Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:06:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524852.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_SRR10524852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:06:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	926,438
Mapped reads	852,135 / 91.98%
Unmapped reads	74,303 / 8.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,178 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	18,574 / 2%
Duplication rate	1.49%
Clipped reads	853,243 / 92.1%

2.2. ACGT Content

Number/percentage of A's	13,161,455 / 26.4%
Number/percentage of C's	9,553,287 / 19.16%
Number/percentage of T's	15,679,701 / 31.45%
Number/percentage of G's	11,456,695 / 22.98%
Number/percentage of N's	6,985 / 0.01%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0161

Standard Deviation	0.1834

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

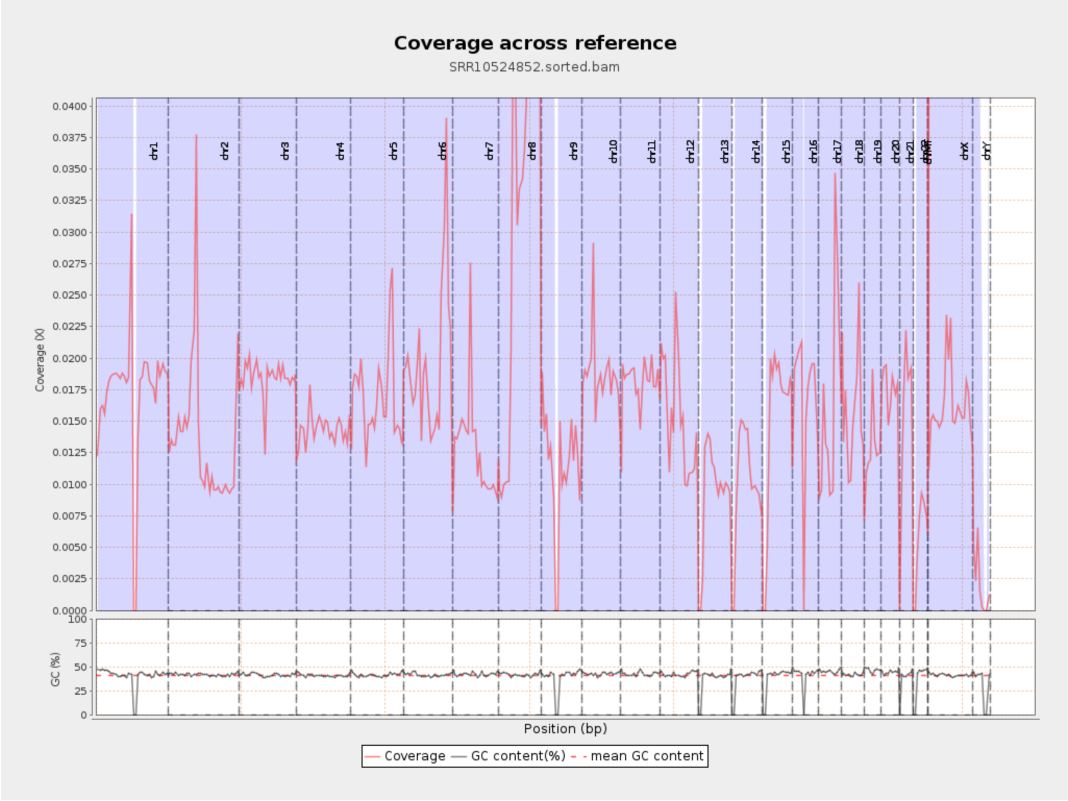
General error rate	0.49%
Mismatches	237,943
Insertions	4,140
Mapped reads with at least one insertion	0.48%
Deletions	9,357
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.24%

2.6. Chromosome stats

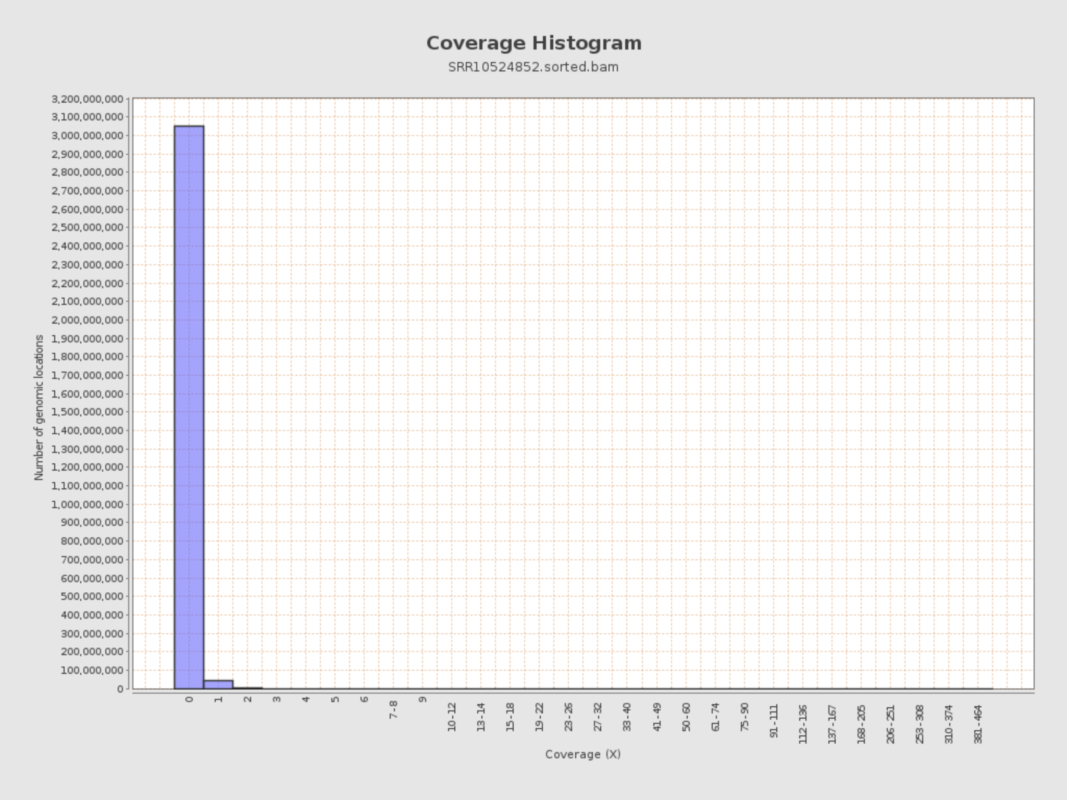
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4286136	0.0172	0.3414
chr2	243199373	3262490	0.0134	0.1811
chr3	198022430	3649900	0.0184	0.1407
chr4	191154276	2744675	0.0144	0.1284
chr5	180915260	3083890	0.017	0.1359
chr6	171115067	3334809	0.0195	0.1554
chr7	159138663	2033367	0.0128	0.2298

chr8	146364022	5508314	0.0376	0.2557
chr9	141213431	1605413	0.0114	0.1393
chr10	135534747	2542707	0.0188	0.1777
chr11	135006516	2455562	0.0182	0.1639
chr12	133851895	2029099	0.0152	0.1303
chr13	115169878	1051652	0.0091	0.1002
chr14	107349540	1079357	0.0101	0.1079
chr15	102531392	1528236	0.0149	0.1277
chr16	90354753	1497816	0.0166	0.1398
chr17	81195210	1356258	0.0167	0.1455
chr18	78077248	1234898	0.0158	0.2499
chr19	59128983	766212	0.013	0.2328
chr20	63025520	1087504	0.0173	0.1381
chr21	48129895	744149	0.0155	0.1323
chr22	51304566	302236	0.0059	0.0792
chrMT	16571	22144	1.3363	1.3248
chrX	155270560	2545876	0.0164	0.1448
chrY	59373566	120122	0.002	0.0588

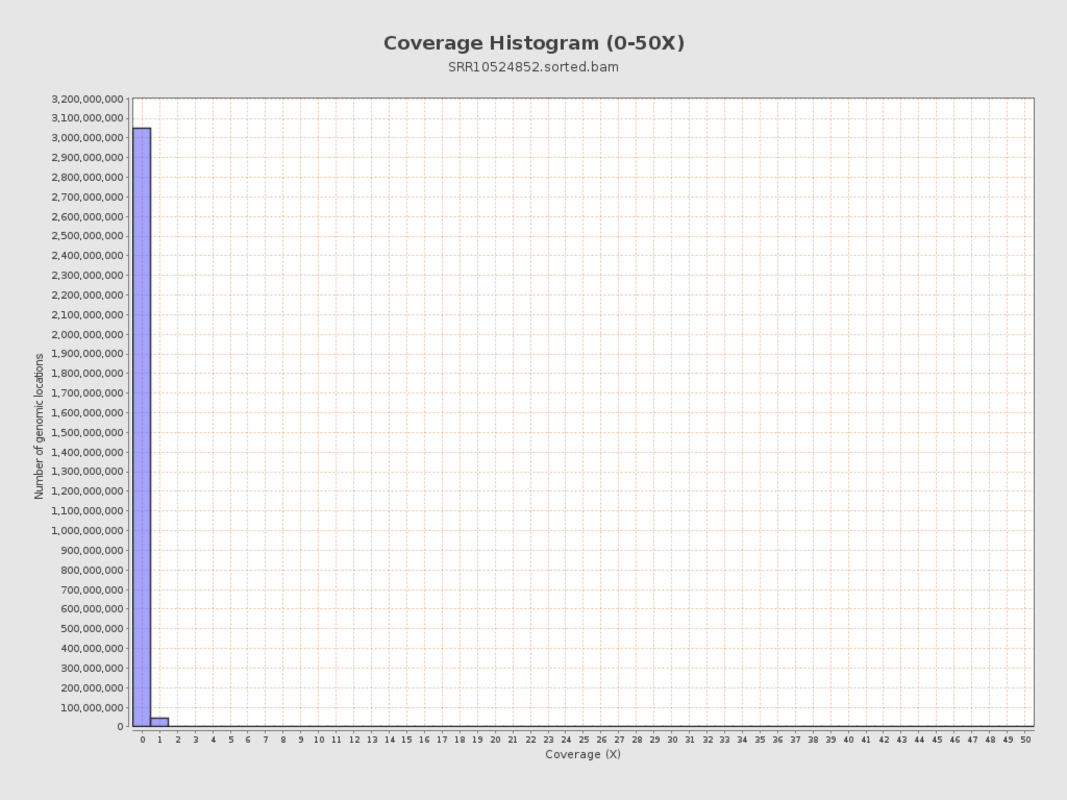
3. Results : Coverage across reference



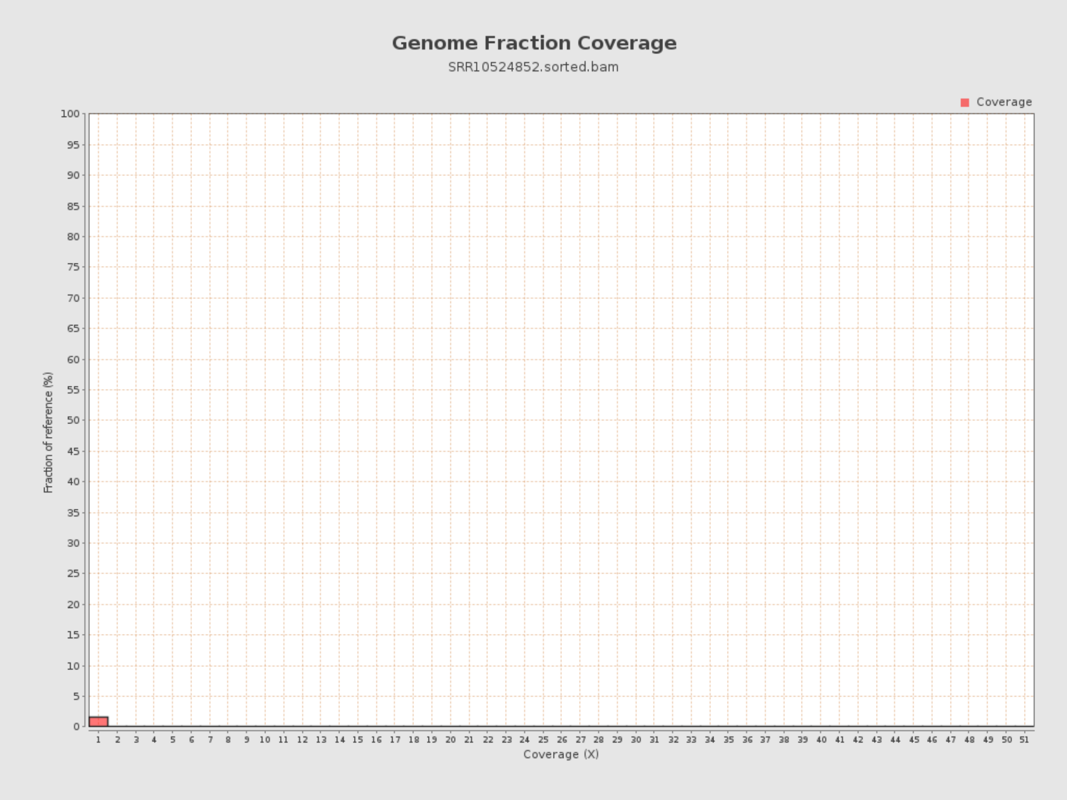
4. Results : Coverage Histogram



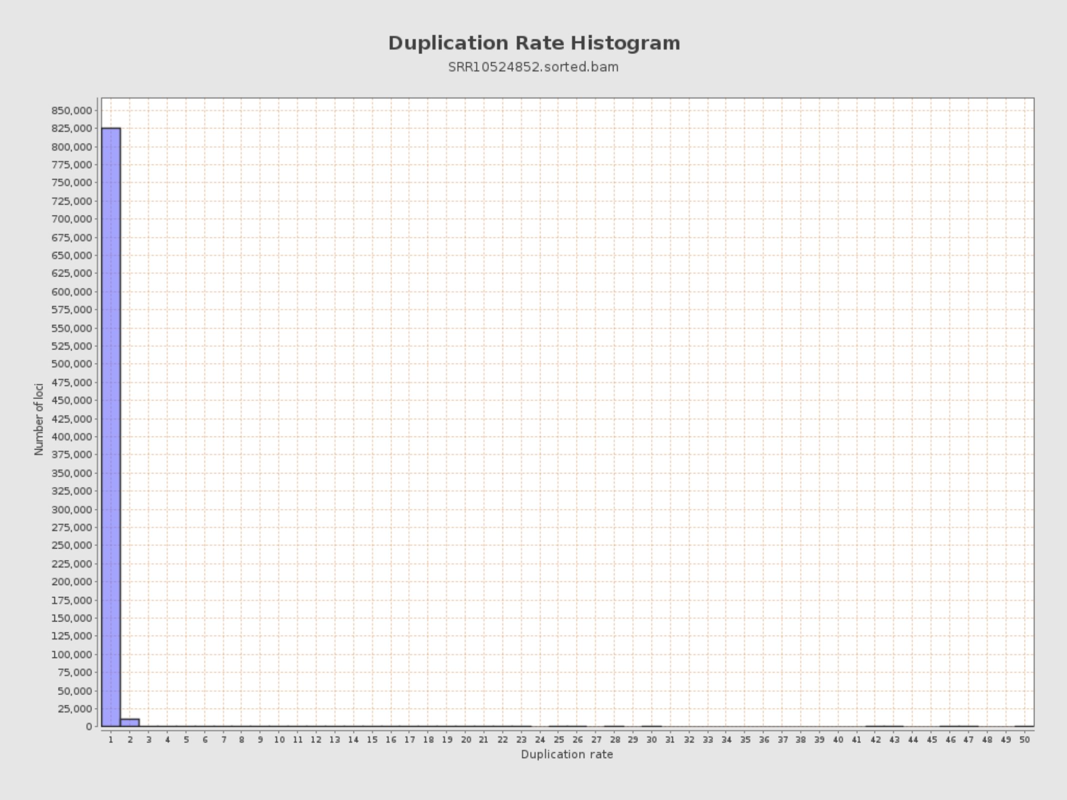
5. Results : Coverage Histogram (0-50X)



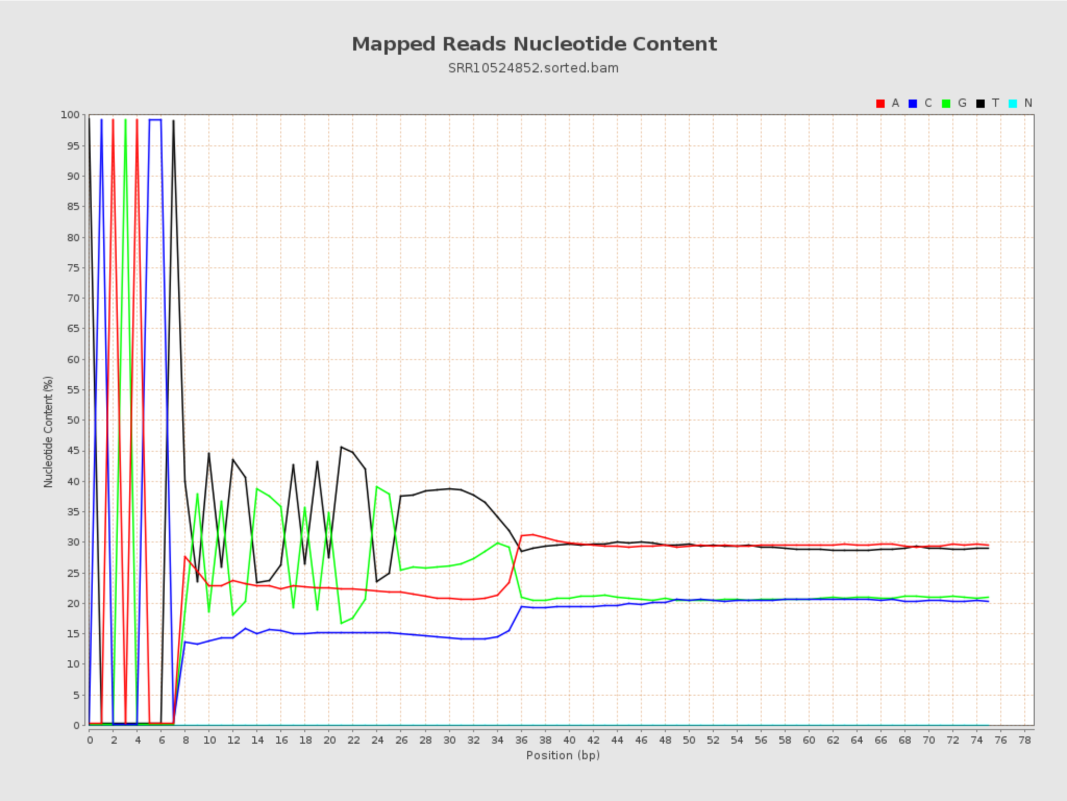
6. Results : Genome Fraction Coverage



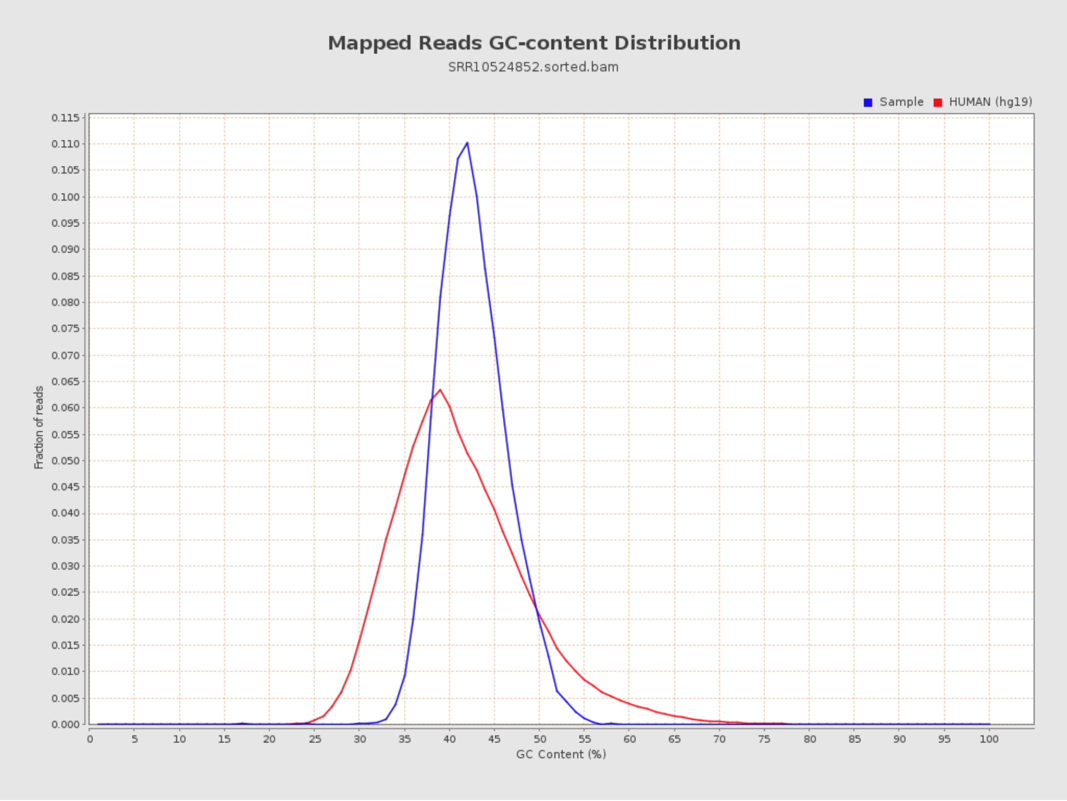
7. Results : Duplication Rate Histogram



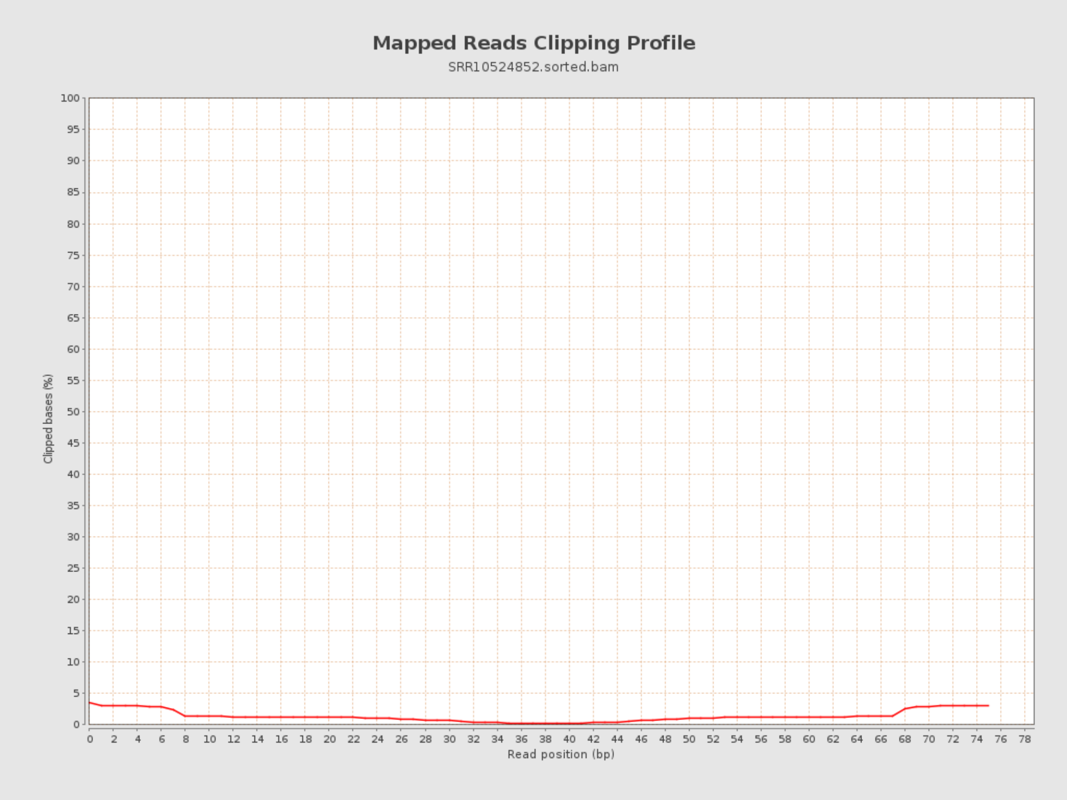
8. Results : Mapped Reads Nucleotide Content



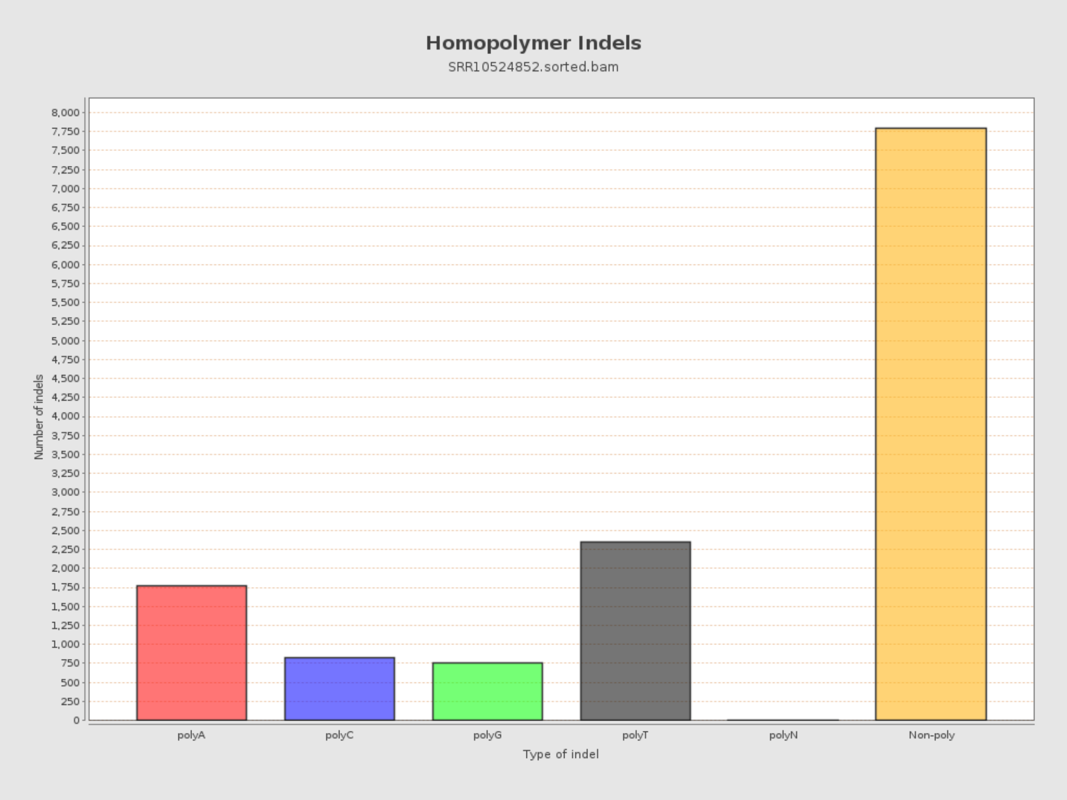
9. Results : Mapped Reads GC-content Distribution



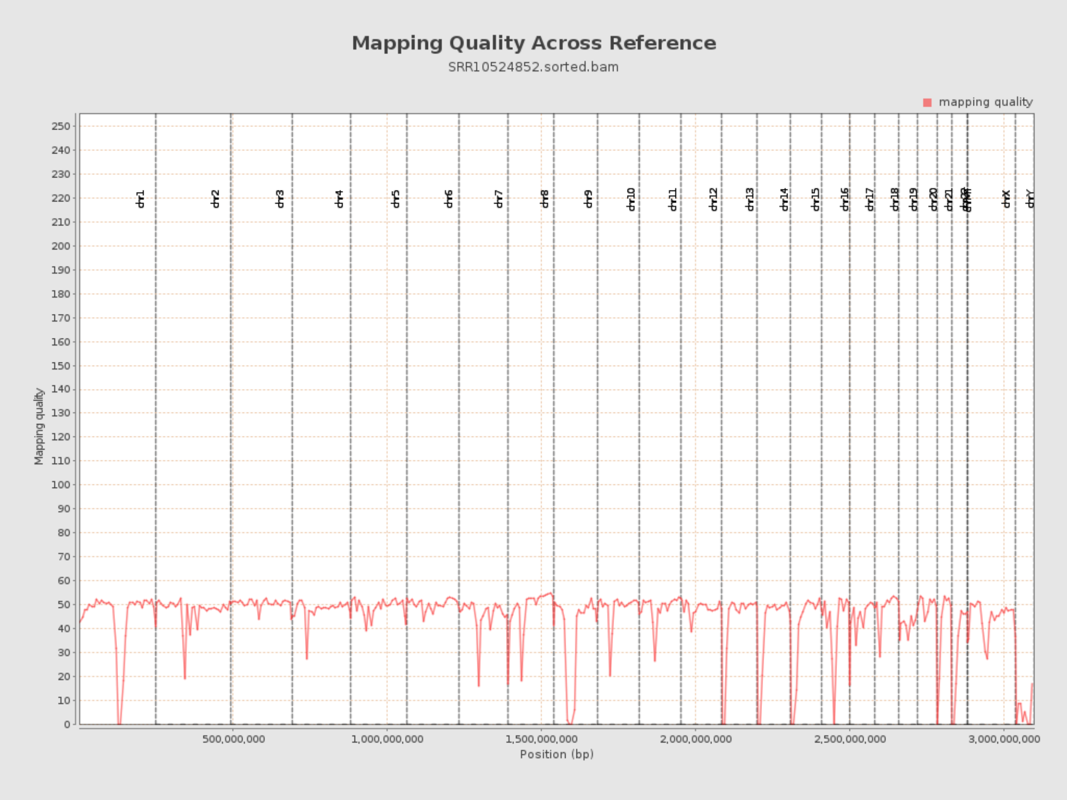
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram