Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 21:31:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524811.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_SRR10524811 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524811.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 21:31:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524811.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	990,561
Mapped reads	908,216 / 91.69%
Unmapped reads	82,345 / 8.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,086 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	23,478 / 2.37%
Duplication rate	1.88%
Clipped reads	908,801 / 91.75%

2.2. ACGT Content

Number/percentage of A's	13,568,796 / 25.75%
Number/percentage of C's	10,473,398 / 19.88%
Number/percentage of T's	16,337,590 / 31.01%
Number/percentage of G's	12,305,295 / 23.36%
Number/percentage of N's	1,164 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.017

Standard Deviation	0.1857

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

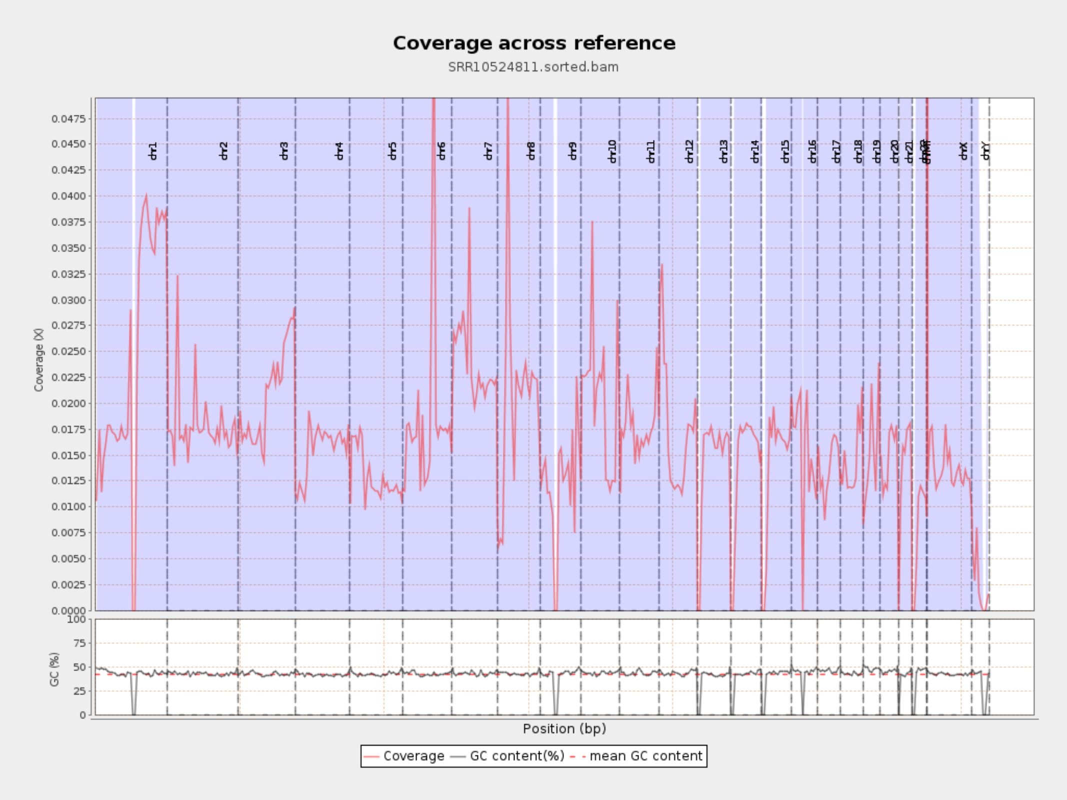
General error rate	0.52%
Mismatches	264,686
Insertions	3,918
Mapped reads with at least one insertion	0.43%
Deletions	11,108
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.82%

2.6. Chromosome stats

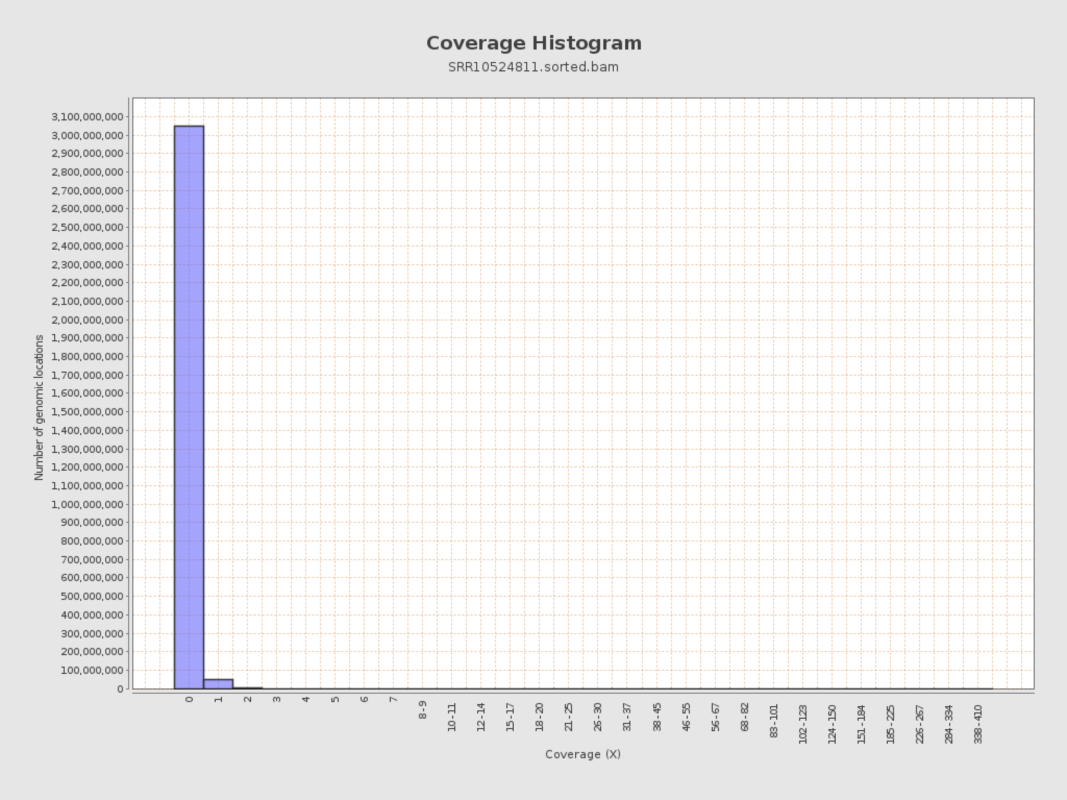
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6061946	0.0243	0.3094
chr2	243199373	4329495	0.0178	0.2221
chr3	198022430	4095878	0.0207	0.1525
chr4	191154276	2981366	0.0156	0.1355
chr5	180915260	2366445	0.0131	0.1207
chr6	171115067	3261931	0.0191	0.156
chr7	159138663	3847659	0.0242	0.3131

chr8	146364022	3058030	0.0209	0.1882
chr9	141213431	1712168	0.0121	0.1365
chr10	135534747	2808203	0.0207	0.2116
chr11	135006516	2384672	0.0177	0.1553
chr12	133851895	2362923	0.0177	0.1408
chr13	115169878	1650496	0.0143	0.1265
chr14	107349540	1510990	0.0141	0.1275
chr15	102531392	1402903	0.0137	0.1249
chr16	90354753	1385006	0.0153	0.1401
chr17	81195210	1124640	0.0139	0.1264
chr18	78077248	1118145	0.0143	0.2205
chr19	59128983	912057	0.0154	0.2234
chr20	63025520	933665	0.0148	0.1279
chr21	48129895	674586	0.014	0.1279
chr22	51304566	402024	0.0078	0.092
chrMT	16571	39837	2.404	2.0381
chrX	155270560	2134567	0.0137	0.1325
chrY	59373566	144310	0.0024	0.075

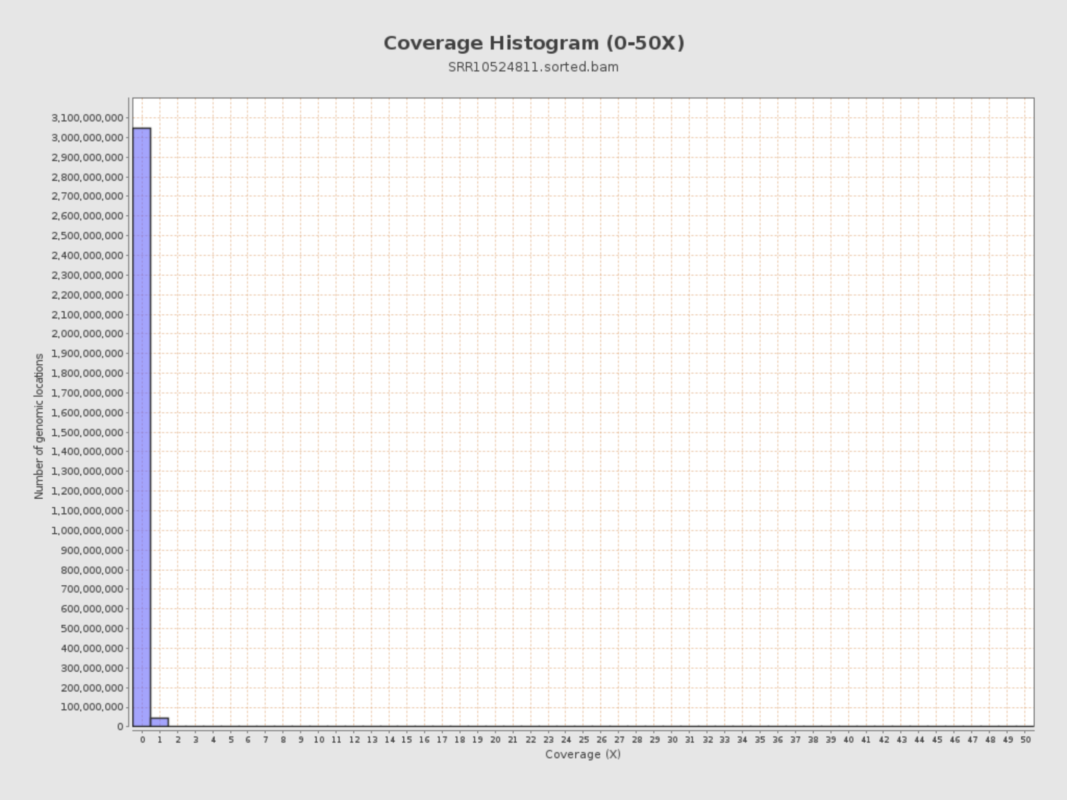
3. Results : Coverage across reference



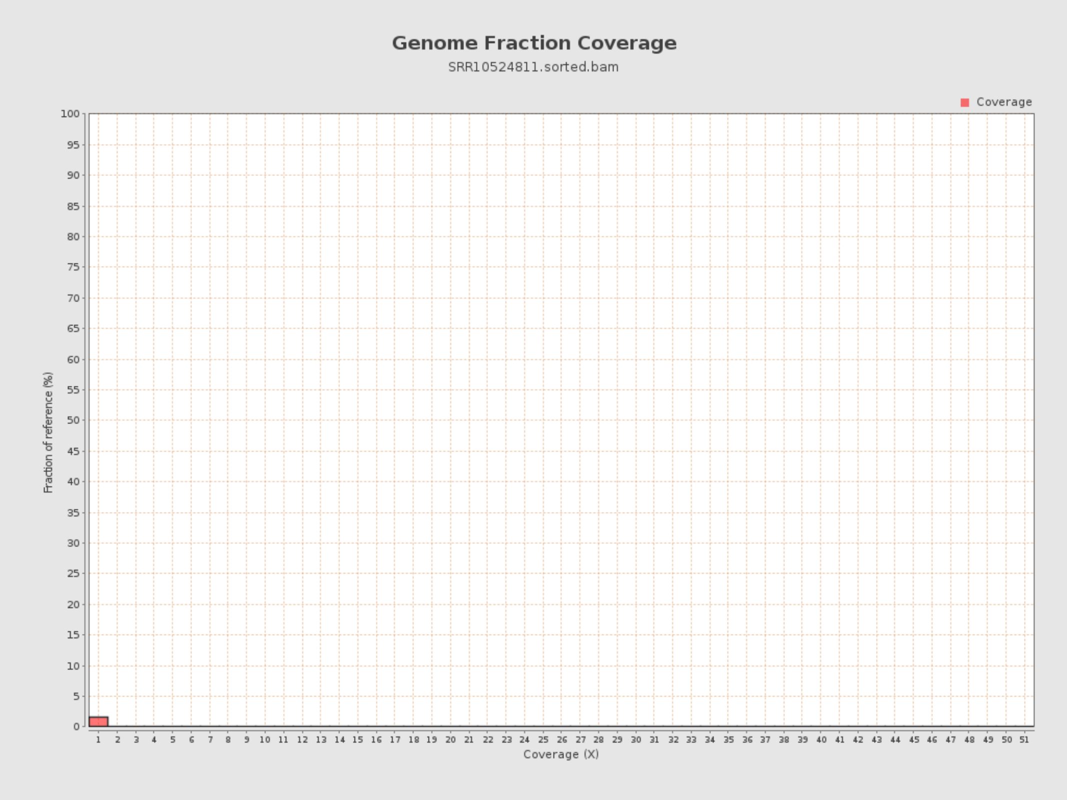
4. Results : Coverage Histogram



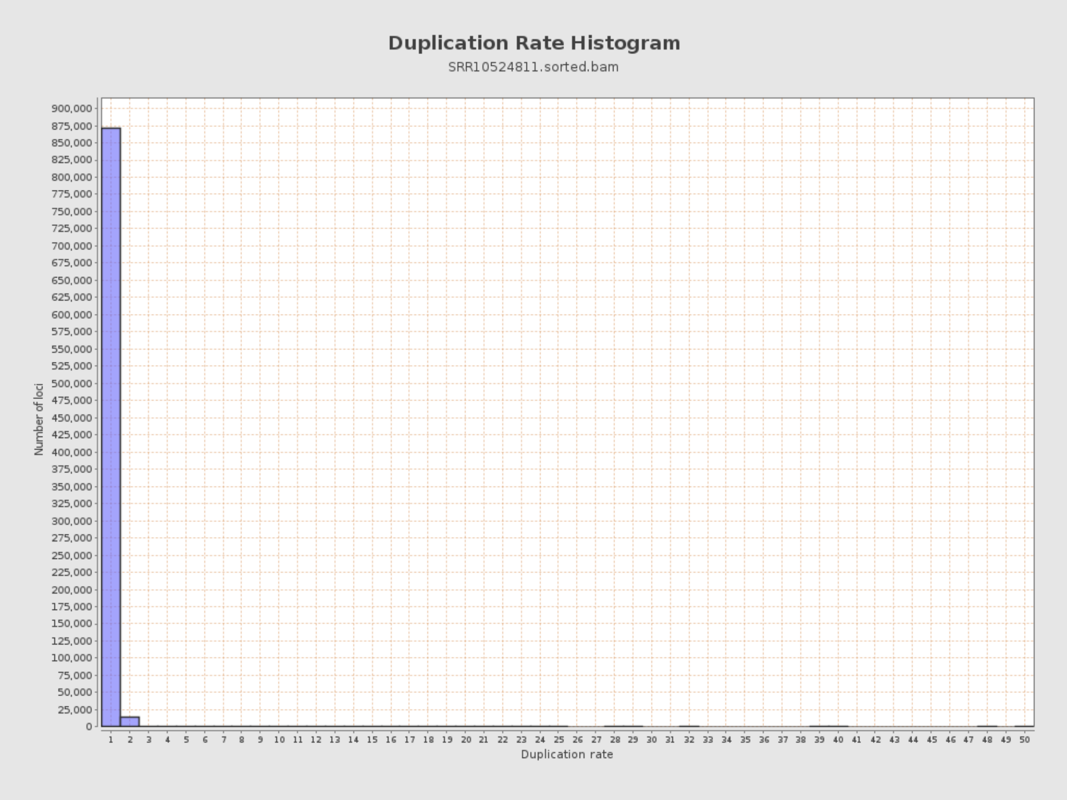
5. Results : Coverage Histogram (0-50X)



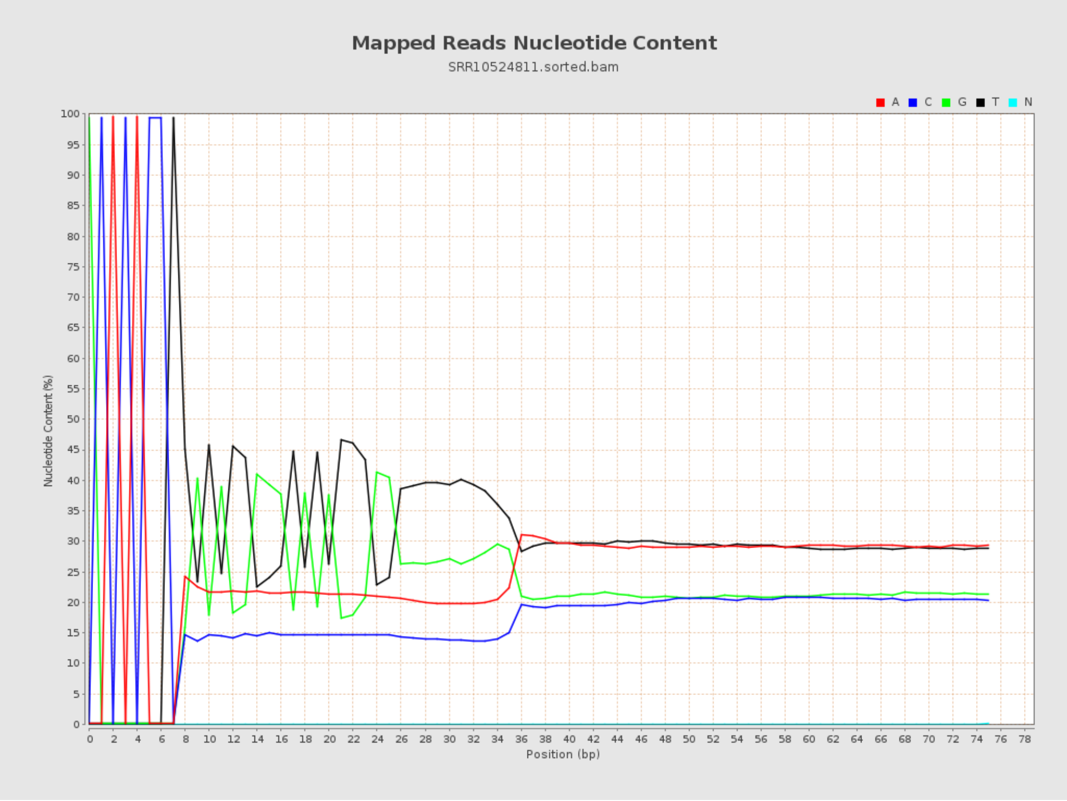
6. Results : Genome Fraction Coverage



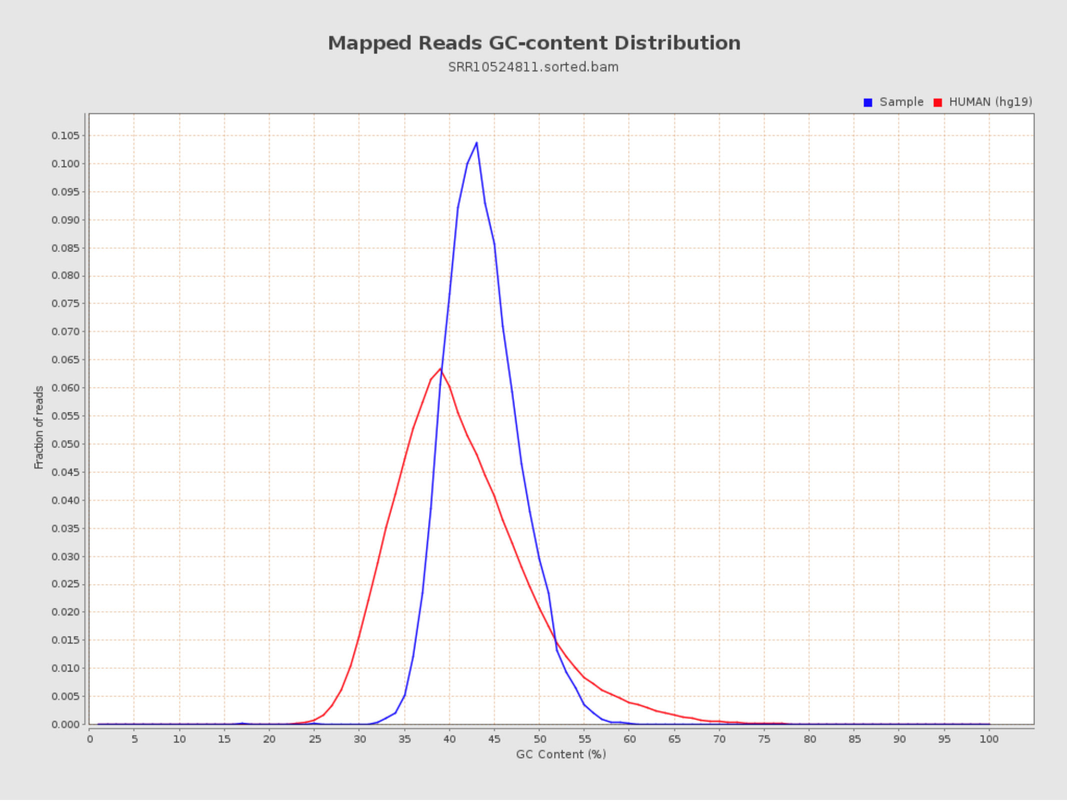
7. Results : Duplication Rate Histogram



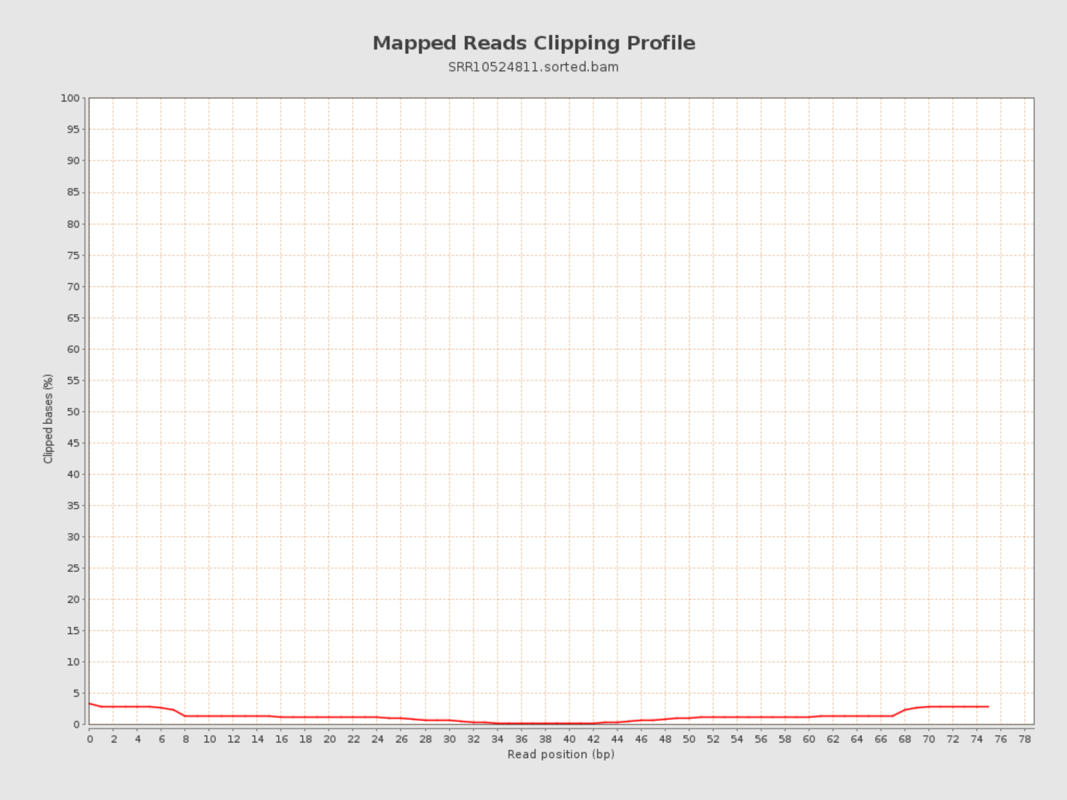
8. Results : Mapped Reads Nucleotide Content



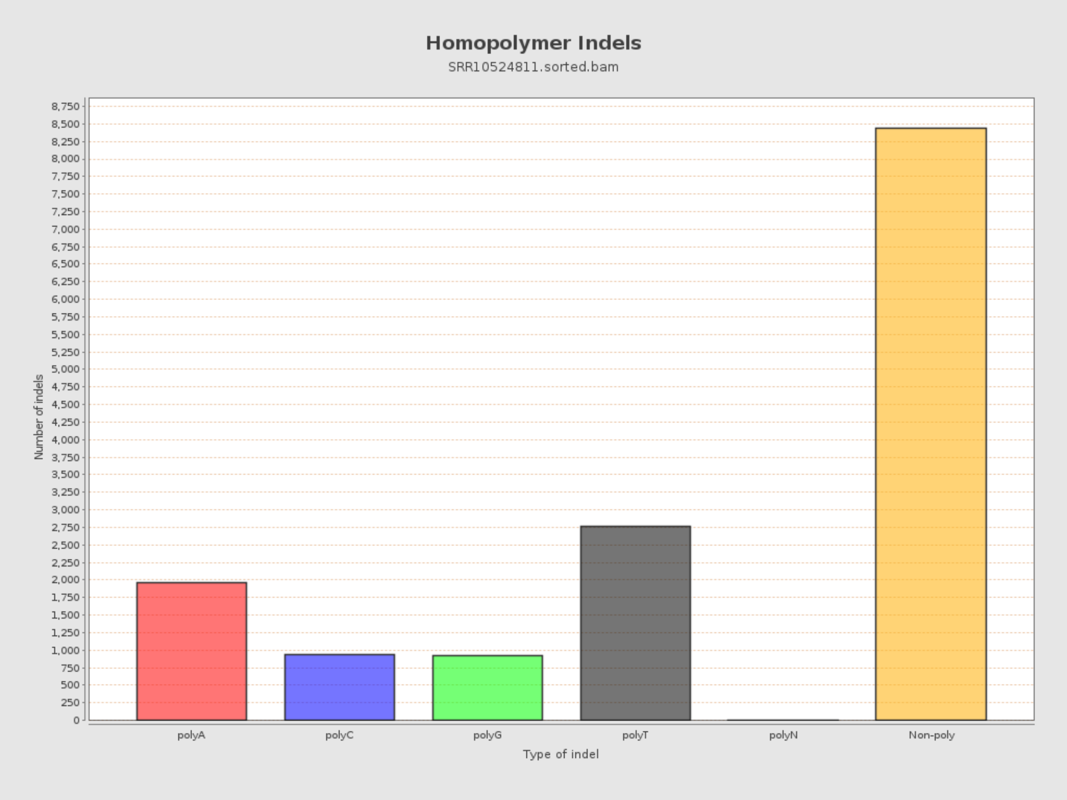
9. Results : Mapped Reads GC-content Distribution



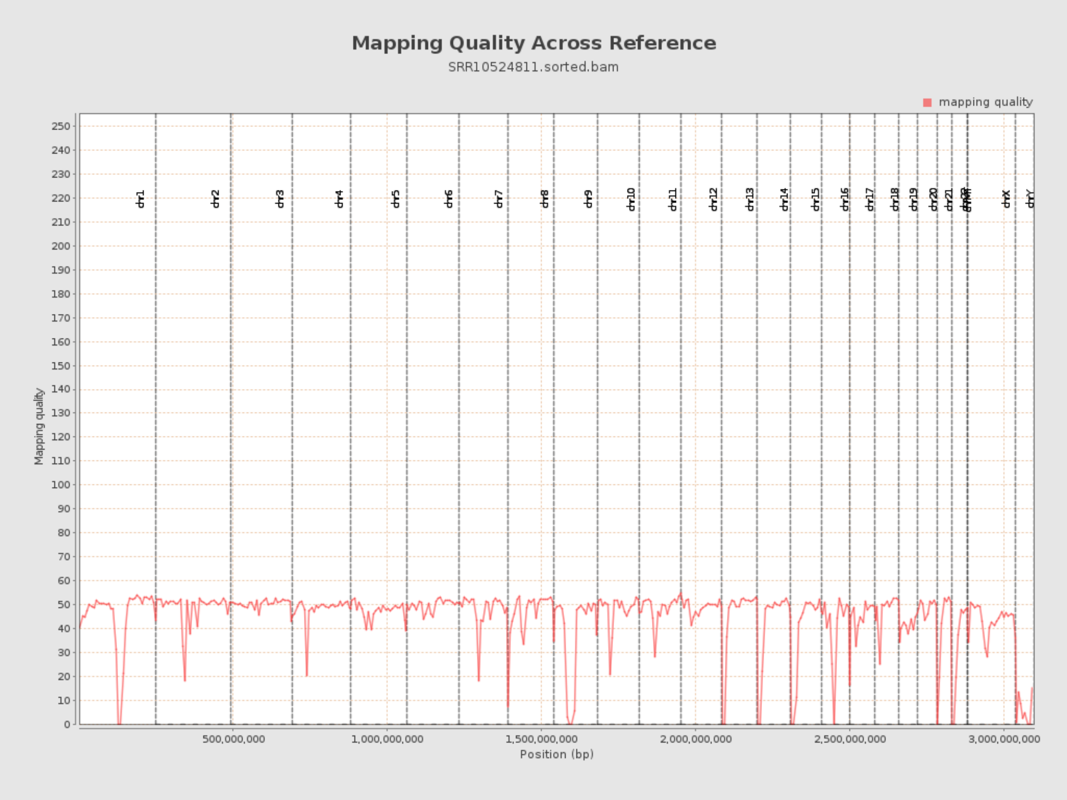
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram