Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 10:28:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038389.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_SRR5038389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038389_1.fastq.gz SRR5038389_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 10:28:15 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,691,028
Mapped reads	16,078,857 / 96.33%
Unmapped reads	612,171 / 3.67%
Mapped paired reads	16,078,857 / 96.33%
Mapped reads, first in pair	8,149,198 / 48.82%
Mapped reads, second in pair	7,929,659 / 47.51%
Mapped reads, both in pair	15,797,748 / 94.65%
Mapped reads, singletons	281,109 / 1.68%
Secondary alignments	0
Supplementary alignments	277,961 / 1.67%
Read min/max/mean length	30 / 150 / 150.83
Duplicated reads (estimated)	3,268,027 / 19.58%
Duplication rate	13.85%
Clipped reads	7,826,246 / 46.89%

2.2. ACGT Content

Number/percentage of A's	621,379,676 / 28.78%
Number/percentage of C's	423,969,446 / 19.64%
Number/percentage of T's	634,656,948 / 29.4%
Number/percentage of G's	478,865,979 / 22.18%
Number/percentage of N's	170,365 / 0.01%

GC Percentage	41.82%

2.3. Coverage

Mean	0.698
Standard Deviation	10.2465

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	82,918.24
Standard Deviation	2,738,052.12
P25/Median/P75	197 / 248 / 314

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	29,178,534
Insertions	409,820
Mapped reads with at least one insertion	2.4%
Deletions	808,688
Mapped reads with at least one deletion	4.83%
Homopolymer indels	46.64%

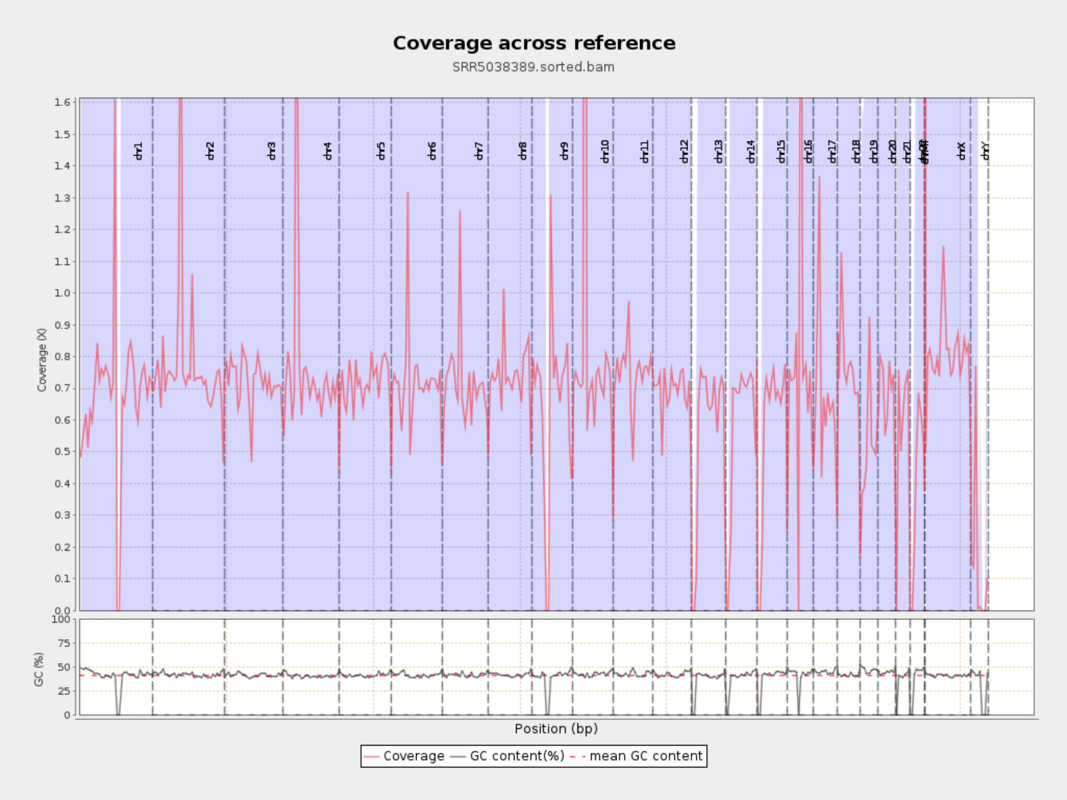
2.7. Chromosome stats

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

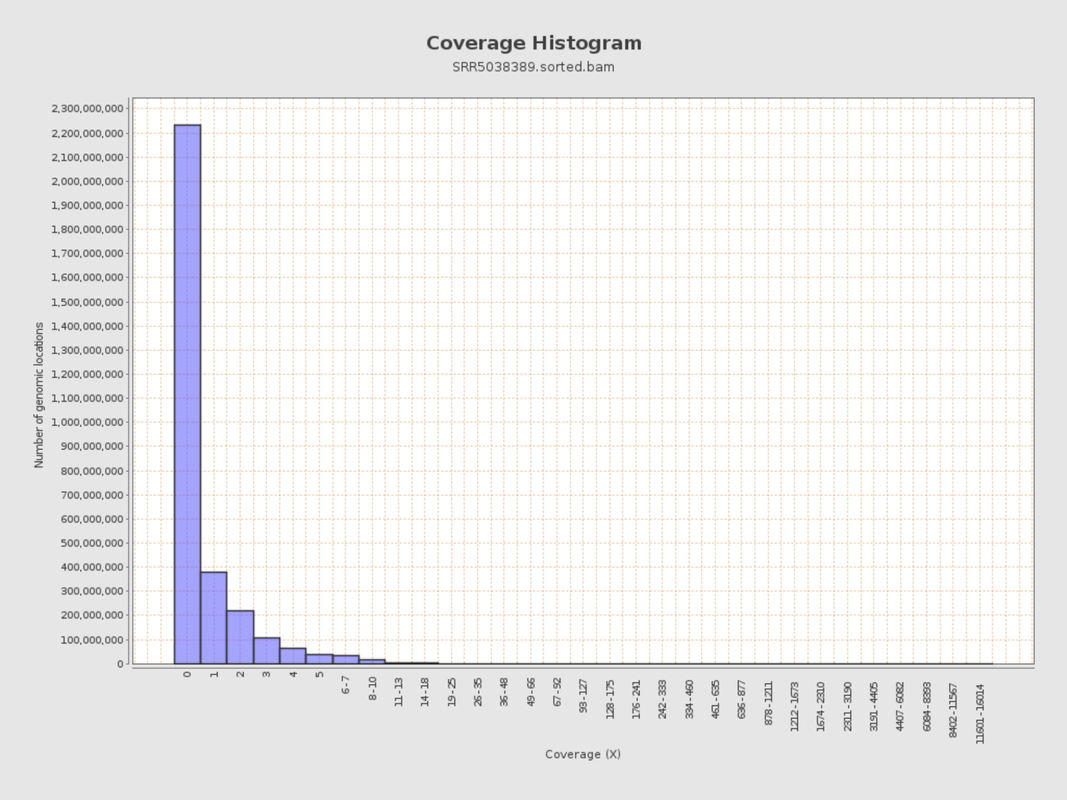
		bases	coverage	deviation
chr1	249250621	169247816	0.679	15.8427
chr2	243199373	191676538	0.7881	10.1054
chr3	198022430	143096146	0.7226	1.653
chr4	191154276	145331225	0.7603	9.7654
chr5	180915260	129358126	0.715	1.5644
chr6	171115067	124674975	0.7286	6.7282
chr7	159138663	113529502	0.7134	9.6304
chr8	146364022	108698350	0.7427	3.2774
chr9	141213431	89980326	0.6372	15.3103
chr10	135534747	122781777	0.9059	27.3311
chr11	135006516	99380888	0.7361	6.4914
chr12	133851895	92466165	0.6908	1.6332
chr13	115169878	65481768	0.5686	1.3544
chr14	107349540	61638121	0.5742	1.5338
chr15	102531392	58007831	0.5658	1.37
chr16	90354753	73319415	0.8115	13.8813
chr17	81195210	53637277	0.6606	11.1802
chr18	78077248	60209676	0.7712	11.7608
chr19	59128983	29930580	0.5062	7.1712
chr20	63025520	42987676	0.6821	3.1039
chr21	48129895	27791120	0.5774	4.6942
chr22	51304566	20075695	0.3913	1.2438
chrMT	16571	3360993	202.8238	103.6127
chrX	155270560	125287049	0.8069	3.3925

chrY	59373566	8735761	0.1471	11.2072

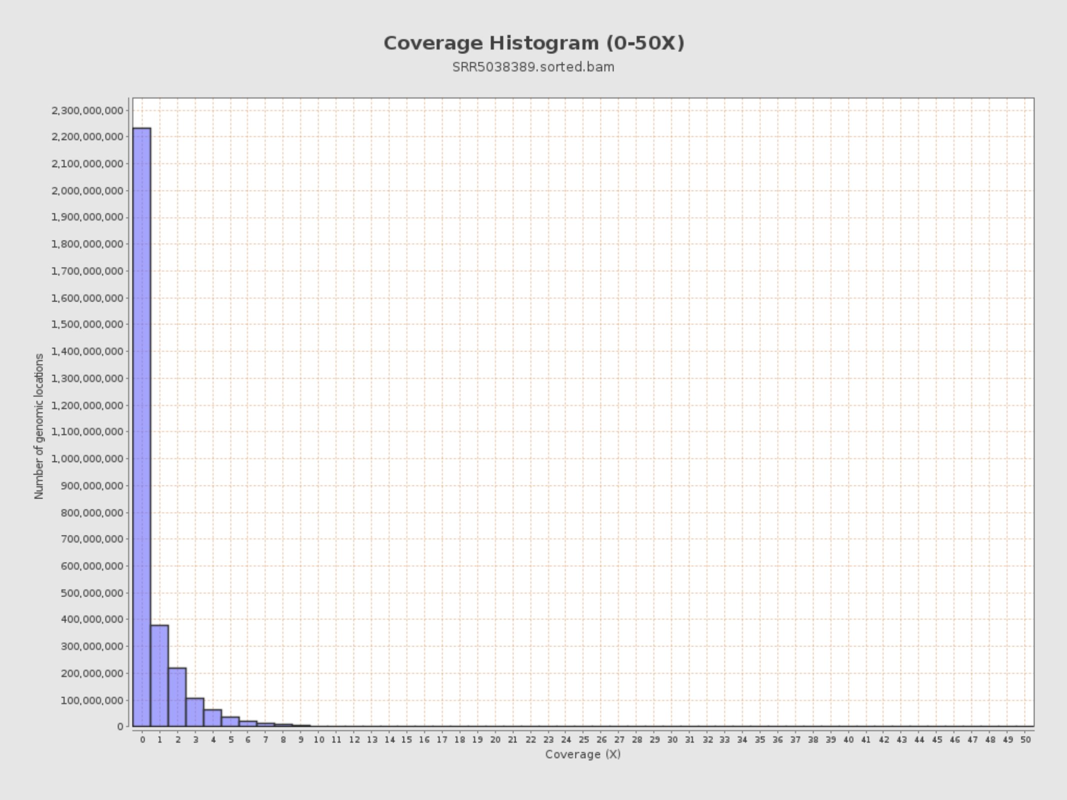
3. Results : Coverage across reference



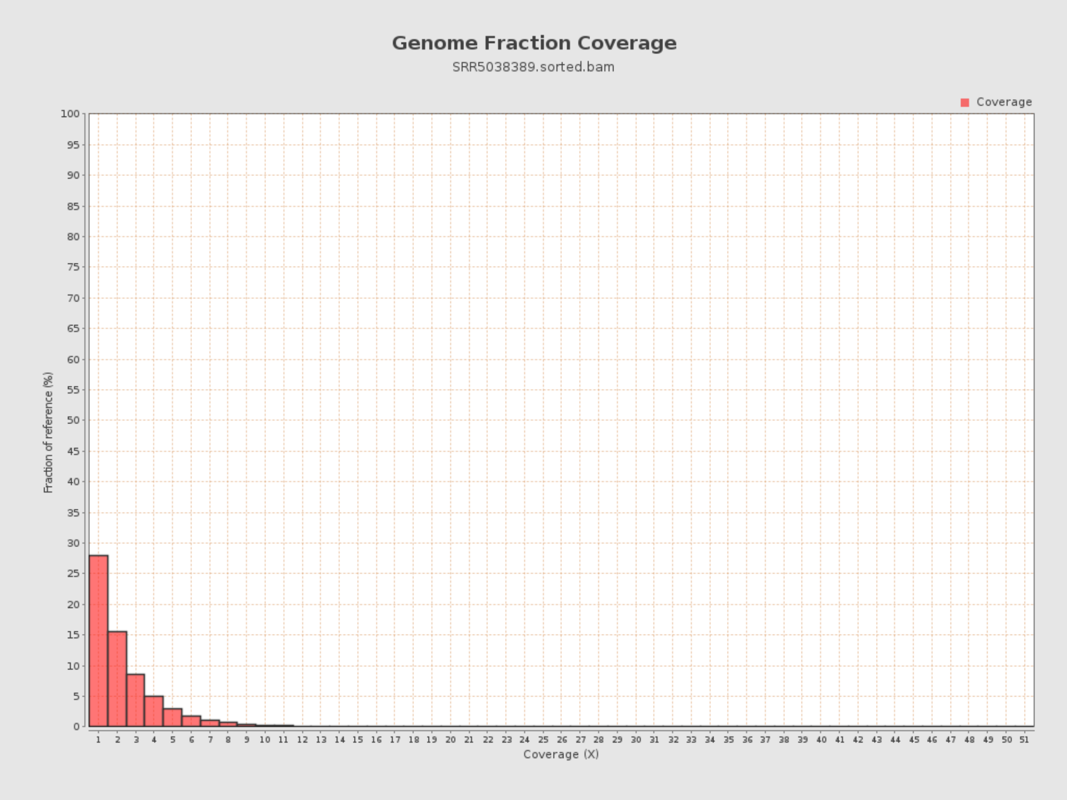
4. Results : Coverage Histogram



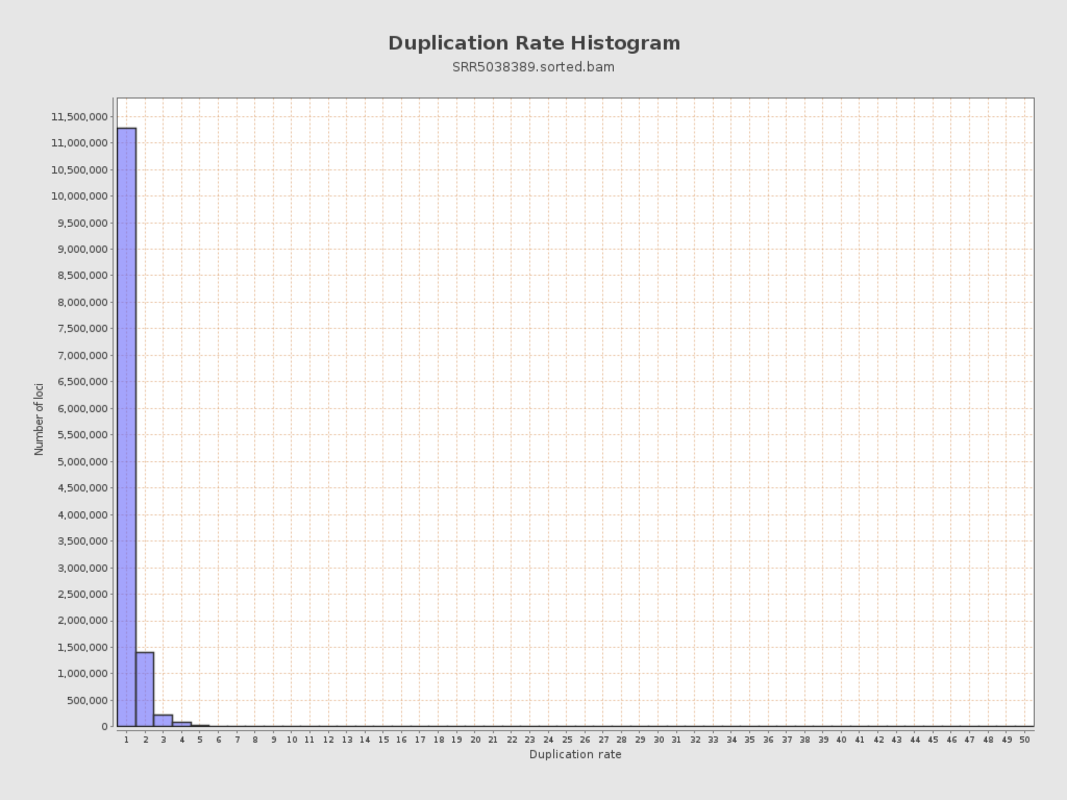
5. Results : Coverage Histogram (0-50X)



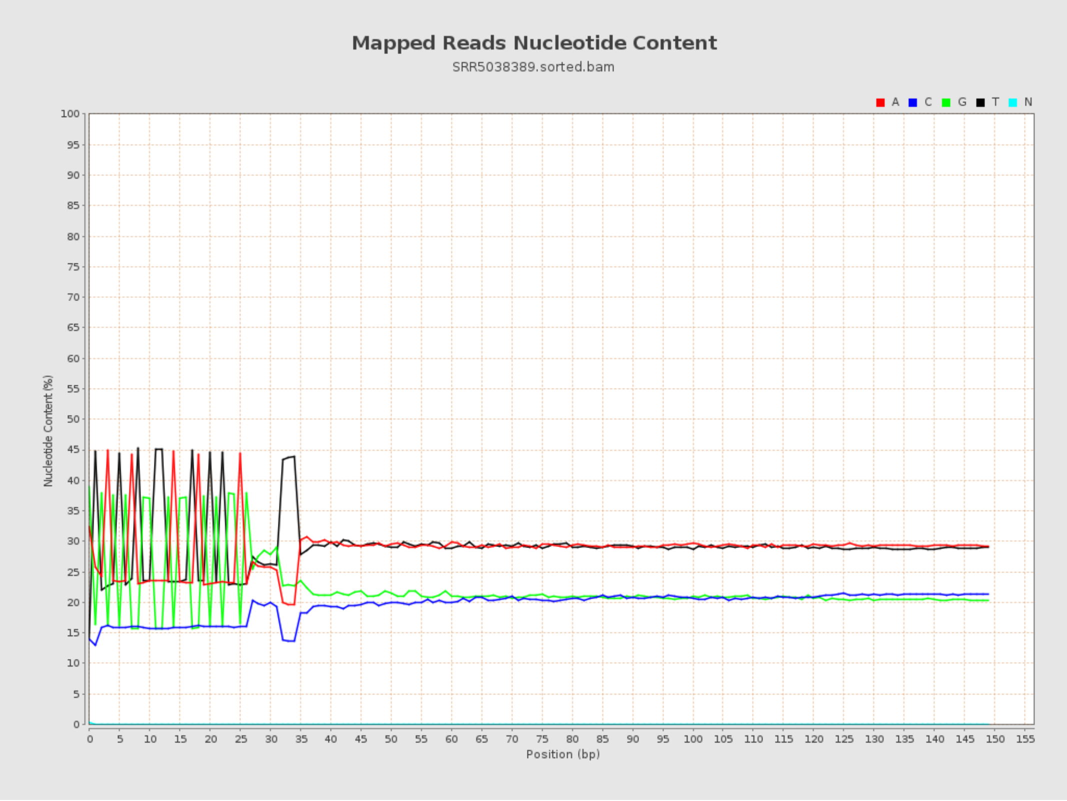
6. Results : Genome Fraction Coverage



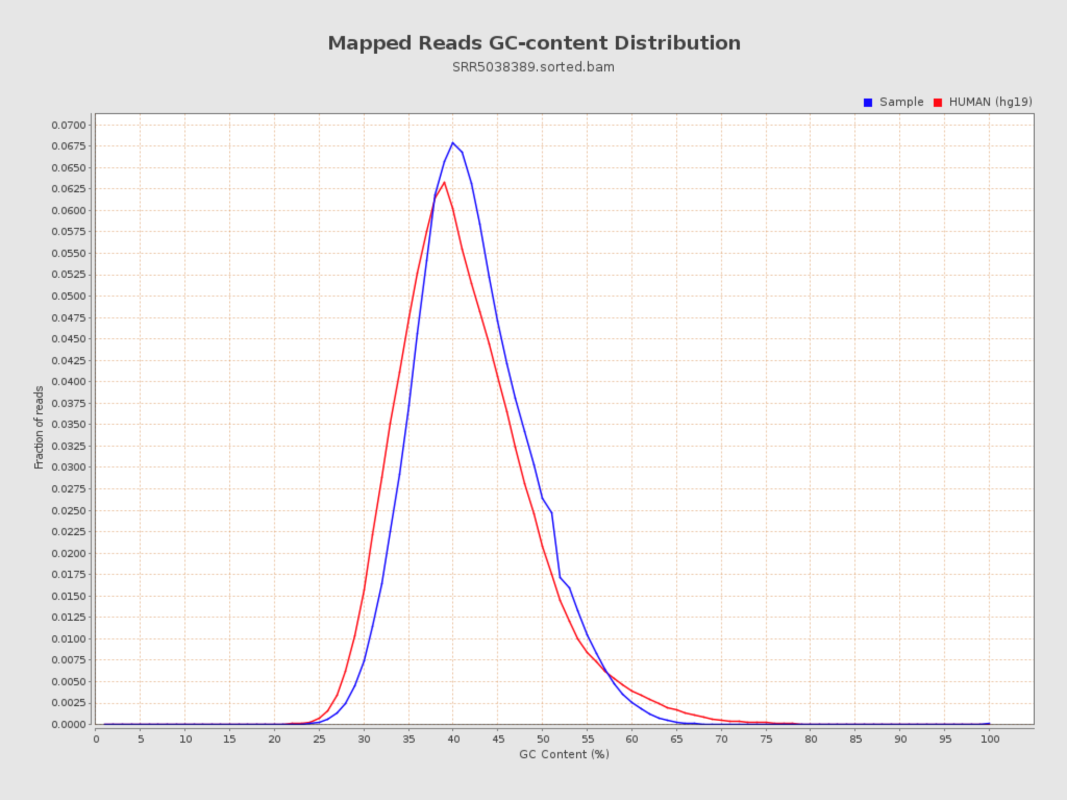
7. Results : Duplication Rate Histogram



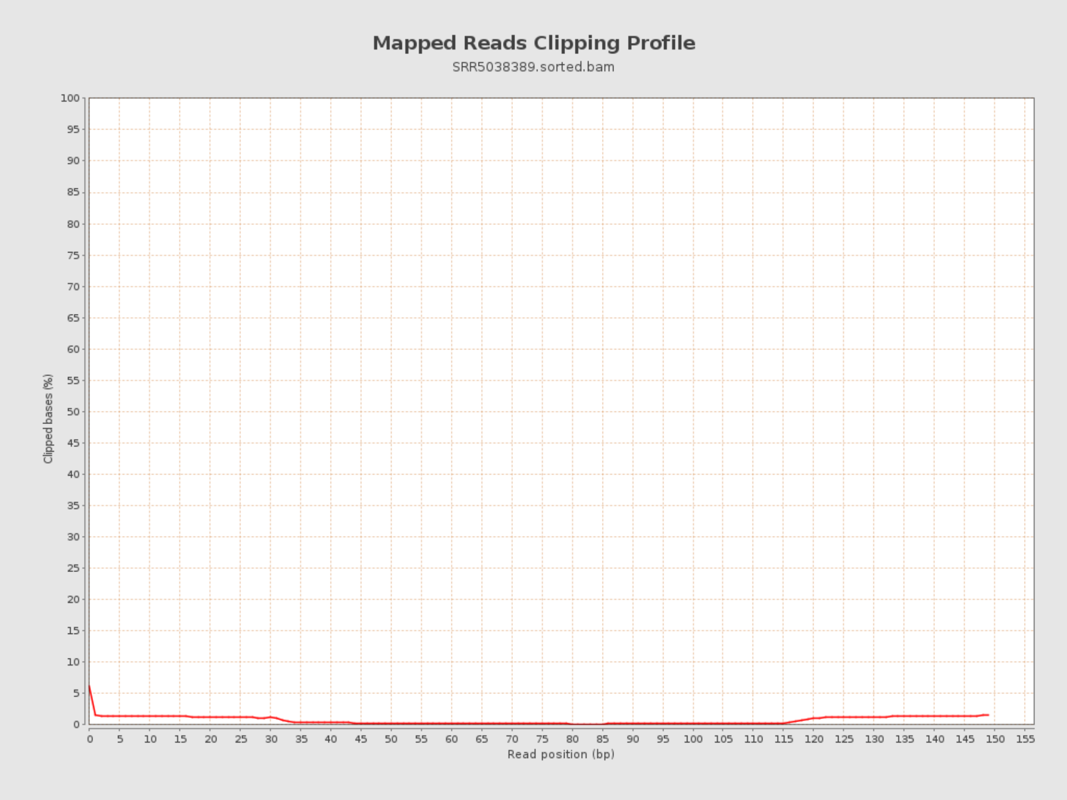
8. Results : Mapped Reads Nucleotide Content



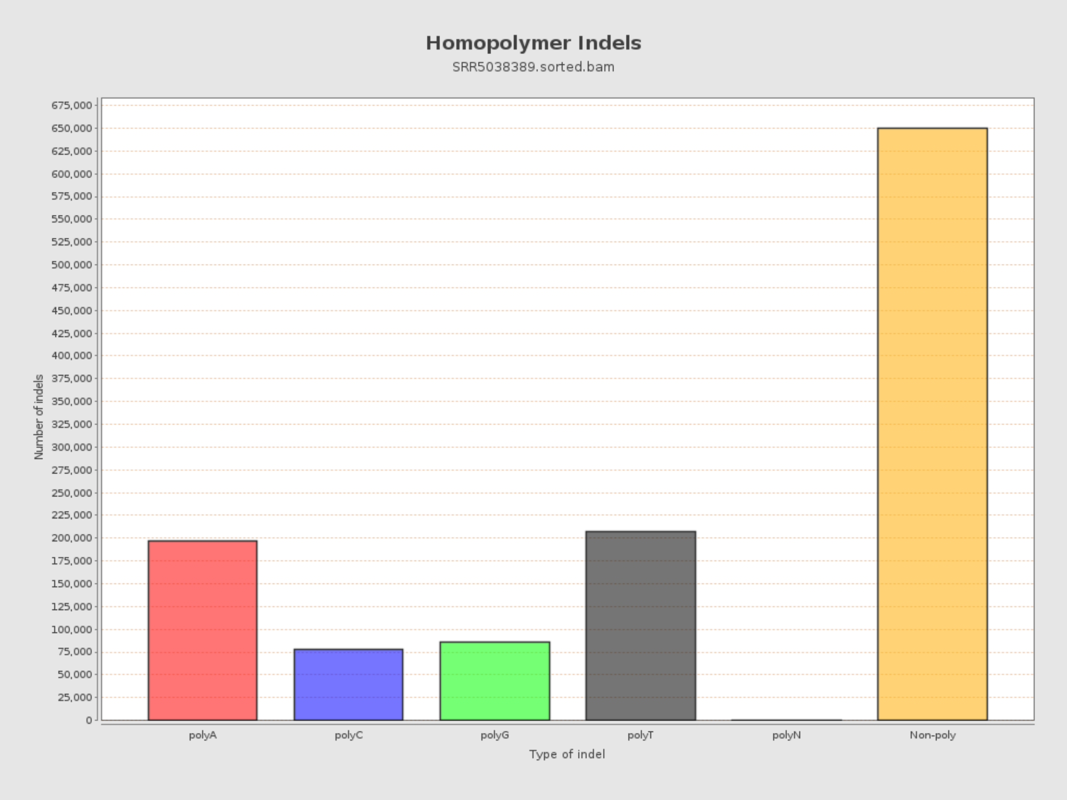
9. Results : Mapped Reads GC-content Distribution



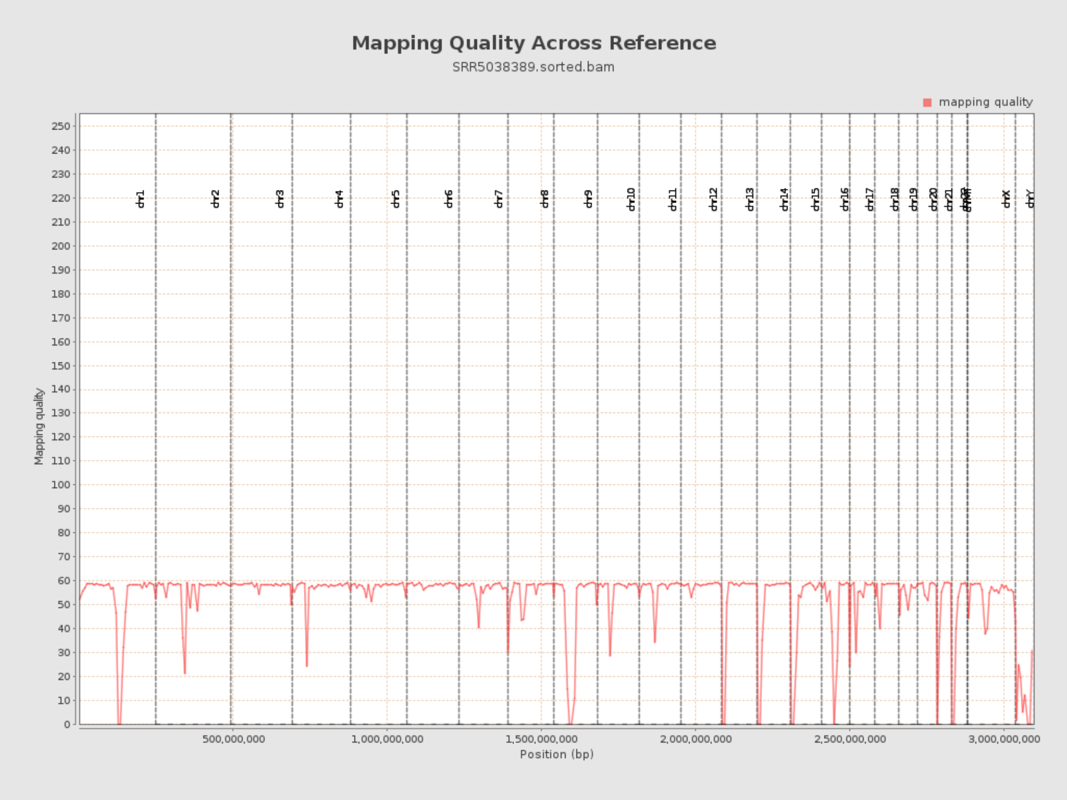
10. Results : Mapped Reads Clipping Profile



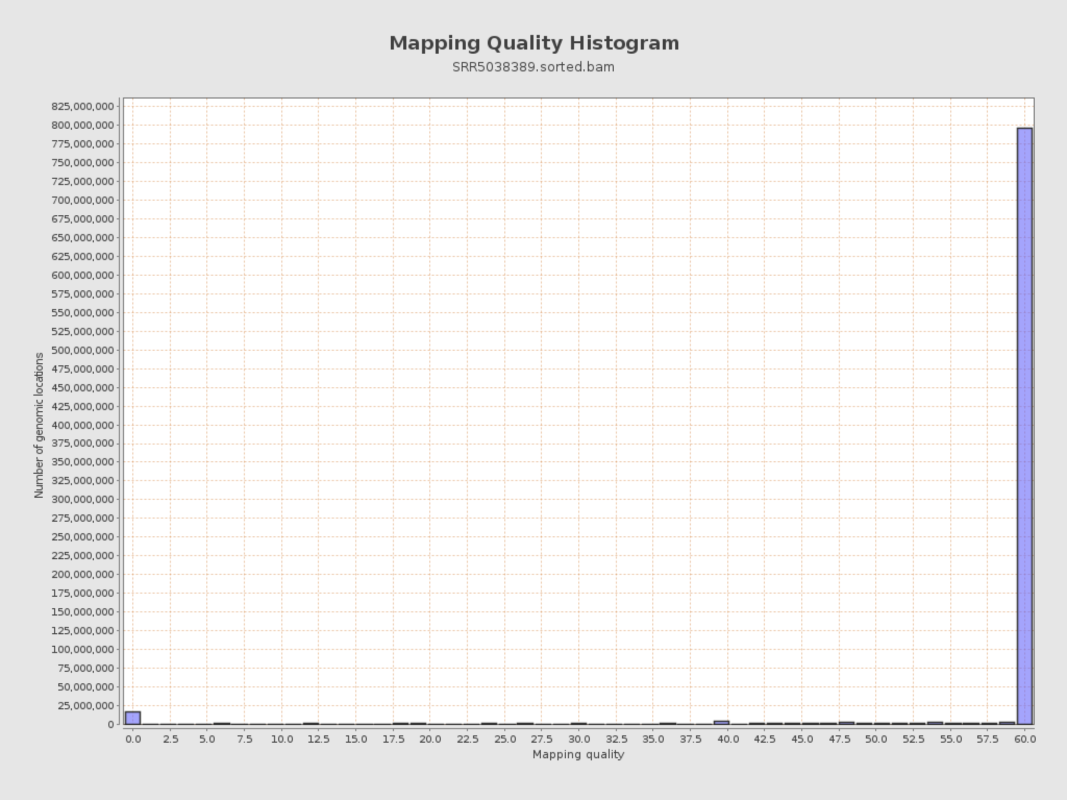
11. Results : Homopolymer Indels



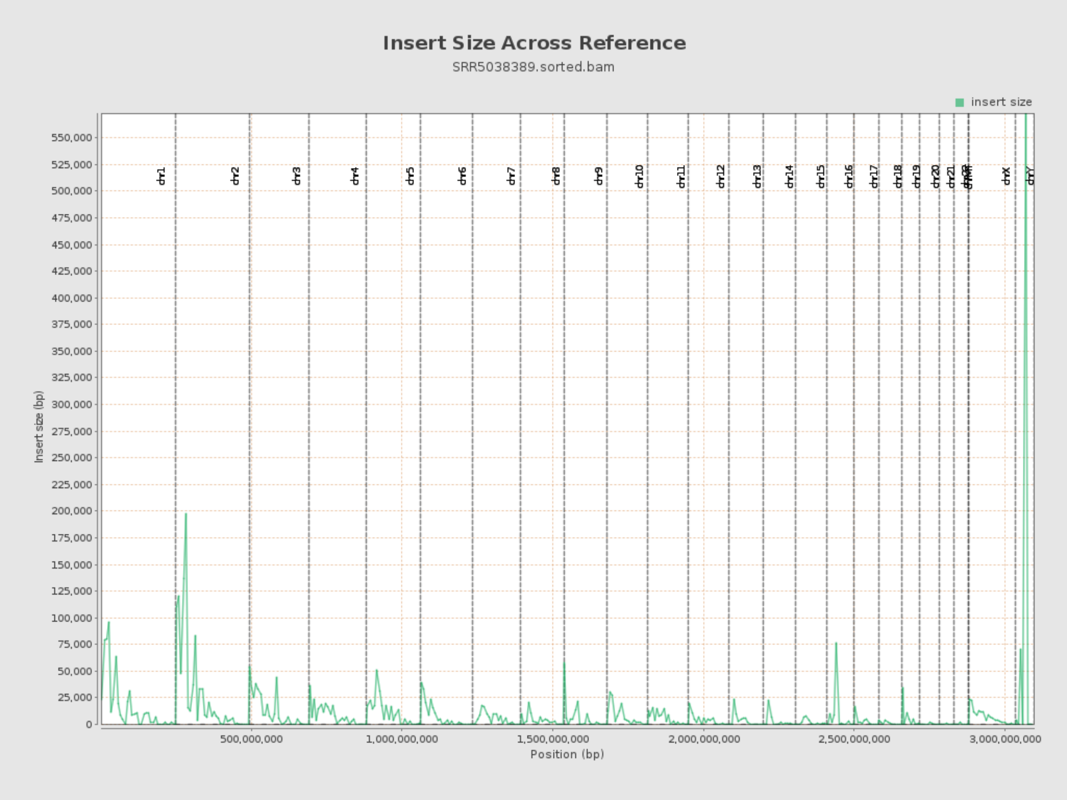
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram