Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 20:00:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038411.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_SRR5038411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038411_1.fastq.gz SRR5038411_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 20:00:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038411.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,397,660
Mapped reads	14,083,609 / 97.82%
Unmapped reads	314,051 / 2.18%
Mapped paired reads	14,083,609 / 97.82%
Mapped reads, first in pair	7,108,793 / 49.37%
Mapped reads, second in pair	6,974,816 / 48.44%
Mapped reads, both in pair	13,931,422 / 96.76%
Mapped reads, singletons	152,187 / 1.06%
Secondary alignments	0
Supplementary alignments	269,940 / 1.87%
Read min/max/mean length	30 / 150 / 150.94
Duplicated reads (estimated)	1,966,448 / 13.66%
Duplication rate	8.72%
Clipped reads	3,371,268 / 23.42%

2.2. ACGT Content

Number/percentage of A's	581,458,337 / 28.89%
Number/percentage of C's	415,000,971 / 20.62%
Number/percentage of T's	582,618,888 / 28.95%
Number/percentage of G's	433,264,501 / 21.53%
Number/percentage of N's	43,268 / 0%

GC Percentage	42.15%

2.3. Coverage

Mean	0.6506
Standard Deviation	8.2178

2.4. Mapping Quality

Mean Mapping Quality	53.78

2.5. Insert size

Mean	106,307.36
Standard Deviation	3,102,667.58
P25/Median/P75	221 / 261 / 312

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	26,807,731
Insertions	392,626
Mapped reads with at least one insertion	2.55%
Deletions	736,934
Mapped reads with at least one deletion	4.98%
Homopolymer indels	45.45%

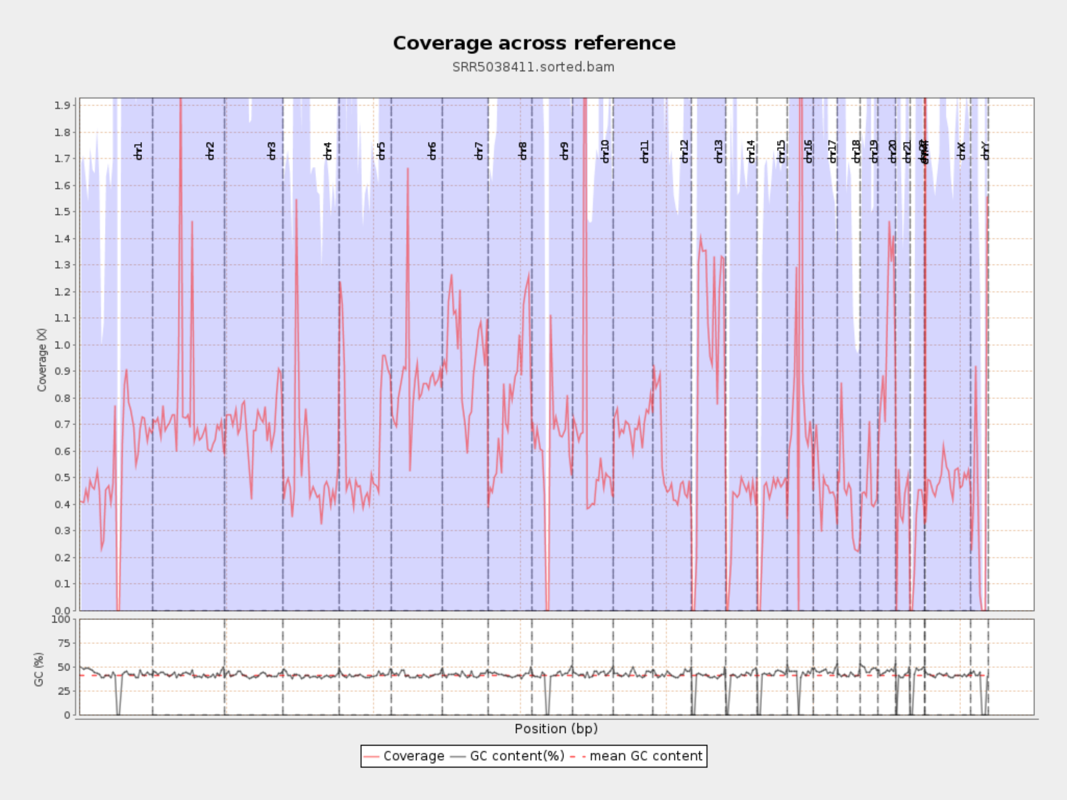
2.7. Chromosome stats

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

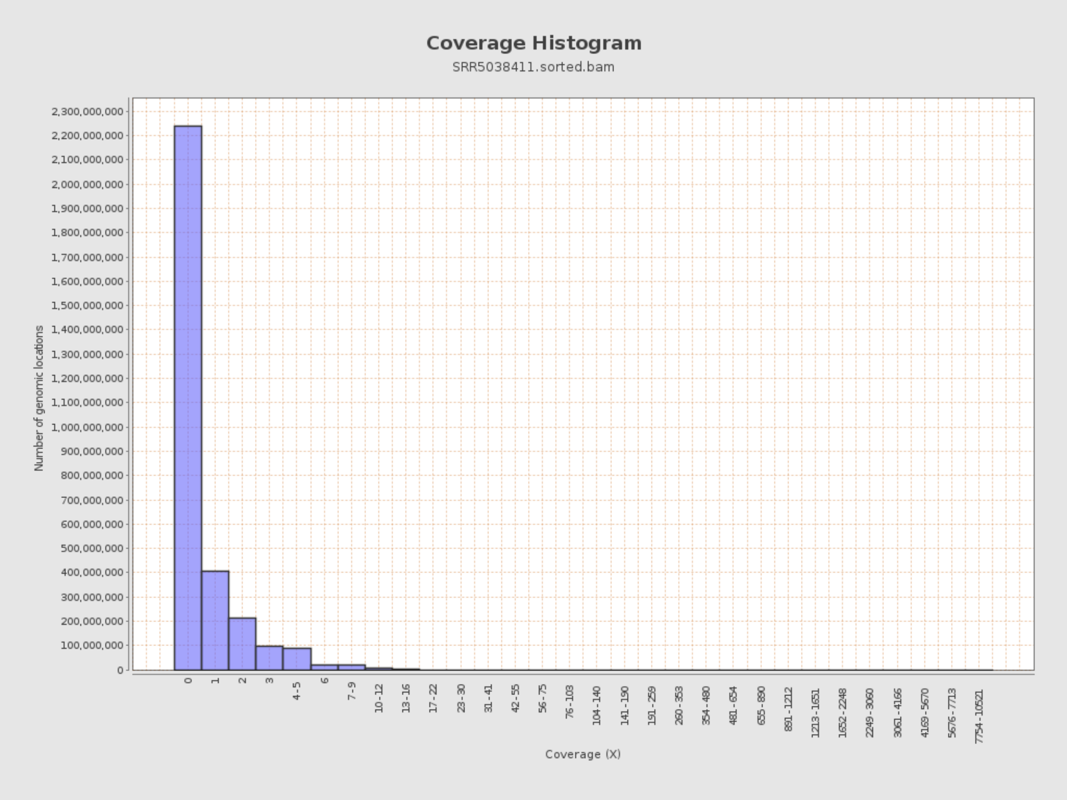
		bases	coverage	deviation
chr1	249250621	132865685	0.5331	5.2135
chr2	243199373	184845329	0.7601	11.0359
chr3	198022430	140284696	0.7084	1.5247
chr4	191154276	101072752	0.5287	6.9471
chr5	180915260	115644950	0.6392	1.6773
chr6	171115067	147696291	0.8631	9.0644
chr7	159138663	153190637	0.9626	8.4486
chr8	146364022	116543994	0.7963	2.3467
chr9	141213431	84480068	0.5982	10.7226
chr10	135534747	91422061	0.6745	21.8596
chr11	135006516	93600324	0.6933	3.4154
chr12	133851895	73570335	0.5496	1.4196
chr13	115169878	114357555	0.9929	1.9645
chr14	107349540	40080292	0.3734	1.3537
chr15	102531392	39759184	0.3878	1.0395
chr16	90354753	83295362	0.9219	18.9757
chr17	81195210	38452295	0.4736	3.5538
chr18	78077248	33134559	0.4244	9.4256
chr19	59128983	26663574	0.4509	3.3536
chr20	63025520	65463308	1.0387	2.8496
chr21	48129895	18534681	0.3851	3.2918
chr22	51304566	14648670	0.2855	1.4829
chrMT	16571	945729	57.0713	25.7328
chrX	155270560	75945418	0.4891	1.5766

chrY	59373566	27481778	0.4629	12.8375

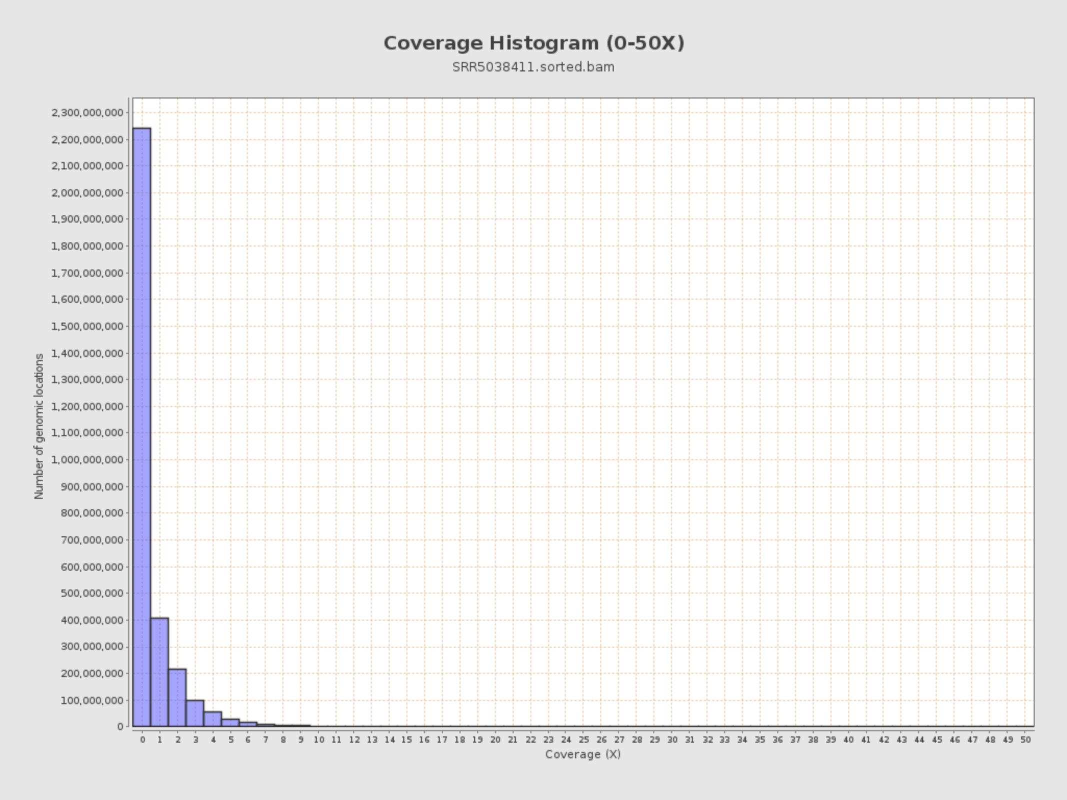
3. Results : Coverage across reference



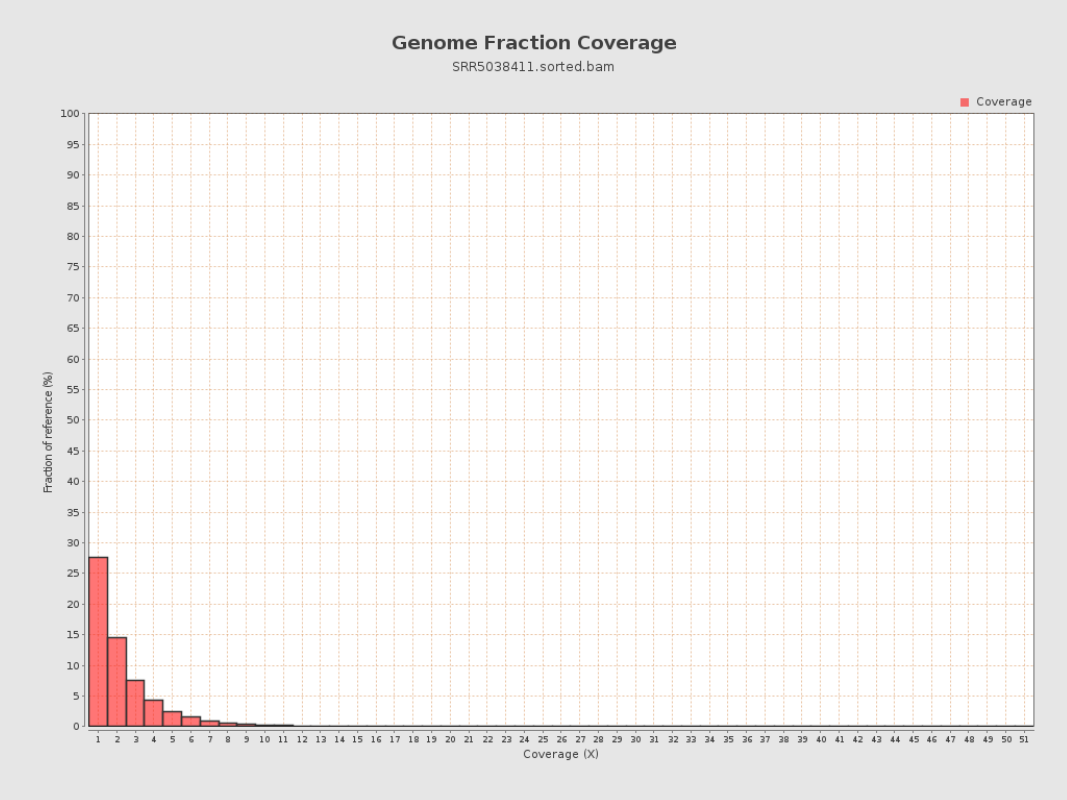
4. Results : Coverage Histogram



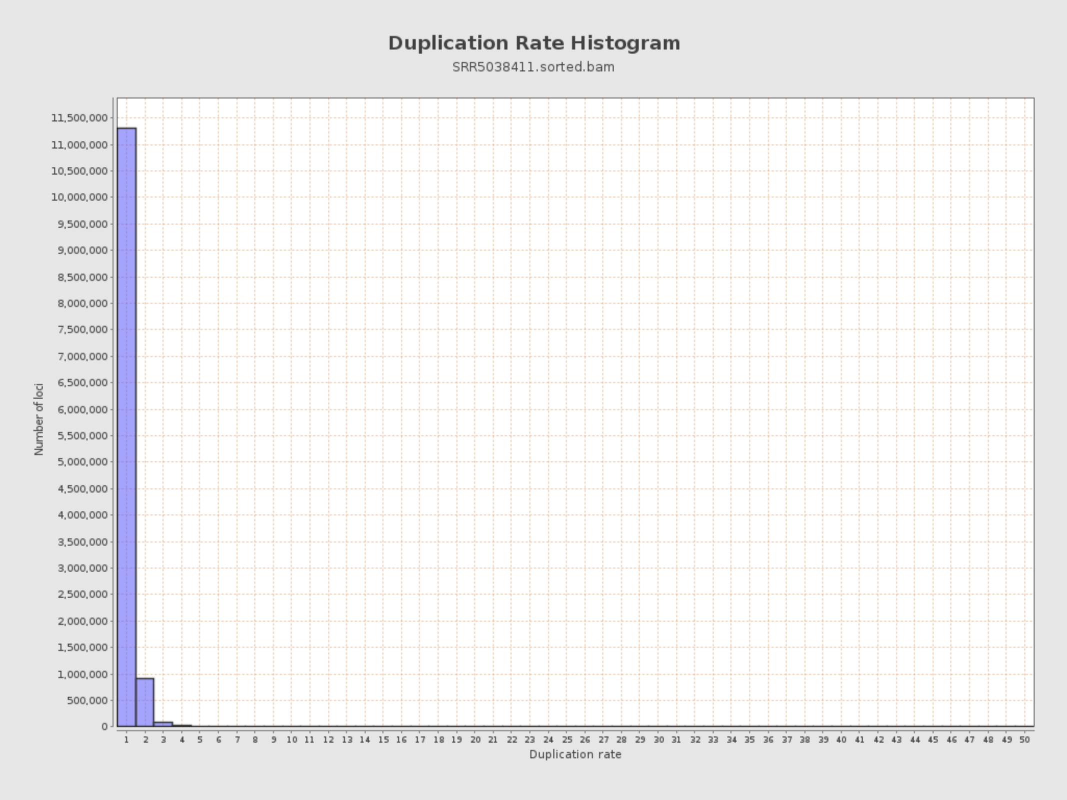
5. Results : Coverage Histogram (0-50X)



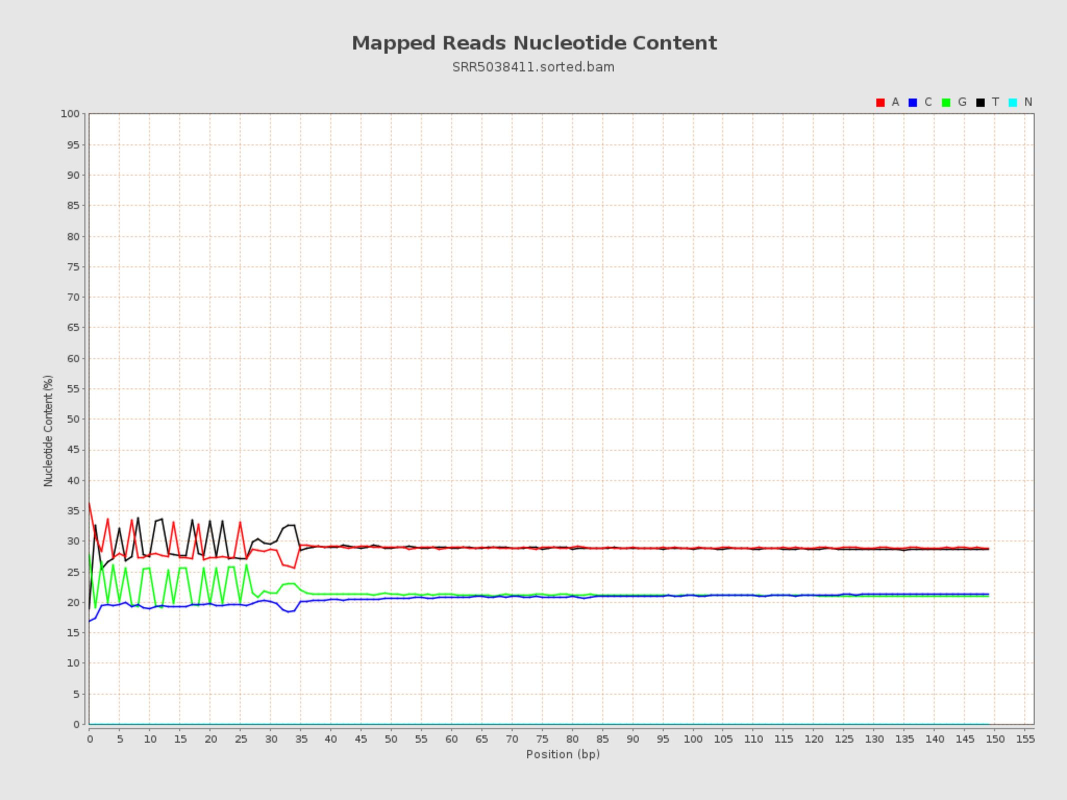
6. Results : Genome Fraction Coverage



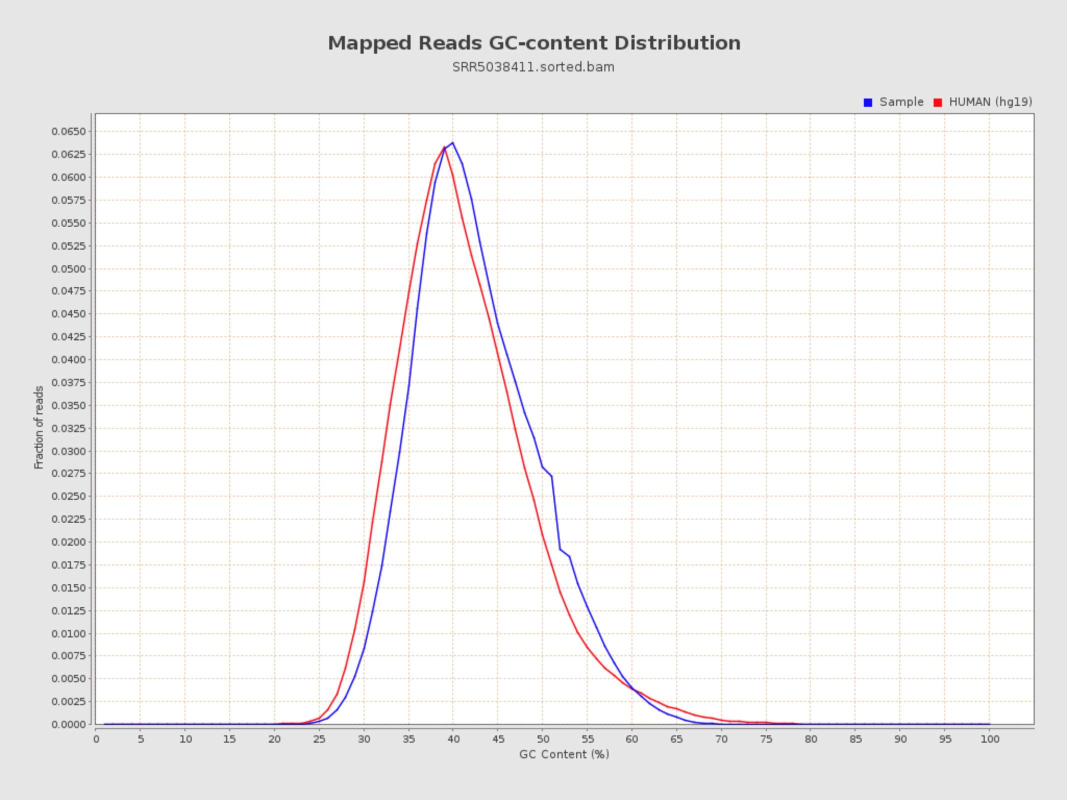
7. Results : Duplication Rate Histogram



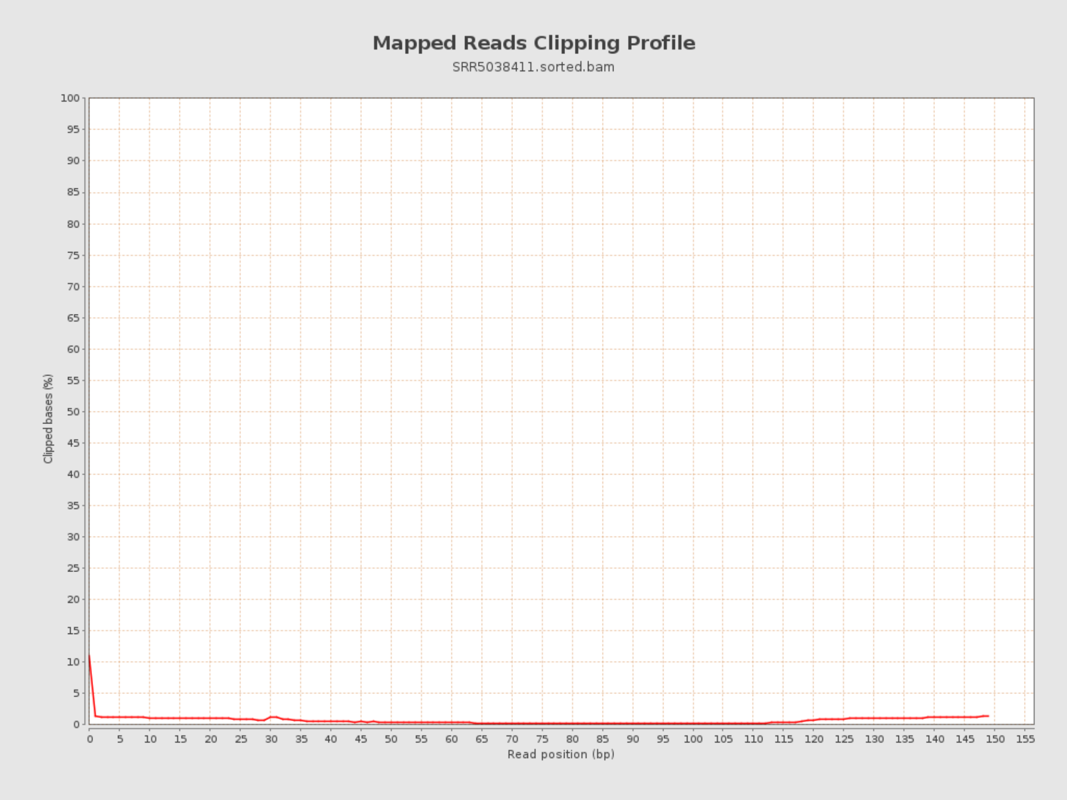
8. Results : Mapped Reads Nucleotide Content



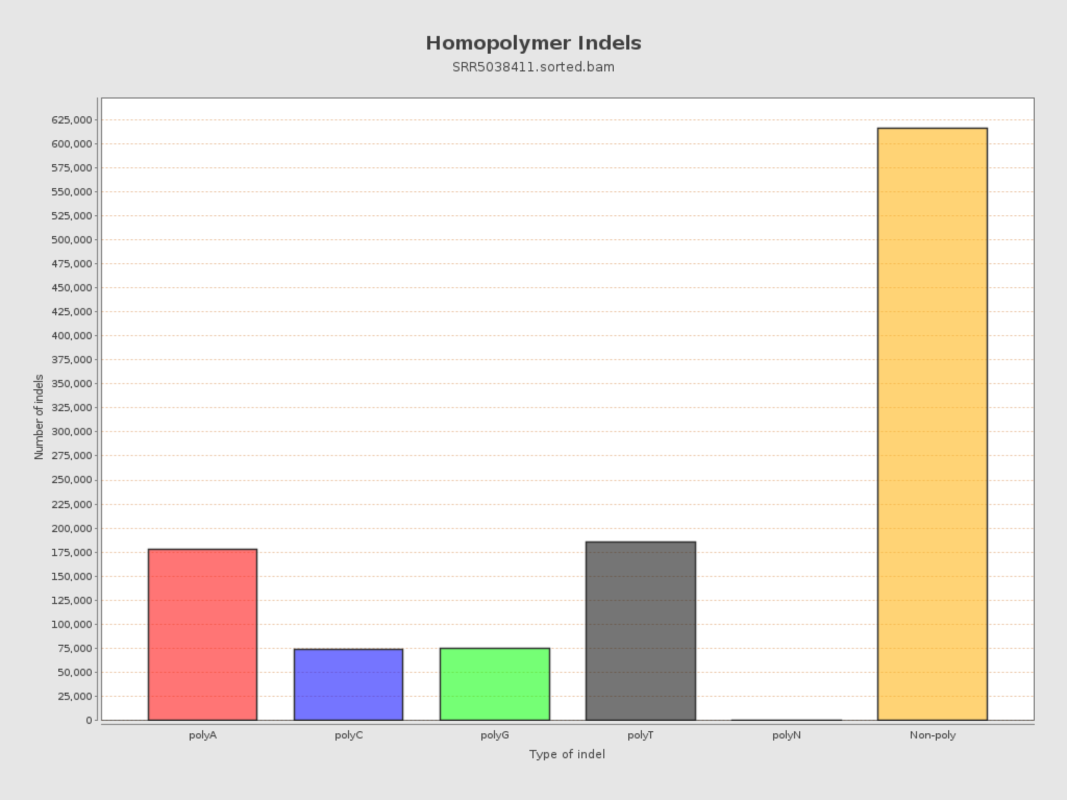
9. Results : Mapped Reads GC-content Distribution



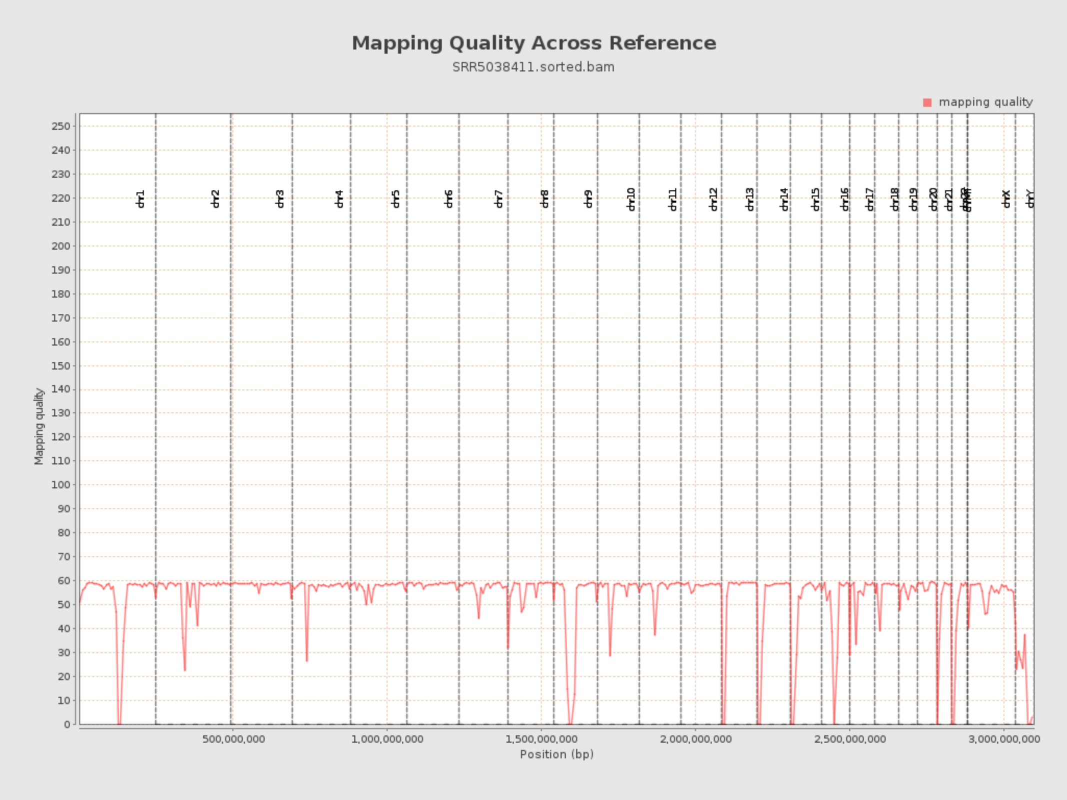
10. Results : Mapped Reads Clipping Profile



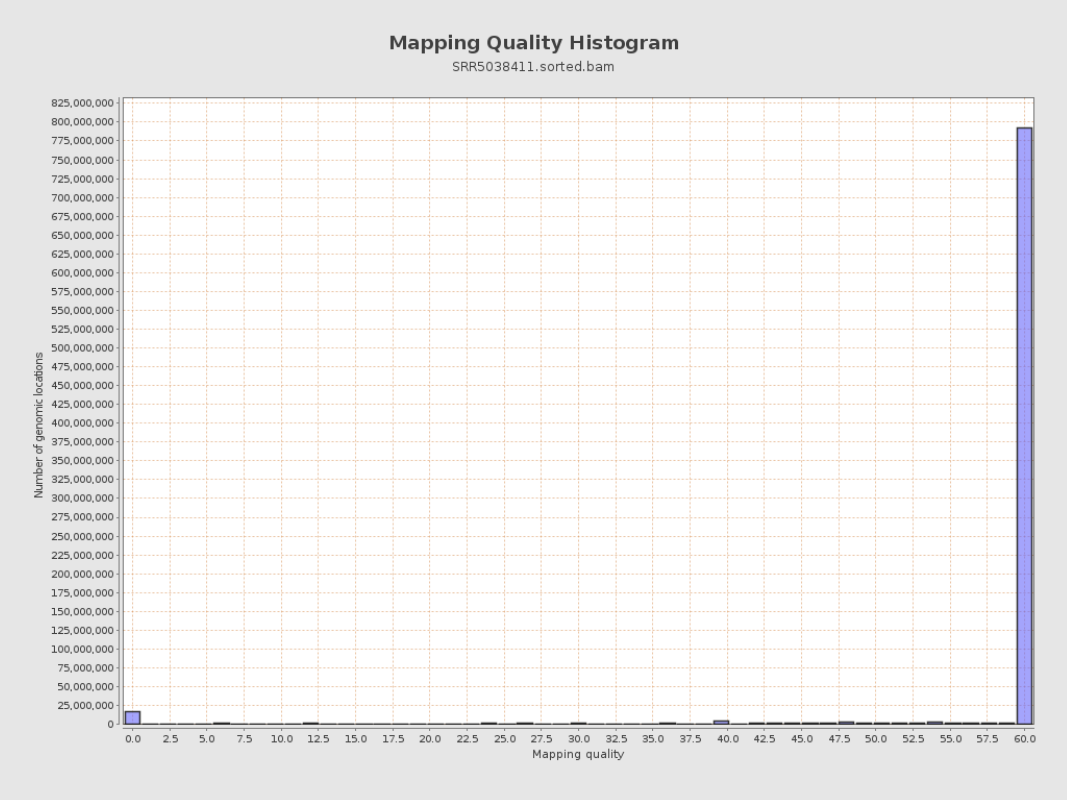
11. Results : Homopolymer Indels



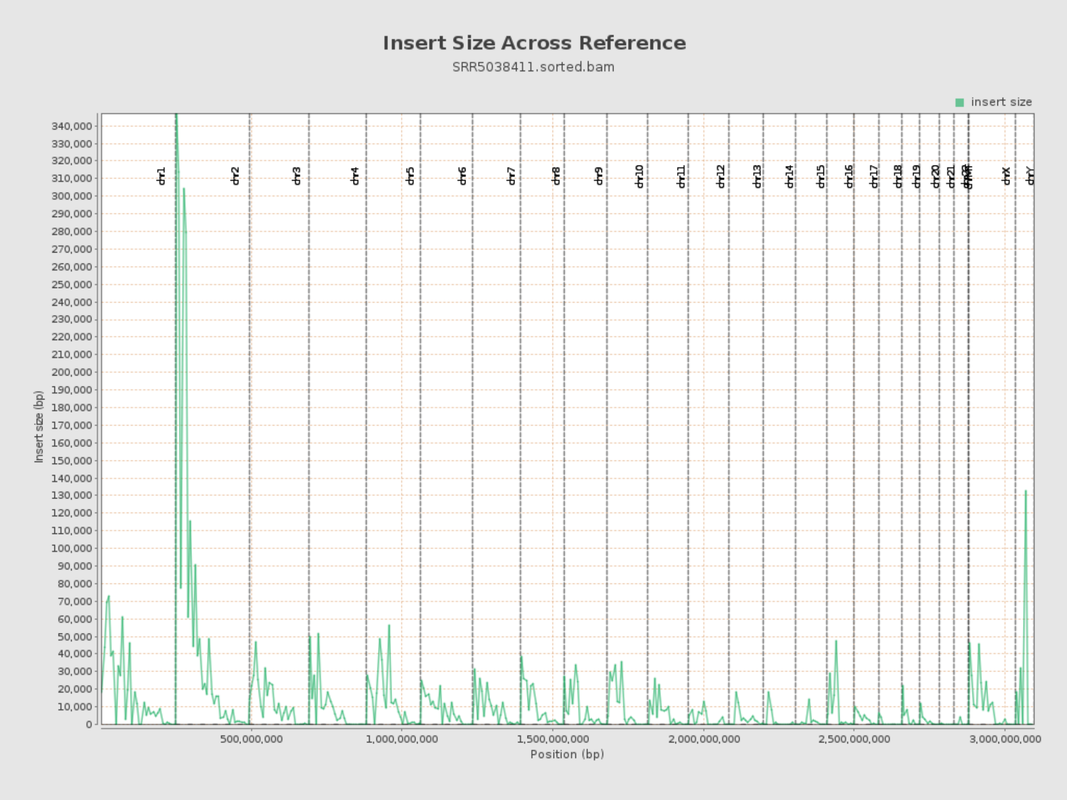
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram