Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:14:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006162.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_SRR1006162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006162_1.fastq.gz SRR1006162_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:14:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,856,636
Mapped reads	4,107,233 / 84.57%
Unmapped reads	749,403 / 15.43%
Mapped paired reads	4,107,233 / 84.57%
Mapped reads, first in pair	2,056,476 / 42.34%
Mapped reads, second in pair	2,050,757 / 42.23%
Mapped reads, both in pair	3,842,048 / 79.11%
Mapped reads, singletons	265,185 / 5.46%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	205,951 / 4.24%
Duplication rate	4.48%
Clipped reads	338,720 / 6.97%

2.2. ACGT Content

Number/percentage of A's	42,258,149 / 26.66%
Number/percentage of C's	36,232,513 / 22.86%
Number/percentage of T's	42,848,167 / 27.03%
Number/percentage of G's	37,149,438 / 23.44%
Number/percentage of N's	19,392 / 0.01%
GC Percentage	46.3%

2.3. Coverage

Mean	0.0512
Standard Deviation	0.3808

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Insert size

Mean	52,353.81
Standard Deviation	2,189,638.97
P25/Median/P75	53 / 75 / 110

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	596,743
Insertions	5,567
Mapped reads with at least one insertion	0.14%
Deletions	14,498
Mapped reads with at least one deletion	0.35%
Homopolymer indels	38.33%

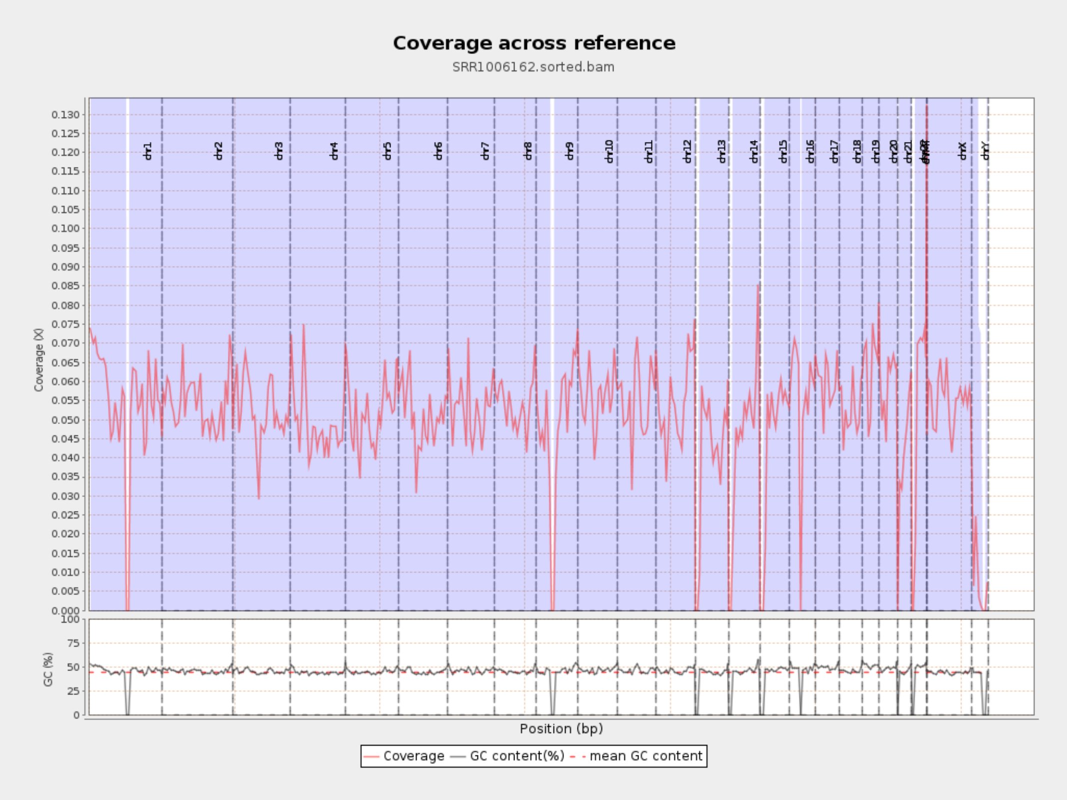
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

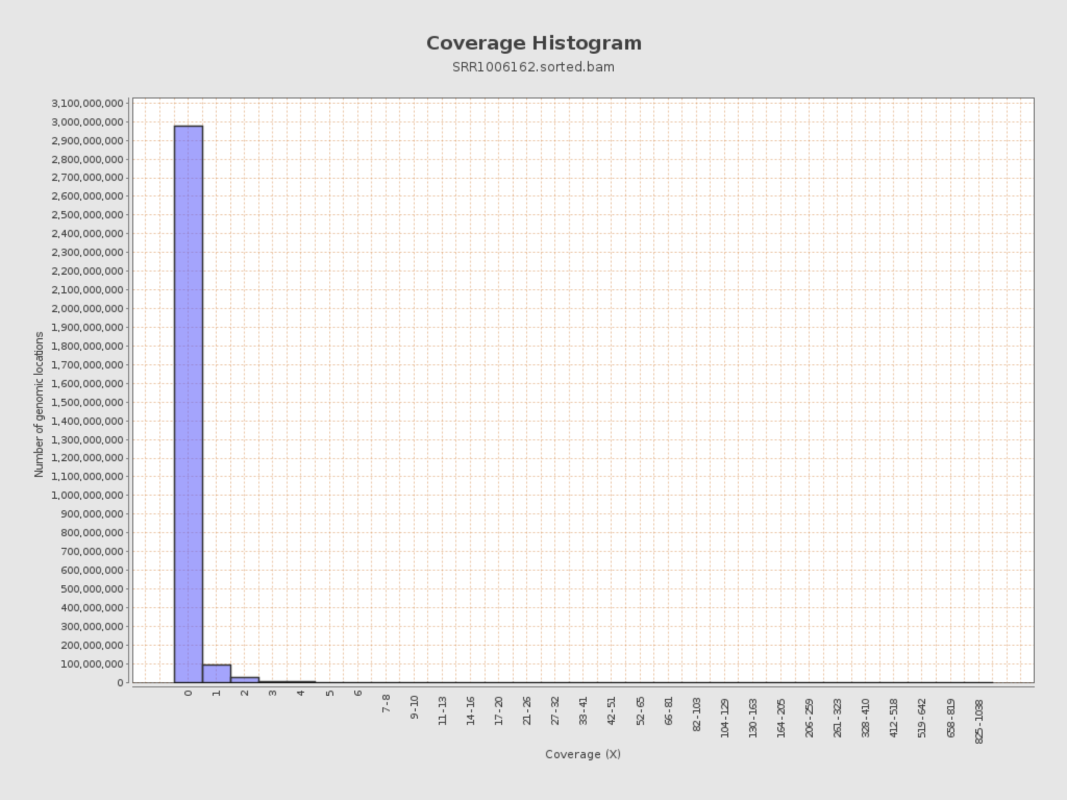
chr1	249250621	13474404	0.0541	0.3827
chr2	243199373	13280238	0.0546	0.3272
chr3	198022430	10370281	0.0524	0.2852
chr4	191154276	9313271	0.0487	0.3002
chr5	180915260	9345632	0.0517	0.2852
chr6	171115067	8748051	0.0511	0.2938
chr7	159138663	8410567	0.0529	0.3407
chr8	146364022	7889966	0.0539	0.5827
chr9	141213431	6562467	0.0465	0.2899
chr10	135534747	7592197	0.056	0.353
chr11	135006516	7403831	0.0548	0.3144
chr12	133851895	7278127	0.0544	0.304
chr13	115169878	4587509	0.0398	0.258
chr14	107349540	4796781	0.0447	1.0142
chr15	102531392	4498191	0.0439	0.2659
chr16	90354753	5074840	0.0562	0.3251
chr17	81195210	4876097	0.0601	0.3209
chr18	78077248	4074745	0.0522	0.3699
chr19	59128983	3787032	0.064	0.3889
chr20	63025520	3726795	0.0591	0.3254
chr21	48129895	1947466	0.0405	0.2948
chr22	51304566	2481576	0.0484	0.4574
chrMT	16571	2196	0.1325	0.5536
chrX	155270560	8547425	0.055	0.298

chrY	59373566	457376	0.0077	0.2041

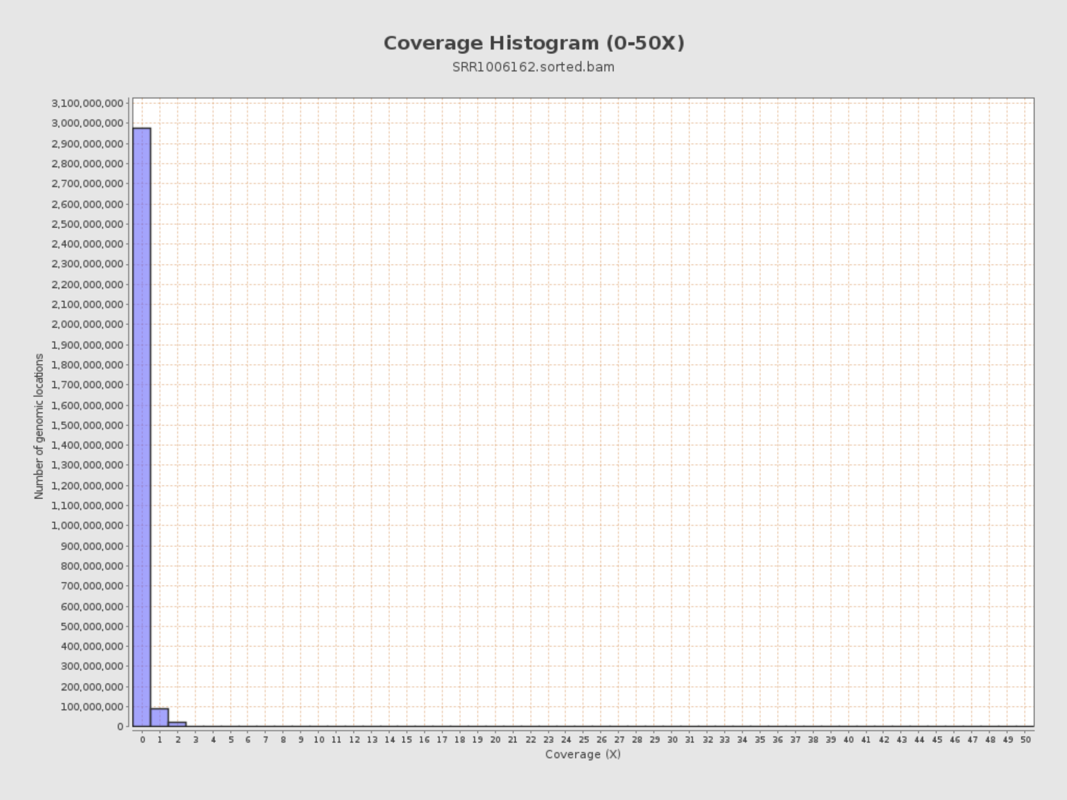
3. Results : Coverage across reference



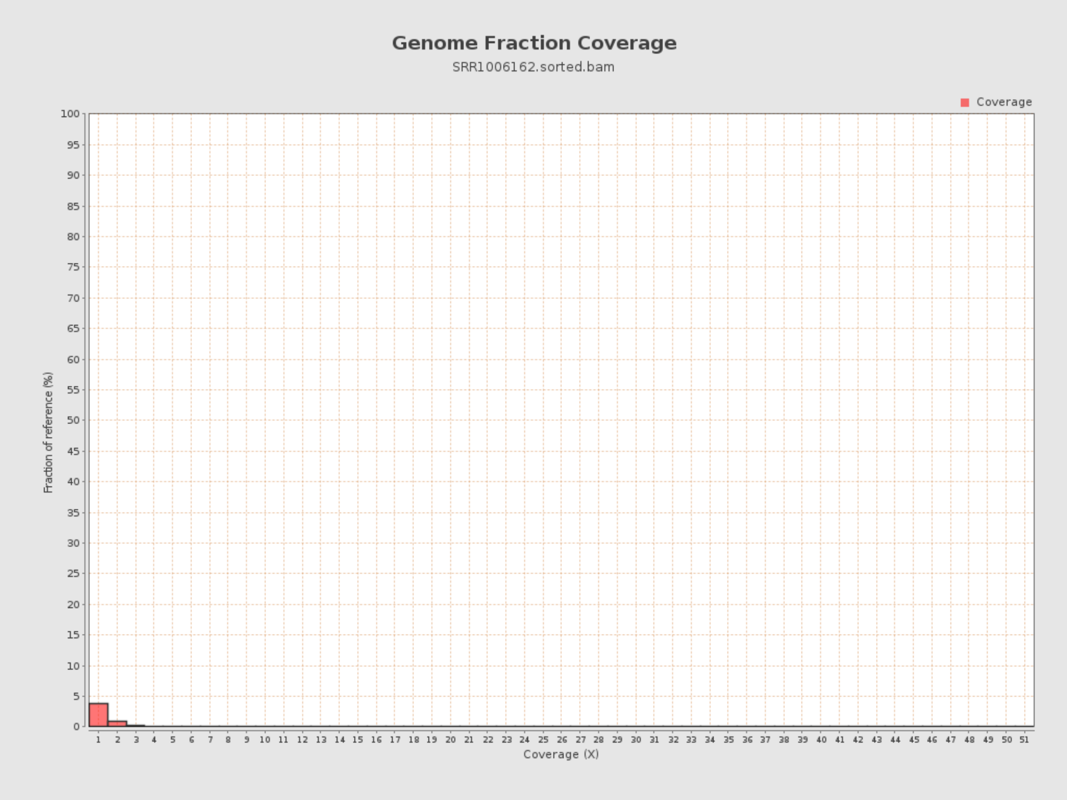
4. Results : Coverage Histogram



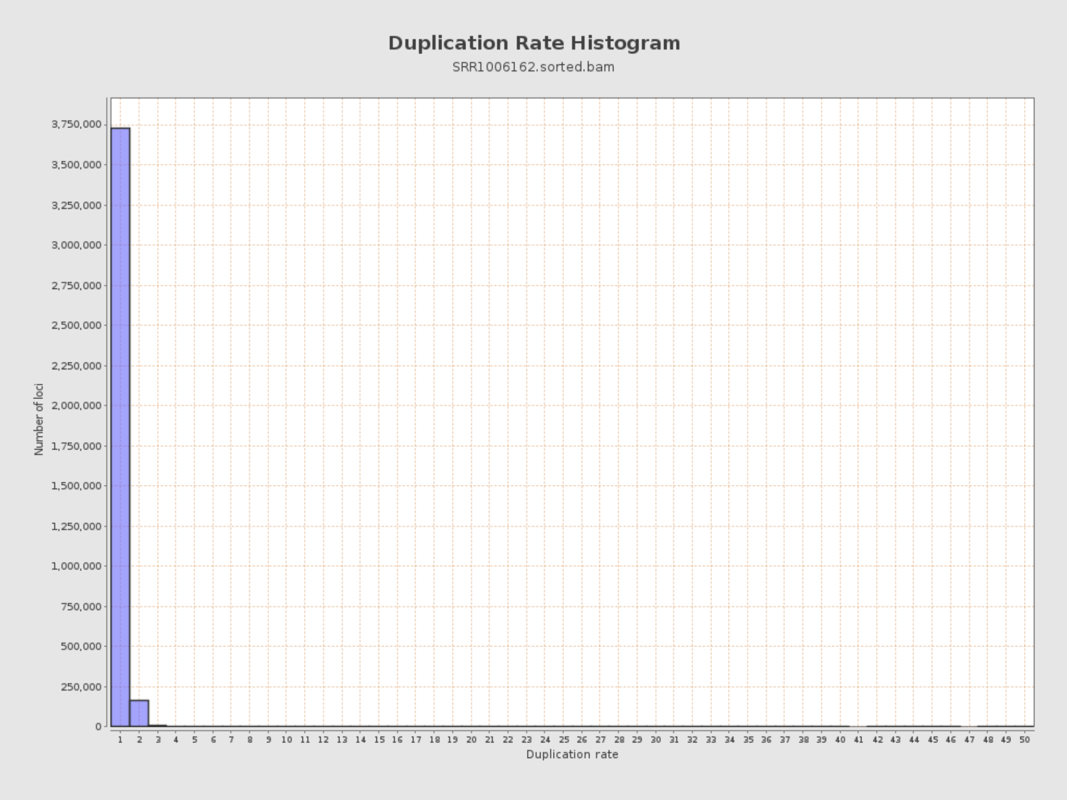
5. Results : Coverage Histogram (0-50X)



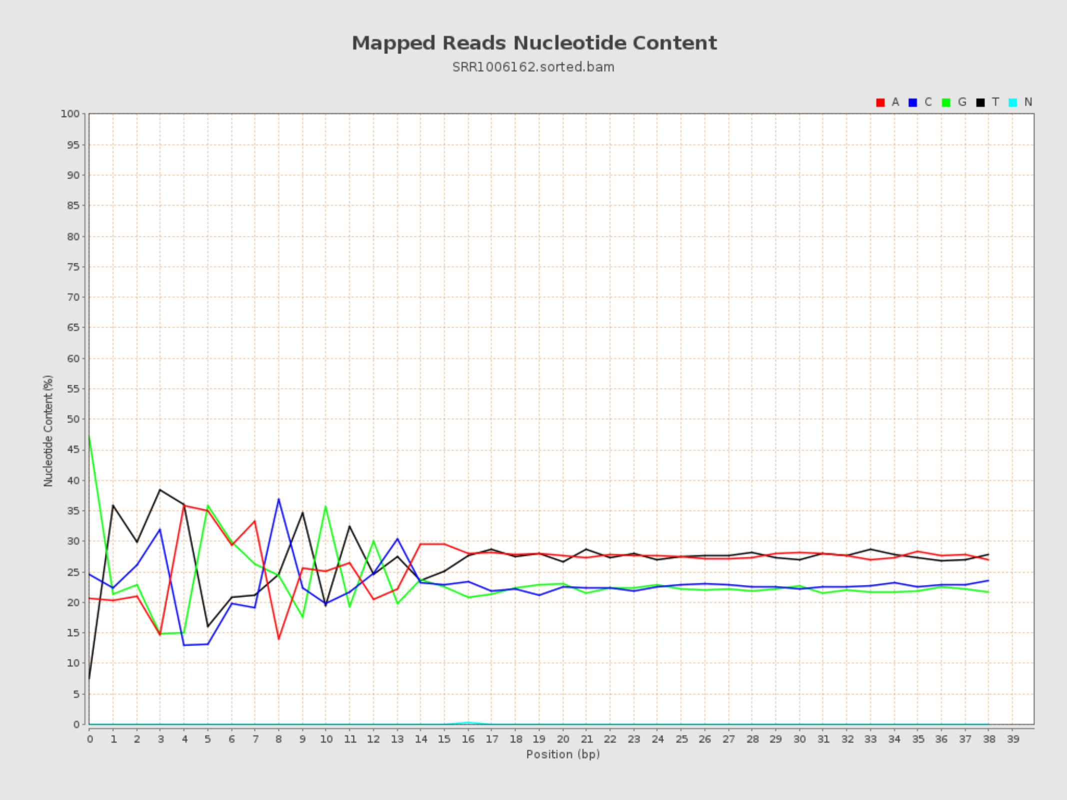
6. Results : Genome Fraction Coverage



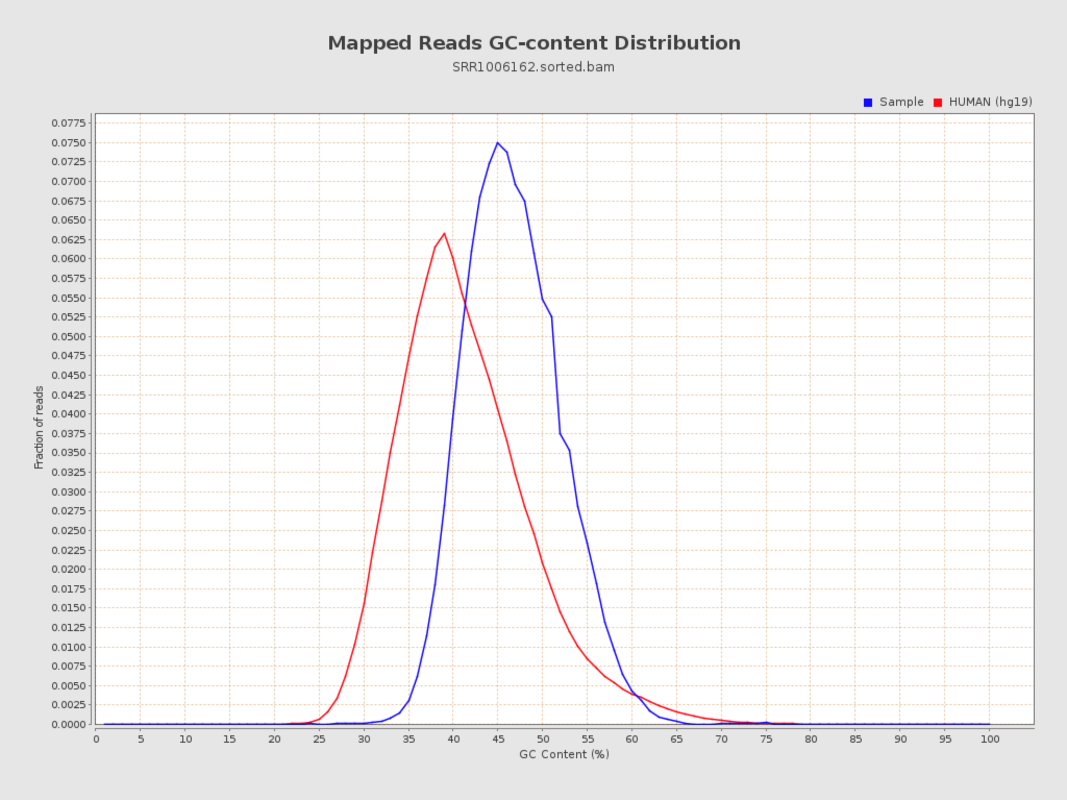
7. Results : Duplication Rate Histogram



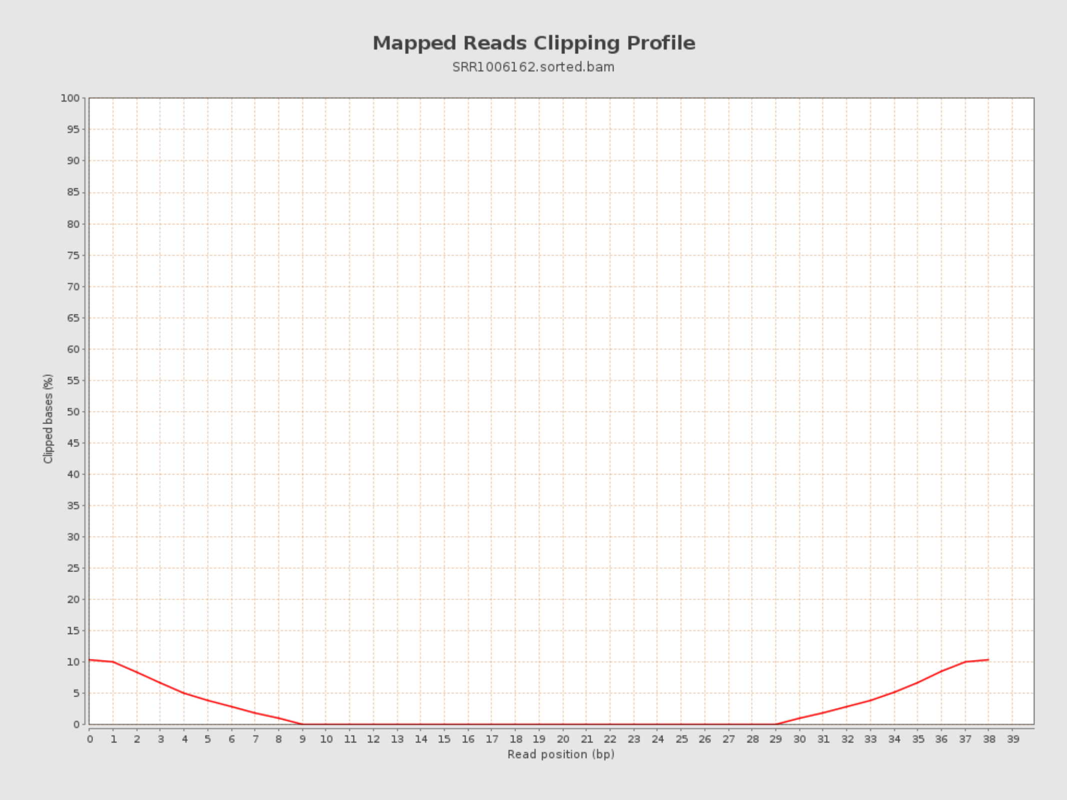
8. Results : Mapped Reads Nucleotide Content



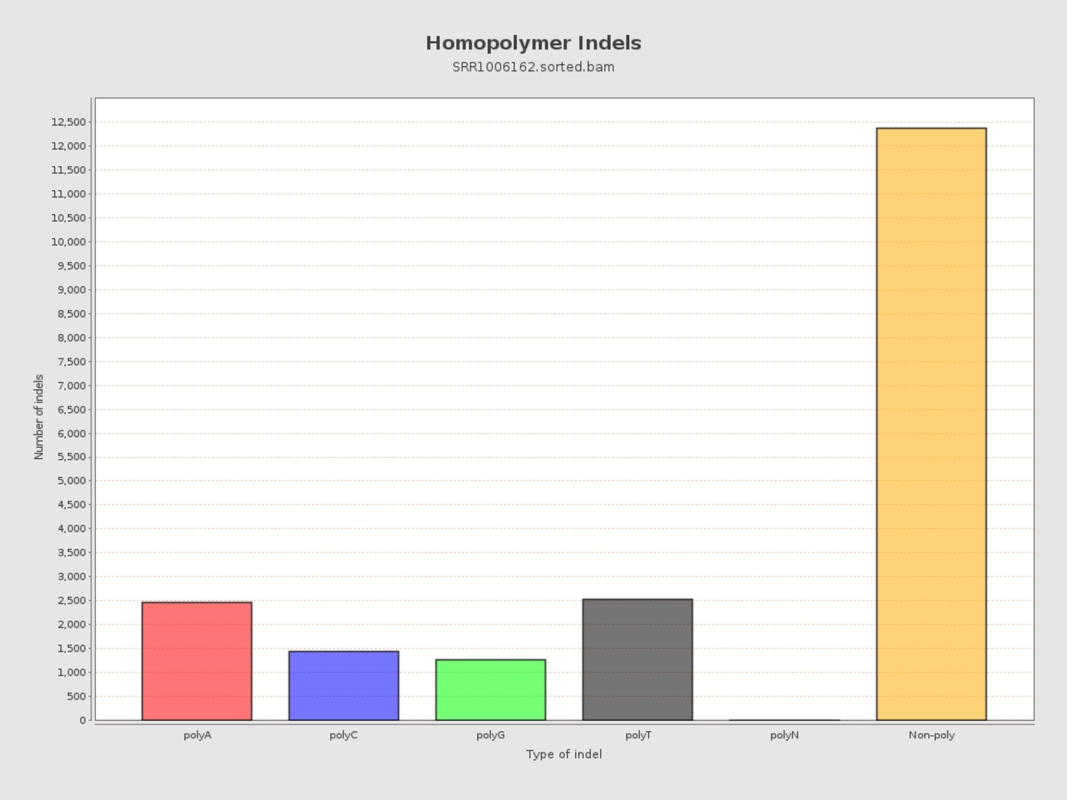
9. Results : Mapped Reads GC-content Distribution



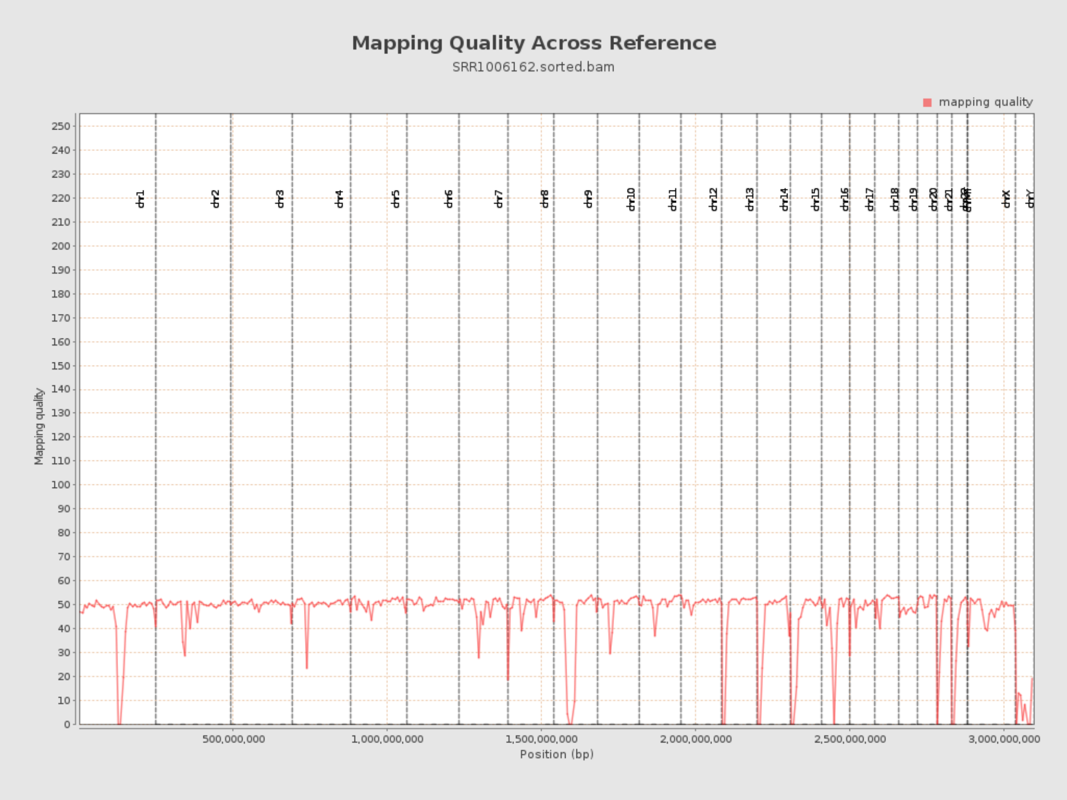
10. Results : Mapped Reads Clipping Profile



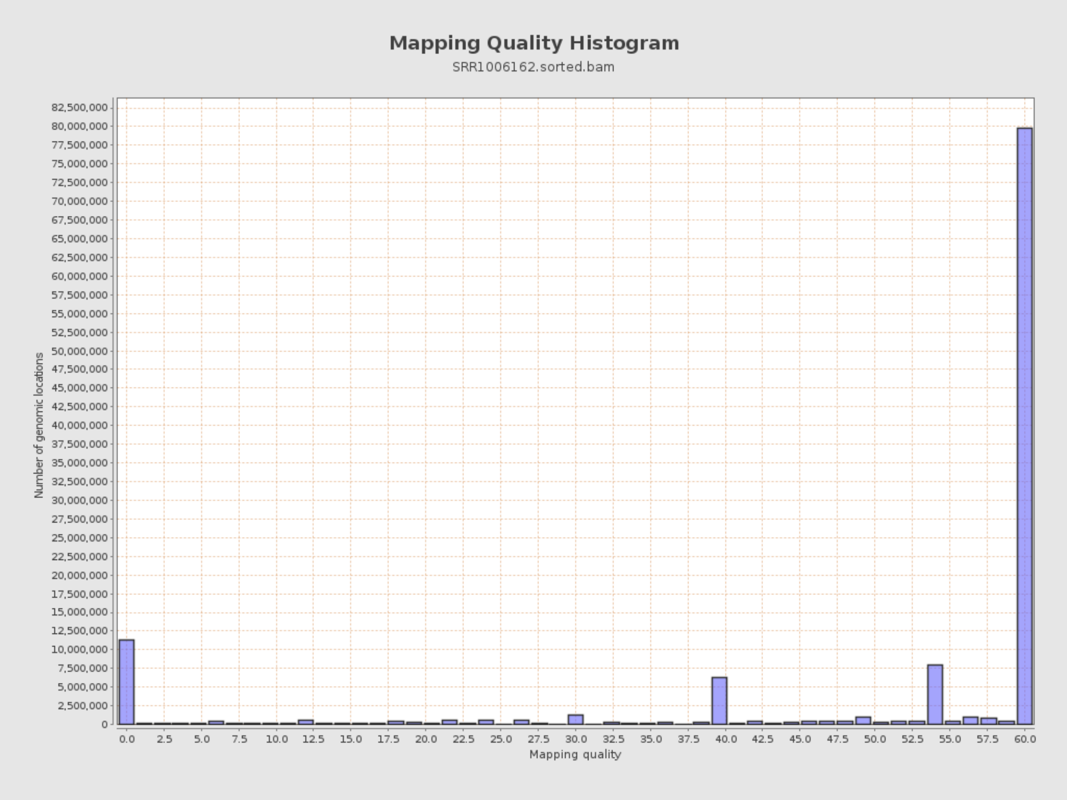
11. Results : Homopolymer Indels



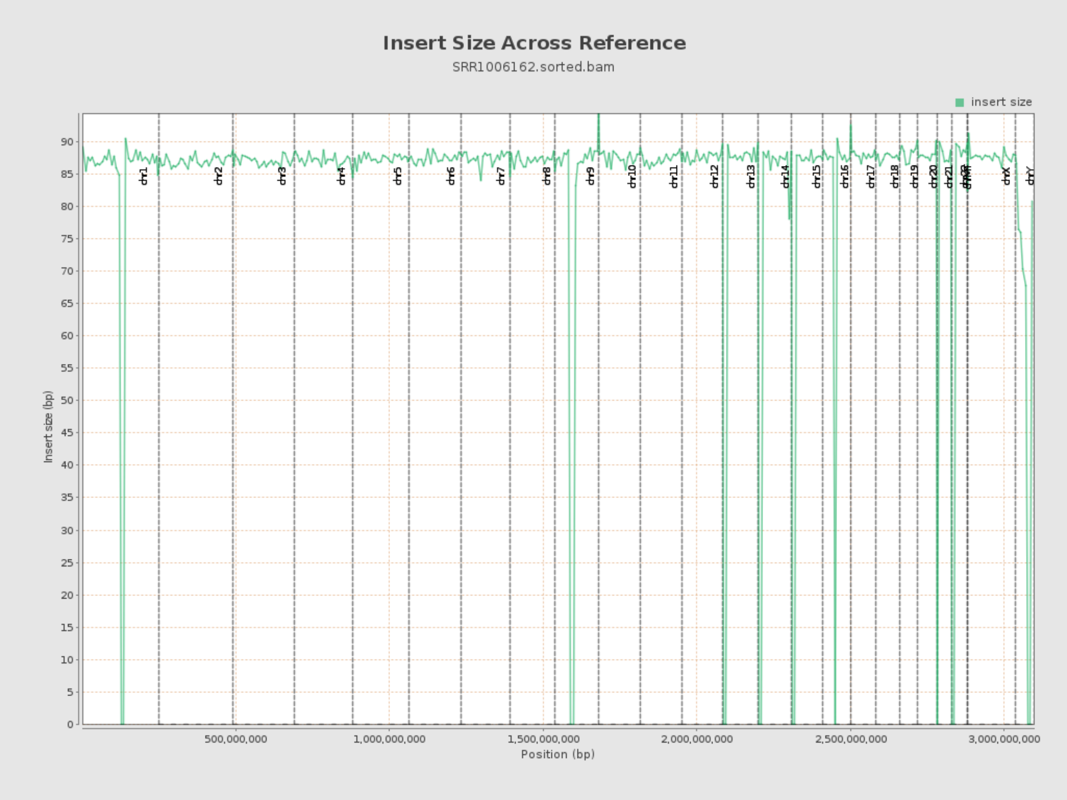
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram