Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006439.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_SRR1006439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006439.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:48:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006439.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,359,907
Mapped reads	1,281,561 / 94.24%
Unmapped reads	78,346 / 5.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,669 / 0.27%
Read min/max/mean length	30 / 59 / 57.14
Duplicated reads (estimated)	28,959 / 2.13%
Duplication rate	1.88%
Clipped reads	163,995 / 12.06%

2.2. ACGT Content

Number/percentage of A's	20,287,549 / 28.36%
Number/percentage of C's	14,885,989 / 20.81%
Number/percentage of T's	20,627,146 / 28.83%
Number/percentage of G's	15,743,155 / 22%
Number/percentage of N's	1,498 / 0%
GC Percentage	42.81%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2277

2.4. Mapping Quality

Mean Mapping Quality	46.44

2.5. Mismatches and indels

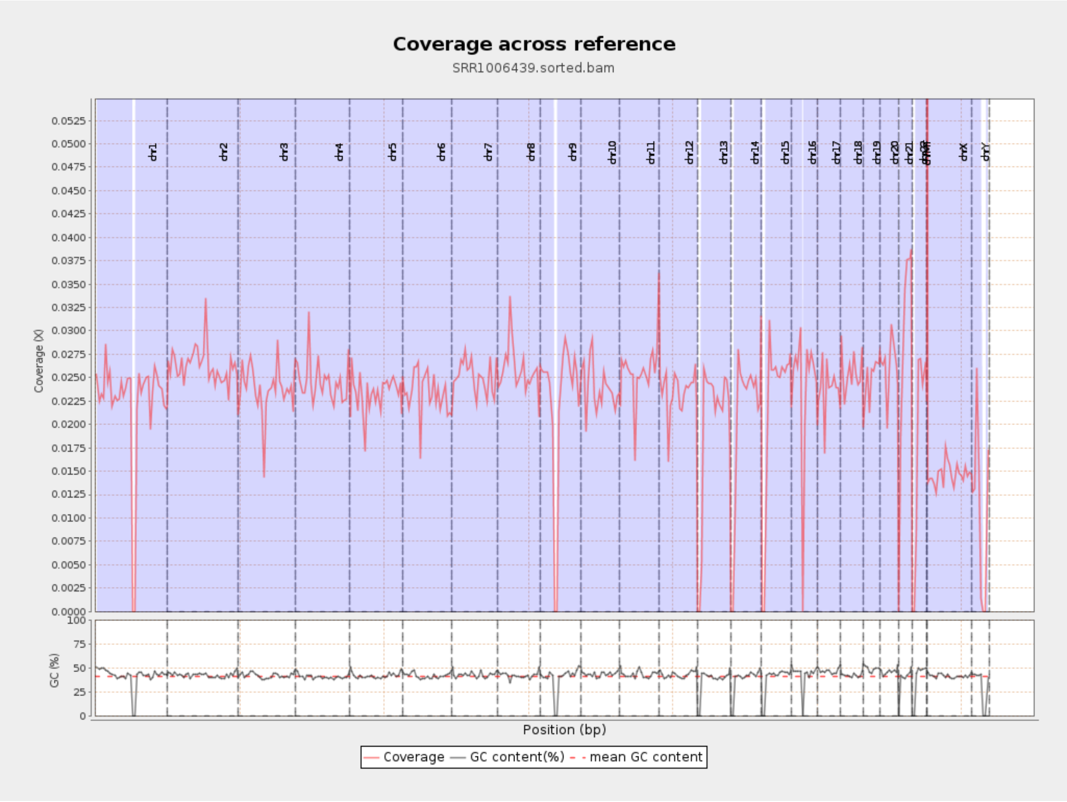
General error rate	0.38%
Mismatches	266,125
Insertions	4,456
Mapped reads with at least one insertion	0.35%
Deletions	11,886
Mapped reads with at least one deletion	0.92%
Homopolymer indels	45.26%

2.6. Chromosome stats

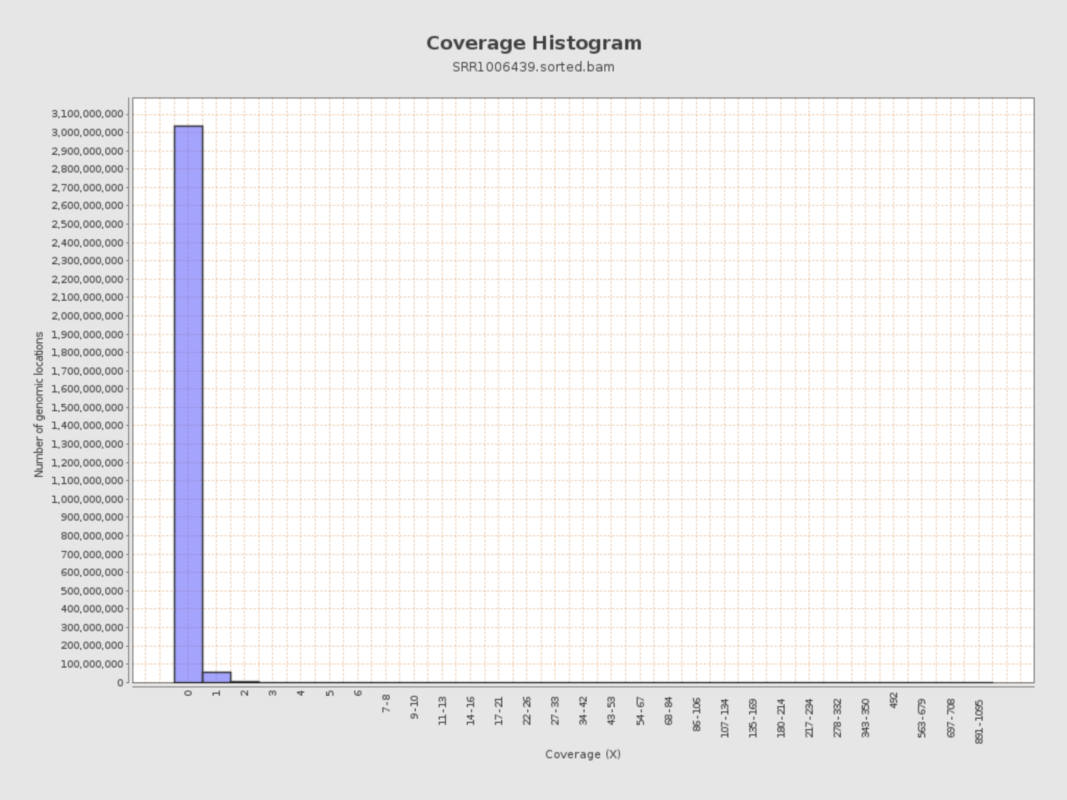
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5574104	0.0224	0.2213
chr2	243199373	6396385	0.0263	0.201
chr3	198022430	4705207	0.0238	0.1742
chr4	191154276	4710228	0.0246	0.1823
chr5	180915260	4252430	0.0235	0.1737
chr6	171115067	4003340	0.0234	0.1763
chr7	159138663	3993800	0.0251	0.2017

chr8	146364022	3782862	0.0258	0.6317
chr9	141213431	3159605	0.0224	0.1806
chr10	135534747	3258342	0.024	0.1989
chr11	135006516	3423444	0.0254	0.1901
chr12	133851895	3141955	0.0235	0.1752
chr13	115169878	2270957	0.0197	0.1587
chr14	107349540	2189274	0.0204	0.1645
chr15	102531392	2220125	0.0217	0.1672
chr16	90354753	2145586	0.0237	0.1837
chr17	81195210	1934577	0.0238	0.1831
chr18	78077248	1996292	0.0256	0.2403
chr19	59128983	1471105	0.0249	0.2061
chr20	63025520	1652911	0.0262	0.1887
chr21	48129895	1394991	0.029	0.2014
chr22	51304566	923972	0.018	0.1579
chrMT	16571	49407	2.9815	2.5698
chrX	155270560	2278806	0.0147	0.1389
chrY	59373566	635094	0.0107	0.148

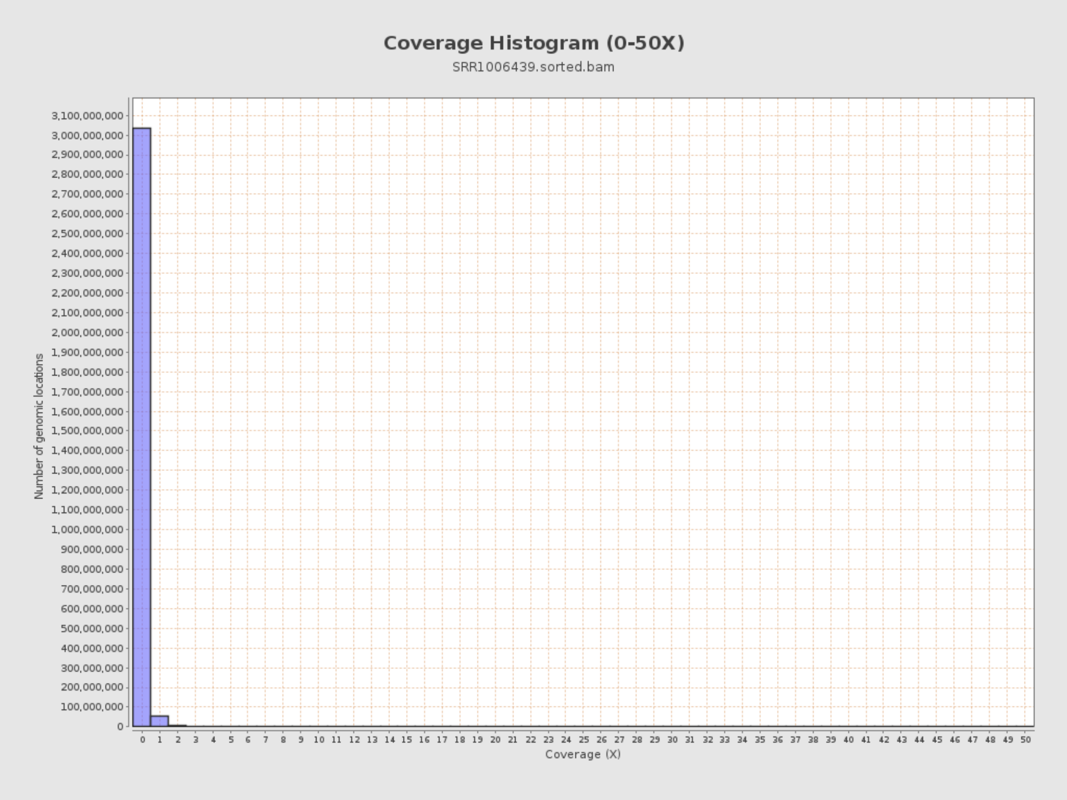
3. Results : Coverage across reference



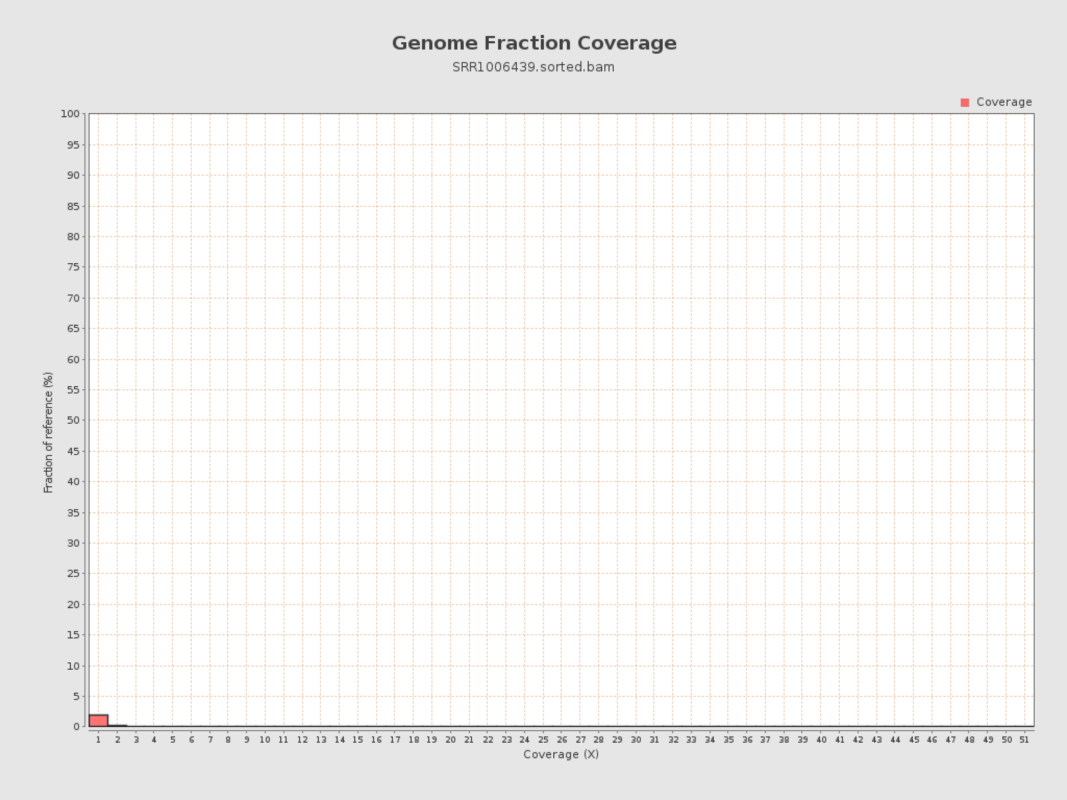
4. Results : Coverage Histogram



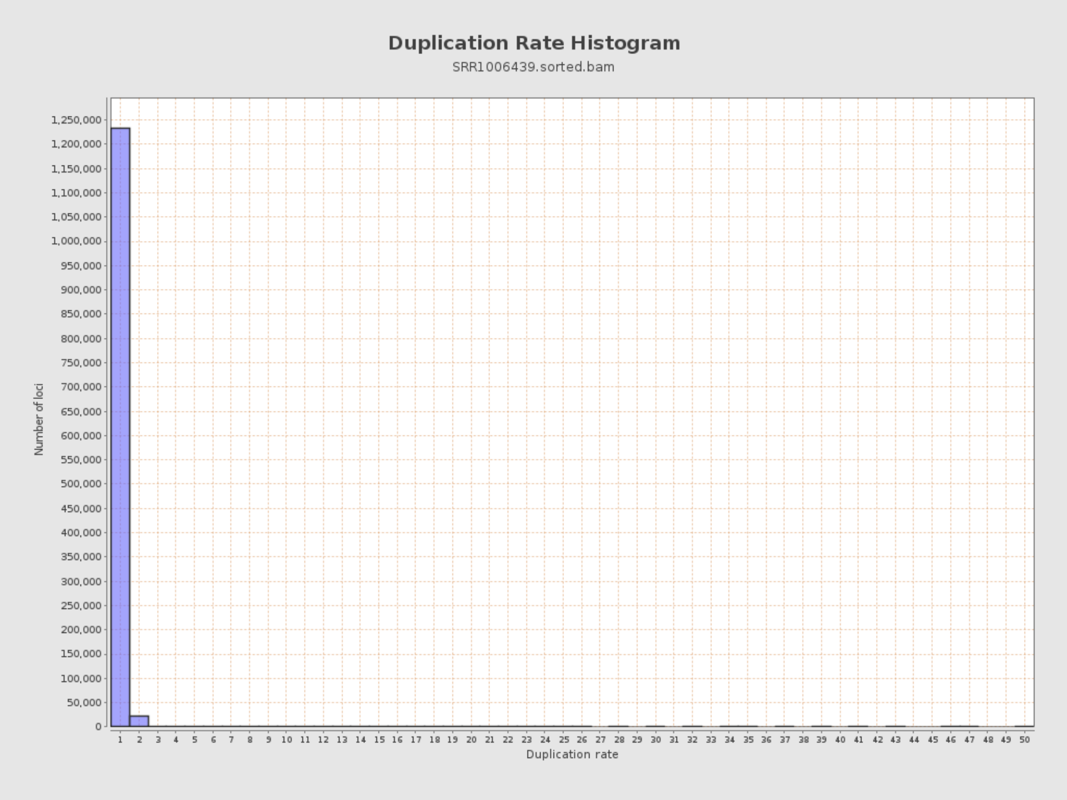
5. Results : Coverage Histogram (0-50X)



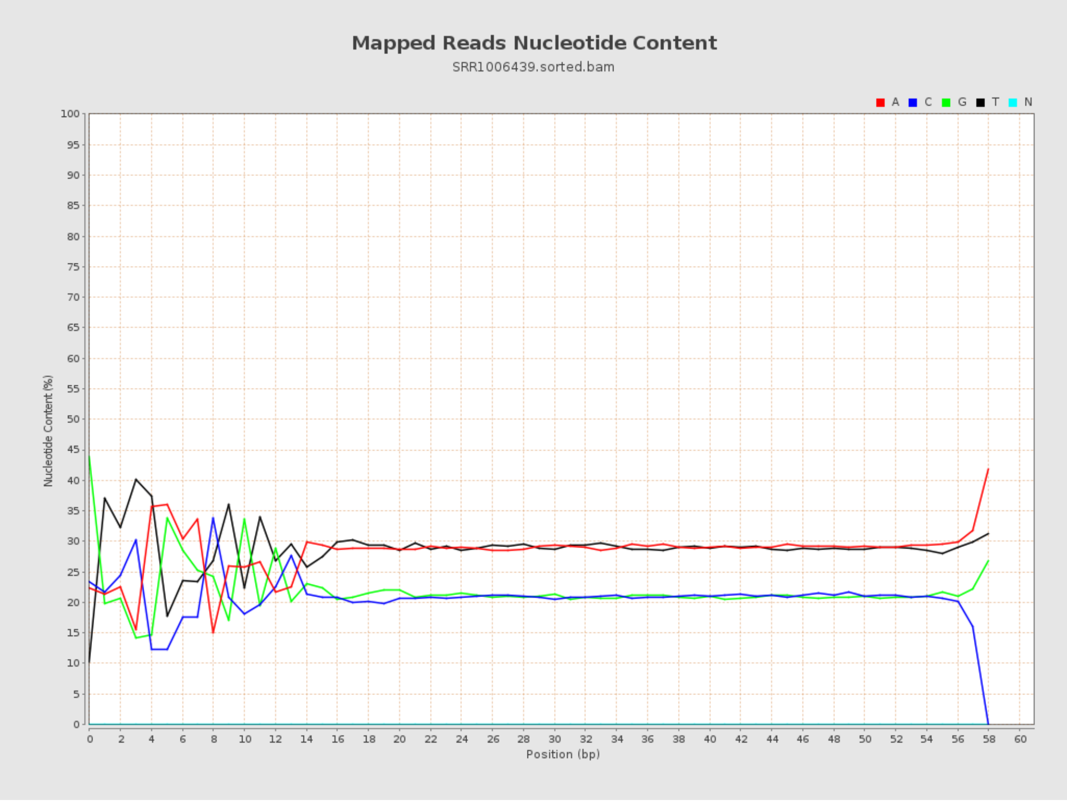
6. Results : Genome Fraction Coverage



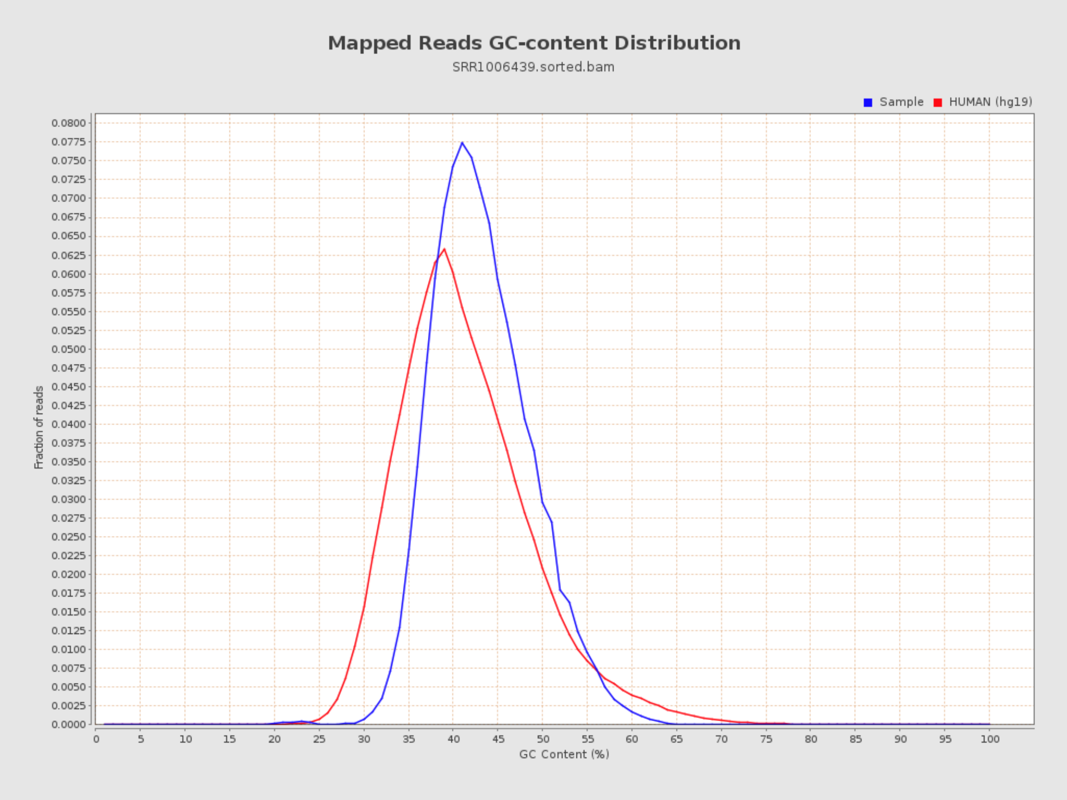
7. Results : Duplication Rate Histogram



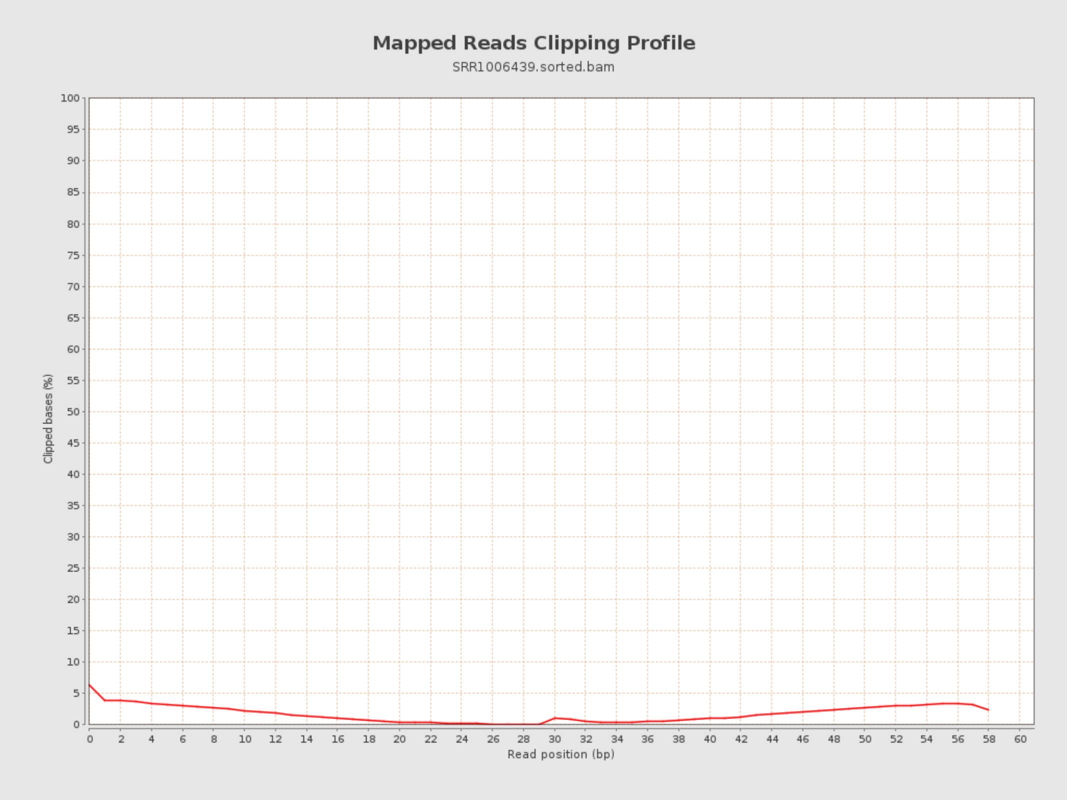
8. Results : Mapped Reads Nucleotide Content



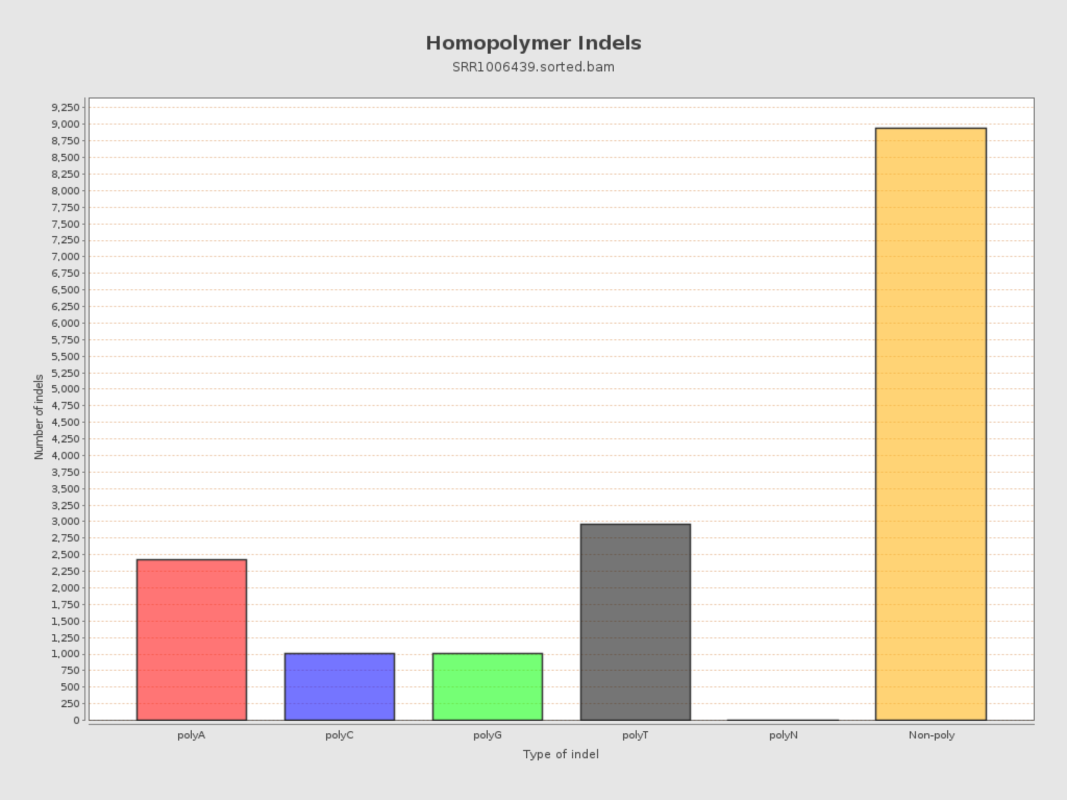
9. Results : Mapped Reads GC-content Distribution



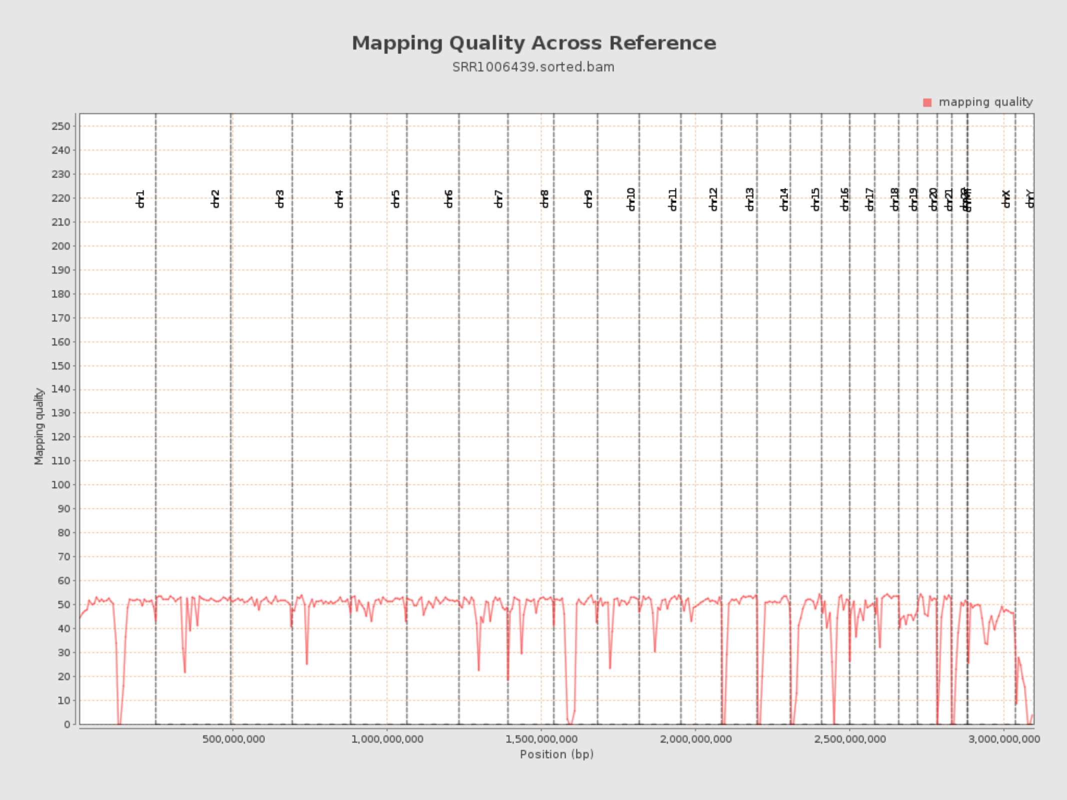
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram