Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 14:55:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038448.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_SRR5038448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038448_1.fastq.gz SRR5038448_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 14:55:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,913,608
Mapped reads	16,972,784 / 89.74%
Unmapped reads	1,940,824 / 10.26%
Mapped paired reads	16,972,784 / 89.74%
Mapped reads, first in pair	8,621,333 / 45.58%
Mapped reads, second in pair	8,351,451 / 44.16%
Mapped reads, both in pair	16,625,526 / 87.9%
Mapped reads, singletons	347,258 / 1.84%
Secondary alignments	0
Supplementary alignments	324,952 / 1.72%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	3,433,612 / 18.15%
Duplication rate	13.35%
Clipped reads	8,239,334 / 43.56%

2.2. ACGT Content

Number/percentage of A's	652,313,315 / 28.7%
Number/percentage of C's	449,854,283 / 19.79%
Number/percentage of T's	665,879,006 / 29.3%
Number/percentage of G's	504,428,604 / 22.2%
Number/percentage of N's	173,543 / 0.01%

GC Percentage	41.99%

2.3. Coverage

Mean	0.7347
Standard Deviation	11.4721

2.4. Mapping Quality

Mean Mapping Quality	53.28

2.5. Insert size

Mean	97,255.53
Standard Deviation	2,957,086.62
P25/Median/P75	199 / 252 / 320

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	31,706,709
Insertions	461,254
Mapped reads with at least one insertion	2.54%
Deletions	841,733
Mapped reads with at least one deletion	4.74%
Homopolymer indels	45.59%

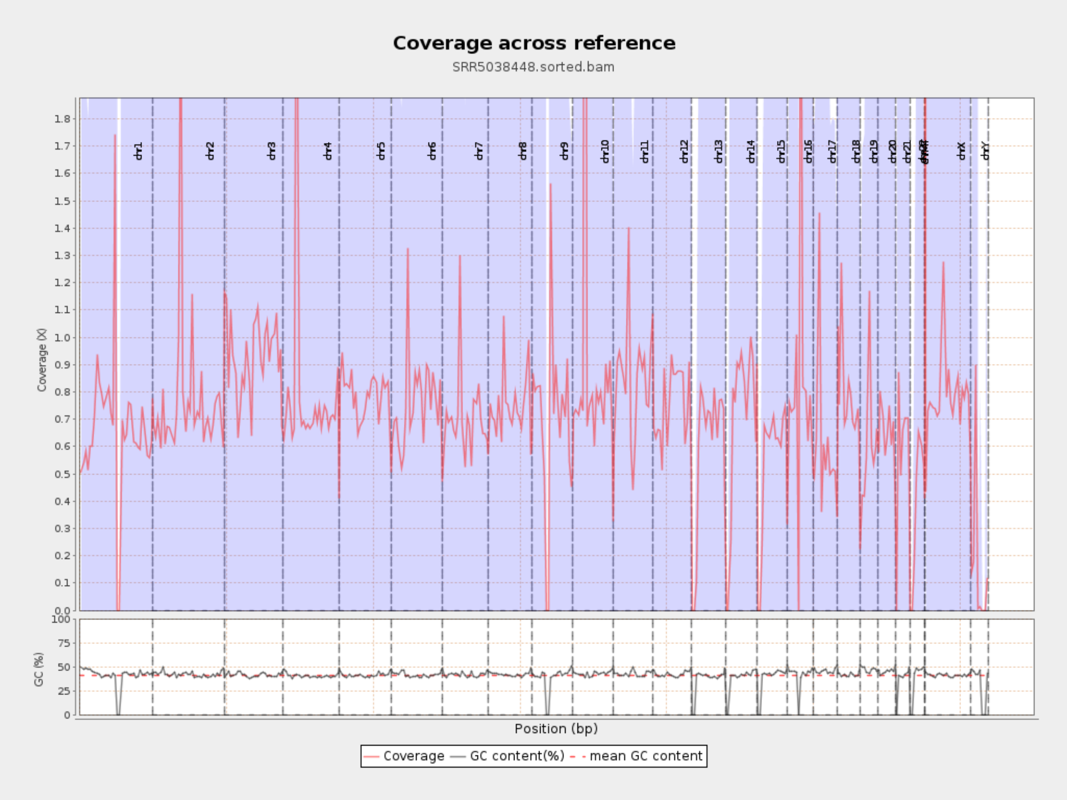
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

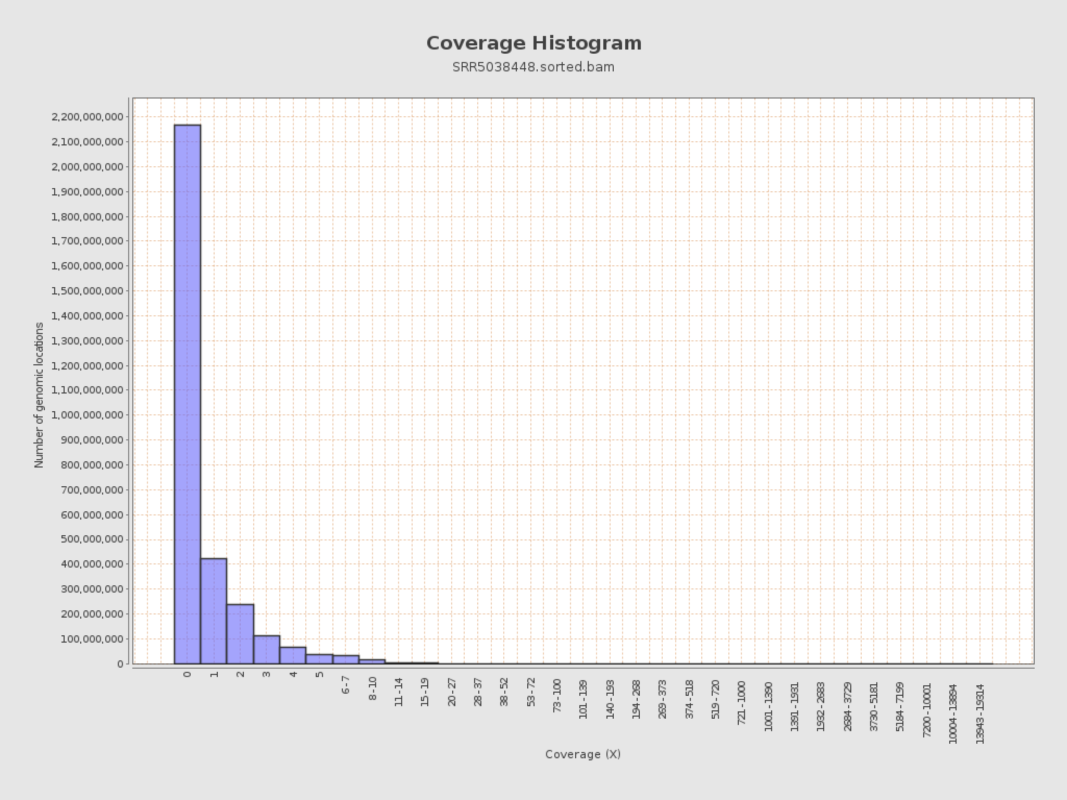
		bases	coverage	deviation
chr1	249250621	165016841	0.6621	18.8482
chr2	243199373	188965143	0.777	11.7671
chr3	198022430	184562193	0.932	1.8425
chr4	191154276	151017623	0.79	12.2935
chr5	180915260	141632795	0.7829	1.6827
chr6	171115067	131437545	0.7681	6.8104
chr7	159138663	111597758	0.7013	9.049
chr8	146364022	109697565	0.7495	3.1571
chr9	141213431	97332840	0.6893	18.4938
chr10	135534747	132573903	0.9782	27.9067
chr11	135006516	111419416	0.8253	8.6719
chr12	133851895	100777015	0.7529	1.7418
chr13	115169878	69031016	0.5994	1.3583
chr14	107349540	74475662	0.6938	1.7864
chr15	102531392	55517205	0.5415	1.2856
chr16	90354753	76990221	0.8521	14.0195
chr17	81195210	49305010	0.6072	12.5172
chr18	78077248	62147558	0.796	14.623
chr19	59128983	35258938	0.5963	9.5074
chr20	63025520	41312250	0.6555	3.6979
chr21	48129895	29099364	0.6046	5.3313
chr22	51304566	19970314	0.3893	1.3121
chrMT	16571	2212757	133.5319	64.6312
chrX	155270560	122951316	0.7919	3.9774

chrY	59373566	10145401	0.1709	12.8827

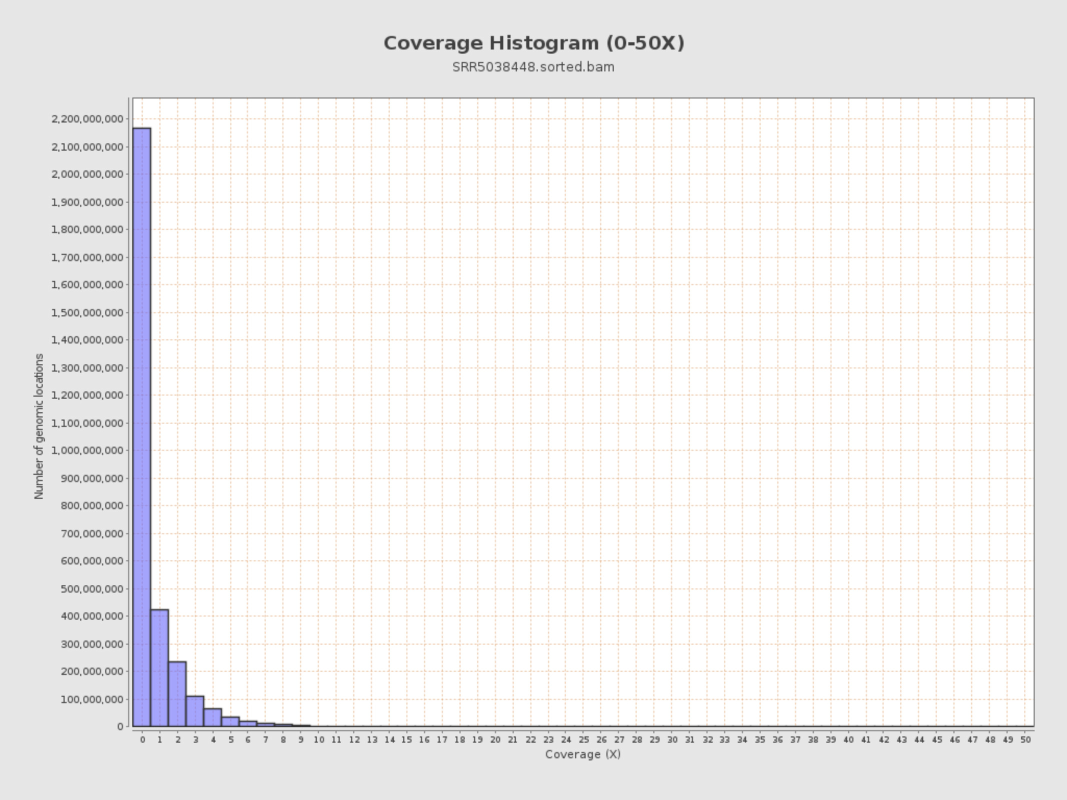
3. Results : Coverage across reference



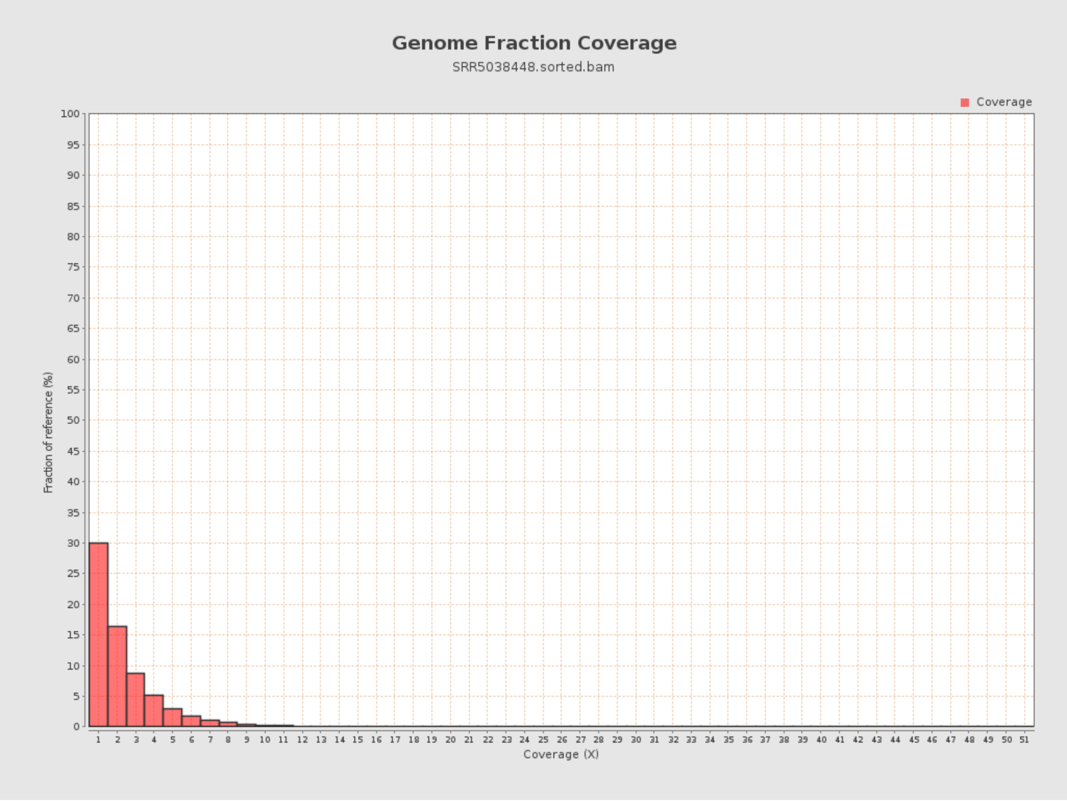
4. Results : Coverage Histogram



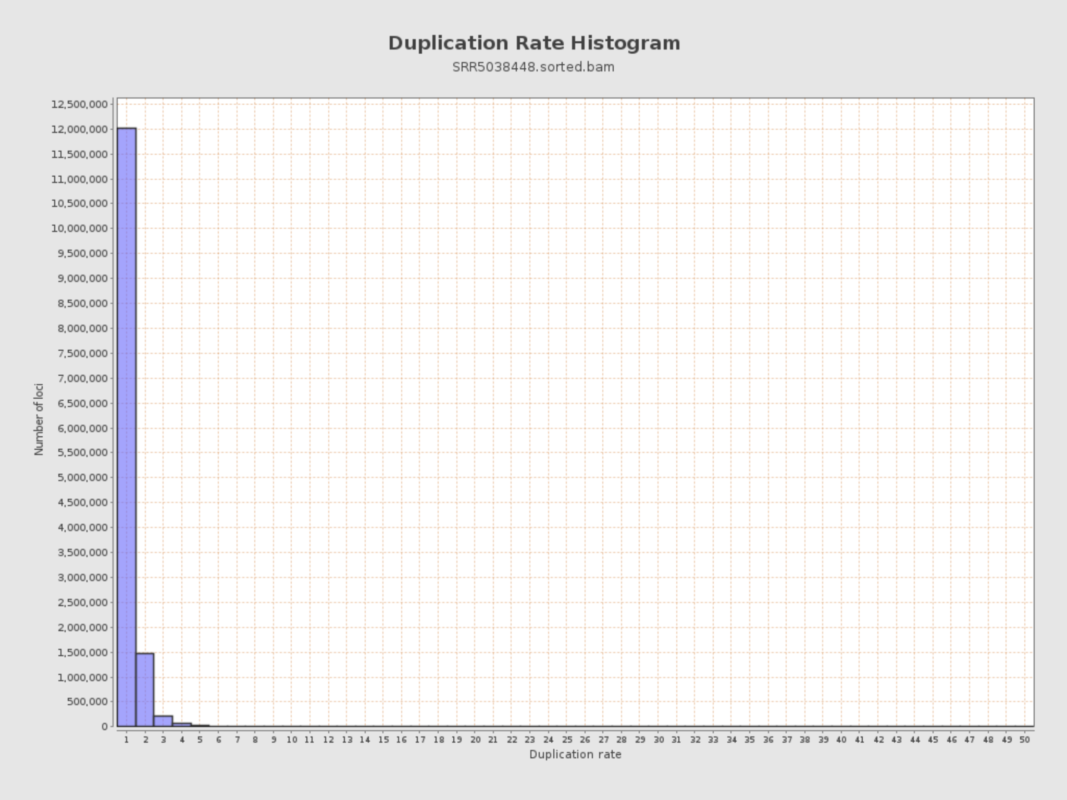
5. Results : Coverage Histogram (0-50X)



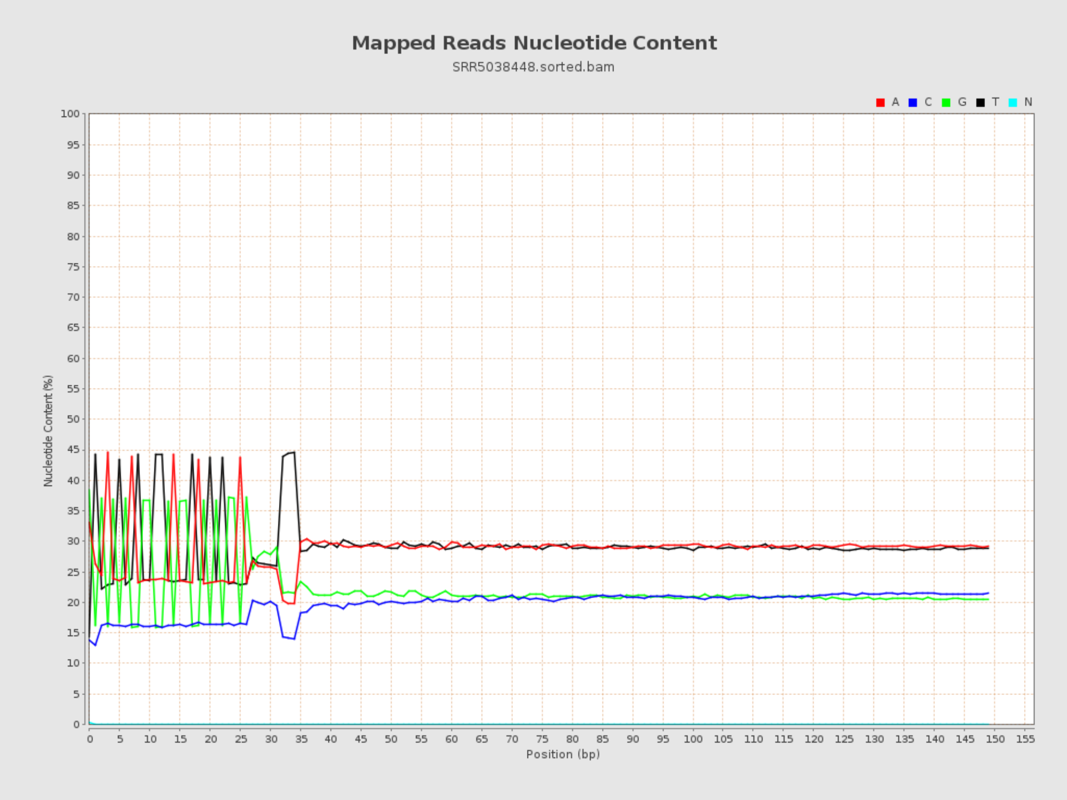
6. Results : Genome Fraction Coverage



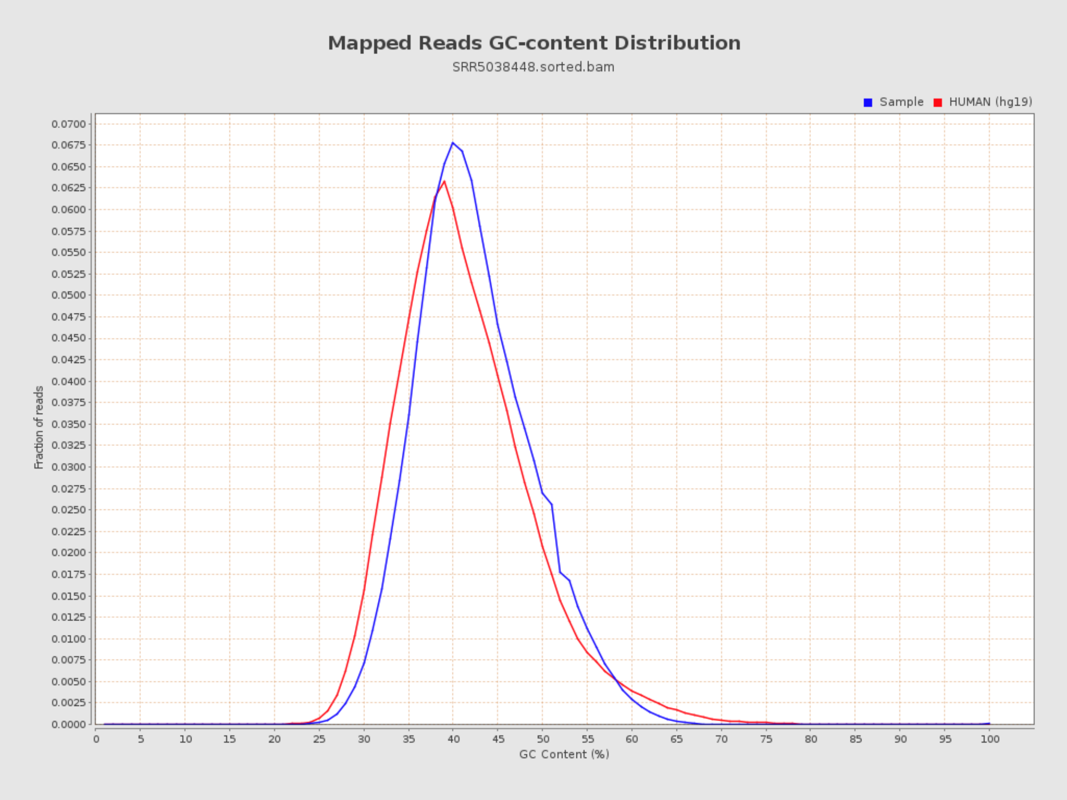
7. Results : Duplication Rate Histogram



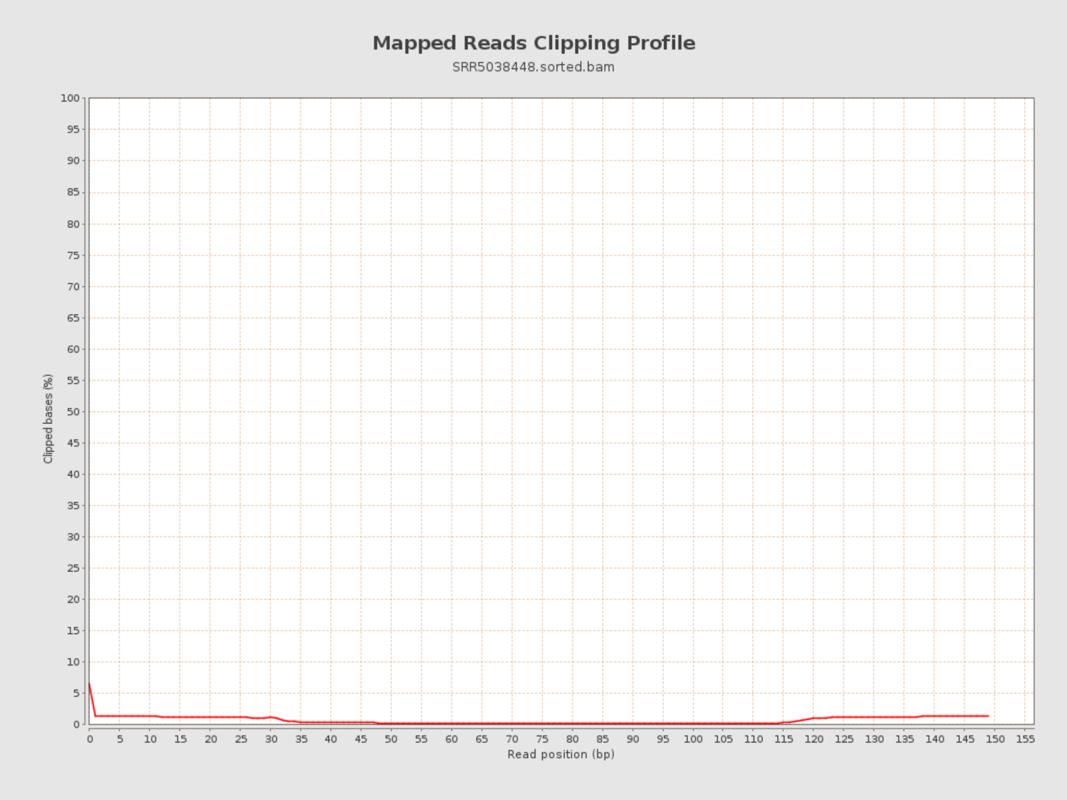
8. Results : Mapped Reads Nucleotide Content



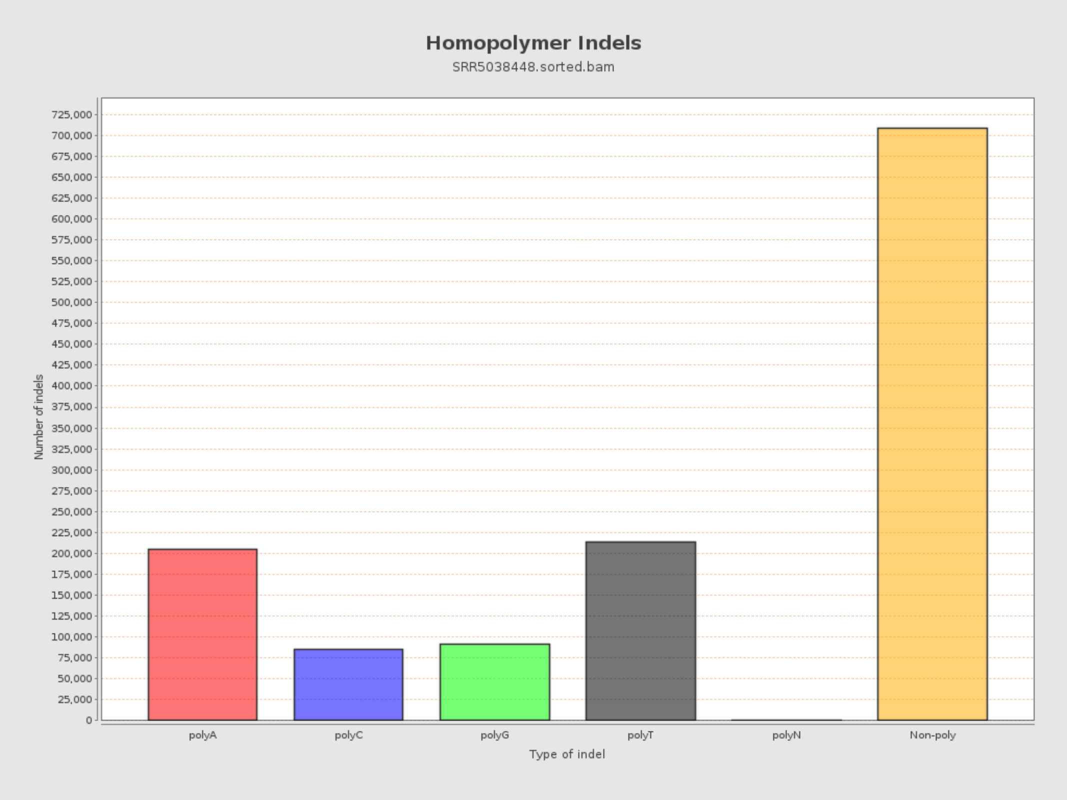
9. Results : Mapped Reads GC-content Distribution



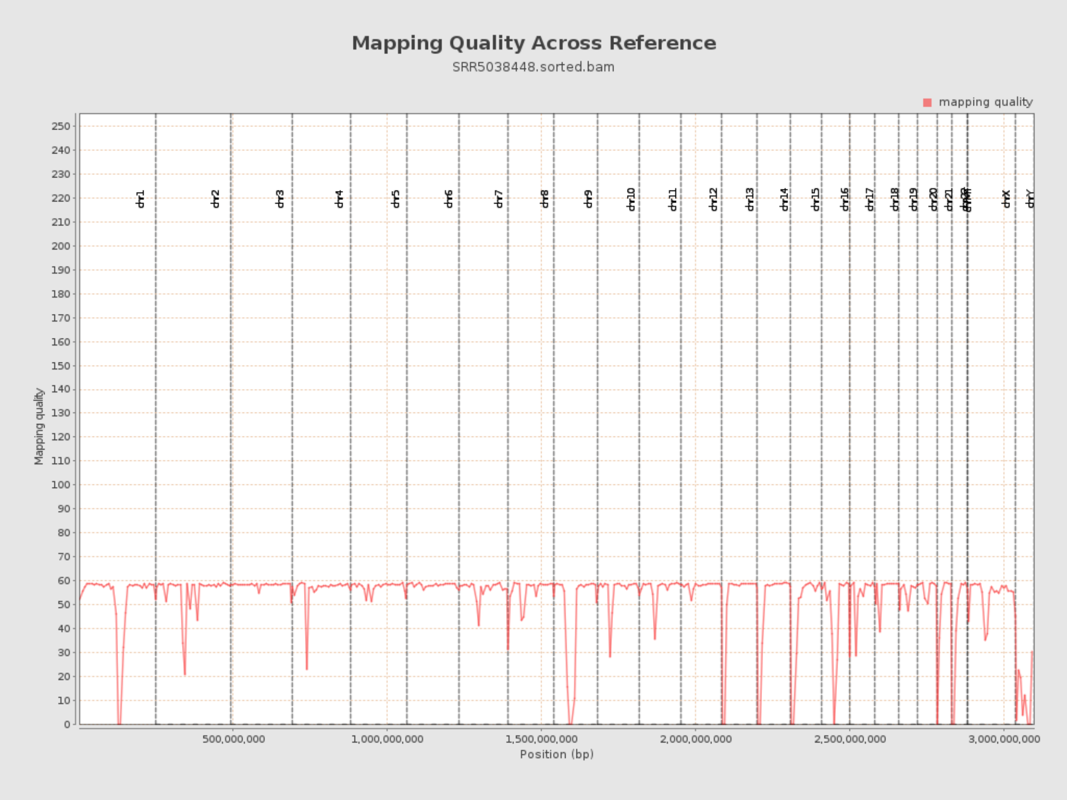
10. Results : Mapped Reads Clipping Profile



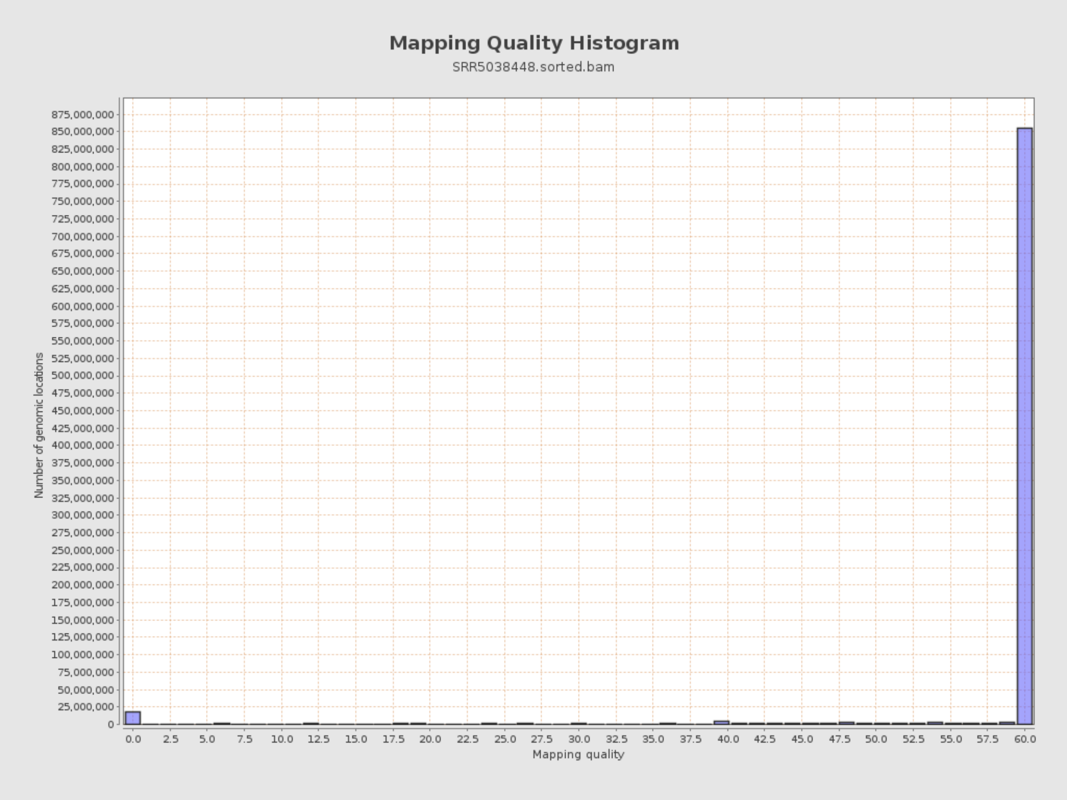
11. Results : Homopolymer Indels



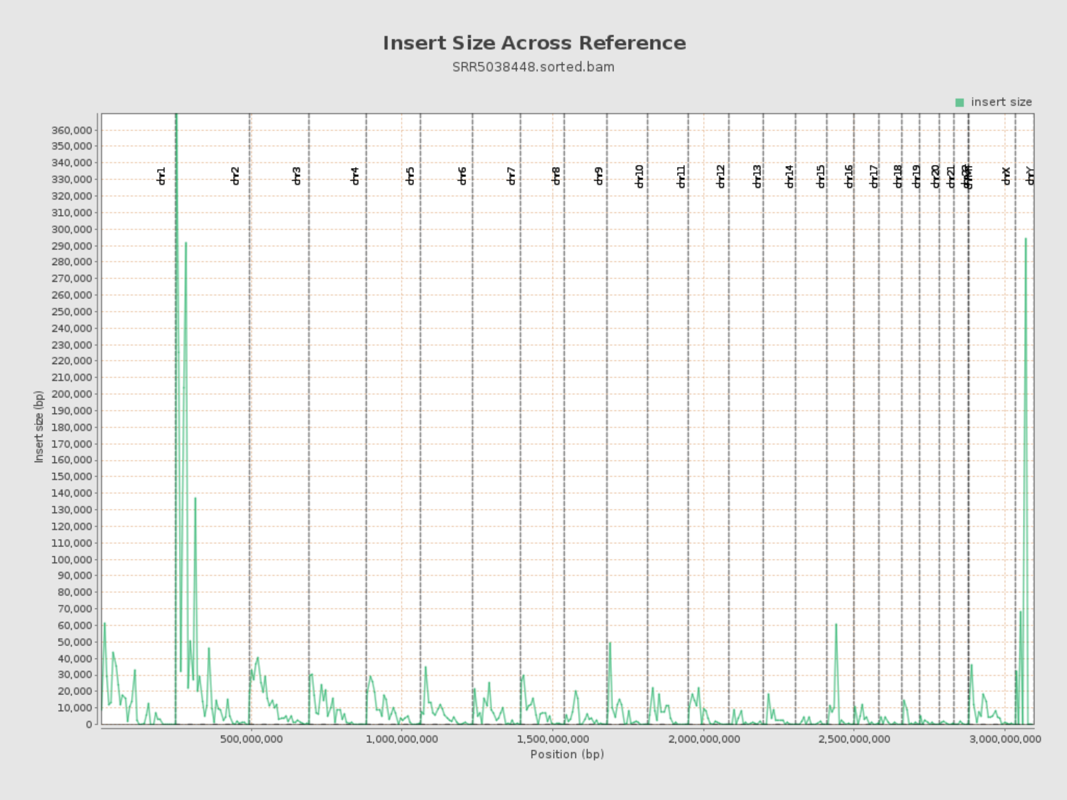
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram