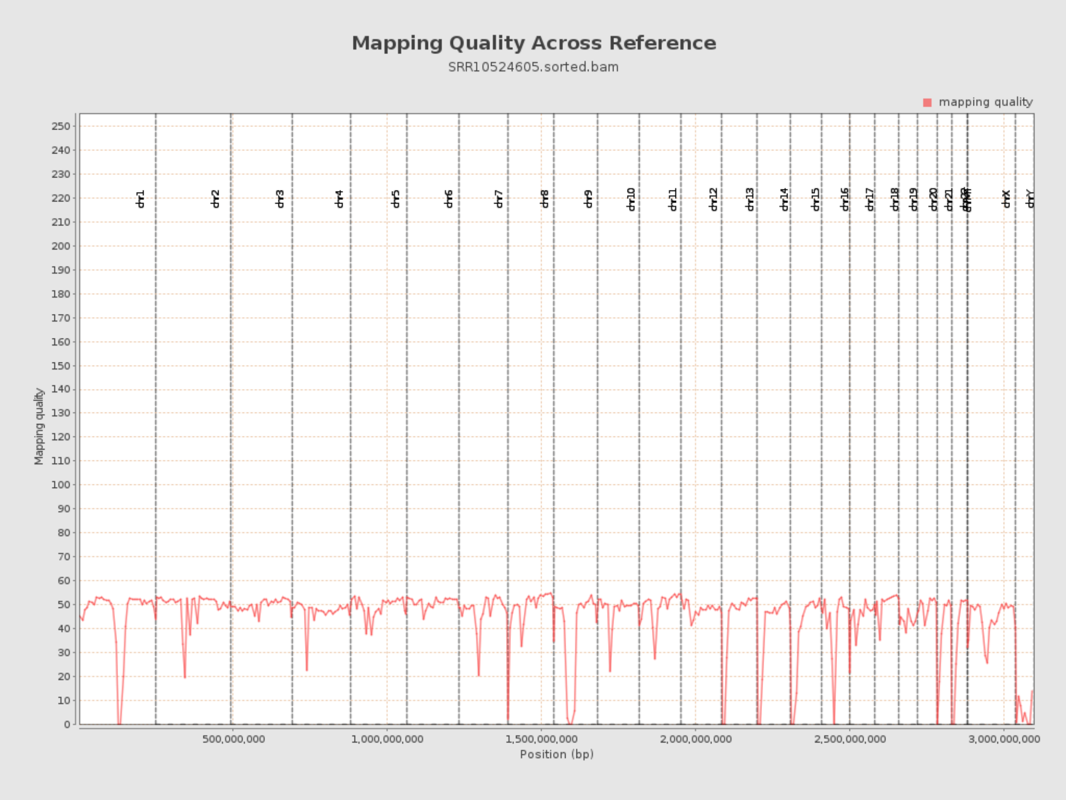
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram