Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 09:11:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038437.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_SRR5038437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038437_1.fastq.gz SRR5038437_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 09:11:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	77,424,954
Mapped reads	76,899,528 / 99.32%
Unmapped reads	525,426 / 0.68%
Mapped paired reads	76,899,528 / 99.32%
Mapped reads, first in pair	38,608,793 / 49.87%
Mapped reads, second in pair	38,290,735 / 49.46%
Mapped reads, both in pair	76,533,412 / 98.85%
Mapped reads, singletons	366,116 / 0.47%
Secondary alignments	0
Supplementary alignments	171,875 / 0.22%
Read min/max/mean length	30 / 150 / 150.11
Duplicated reads (estimated)	30,104,399 / 38.88%
Duplication rate	36.32%
Clipped reads	5,264,357 / 6.8%

2.2. ACGT Content

Number/percentage of A's	2,811,067,667 / 24.63%
Number/percentage of C's	2,896,945,565 / 25.38%
Number/percentage of T's	2,830,387,286 / 24.8%
Number/percentage of G's	2,875,291,589 / 25.19%
Number/percentage of N's	1,058,970 / 0.01%

GC Percentage	50.57%

2.3. Coverage

Mean	3.6879
Standard Deviation	24.4307

2.4. Mapping Quality

Mean Mapping Quality	55.81

2.5. Insert size

Mean	23,156.77
Standard Deviation	1,601,124.73
P25/Median/P75	197 / 228 / 266

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	69,884,392
Insertions	598,933
Mapped reads with at least one insertion	0.74%
Deletions	705,031
Mapped reads with at least one deletion	0.89%
Homopolymer indels	45.76%

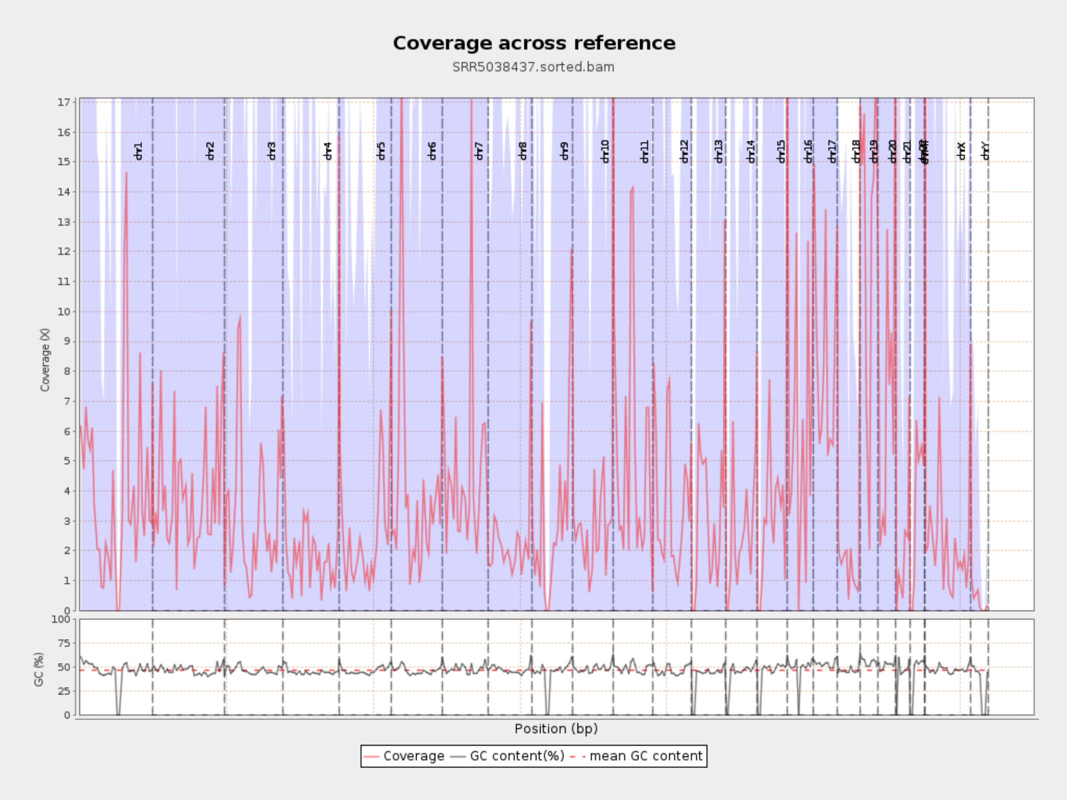
2.7. Chromosome stats

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

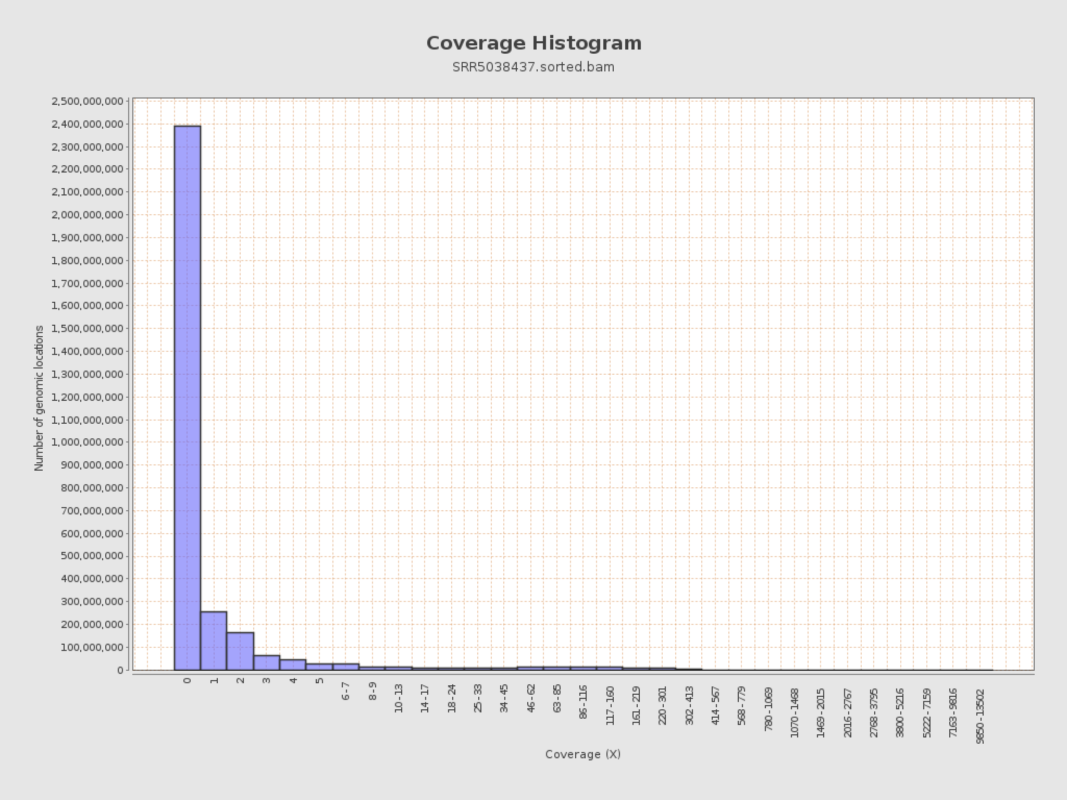
		bases	coverage	deviation
chr1	249250621	991474498	3.9778	23.9137
chr2	243199373	948002780	3.898	25.9642
chr3	198022430	644569625	3.255	21.4283
chr4	191154276	356642348	1.8657	14.1879
chr5	180915260	493448174	2.7275	20.7208
chr6	171115067	661442228	3.8655	25.9294
chr7	159138663	754931554	4.7439	32.7618
chr8	146364022	344878928	2.3563	16.9586
chr9	141213431	450668937	3.1914	21.3987
chr10	135534747	354400665	2.6148	16.3974
chr11	135006516	770547295	5.7075	33.9818
chr12	133851895	484804838	3.6219	20.3686
chr13	115169878	351220077	3.0496	25.4544
chr14	107349540	272322049	2.5368	16.4193
chr15	102531392	299515702	2.9212	17.3824
chr16	90354753	579753208	6.4164	34.0384
chr17	81195210	696300230	8.5756	37.4102
chr18	78077248	110011918	1.409	10.6134
chr19	59128983	754510839	12.7604	45.3842
chr20	63025520	443485123	7.0366	40.2503
chr21	48129895	94070148	1.9545	25.3594
chr22	51304566	195375891	3.8082	20.3024
chrMT	16571	1213218	73.2133	27.8837
chrX	155270560	342857758	2.2081	16.5212

chrY	59373566	20283219	0.3416	4.9626

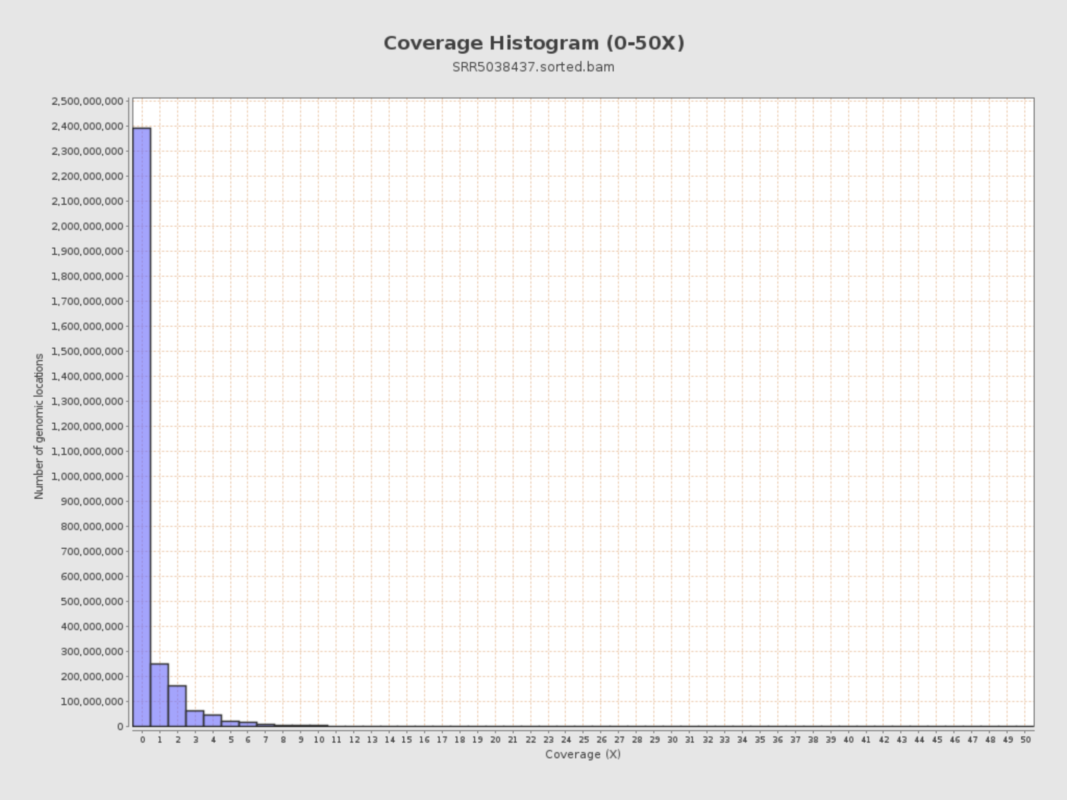
3. Results : Coverage across reference



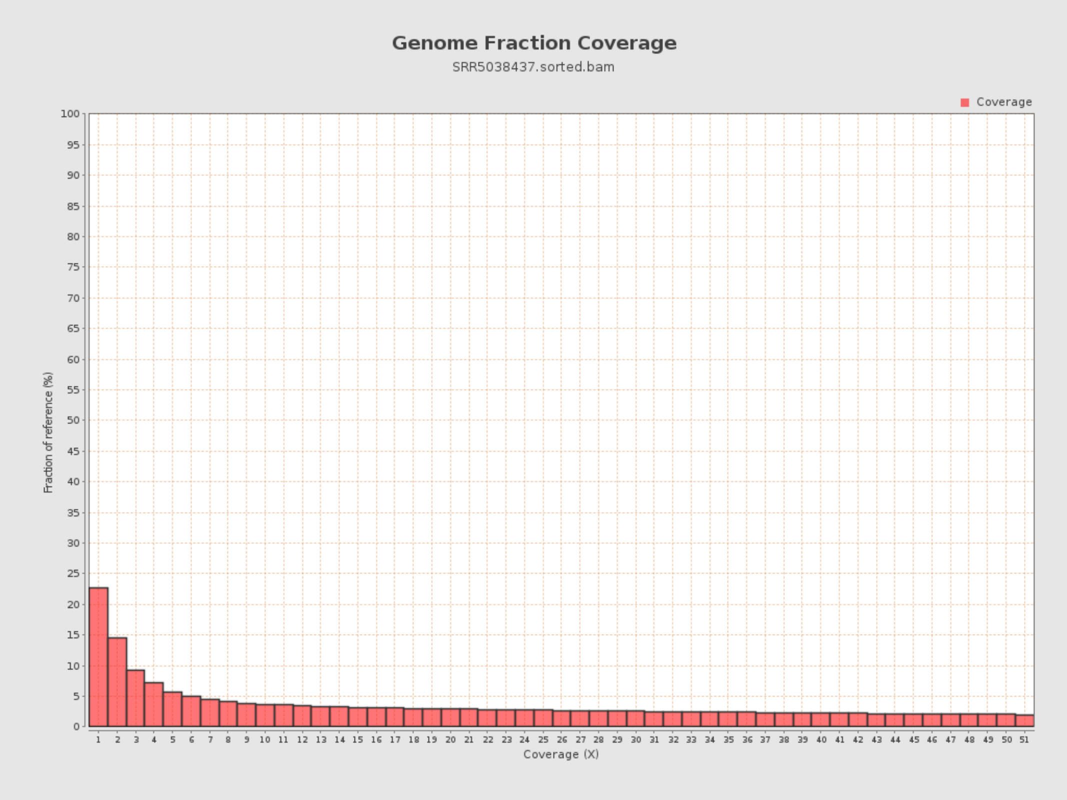
4. Results : Coverage Histogram



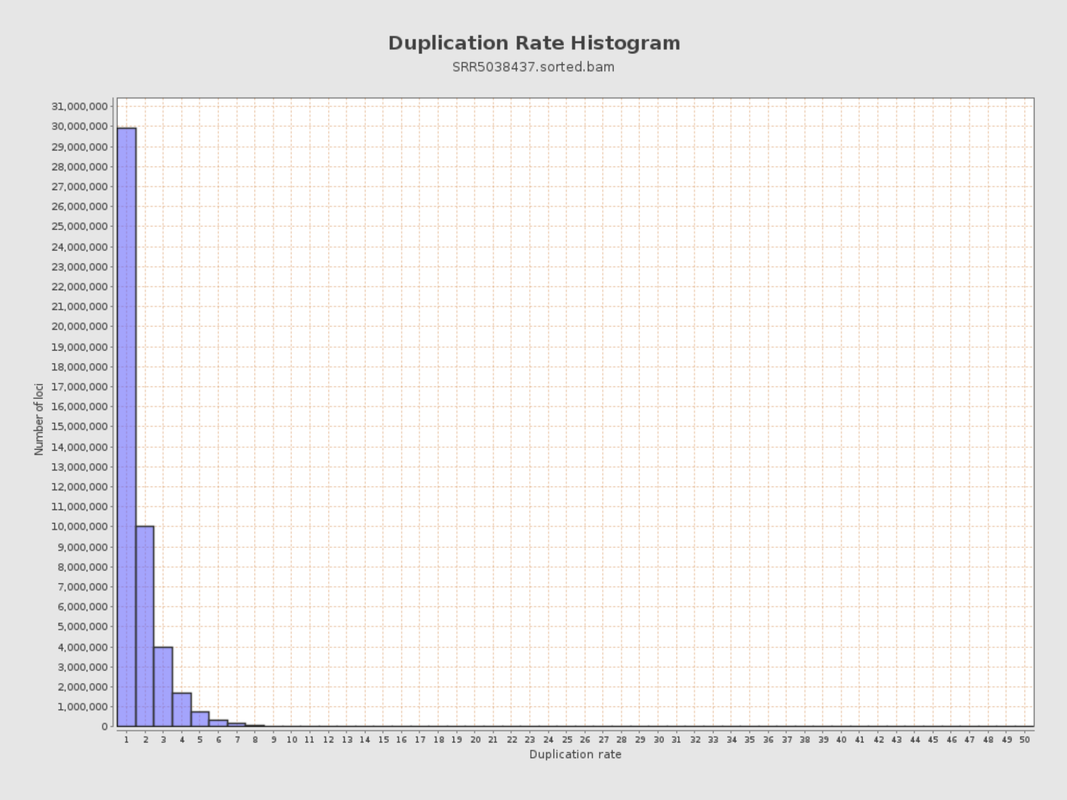
5. Results : Coverage Histogram (0-50X)



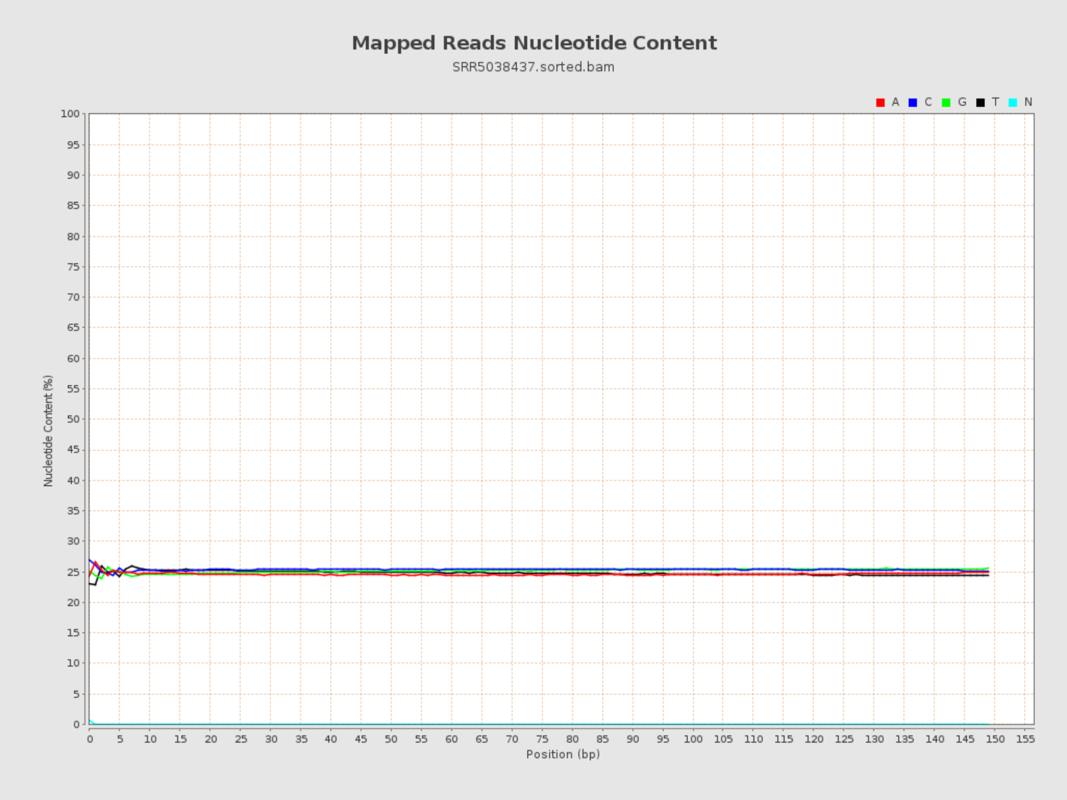
6. Results : Genome Fraction Coverage



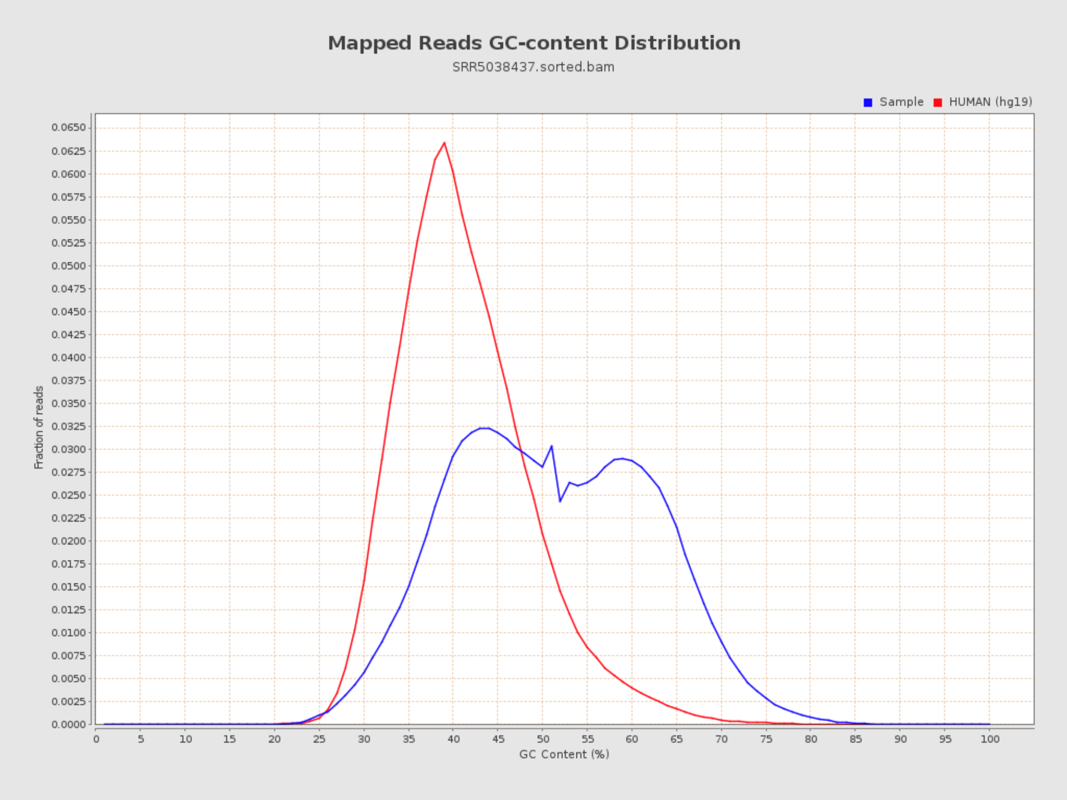
7. Results : Duplication Rate Histogram



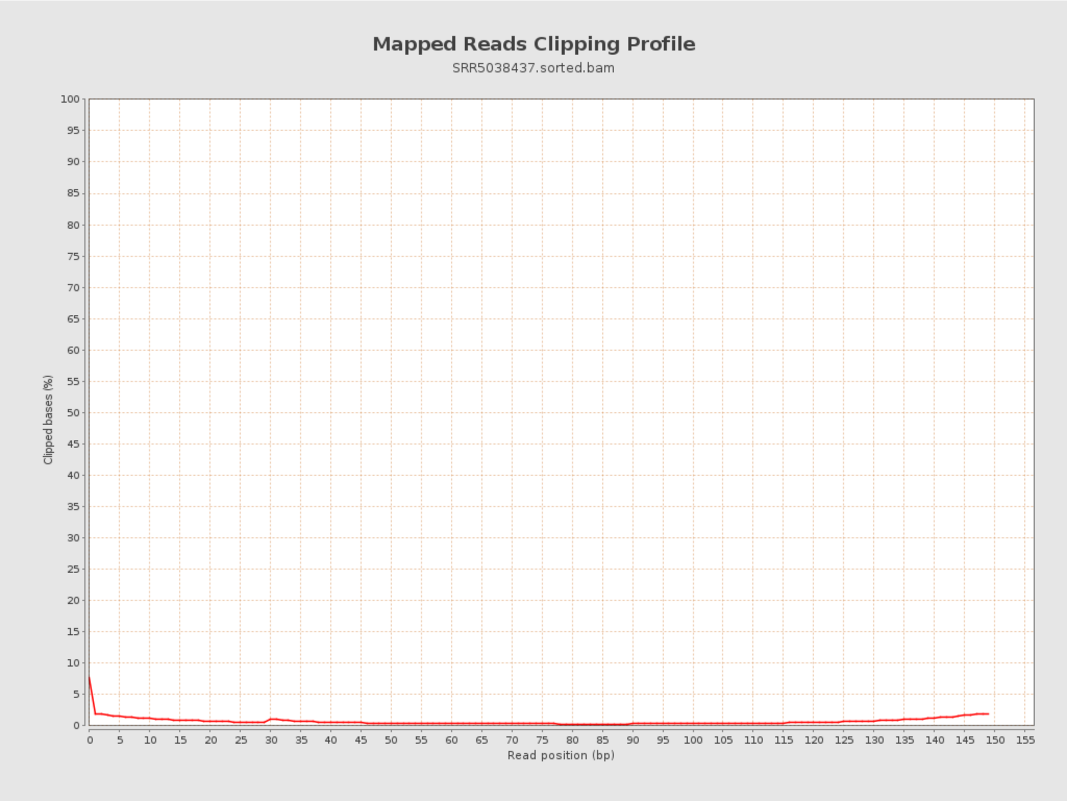
8. Results : Mapped Reads Nucleotide Content



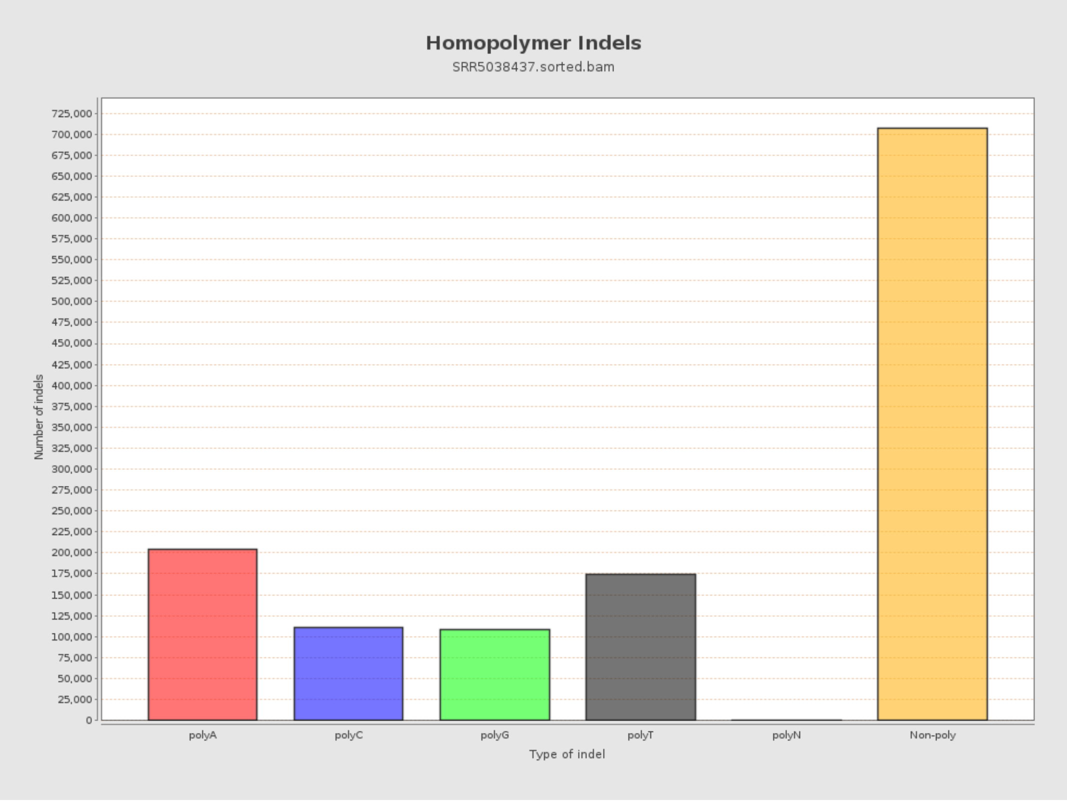
9. Results : Mapped Reads GC-content Distribution



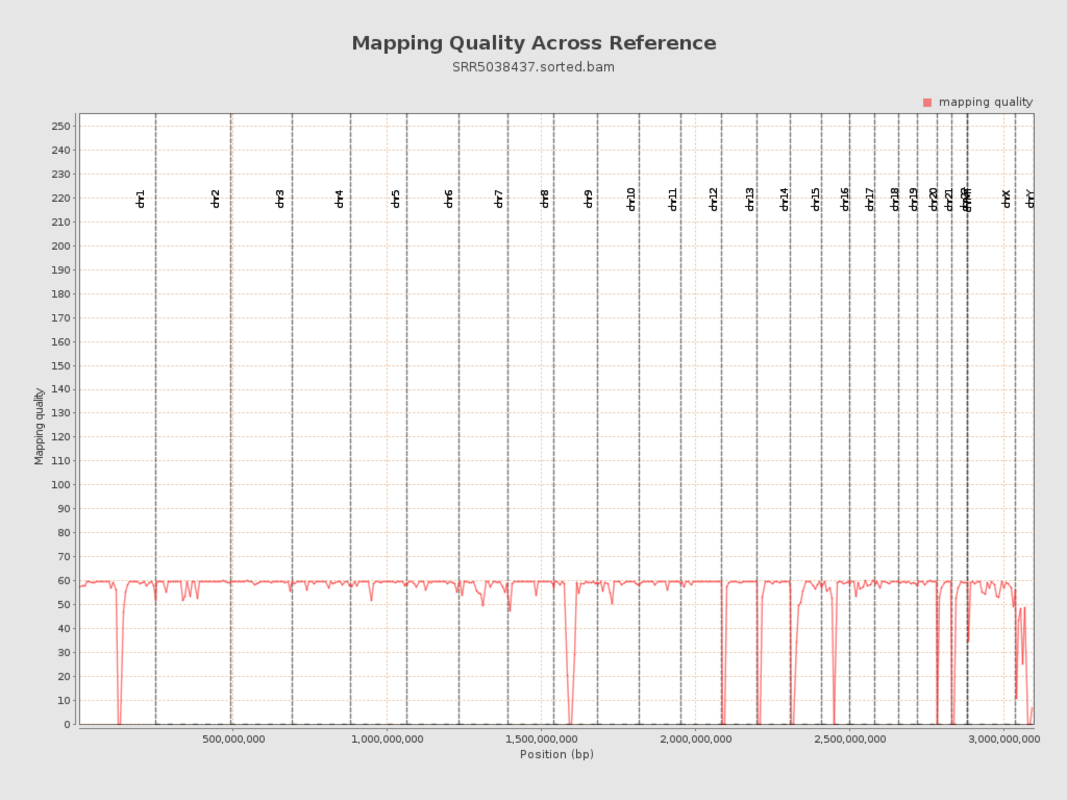
10. Results : Mapped Reads Clipping Profile



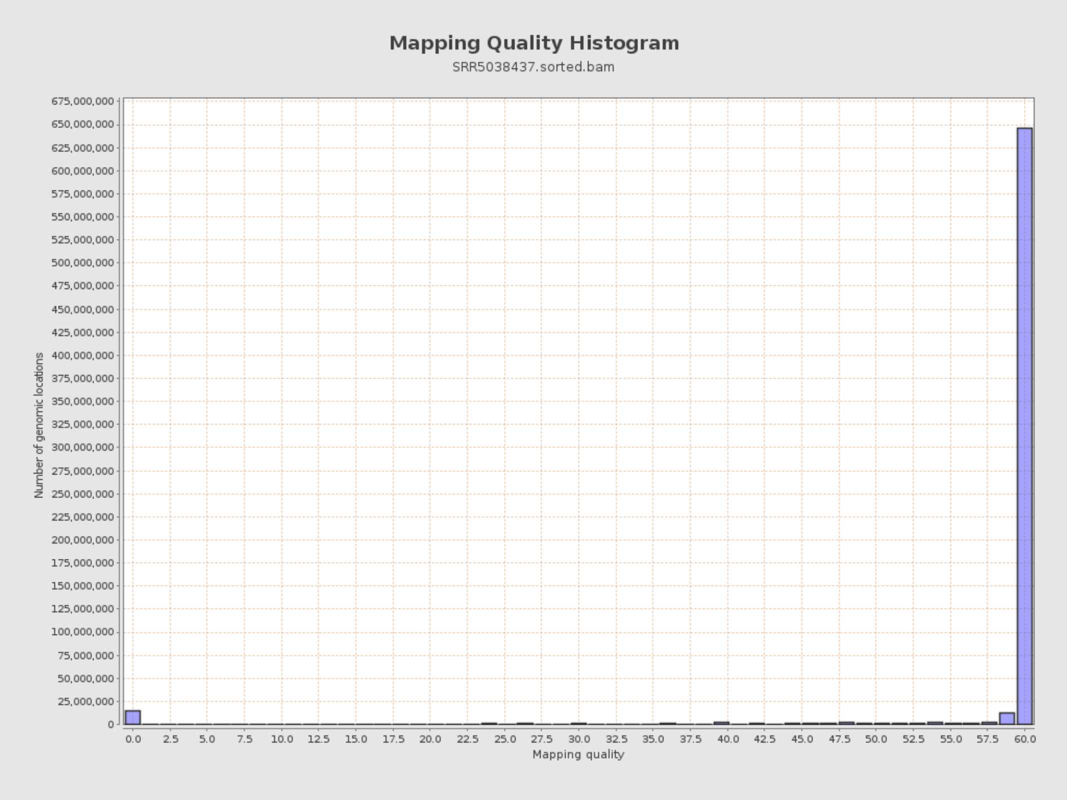
11. Results : Homopolymer Indels



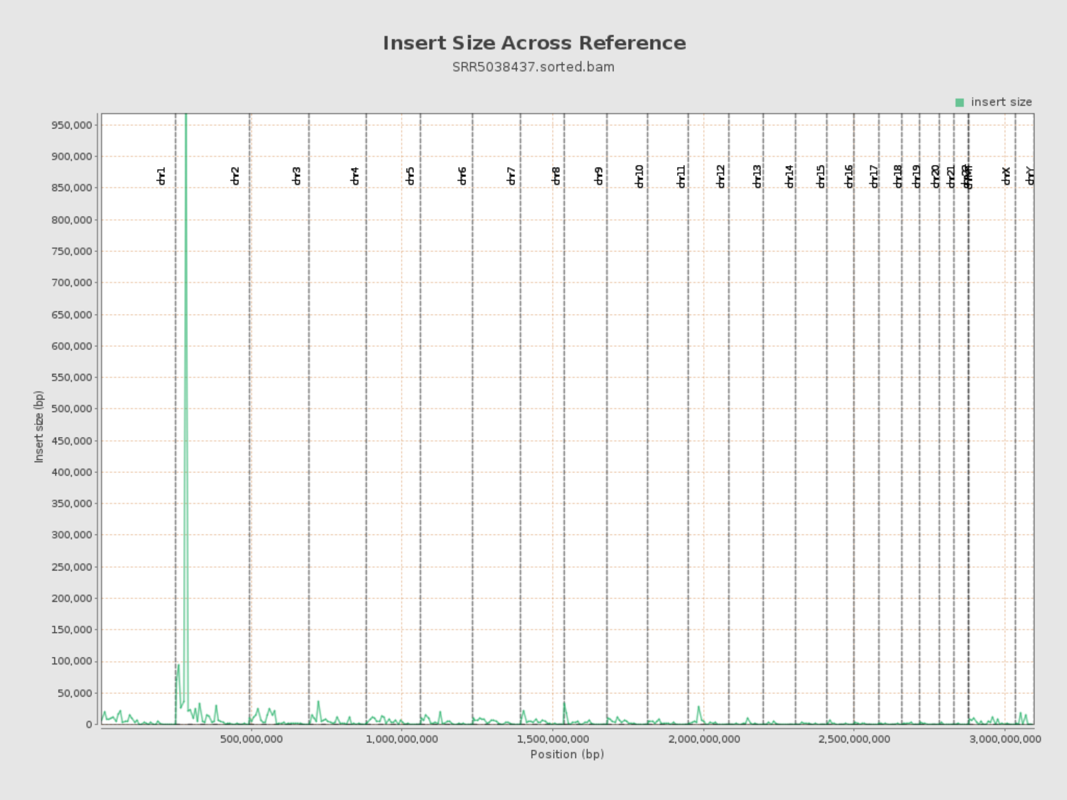
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram