Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:59:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524697.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_SRR10524697 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524697.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:59:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524697.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,556,636
Mapped reads	1,438,906 / 92.44%
Unmapped reads	117,730 / 7.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,773 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	50,862 / 3.27%
Duplication rate	2.54%
Clipped reads	1,440,112 / 92.51%

2.2. ACGT Content

Number/percentage of A's	21,754,458 / 25.52%
Number/percentage of C's	15,240,516 / 17.88%
Number/percentage of T's	27,971,772 / 32.81%
Number/percentage of G's	20,275,486 / 23.78%
Number/percentage of N's	12,810 / 0.02%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2696

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

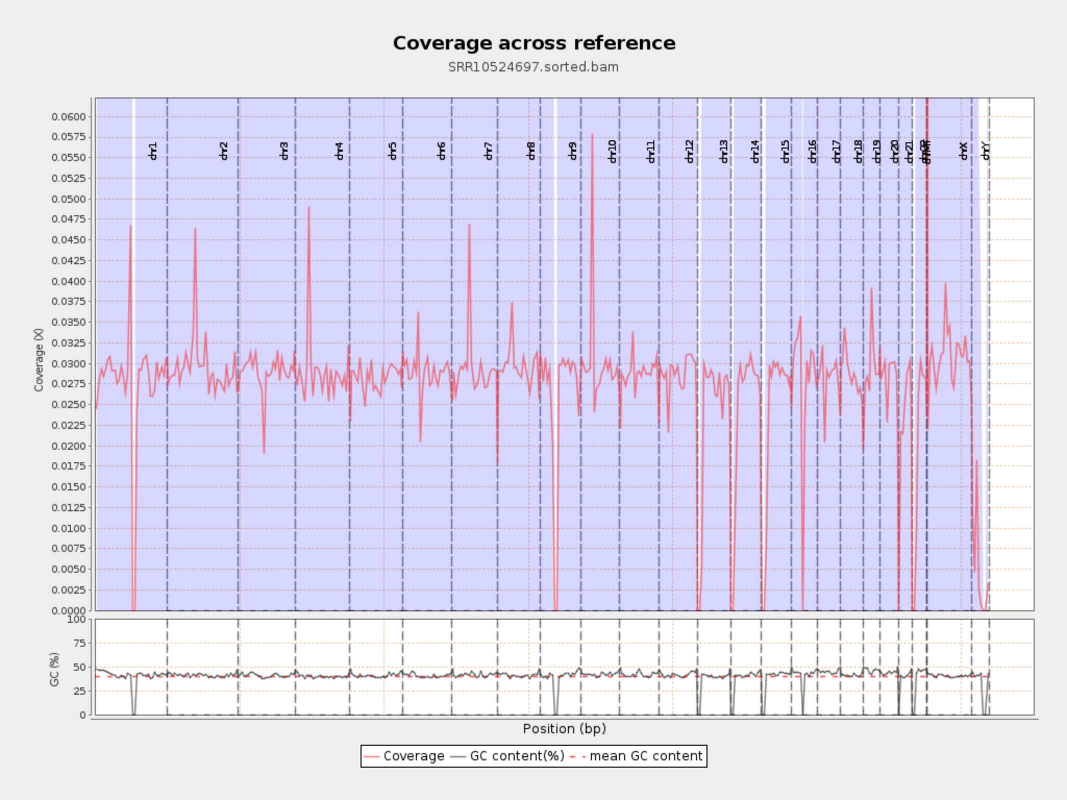
General error rate	0.52%
Mismatches	427,102
Insertions	7,175
Mapped reads with at least one insertion	0.5%
Deletions	16,159
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.73%

2.6. Chromosome stats

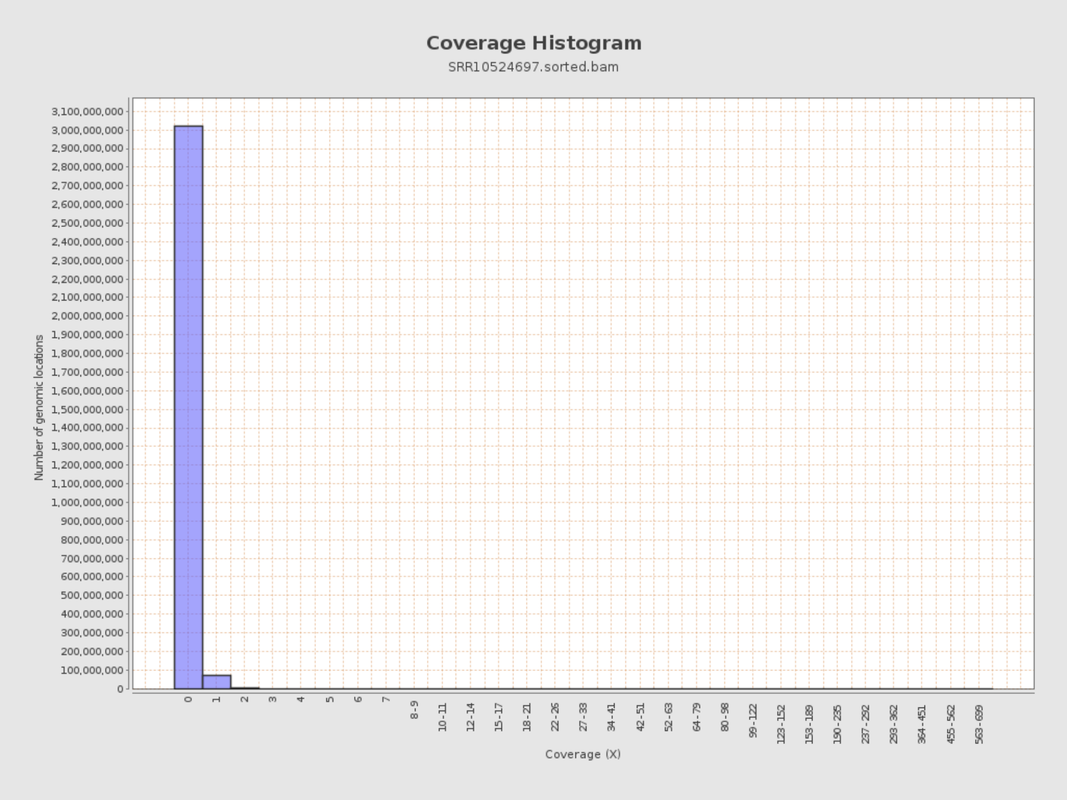
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6819430	0.0274	0.4756
chr2	243199373	7199152	0.0296	0.3629
chr3	198022430	5728289	0.0289	0.1845
chr4	191154276	5558905	0.0291	0.2085
chr5	180915260	5137559	0.0284	0.1829
chr6	171115067	4945669	0.0289	0.2068
chr7	159138663	4688068	0.0295	0.312

chr8	146364022	4345874	0.0297	0.3017
chr9	141213431	3598950	0.0255	0.2242
chr10	135534747	4116394	0.0304	0.2872
chr11	135006516	3900205	0.0289	0.2338
chr12	133851895	3850217	0.0288	0.1833
chr13	115169878	2663708	0.0231	0.1636
chr14	107349540	2546214	0.0237	0.1701
chr15	102531392	2396978	0.0234	0.1648
chr16	90354753	2484118	0.0275	0.195
chr17	81195210	2290810	0.0282	0.1913
chr18	78077248	2249897	0.0288	0.3961
chr19	59128983	1758078	0.0297	0.3635
chr20	63025520	1786309	0.0283	0.1845
chr21	48129895	1111628	0.0231	0.186
chr22	51304566	996784	0.0194	0.1501
chrMT	16571	30646	1.8494	1.641
chrX	155270560	4788672	0.0308	0.2057
chrY	59373566	288251	0.0049	0.1901

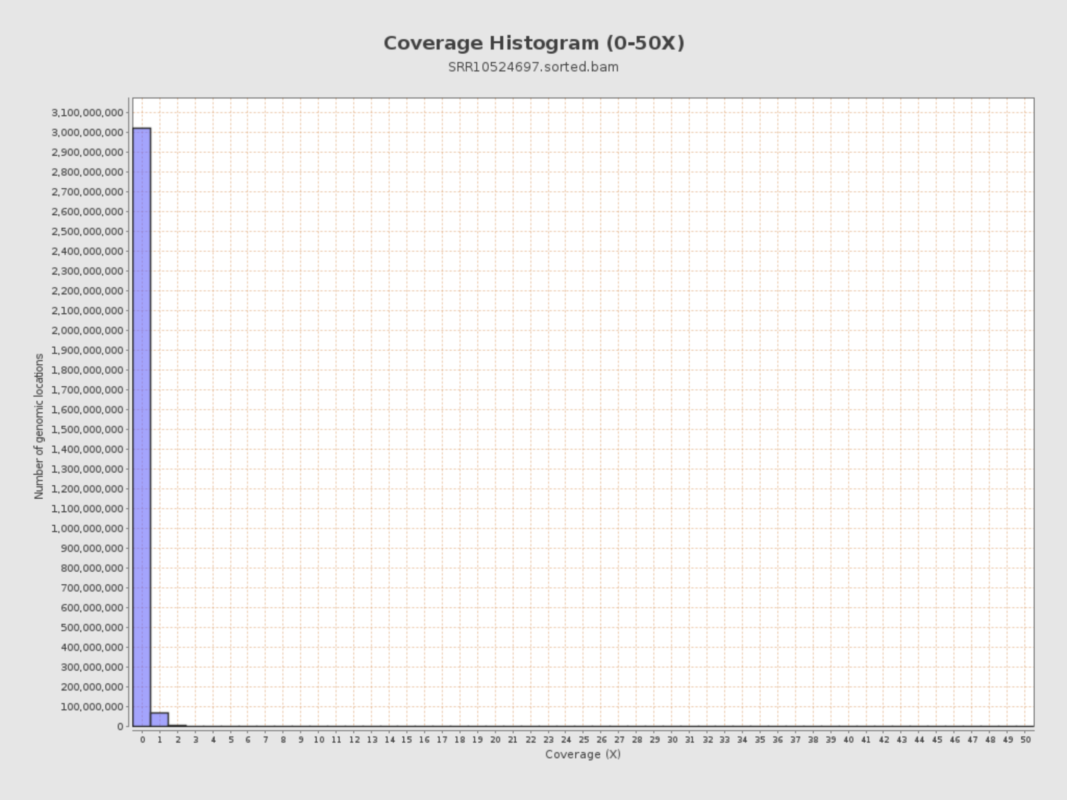
3. Results : Coverage across reference



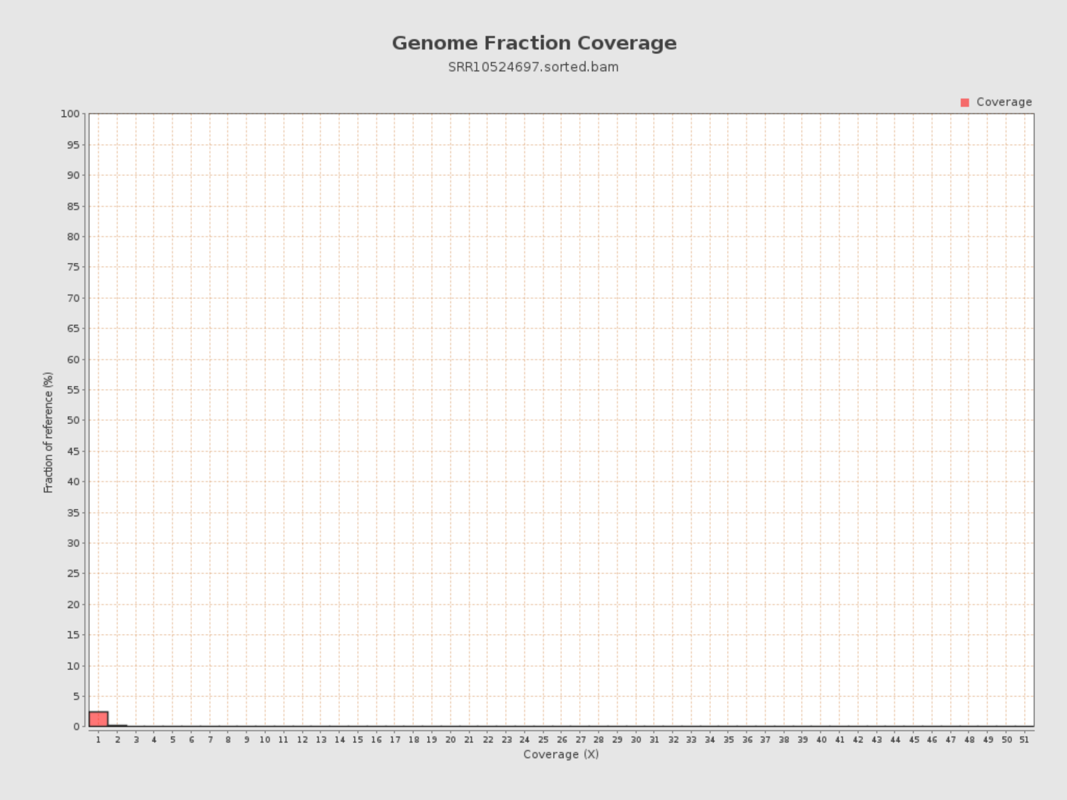
4. Results : Coverage Histogram



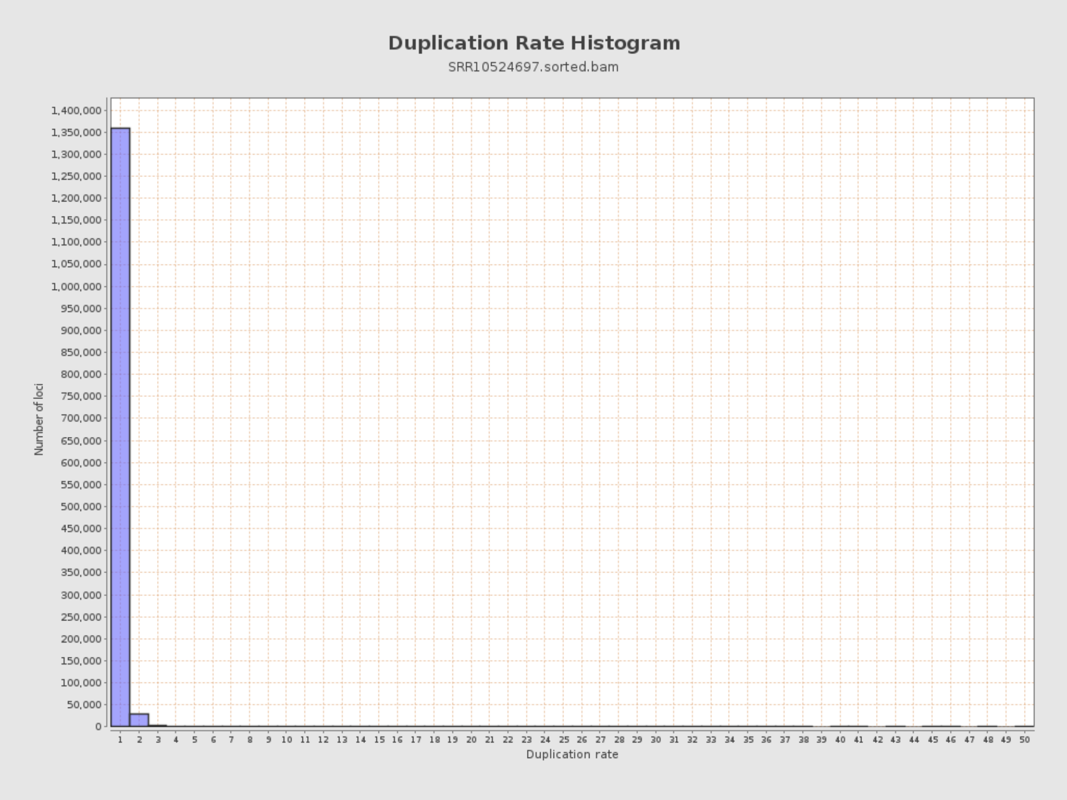
5. Results : Coverage Histogram (0-50X)



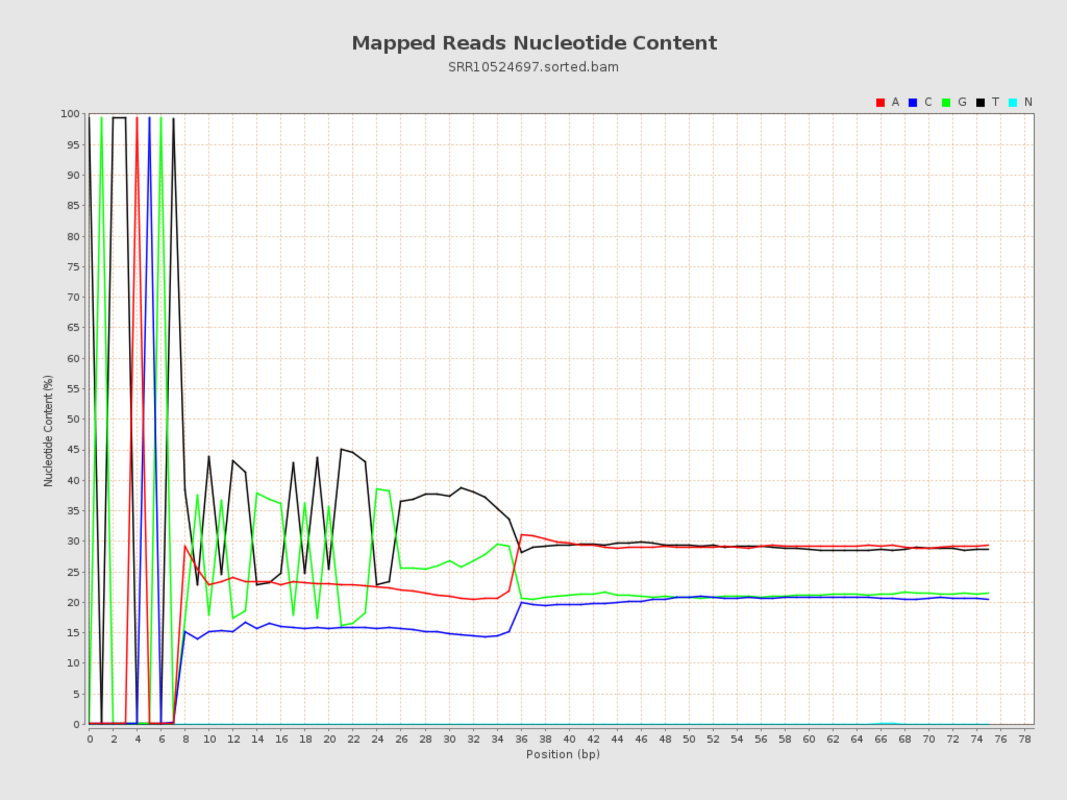
6. Results : Genome Fraction Coverage



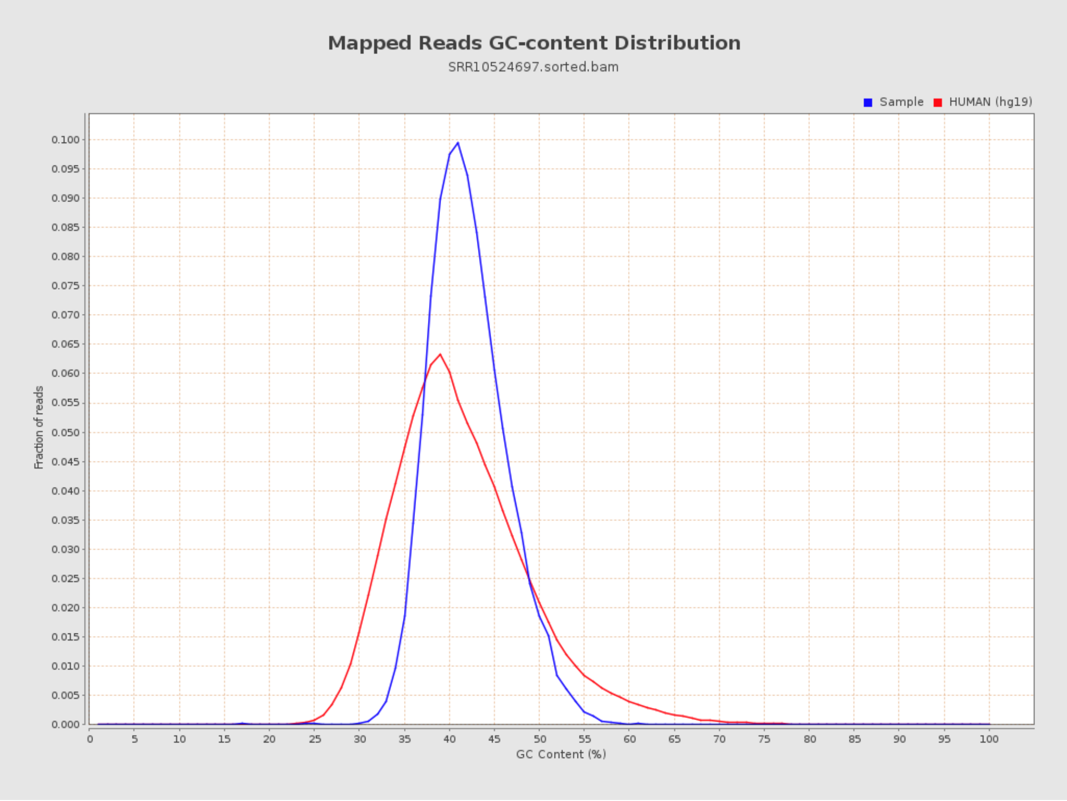
7. Results : Duplication Rate Histogram



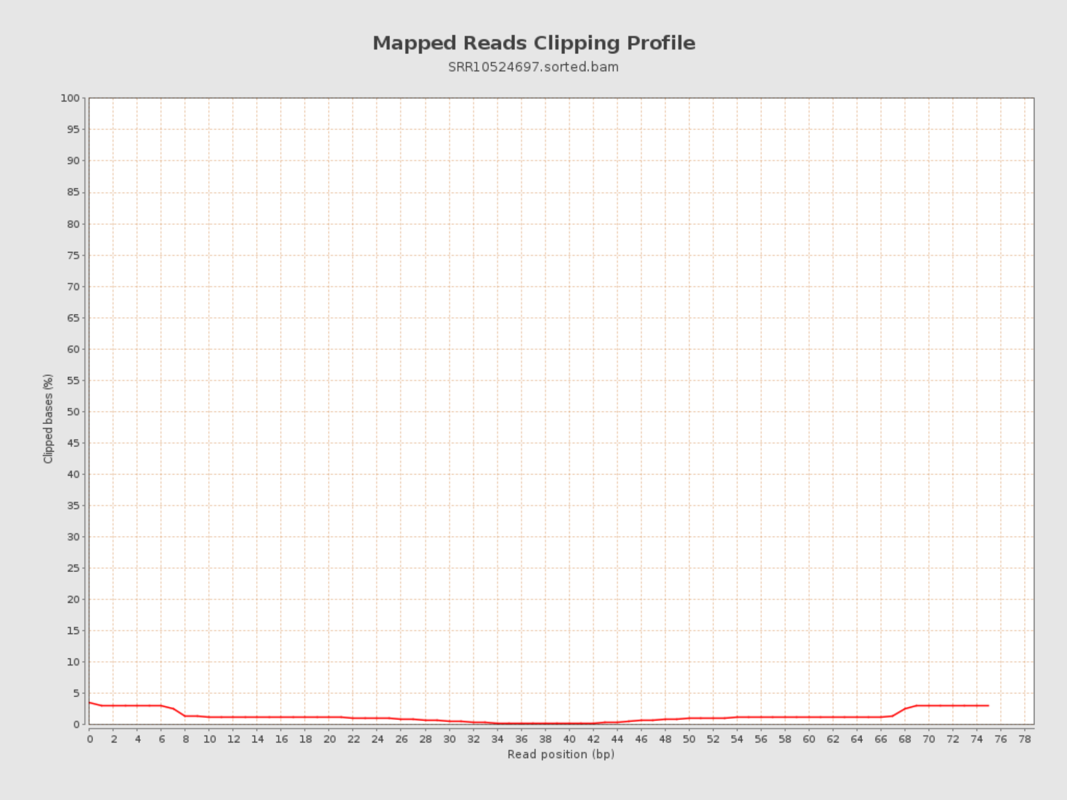
8. Results : Mapped Reads Nucleotide Content



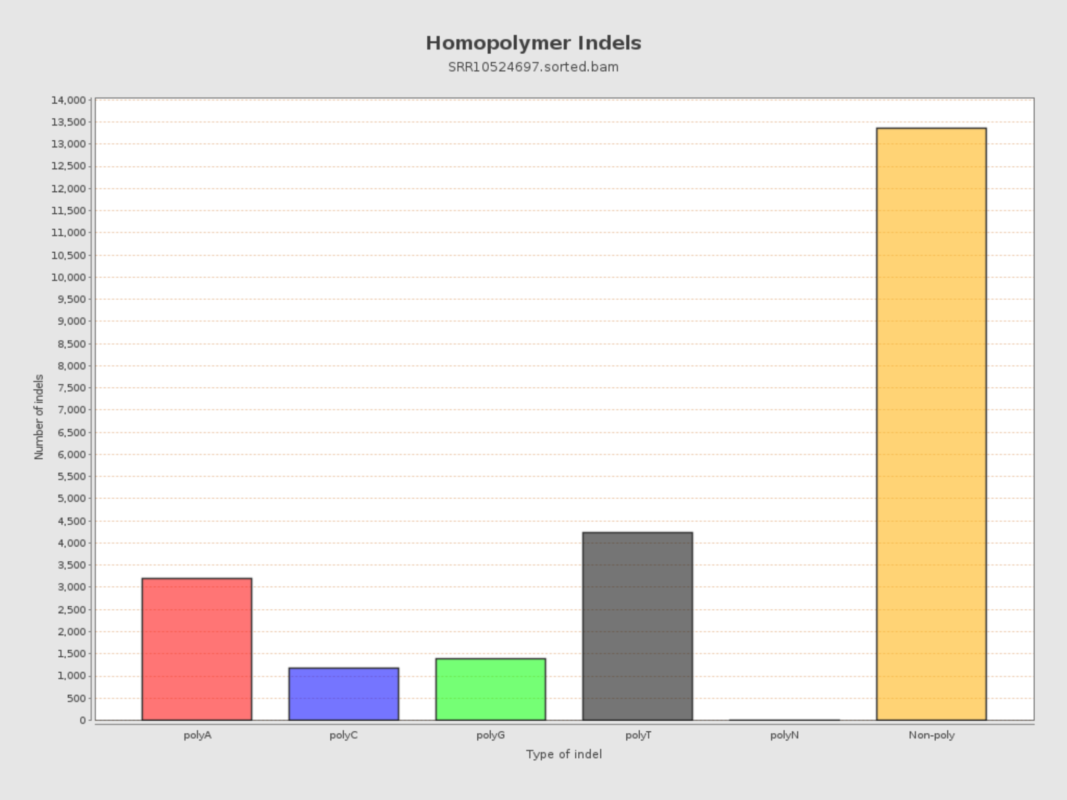
9. Results : Mapped Reads GC-content Distribution



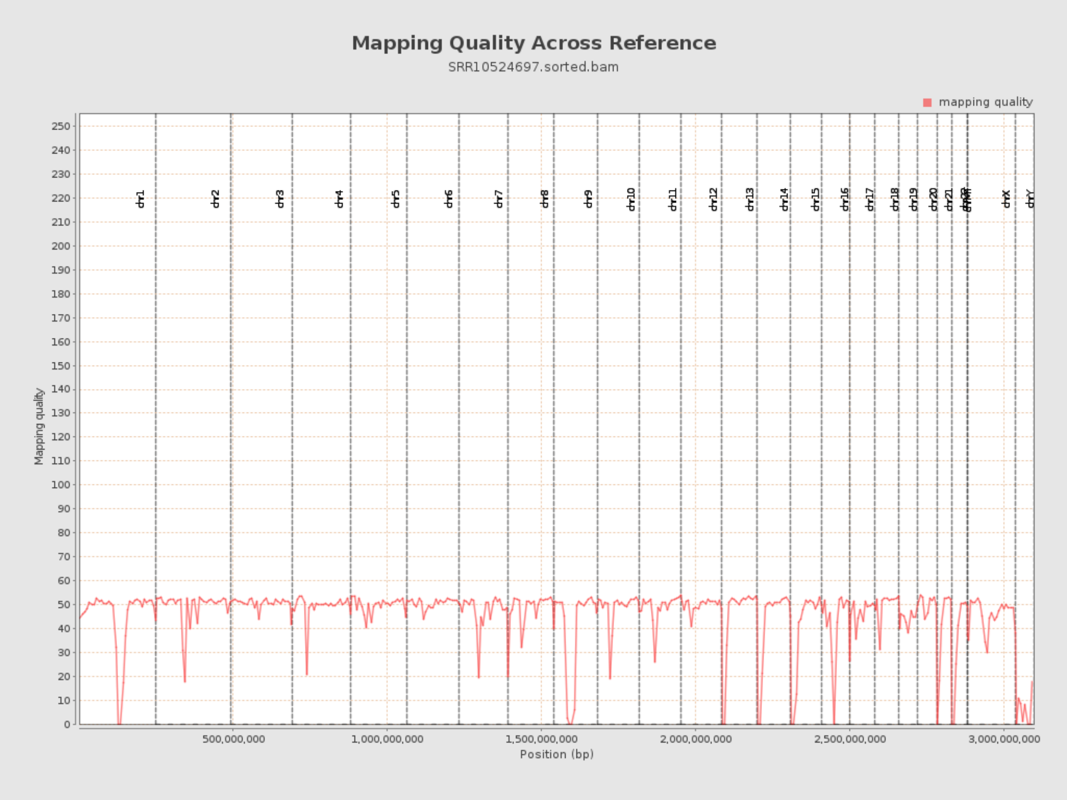
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram