Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:37:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524603.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_SRR10524603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524603.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:37:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	913,009
Mapped reads	848,344 / 92.92%
Unmapped reads	64,665 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,804 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	26,040 / 2.85%
Duplication rate	2.39%
Clipped reads	847,254 / 92.8%

2.2. ACGT Content

Number/percentage of A's	12,685,676 / 25.67%
Number/percentage of C's	9,506,921 / 19.24%
Number/percentage of T's	15,563,603 / 31.5%
Number/percentage of G's	11,653,028 / 23.58%
Number/percentage of N's	311 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.016

Standard Deviation	0.1708

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

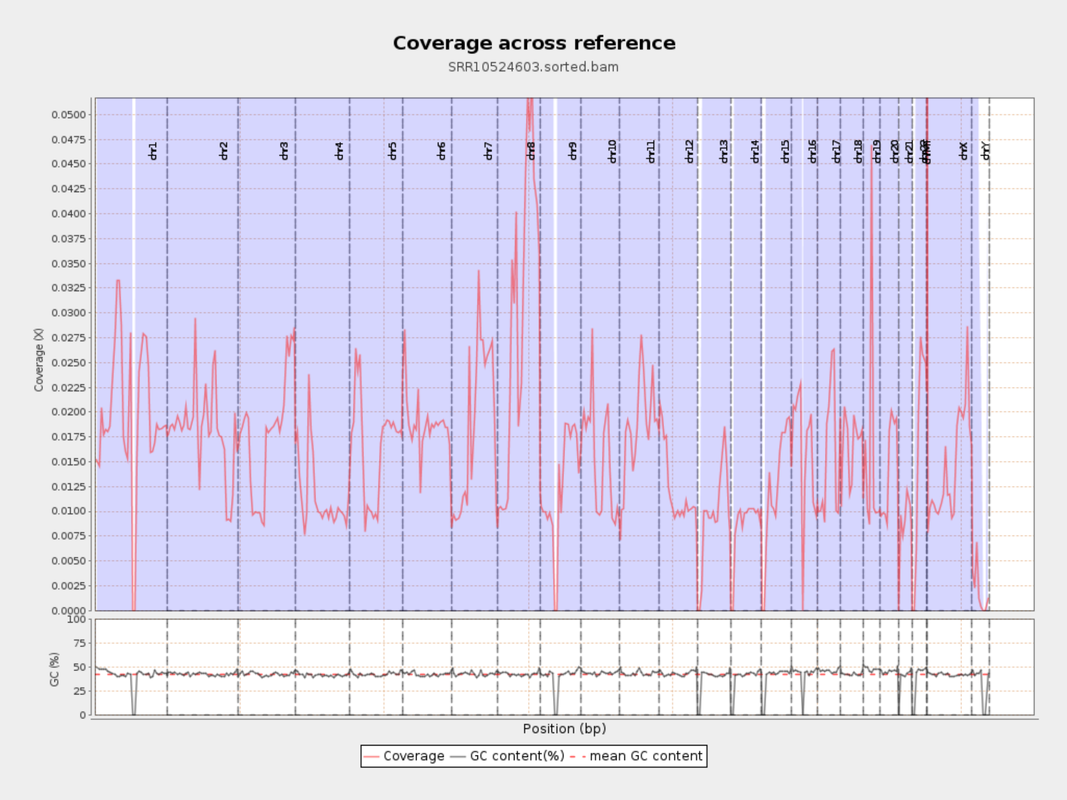
General error rate	0.49%
Mismatches	236,801
Insertions	3,844
Mapped reads with at least one insertion	0.45%
Deletions	9,589
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.01%

2.6. Chromosome stats

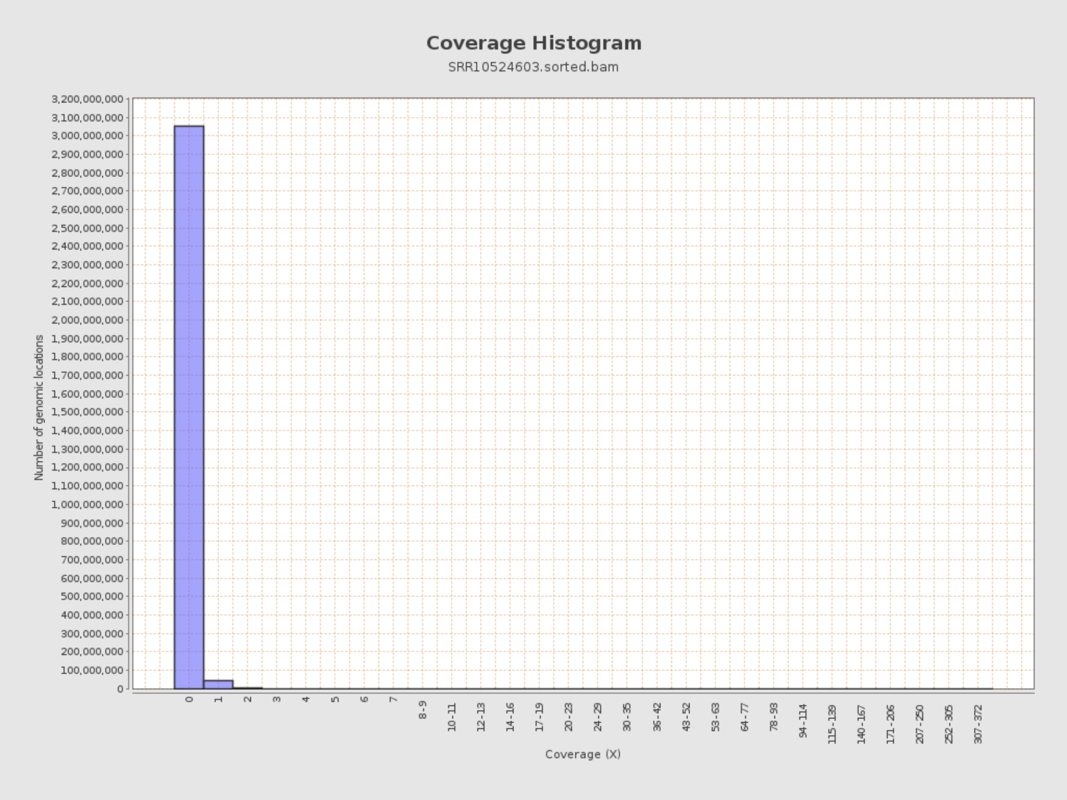
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4924810	0.0198	0.2895
chr2	243199373	4406916	0.0181	0.1905
chr3	198022430	3519684	0.0178	0.1416
chr4	191154276	2223738	0.0116	0.1255
chr5	180915260	3013918	0.0167	0.1371
chr6	171115067	3219523	0.0188	0.1528
chr7	159138663	2975277	0.0187	0.2102

chr8	146364022	4423175	0.0302	0.2296
chr9	141213431	1736101	0.0123	0.1454
chr10	135534747	2110793	0.0156	0.1636
chr11	135006516	2509061	0.0186	0.166
chr12	133851895	1636707	0.0122	0.1192
chr13	115169878	1100625	0.0096	0.1052
chr14	107349540	906150	0.0084	0.1008
chr15	102531392	1251289	0.0122	0.1209
chr16	90354753	1433716	0.0159	0.1371
chr17	81195210	1252373	0.0154	0.1339
chr18	78077248	1298156	0.0166	0.2245
chr19	59128983	930935	0.0157	0.203
chr20	63025520	910255	0.0144	0.1302
chr21	48129895	422068	0.0088	0.1061
chr22	51304566	851755	0.0166	0.137
chrMT	16571	2234	0.1348	0.3963
chrX	155270560	2253531	0.0145	0.1384
chrY	59373566	113183	0.0019	0.0645

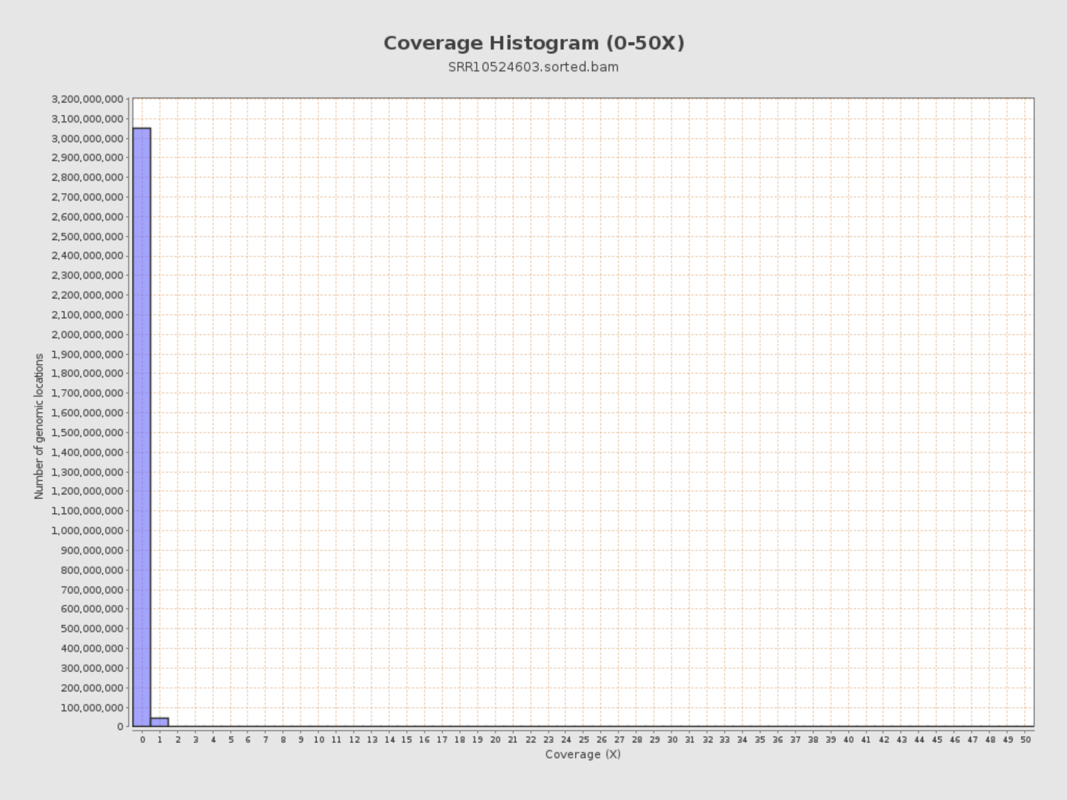
3. Results : Coverage across reference



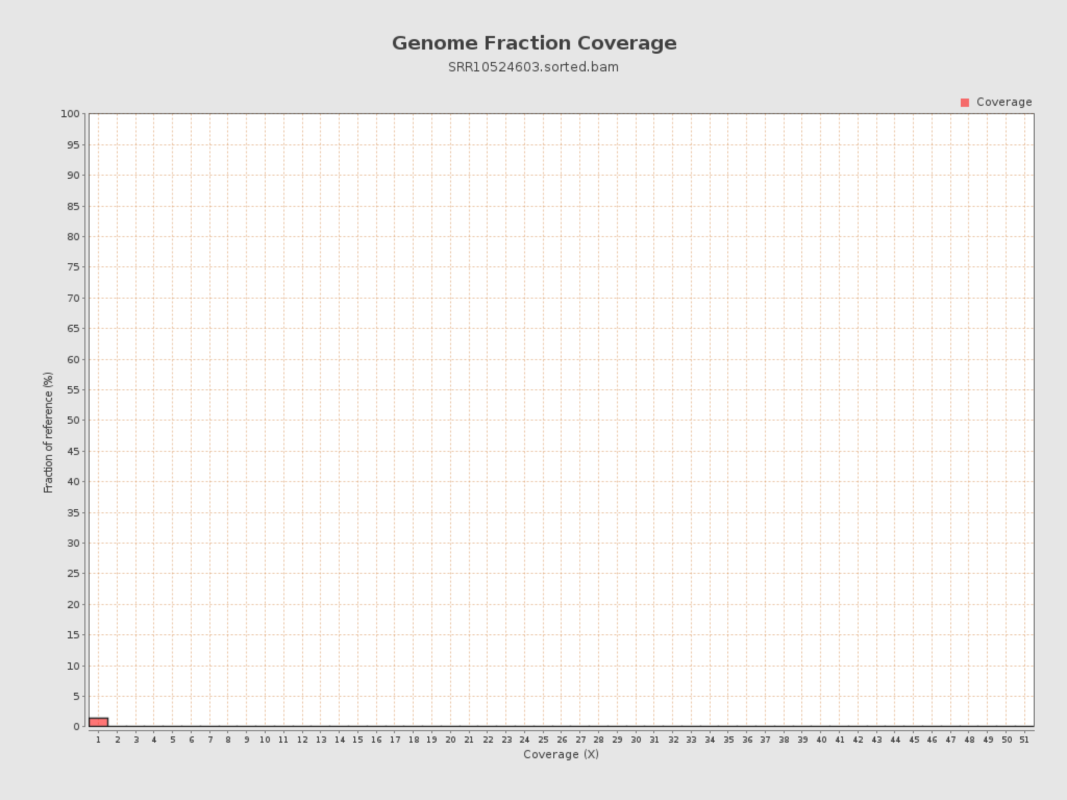
4. Results : Coverage Histogram



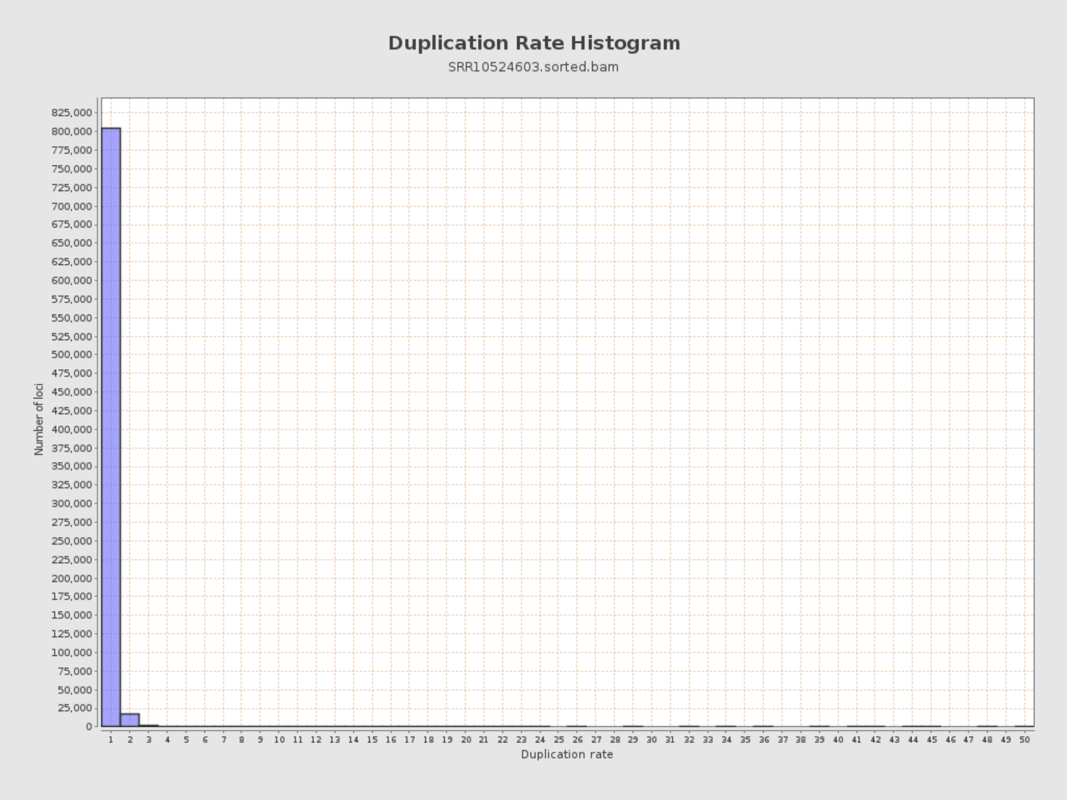
5. Results : Coverage Histogram (0-50X)



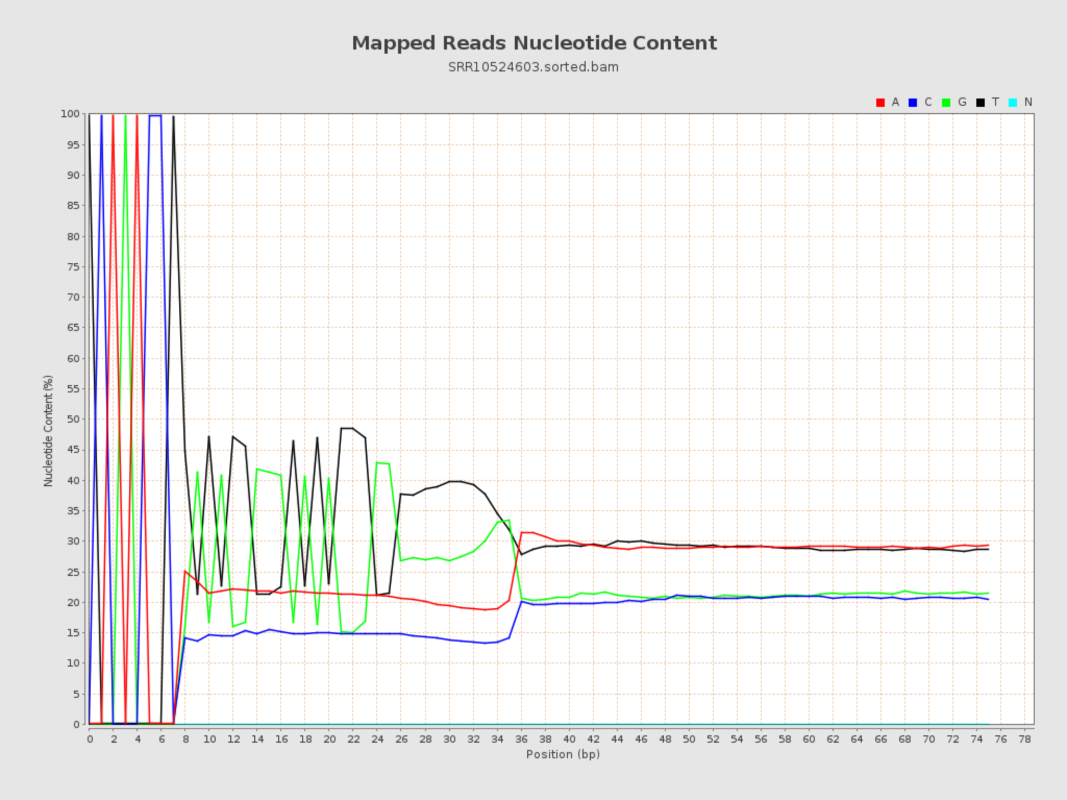
6. Results : Genome Fraction Coverage



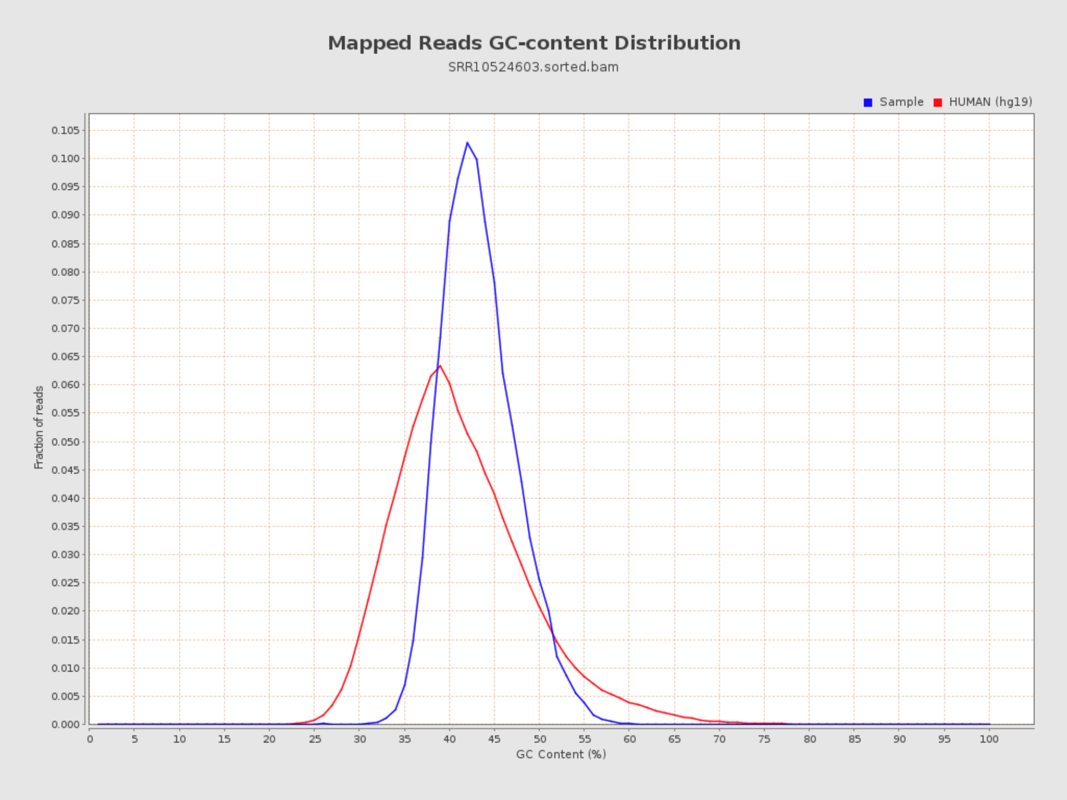
7. Results : Duplication Rate Histogram



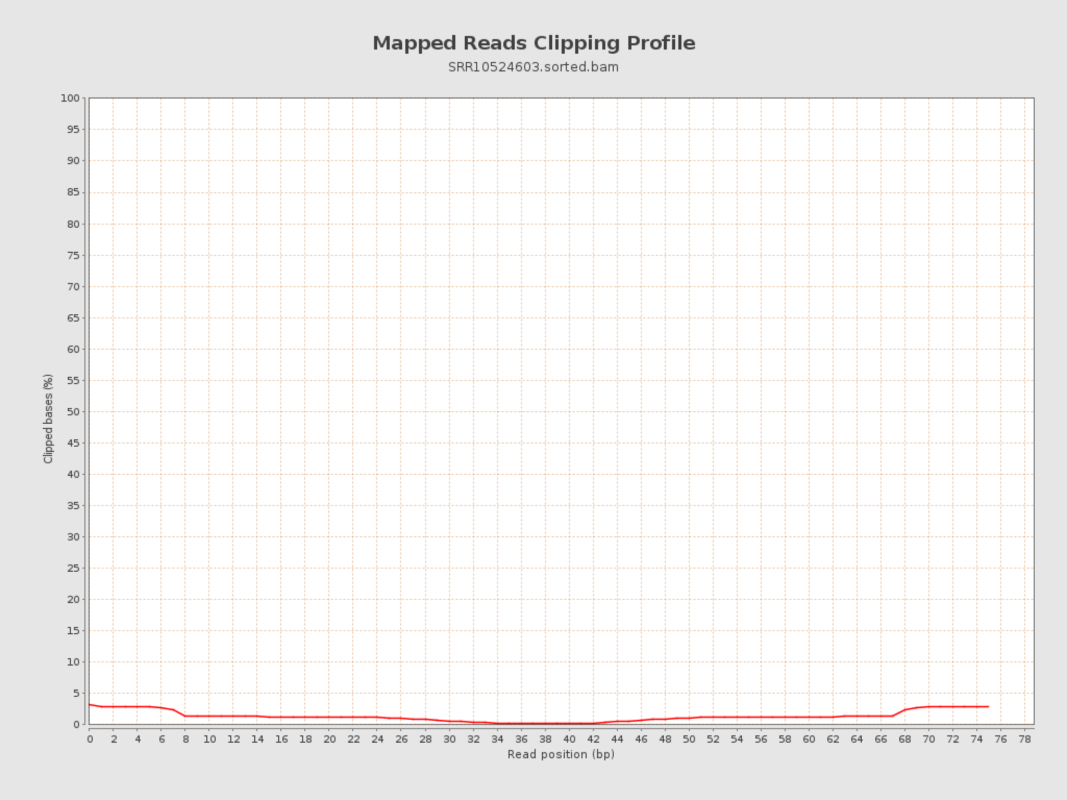
8. Results : Mapped Reads Nucleotide Content



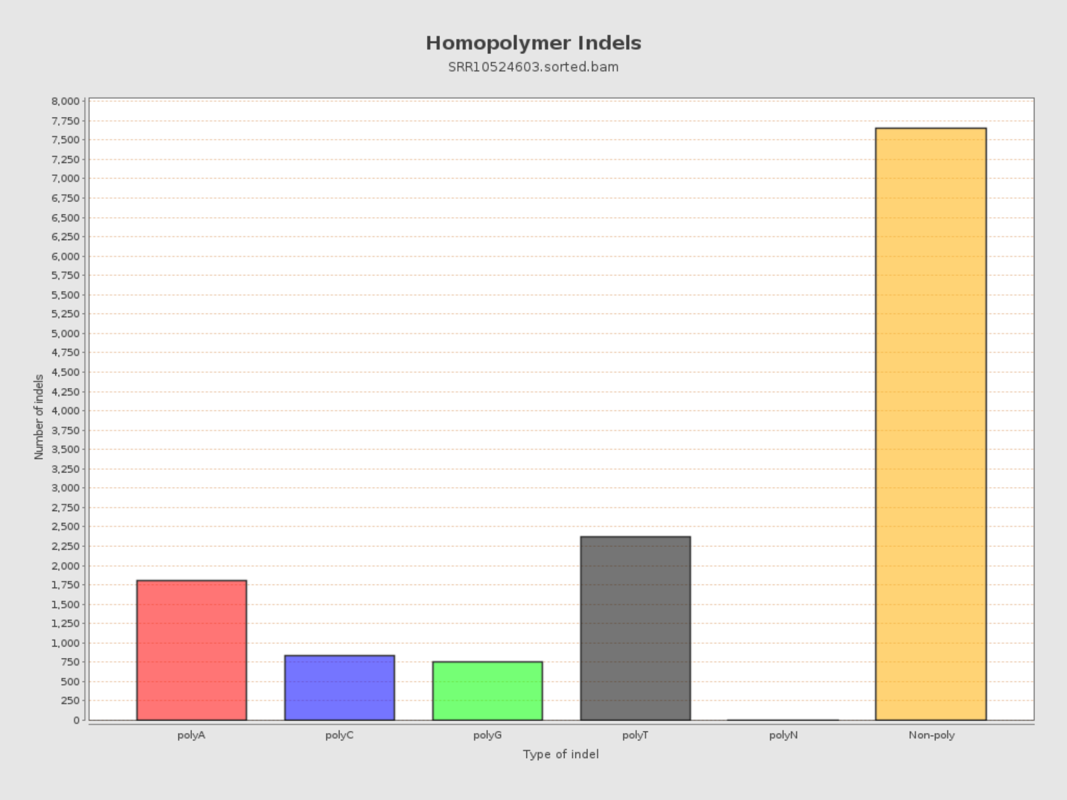
9. Results : Mapped Reads GC-content Distribution



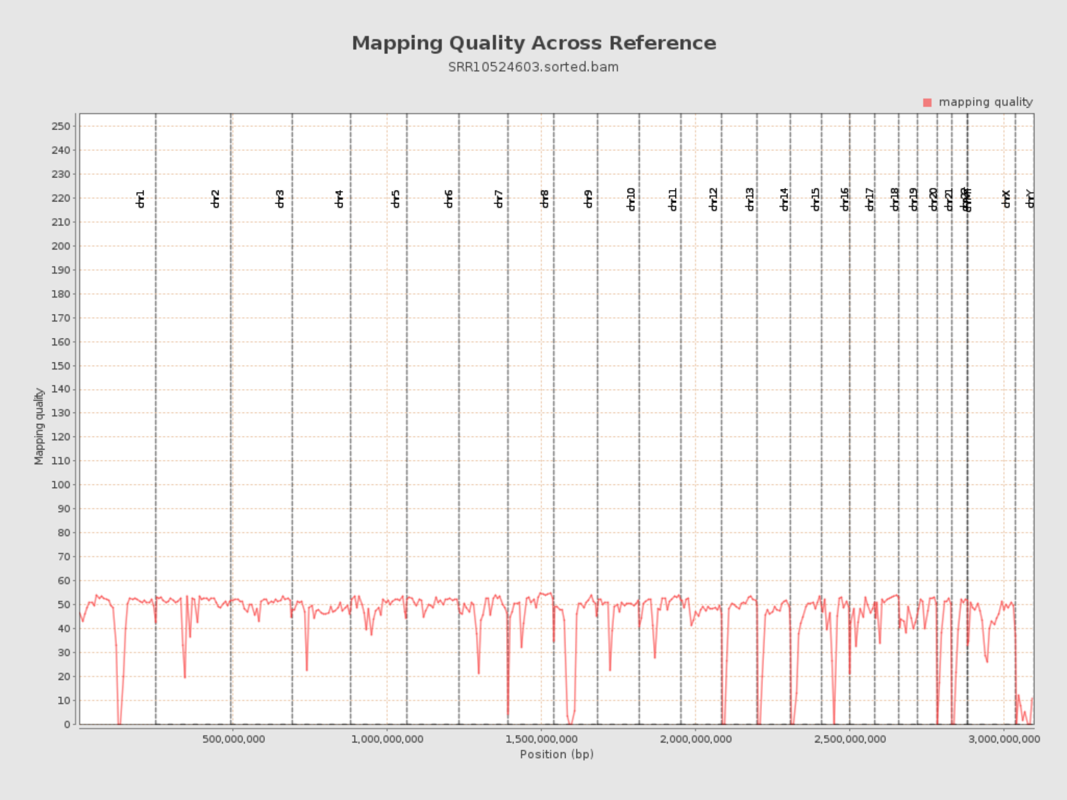
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram