Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:39:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006433.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_SRR1006433 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006433.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:39:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006433.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,772,723
Mapped reads	3,040,739 / 80.6%
Unmapped reads	731,984 / 19.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,760 / 0.21%
Read min/max/mean length	30 / 59 / 59.06
Duplicated reads (estimated)	543,548 / 14.41%
Duplication rate	17.14%
Clipped reads	865,977 / 22.95%

2.2. ACGT Content

Number/percentage of A's	47,139,611 / 27.98%
Number/percentage of C's	36,026,838 / 21.39%
Number/percentage of T's	48,994,736 / 29.09%
Number/percentage of G's	36,280,549 / 21.54%
Number/percentage of N's	7,581 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.6768

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

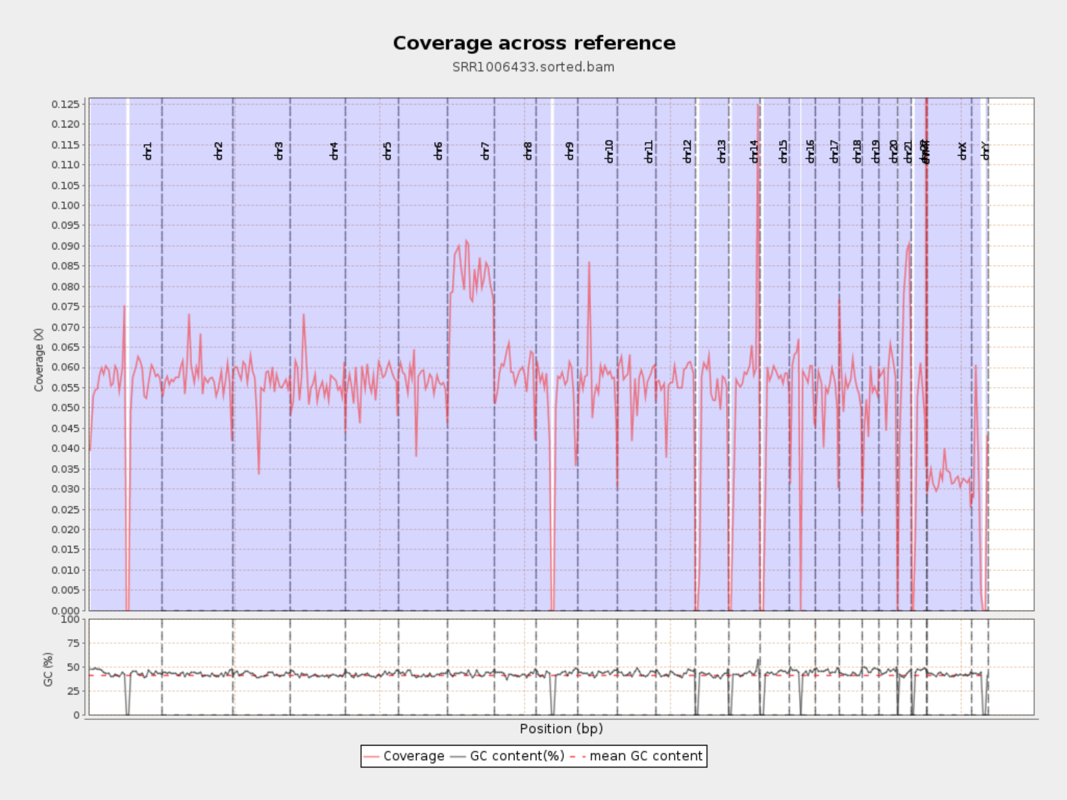
General error rate	0.44%
Mismatches	715,337
Insertions	12,694
Mapped reads with at least one insertion	0.42%
Deletions	31,780
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.33%

2.6. Chromosome stats

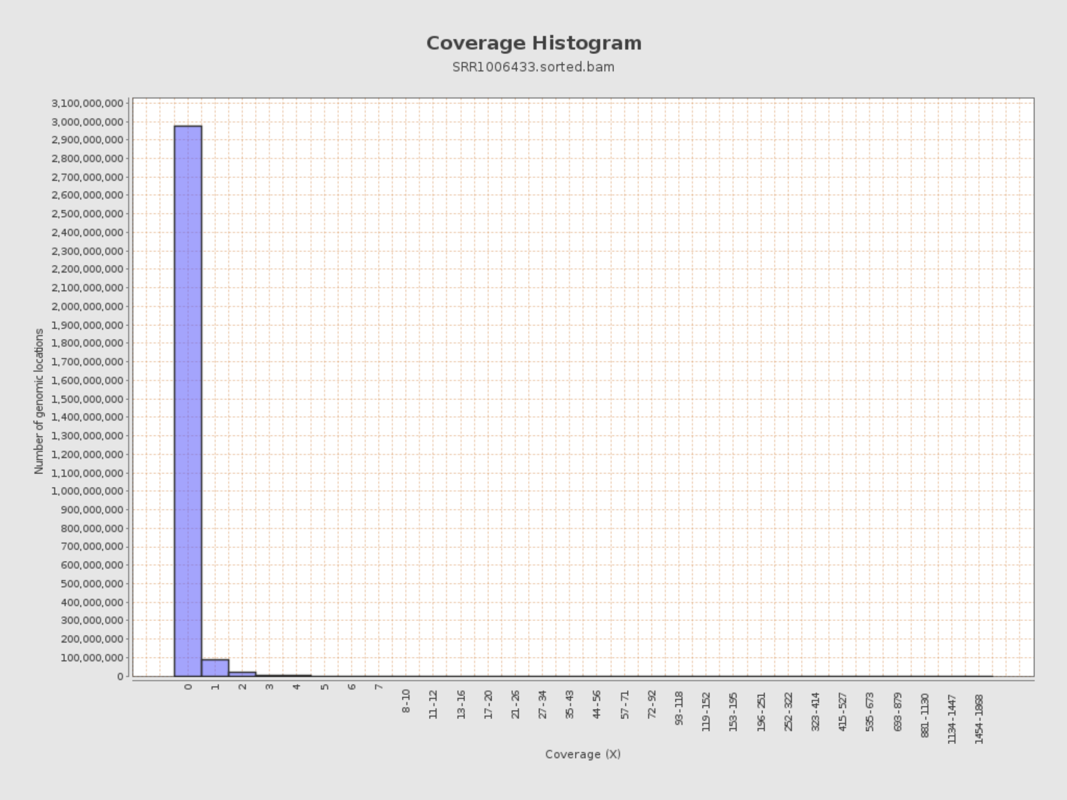
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13433920	0.0539	0.5208
chr2	243199373	14022953	0.0577	0.3906
chr3	198022430	11170054	0.0564	0.3119
chr4	191154276	10743021	0.0562	0.3291
chr5	180915260	10222786	0.0565	0.3122
chr6	171115067	9672829	0.0565	0.4089
chr7	159138663	13115177	0.0824	0.5497

chr8	146364022	8554423	0.0584	0.9635
chr9	141213431	6898925	0.0489	0.3633
chr10	135534747	7837755	0.0578	0.4187
chr11	135006516	7621211	0.0565	0.3555
chr12	133851895	7474664	0.0558	0.3138
chr13	115169878	5382706	0.0467	0.2854
chr14	107349540	5737163	0.0534	2.7999
chr15	102531392	4879681	0.0476	0.2885
chr16	90354753	4772735	0.0528	0.3368
chr17	81195210	4265641	0.0525	0.3342
chr18	78077248	4438649	0.0568	0.4786
chr19	59128983	2998906	0.0507	0.4784
chr20	63025520	3560653	0.0565	0.6172
chr21	48129895	3067492	0.0637	0.3633
chr22	51304566	1886582	0.0368	0.3634
chrMT	16571	253098	15.2736	13.9739
chrX	155270560	5034967	0.0324	0.2474
chrY	59373566	1454425	0.0245	0.3264

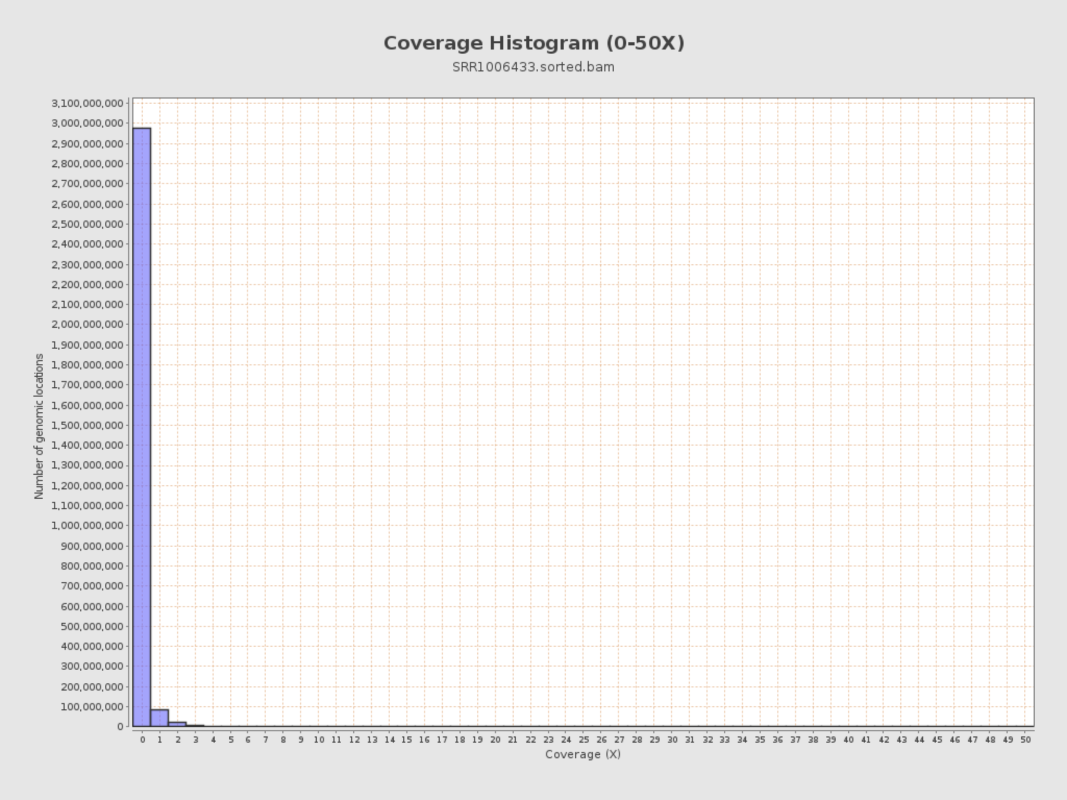
3. Results : Coverage across reference



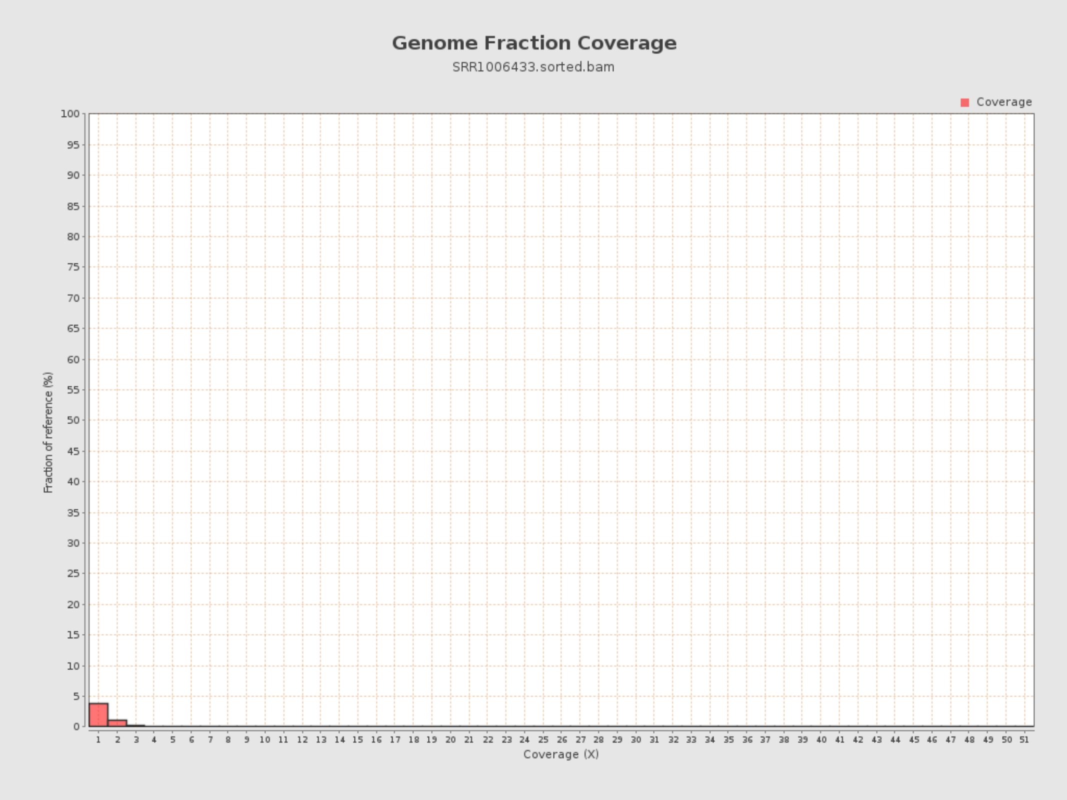
4. Results : Coverage Histogram



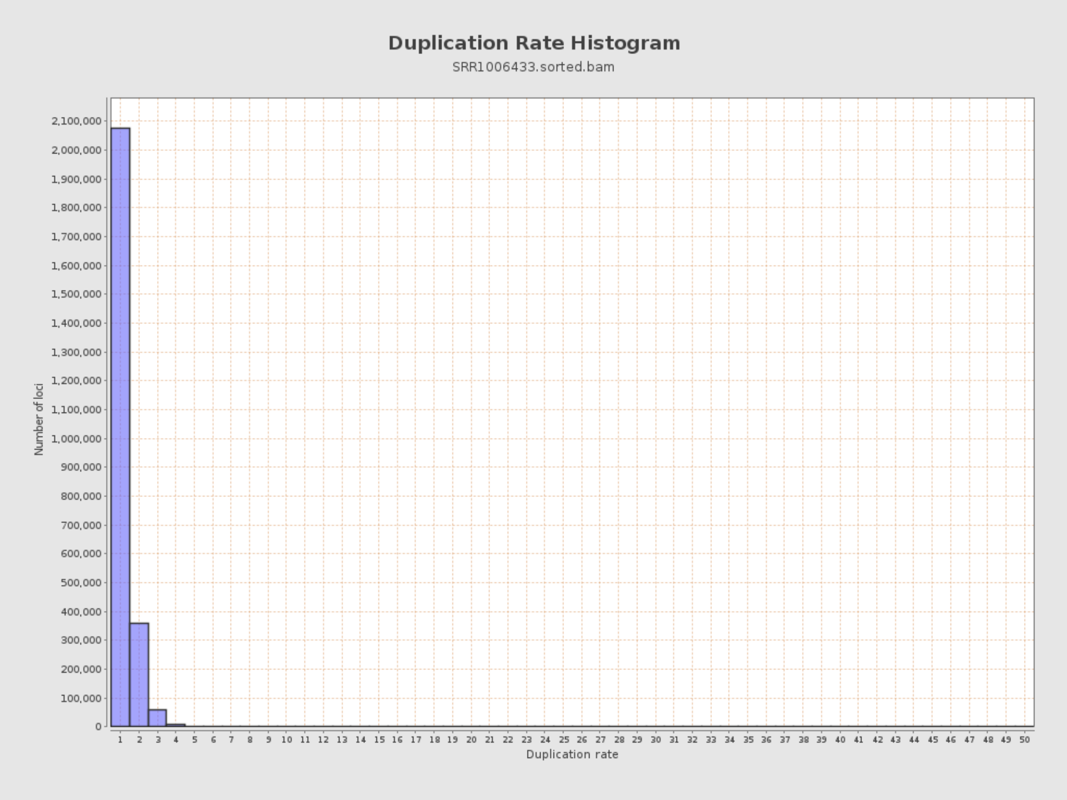
5. Results : Coverage Histogram (0-50X)



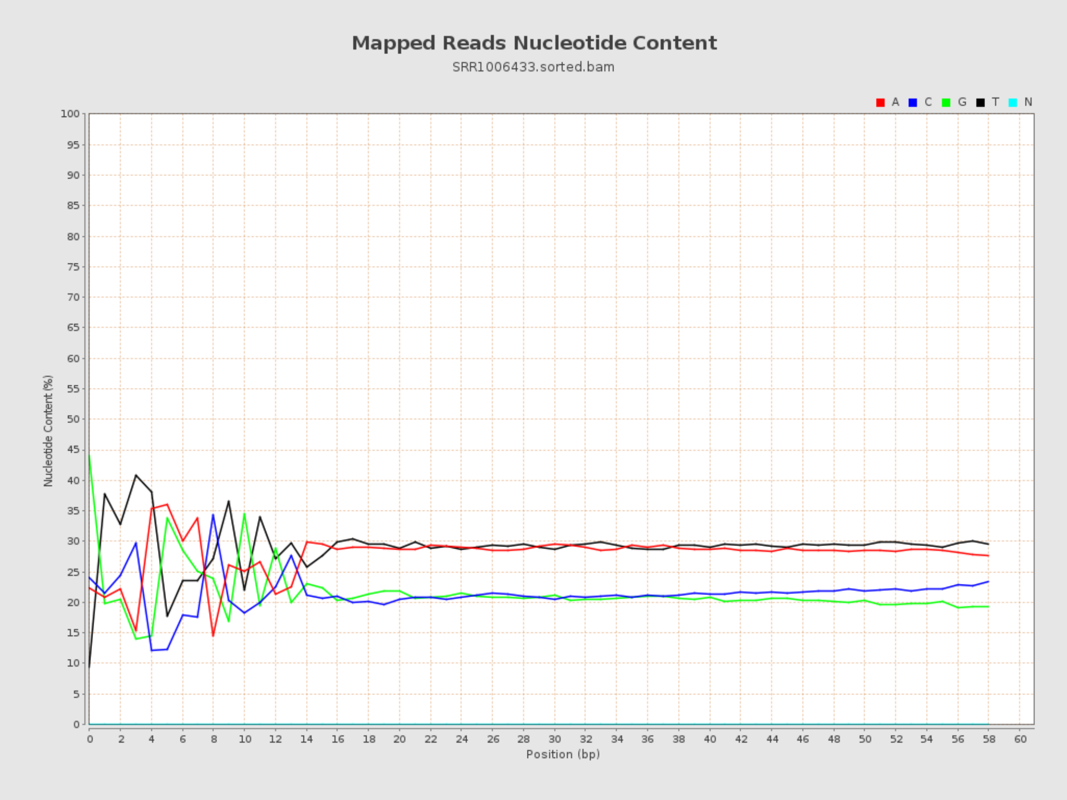
6. Results : Genome Fraction Coverage



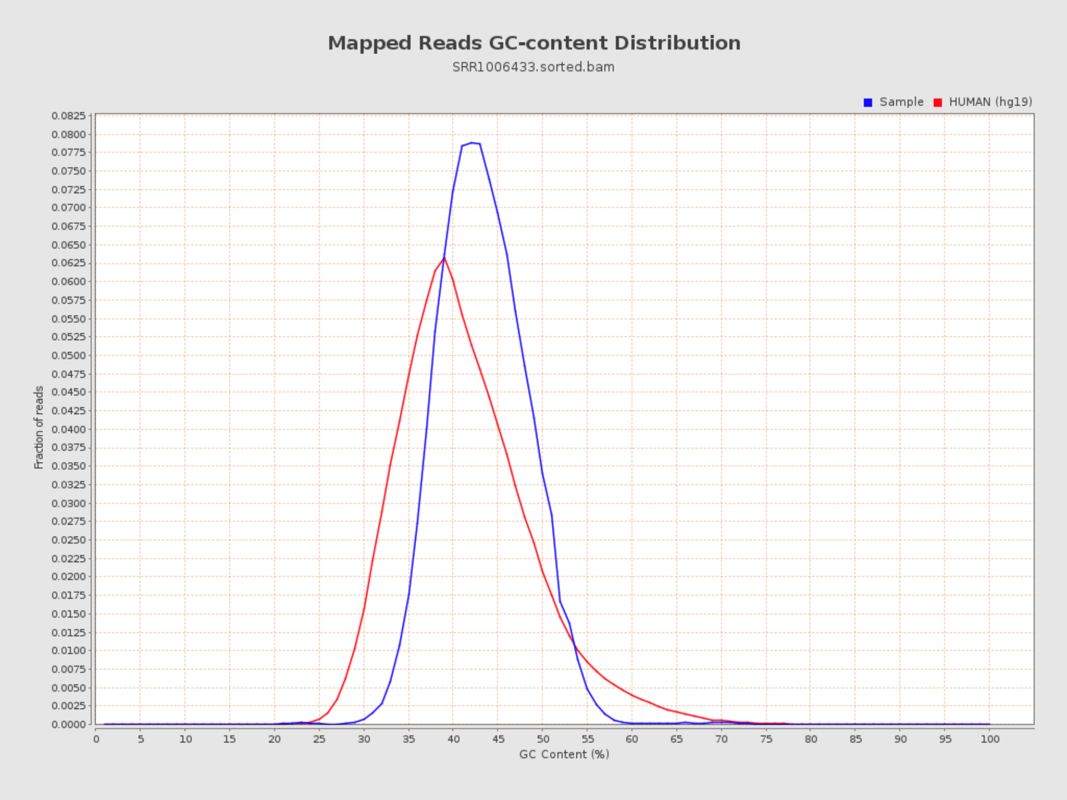
7. Results : Duplication Rate Histogram



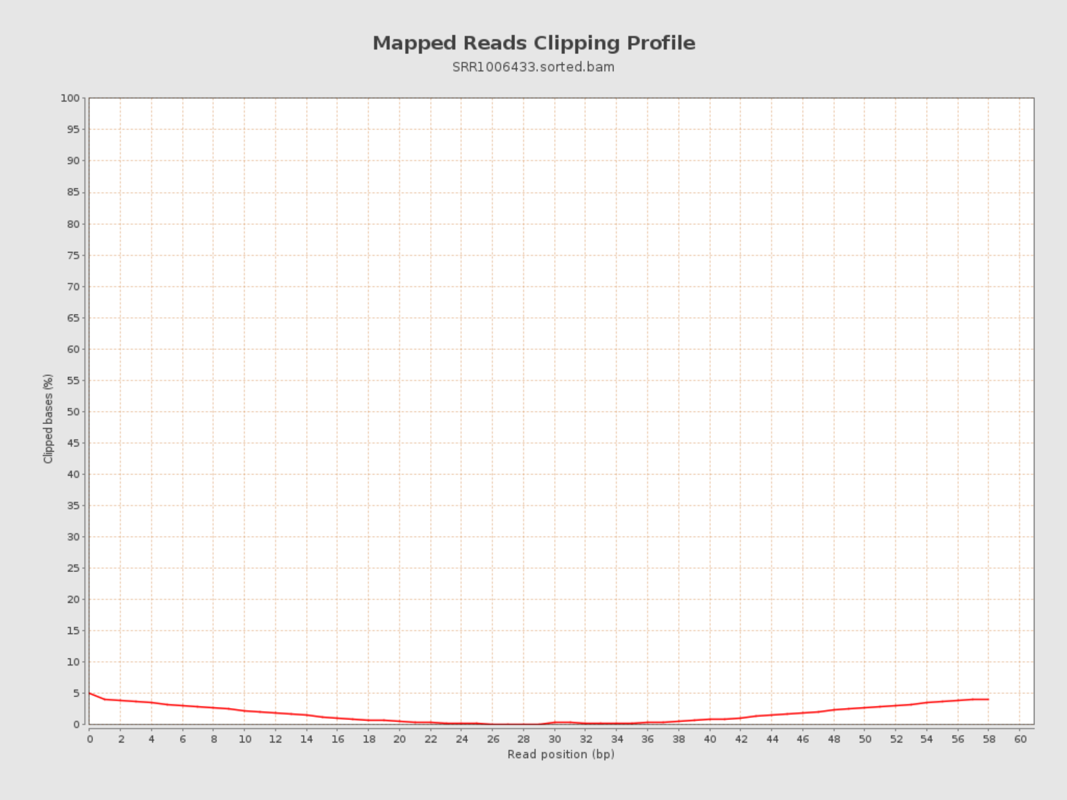
8. Results : Mapped Reads Nucleotide Content



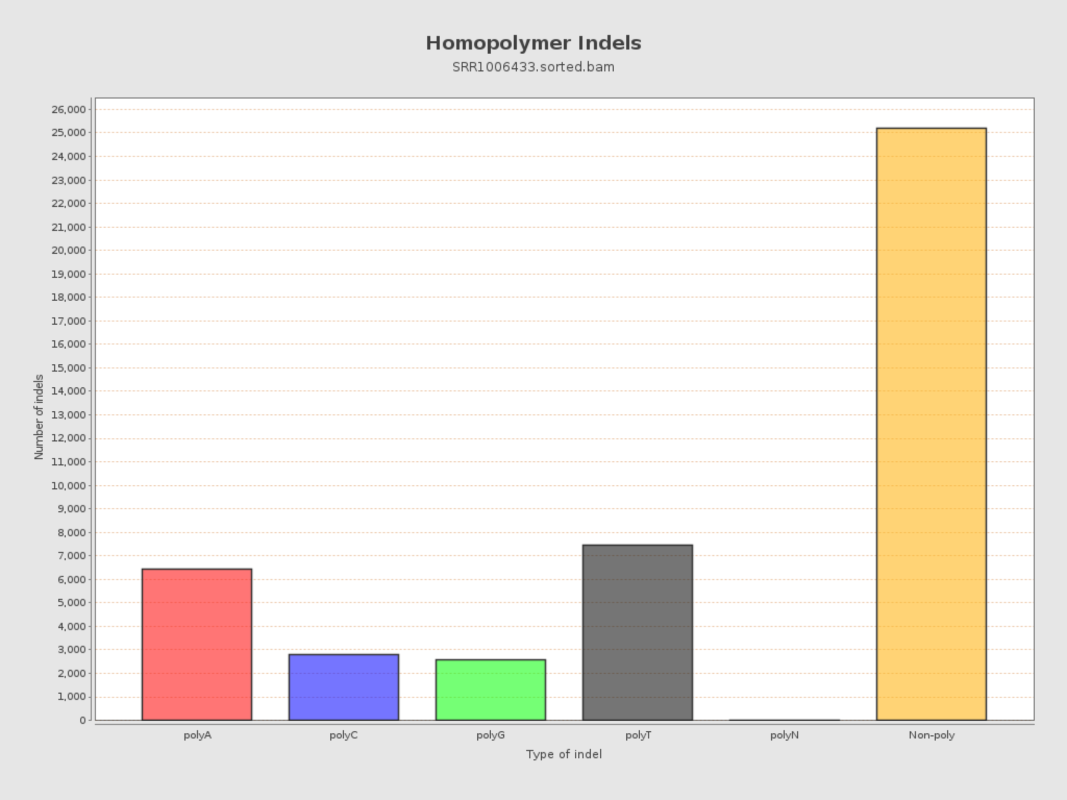
9. Results : Mapped Reads GC-content Distribution



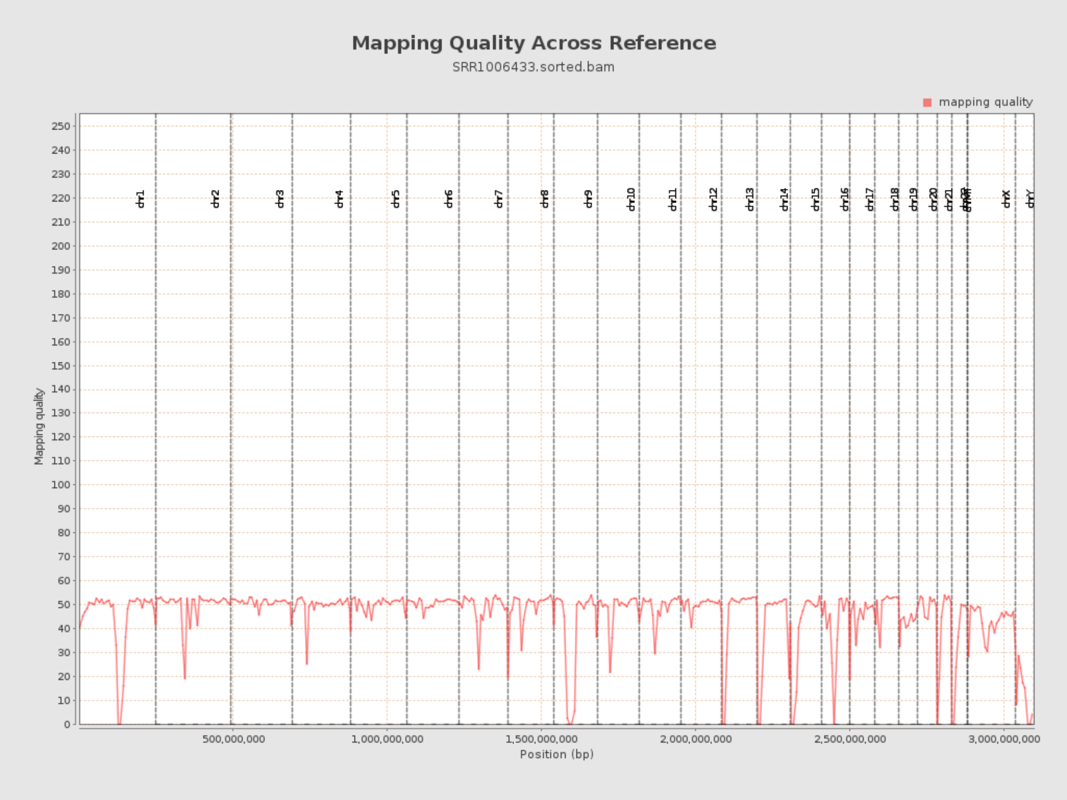
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram