Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 22:57:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038466.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_SRR5038466 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038466_1.fastq.gz SRR5038466_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 22:57:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038466.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,357,846
Mapped reads	13,702,088 / 95.43%
Unmapped reads	655,758 / 4.57%
Mapped paired reads	13,702,088 / 95.43%
Mapped reads, first in pair	6,926,263 / 48.24%
Mapped reads, second in pair	6,775,825 / 47.19%
Mapped reads, both in pair	13,530,202 / 94.24%
Mapped reads, singletons	171,886 / 1.2%
Secondary alignments	0
Supplementary alignments	238,608 / 1.66%
Read min/max/mean length	30 / 150 / 150.84
Duplicated reads (estimated)	2,142,685 / 14.92%
Duplication rate	9.5%
Clipped reads	3,044,762 / 21.21%

2.2. ACGT Content

Number/percentage of A's	582,838,113 / 29.65%
Number/percentage of C's	394,562,189 / 20.07%
Number/percentage of T's	582,002,507 / 29.6%
Number/percentage of G's	406,471,030 / 20.68%
Number/percentage of N's	41,496 / 0%

GC Percentage	40.75%

2.3. Coverage

Mean	0.6355
Standard Deviation	9.397

2.4. Mapping Quality

Mean Mapping Quality	53.73

2.5. Insert size

Mean	86,053.61
Standard Deviation	2,783,683.62
P25/Median/P75	210 / 255 / 312

2.6. Mismatches and indels

General error rate	1.53%
Mismatches	28,969,100
Insertions	405,215
Mapped reads with at least one insertion	2.74%
Deletions	769,385
Mapped reads with at least one deletion	5.36%
Homopolymer indels	46.65%

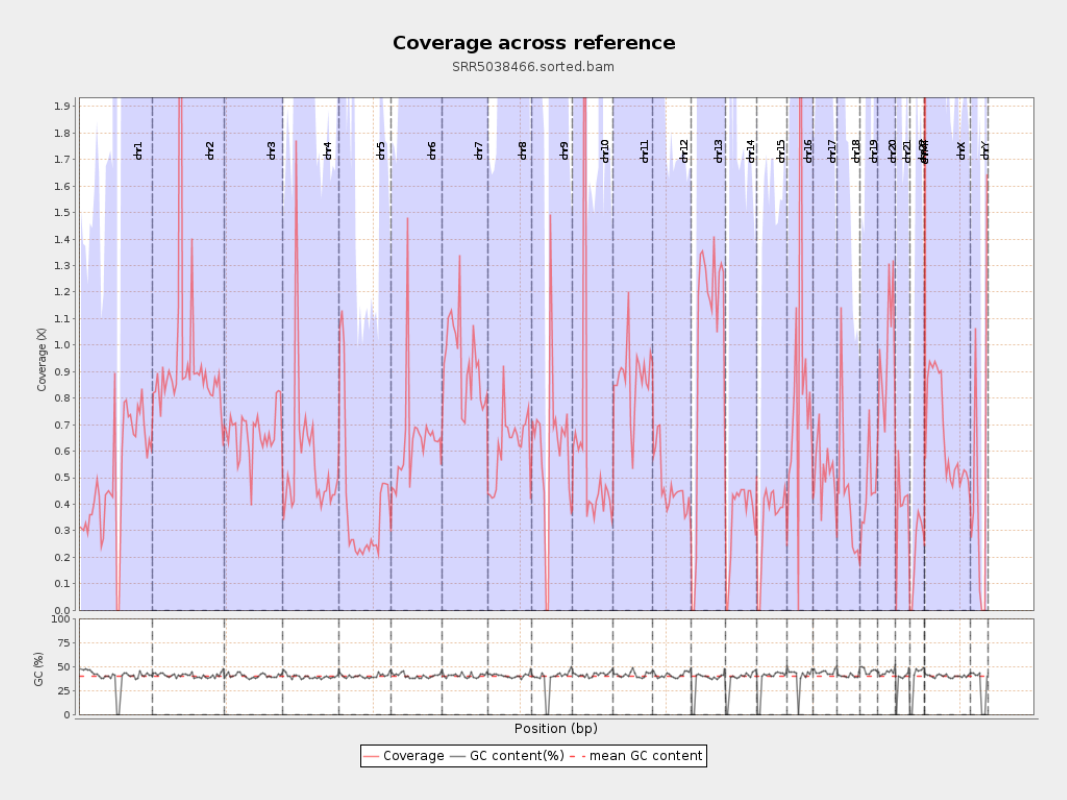
2.7. Chromosome stats

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

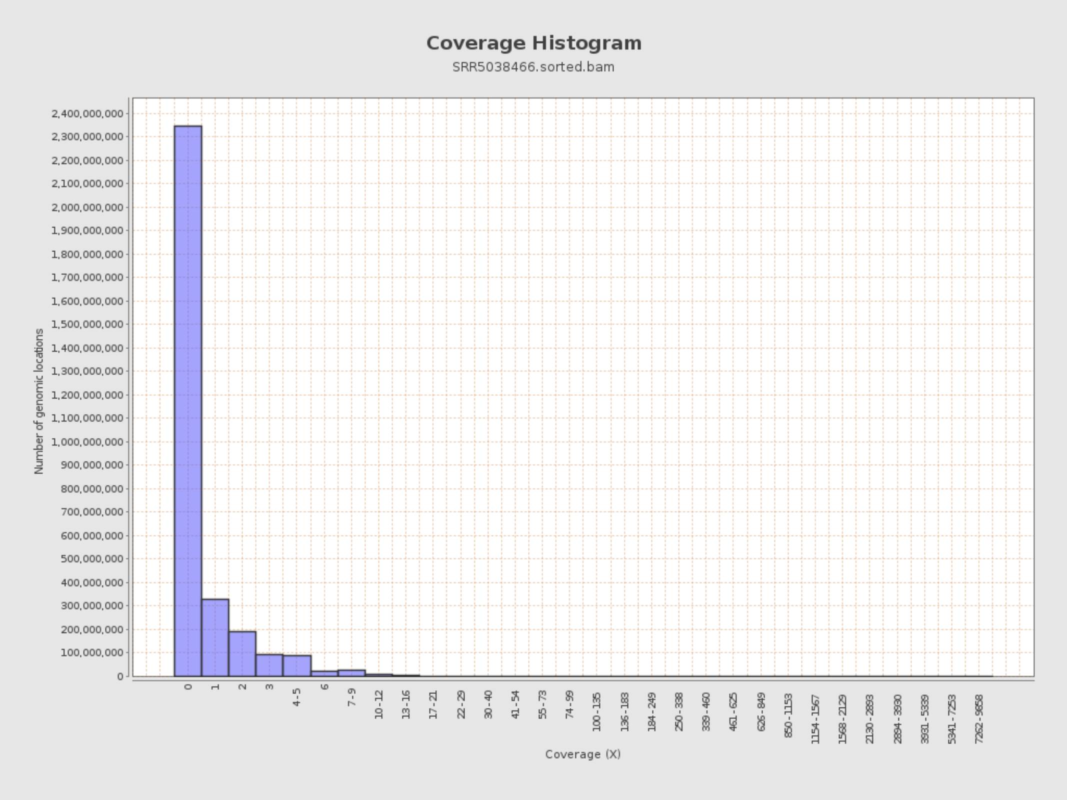
		bases	coverage	deviation
chr1	249250621	127365671	0.511	7.5224
chr2	243199373	234030600	0.9623	15.3332
chr3	198022430	132958604	0.6714	1.606
chr4	191154276	107188796	0.5607	8.5574
chr5	180915260	72383349	0.4001	1.3975
chr6	171115067	110240053	0.6442	9.2607
chr7	159138663	147661234	0.9279	9.4931
chr8	146364022	90330738	0.6172	2.9456
chr9	141213431	84688422	0.5997	16.4029
chr10	135534747	84385398	0.6226	20.195
chr11	135006516	116249221	0.8611	6.846
chr12	133851895	63093888	0.4714	1.3638
chr13	115169878	119022511	1.0335	2.1317
chr14	107349540	37568849	0.35	1.3656
chr15	102531392	34913996	0.3405	1.0507
chr16	90354753	79041220	0.8748	15.7565
chr17	81195210	41873518	0.5157	5.8553
chr18	78077248	33729259	0.432	13.5953
chr19	59128983	26018507	0.44	4.6313
chr20	63025520	60978693	0.9675	3.3687
chr21	48129895	18769454	0.39	4.3072
chr22	51304566	11523295	0.2246	1.169
chrMT	16571	1439828	86.8884	53.9834
chrX	155270560	102580632	0.6607	2.326

chrY	59373566	29428723	0.4957	14.5141

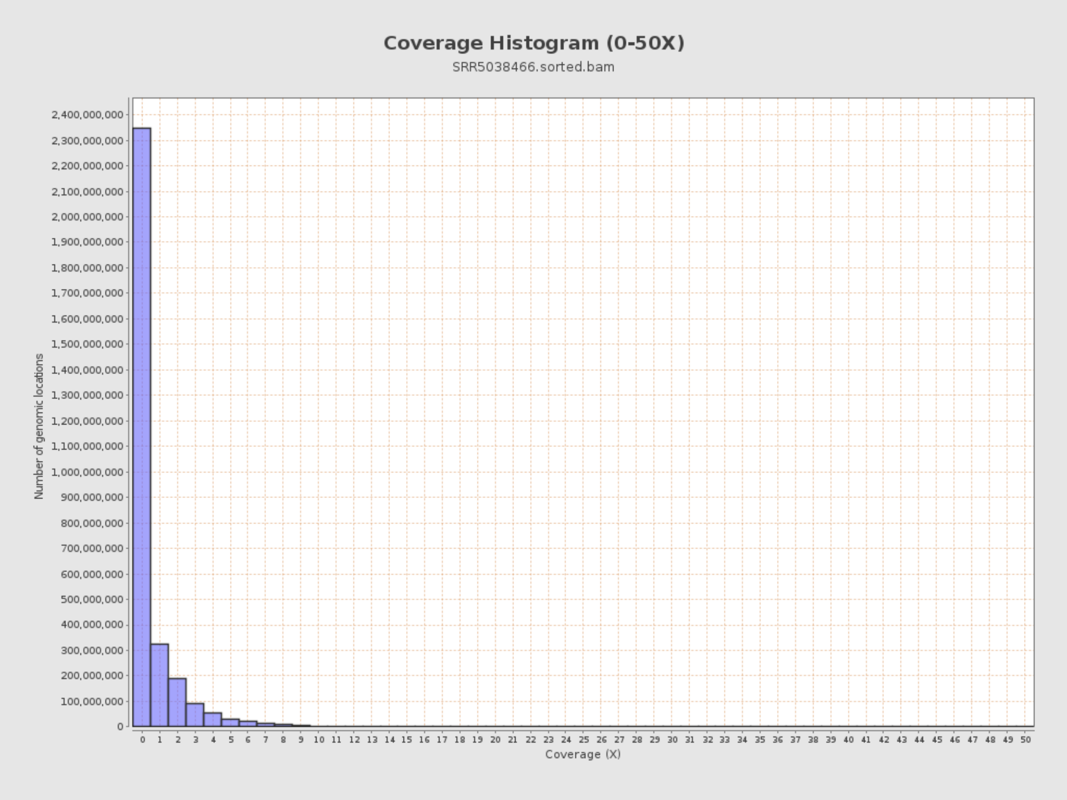
3. Results : Coverage across reference



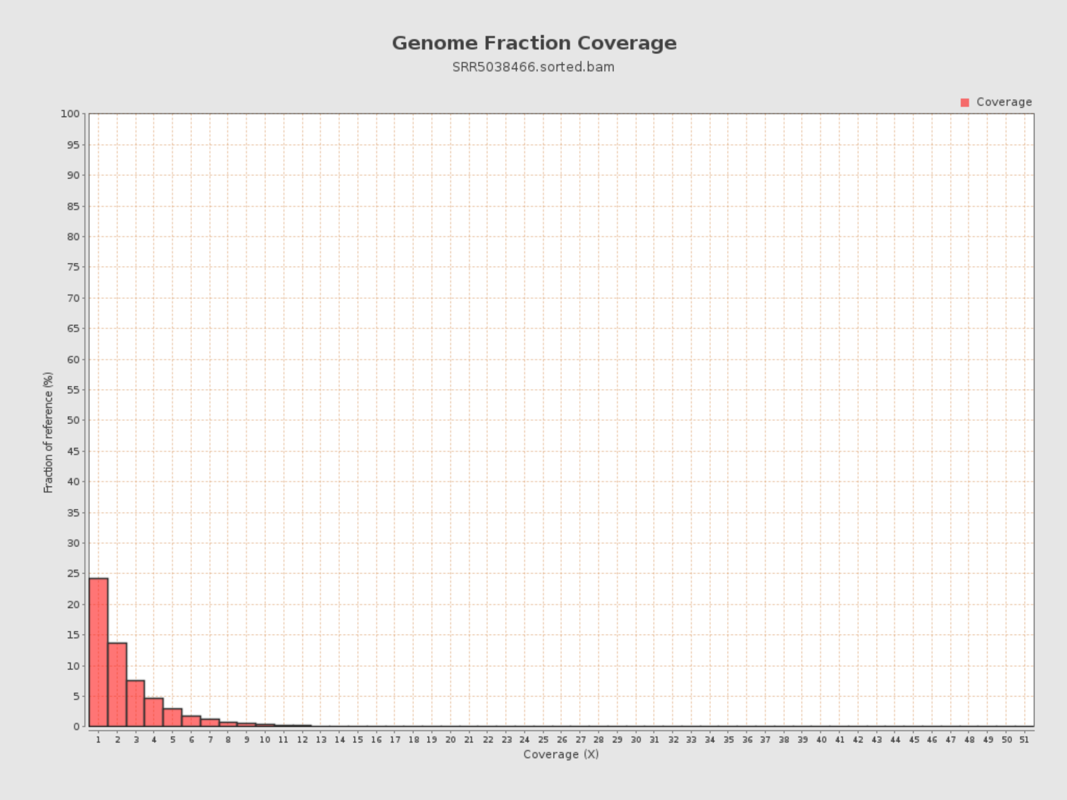
4. Results : Coverage Histogram



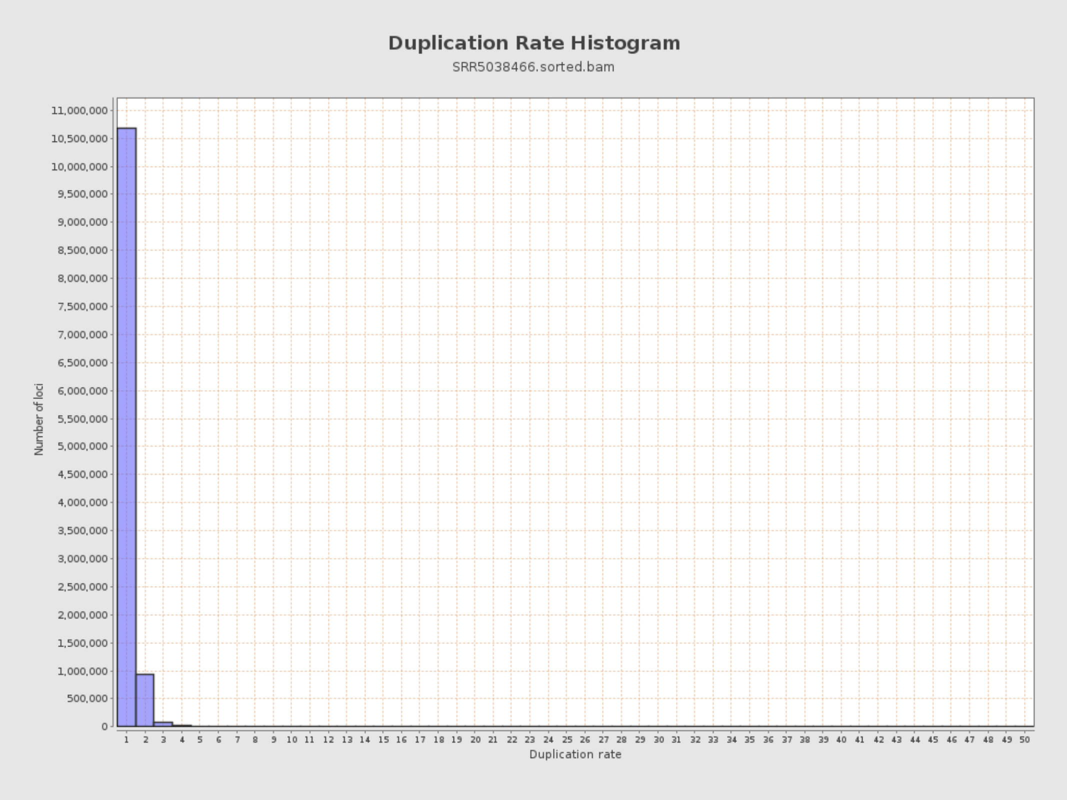
5. Results : Coverage Histogram (0-50X)



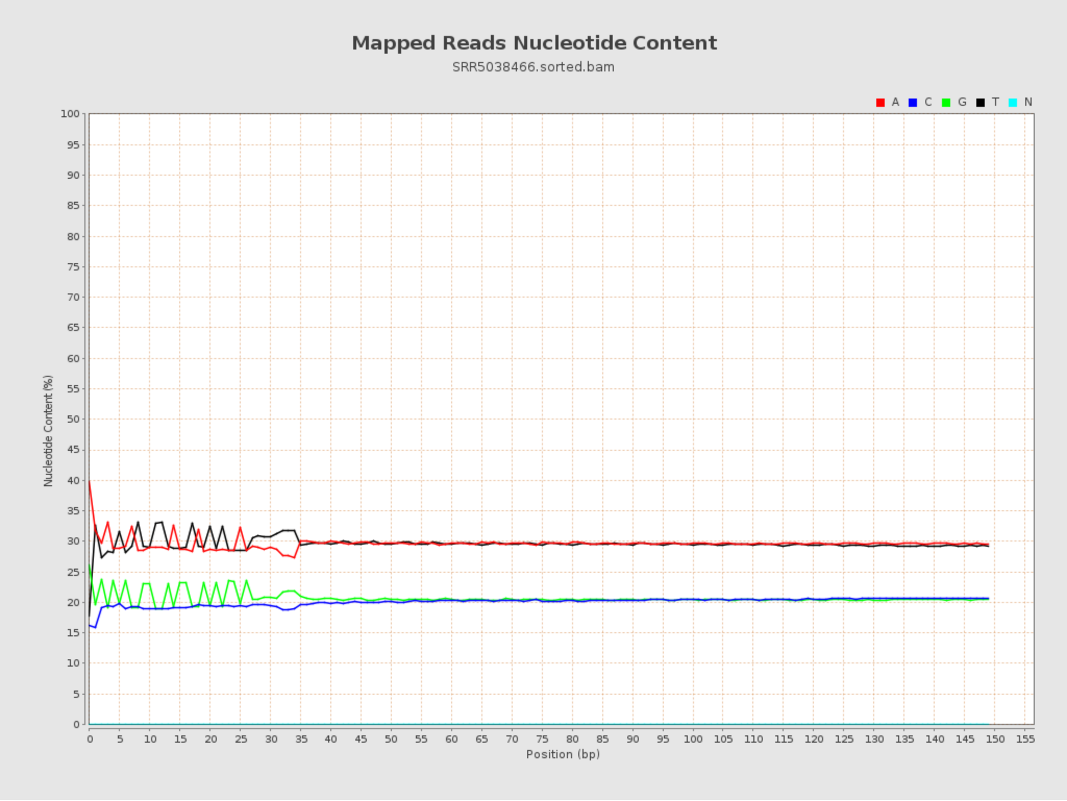
6. Results : Genome Fraction Coverage



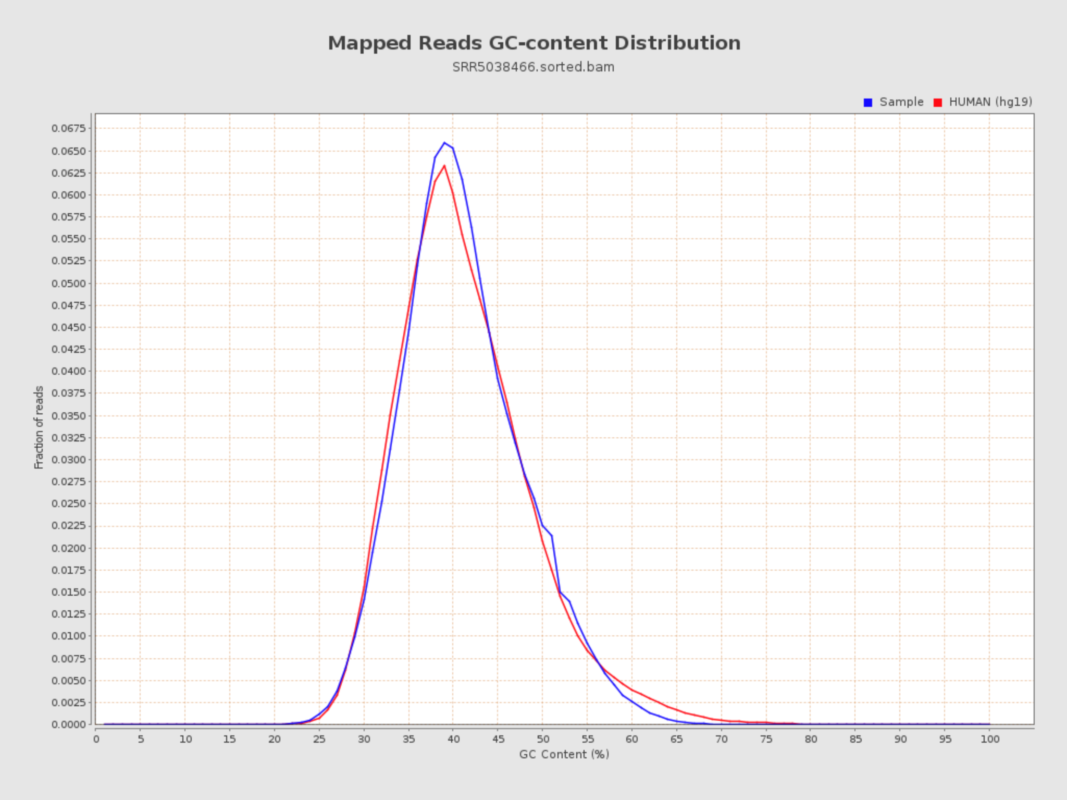
7. Results : Duplication Rate Histogram



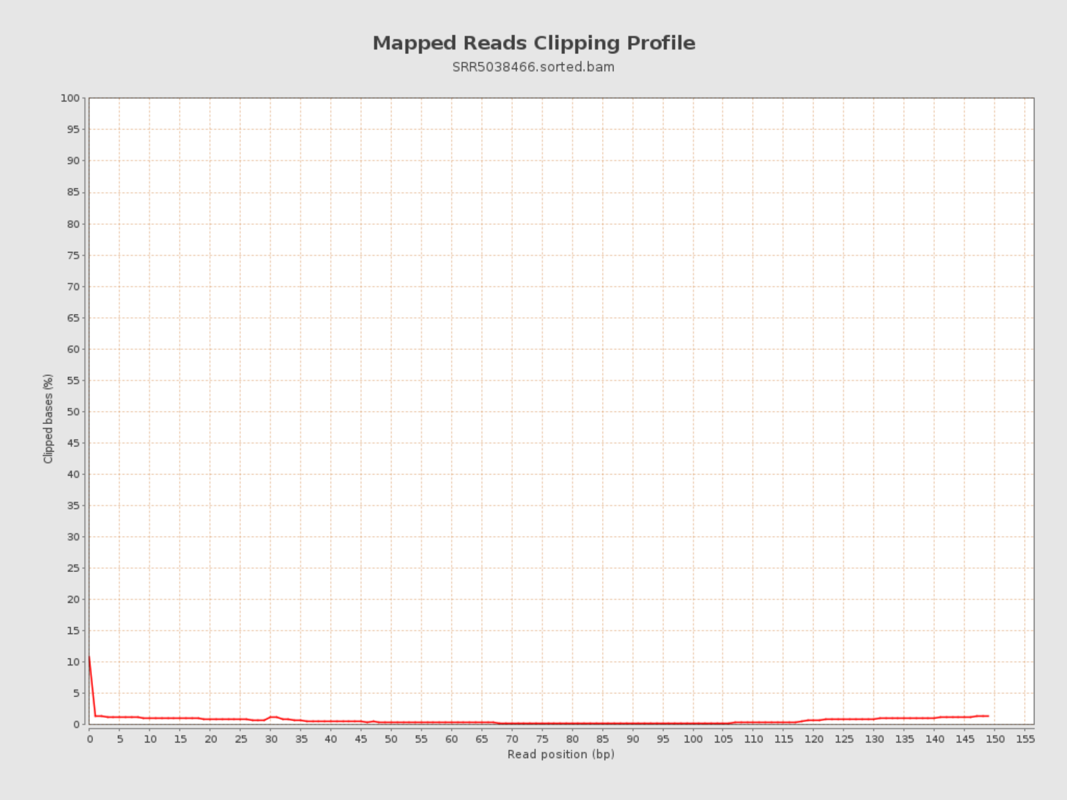
8. Results : Mapped Reads Nucleotide Content



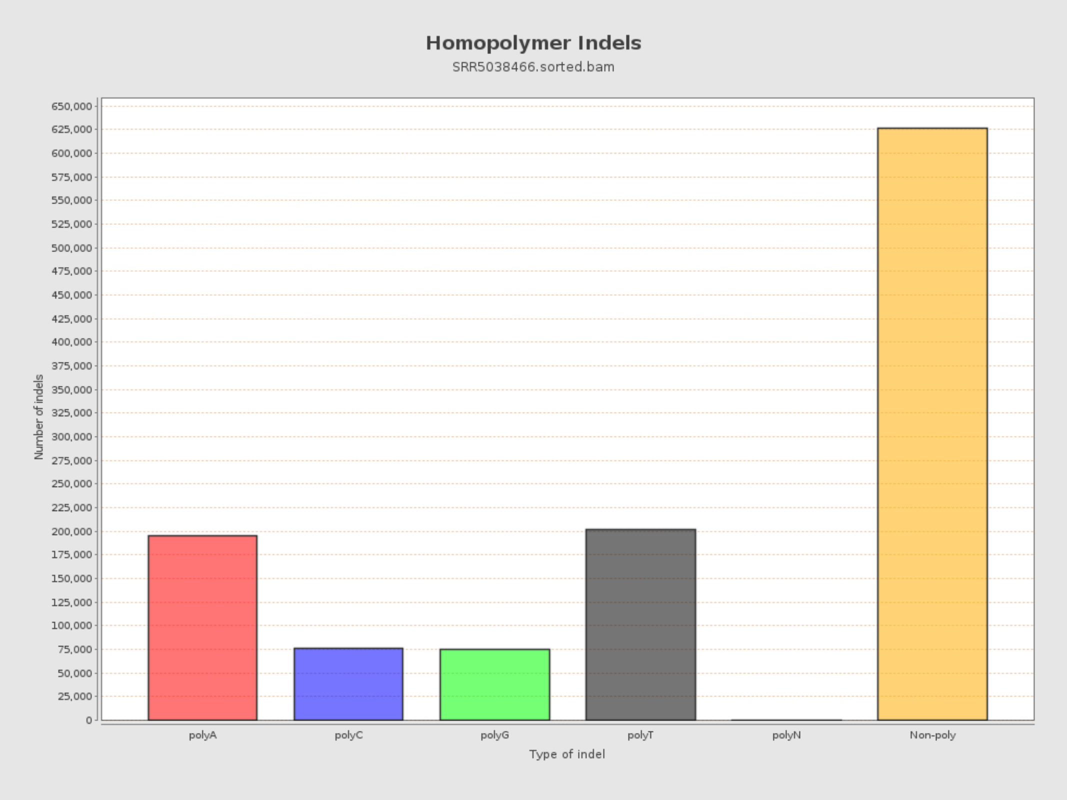
9. Results : Mapped Reads GC-content Distribution



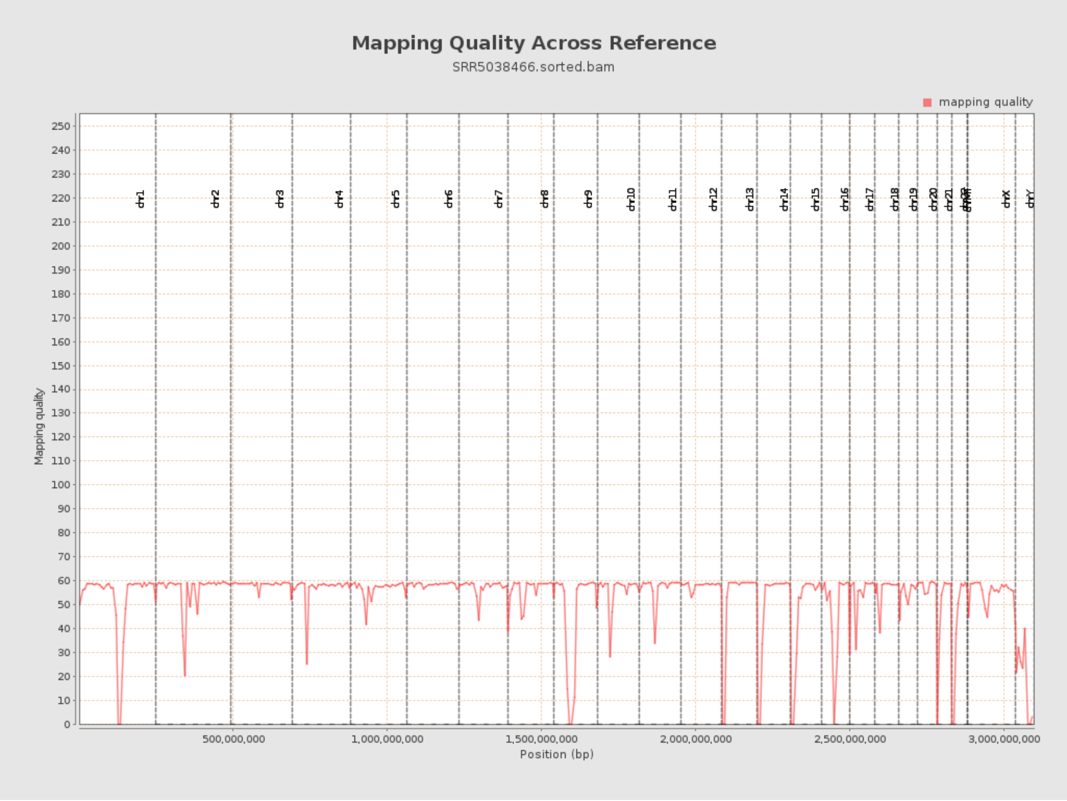
10. Results : Mapped Reads Clipping Profile



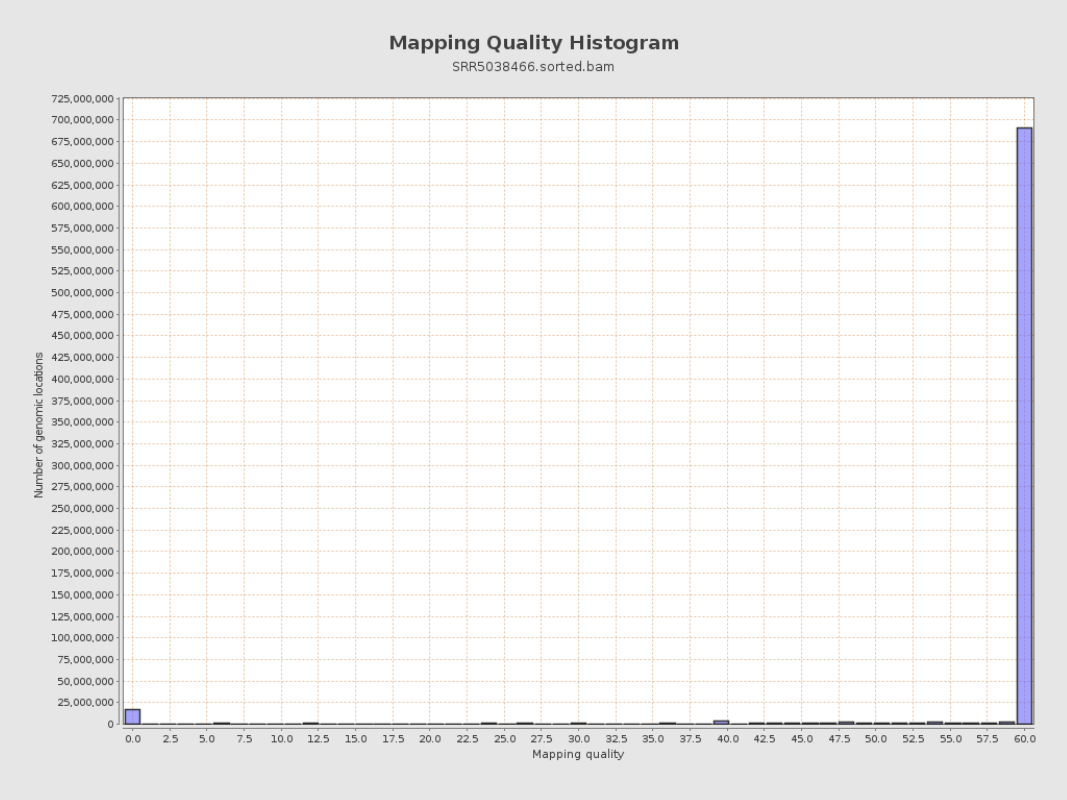
11. Results : Homopolymer Indels



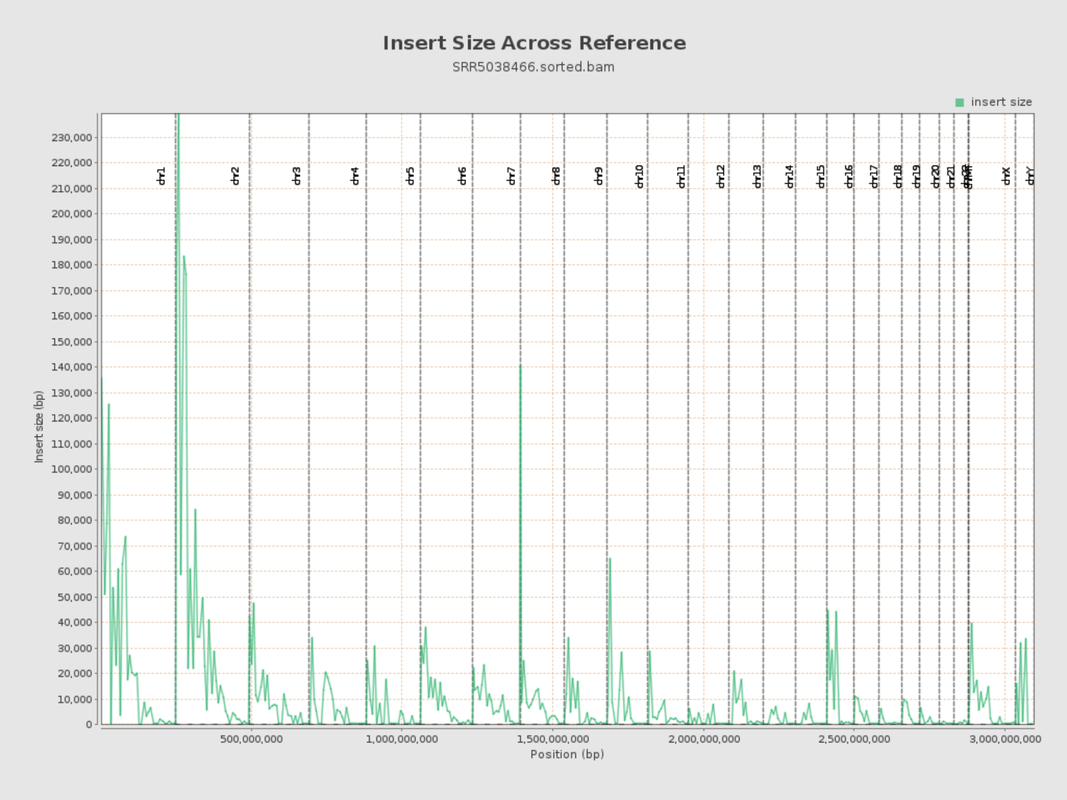
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram