Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 17:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038454.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_SRR5038454 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038454_1.fastq.gz SRR5038454_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 17:17:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038454.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,421,516
Mapped reads	14,013,680 / 97.17%
Unmapped reads	407,836 / 2.83%
Mapped paired reads	14,013,680 / 97.17%
Mapped reads, first in pair	7,076,612 / 49.07%
Mapped reads, second in pair	6,937,068 / 48.1%
Mapped reads, both in pair	13,845,674 / 96.01%
Mapped reads, singletons	168,006 / 1.16%
Secondary alignments	0
Supplementary alignments	371,073 / 2.57%
Read min/max/mean length	30 / 150 / 151.32
Duplicated reads (estimated)	2,614,097 / 18.13%
Duplication rate	10.03%
Clipped reads	4,149,500 / 28.77%

2.2. ACGT Content

Number/percentage of A's	578,764,494 / 29.29%
Number/percentage of C's	397,145,534 / 20.1%
Number/percentage of T's	584,170,906 / 29.56%
Number/percentage of G's	415,992,633 / 21.05%
Number/percentage of N's	41,839 / 0%

GC Percentage	41.15%

2.3. Coverage

Mean	0.6389
Standard Deviation	12.682

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	147,583.24
Standard Deviation	3,565,081.3
P25/Median/P75	215 / 256 / 307

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	30,839,740
Insertions	445,206
Mapped reads with at least one insertion	2.93%
Deletions	764,891
Mapped reads with at least one deletion	5.2%
Homopolymer indels	45.12%

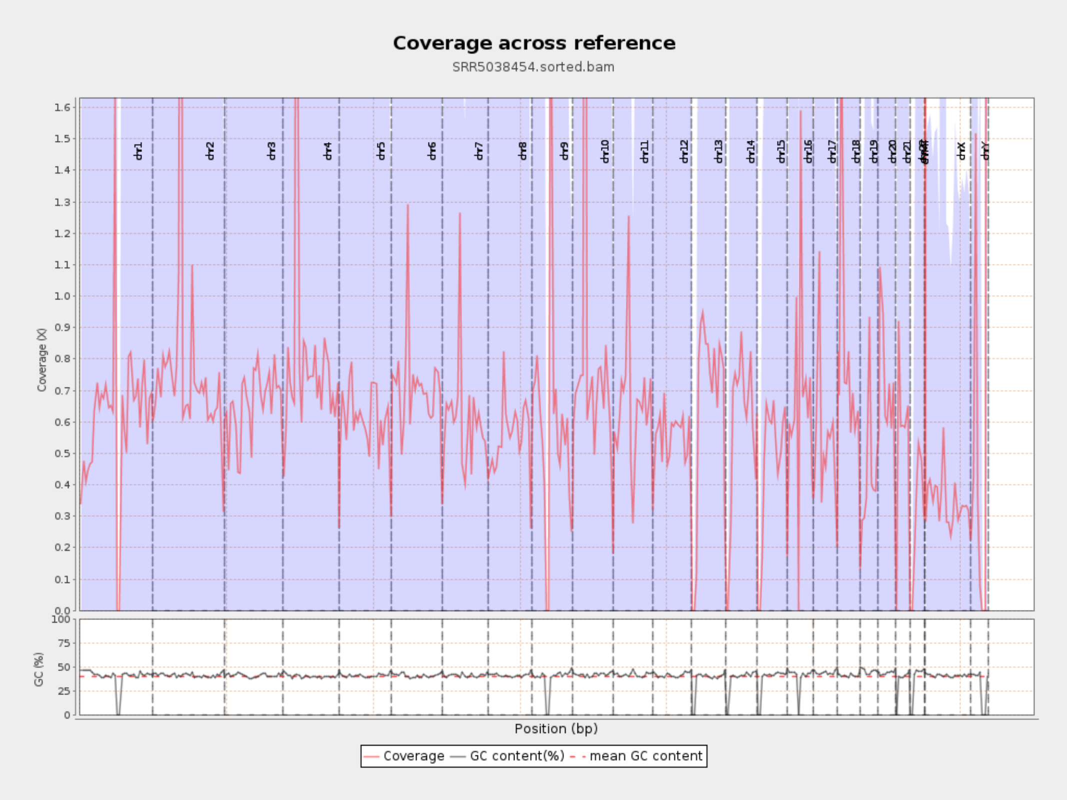
2.7. Chromosome stats

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

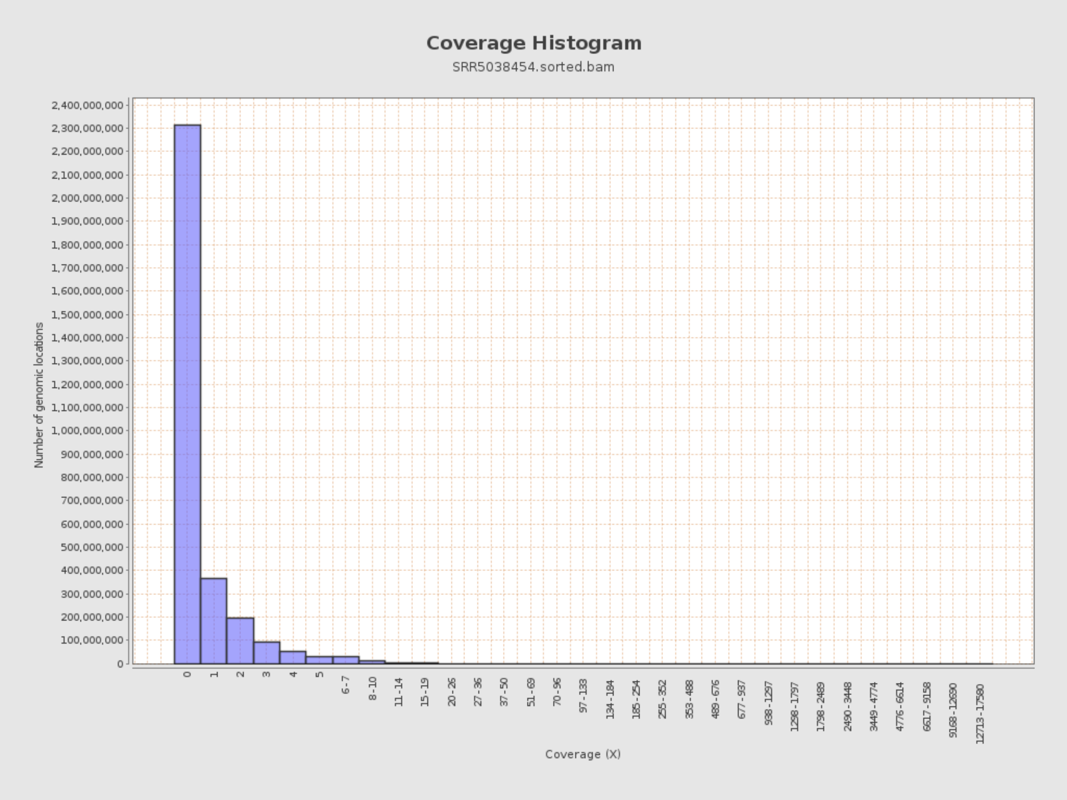
		bases	coverage	deviation
chr1	249250621	153813434	0.6171	15.5568
chr2	243199373	196343206	0.8073	17.6382
chr3	198022430	130684224	0.6599	1.5585
chr4	191154276	153266597	0.8018	13.5853
chr5	180915260	109028153	0.6026	1.7037
chr6	171115067	122562759	0.7163	5.9912
chr7	159138663	96030253	0.6034	8.9516
chr8	146364022	80989739	0.5533	3.2454
chr9	141213431	83440354	0.5909	28.357
chr10	135534747	117753917	0.8688	22.9314
chr11	135006516	86256836	0.6389	8.8901
chr12	133851895	73747075	0.551	1.4796
chr13	115169878	76555827	0.6647	1.5252
chr14	107349540	61618723	0.574	1.7592
chr15	102531392	47202713	0.4604	1.2335
chr16	90354753	59143263	0.6546	8.4105
chr17	81195210	43625896	0.5373	9.9014
chr18	78077248	62412611	0.7994	23.4423
chr19	59128983	24913366	0.4213	8.1895
chr20	63025520	44636069	0.7082	4.4083
chr21	48129895	27143574	0.564	6.3371
chr22	51304566	14980857	0.292	1.3424
chrMT	16571	6604323	398.547	224.3424
chrX	155270560	53288254	0.3432	2.539

chrY	59373566	51736226	0.8714	25.8443

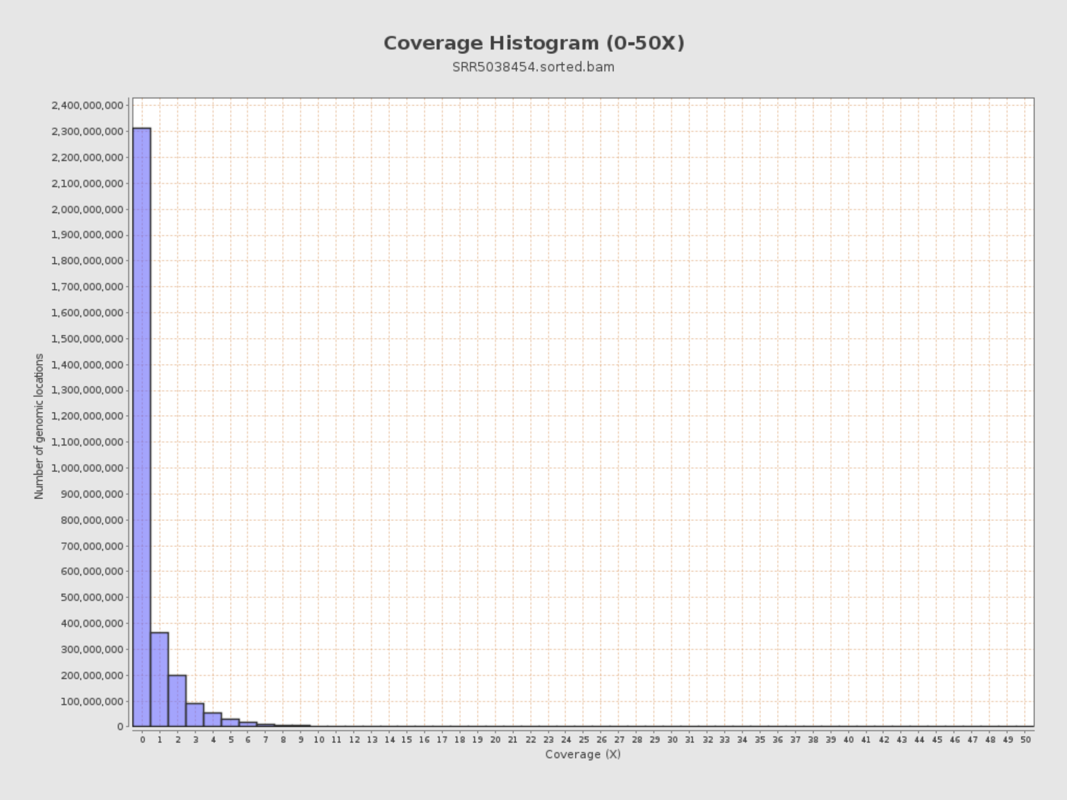
3. Results : Coverage across reference



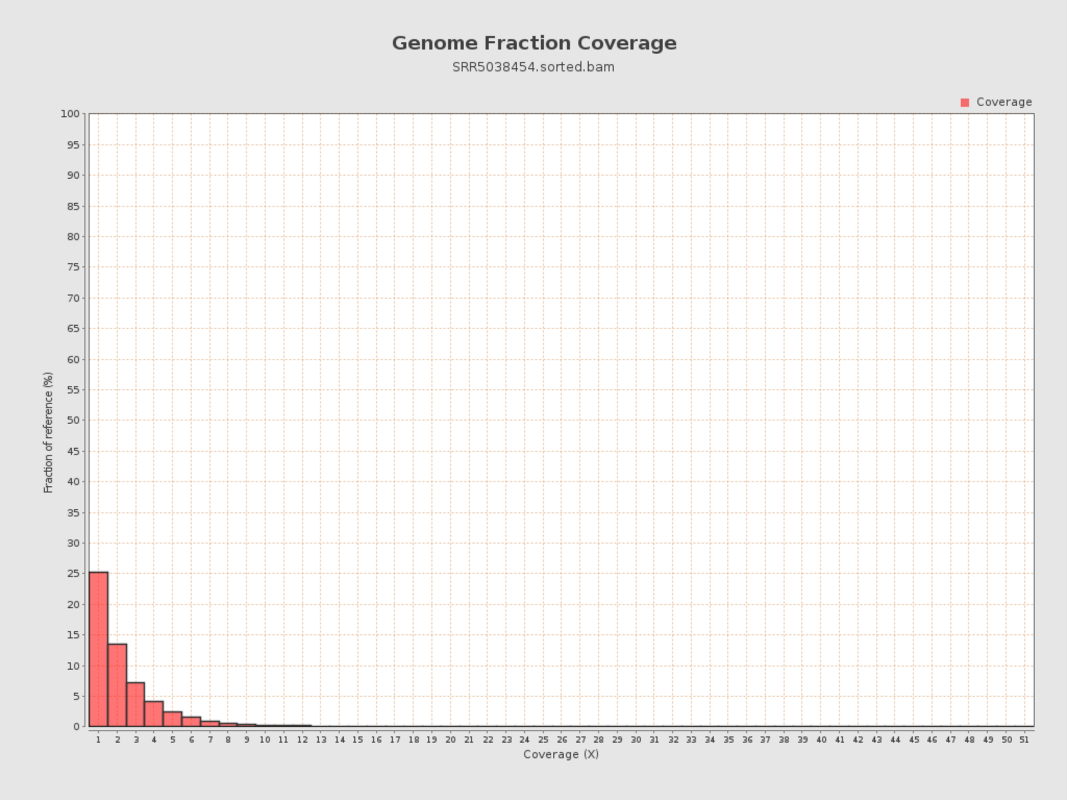
4. Results : Coverage Histogram



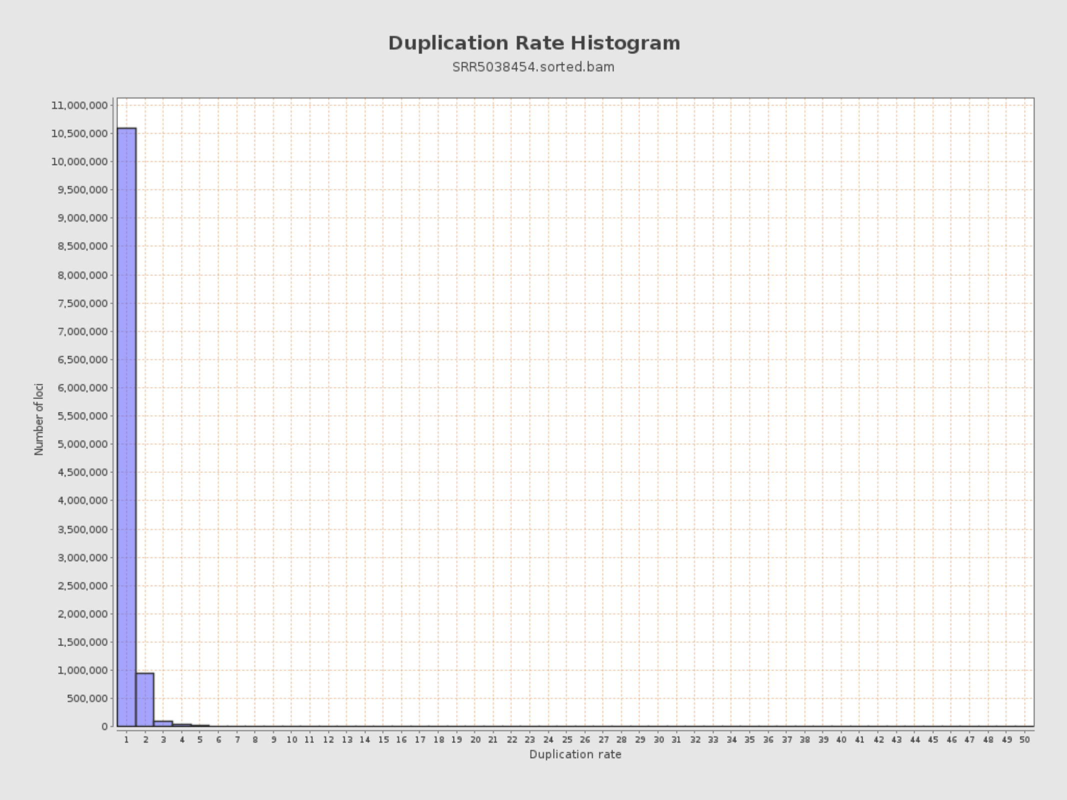
5. Results : Coverage Histogram (0-50X)



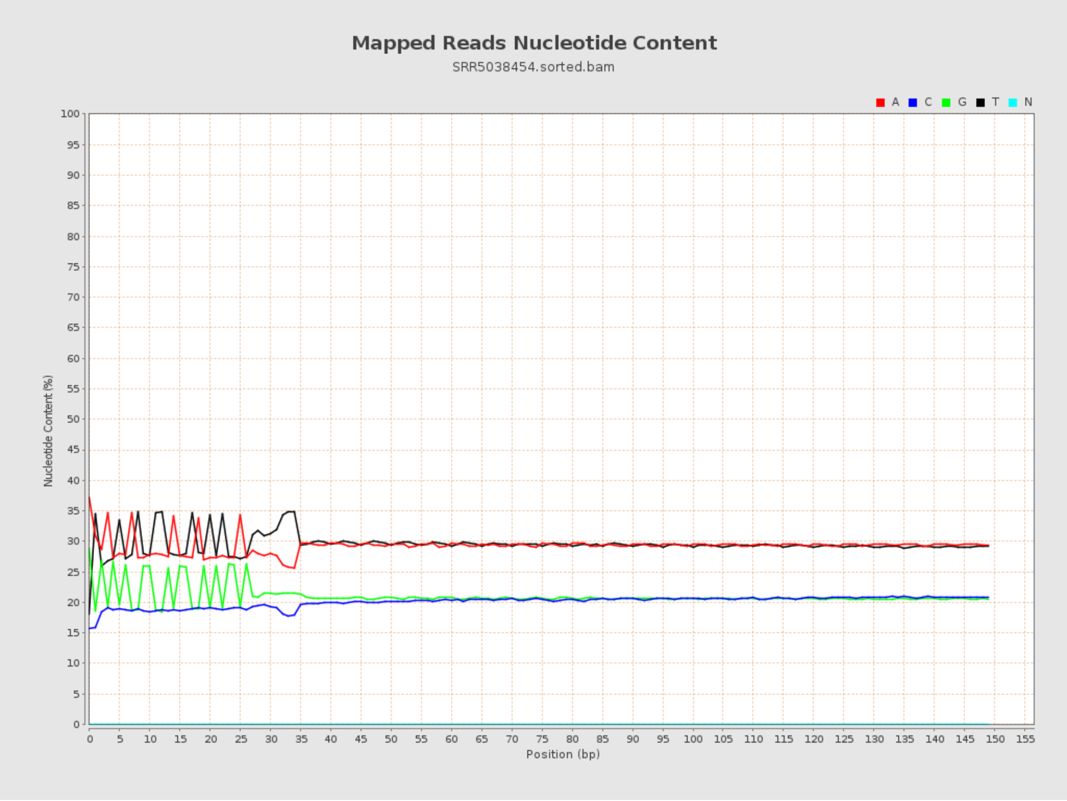
6. Results : Genome Fraction Coverage



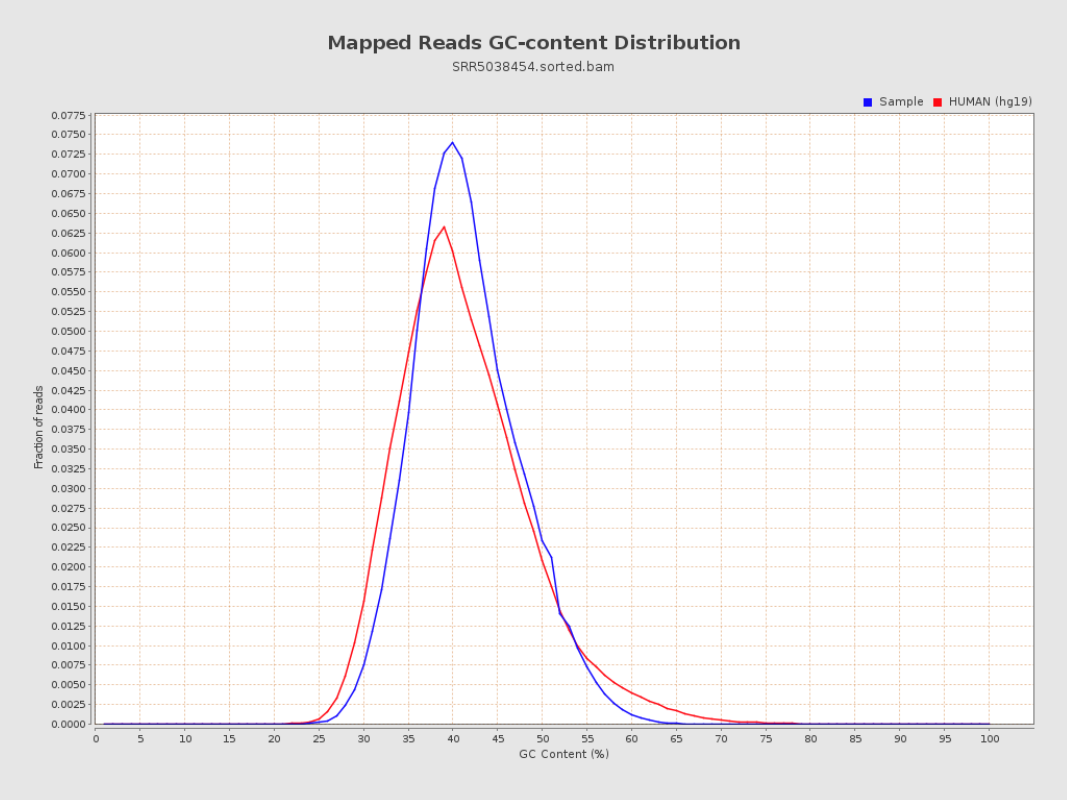
7. Results : Duplication Rate Histogram



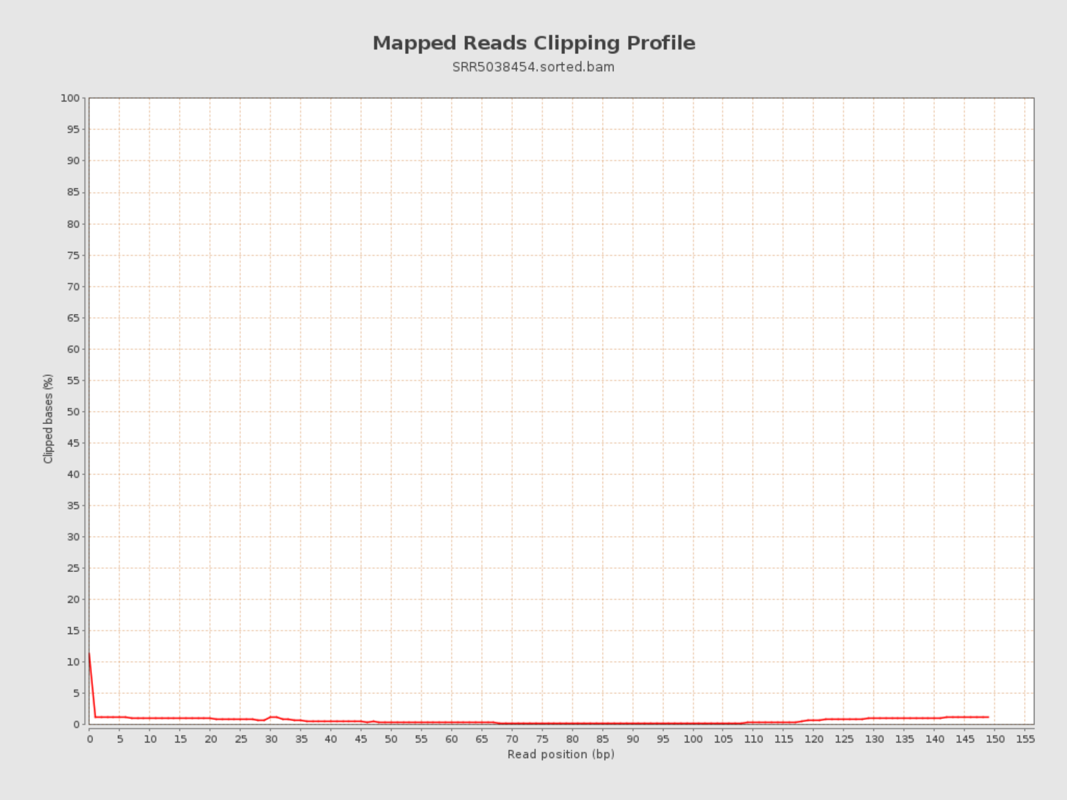
8. Results : Mapped Reads Nucleotide Content



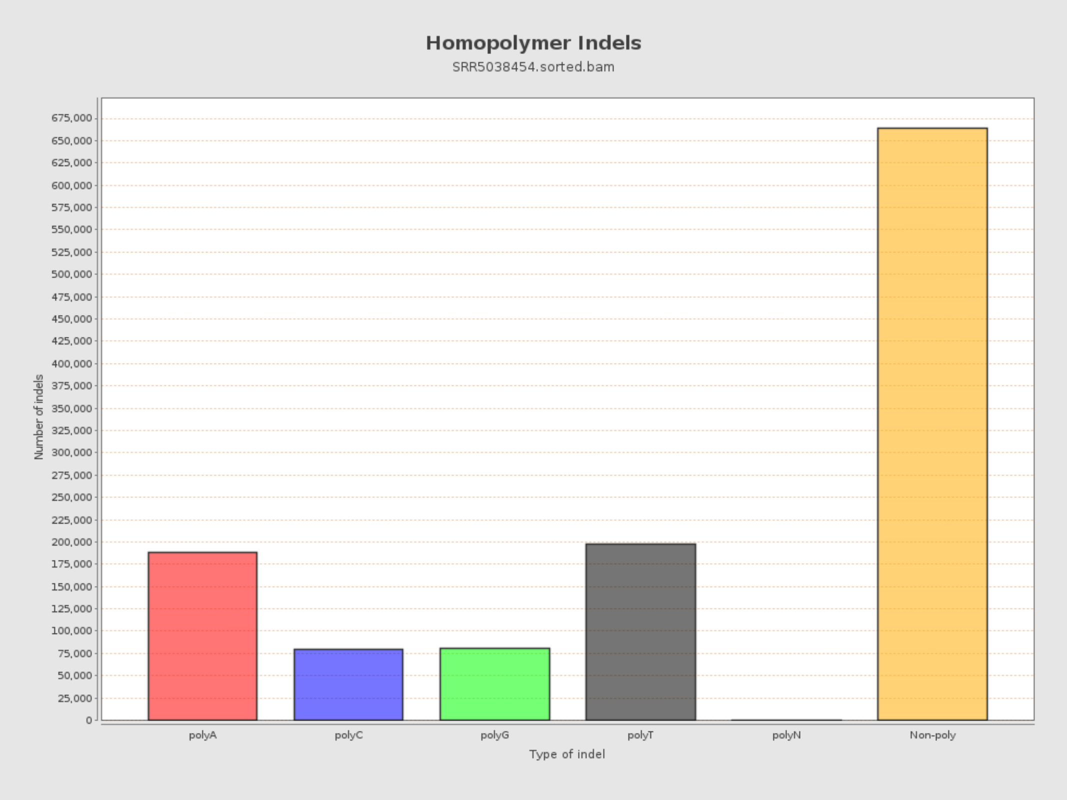
9. Results : Mapped Reads GC-content Distribution



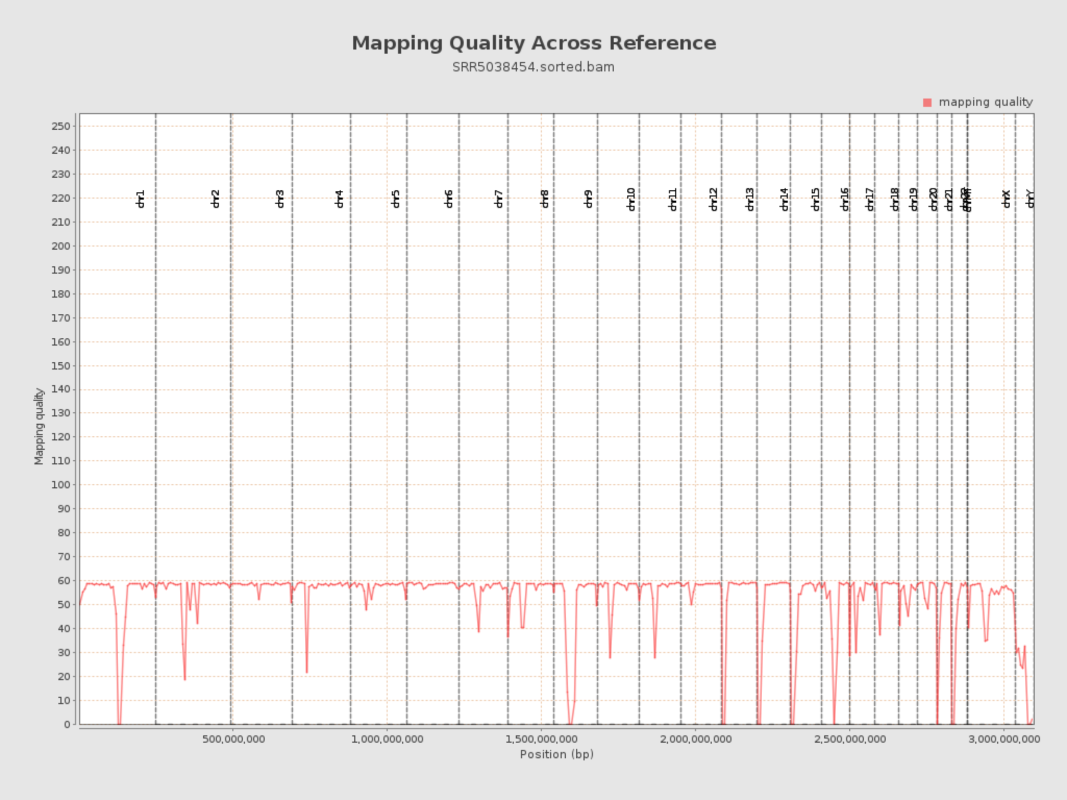
10. Results : Mapped Reads Clipping Profile



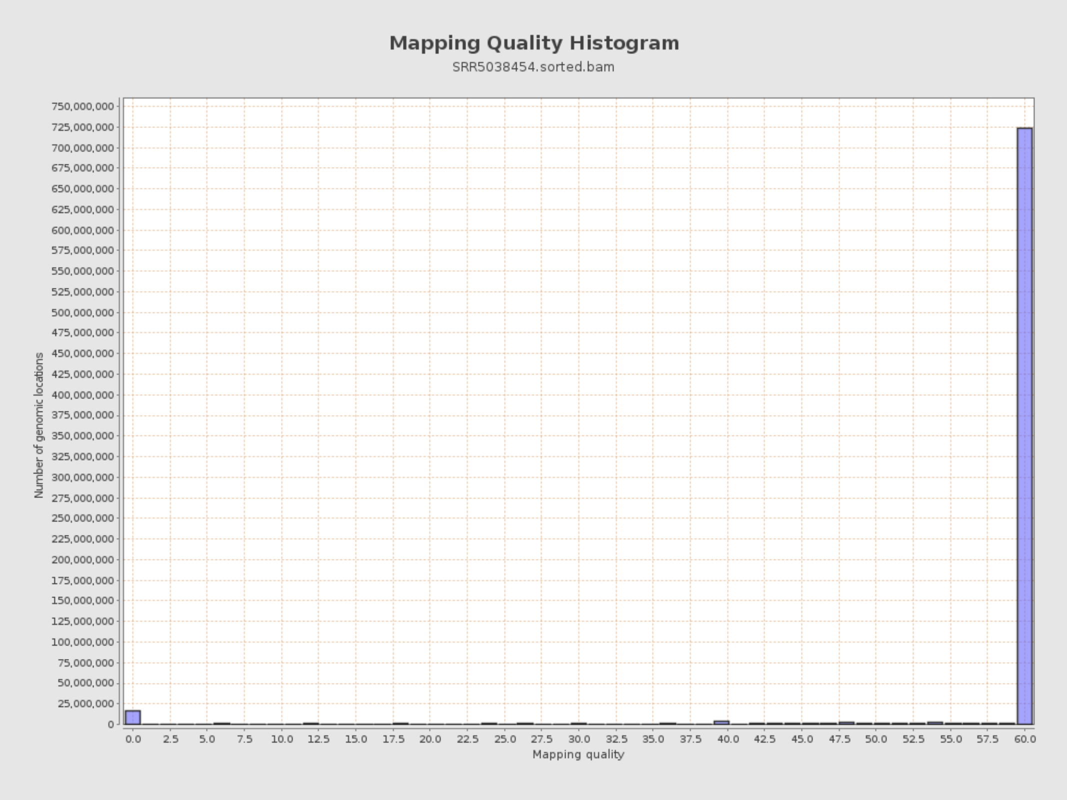
11. Results : Homopolymer Indels



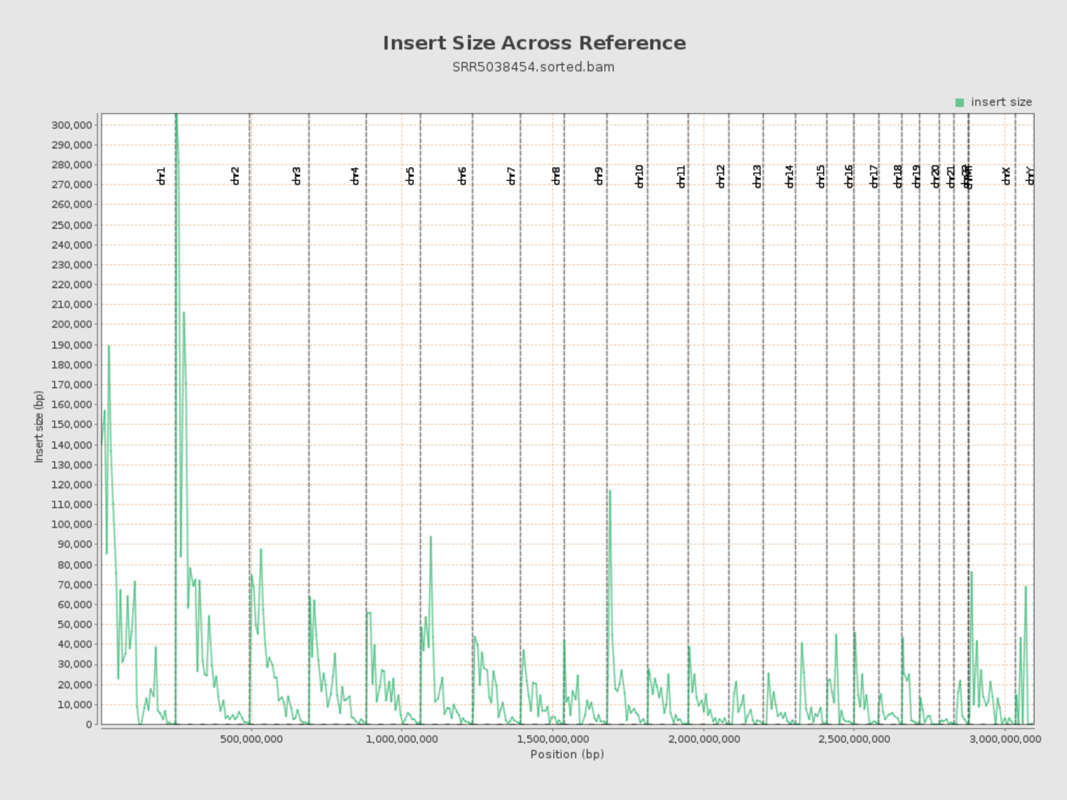
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram