Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:15:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006448.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_SRR1006448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006448.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:15:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,115,082
Mapped reads	1,995,361 / 94.34%
Unmapped reads	119,721 / 5.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,872 / 0.32%
Read min/max/mean length	30 / 59 / 57.24
Duplicated reads (estimated)	36,579 / 1.73%
Duplication rate	1.25%
Clipped reads	271,932 / 12.86%

2.2. ACGT Content

Number/percentage of A's	31,637,900 / 28.42%
Number/percentage of C's	23,331,356 / 20.96%
Number/percentage of T's	32,054,701 / 28.79%
Number/percentage of G's	24,305,673 / 21.83%
Number/percentage of N's	2,338 / 0%
GC Percentage	42.79%

2.3. Coverage

Mean	0.036

Standard Deviation	0.2897

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

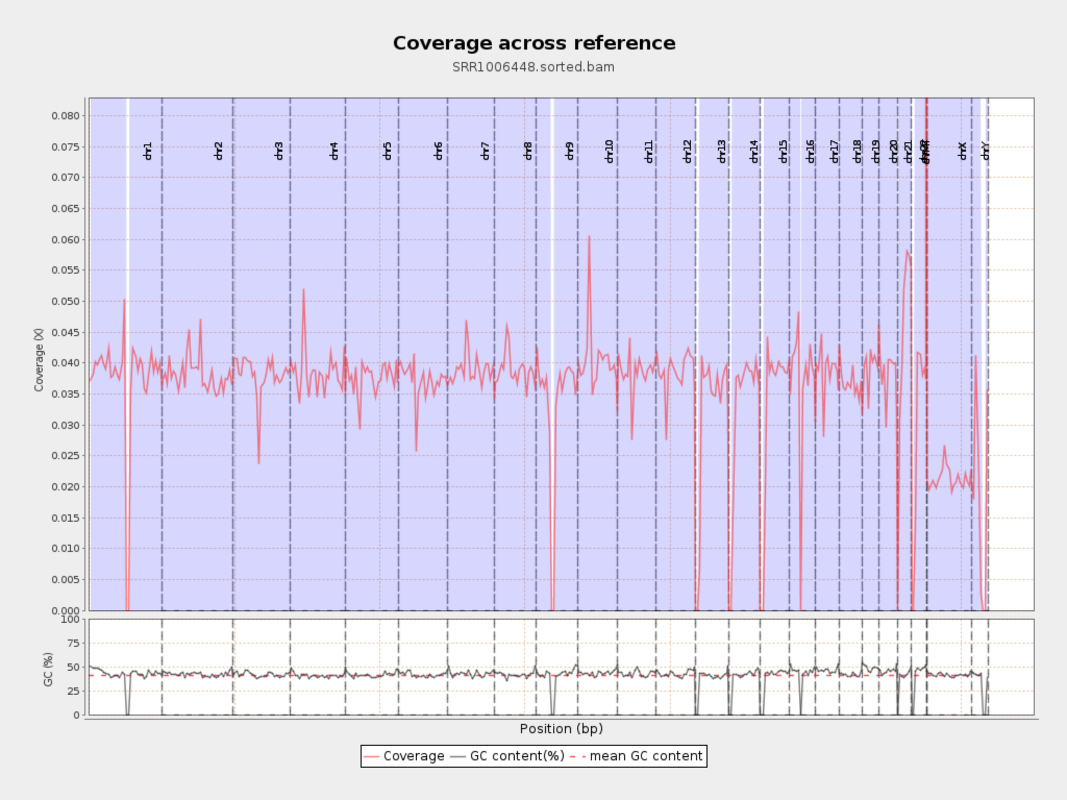
General error rate	0.42%
Mismatches	453,343
Insertions	7,167
Mapped reads with at least one insertion	0.36%
Deletions	19,444
Mapped reads with at least one deletion	0.97%
Homopolymer indels	45.67%

2.6. Chromosome stats

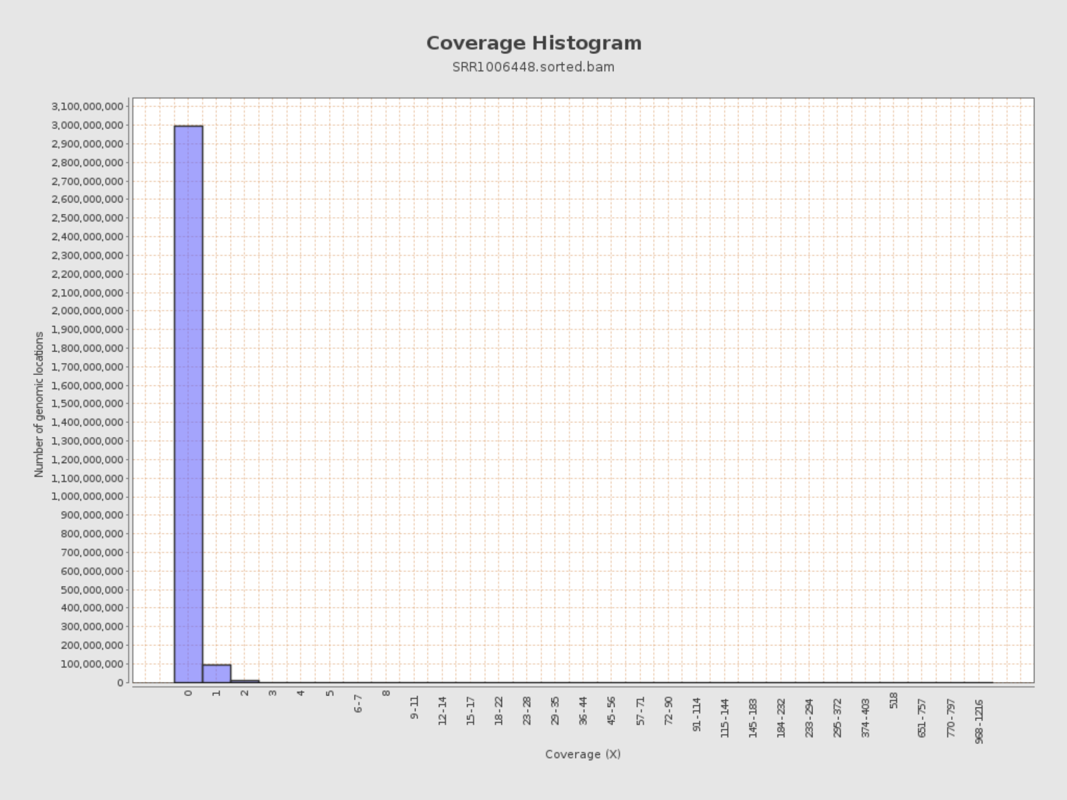
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9239025	0.0371	0.3881
chr2	243199373	9294277	0.0382	0.2545
chr3	198022430	7535332	0.0381	0.2091
chr4	191154276	7344531	0.0384	0.2251
chr5	180915260	6807406	0.0376	0.2079
chr6	171115067	6366403	0.0372	0.2177
chr7	159138663	6215867	0.0391	0.2879

chr8	146364022	5686086	0.0388	0.7121
chr9	141213431	4628974	0.0328	0.2232
chr10	135534747	5508883	0.0406	0.2944
chr11	135006516	5193743	0.0385	0.2379
chr12	133851895	5185464	0.0387	0.213
chr13	115169878	3595735	0.0312	0.1889
chr14	107349540	3410587	0.0318	0.2005
chr15	102531392	3325878	0.0324	0.1935
chr16	90354753	3328538	0.0368	0.2356
chr17	81195210	3139054	0.0387	0.2312
chr18	78077248	2873105	0.0368	0.3314
chr19	59128983	2328160	0.0394	0.324
chr20	63025520	2403578	0.0381	0.213
chr21	48129895	2106931	0.0438	0.2465
chr22	51304566	1418190	0.0276	0.1946
chrMT	16571	86642	5.2285	3.4582
chrX	155270560	3318347	0.0214	0.1626
chrY	59373566	1023463	0.0172	0.237

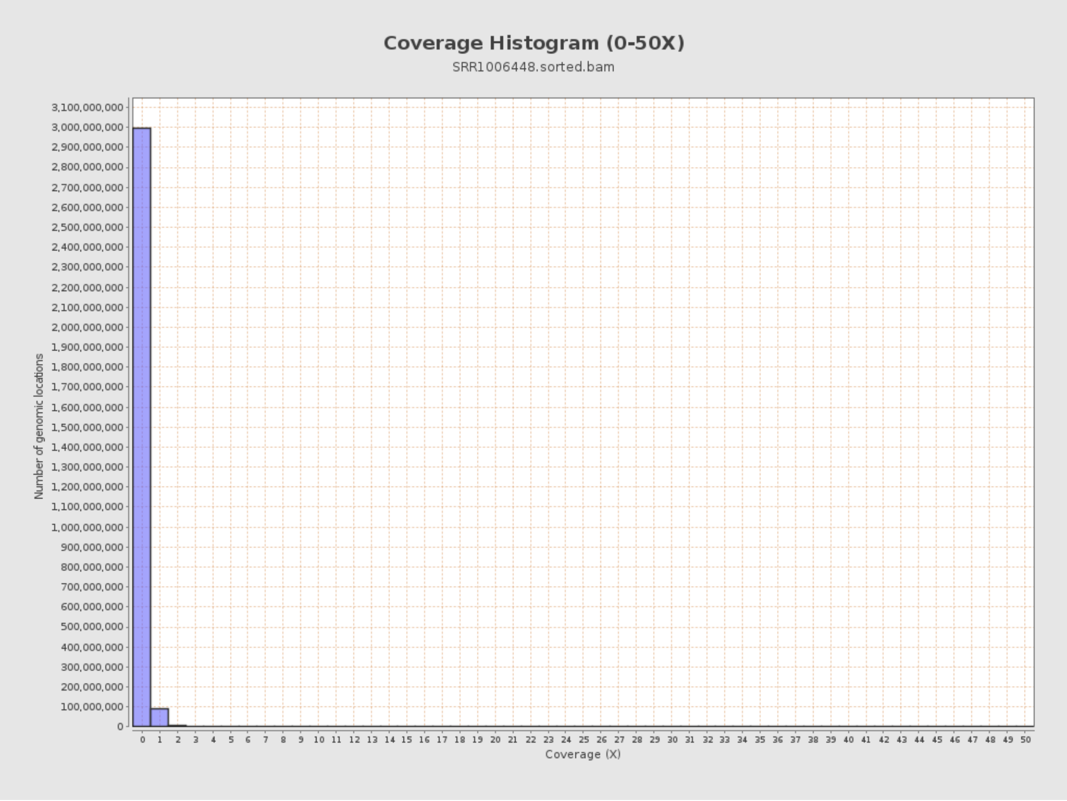
3. Results : Coverage across reference



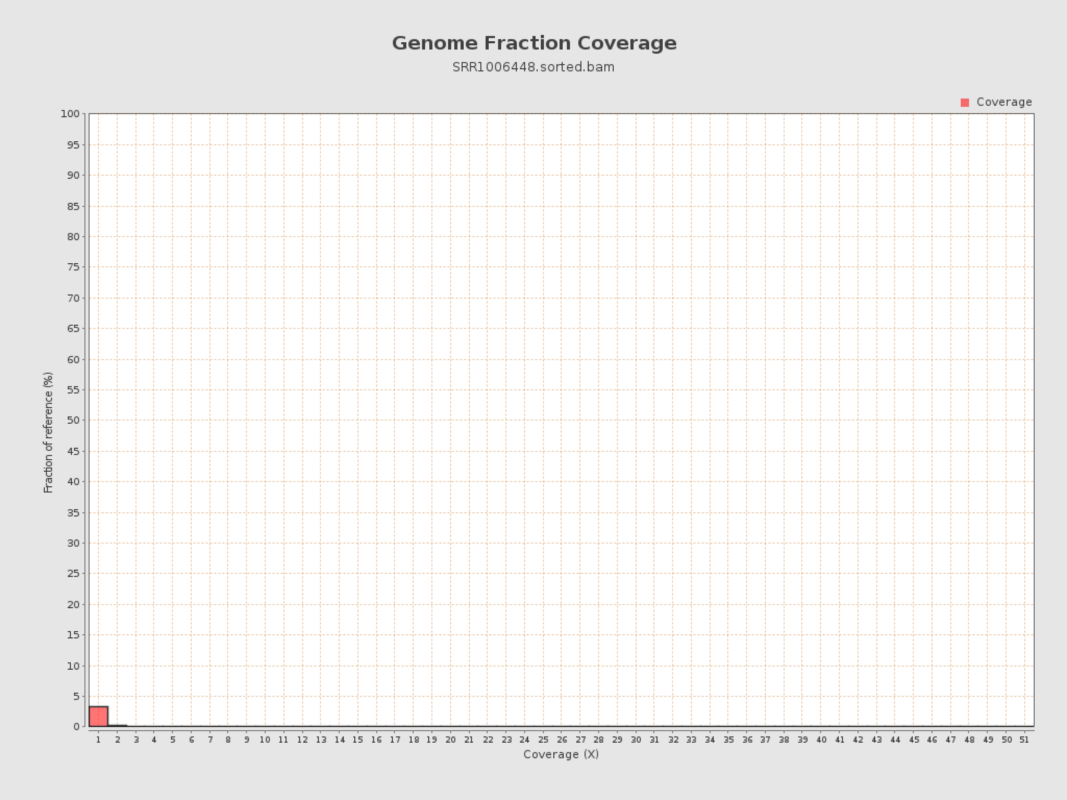
4. Results : Coverage Histogram



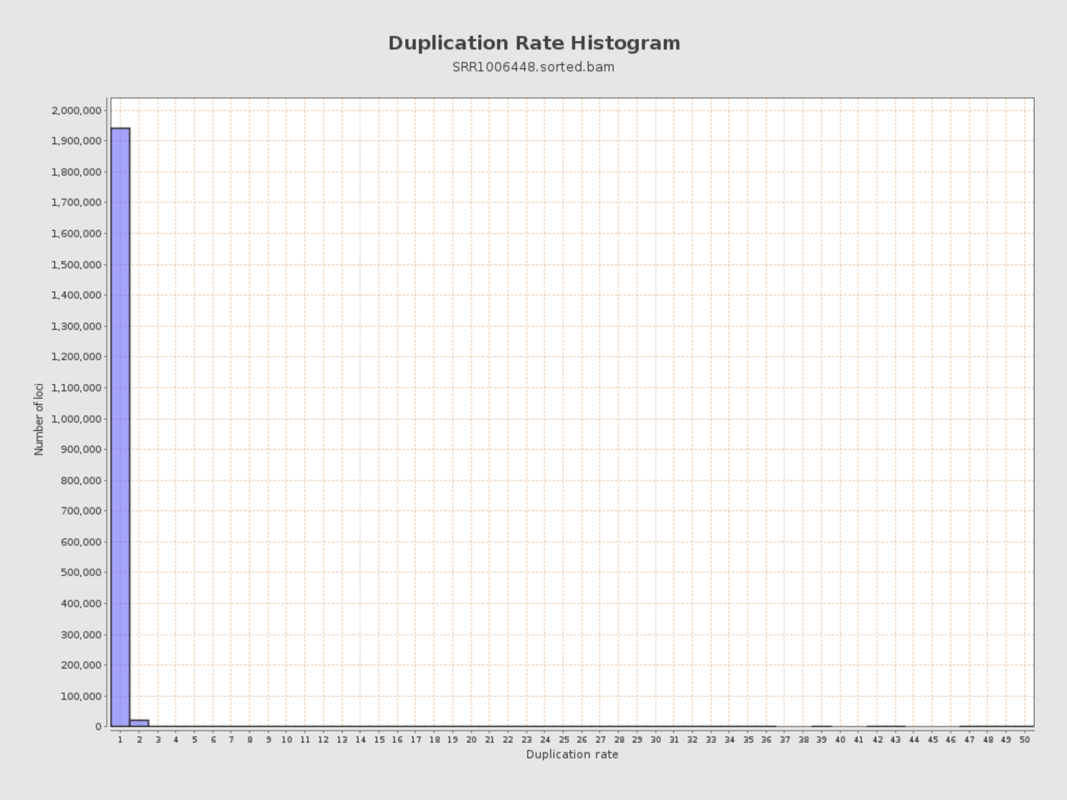
5. Results : Coverage Histogram (0-50X)



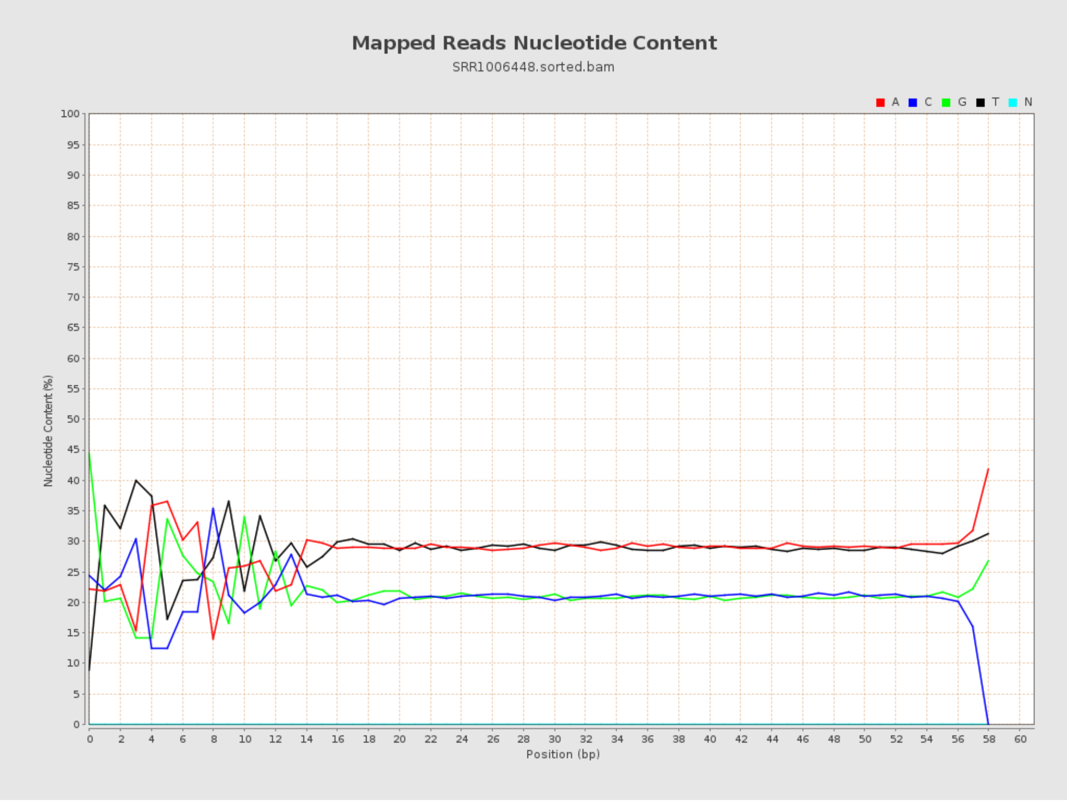
6. Results : Genome Fraction Coverage



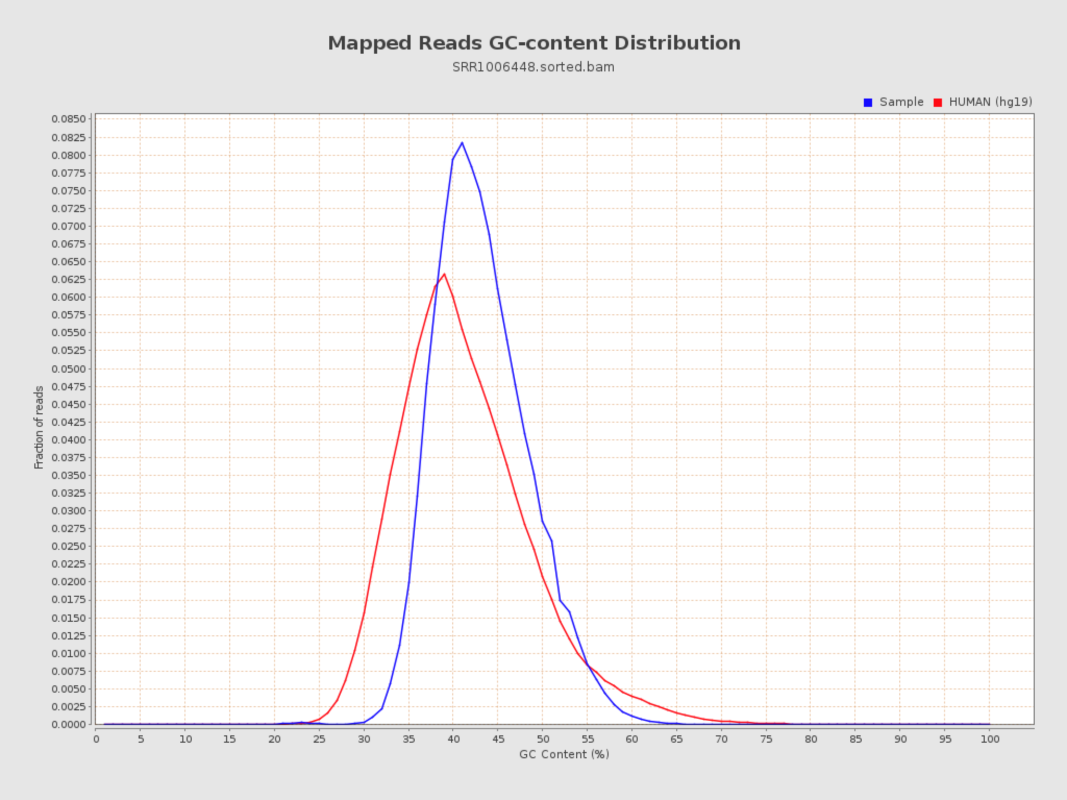
7. Results : Duplication Rate Histogram



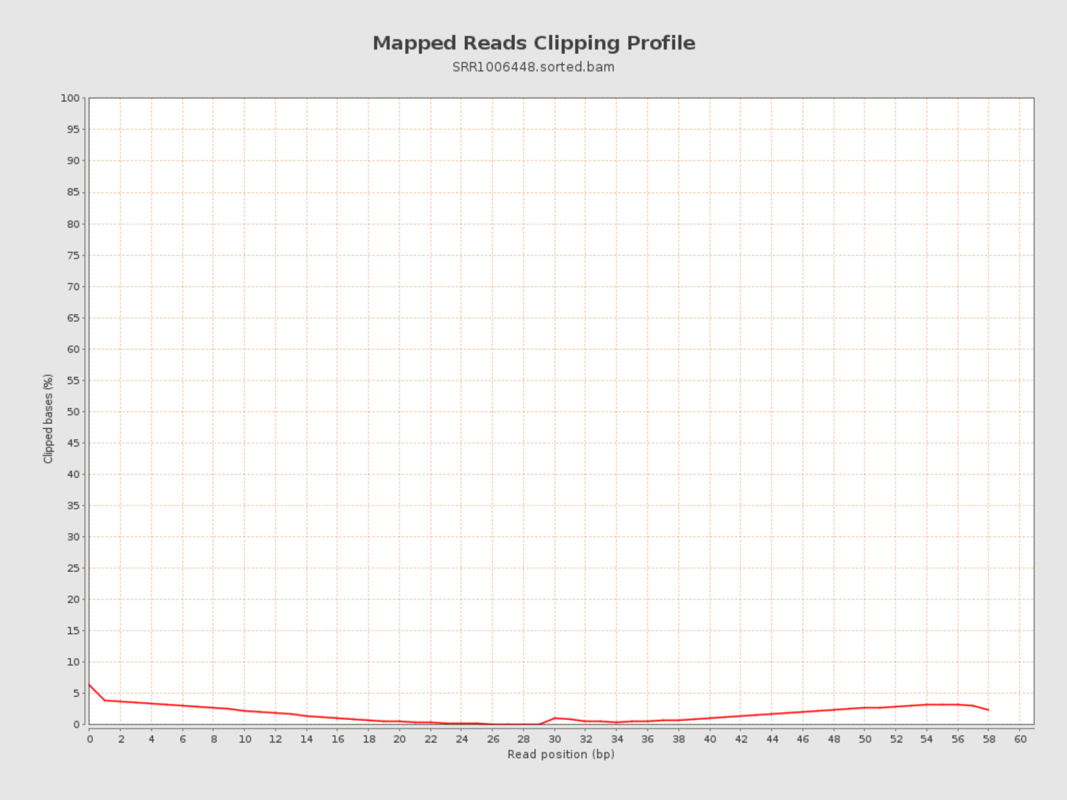
8. Results : Mapped Reads Nucleotide Content



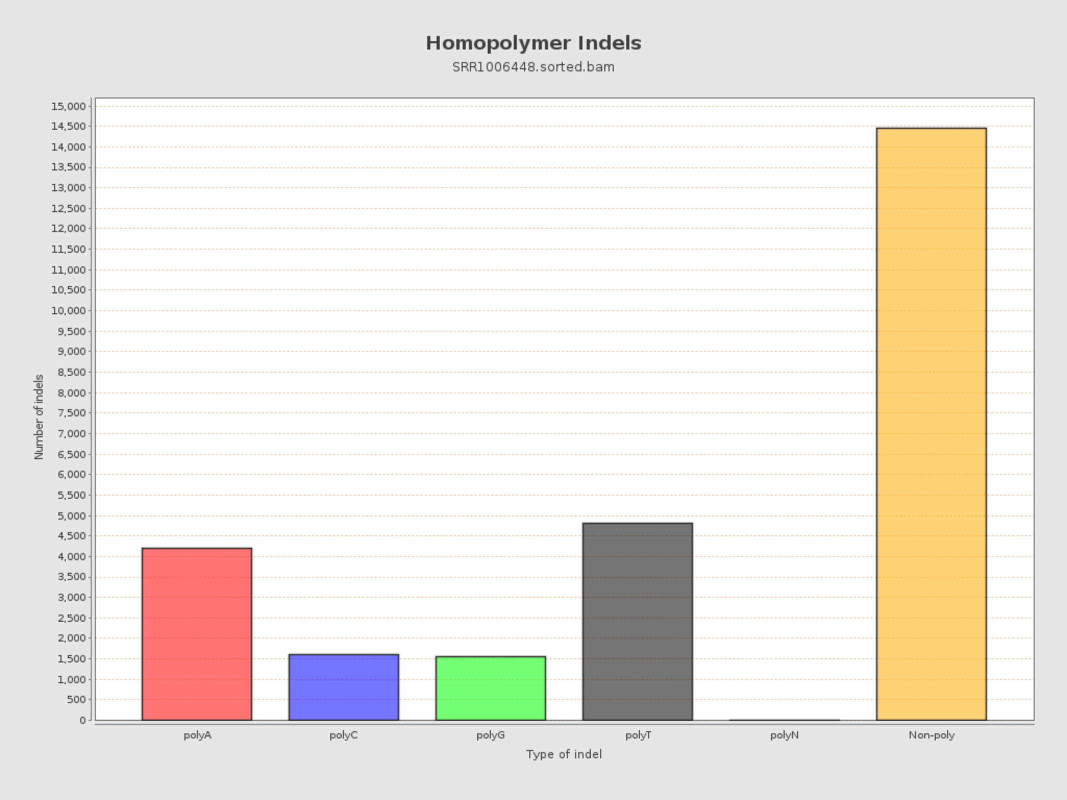
9. Results : Mapped Reads GC-content Distribution



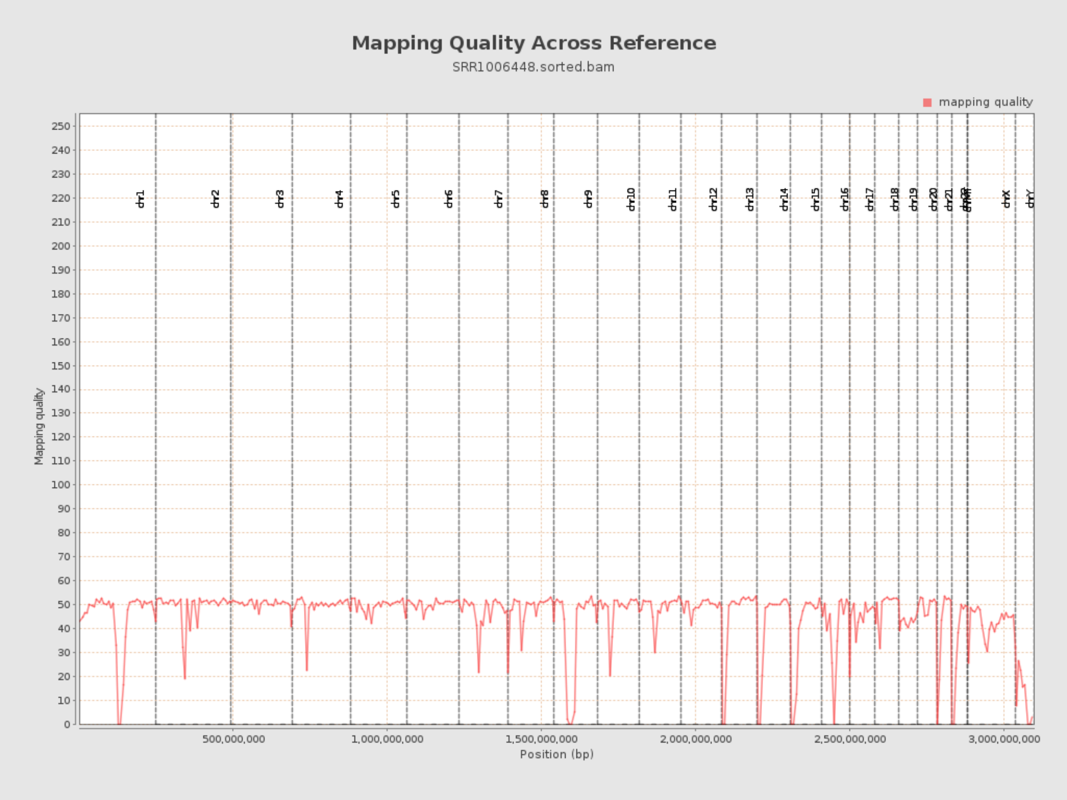
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram