Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:13:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006447.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_SRR1006447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006447.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:13:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,221,121
Mapped reads	1,162,449 / 95.2%
Unmapped reads	58,672 / 4.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,243 / 0.27%
Read min/max/mean length	30 / 59 / 57.25
Duplicated reads (estimated)	15,873 / 1.3%
Duplication rate	1.01%
Clipped reads	141,078 / 11.55%

2.2. ACGT Content

Number/percentage of A's	18,432,094 / 28.34%
Number/percentage of C's	13,764,778 / 21.16%
Number/percentage of T's	18,480,520 / 28.42%
Number/percentage of G's	14,357,676 / 22.08%
Number/percentage of N's	1,902 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.021

Standard Deviation	0.1793

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

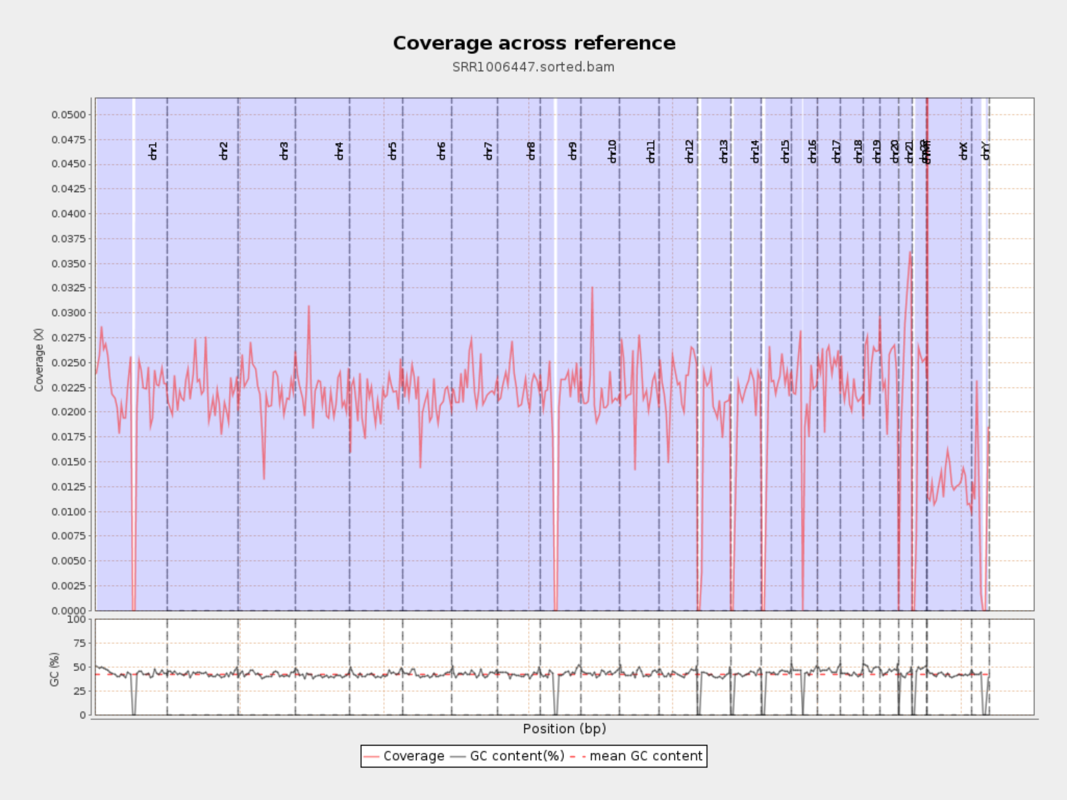
General error rate	0.43%
Mismatches	270,782
Insertions	4,264
Mapped reads with at least one insertion	0.37%
Deletions	11,377
Mapped reads with at least one deletion	0.97%
Homopolymer indels	45.95%

2.6. Chromosome stats

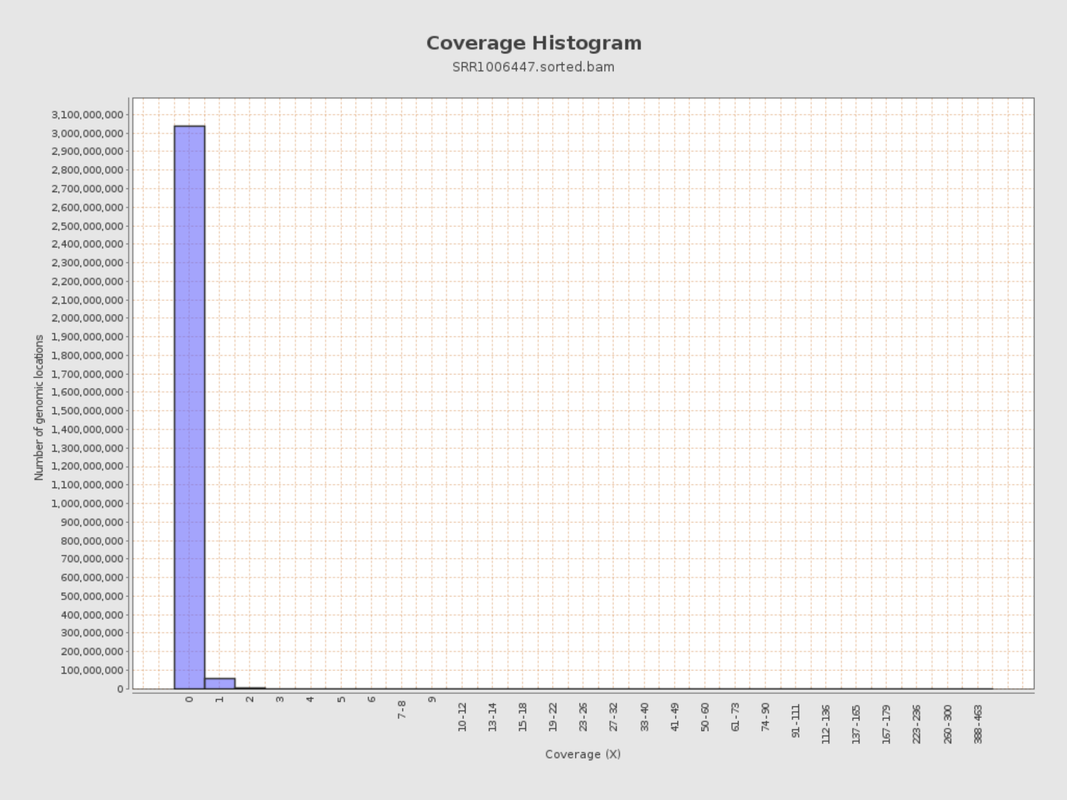
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5351248	0.0215	0.2159
chr2	243199373	5319410	0.0219	0.1787
chr3	198022430	4397177	0.0222	0.1577
chr4	191154276	4236916	0.0222	0.1642
chr5	180915260	3895780	0.0215	0.1551
chr6	171115067	3653784	0.0214	0.1594
chr7	159138663	3602564	0.0226	0.1914

chr8	146364022	3325387	0.0227	0.3081
chr9	141213431	2824449	0.02	0.1623
chr10	135534747	2968092	0.0219	0.184
chr11	135006516	3086948	0.0229	0.1676
chr12	133851895	3062937	0.0229	0.1612
chr13	115169878	2052431	0.0178	0.141
chr14	107349540	2010013	0.0187	0.1477
chr15	102531392	1987132	0.0194	0.1477
chr16	90354753	1854214	0.0205	0.1679
chr17	81195210	1991948	0.0245	0.1733
chr18	78077248	1714764	0.022	0.2103
chr19	59128983	1503390	0.0254	0.2101
chr20	63025520	1496981	0.0238	0.1651
chr21	48129895	1235616	0.0257	0.1817
chr22	51304566	901392	0.0176	0.1471
chrMT	16571	31741	1.9155	1.7812
chrX	155270560	1962524	0.0126	0.1219
chrY	59373566	589073	0.0099	0.147

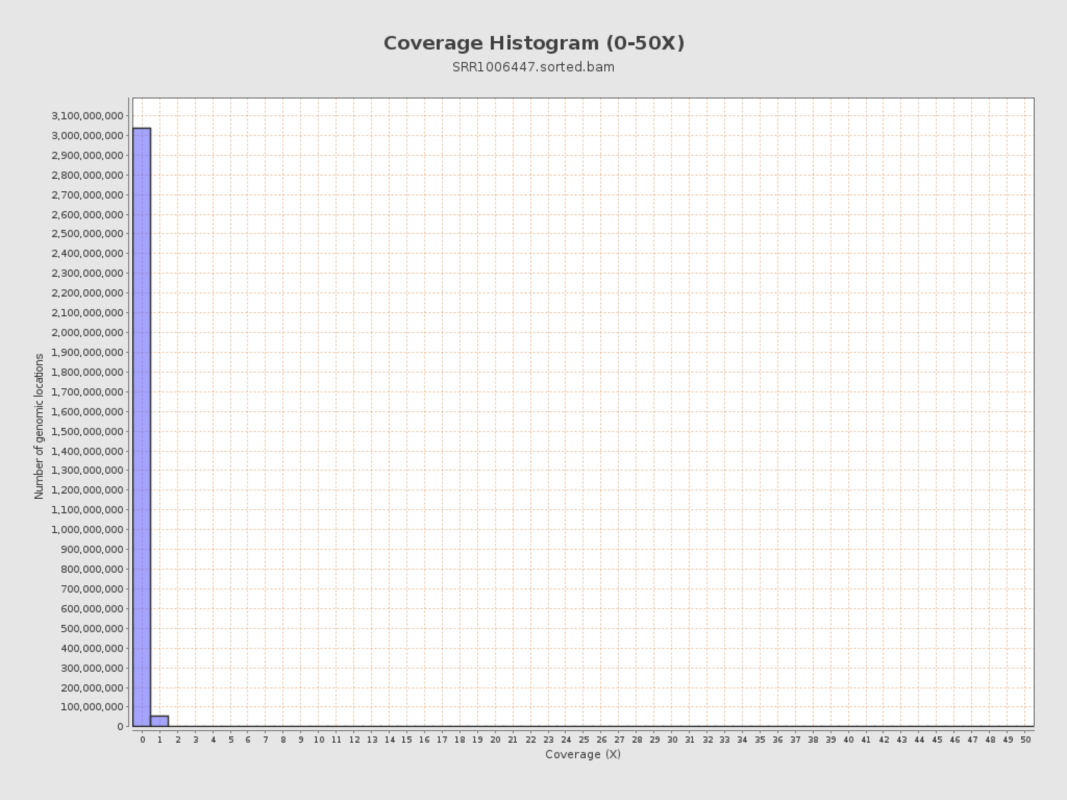
3. Results : Coverage across reference



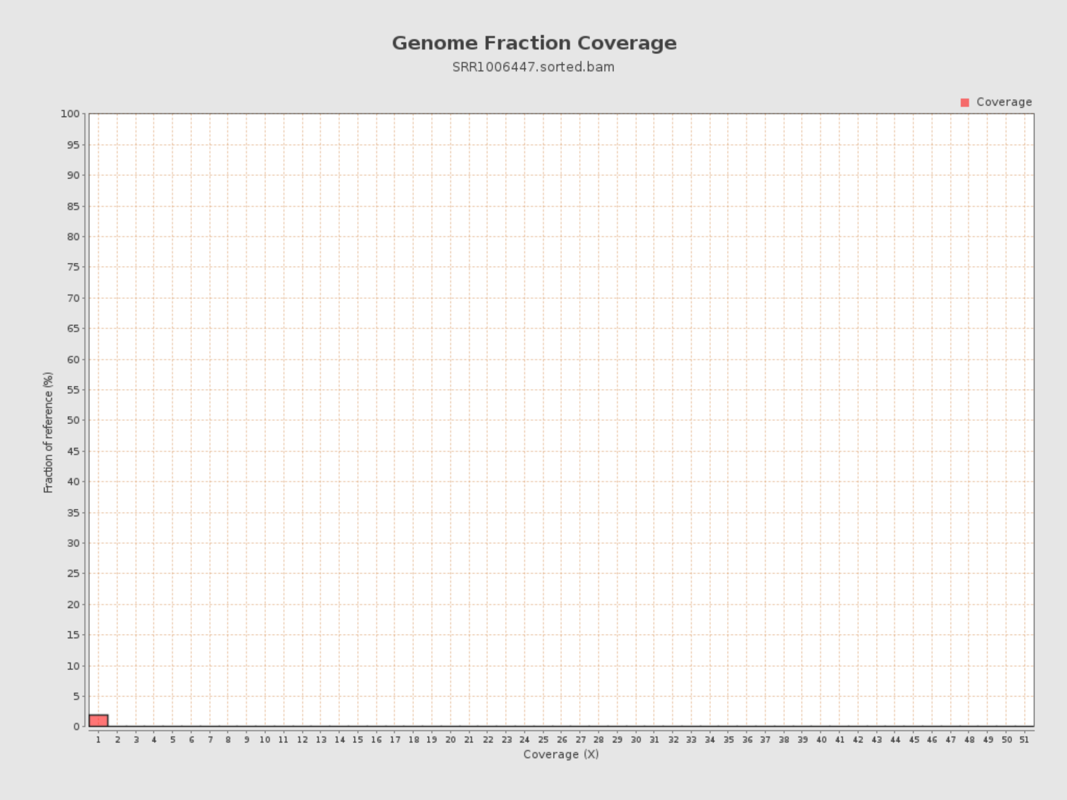
4. Results : Coverage Histogram



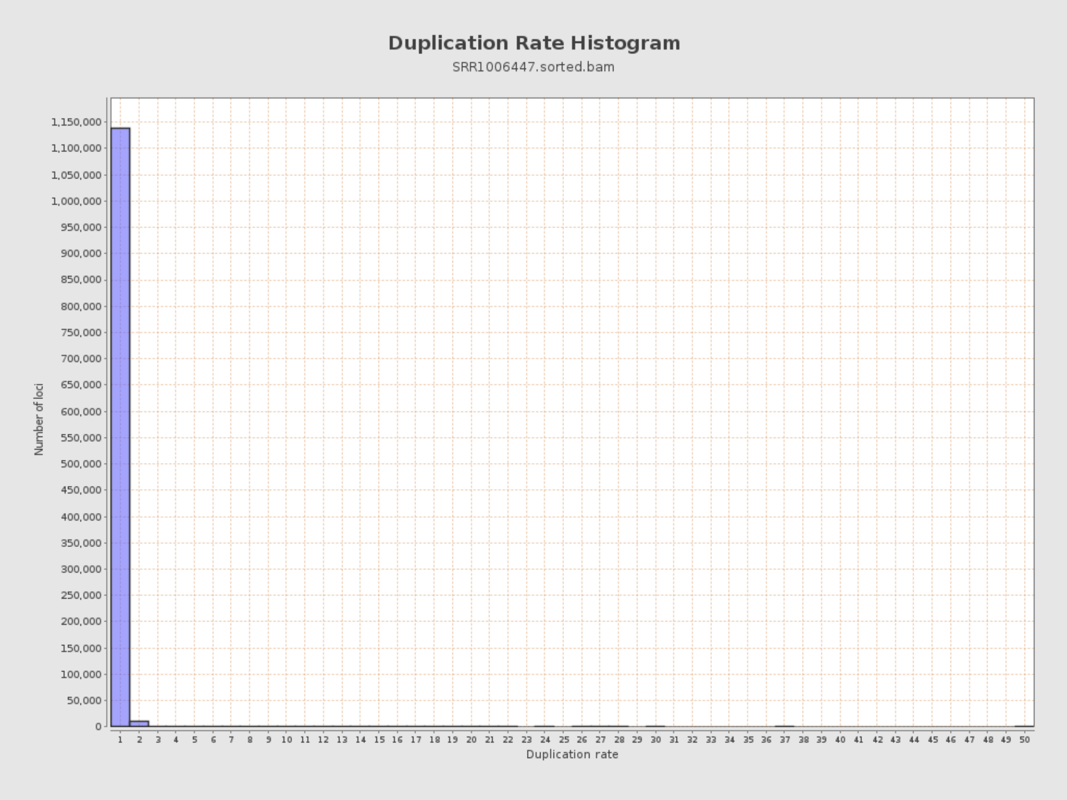
5. Results : Coverage Histogram (0-50X)



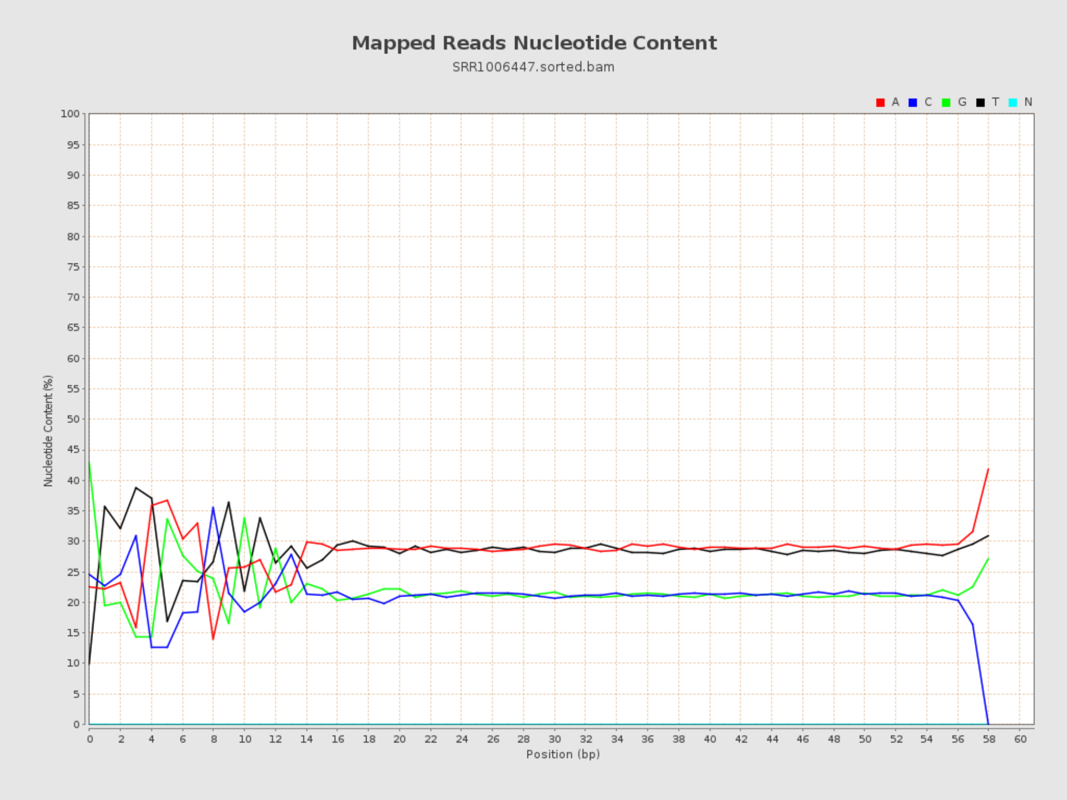
6. Results : Genome Fraction Coverage



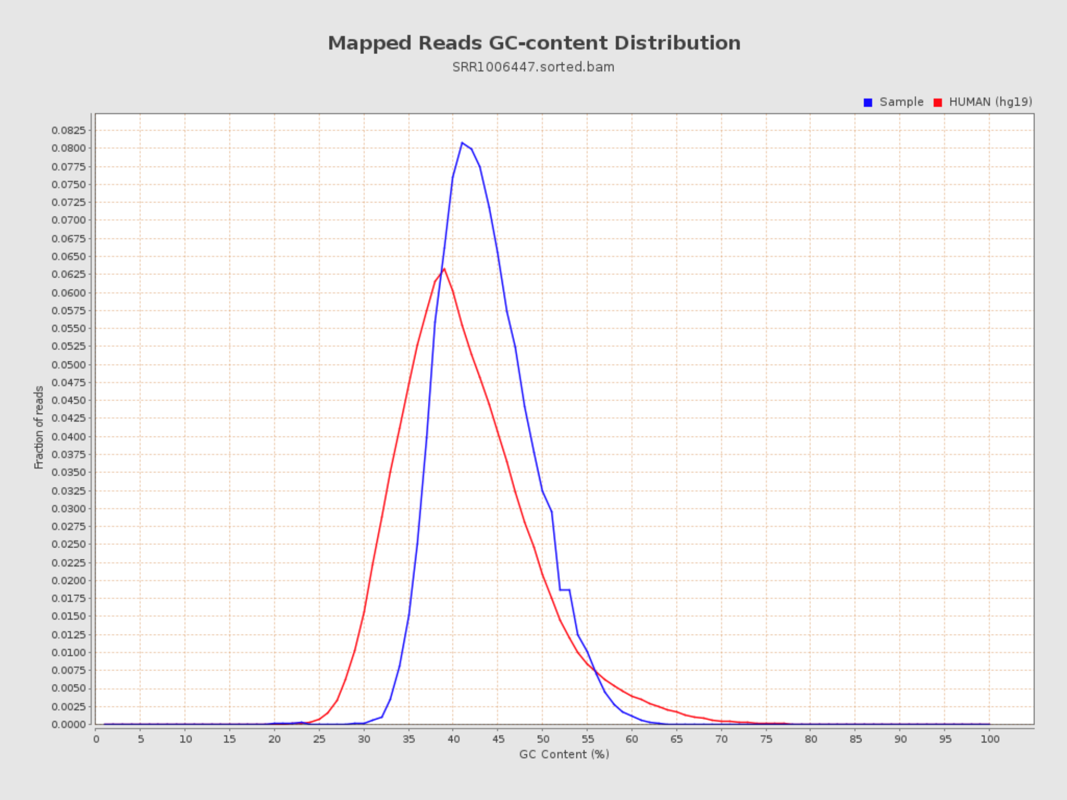
7. Results : Duplication Rate Histogram



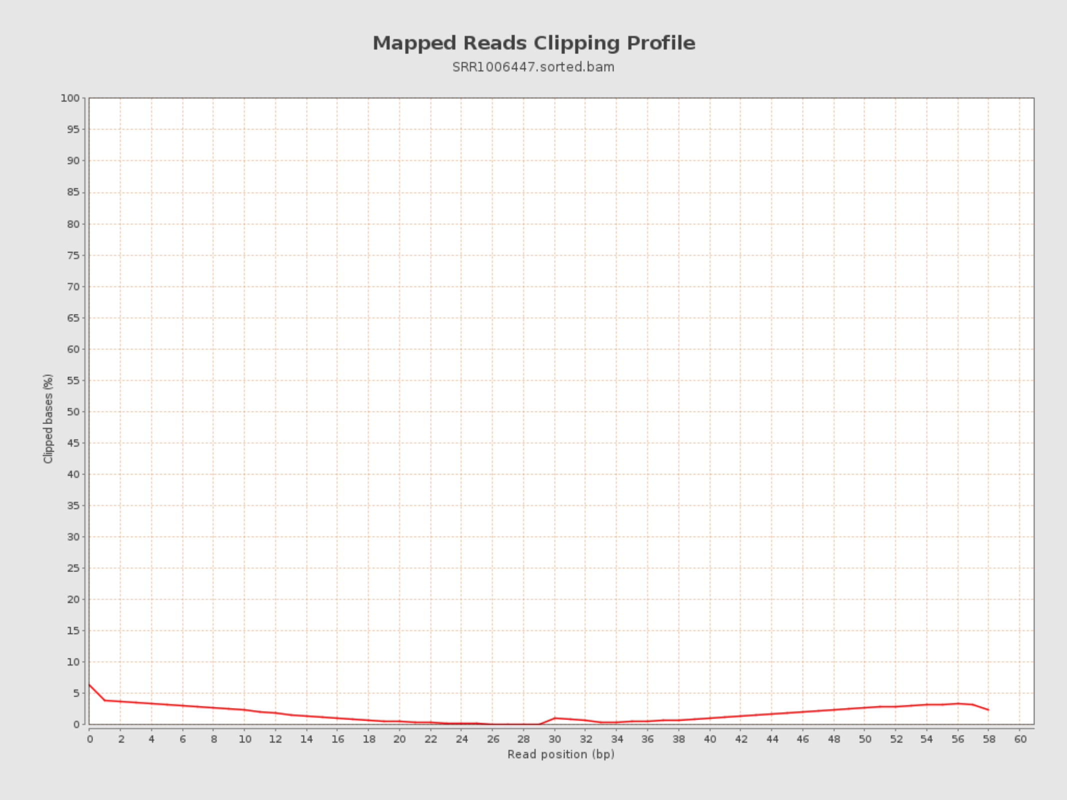
8. Results : Mapped Reads Nucleotide Content



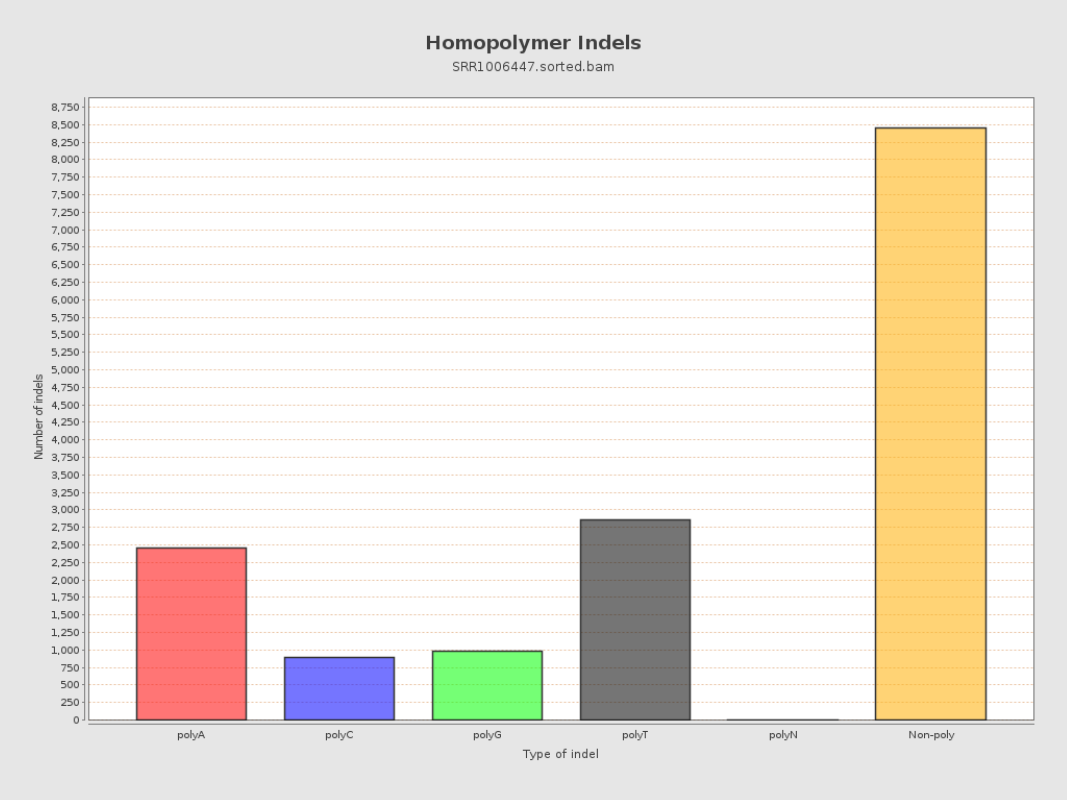
9. Results : Mapped Reads GC-content Distribution



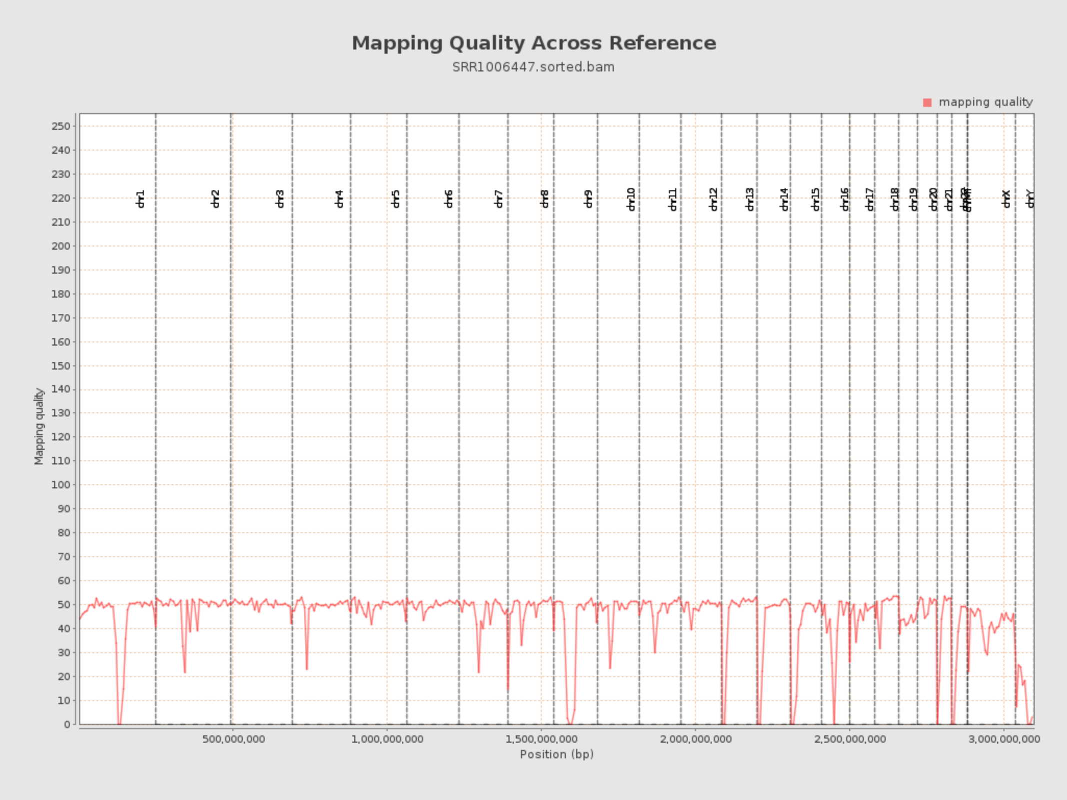
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram