Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 17:29:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038407.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_SRR5038407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038407_1.fastq.gz SRR5038407_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 17:29:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,166,426
Mapped reads	12,845,078 / 97.56%
Unmapped reads	321,348 / 2.44%
Mapped paired reads	12,845,078 / 97.56%
Mapped reads, first in pair	6,488,378 / 49.28%
Mapped reads, second in pair	6,356,700 / 48.28%
Mapped reads, both in pair	12,689,582 / 96.38%
Mapped reads, singletons	155,496 / 1.18%
Secondary alignments	0
Supplementary alignments	305,774 / 2.32%
Read min/max/mean length	30 / 150 / 151.2
Duplicated reads (estimated)	2,326,250 / 17.67%
Duplication rate	9.23%
Clipped reads	3,534,181 / 26.84%

2.2. ACGT Content

Number/percentage of A's	525,488,491 / 28.88%
Number/percentage of C's	375,868,565 / 20.66%
Number/percentage of T's	527,205,023 / 28.97%
Number/percentage of G's	390,936,329 / 21.49%
Number/percentage of N's	39,930 / 0%

GC Percentage	42.14%

2.3. Coverage

Mean	0.5882
Standard Deviation	12.418

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	103,325.49
Standard Deviation	3,009,612.34
P25/Median/P75	215 / 256 / 308

2.6. Mismatches and indels

General error rate	1.62%
Mismatches	28,142,626
Insertions	377,637
Mapped reads with at least one insertion	2.72%
Deletions	644,070
Mapped reads with at least one deletion	4.79%
Homopolymer indels	45.03%

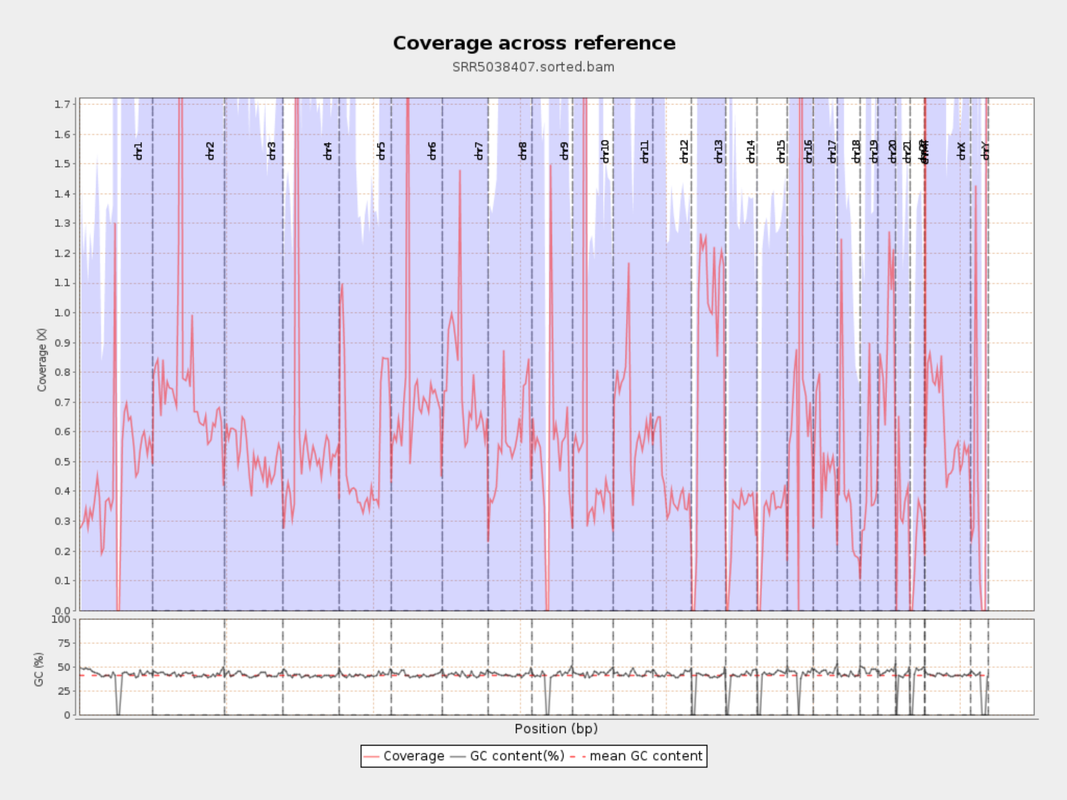
2.7. Chromosome stats

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

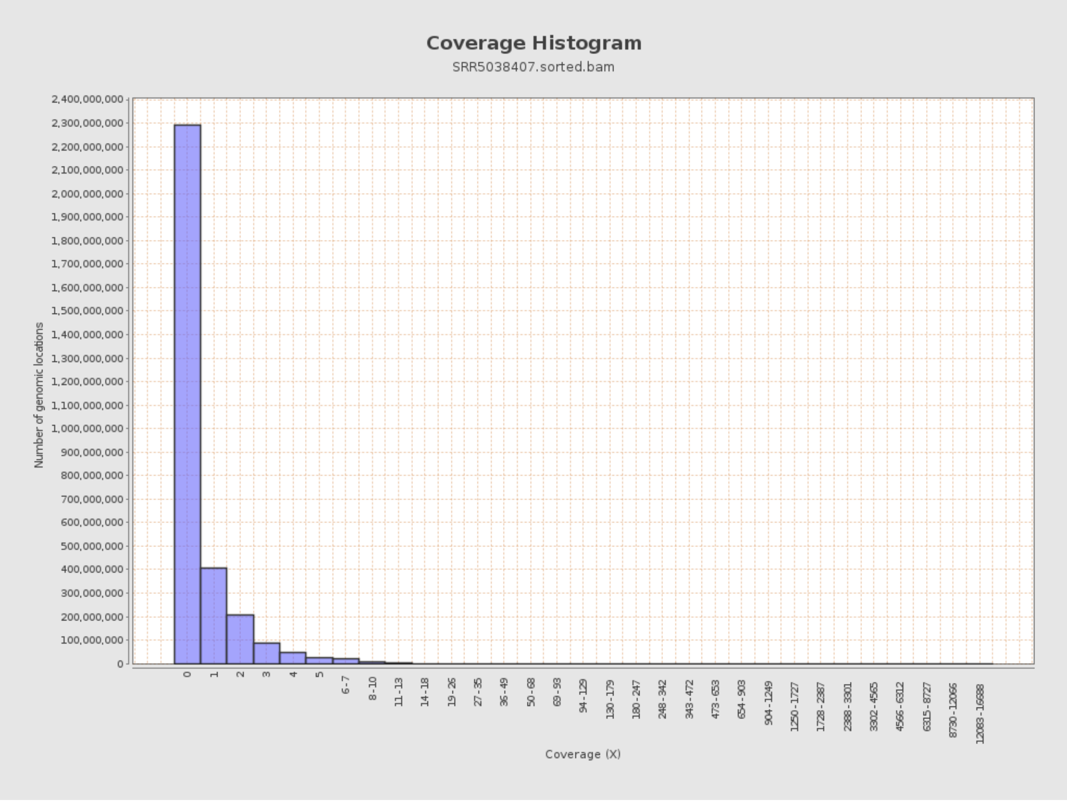
		bases	coverage	deviation
chr1	249250621	111132514	0.4459	14.8502
chr2	243199373	196958440	0.8099	15.2933
chr3	198022430	103451063	0.5224	1.2672
chr4	191154276	110486466	0.578	15.0645
chr5	180915260	99677639	0.551	1.4329
chr6	171115067	127305857	0.744	17.4374
chr7	159138663	120683910	0.7584	12.4764
chr8	146364022	83422397	0.57	3.1731
chr9	141213431	73591782	0.5211	18.3816
chr10	135534747	85332811	0.6296	26.5316
chr11	135006516	88403044	0.6548	8.2076
chr12	133851895	57252813	0.4277	1.1205
chr13	115169878	106300942	0.923	1.7409
chr14	107349540	32326247	0.3011	1.1636
chr15	102531392	30698833	0.2994	0.8469
chr16	90354753	75423212	0.8347	17.5583
chr17	81195210	41334926	0.5091	6.9283
chr18	78077248	31275152	0.4006	16.0415
chr19	59128983	23474041	0.397	8.2135
chr20	63025520	56920568	0.9031	4.6302
chr21	48129895	16803014	0.3491	6.372
chr22	51304566	10660668	0.2078	0.829
chrMT	16571	1386193	83.6517	44.8951
chrX	155270560	95460149	0.6148	2.415

chrY	59373566	41224055	0.6943	22.4476

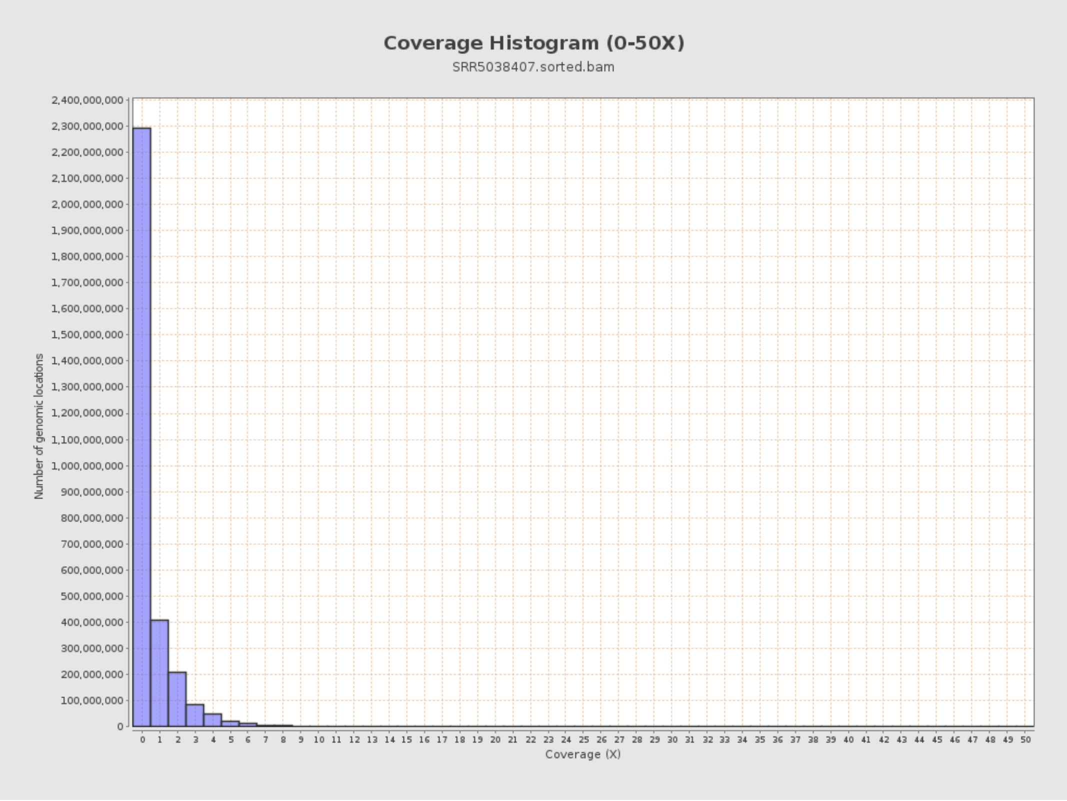
3. Results : Coverage across reference



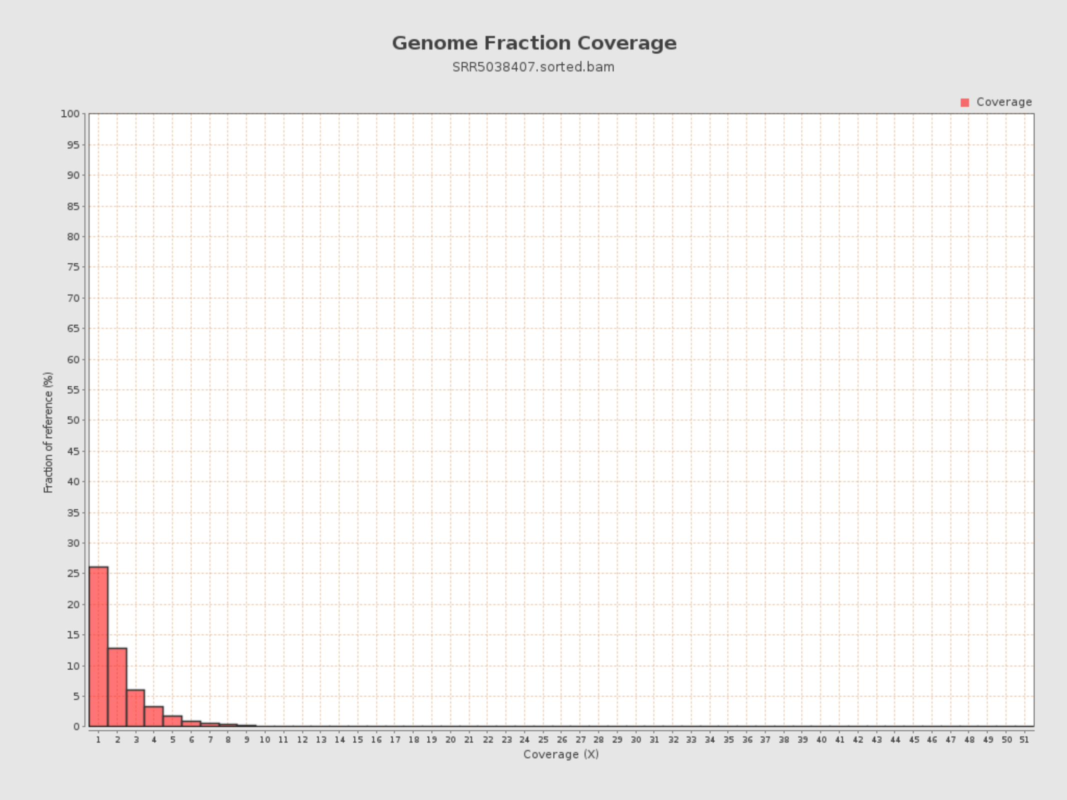
4. Results : Coverage Histogram



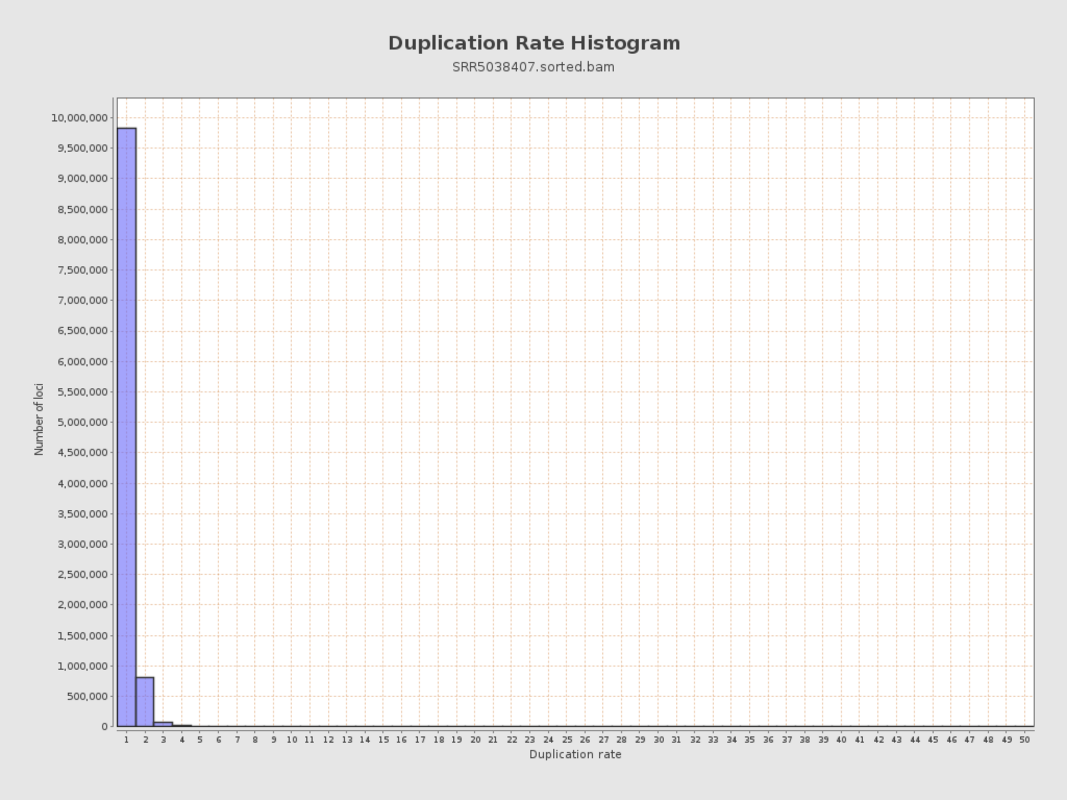
5. Results : Coverage Histogram (0-50X)



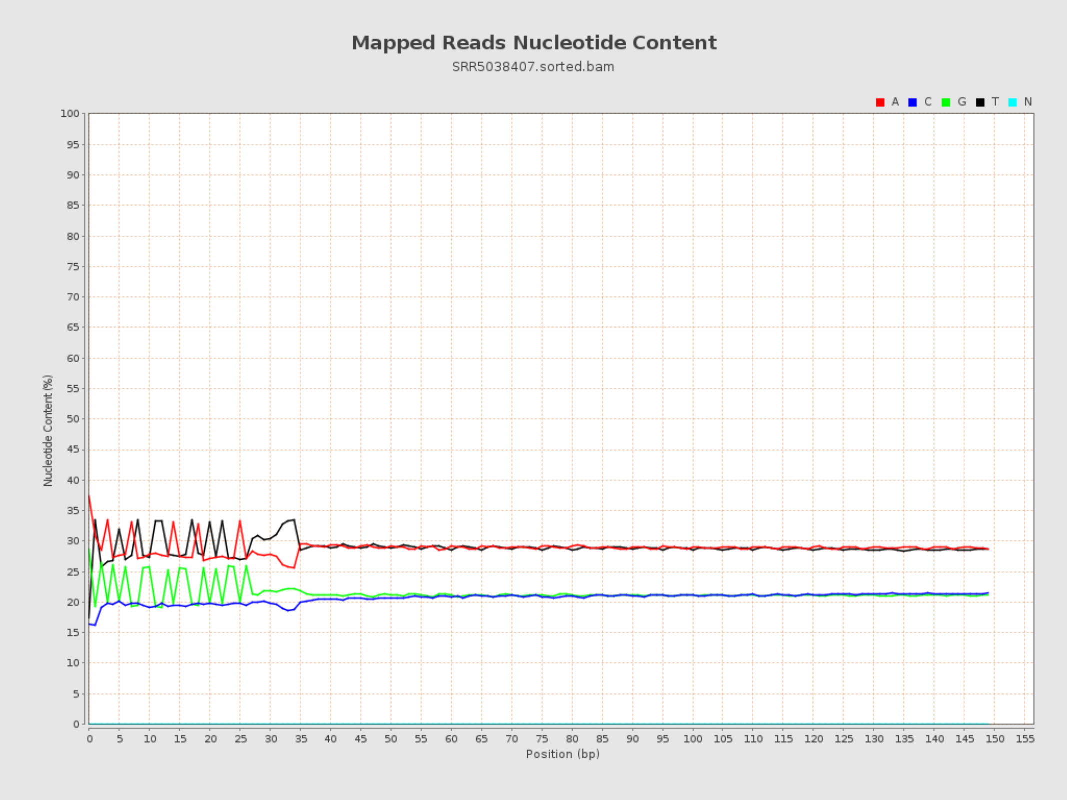
6. Results : Genome Fraction Coverage



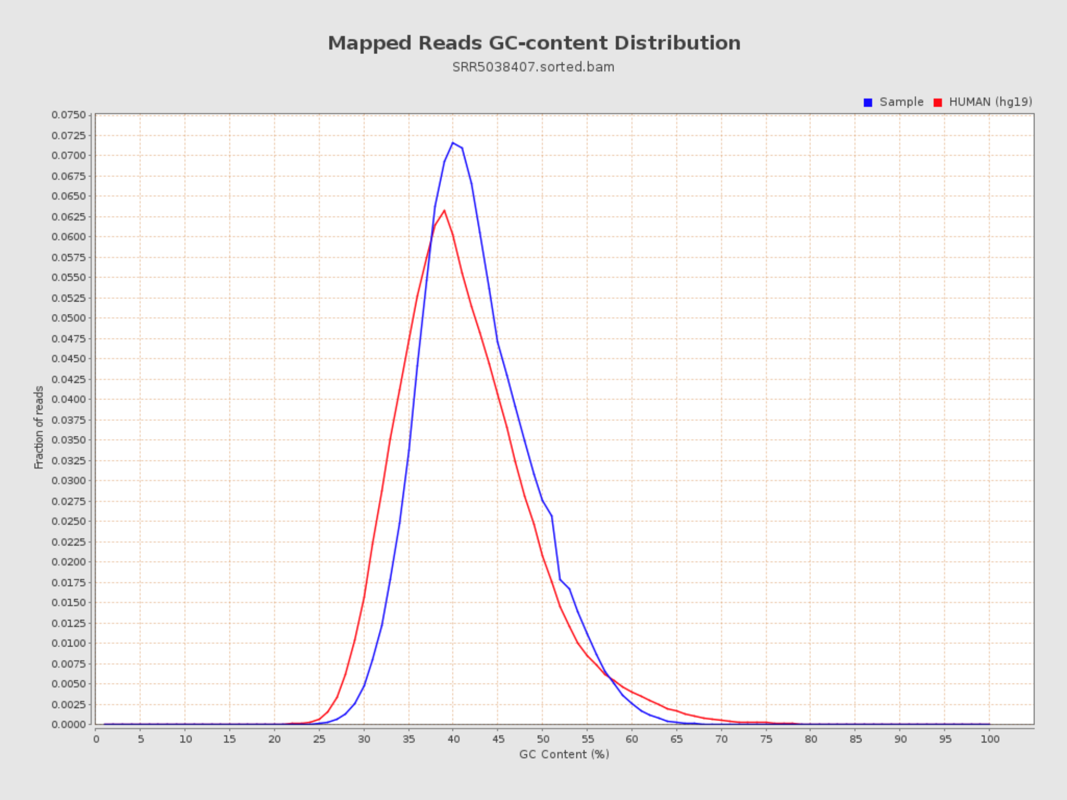
7. Results : Duplication Rate Histogram



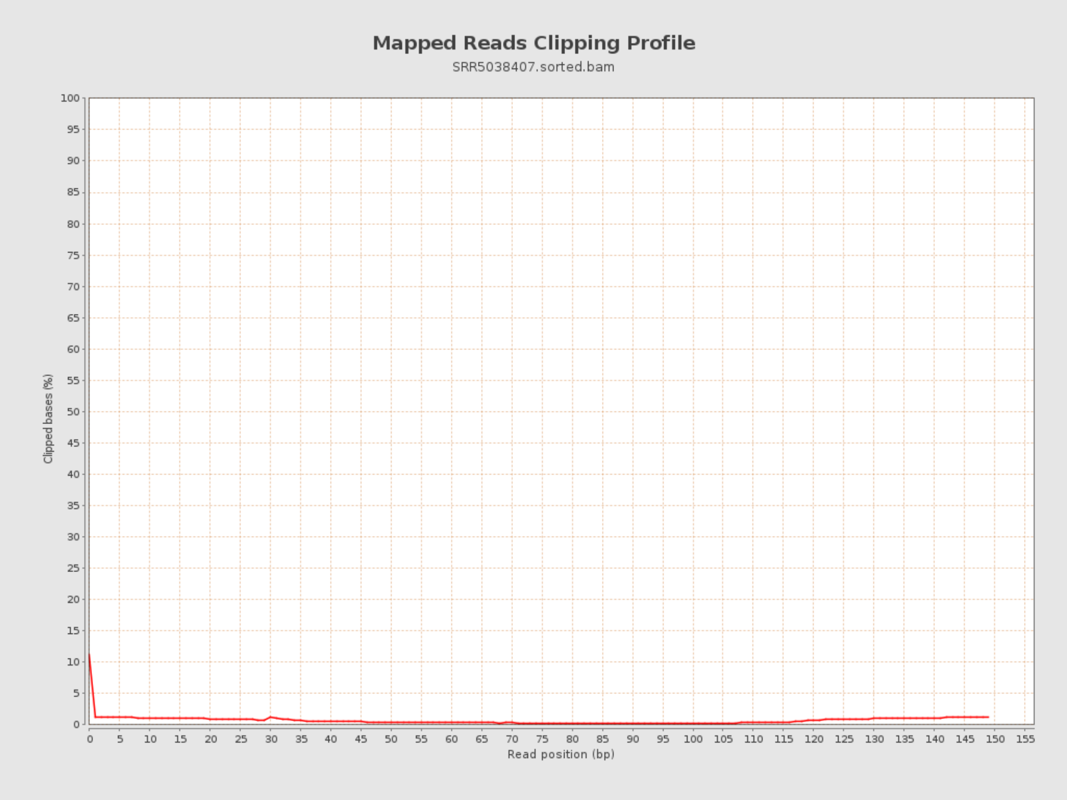
8. Results : Mapped Reads Nucleotide Content



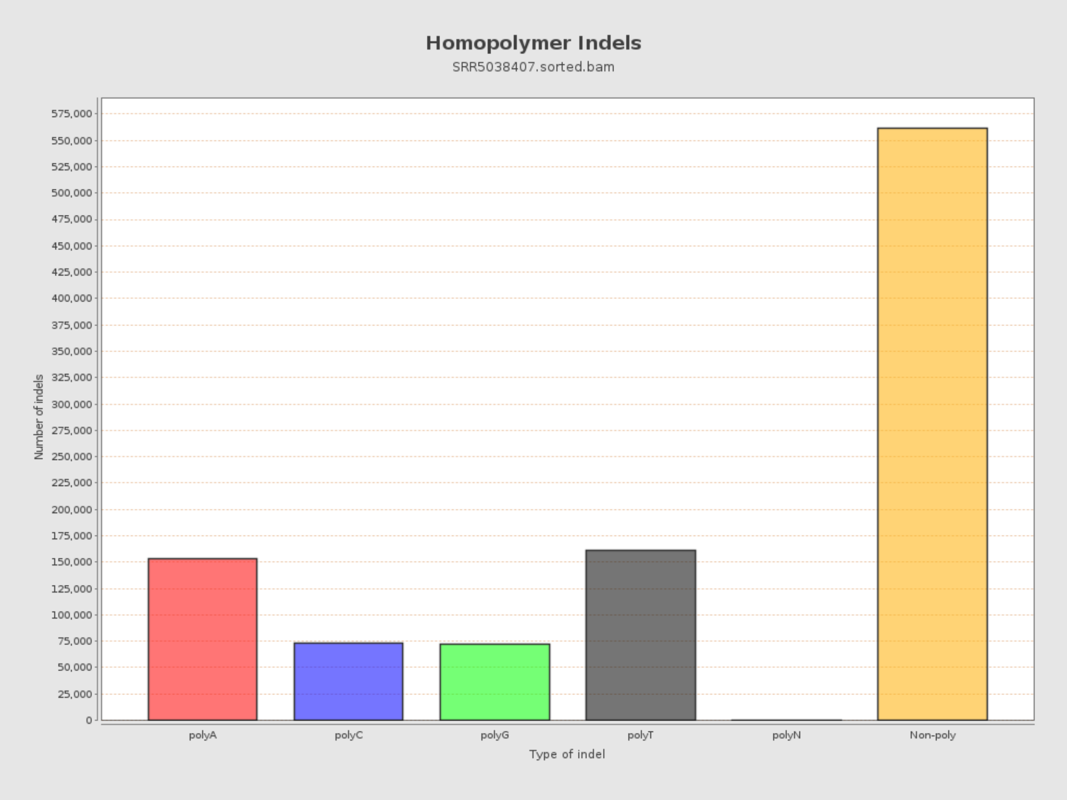
9. Results : Mapped Reads GC-content Distribution



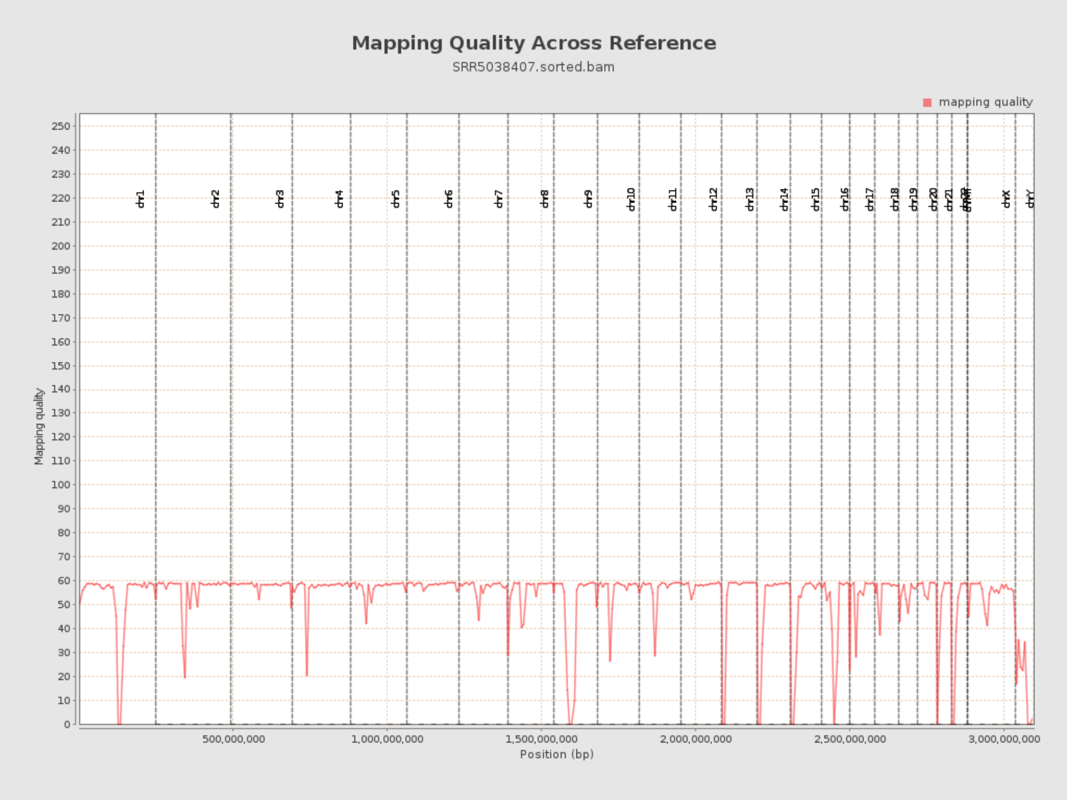
10. Results : Mapped Reads Clipping Profile



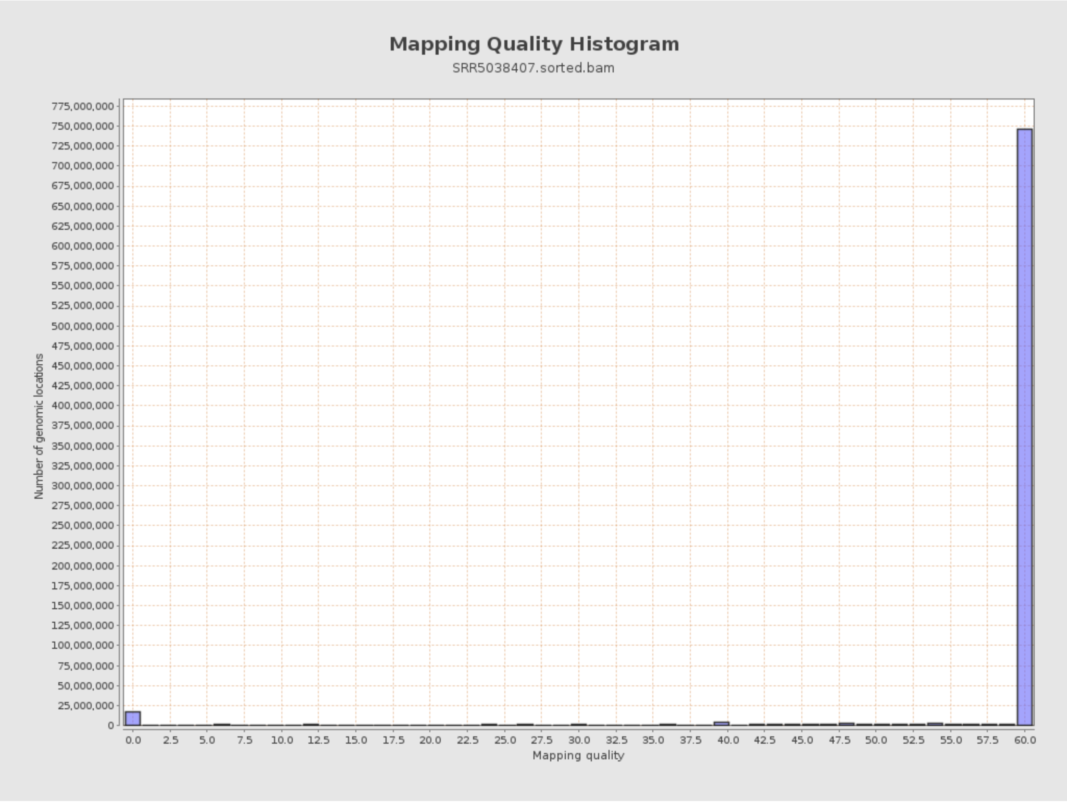
11. Results : Homopolymer Indels



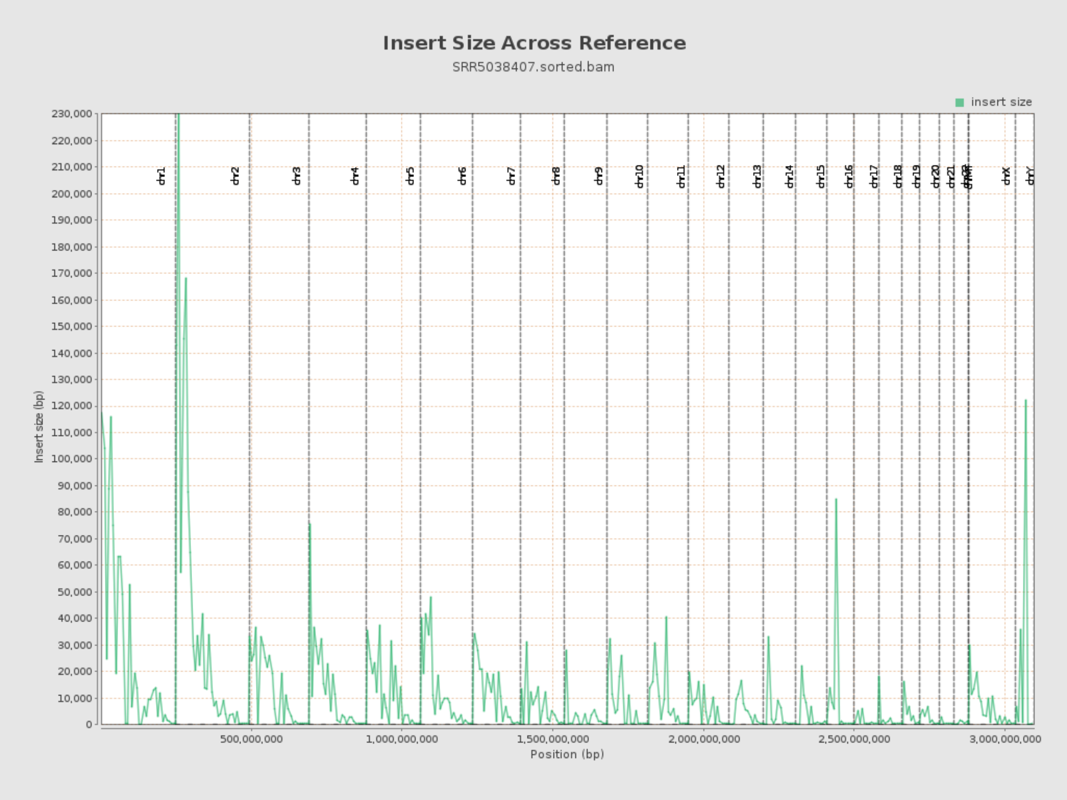
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram