Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 16:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038452.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_SRR5038452 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038452_1.fastq.gz SRR5038452_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 16:31:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038452.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,852,774
Mapped reads	13,463,241 / 97.19%
Unmapped reads	389,533 / 2.81%
Mapped paired reads	13,463,241 / 97.19%
Mapped reads, first in pair	6,808,782 / 49.15%
Mapped reads, second in pair	6,654,459 / 48.04%
Mapped reads, both in pair	13,291,280 / 95.95%
Mapped reads, singletons	171,961 / 1.24%
Secondary alignments	0
Supplementary alignments	219,429 / 1.58%
Read min/max/mean length	30 / 150 / 150.81
Duplicated reads (estimated)	2,117,737 / 15.29%
Duplication rate	9.99%
Clipped reads	3,115,249 / 22.49%

2.2. ACGT Content

Number/percentage of A's	574,219,895 / 29.78%
Number/percentage of C's	383,731,535 / 19.9%
Number/percentage of T's	574,358,638 / 29.79%
Number/percentage of G's	395,949,766 / 20.53%
Number/percentage of N's	39,182 / 0%

GC Percentage	40.43%

2.3. Coverage

Mean	0.6234
Standard Deviation	8.8835

2.4. Mapping Quality

Mean Mapping Quality	53.74

2.5. Insert size

Mean	73,747.25
Standard Deviation	2,560,790.71
P25/Median/P75	203 / 248 / 306

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	27,697,252
Insertions	386,780
Mapped reads with at least one insertion	2.67%
Deletions	740,972
Mapped reads with at least one deletion	5.27%
Homopolymer indels	46.9%

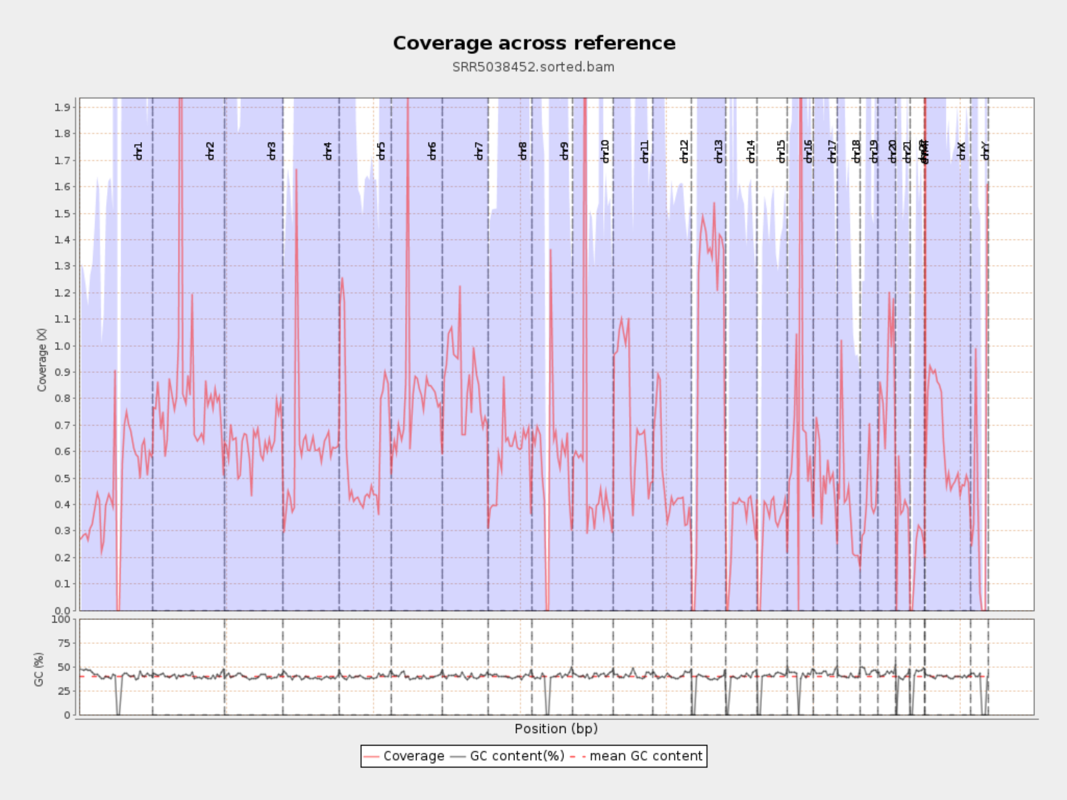
2.7. Chromosome stats

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

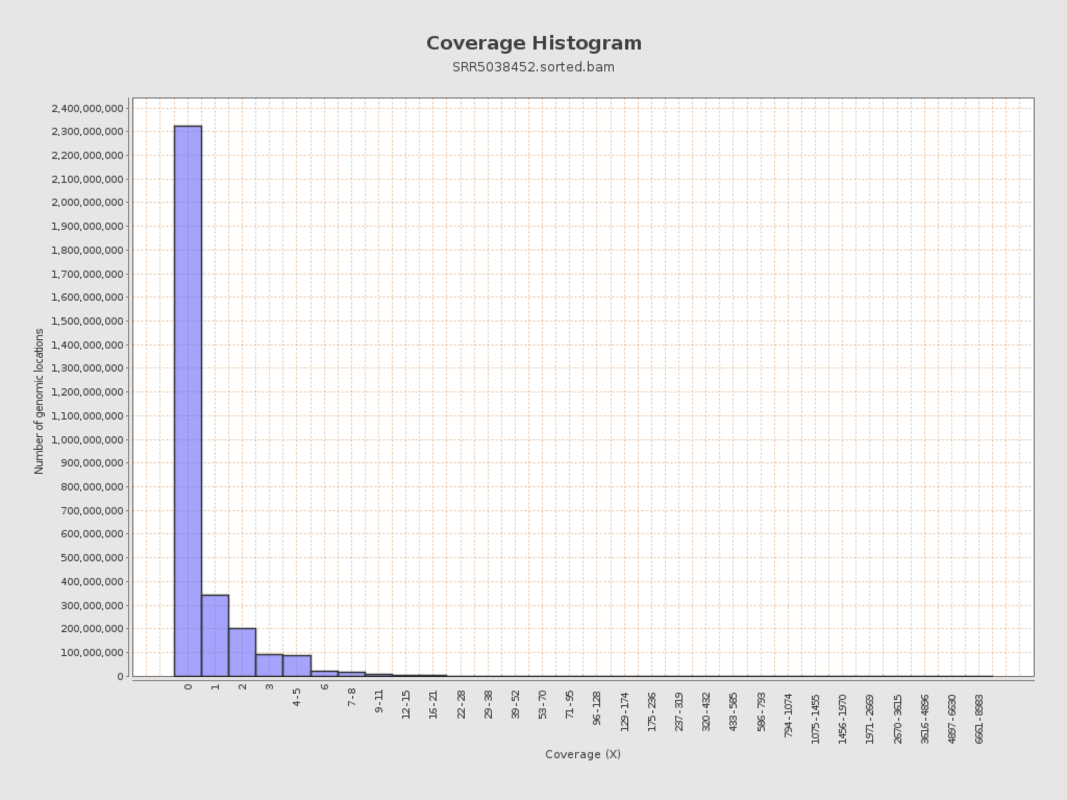
		bases	**coverage**	**deviation**
chr1	249250621	114307309	0.4586	8.206
chr2	243199373	206549056	0.8493	13.6865
chr3	198022430	125363025	0.6331	1.4688
chr4	191154276	116344475	0.6086	8.0749
chr5	180915260	111440053	0.616	1.6109
chr6	171115067	140639909	0.8219	12.7418
chr7	159138663	137343346	0.863	8.6153
chr8	146364022	85049674	0.5811	2.808
chr9	141213431	78144749	0.5534	14.9232
chr10	135534747	77817627	0.5742	17.9496
chr11	135006516	100852925	0.747	6.6353
chr12	133851895	65825424	0.4918	1.3435
chr13	115169878	131630785	1.1429	2.1823
chr14	107349540	35038231	0.3264	1.2705
chr15	102531392	32296789	0.315	0.9654
chr16	90354753	66111879	0.7317	13.6852
chr17	81195210	40629507	0.5004	5.0601
chr18	78077248	31375762	0.4019	12.3832
chr19	59128983	23405691	0.3958	4.9855
chr20	63025520	55575310	0.8818	2.9887
chr21	48129895	17638781	0.3665	4.0113
chr22	51304566	10268946	0.2002	1.0339
chrMT	16571	1281155	77.3131	50.6088
chrX	155270560	97134315	0.6256	2.2006

chrY	59373566	27713582	0.4668	13.5406

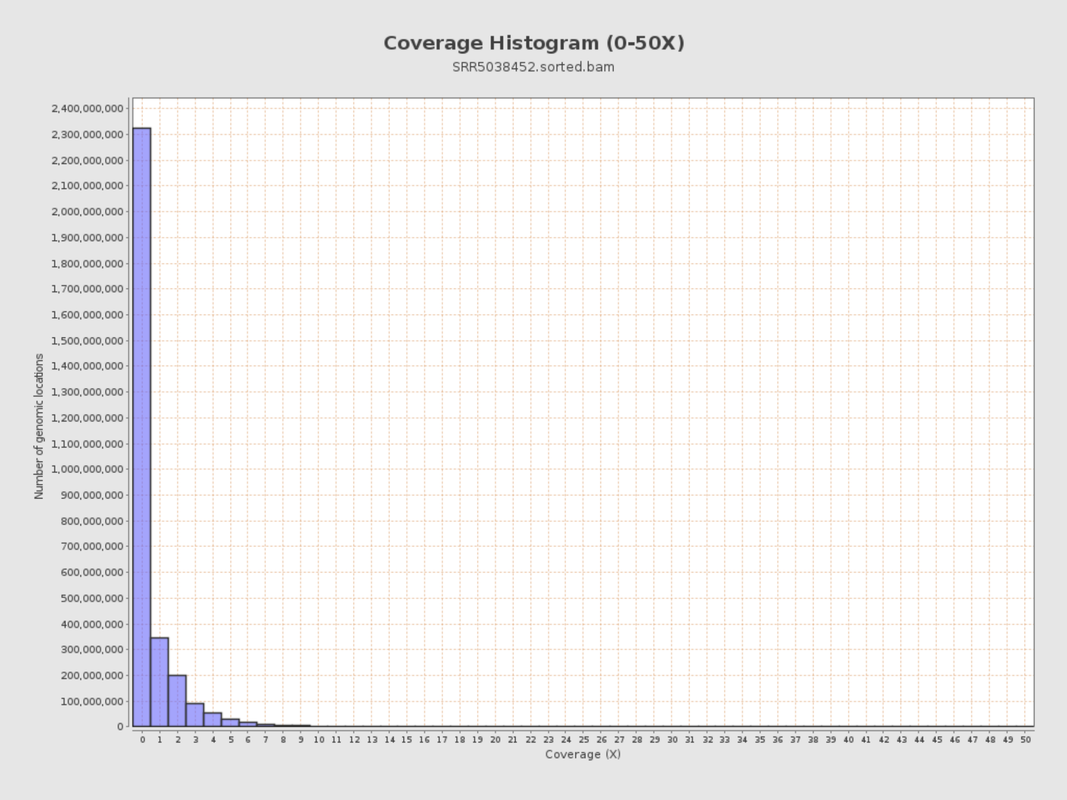
3. Results : Coverage across reference



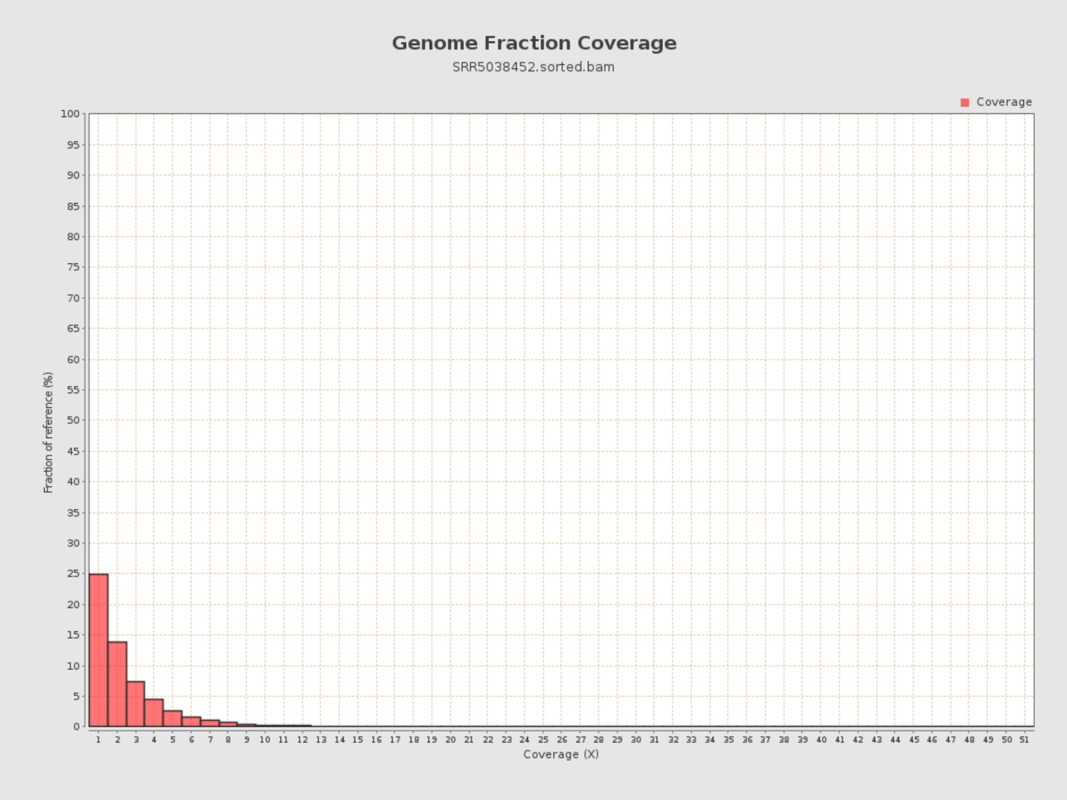
4. Results : Coverage Histogram



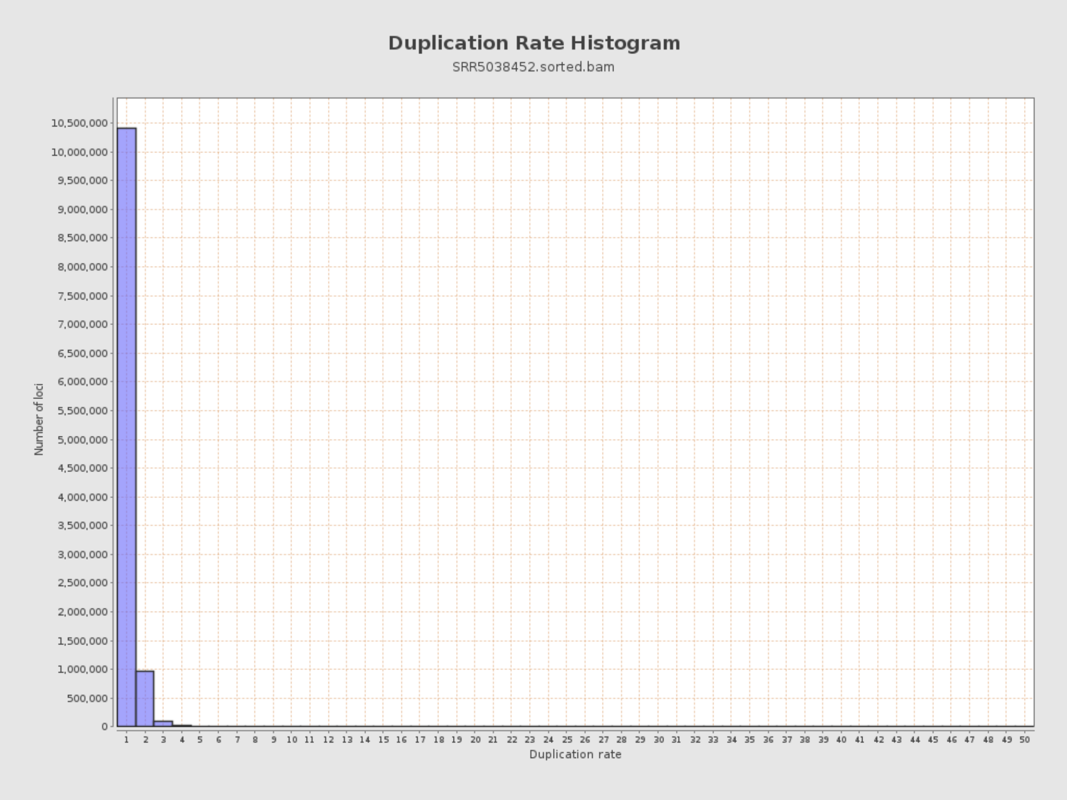
5. Results : Coverage Histogram (0-50X)



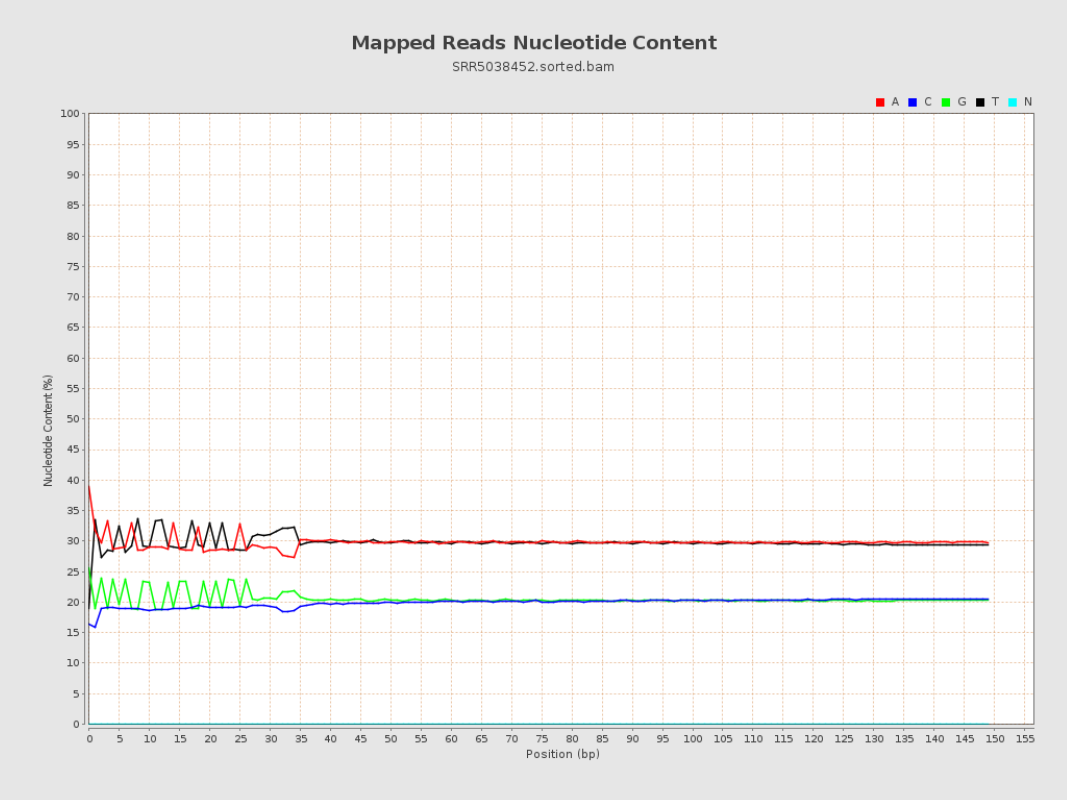
6. Results : Genome Fraction Coverage



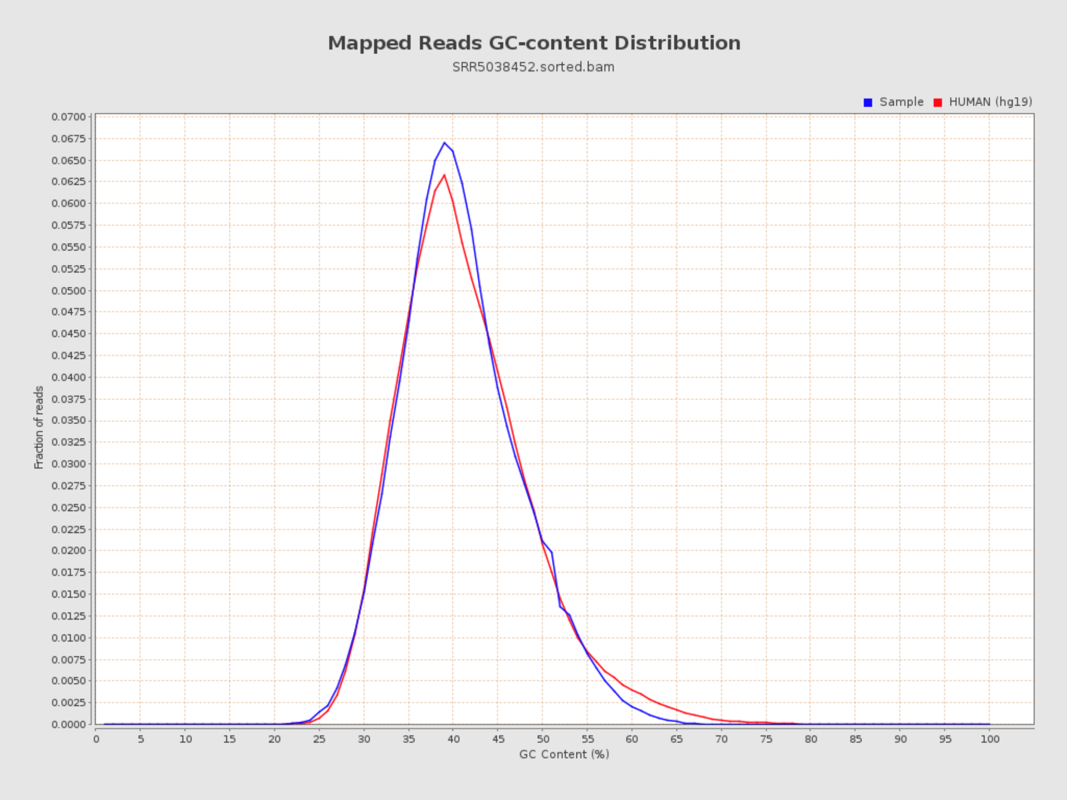
7. Results : Duplication Rate Histogram



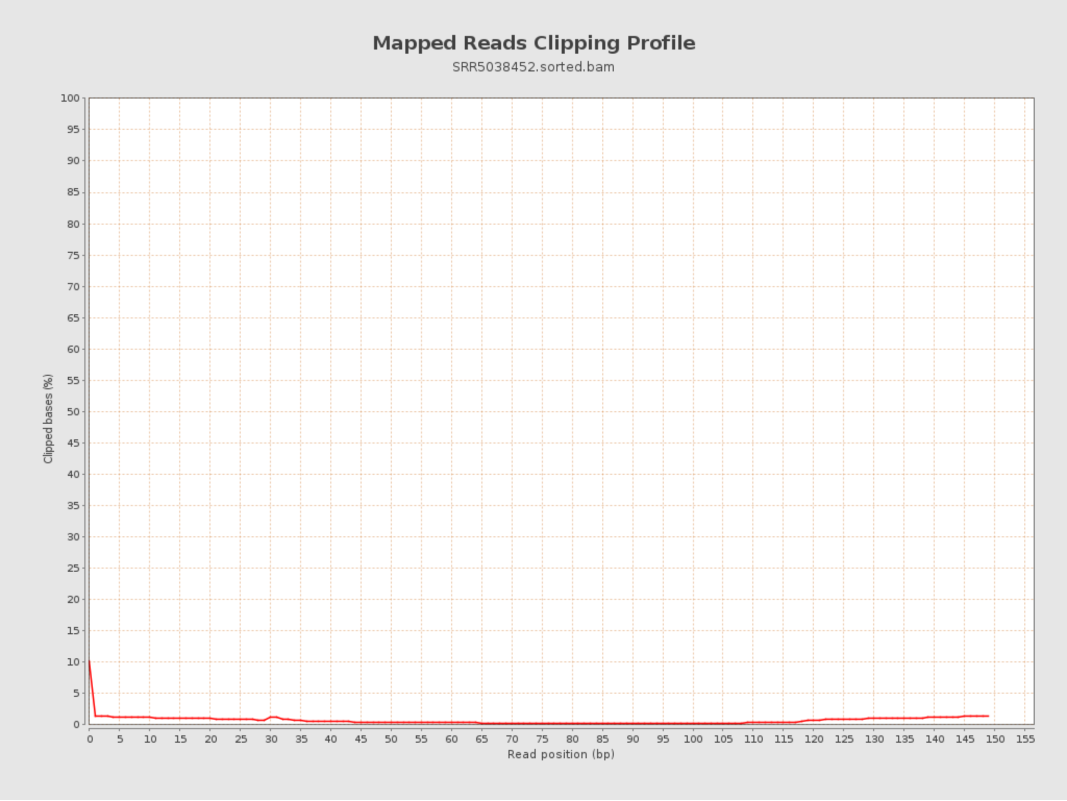
8. Results : Mapped Reads Nucleotide Content



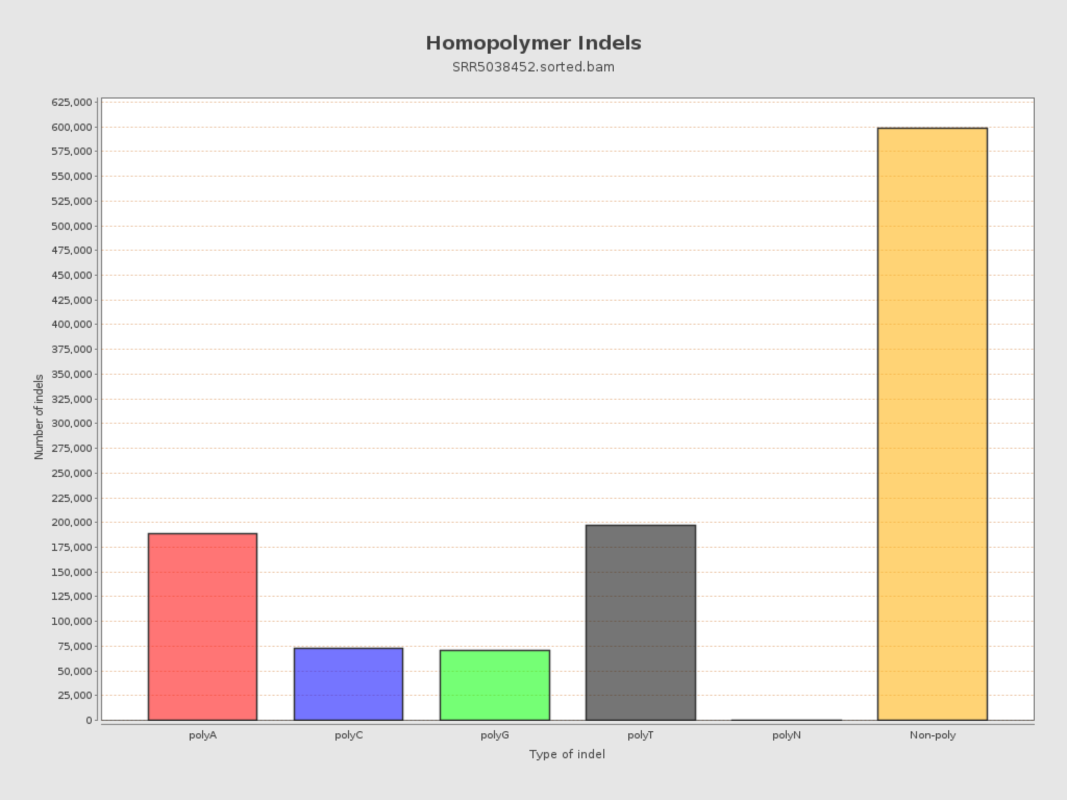
9. Results : Mapped Reads GC-content Distribution



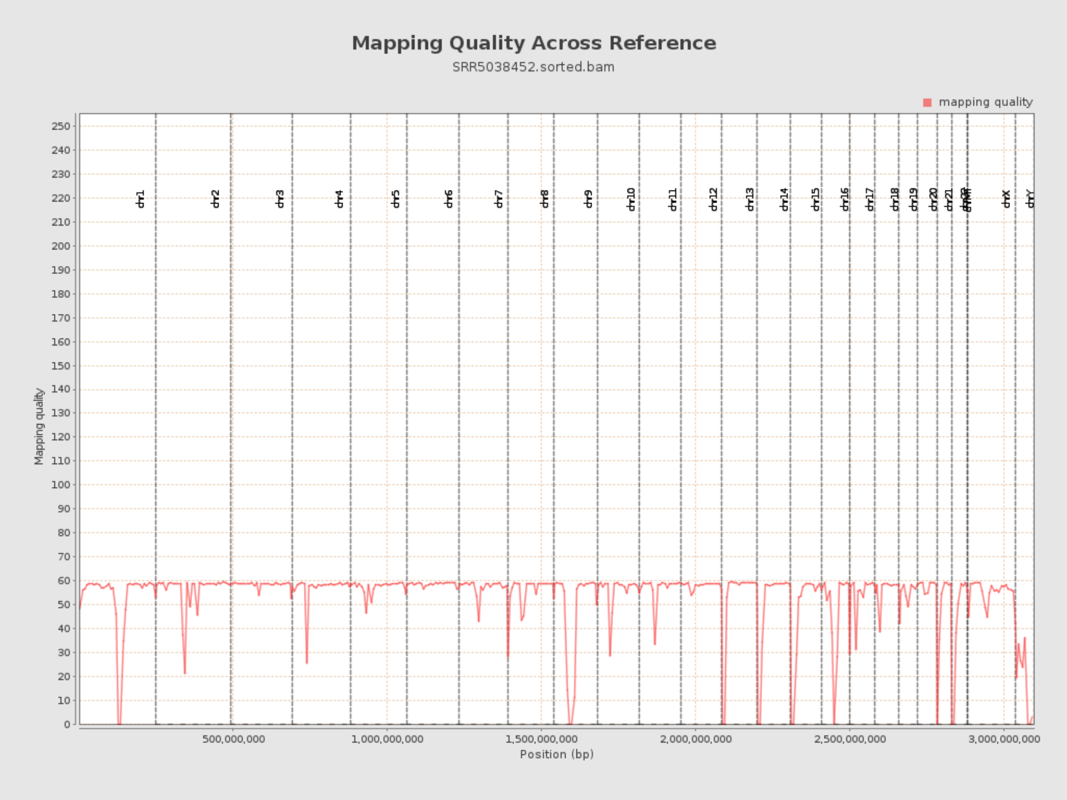
10. Results : Mapped Reads Clipping Profile



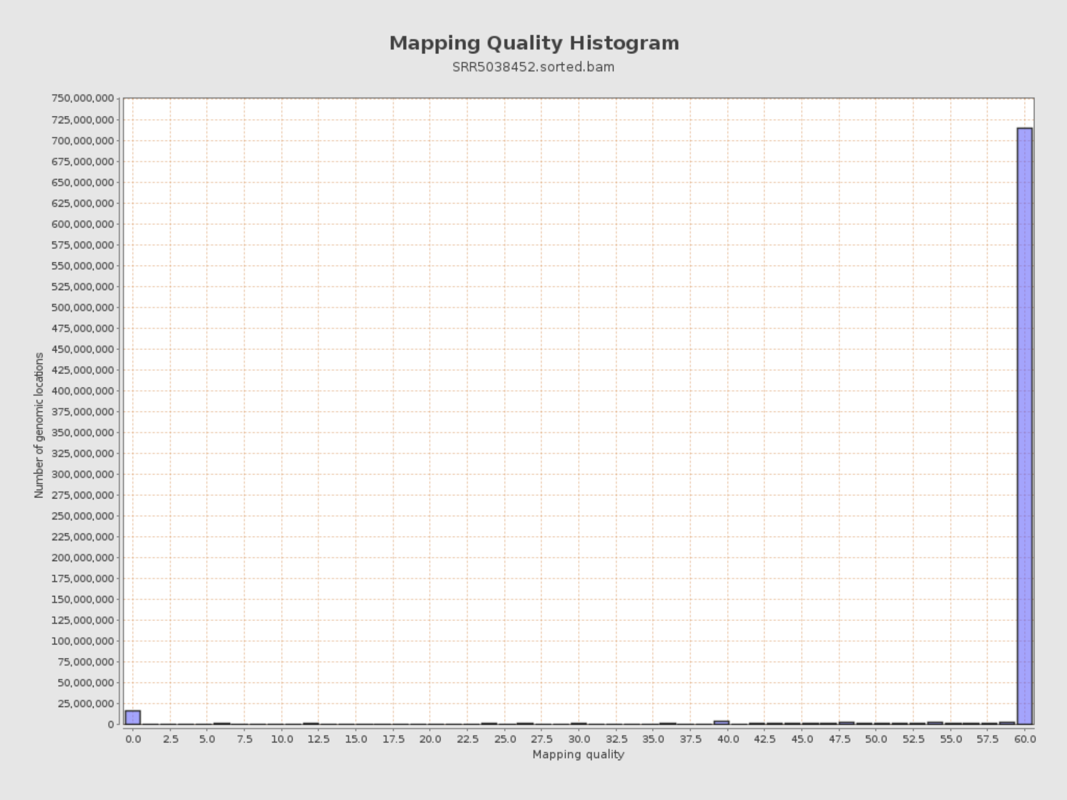
11. Results : Homopolymer Indels



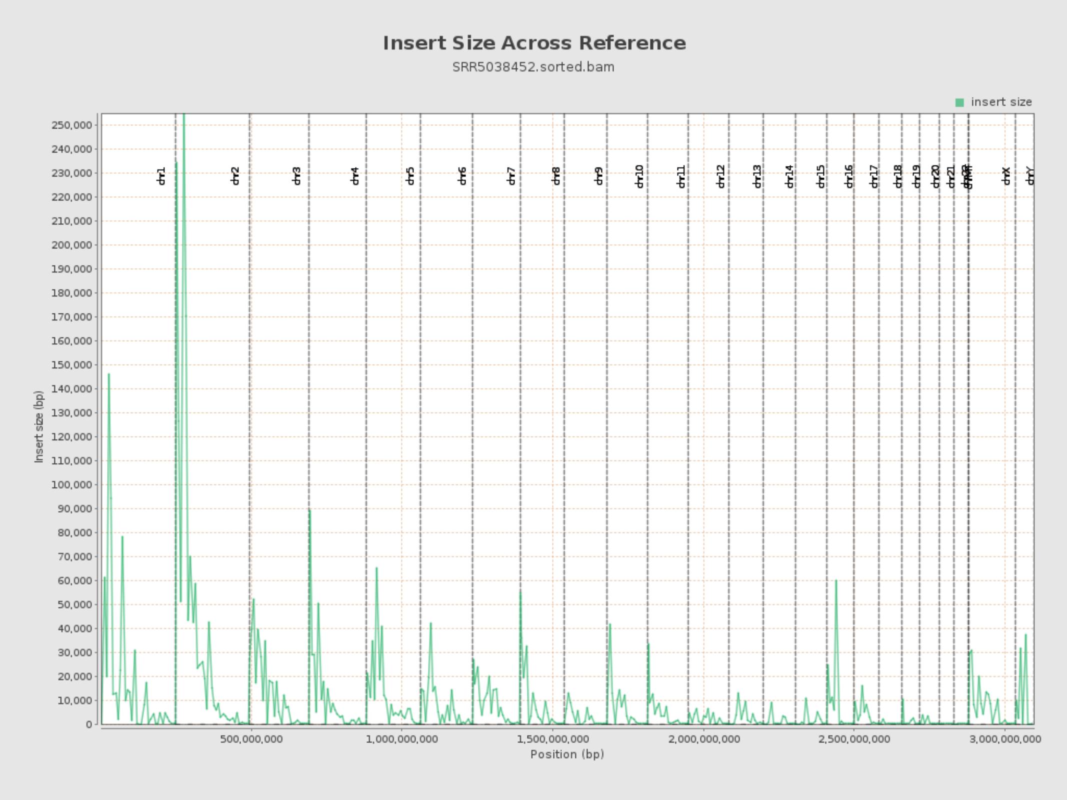
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram