Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:51:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524670.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_SRR10524670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524670.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:51:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	662,362
Mapped reads	613,933 / 92.69%
Unmapped reads	48,429 / 7.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,620 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	13,750 / 2.08%
Duplication rate	1.66%
Clipped reads	616,103 / 93.02%

2.2. ACGT Content

Number/percentage of A's	8,879,354 / 24.42%
Number/percentage of C's	6,876,974 / 18.91%
Number/percentage of T's	11,542,338 / 31.74%
Number/percentage of G's	9,061,540 / 24.92%
Number/percentage of N's	4,689 / 0.01%
GC Percentage	43.83%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.1396

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

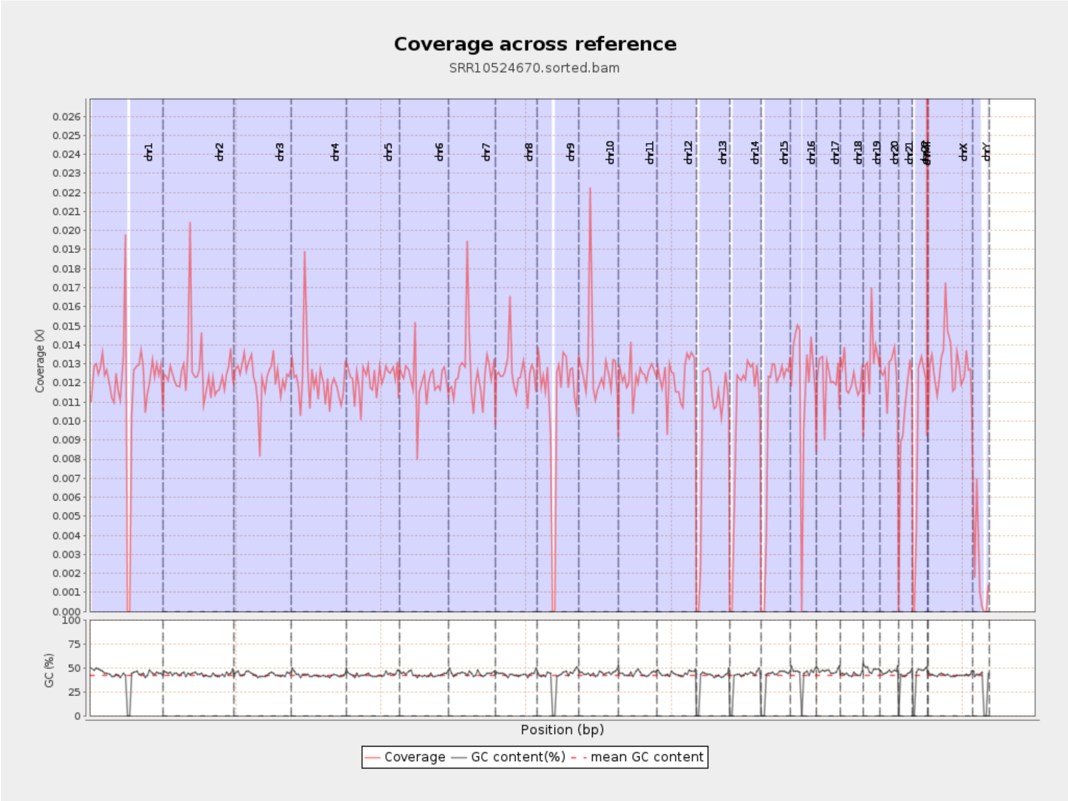
General error rate	0.51%
Mismatches	180,237
Insertions	2,150
Mapped reads with at least one insertion	0.35%
Deletions	6,698
Mapped reads with at least one deletion	1.08%
Homopolymer indels	44.53%

2.6. Chromosome stats

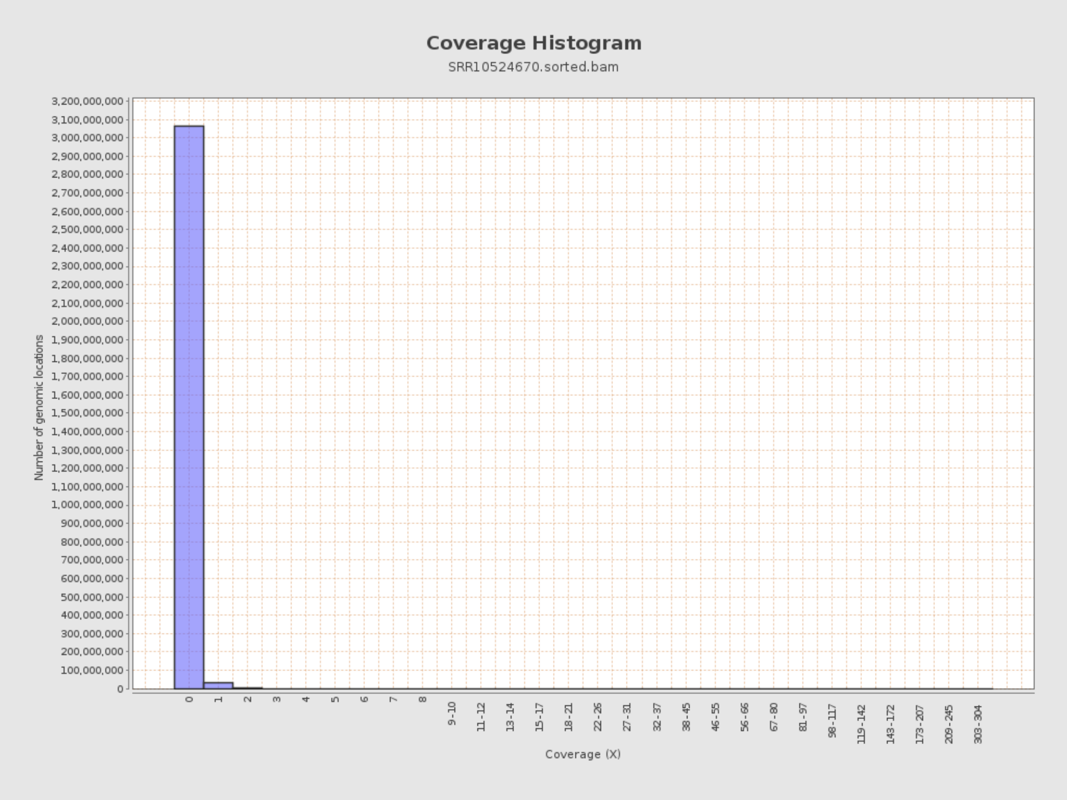
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2931935	0.0118	0.2137
chr2	243199373	3058398	0.0126	0.1763
chr3	198022430	2433569	0.0123	0.1149
chr4	191154276	2318747	0.0121	0.1201
chr5	180915260	2212823	0.0122	0.1149
chr6	171115067	2074199	0.0121	0.121
chr7	159138663	2009039	0.0126	0.1644

chr8	146364022	1835338	0.0125	0.1418
chr9	141213431	1531777	0.0108	0.1241
chr10	135534747	1740240	0.0128	0.1419
chr11	135006516	1663719	0.0123	0.1287
chr12	133851895	1635805	0.0122	0.1157
chr13	115169878	1124930	0.0098	0.1029
chr14	107349540	1104443	0.0103	0.1075
chr15	102531392	1040819	0.0102	0.1049
chr16	90354753	1086137	0.012	0.1176
chr17	81195210	990450	0.0122	0.1184
chr18	78077248	953792	0.0122	0.176
chr19	59128983	785227	0.0133	0.1802
chr20	63025520	785424	0.0125	0.1165
chr21	48129895	479205	0.01	0.1085
chr22	51304566	447060	0.0087	0.097
chrMT	16571	9349	0.5642	0.7982
chrX	155270560	2009401	0.0129	0.1227
chrY	59373566	113625	0.0019	0.077

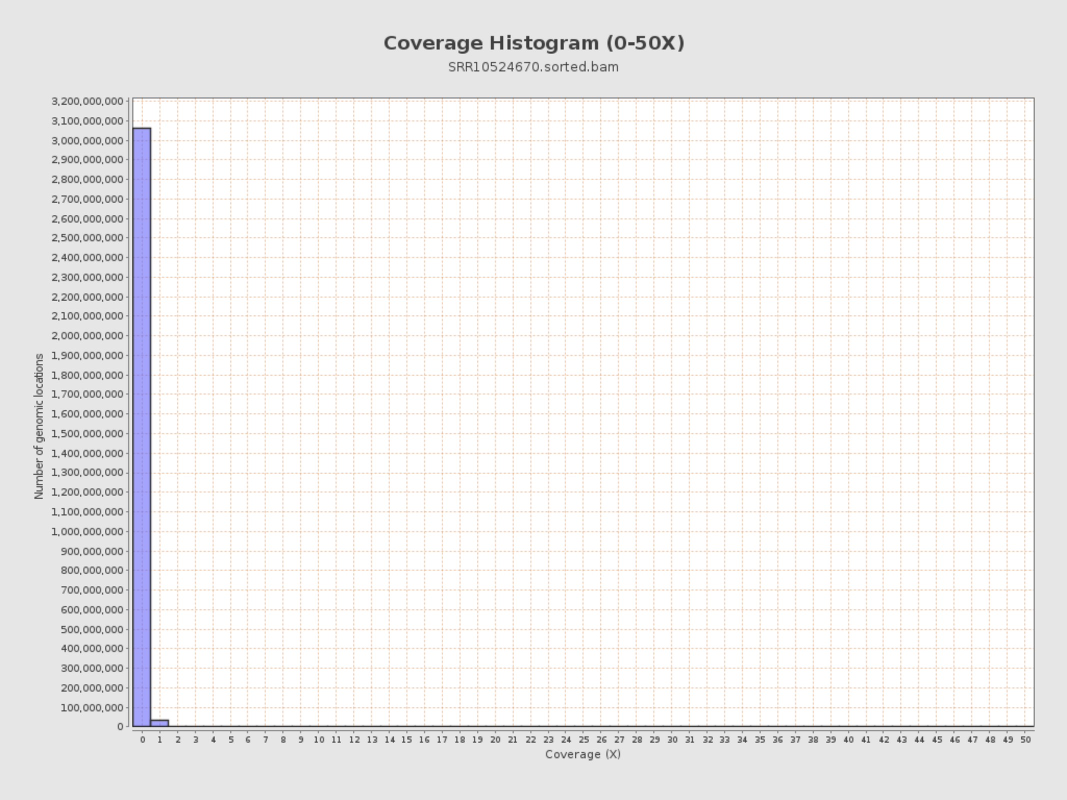
3. Results : Coverage across reference



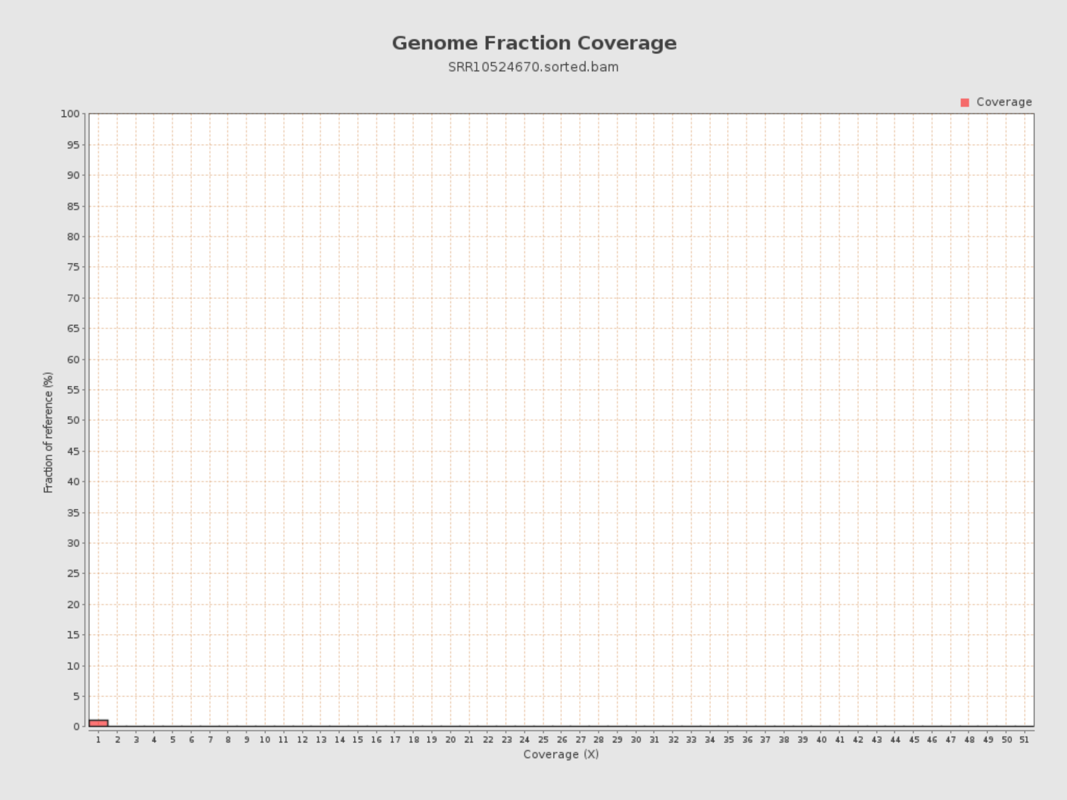
4. Results : Coverage Histogram



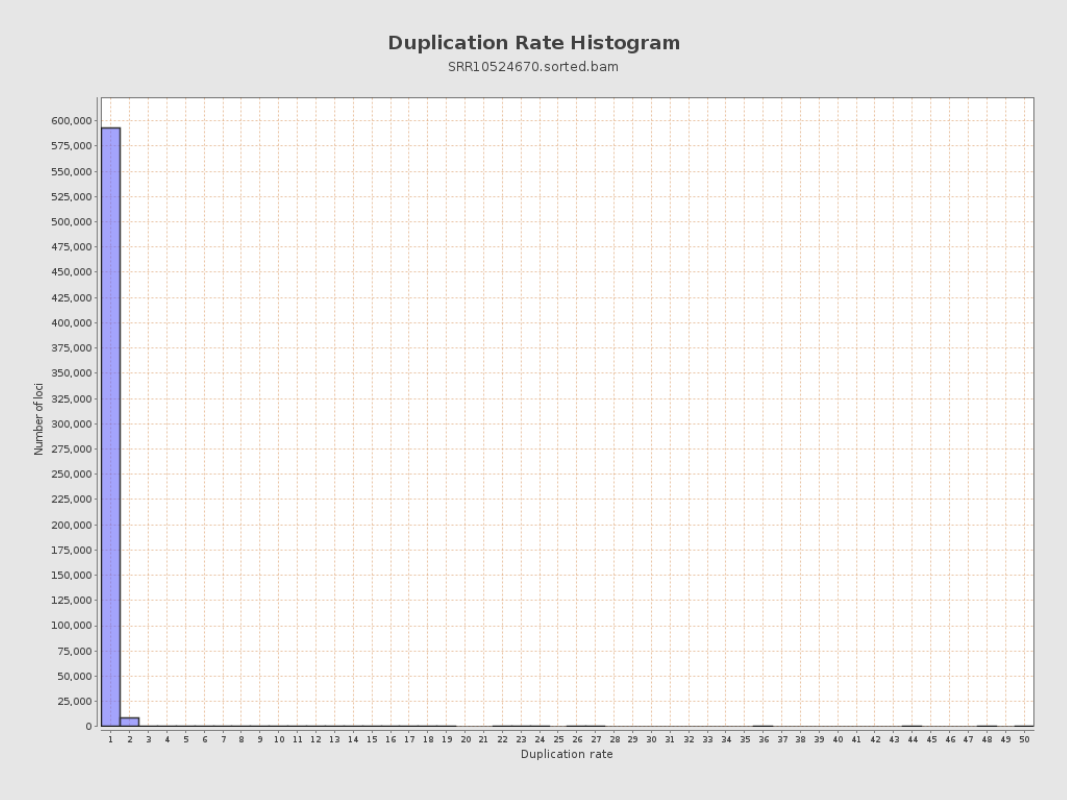
5. Results : Coverage Histogram (0-50X)



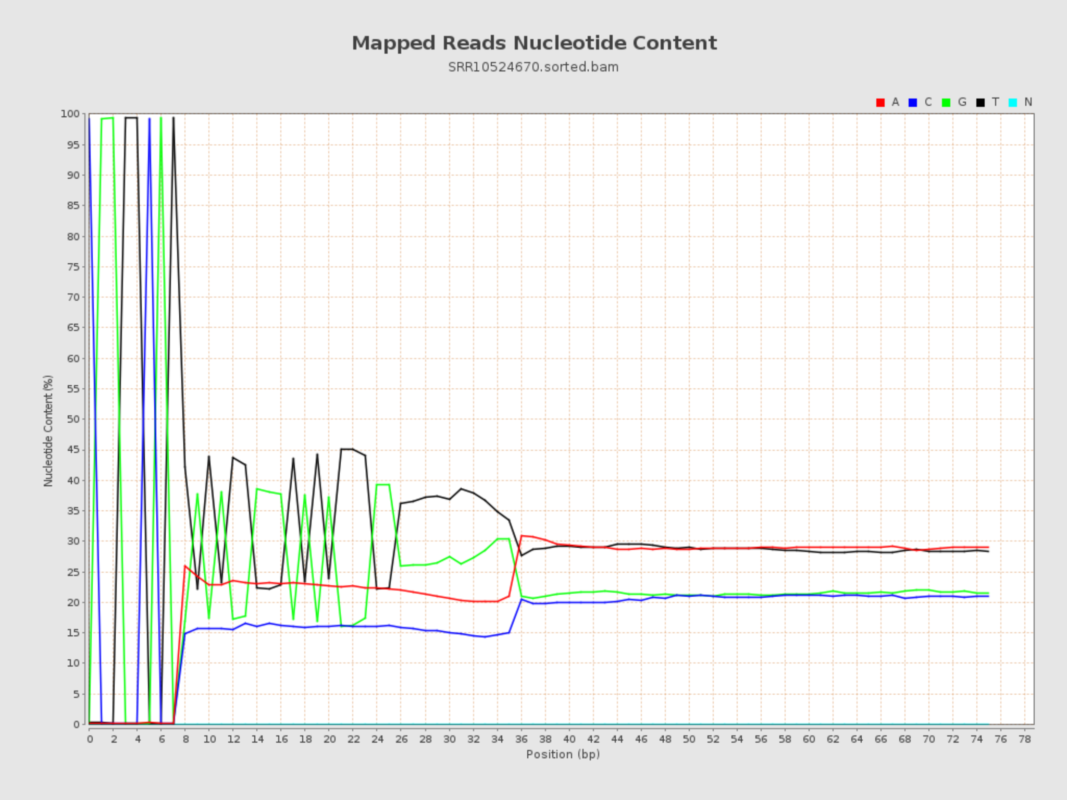
6. Results : Genome Fraction Coverage



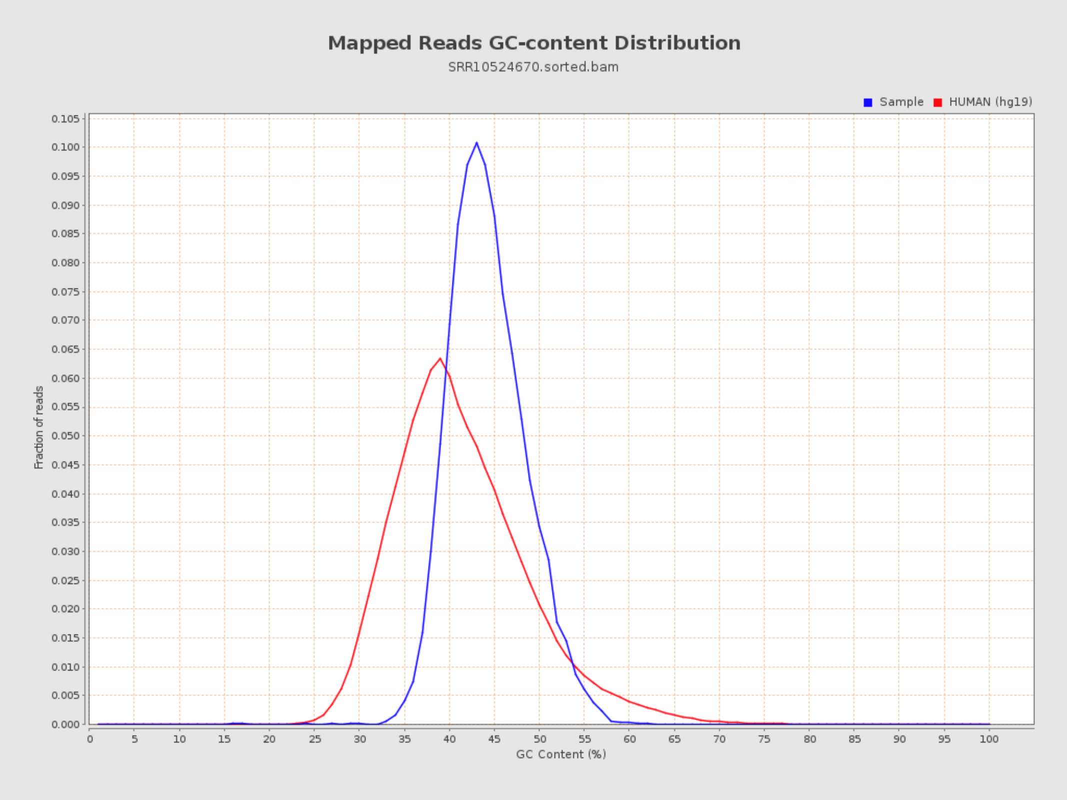
7. Results : Duplication Rate Histogram



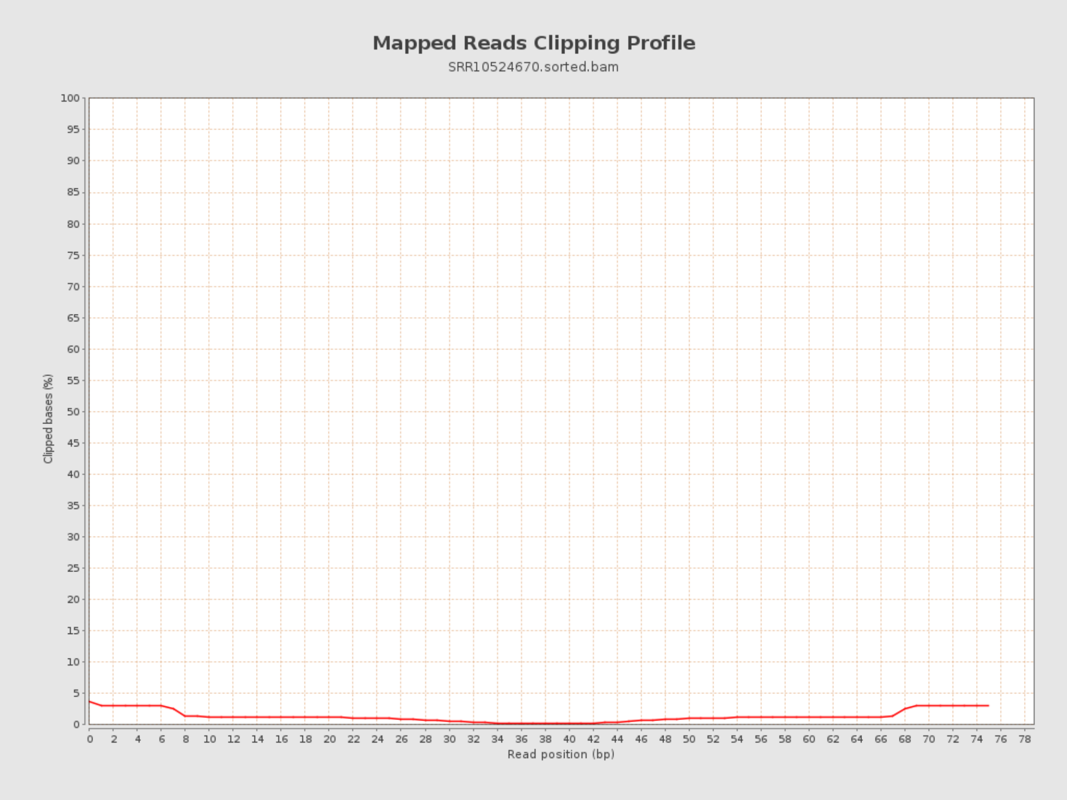
8. Results : Mapped Reads Nucleotide Content



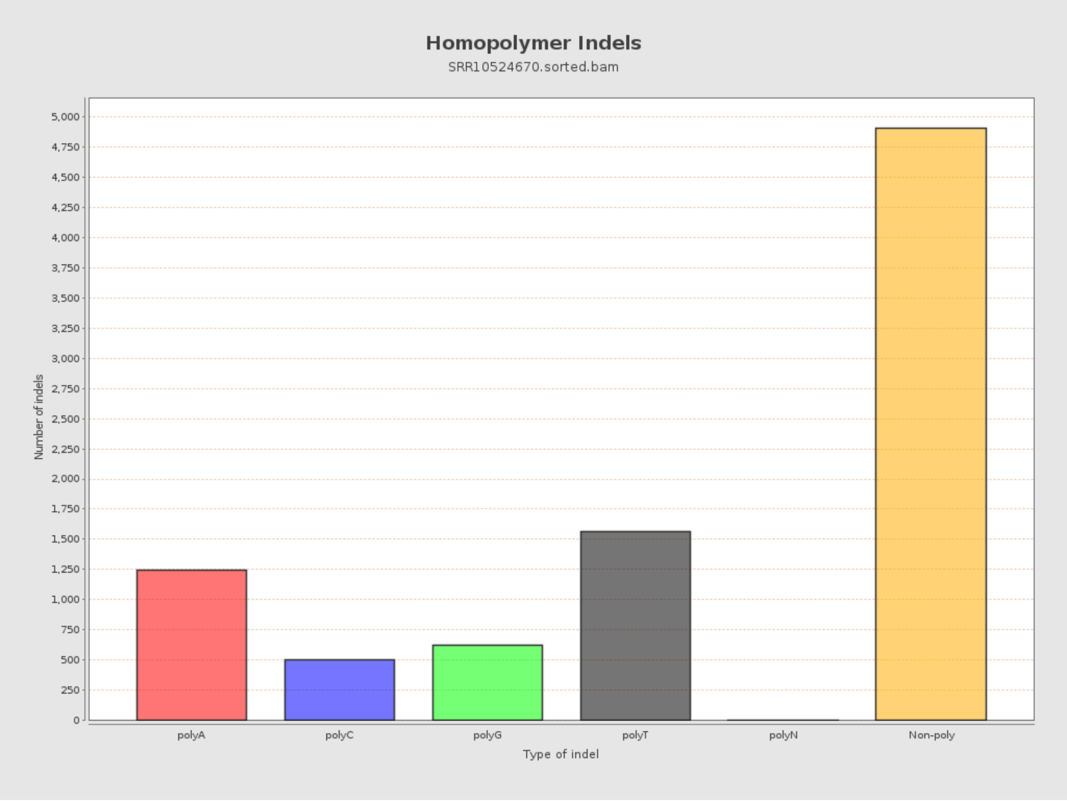
9. Results : Mapped Reads GC-content Distribution



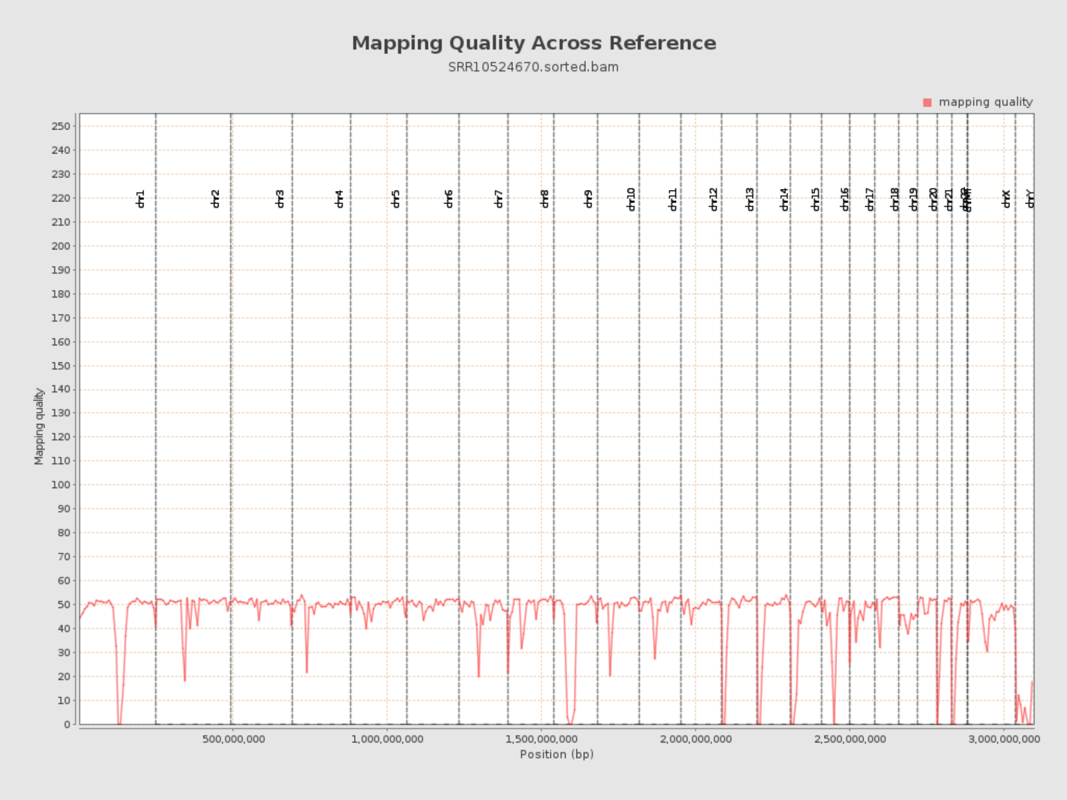
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram