Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:02:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524849.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_SRR10524849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:02:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	880,933
Mapped reads	811,948 / 92.17%
Unmapped reads	68,985 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,562 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	17,390 / 1.97%
Duplication rate	1.48%
Clipped reads	814,116 / 92.42%

2.2. ACGT Content

Number/percentage of A's	11,824,747 / 24.85%
Number/percentage of C's	8,704,723 / 18.3%
Number/percentage of T's	15,407,827 / 32.38%
Number/percentage of G's	11,636,189 / 24.46%
Number/percentage of N's	6,222 / 0.01%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1733

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

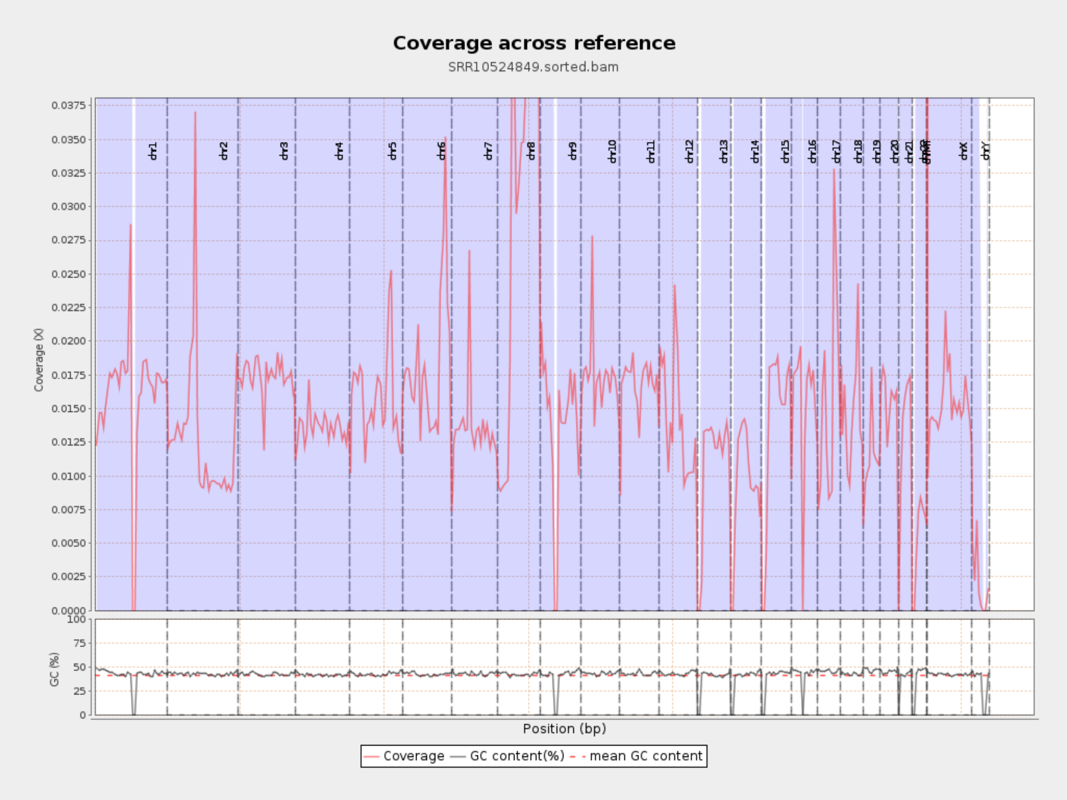
General error rate	0.5%
Mismatches	230,776
Insertions	3,352
Mapped reads with at least one insertion	0.41%
Deletions	9,173
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.39%

2.6. Chromosome stats

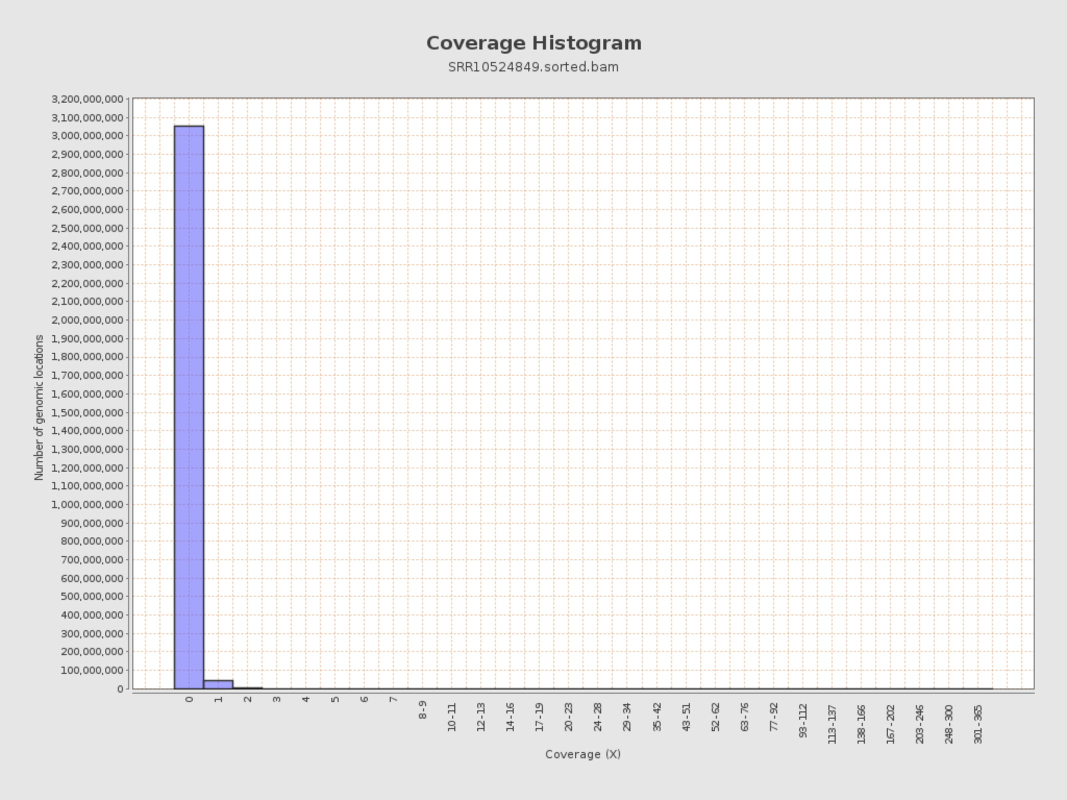
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3973592	0.0159	0.2973
chr2	243199373	3074510	0.0126	0.1707
chr3	198022430	3444362	0.0174	0.137
chr4	191154276	2598720	0.0136	0.1258
chr5	180915260	2895126	0.016	0.1317
chr6	171115067	3094500	0.0181	0.1467
chr7	159138663	2177276	0.0137	0.2221

chr8	146364022	5191220	0.0355	0.2434
chr9	141213431	1954039	0.0138	0.1486
chr10	135534747	2358267	0.0174	0.1684
chr11	135006516	2280211	0.0169	0.1581
chr12	133851895	1884656	0.0141	0.1243
chr13	115169878	1233874	0.0107	0.1073
chr14	107349540	1003962	0.0094	0.1057
chr15	102531392	1429611	0.0139	0.1233
chr16	90354753	1363126	0.0151	0.1342
chr17	81195210	1292163	0.0159	0.1402
chr18	78077248	1159040	0.0148	0.2456
chr19	59128983	681686	0.0115	0.2244
chr20	63025520	976260	0.0155	0.1301
chr21	48129895	630773	0.0131	0.1235
chr22	51304566	279550	0.0054	0.076
chrMT	16571	105475	6.365	4.0219
chrX	155270560	2392159	0.0154	0.1405
chrY	59373566	119977	0.002	0.059

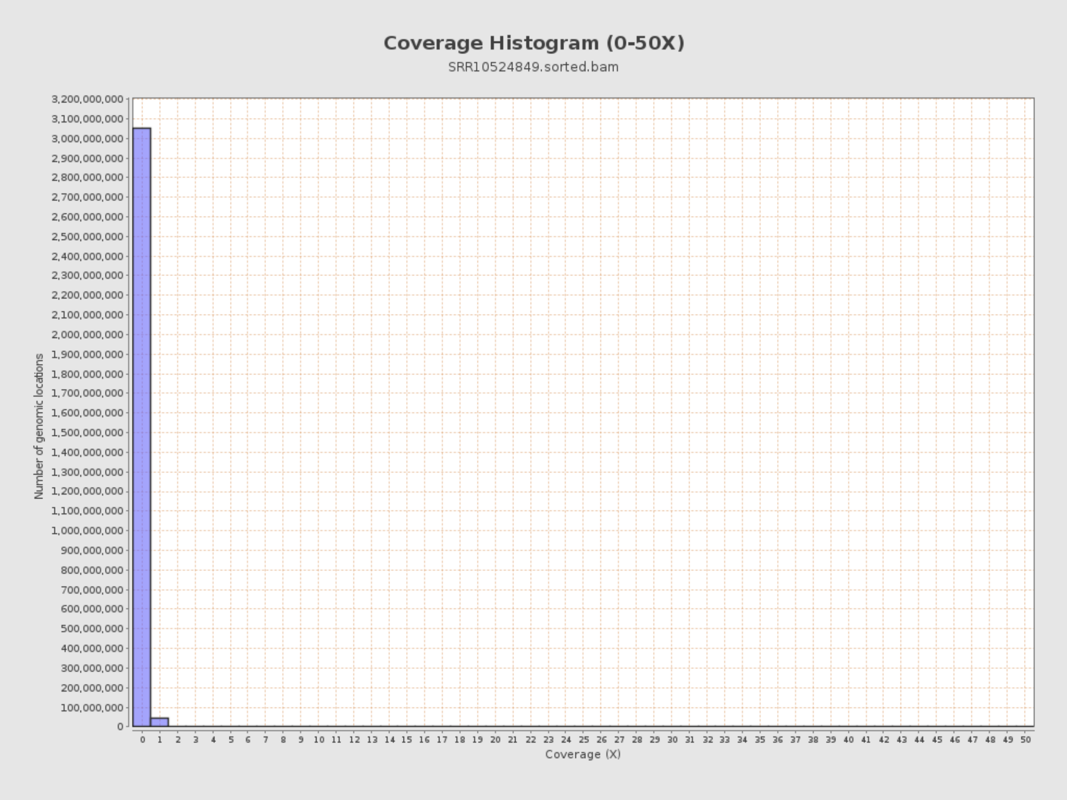
3. Results : Coverage across reference



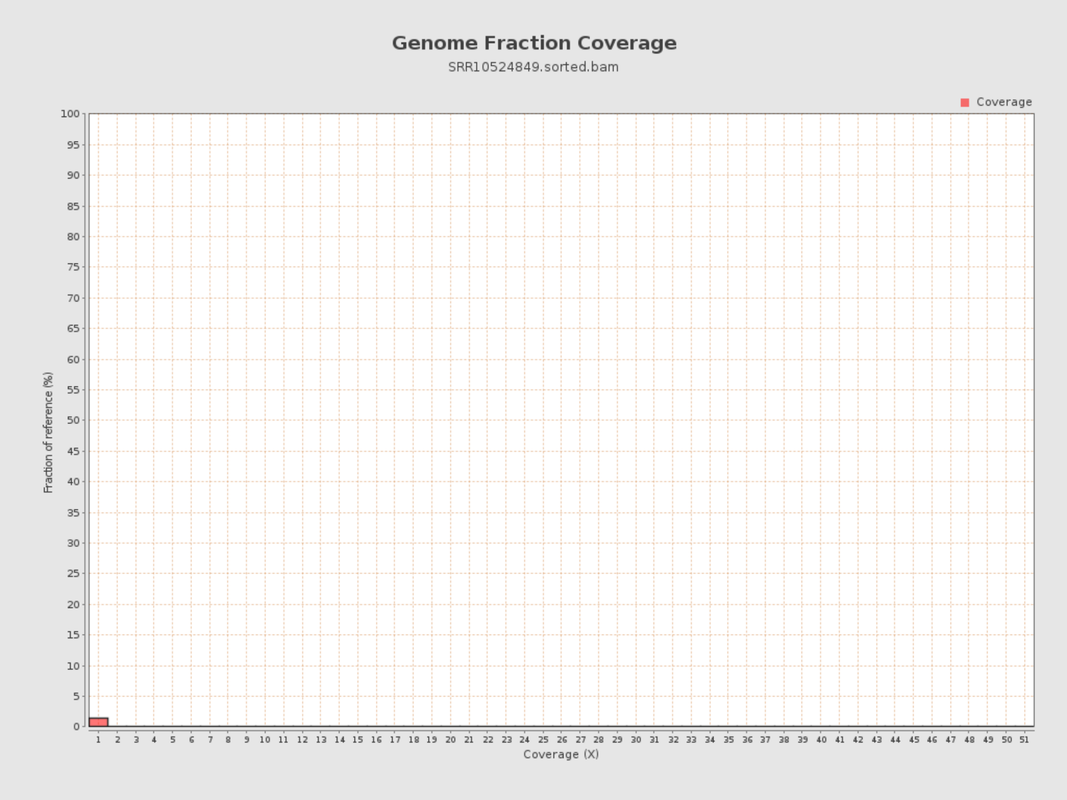
4. Results : Coverage Histogram



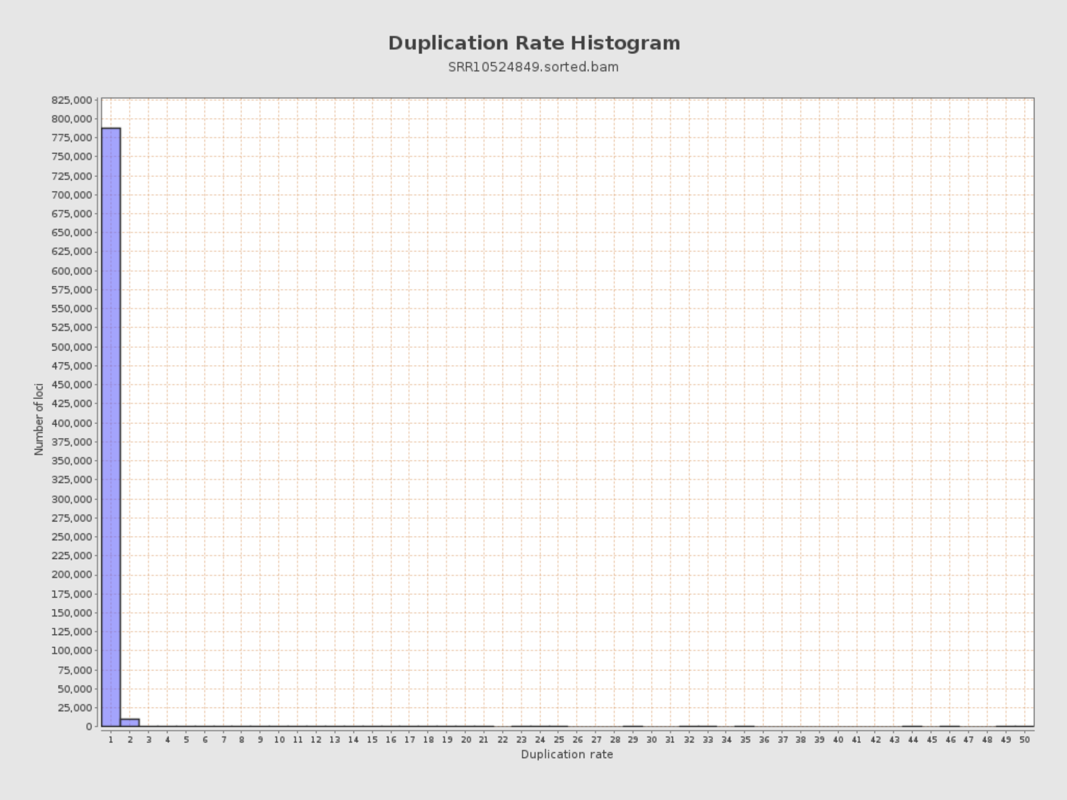
5. Results : Coverage Histogram (0-50X)



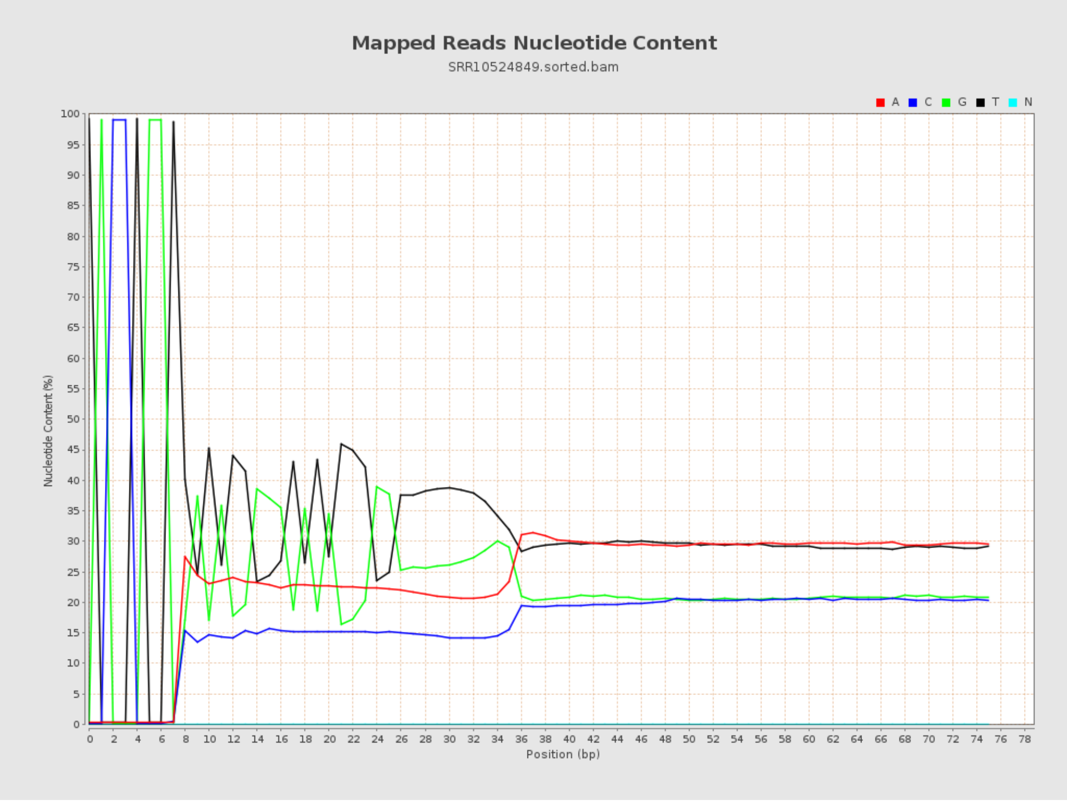
6. Results : Genome Fraction Coverage



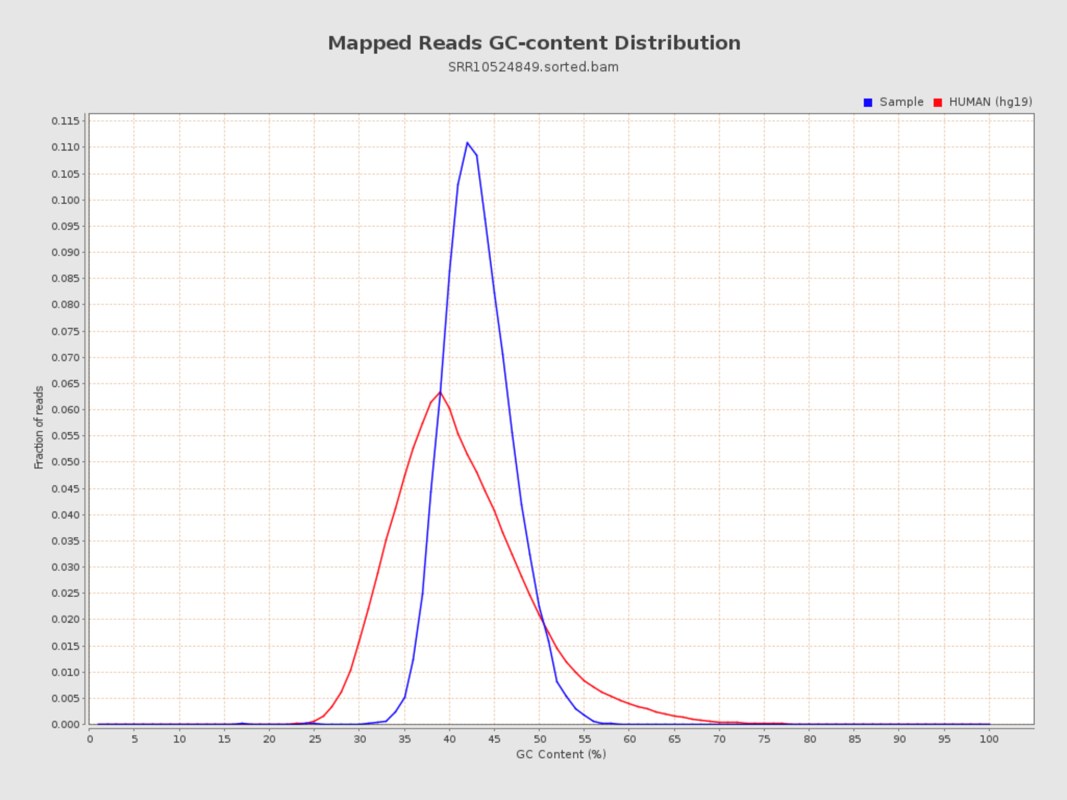
7. Results : Duplication Rate Histogram



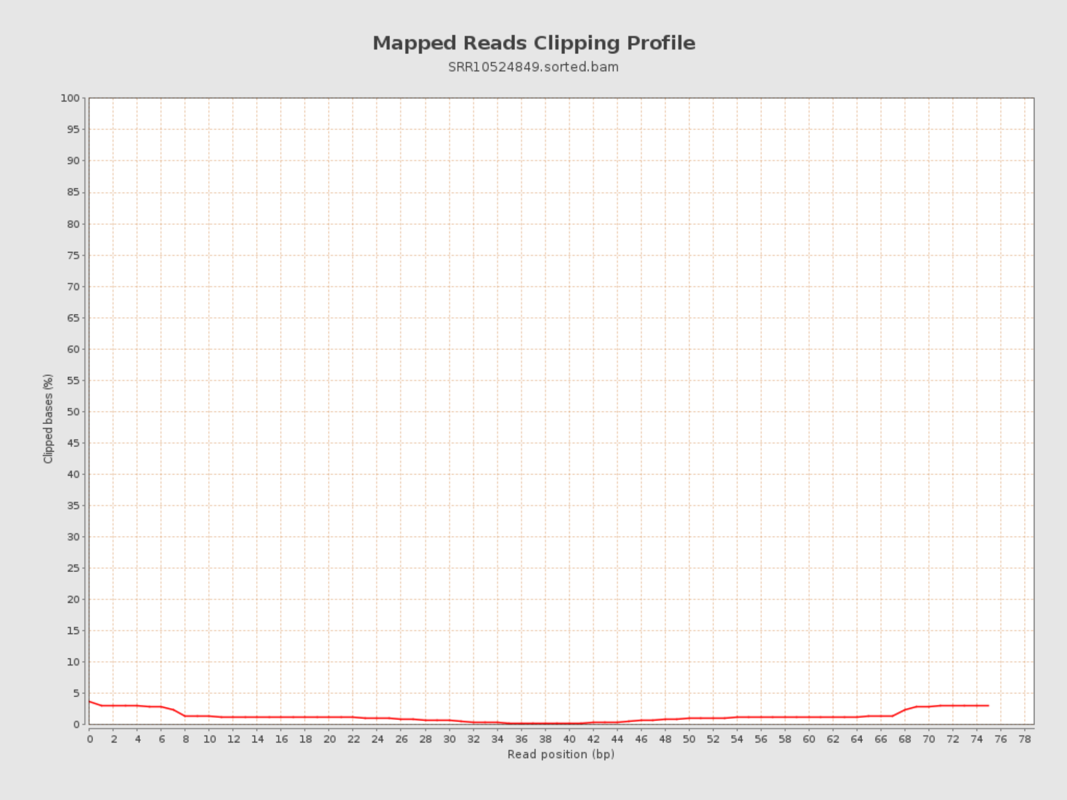
8. Results : Mapped Reads Nucleotide Content



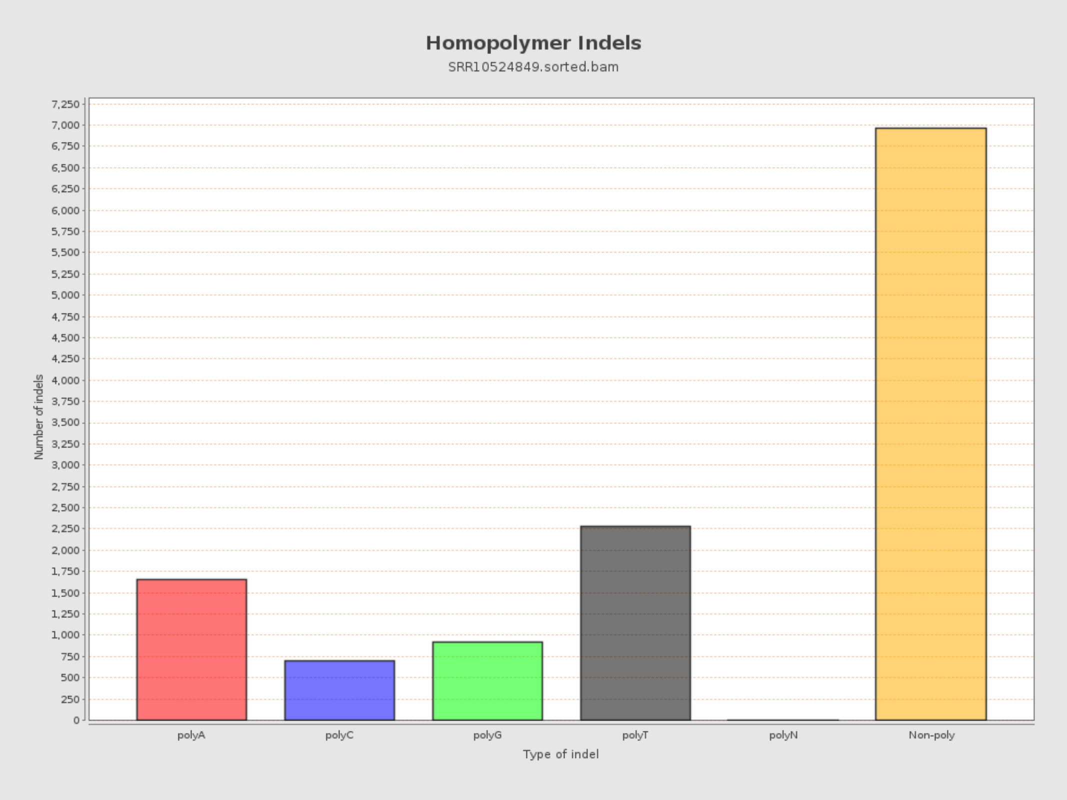
9. Results : Mapped Reads GC-content Distribution



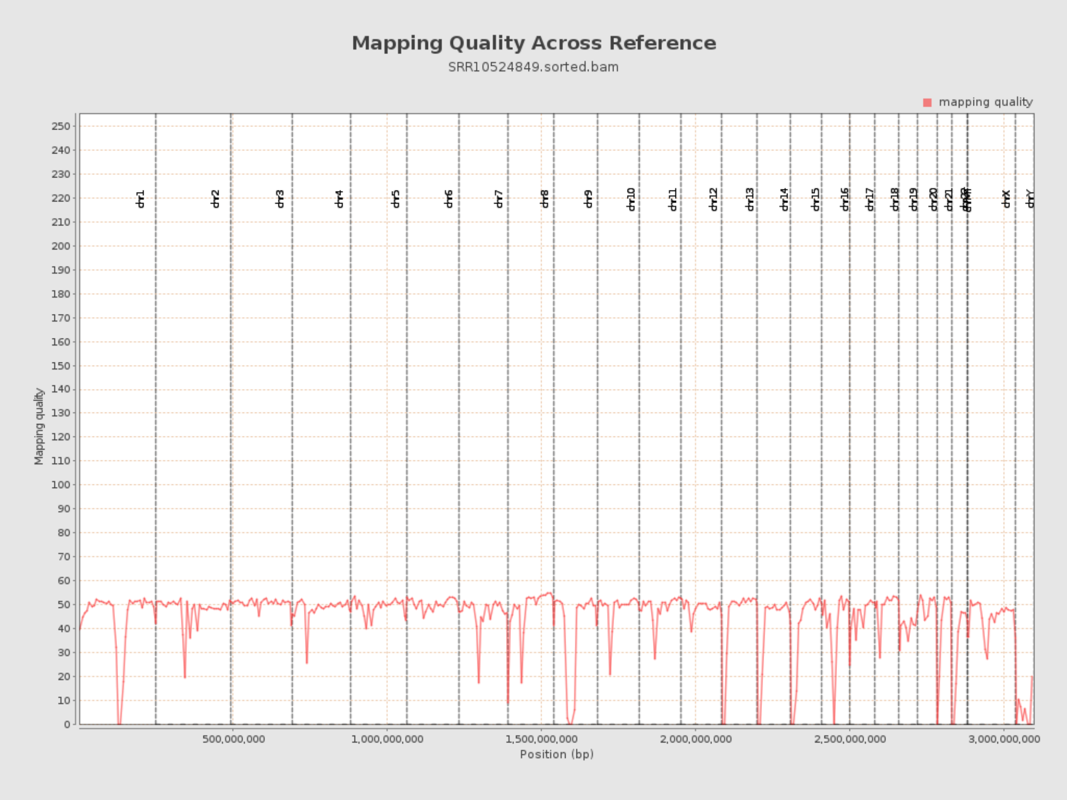
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram