Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:02:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524676.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_SRR10524676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524676.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:02:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	561,534
Mapped reads	516,879 / 92.05%
Unmapped reads	44,655 / 7.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,298 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	10,351 / 1.84%
Duplication rate	1.47%
Clipped reads	517,750 / 92.2%

2.2. ACGT Content

Number/percentage of A's	7,978,887 / 26.17%
Number/percentage of C's	5,942,984 / 19.49%
Number/percentage of T's	9,532,689 / 31.27%
Number/percentage of G's	7,028,169 / 23.05%
Number/percentage of N's	4,102 / 0.01%
GC Percentage	42.55%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1265

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

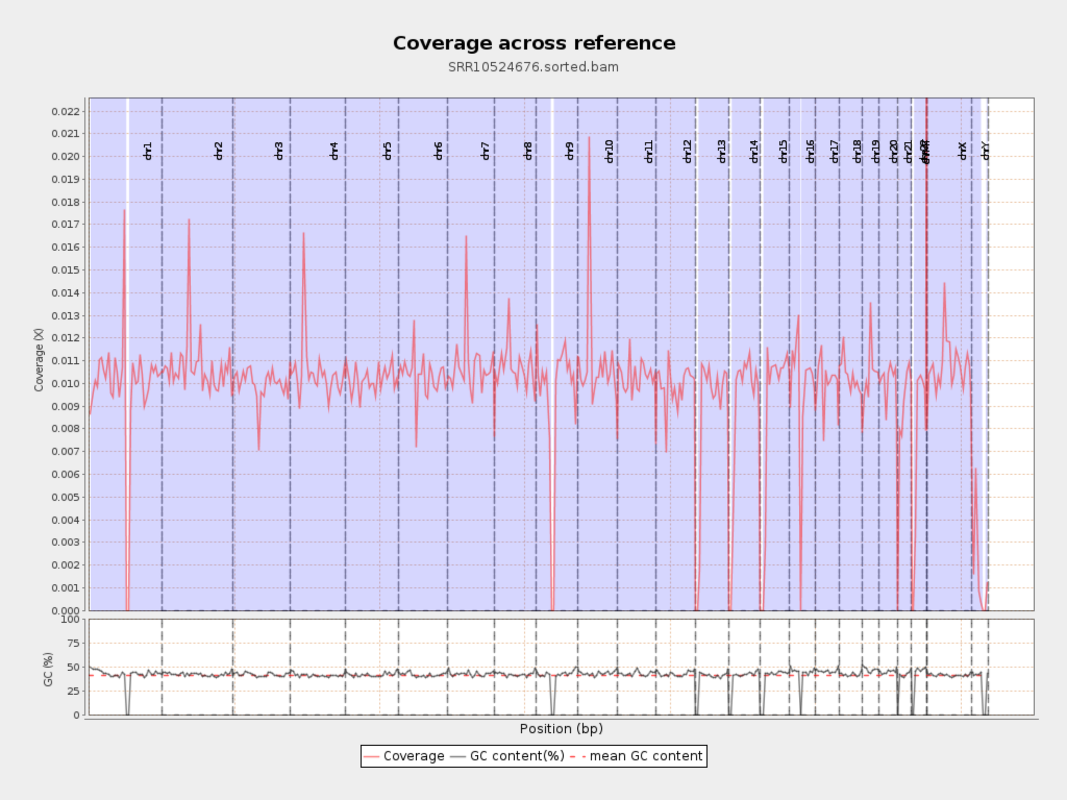
General error rate	0.52%
Mismatches	154,457
Insertions	2,155
Mapped reads with at least one insertion	0.41%
Deletions	5,905
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.11%

2.6. Chromosome stats

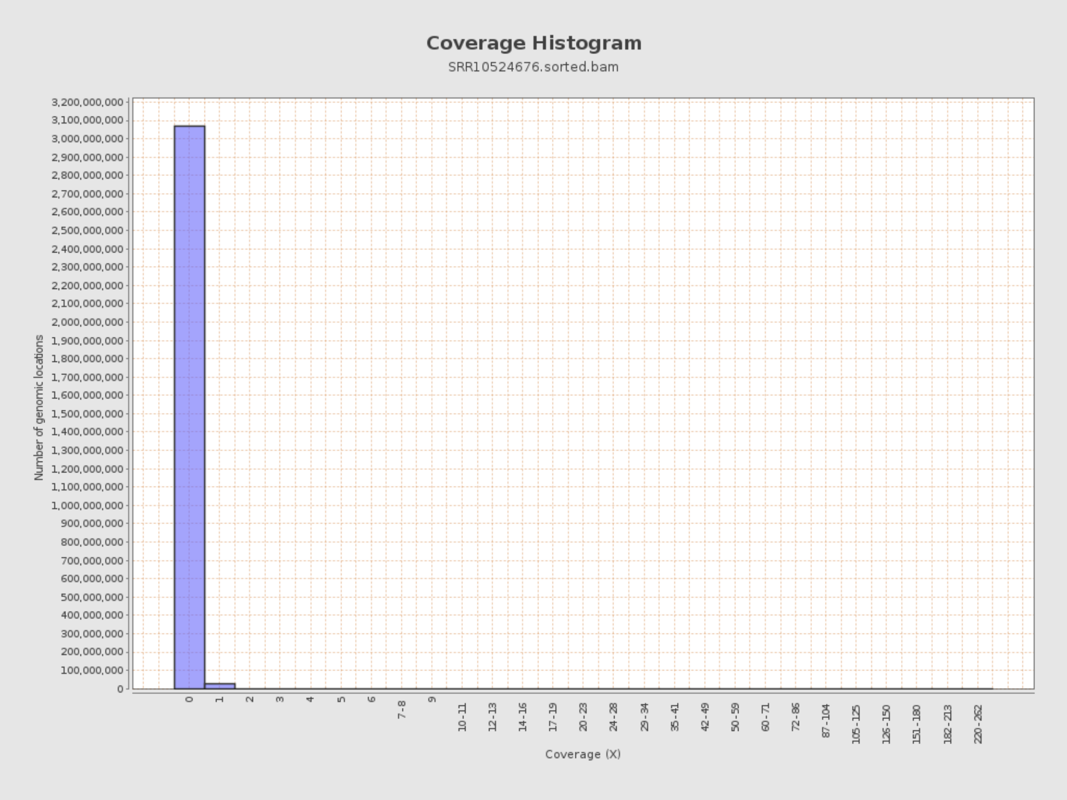
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2442667	0.0098	0.1966
chr2	243199373	2618323	0.0108	0.1559
chr3	198022430	1970937	0.01	0.1029
chr4	191154276	2002071	0.0105	0.111
chr5	180915260	1841096	0.0102	0.104
chr6	171115067	1767779	0.0103	0.1111
chr7	159138663	1721364	0.0108	0.1405

chr8	146364022	1566706	0.0107	0.1403
chr9	141213431	1292699	0.0092	0.1102
chr10	135534747	1482232	0.0109	0.1333
chr11	135006516	1386285	0.0103	0.1158
chr12	133851895	1329703	0.0099	0.1028
chr13	115169878	969734	0.0084	0.0954
chr14	107349540	923603	0.0086	0.0962
chr15	102531392	886105	0.0086	0.0957
chr16	90354753	882935	0.0098	0.1051
chr17	81195210	811484	0.01	0.1069
chr18	78077248	809283	0.0104	0.1659
chr19	59128983	618249	0.0105	0.1494
chr20	63025520	637498	0.0101	0.1046
chr21	48129895	408885	0.0085	0.0988
chr22	51304566	353379	0.0069	0.0855
chrMT	16571	601	0.0363	0.2232
chrX	155270560	1673958	0.0108	0.1106
chrY	59373566	98541	0.0017	0.0674

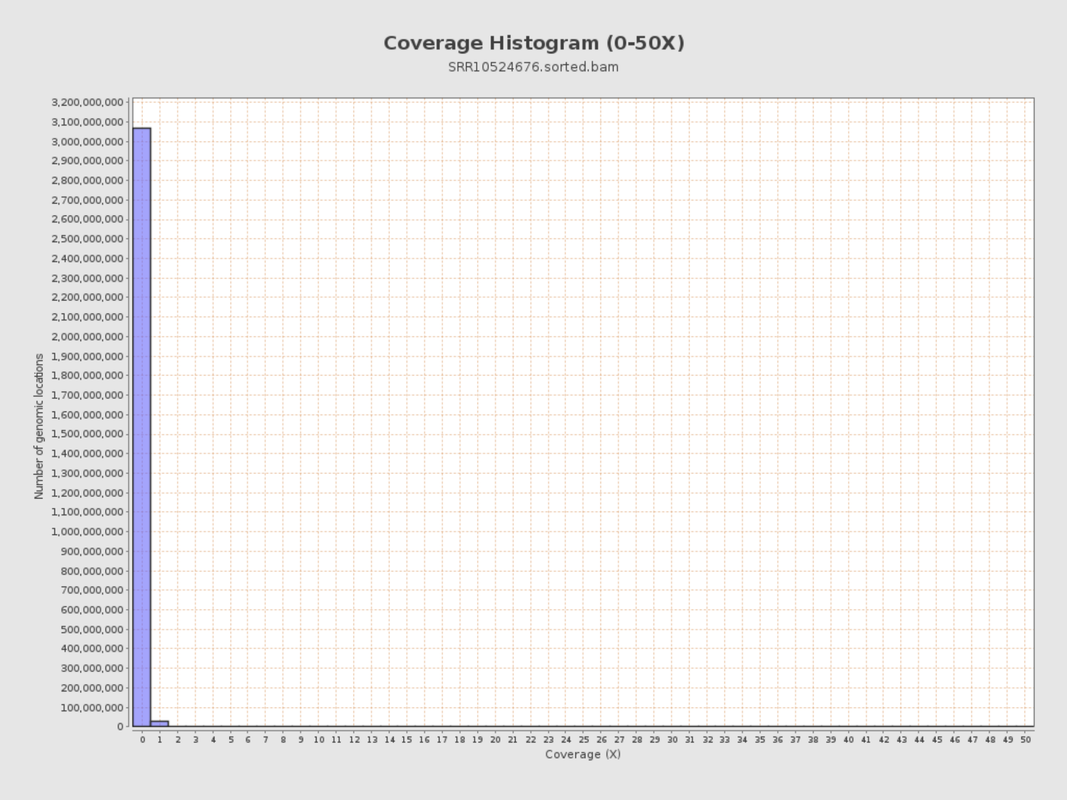
3. Results : Coverage across reference



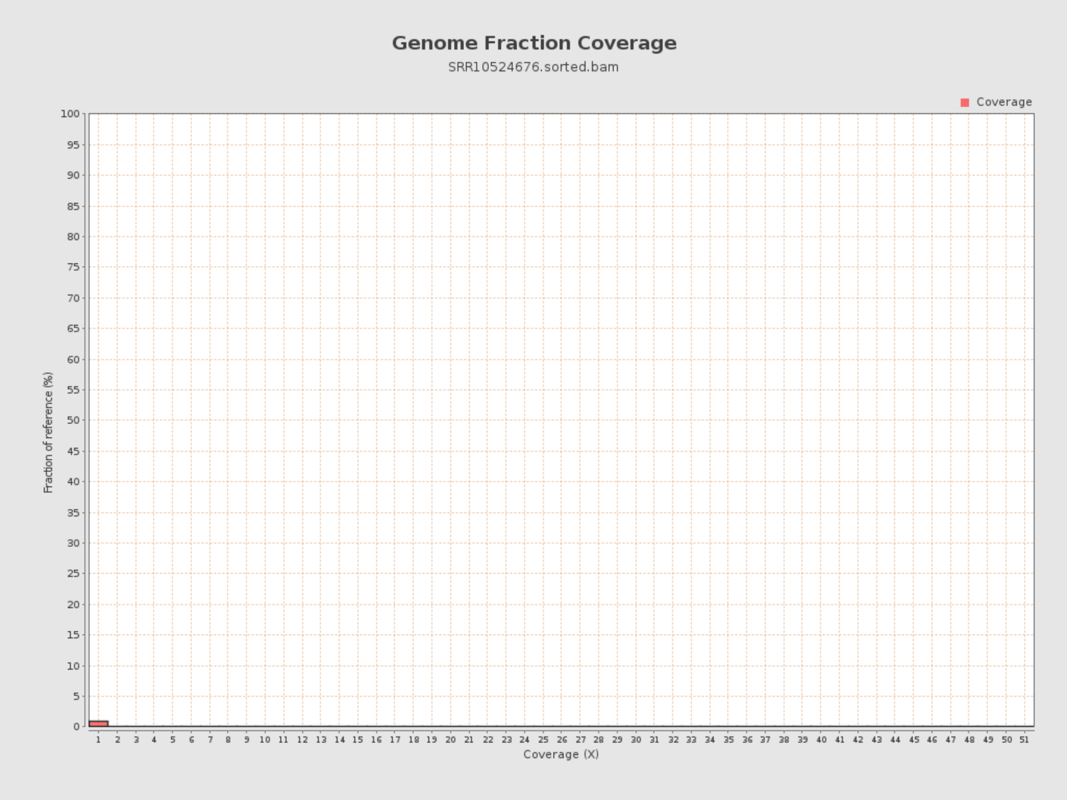
4. Results : Coverage Histogram



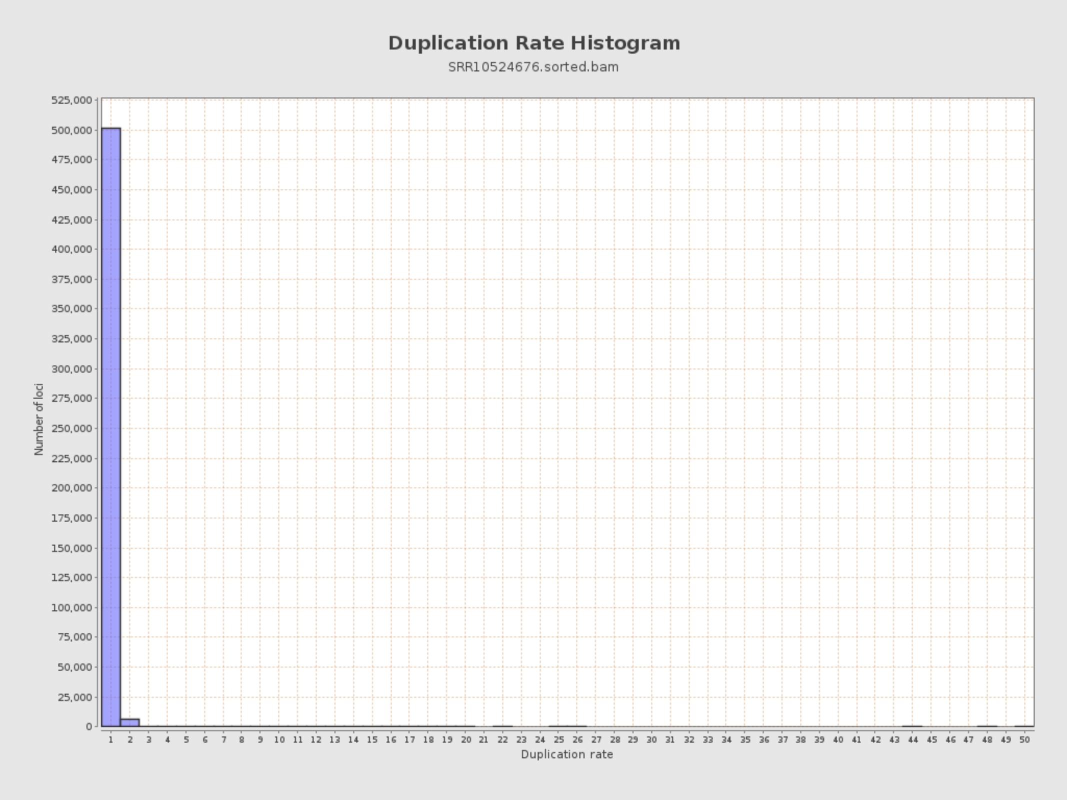
5. Results : Coverage Histogram (0-50X)



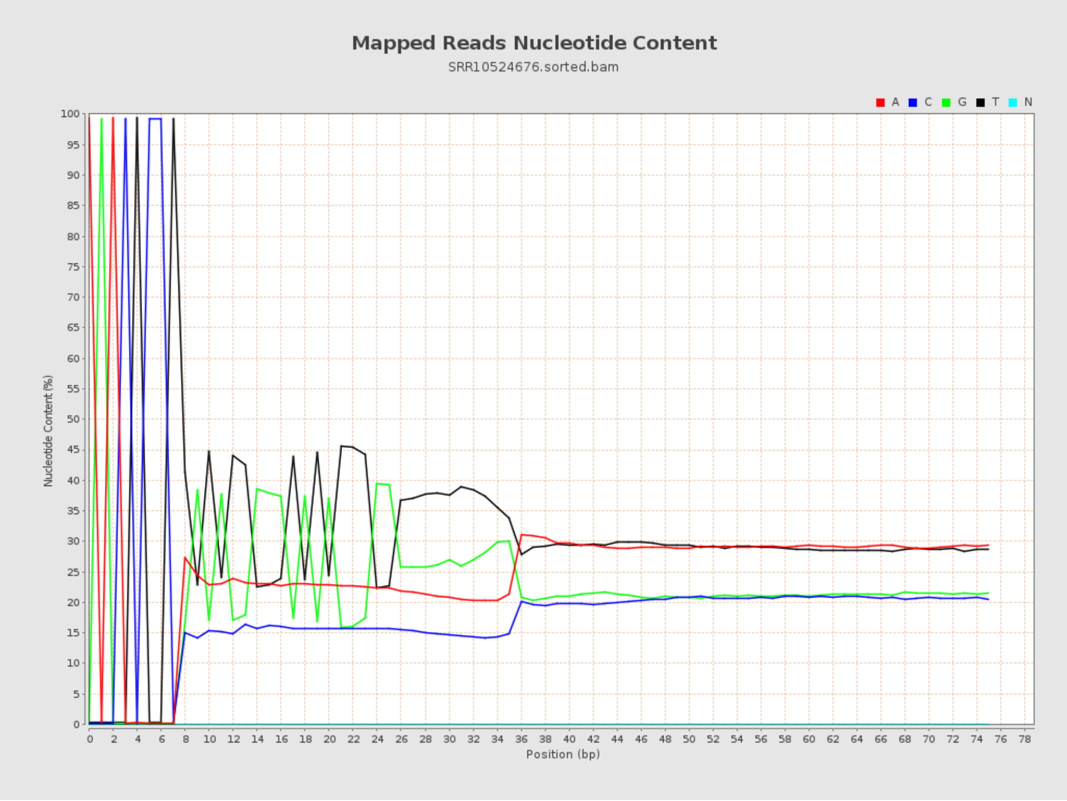
6. Results : Genome Fraction Coverage



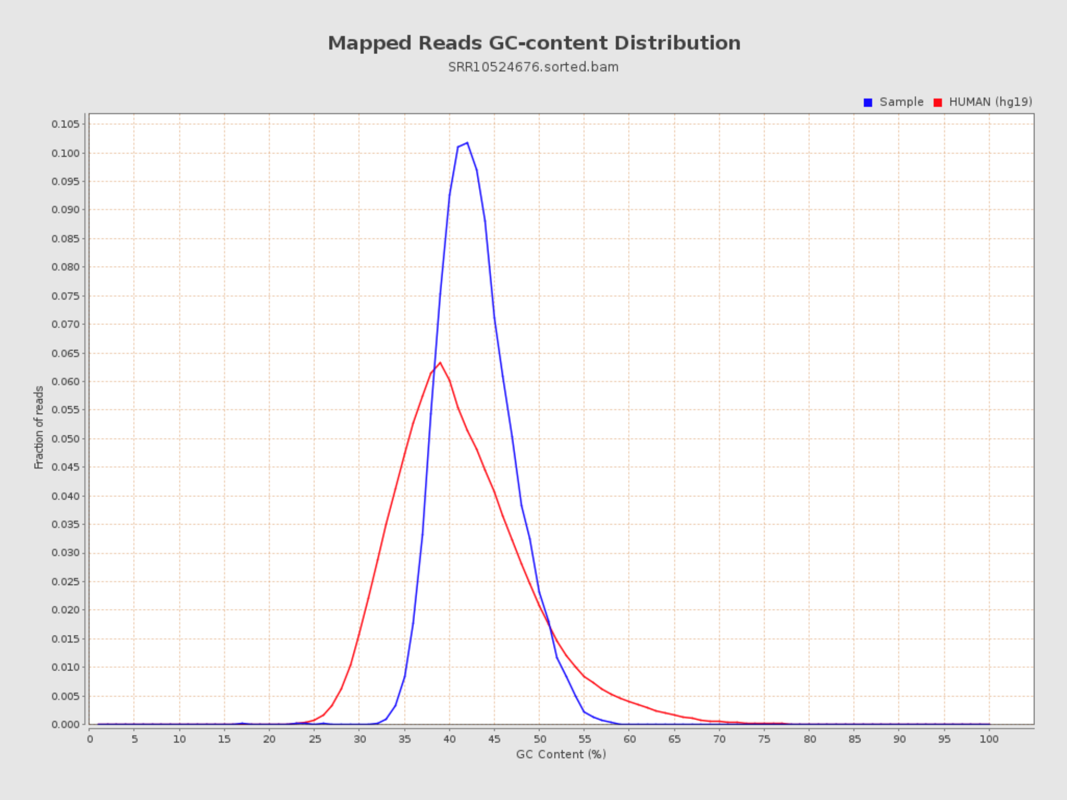
7. Results : Duplication Rate Histogram



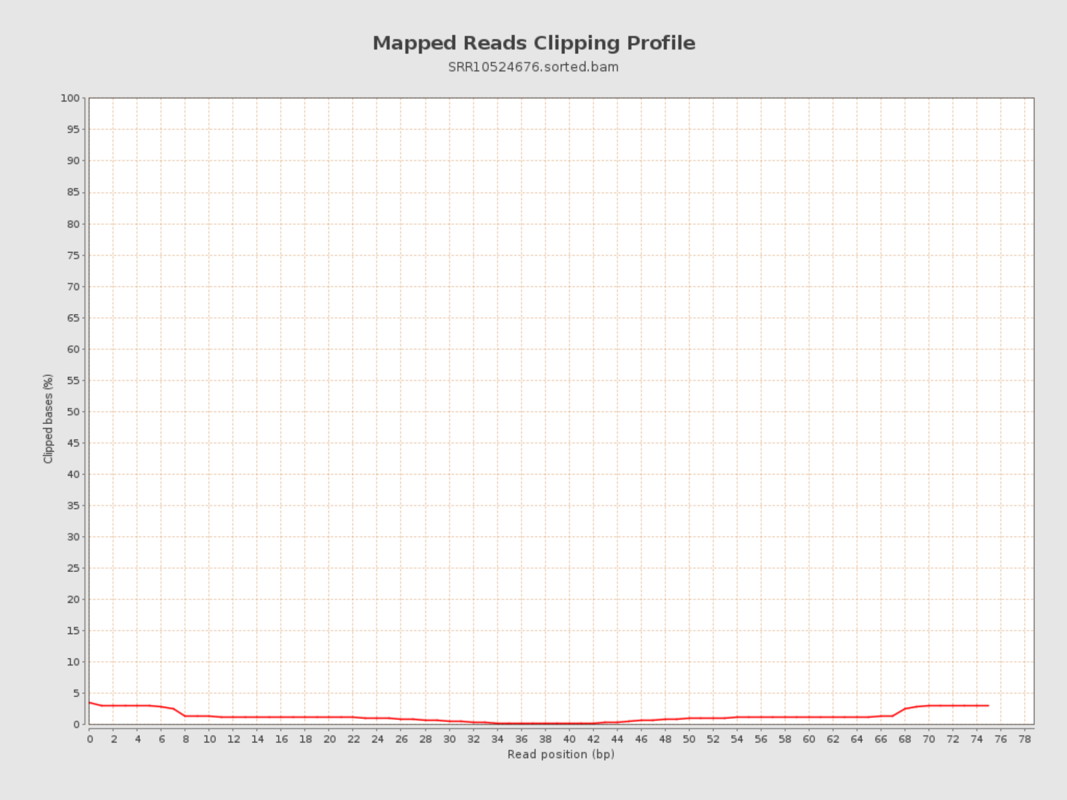
8. Results : Mapped Reads Nucleotide Content



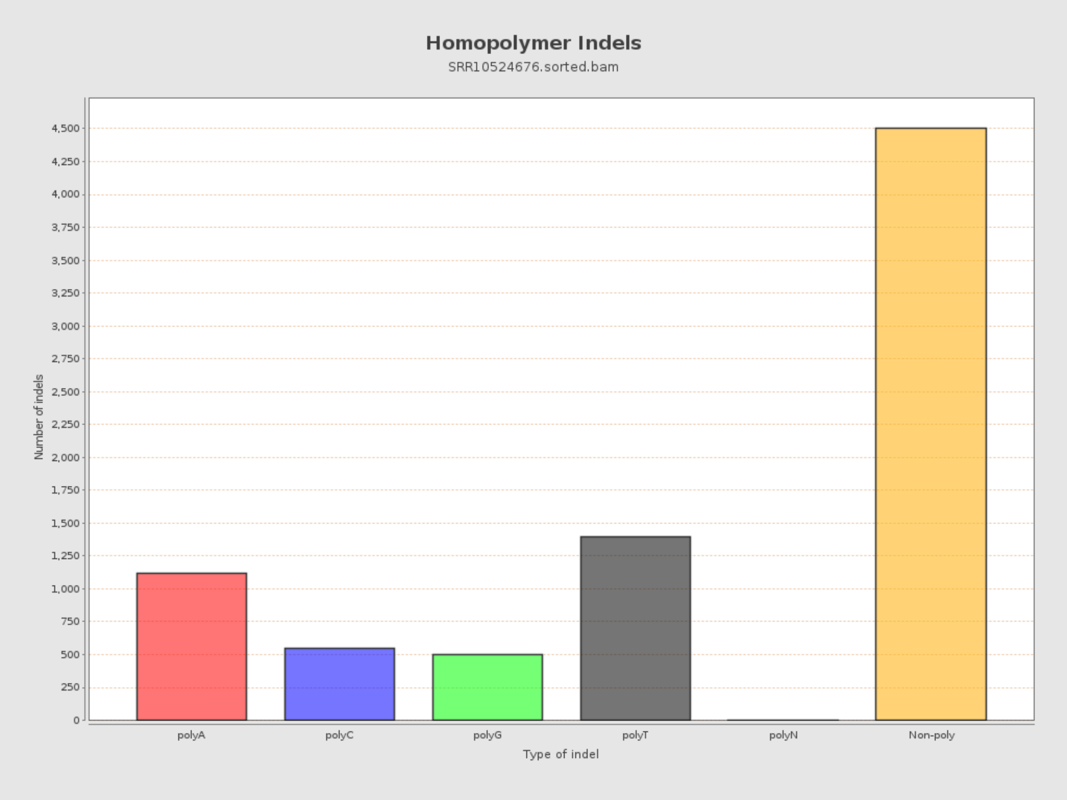
9. Results : Mapped Reads GC-content Distribution



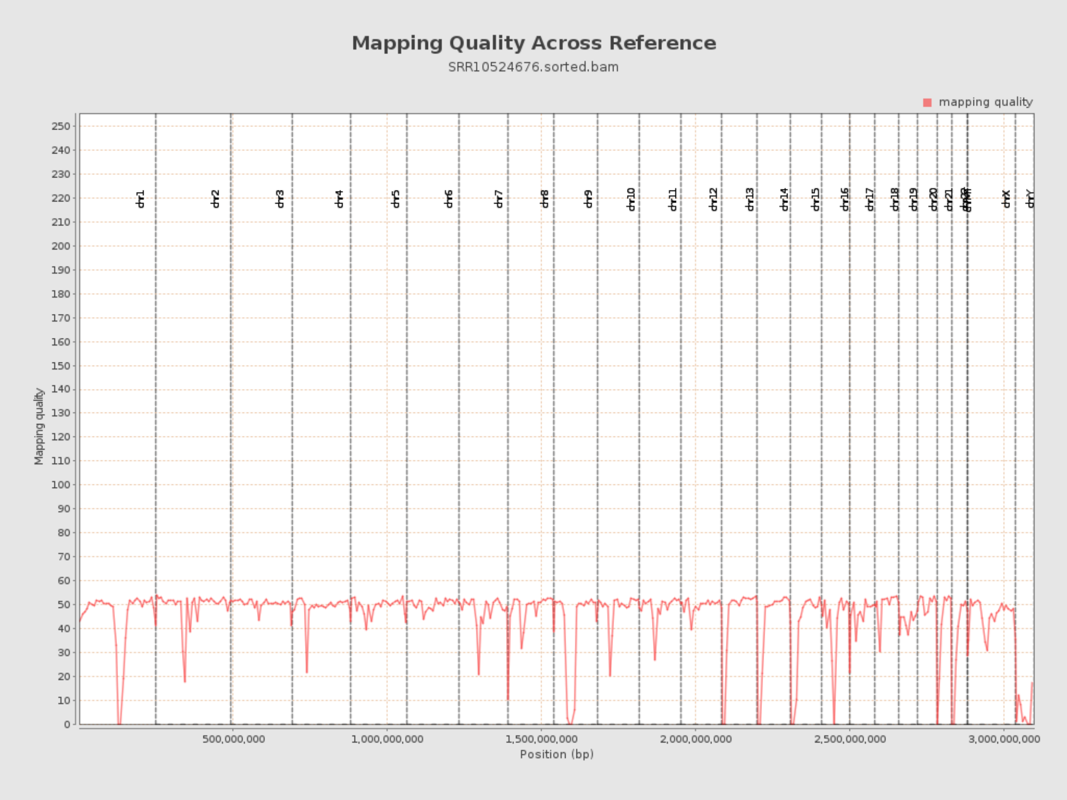
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram