Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:04:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006443.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_SRR1006443 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006443.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:04:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006443.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,496,869
Mapped reads	1,416,105 / 94.6%
Unmapped reads	80,764 / 5.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,664 / 0.31%
Read min/max/mean length	30 / 59 / 57.12
Duplicated reads (estimated)	25,610 / 1.71%
Duplication rate	1.26%
Clipped reads	183,202 / 12.24%

2.2. ACGT Content

Number/percentage of A's	22,583,757 / 28.6%
Number/percentage of C's	16,318,274 / 20.67%
Number/percentage of T's	23,016,341 / 29.15%
Number/percentage of G's	17,043,980 / 21.58%
Number/percentage of N's	1,724 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2489

2.4. Mapping Quality

Mean Mapping Quality	45.5

2.5. Mismatches and indels

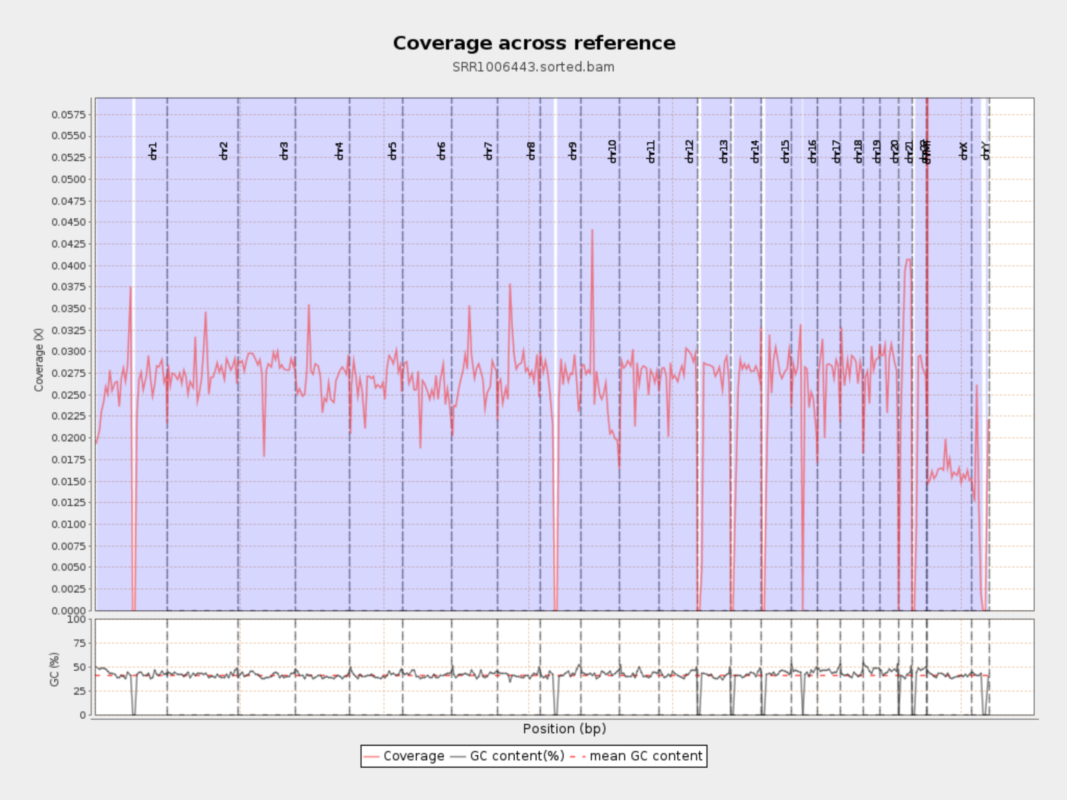
General error rate	0.42%
Mismatches	321,652
Insertions	4,877
Mapped reads with at least one insertion	0.34%
Deletions	15,047
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.01%

2.6. Chromosome stats

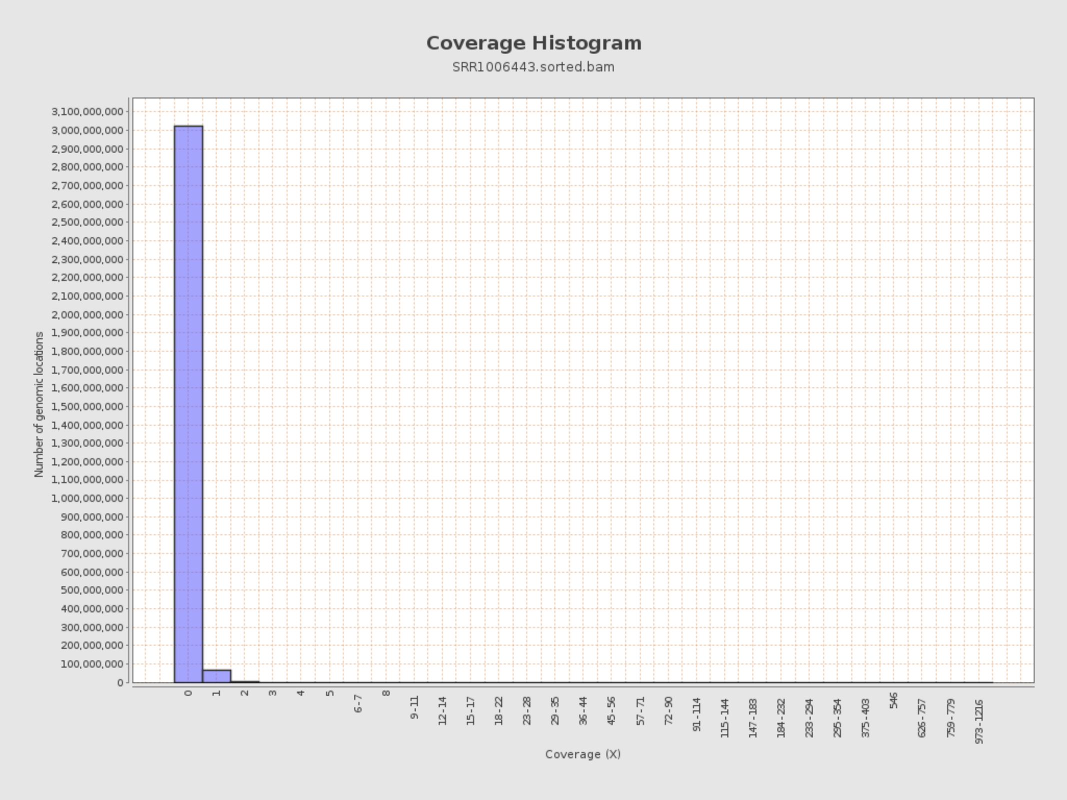
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6169105	0.0248	0.3105
chr2	243199373	6719701	0.0276	0.2072
chr3	198022430	5607210	0.0283	0.1771
chr4	191154276	5138352	0.0269	0.1804
chr5	180915260	4866991	0.0269	0.1729
chr6	171115067	4414948	0.0258	0.1746
chr7	159138663	4331659	0.0272	0.2274

chr8	146364022	4122499	0.0282	0.697
chr9	141213431	3382045	0.0239	0.1843
chr10	135534747	3465748	0.0256	0.2247
chr11	135006516	3707201	0.0275	0.1963
chr12	133851895	3706365	0.0277	0.1769
chr13	115169878	2684112	0.0233	0.1606
chr14	107349540	2486586	0.0232	0.1637
chr15	102531392	2416524	0.0236	0.1617
chr16	90354753	2192952	0.0243	0.1813
chr17	81195210	2232187	0.0275	0.1871
chr18	78077248	2218319	0.0284	0.2658
chr19	59128983	1632411	0.0276	0.2613
chr20	63025520	1783002	0.0283	0.1798
chr21	48129895	1530661	0.0318	0.2005
chr22	51304566	1002615	0.0195	0.1581
chrMT	16571	28500	1.7199	1.5217
chrX	155270560	2495650	0.0161	0.1394
chrY	59373566	653650	0.011	0.1647

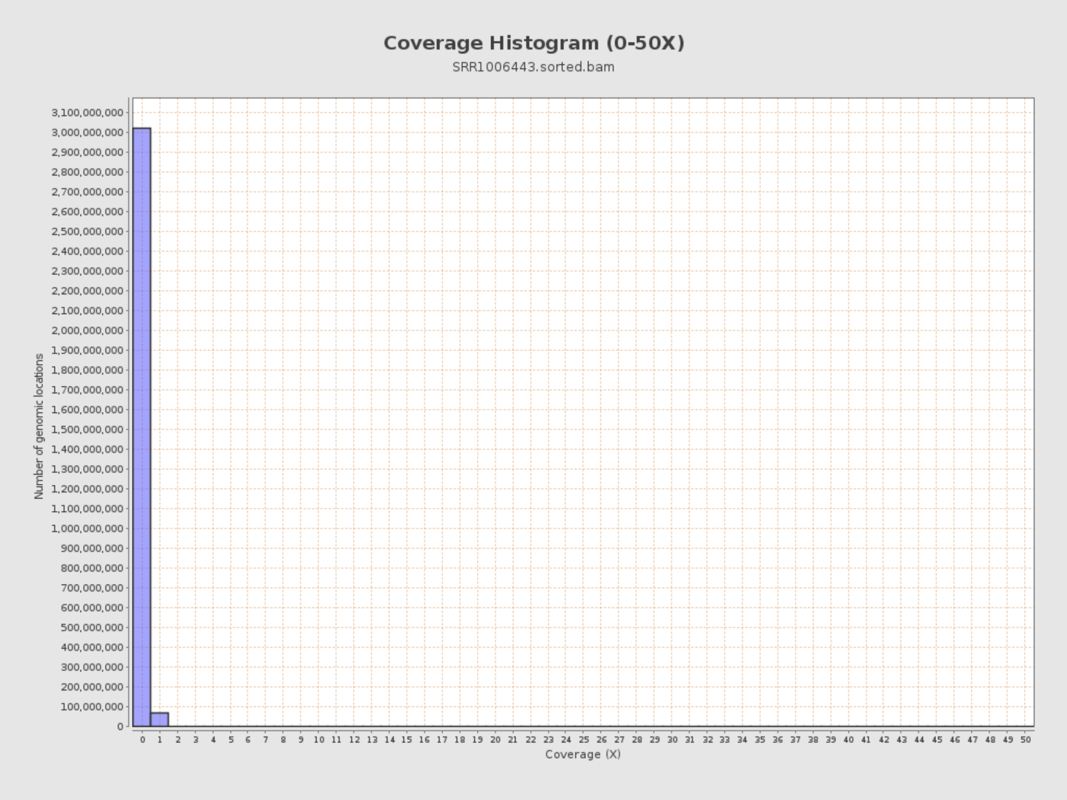
3. Results : Coverage across reference



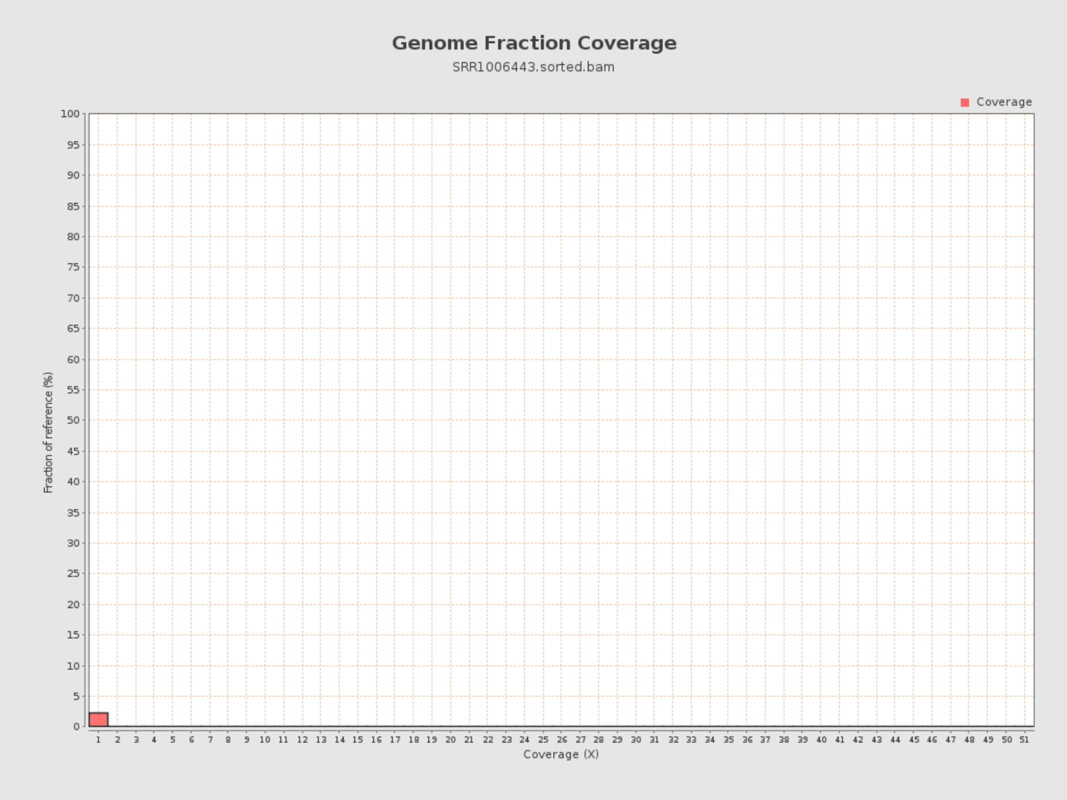
4. Results : Coverage Histogram



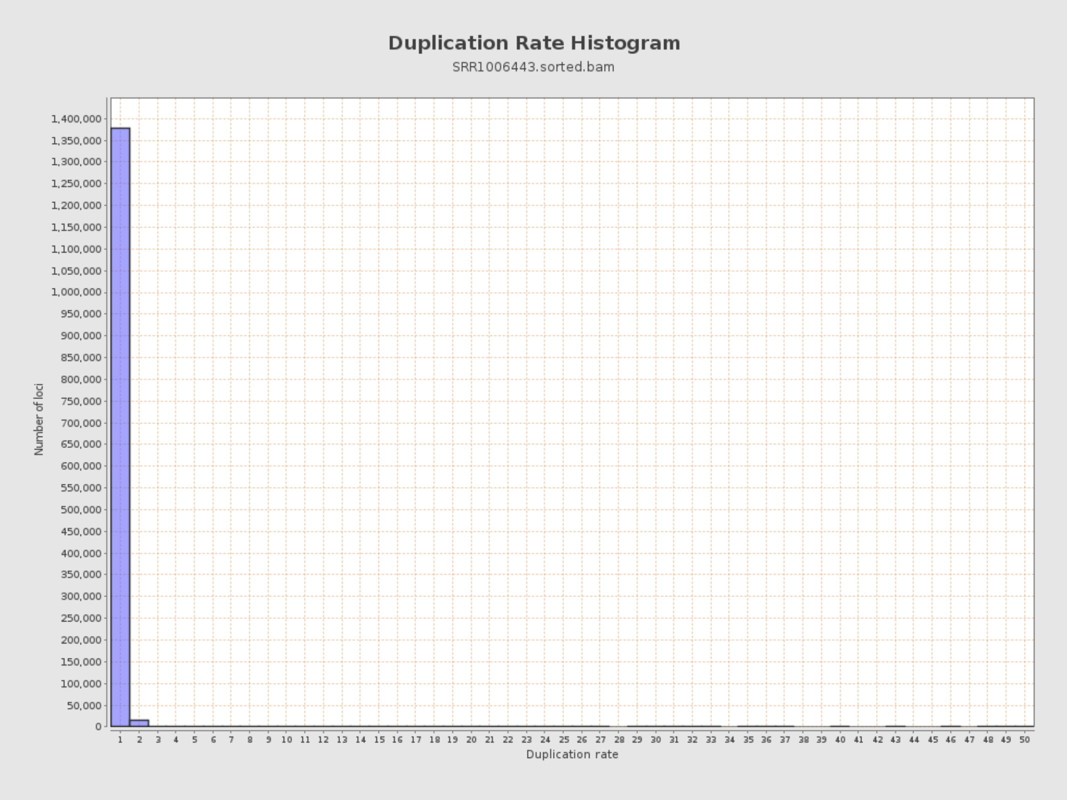
5. Results : Coverage Histogram (0-50X)



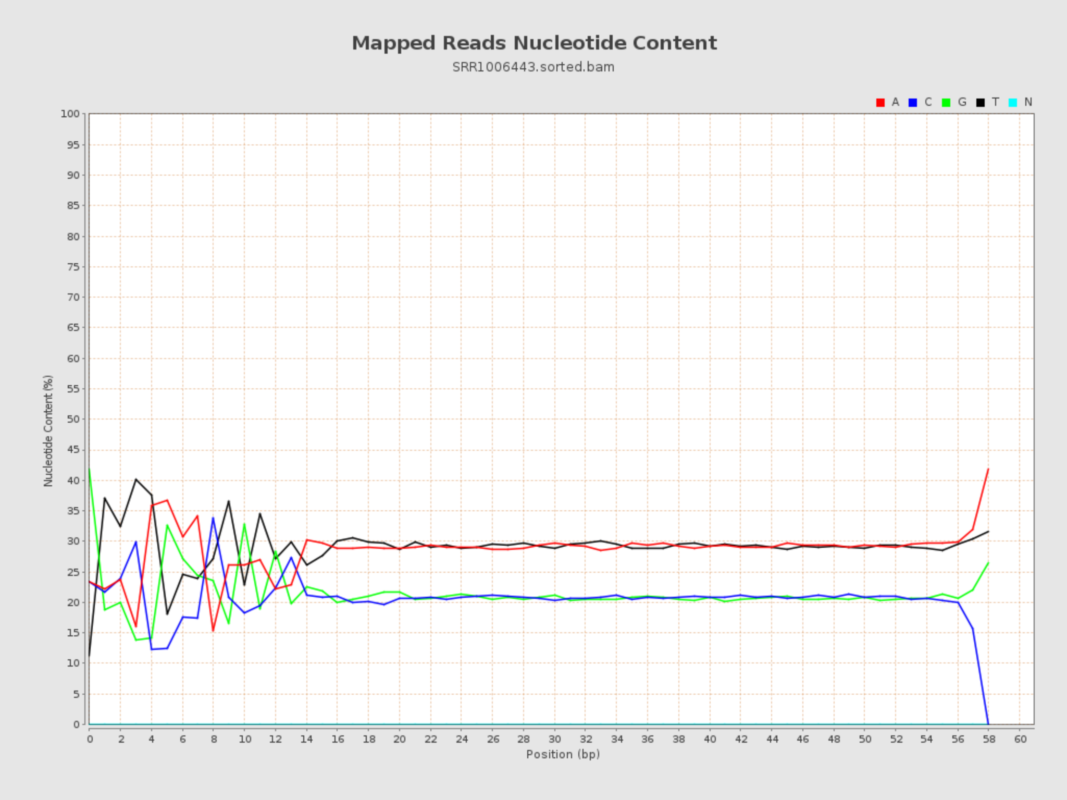
6. Results : Genome Fraction Coverage



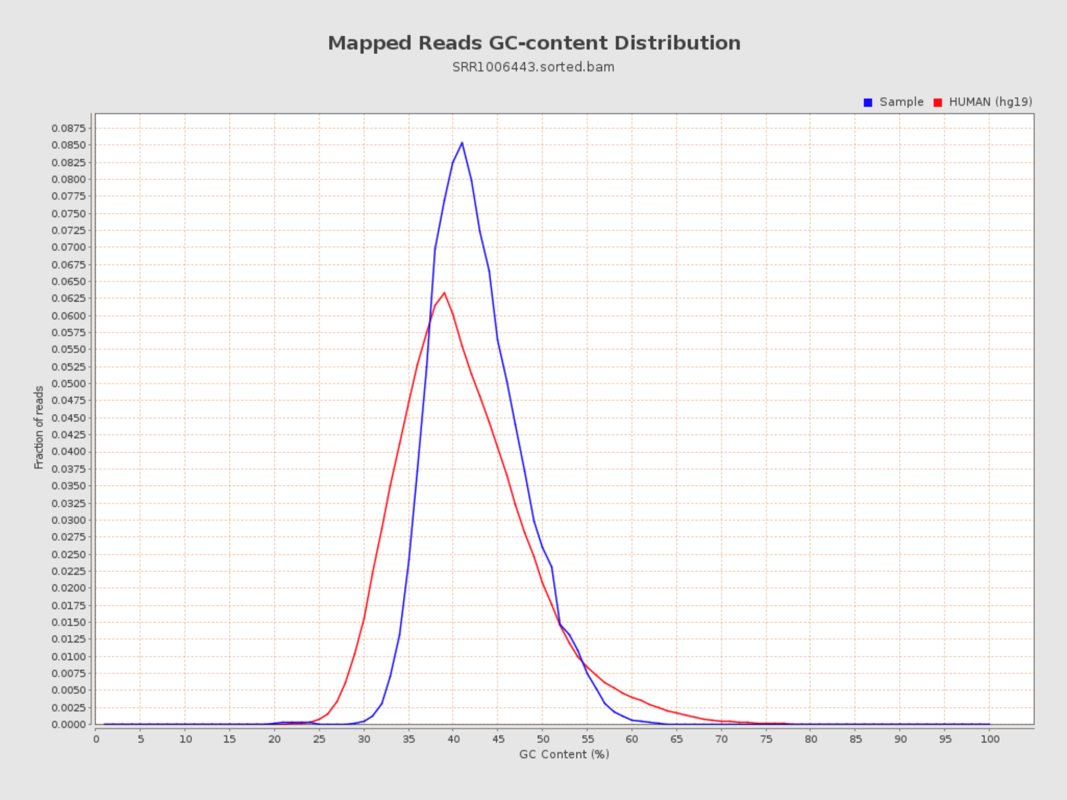
7. Results : Duplication Rate Histogram



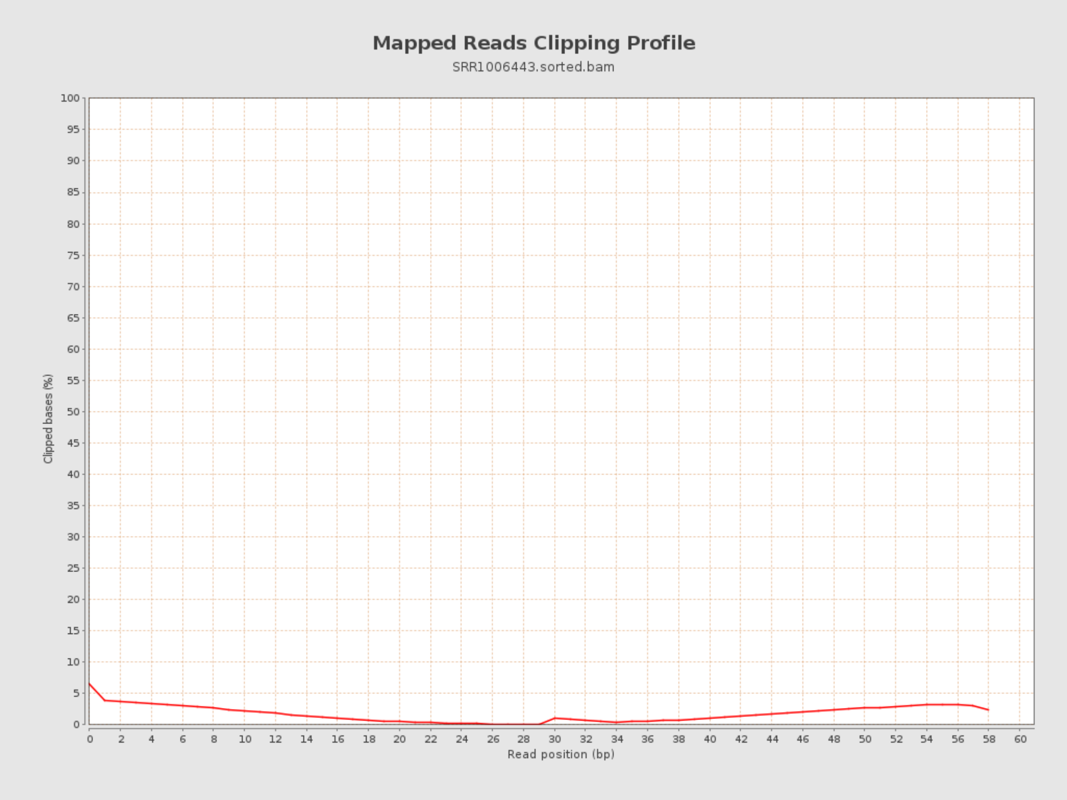
8. Results : Mapped Reads Nucleotide Content



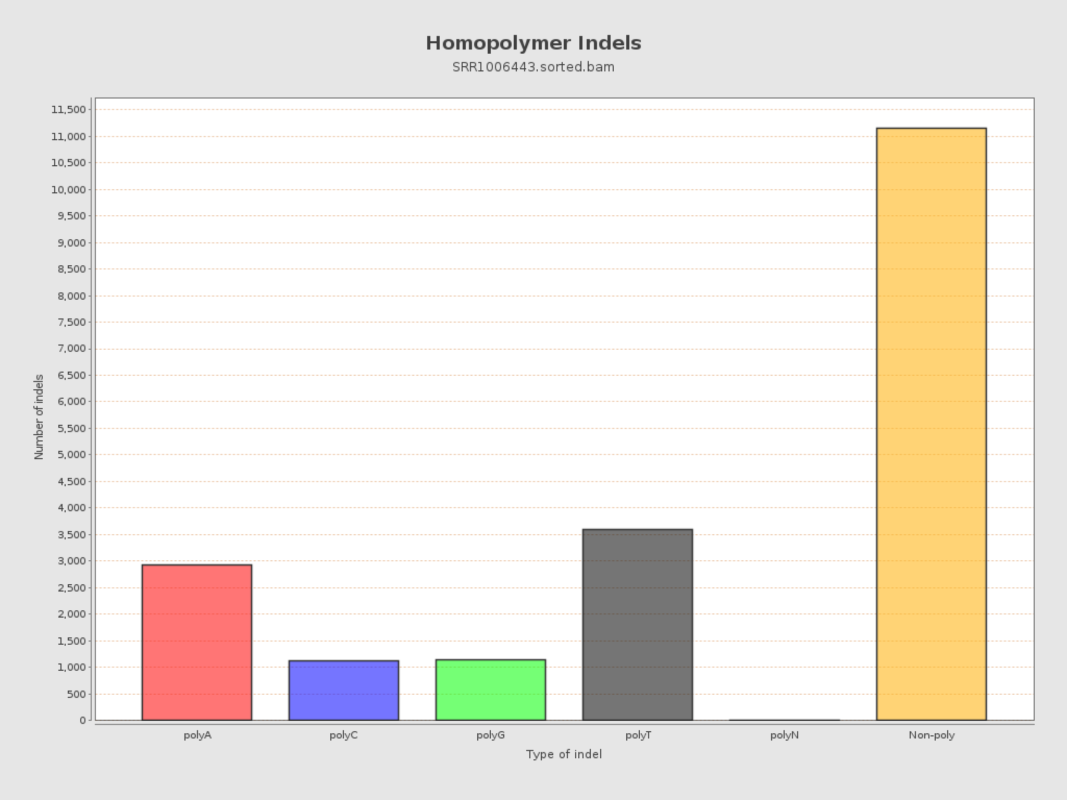
9. Results : Mapped Reads GC-content Distribution



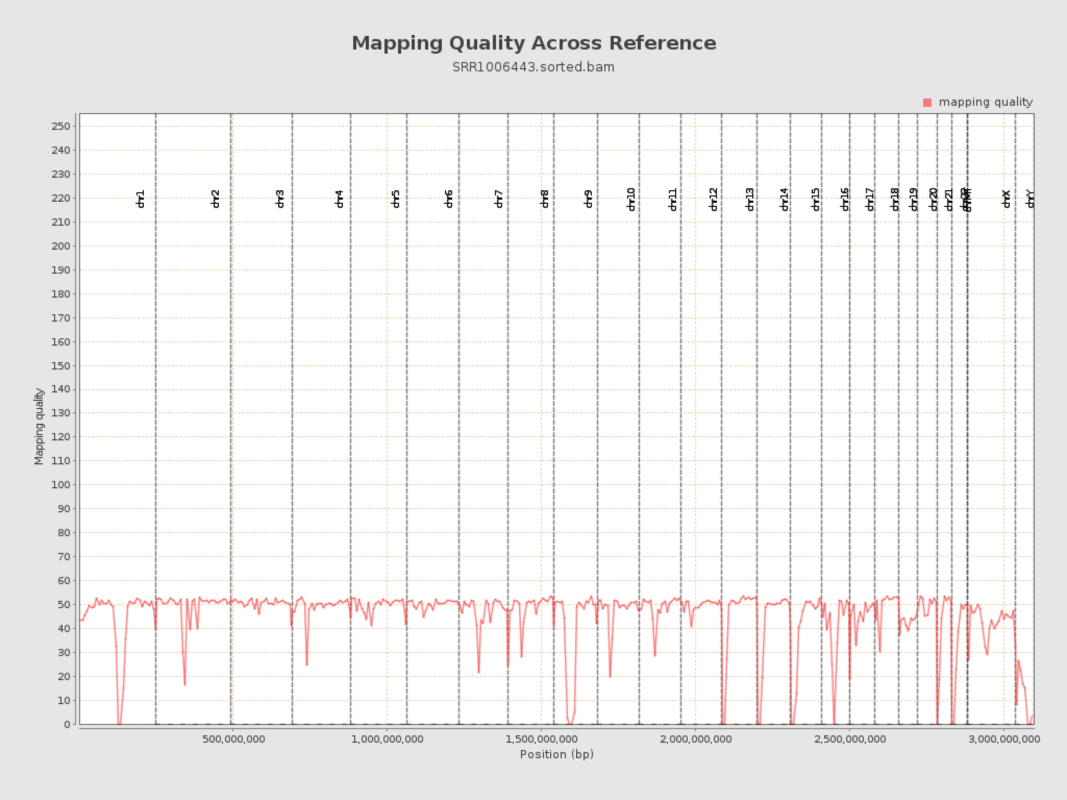
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram