

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:55:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524453.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_SRR10524453 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524453.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:55:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524453.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,133,329
Mapped reads	1,036,837 / 91.49%
Unmapped reads	96,492 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,353 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	36,794 / 3.25%
Duplication rate	2.77%
Clipped reads	1,036,032 / 91.41%

2.2. ACGT Content

Number/percentage of A's	15,781,206 / 26.27%
Number/percentage of C's	11,118,579 / 18.51%
Number/percentage of T's	18,312,388 / 30.48%
Number/percentage of G's	14,861,351 / 24.74%
Number/percentage of N's	1,235 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.1959
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.21
----------------------	-------

2.5. Mismatches and indels

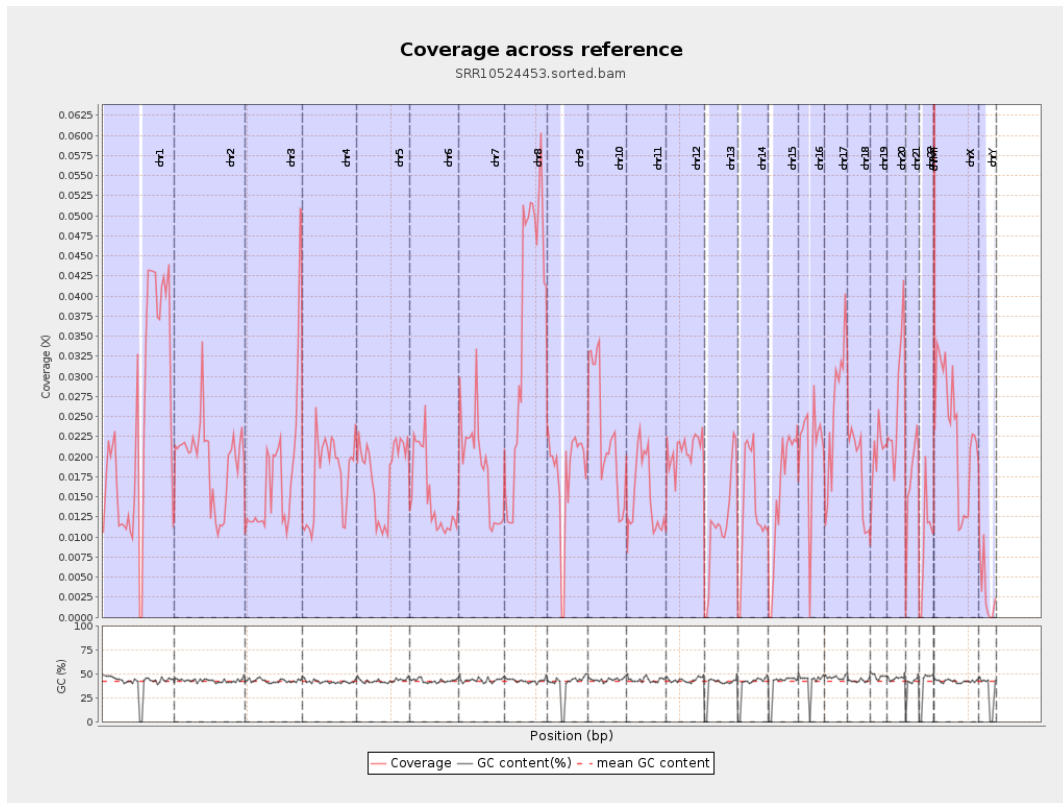
General error rate	0.49%
Mismatches	284,986
Insertions	4,347
Mapped reads with at least one insertion	0.42%
Deletions	11,074
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.38%

2.6. Chromosome stats

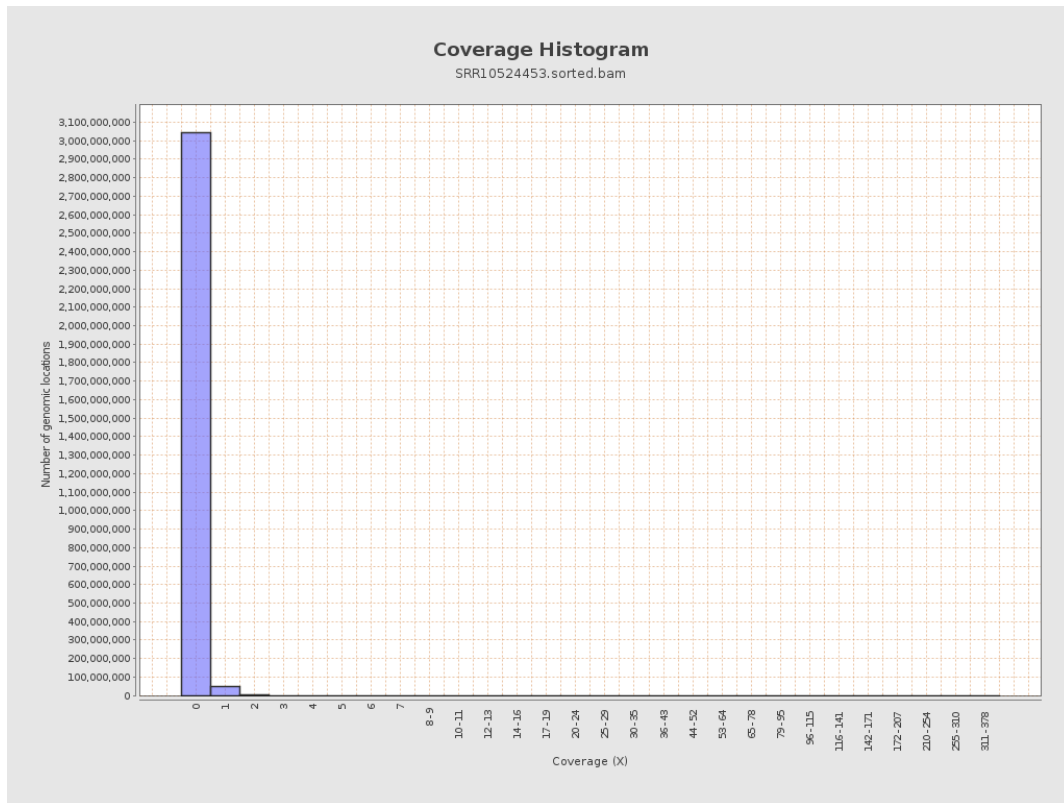
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5948158	0.0239	0.3197
chr2	243199373	4742655	0.0195	0.2237
chr3	198022430	3506104	0.0177	0.1439
chr4	191154276	3373021	0.0176	0.1554
chr5	180915260	3252132	0.018	0.1452
chr6	171115067	2593109	0.0152	0.1576
chr7	159138663	2995096	0.0188	0.2544

chr8	146364022	5340119	0.0365	0.2285
chr9	141213431	2508240	0.0178	0.1748
chr10	135534747	3136028	0.0231	0.2
chr11	135006516	2058107	0.0152	0.1875
chr12	133851895	2790890	0.0209	0.1561
chr13	115169878	1358697	0.0118	0.1181
chr14	107349540	1447623	0.0135	0.1258
chr15	102531392	1606164	0.0157	0.1446
chr16	90354753	1879564	0.0208	0.165
chr17	81195210	2098666	0.0258	0.177
chr18	78077248	1415079	0.0181	0.2748
chr19	59128983	1213969	0.0205	0.2308
chr20	63025520	1708939	0.0271	0.1787
chr21	48129895	833817	0.0173	0.1493
chr22	51304566	495640	0.0097	0.1053
chrMT	16571	4834	0.2917	0.5919
chrX	155270560	3600069	0.0232	0.1786
chrY	59373566	187145	0.0032	0.0857

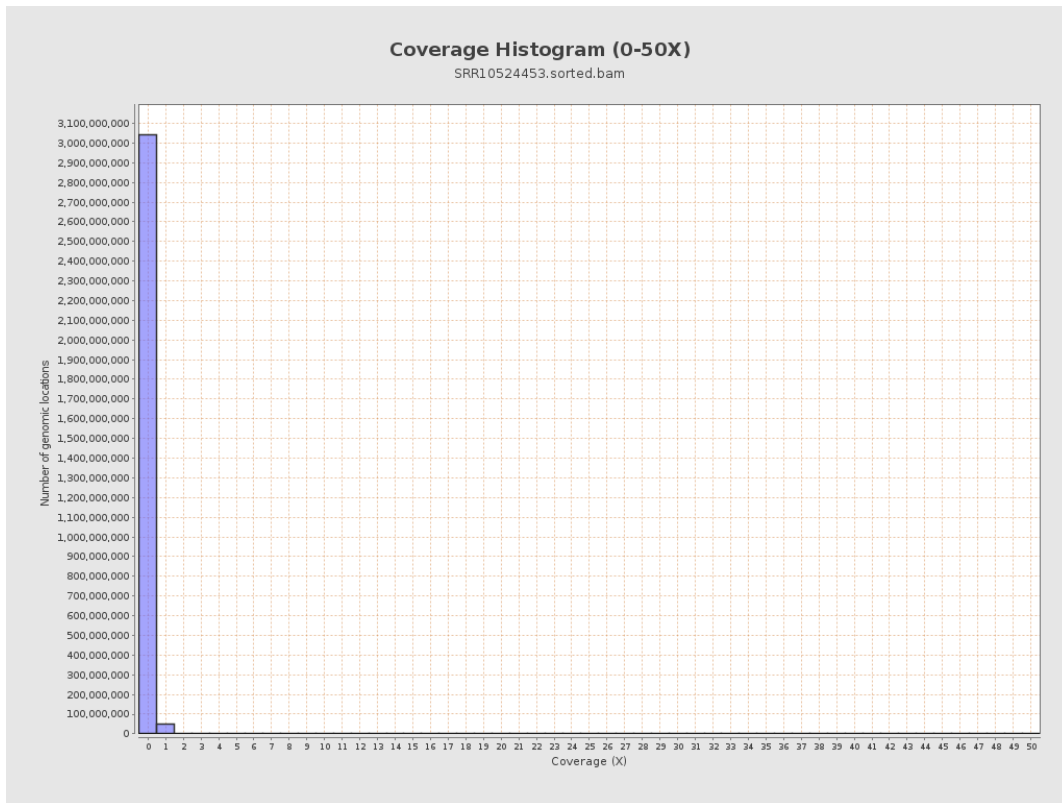
3. Results : Coverage across reference



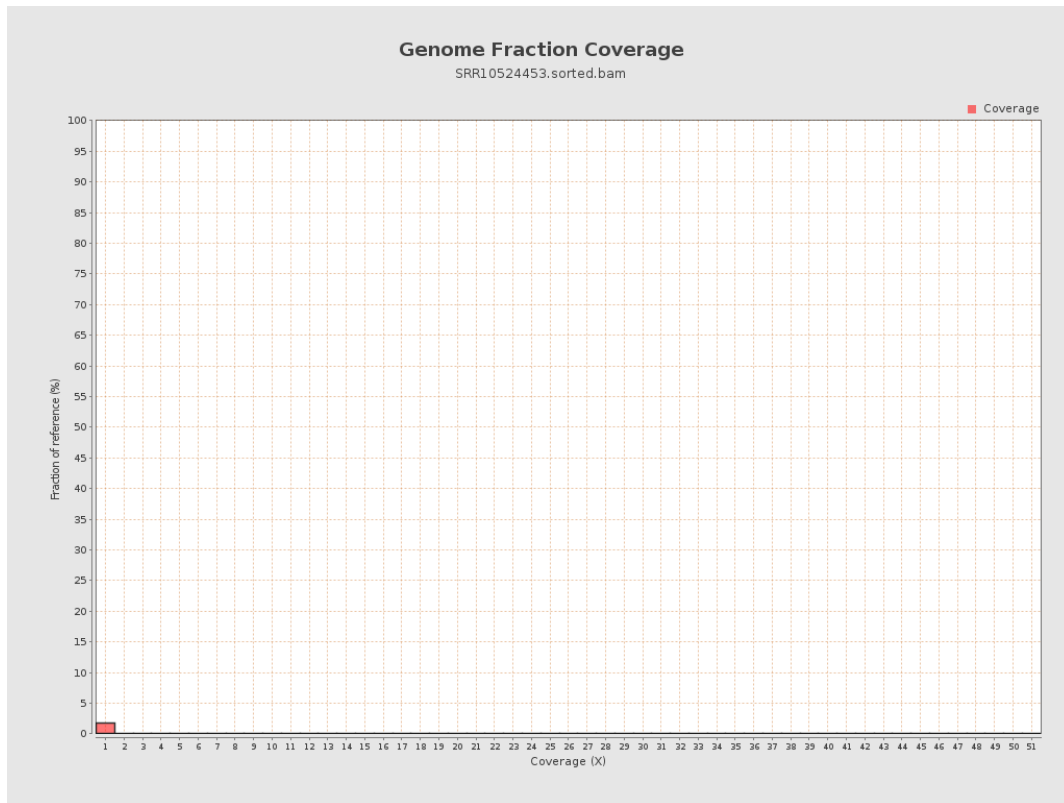
4. Results : Coverage Histogram



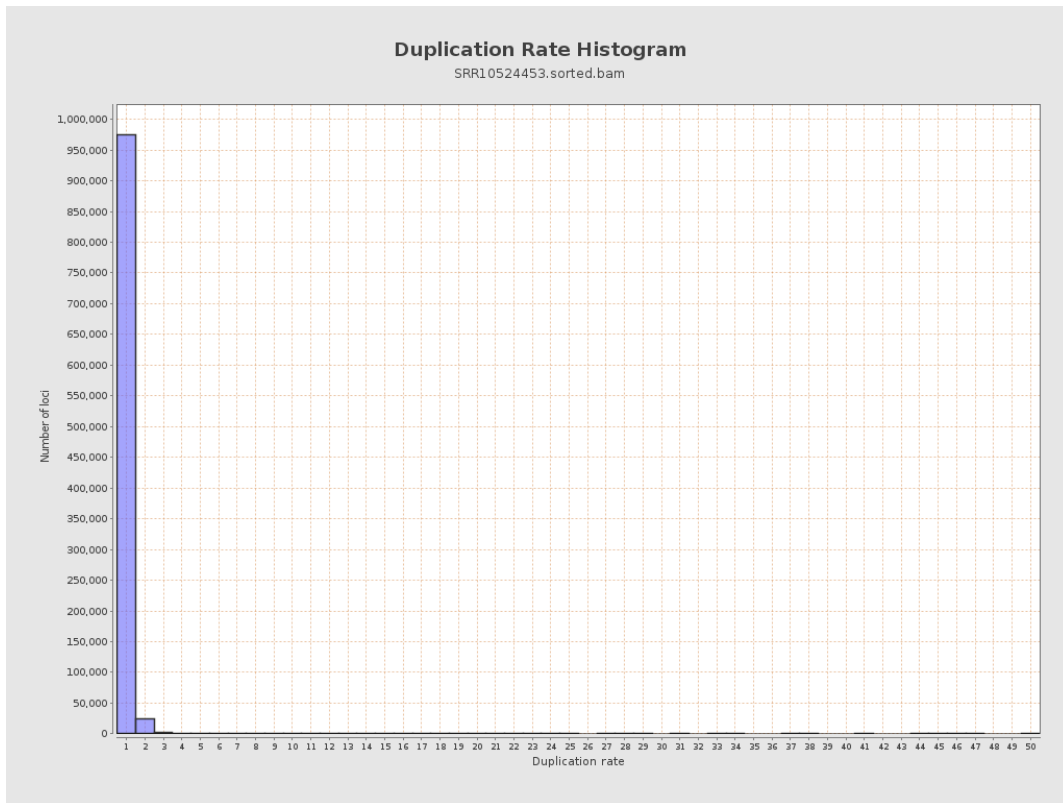
5. Results : Coverage Histogram (0-50X)



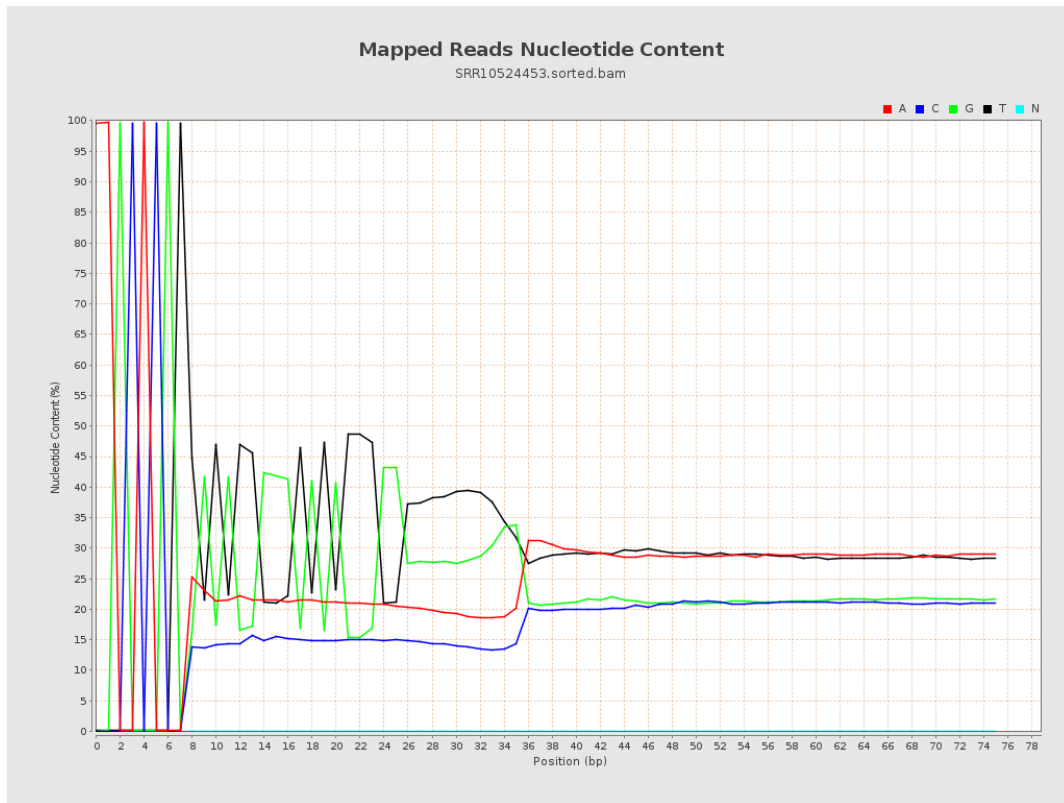
6. Results : Genome Fraction Coverage



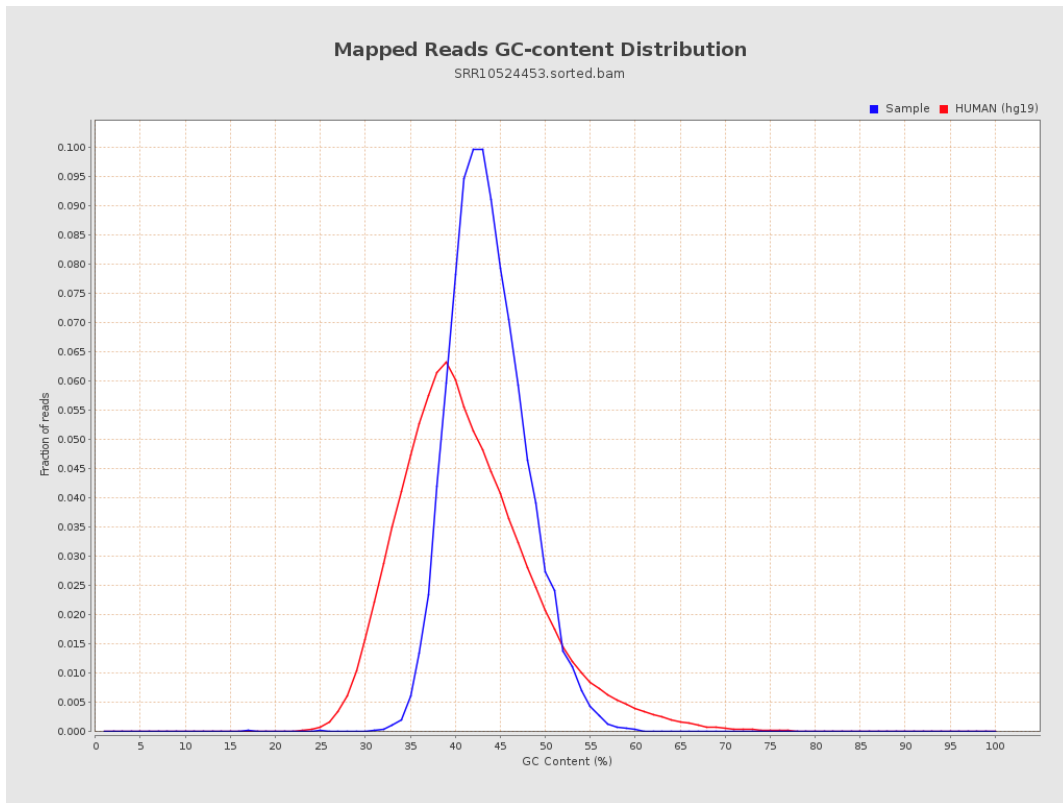
7. Results : Duplication Rate Histogram



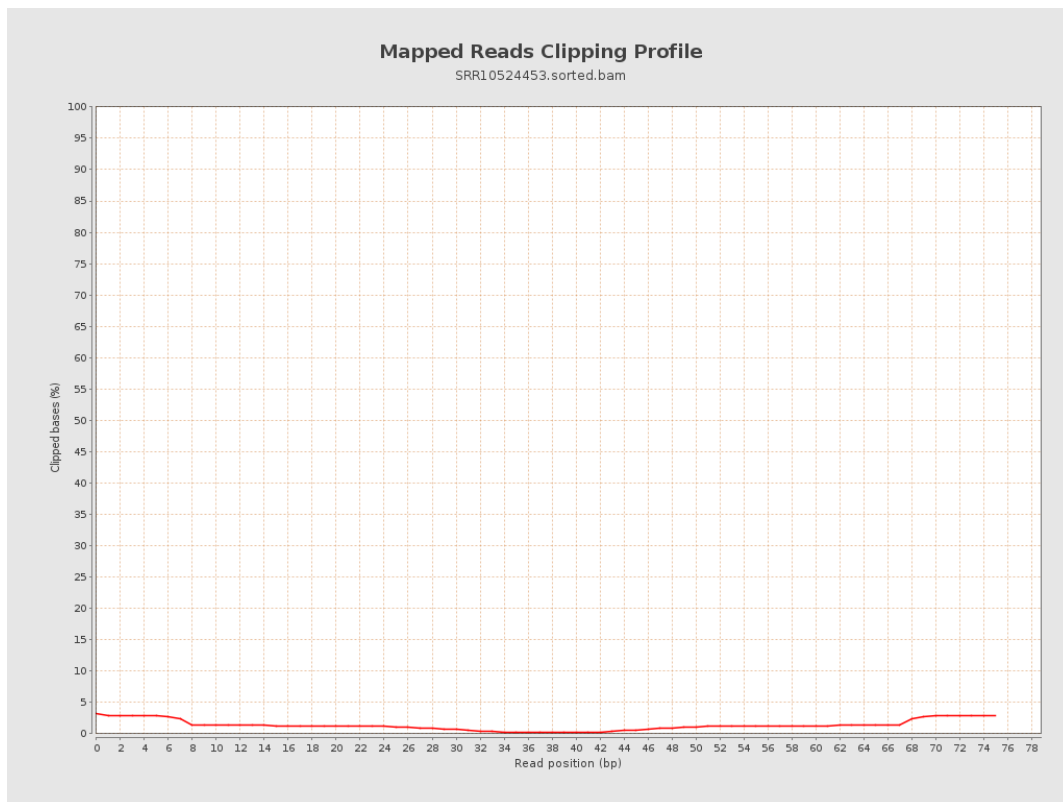
8. Results : Mapped Reads Nucleotide Content



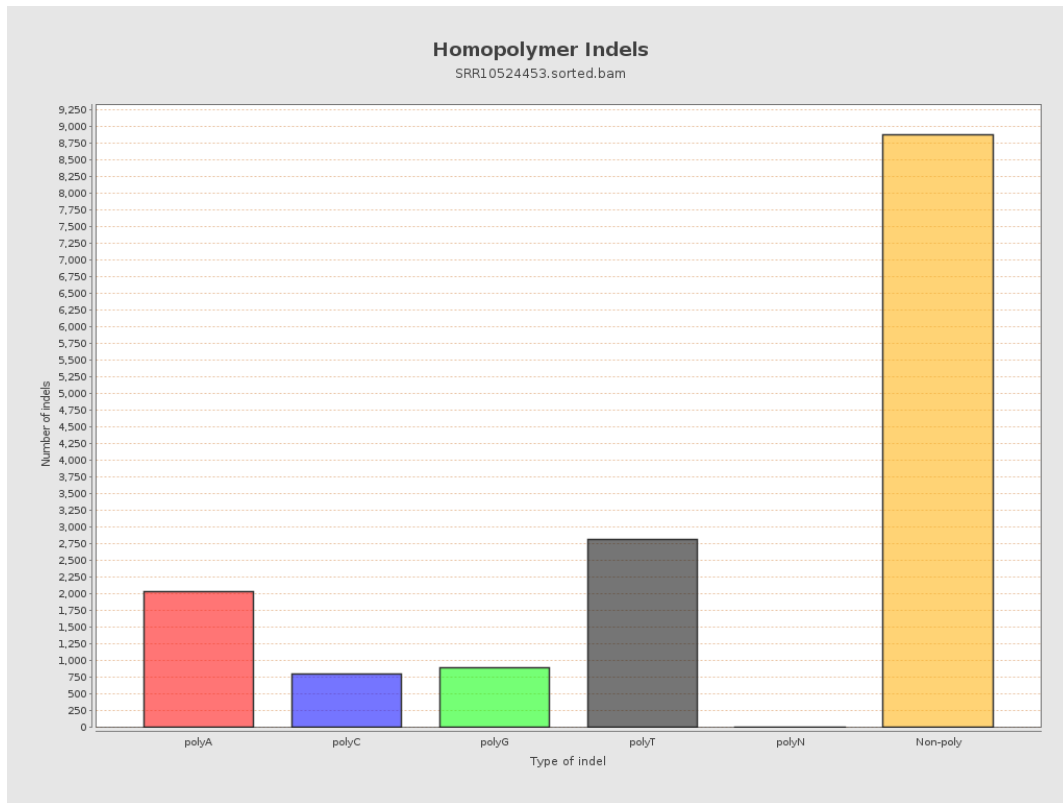
9. Results : Mapped Reads GC-content Distribution



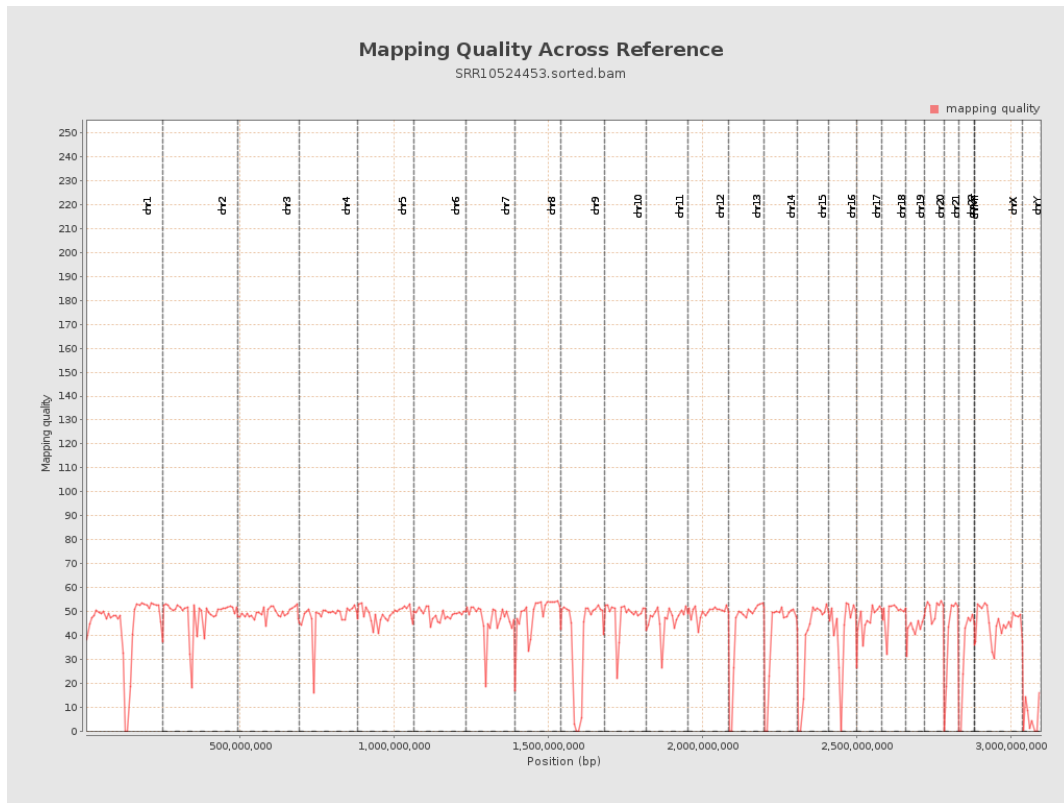
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

