Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 22:59:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038417.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_SRR5038417 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038417_1.fastq.gz SRR5038417_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 22:59:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038417.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,753,886
Mapped reads	19,158,425 / 96.99%
Unmapped reads	595,461 / 3.01%
Mapped paired reads	19,158,425 / 96.99%
Mapped reads, first in pair	9,641,192 / 48.81%
Mapped reads, second in pair	9,517,233 / 48.18%
Mapped reads, both in pair	19,012,656 / 96.25%
Mapped reads, singletons	145,769 / 0.74%
Secondary alignments	0
Supplementary alignments	200,147 / 1.01%
Read min/max/mean length	30 / 150 / 150.52
Duplicated reads (estimated)	1,976,777 / 10.01%
Duplication rate	7.87%
Clipped reads	1,906,134 / 9.65%

2.2. ACGT Content

Number/percentage of A's	809,624,113 / 28.7%
Number/percentage of C's	603,978,764 / 21.41%
Number/percentage of T's	803,860,627 / 28.49%
Number/percentage of G's	603,568,436 / 21.39%
Number/percentage of N's	269,000 / 0.01%

GC Percentage	42.8%

2.3. Coverage

Mean	0.9117
Standard Deviation	8.9884

2.4. Mapping Quality

Mean Mapping Quality	54.33

2.5. Insert size

Mean	106,993.28
Standard Deviation	3,286,462.46
P25/Median/P75	231 / 283 / 351

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	25,240,713
Insertions	334,576
Mapped reads with at least one insertion	1.65%
Deletions	359,072
Mapped reads with at least one deletion	1.79%
Homopolymer indels	44.27%

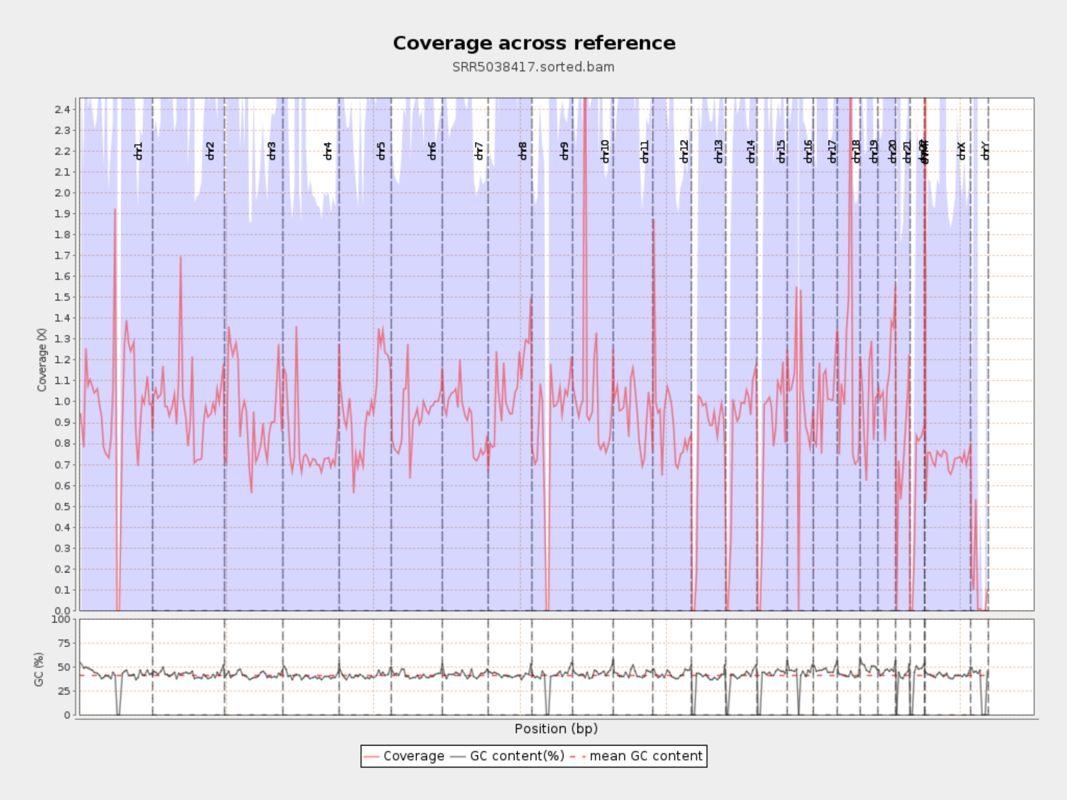
2.7. Chromosome stats

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

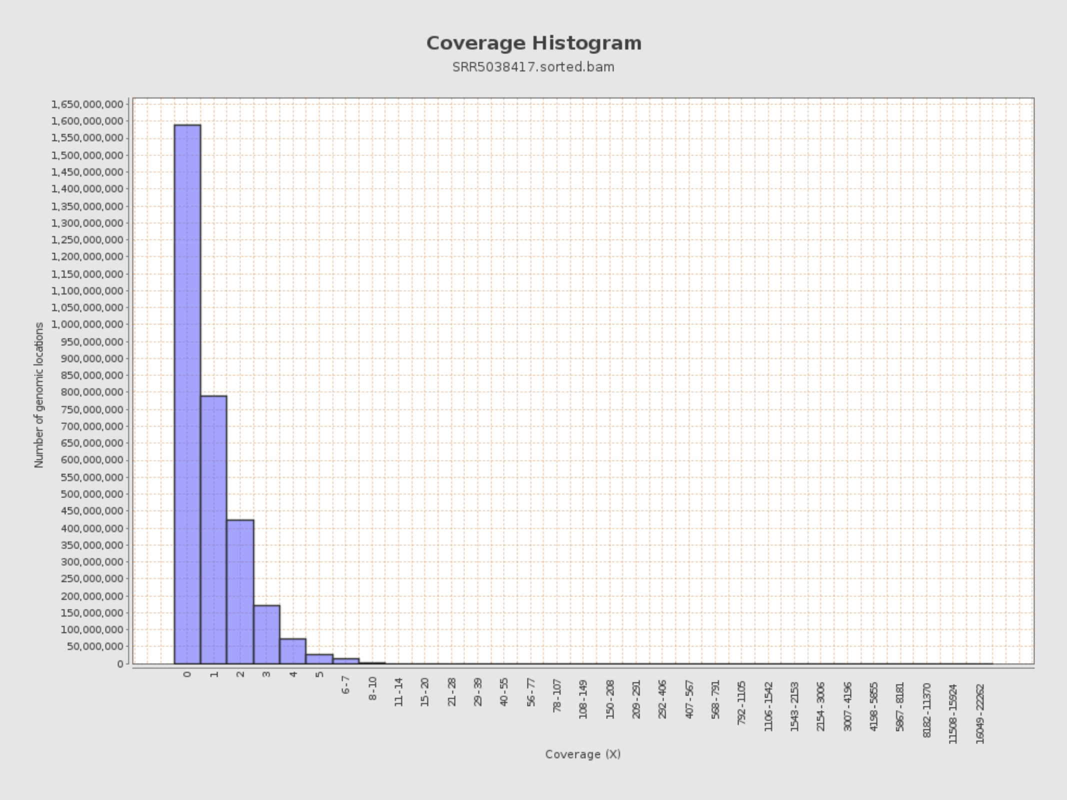
		bases	coverage	deviation
chr1	249250621	243202996	0.9757	22.3874
chr2	243199373	240034696	0.987	7.4263
chr3	198022430	186149920	0.94	1.3017
chr4	191154276	150142001	0.7854	6.0609
chr5	180915260	178315413	0.9856	1.2891
chr6	171115067	159897141	0.9344	4.0608
chr7	159138663	147003848	0.9237	7.3217
chr8	146364022	156436309	1.0688	5.6361
chr9	141213431	120773813	0.8553	10.0547
chr10	135534747	145193610	1.0713	19.5899
chr11	135006516	130358253	0.9656	3.9621
chr12	133851895	122594483	0.9159	1.4096
chr13	115169878	90757584	0.788	1.1531
chr14	107349540	89393192	0.8327	1.243
chr15	102531392	80754596	0.7876	1.1706
chr16	90354753	90076420	0.9969	5.1248
chr17	81195210	83257586	1.0254	5.1348
chr18	78077248	90615142	1.1606	8.185
chr19	59128983	58792519	0.9943	9.0089
chr20	63025520	71575628	1.1357	2.3246
chr21	48129895	35537830	0.7384	3.258
chr22	51304566	29846866	0.5818	1.0345
chrMT	16571	3019880	182.2389	24.6716
chrX	155270560	111854480	0.7204	1.9058

chrY	59373566	6694206	0.1127	6.263

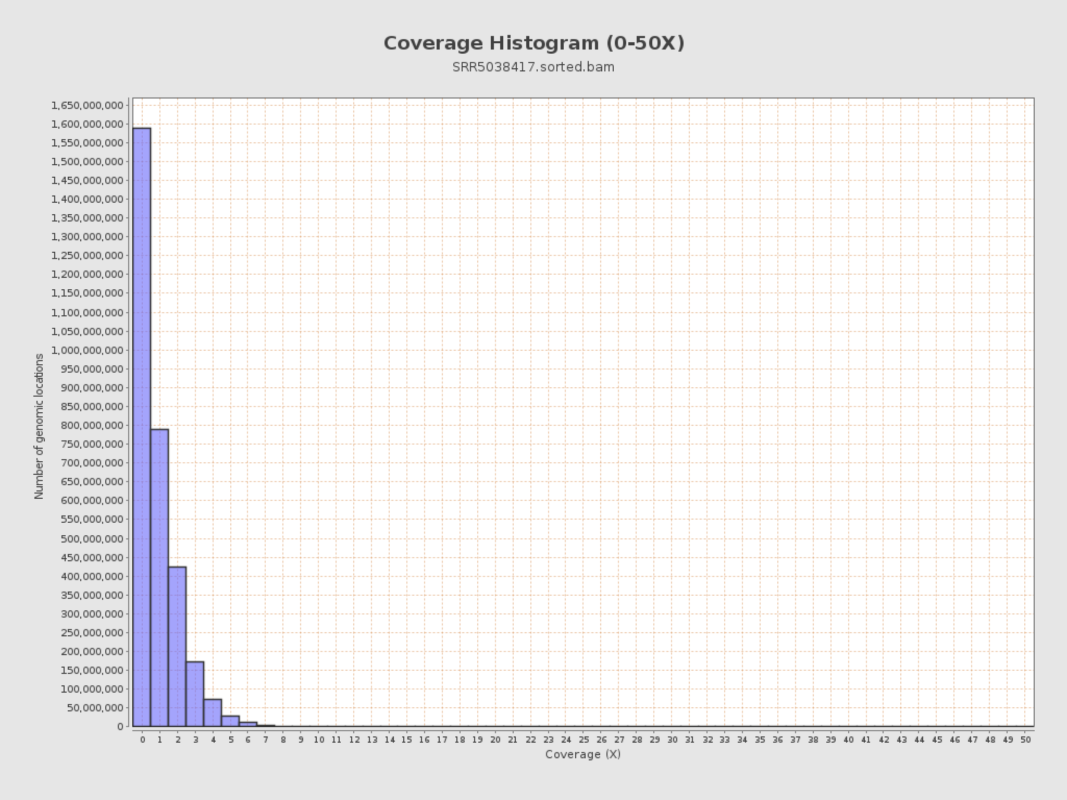
3. Results : Coverage across reference



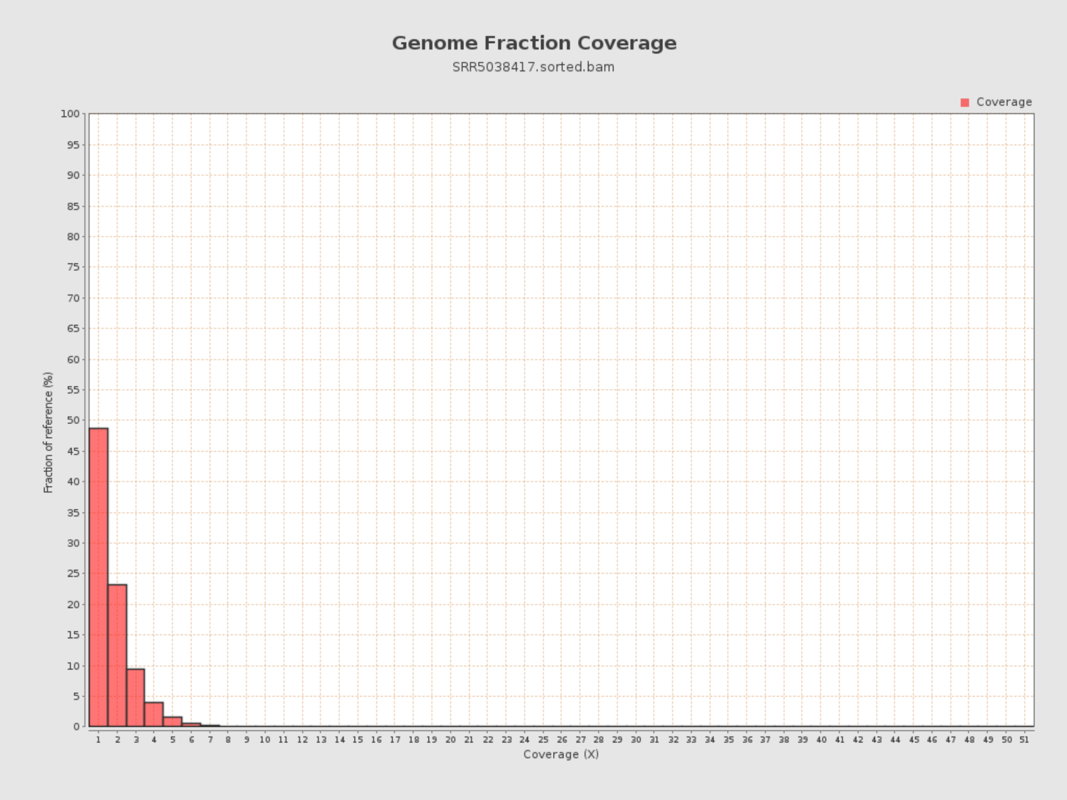
4. Results : Coverage Histogram



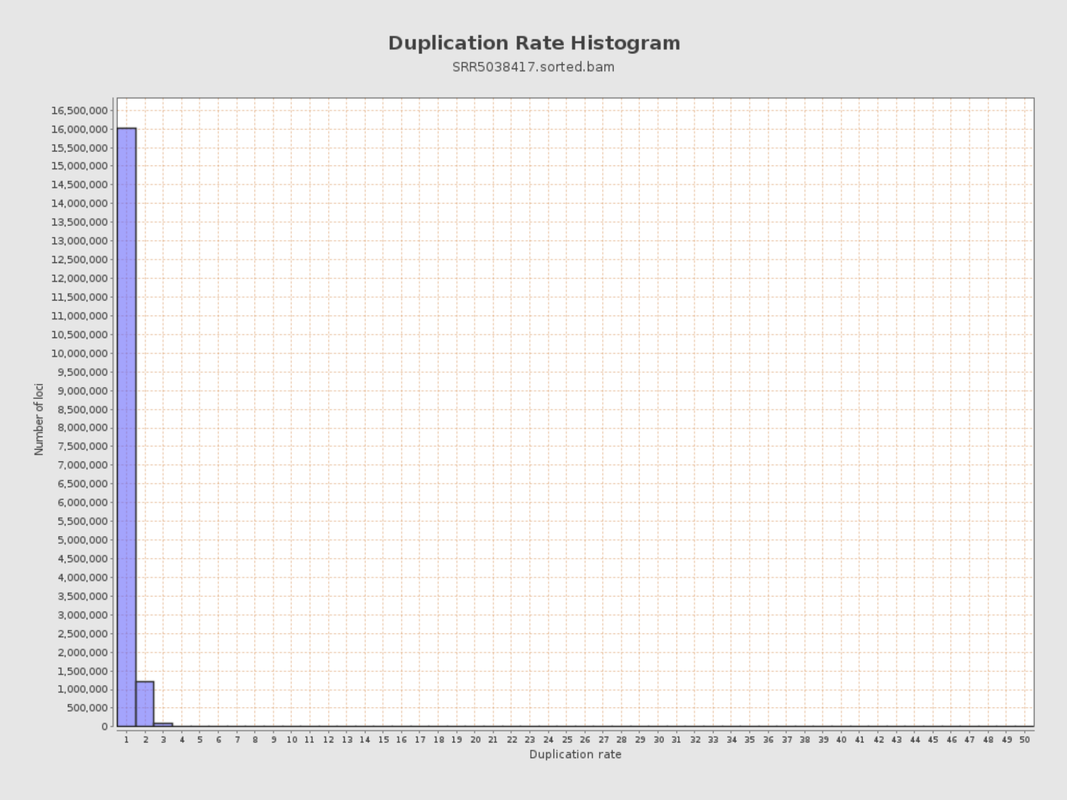
5. Results : Coverage Histogram (0-50X)



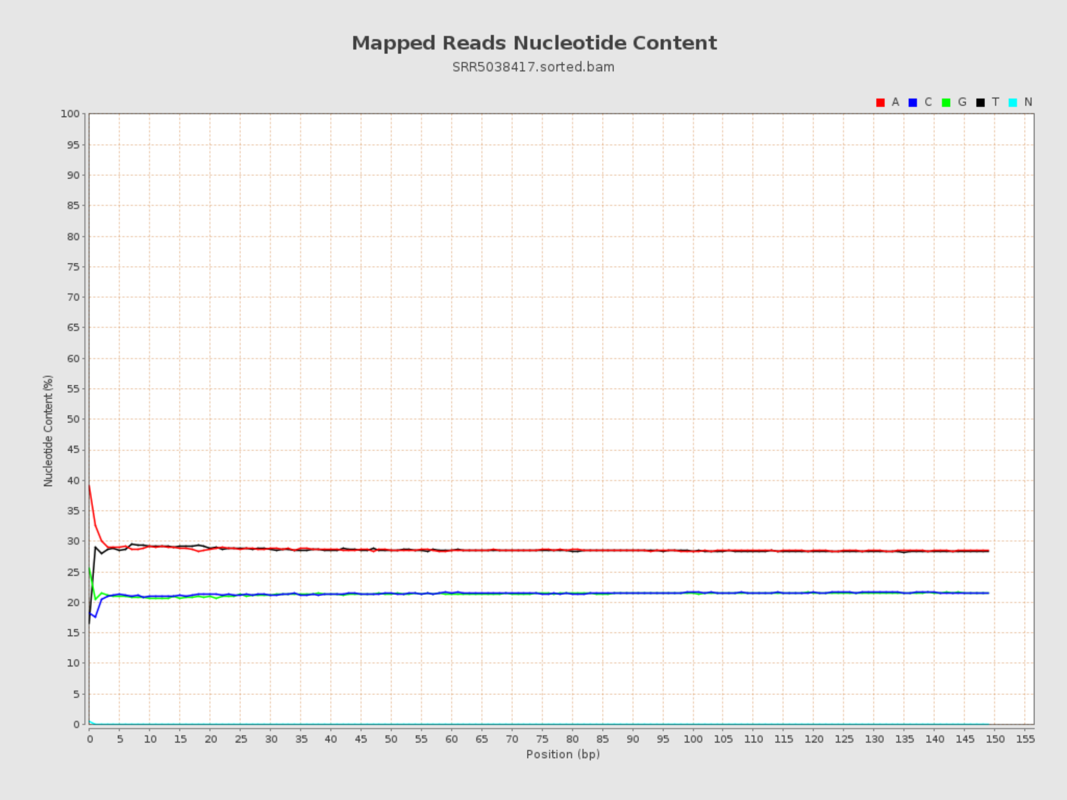
6. Results : Genome Fraction Coverage



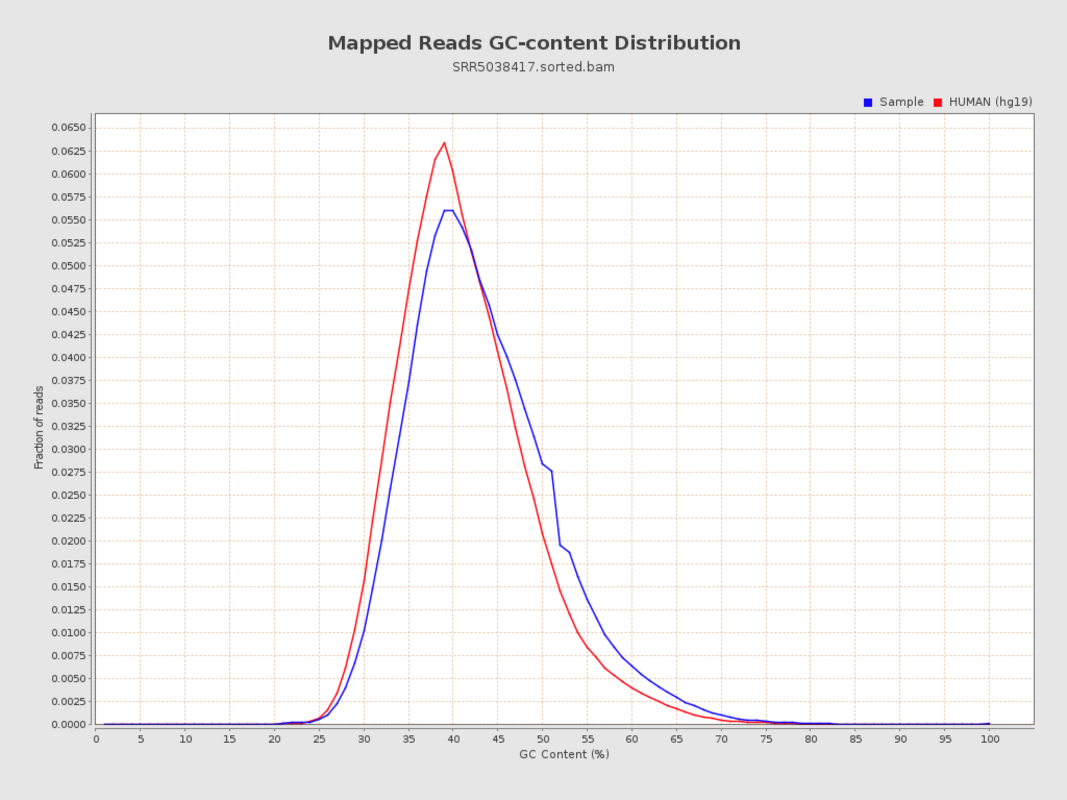
7. Results : Duplication Rate Histogram



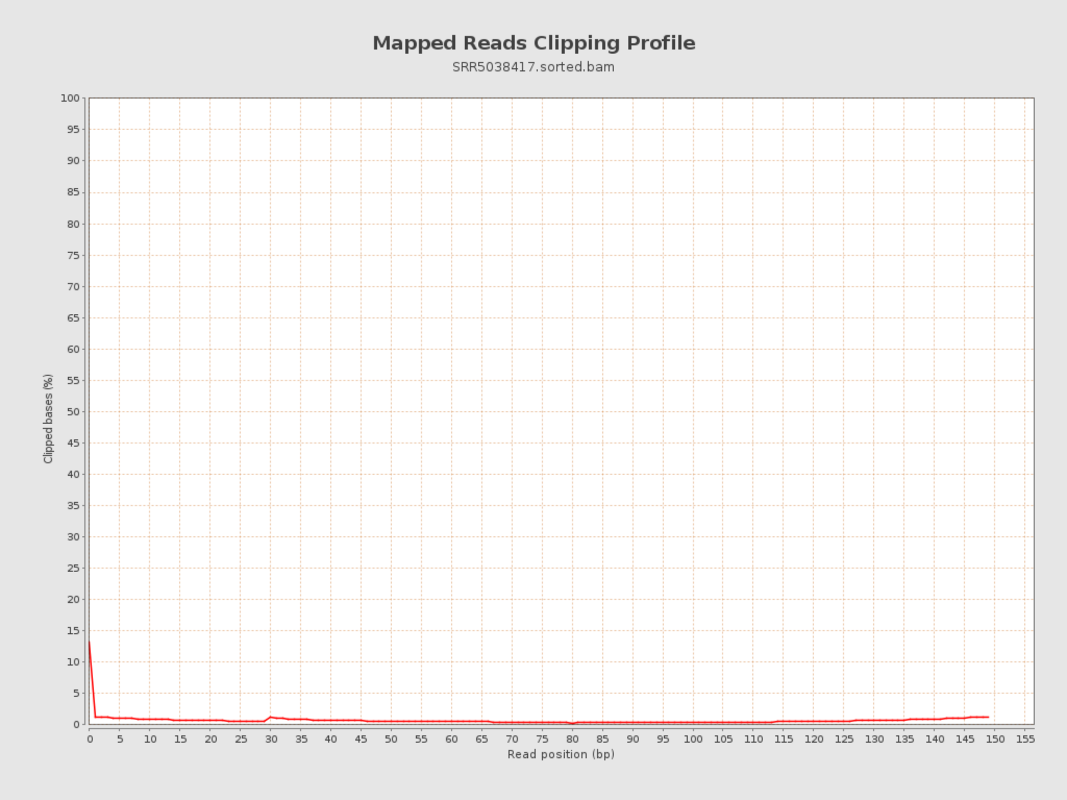
8. Results : Mapped Reads Nucleotide Content



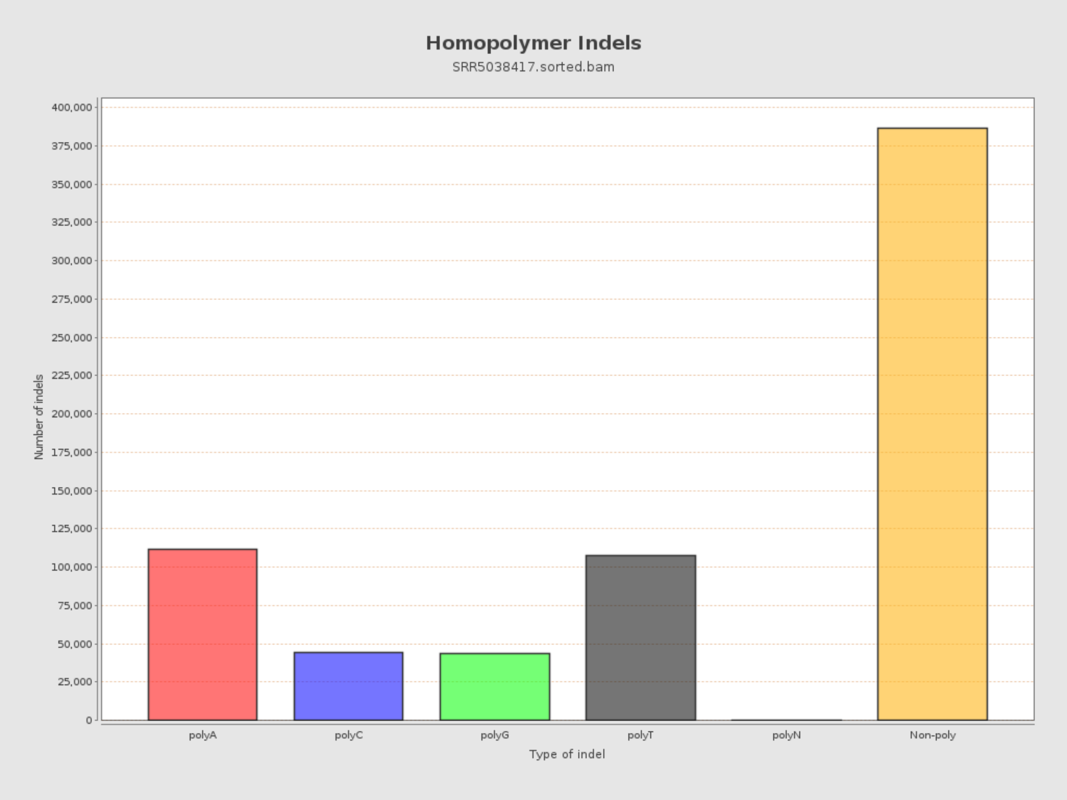
9. Results : Mapped Reads GC-content Distribution



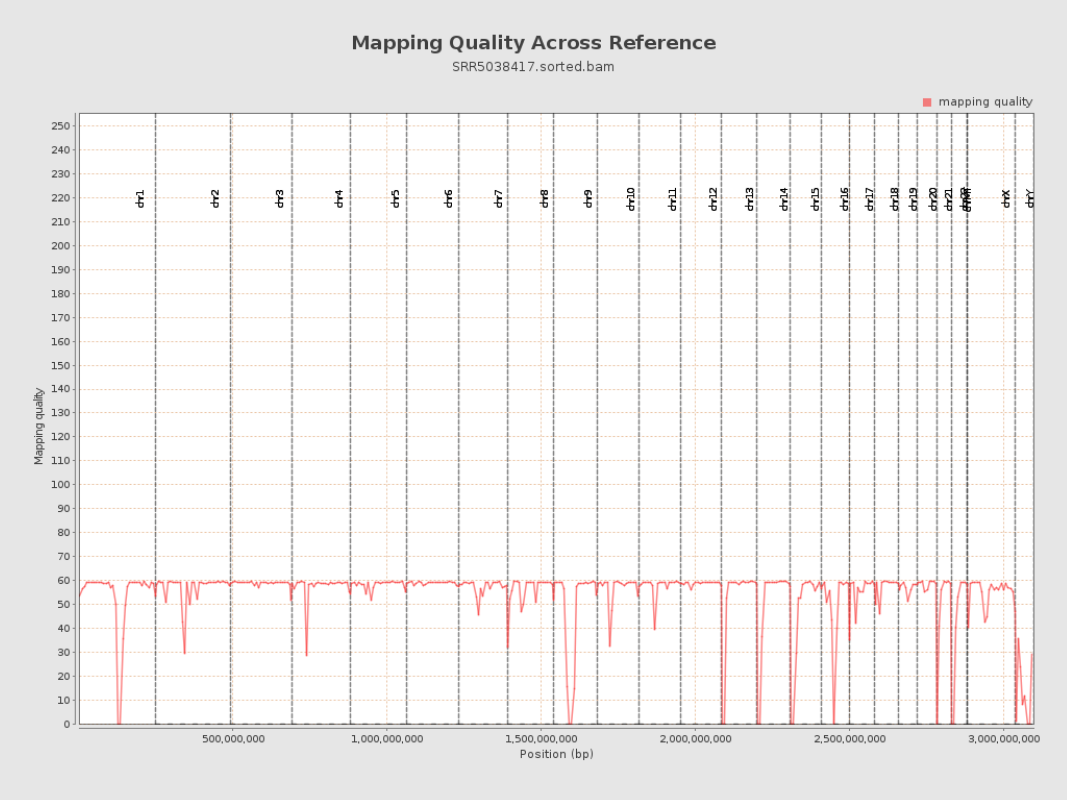
10. Results : Mapped Reads Clipping Profile



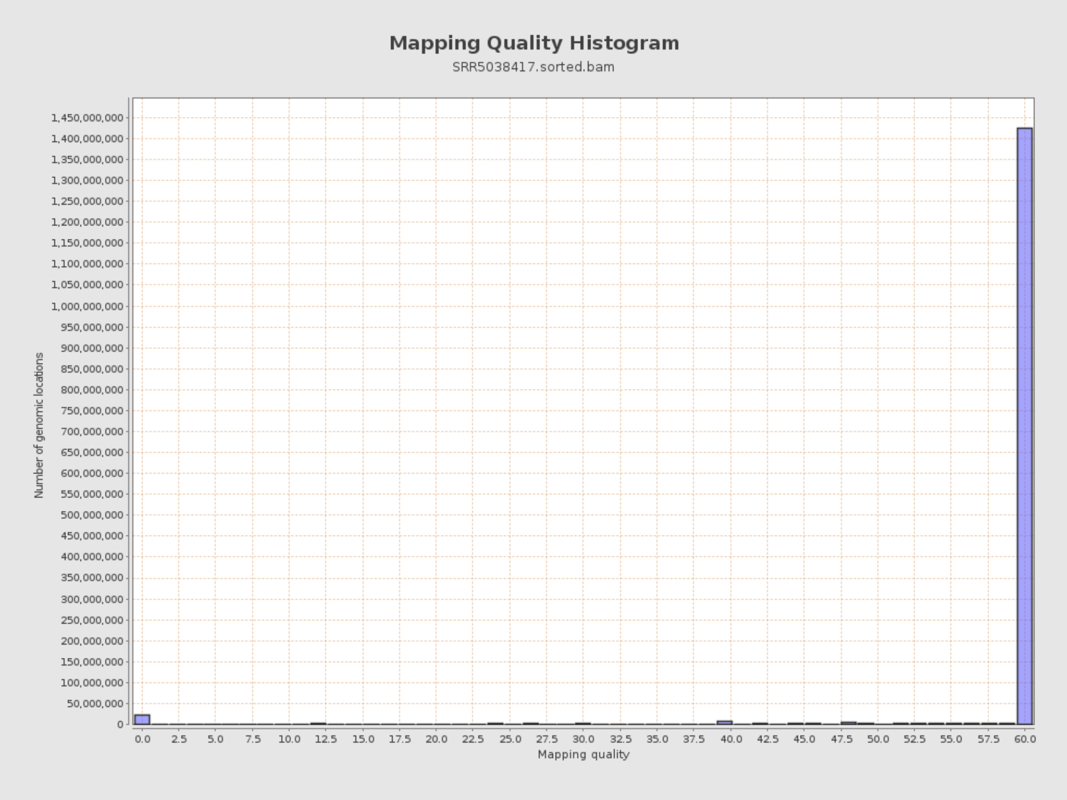
11. Results : Homopolymer Indels



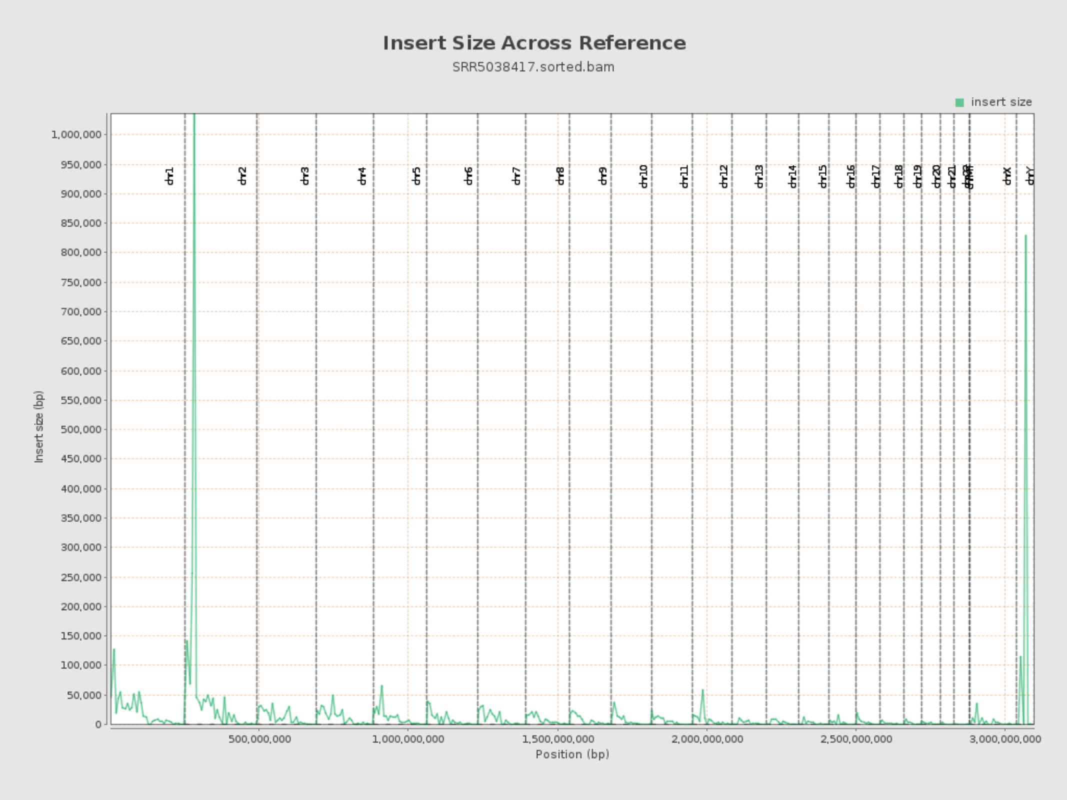
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram