Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:17:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524733.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_SRR10524733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524733.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:17:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,647,393
Mapped reads	1,515,296 / 91.98%
Unmapped reads	132,097 / 8.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,026 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	54,680 / 3.32%
Duplication rate	2.65%
Clipped reads	1,517,774 / 92.13%

2.2. ACGT Content

Number/percentage of A's	22,143,126 / 25.09%
Number/percentage of C's	16,860,479 / 19.1%
Number/percentage of T's	28,159,528 / 31.9%
Number/percentage of G's	21,105,279 / 23.91%
Number/percentage of N's	1,875 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2779

2.4. Mapping Quality

Mean Mapping Quality	45.32

2.5. Mismatches and indels

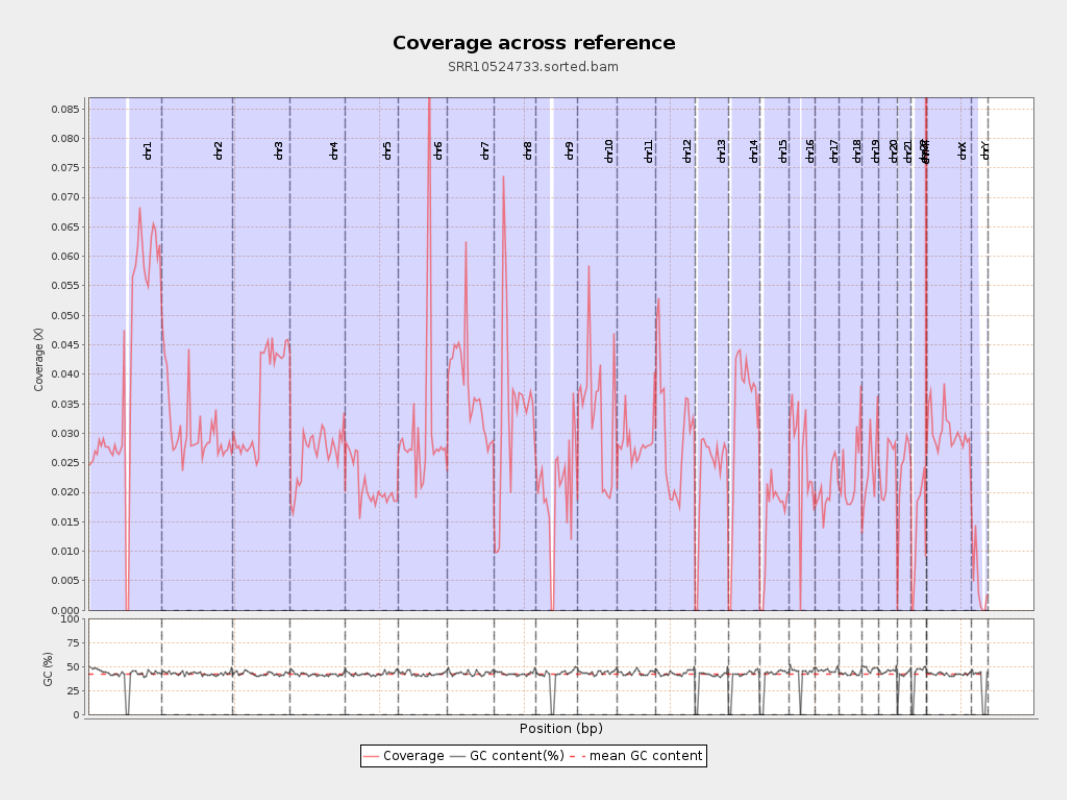
General error rate	0.51%
Mismatches	442,957
Insertions	5,924
Mapped reads with at least one insertion	0.39%
Deletions	19,104
Mapped reads with at least one deletion	1.25%
Homopolymer indels	42.67%

2.6. Chromosome stats

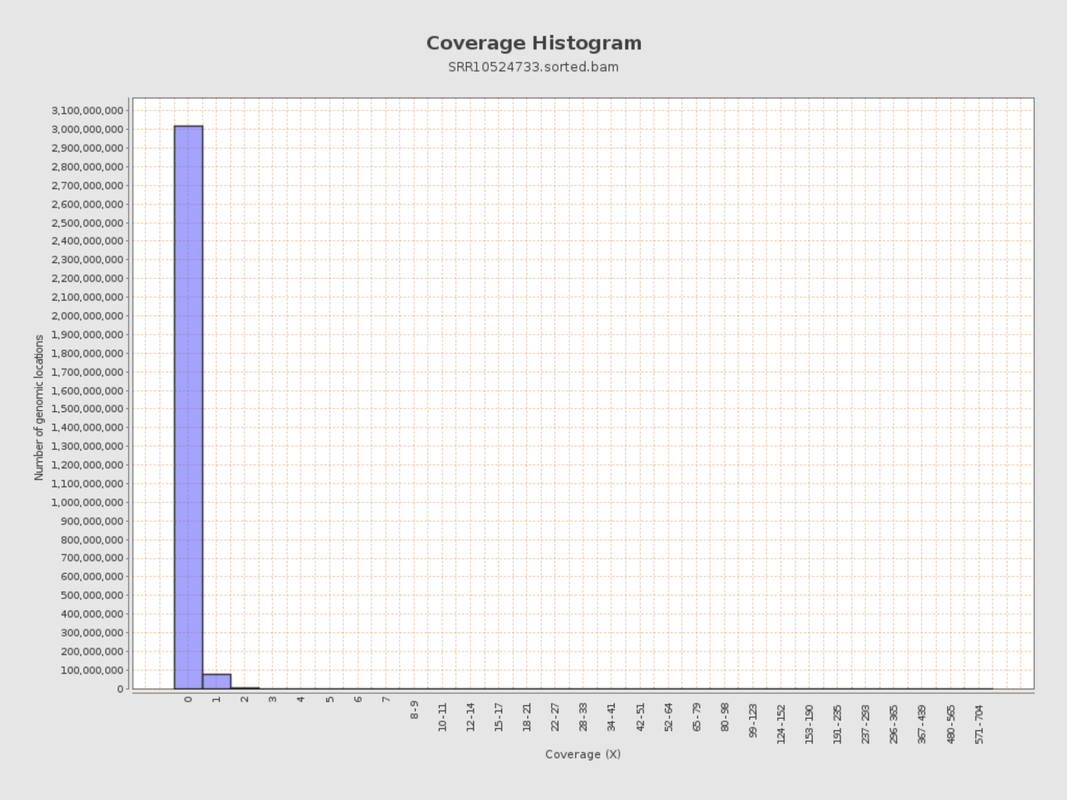
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10005281	0.0401	0.4952
chr2	243199373	7433457	0.0306	0.348
chr3	198022430	7107404	0.0359	0.2039
chr4	191154276	5056783	0.0265	0.1867
chr5	180915260	3822587	0.0211	0.1577
chr6	171115067	5396232	0.0315	0.2144
chr7	159138663	6011838	0.0378	0.467

chr8	146364022	4828615	0.033	0.2957
chr9	141213431	2826459	0.02	0.2005
chr10	135534747	4525376	0.0334	0.2831
chr11	135006516	3863817	0.0286	0.2212
chr12	133851895	3970867	0.0297	0.1873
chr13	115169878	2667772	0.0232	0.165
chr14	107349540	3514848	0.0327	0.1999
chr15	102531392	1614425	0.0157	0.1369
chr16	90354753	2293023	0.0254	0.1887
chr17	81195210	1668574	0.0206	0.1592
chr18	78077248	1798792	0.023	0.3682
chr19	59128983	1436277	0.0243	0.354
chr20	63025520	1518986	0.0241	0.1702
chr21	48129895	1109820	0.0231	0.1726
chr22	51304566	728078	0.0142	0.1269
chrMT	16571	147937	8.9275	5.5186
chrX	155270560	4693354	0.0302	0.2022
chrY	59373566	260283	0.0044	0.1219

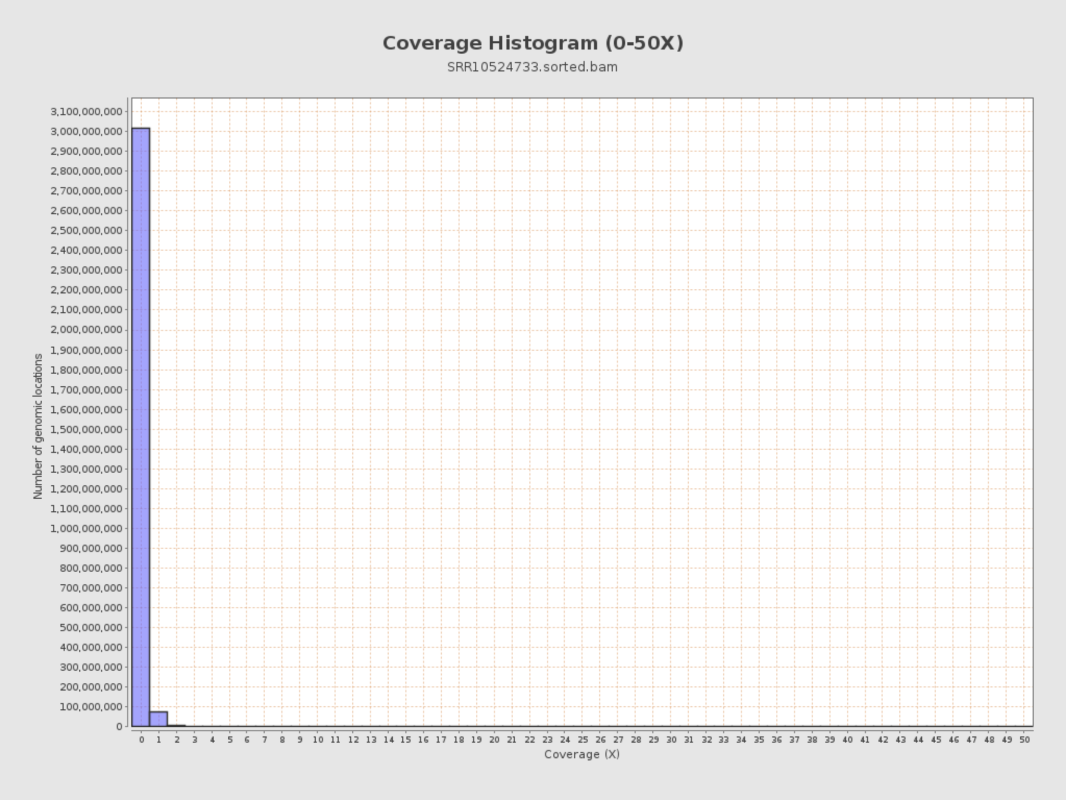
3. Results : Coverage across reference



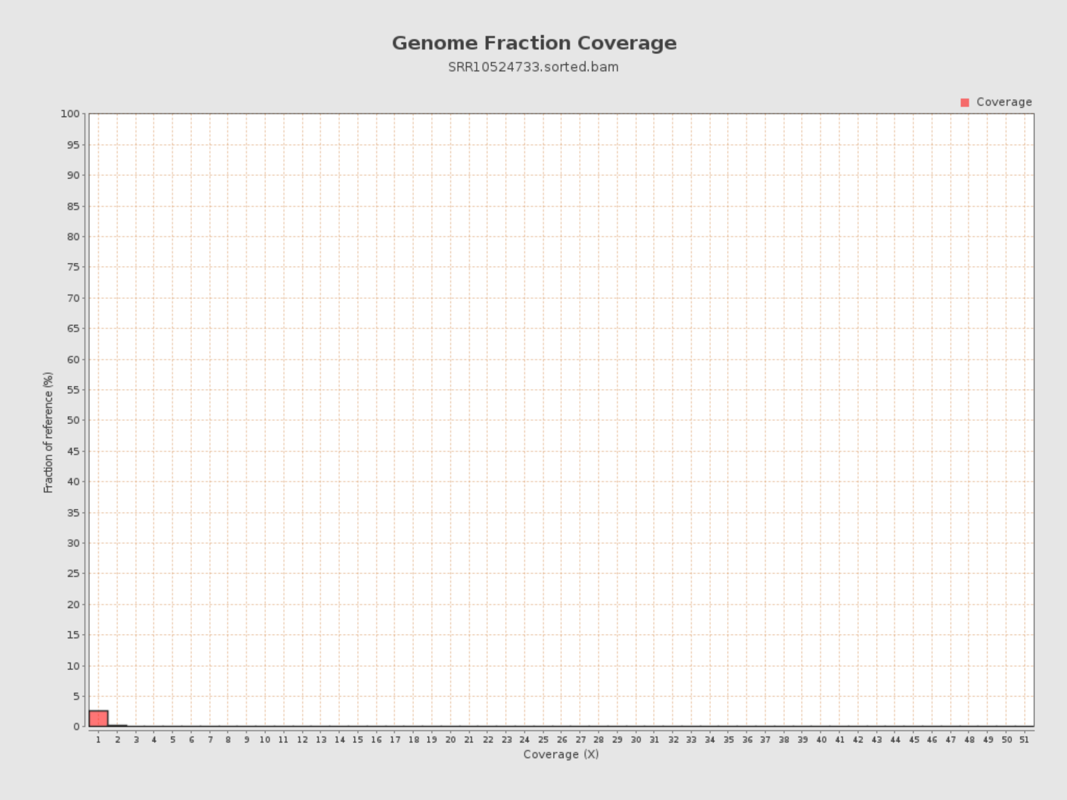
4. Results : Coverage Histogram



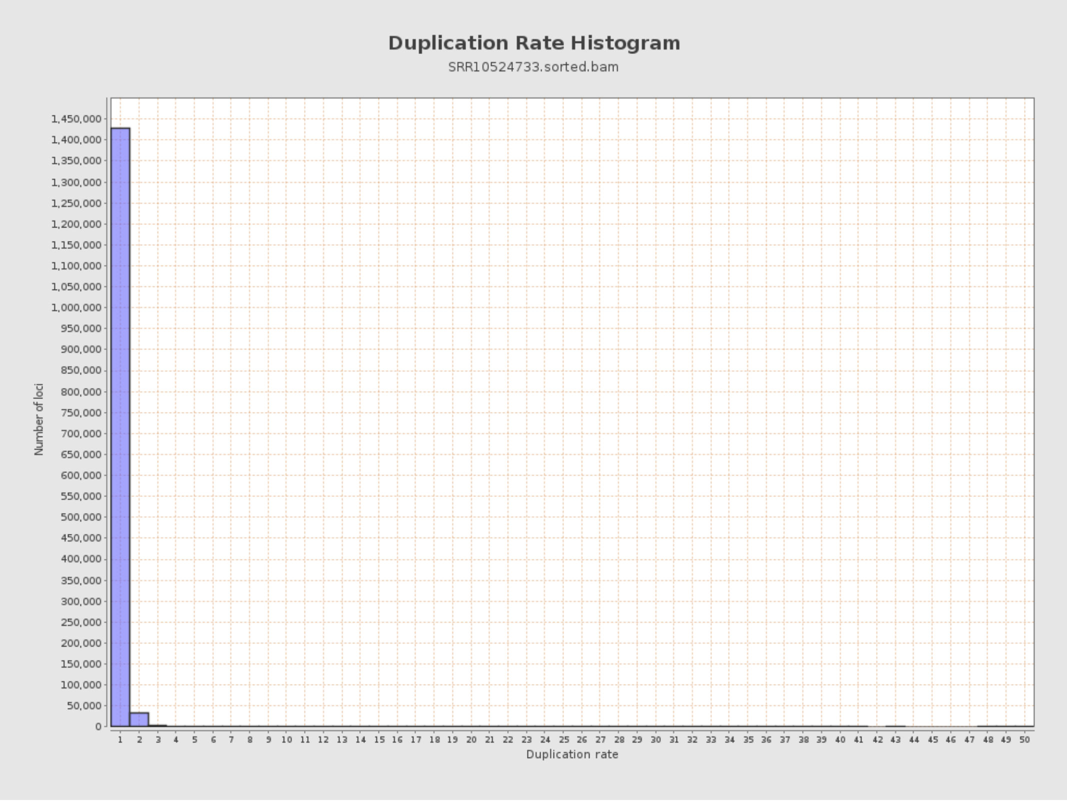
5. Results : Coverage Histogram (0-50X)



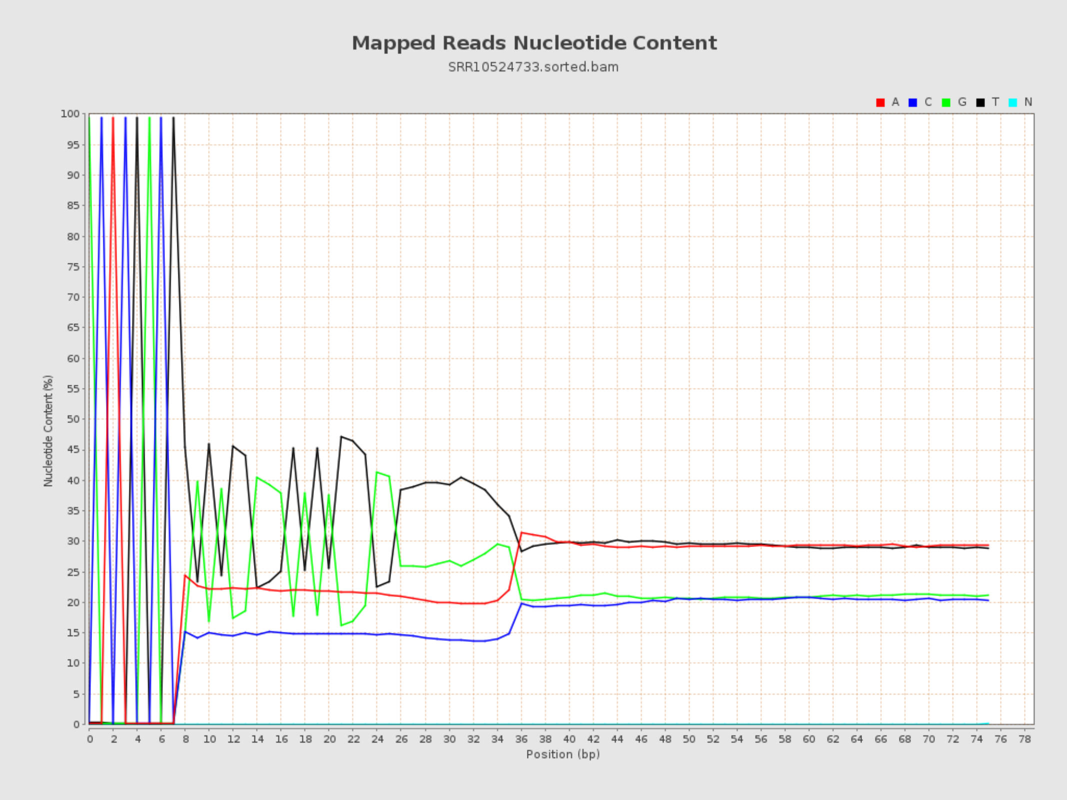
6. Results : Genome Fraction Coverage



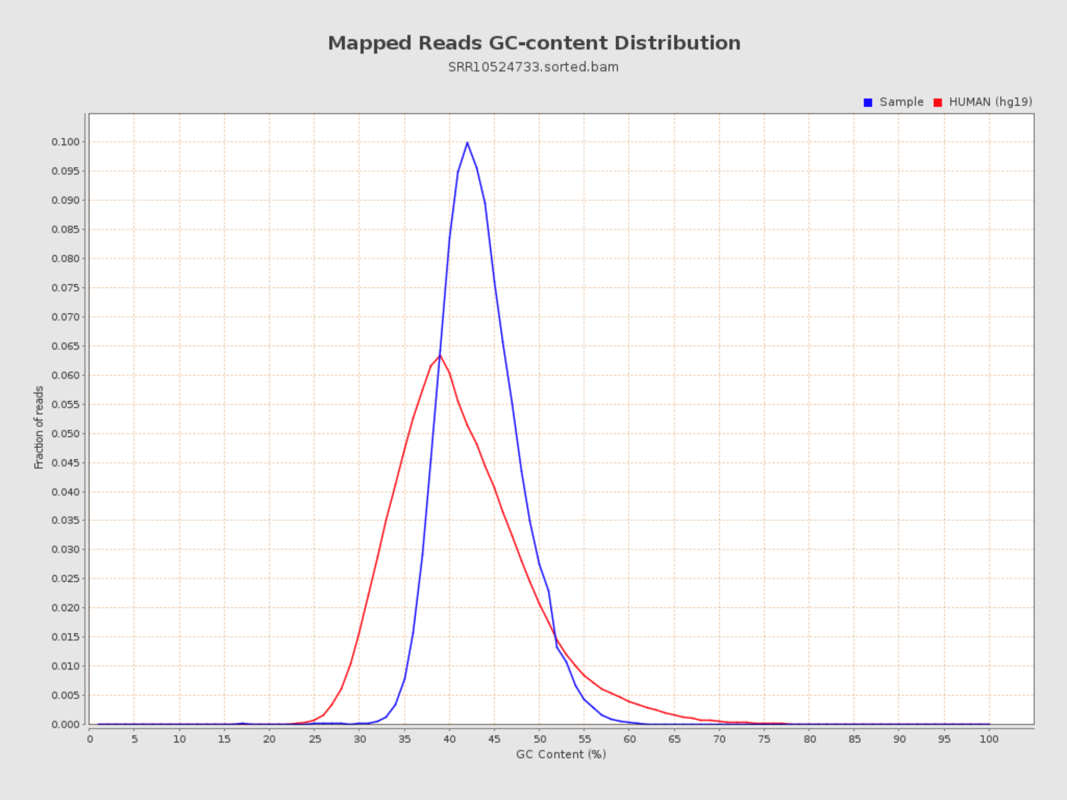
7. Results : Duplication Rate Histogram



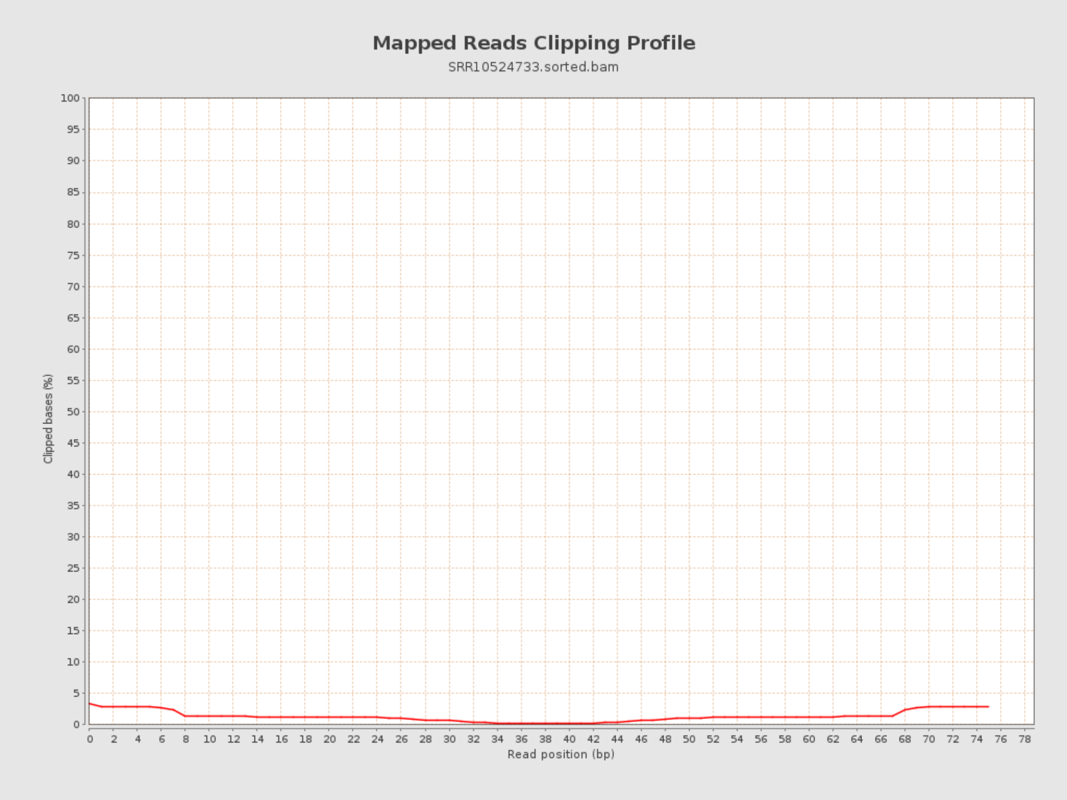
8. Results : Mapped Reads Nucleotide Content



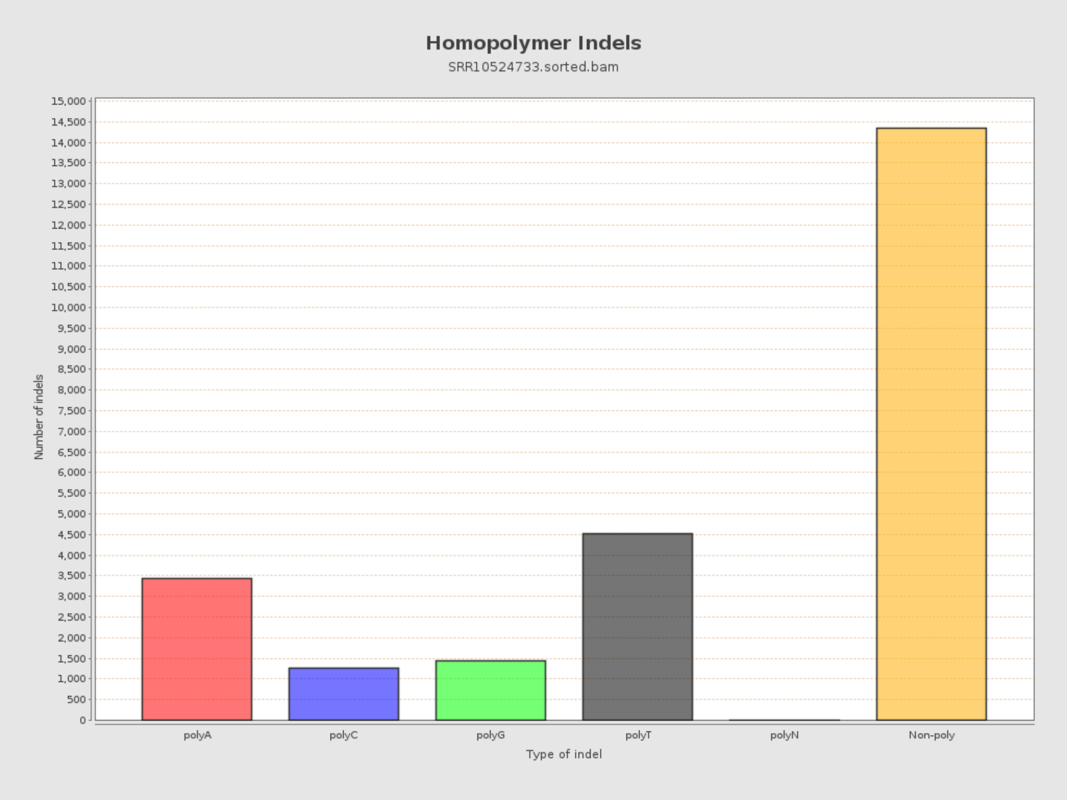
9. Results : Mapped Reads GC-content Distribution



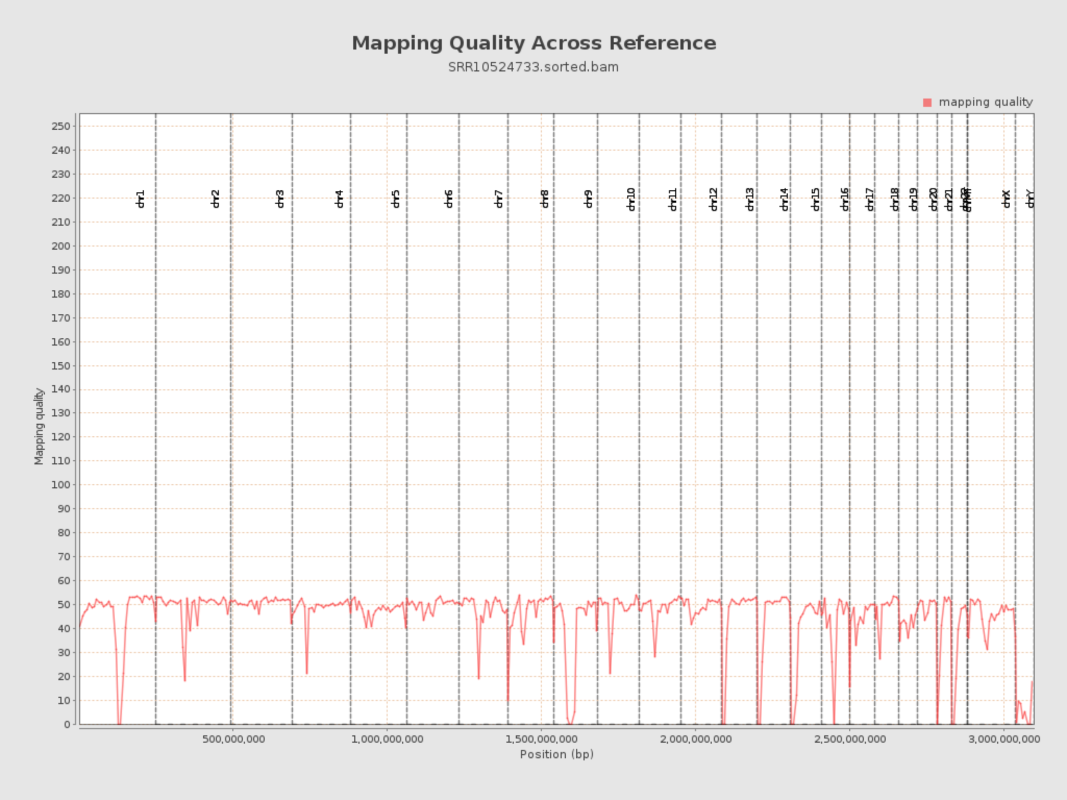
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram