Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:33:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524740.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_SRR10524740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:33:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,644,275
Mapped reads	1,505,537 / 91.56%
Unmapped reads	138,738 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,361 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	59,228 / 3.6%
Duplication rate	2.98%
Clipped reads	1,507,800 / 91.7%

2.2. ACGT Content

Number/percentage of A's	20,924,172 / 24.15%
Number/percentage of C's	16,867,139 / 19.47%
Number/percentage of T's	27,270,906 / 31.47%
Number/percentage of G's	21,576,626 / 24.9%
Number/percentage of N's	10,613 / 0.01%
GC Percentage	44.37%

2.3. Coverage

Mean	0.028

Standard Deviation	0.2504

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

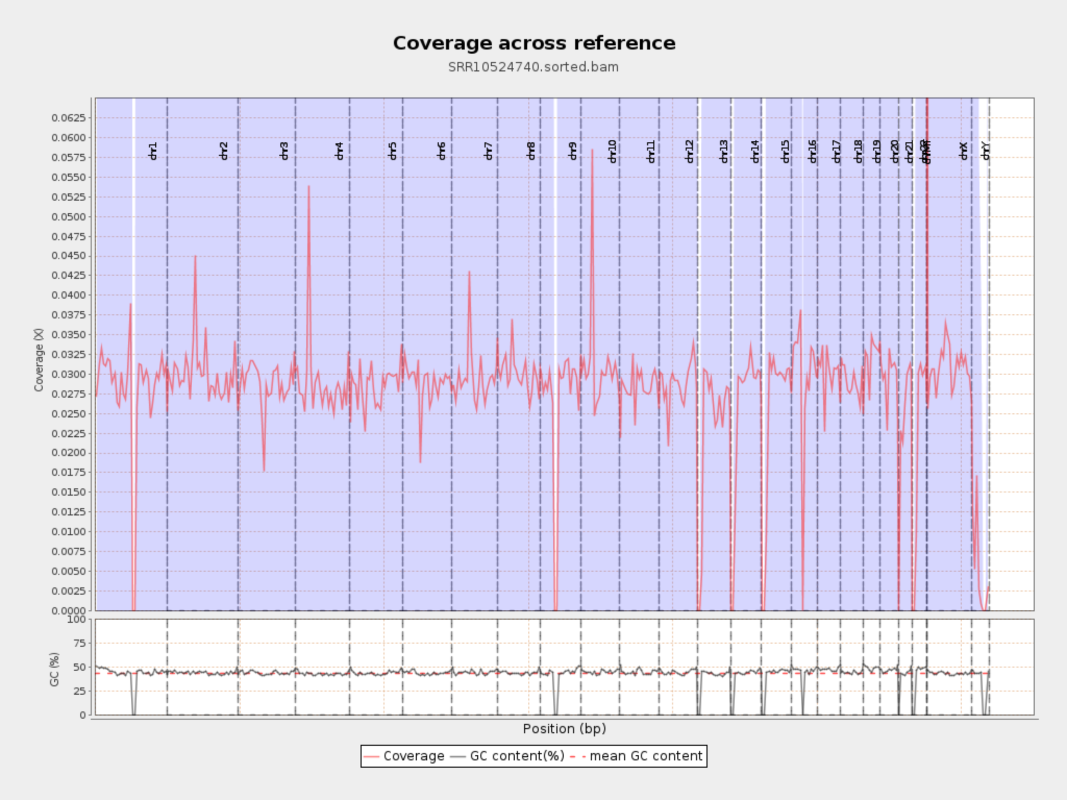
General error rate	0.52%
Mismatches	443,081
Insertions	5,869
Mapped reads with at least one insertion	0.39%
Deletions	17,808
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.78%

2.6. Chromosome stats

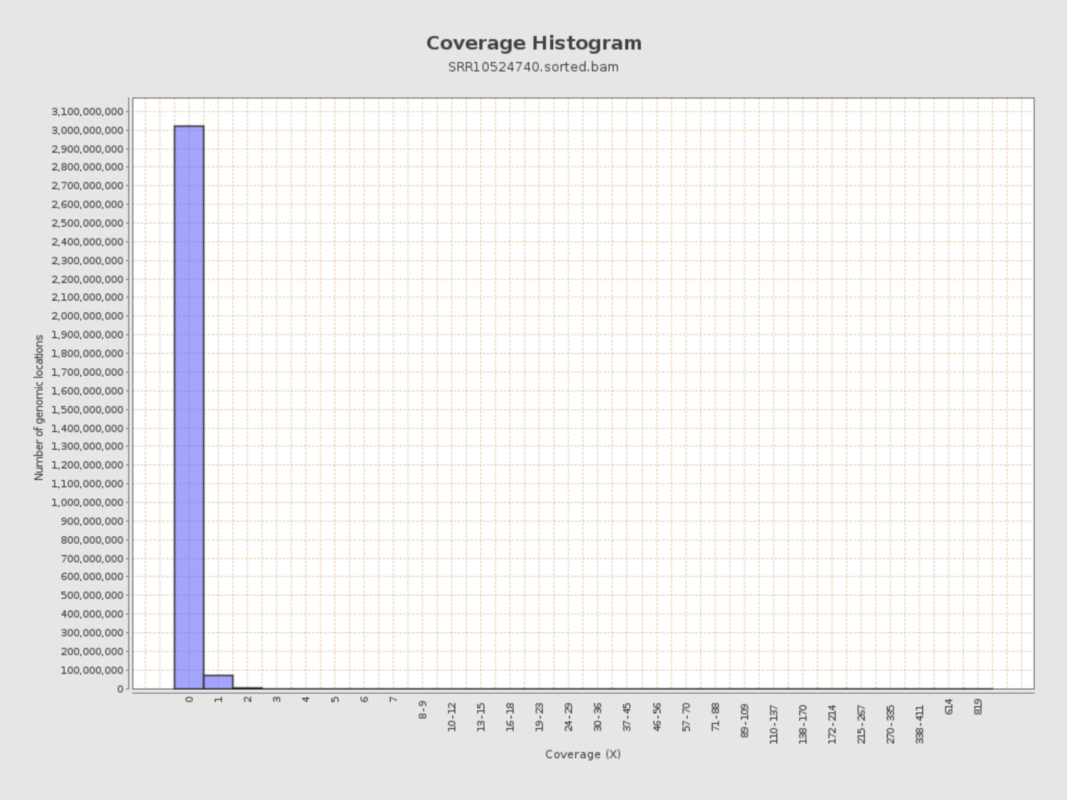
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6947746	0.0279	0.351
chr2	243199373	7328220	0.0301	0.3971
chr3	198022430	5679678	0.0287	0.1884
chr4	191154276	5558232	0.0291	0.2144
chr5	180915260	5195998	0.0287	0.1863
chr6	171115067	4928574	0.0288	0.2053
chr7	159138663	4703199	0.0296	0.3013

chr8	146364022	4394306	0.03	0.2324
chr9	141213431	3684561	0.0261	0.2121
chr10	135534747	4239556	0.0313	0.2937
chr11	135006516	3855507	0.0286	0.221
chr12	133851895	3863236	0.0289	0.1896
chr13	115169878	2612866	0.0227	0.1662
chr14	107349540	2685363	0.025	0.1781
chr15	102531392	2527190	0.0246	0.1726
chr16	90354753	2613255	0.0289	0.2063
chr17	81195210	2456819	0.0303	0.1995
chr18	78077248	2265497	0.029	0.3343
chr19	59128983	1899741	0.0321	0.2853
chr20	63025520	1869227	0.0297	0.1959
chr21	48129895	1167919	0.0243	0.1904
chr22	51304566	1078426	0.021	0.1604
chrMT	16571	30847	1.8615	1.7559
chrX	155270560	4802916	0.0309	0.2096
chrY	59373566	289464	0.0049	0.1411

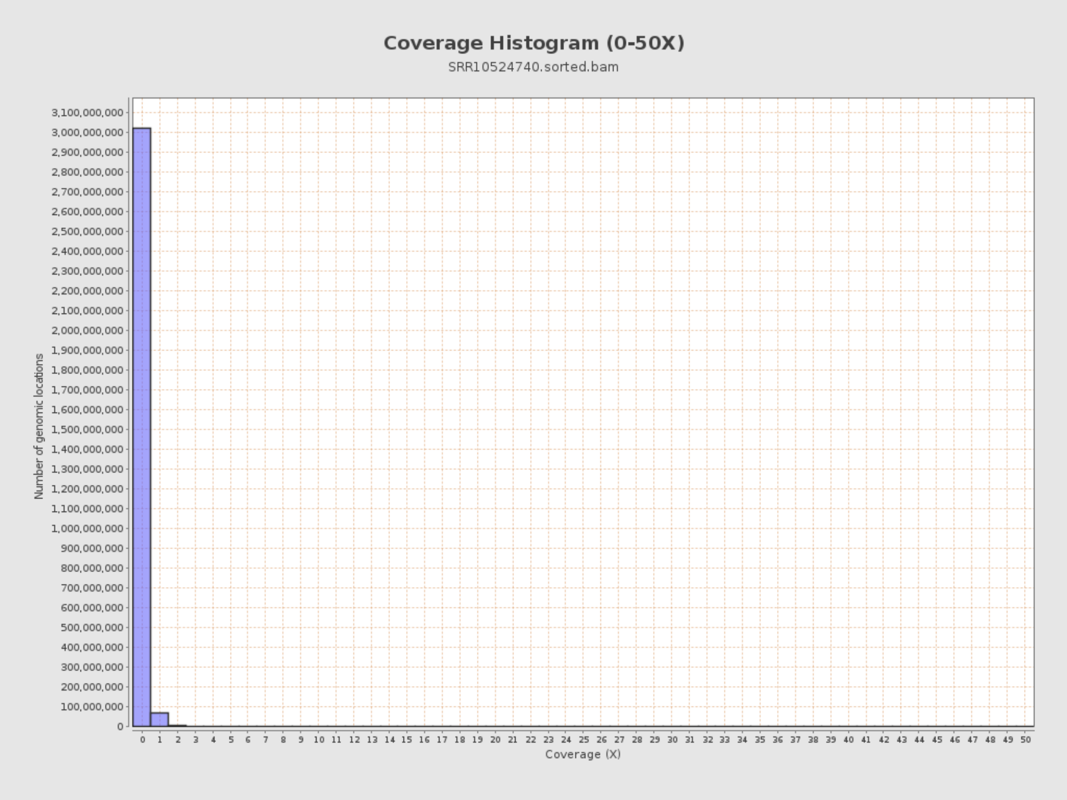
3. Results : Coverage across reference



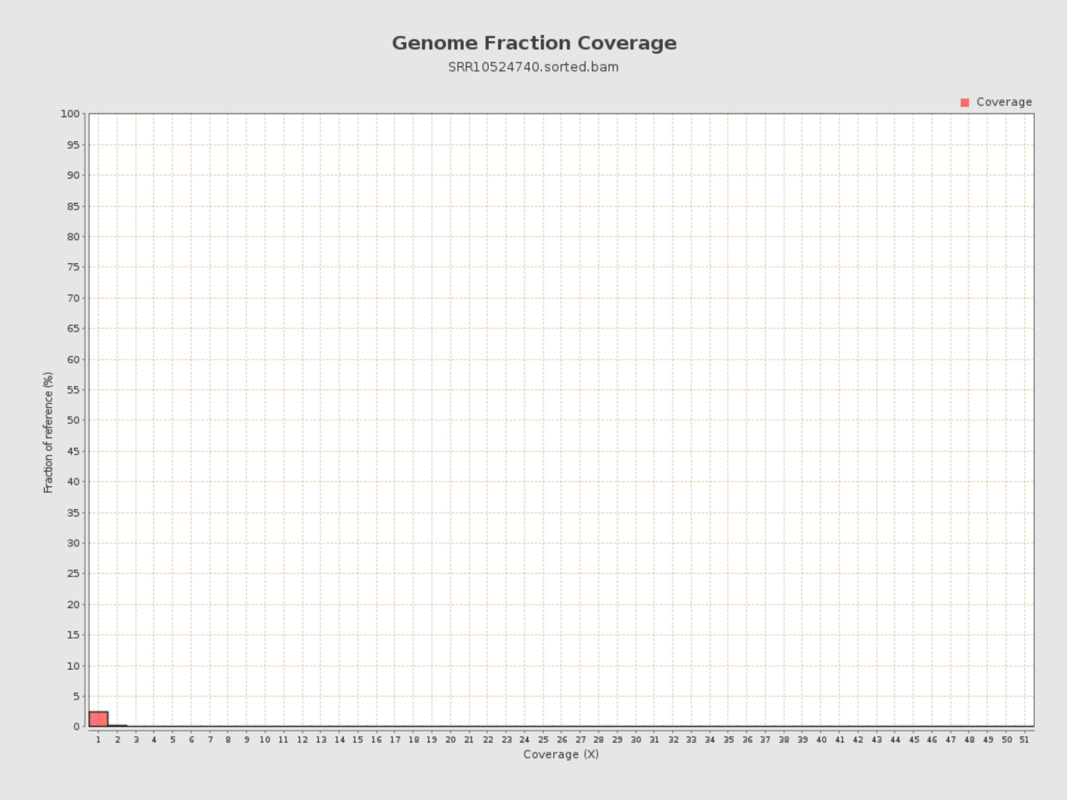
4. Results : Coverage Histogram



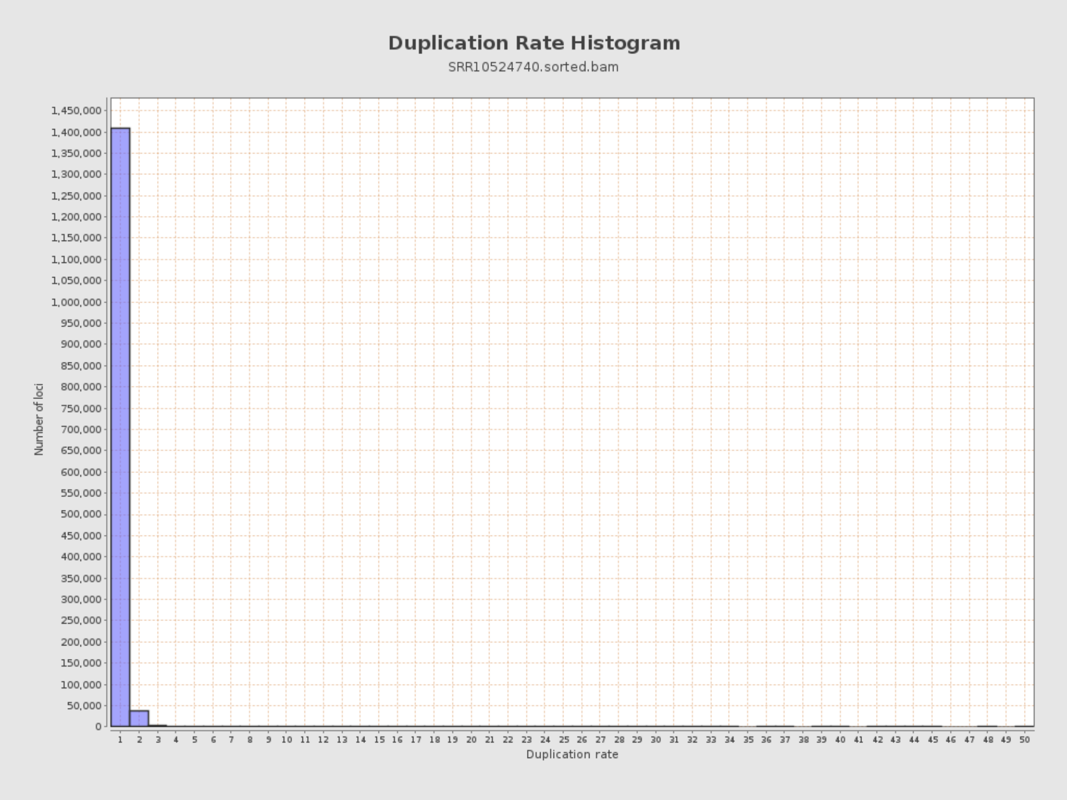
5. Results : Coverage Histogram (0-50X)



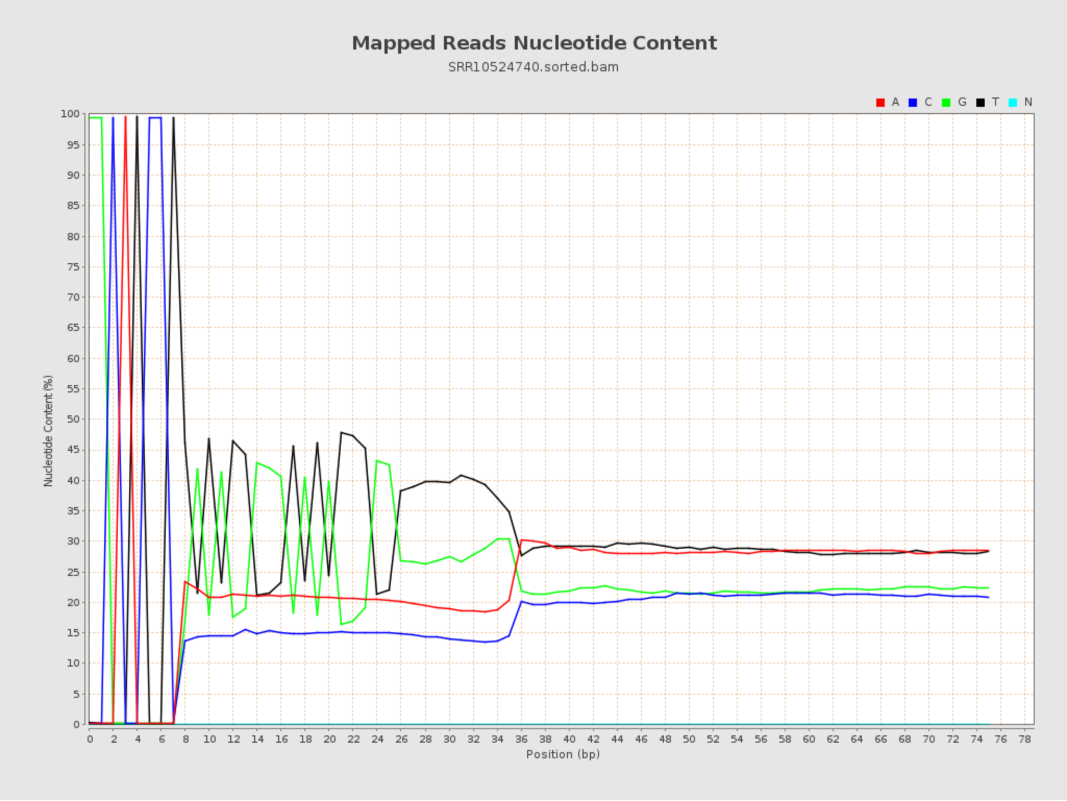
6. Results : Genome Fraction Coverage



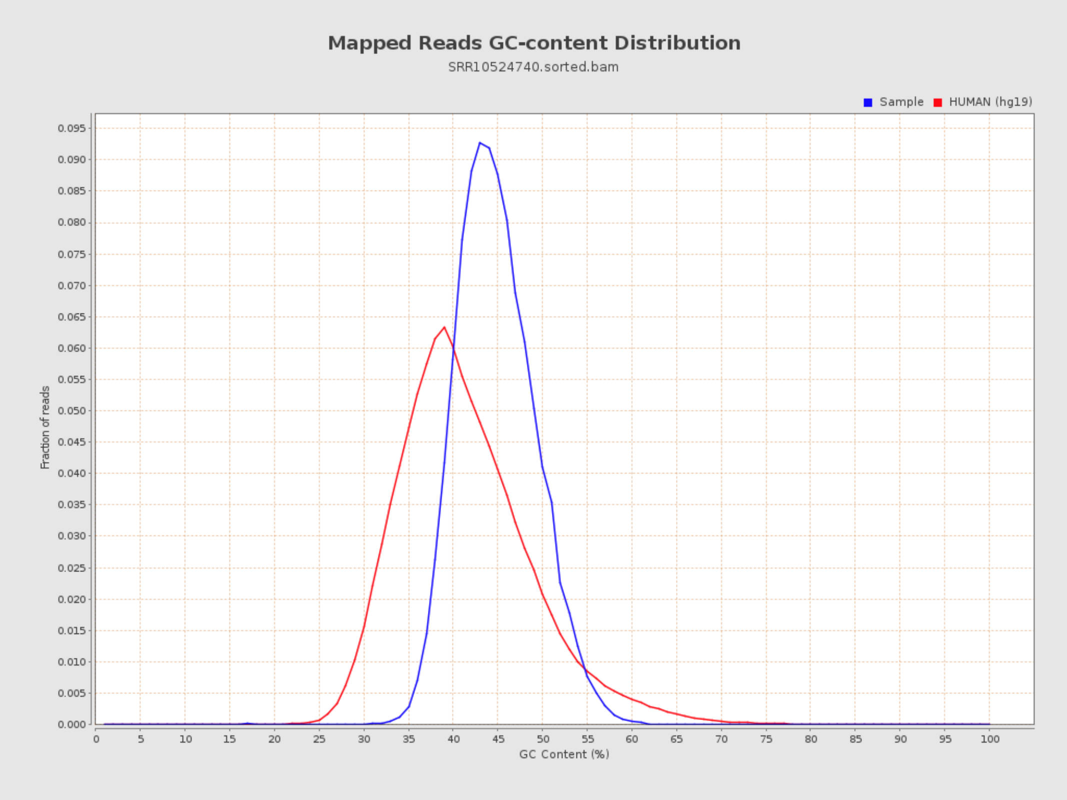
7. Results : Duplication Rate Histogram



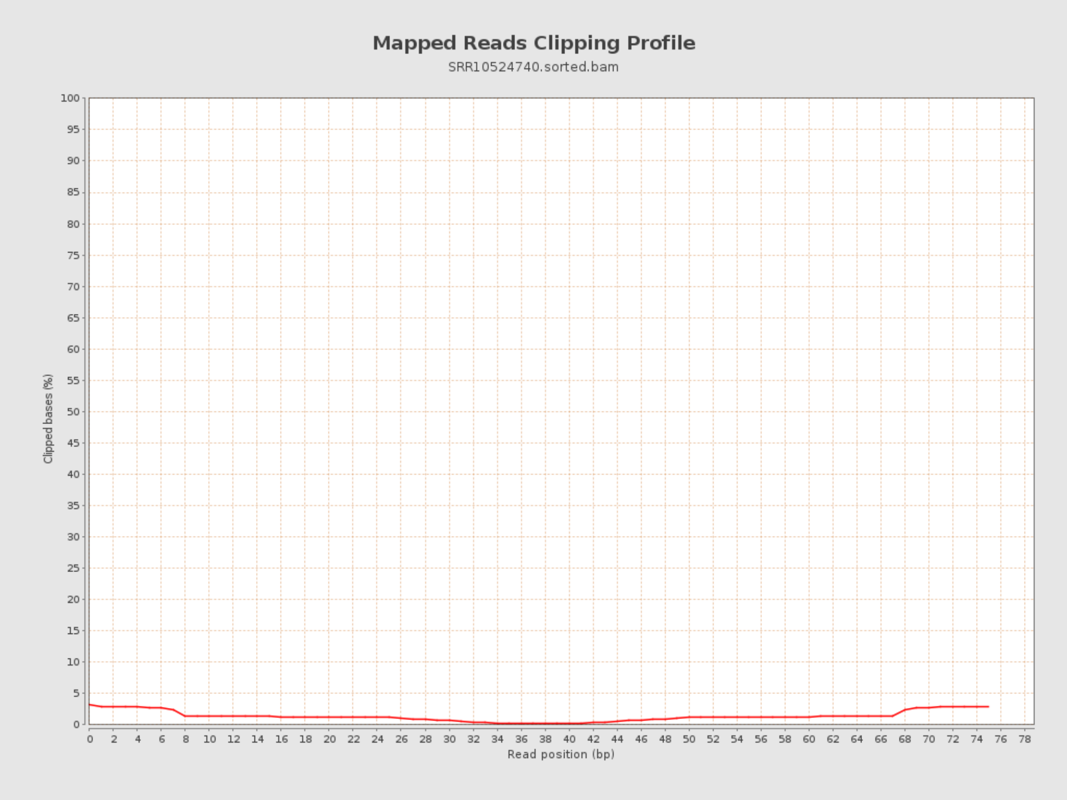
8. Results : Mapped Reads Nucleotide Content



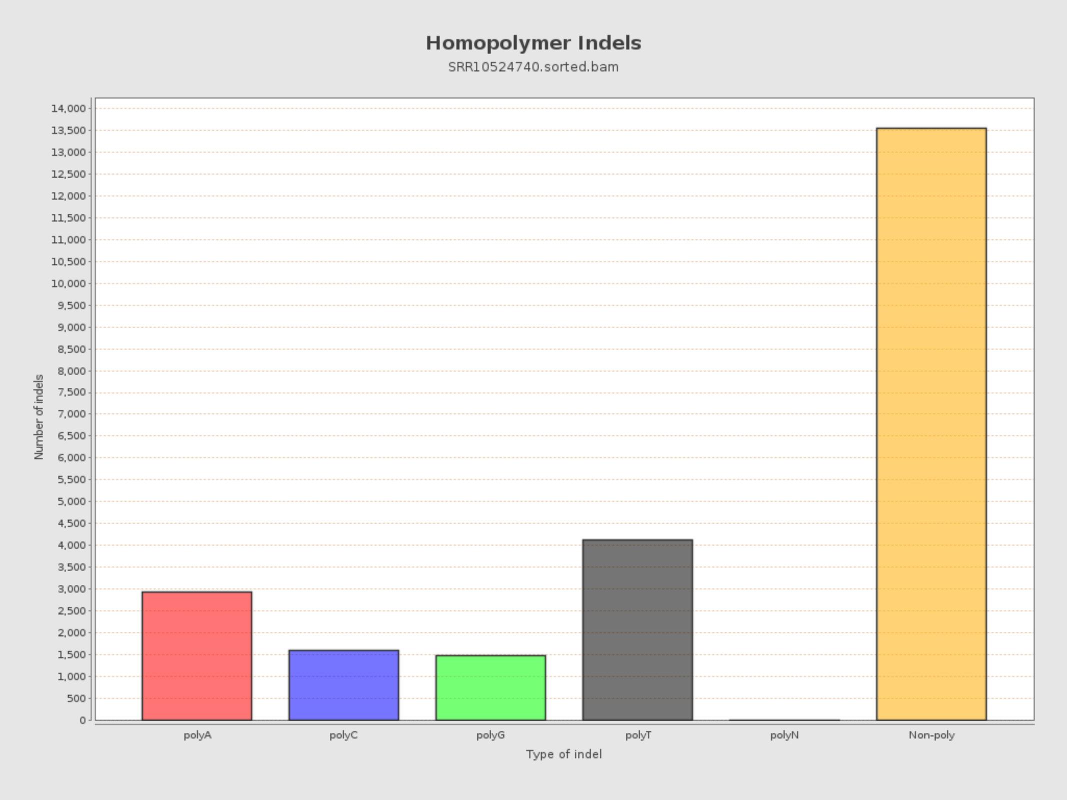
9. Results : Mapped Reads GC-content Distribution



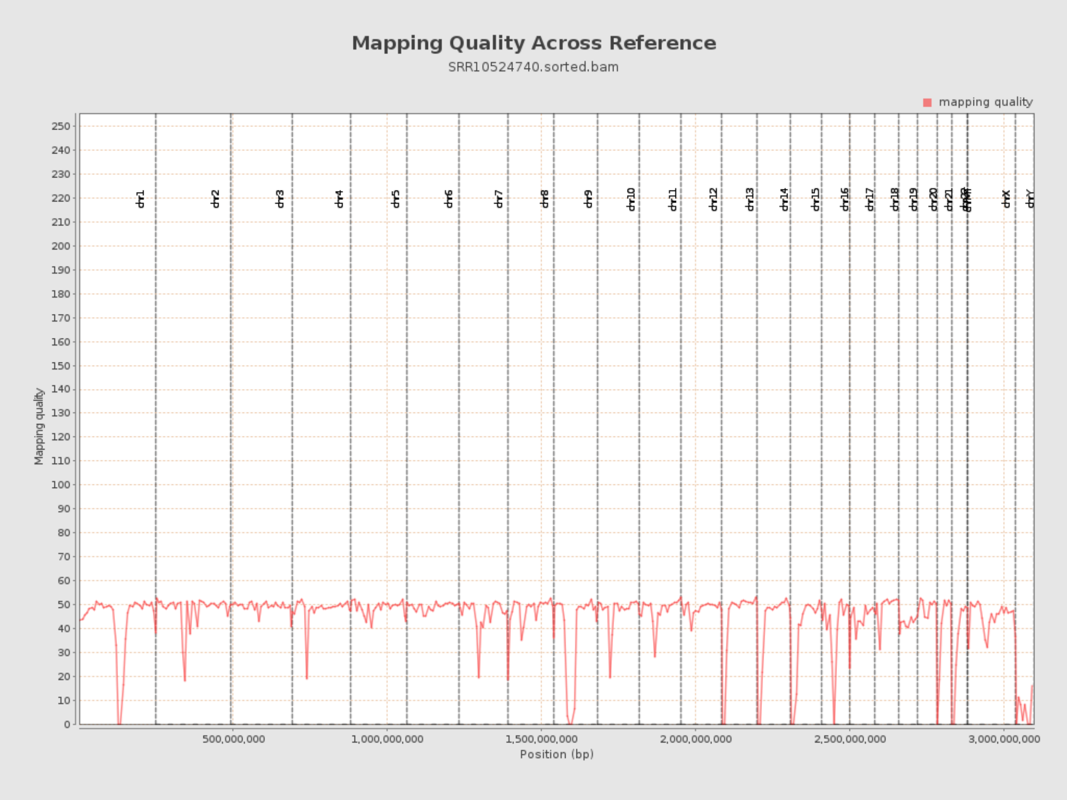
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram