Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 10:01:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038438.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_SRR5038438 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038438_1.fastq.gz SRR5038438_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 10:01:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038438.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,556,840
Mapped reads	14,224,308 / 97.72%
Unmapped reads	332,532 / 2.28%
Mapped paired reads	14,224,308 / 97.72%
Mapped reads, first in pair	7,174,458 / 49.29%
Mapped reads, second in pair	7,049,850 / 48.43%
Mapped reads, both in pair	14,086,124 / 96.77%
Mapped reads, singletons	138,184 / 0.95%
Secondary alignments	0
Supplementary alignments	213,993 / 1.47%
Read min/max/mean length	30 / 150 / 150.77
Duplicated reads (estimated)	1,987,140 / 13.65%
Duplication rate	9.25%
Clipped reads	3,493,326 / 24%

2.2. ACGT Content

Number/percentage of A's	593,344,965 / 29.22%
Number/percentage of C's	411,200,418 / 20.25%
Number/percentage of T's	594,298,610 / 29.26%
Number/percentage of G's	431,992,385 / 21.27%
Number/percentage of N's	42,069 / 0%

GC Percentage	41.52%

2.3. Coverage

Mean	0.6564
Standard Deviation	9.4689

2.4. Mapping Quality

Mean Mapping Quality	53.61

2.5. Insert size

Mean	84,108.91
Standard Deviation	2,716,429.31
P25/Median/P75	221 / 261 / 310

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	25,920,595
Insertions	311,845
Mapped reads with at least one insertion	2.1%
Deletions	671,114
Mapped reads with at least one deletion	4.56%
Homopolymer indels	48.45%

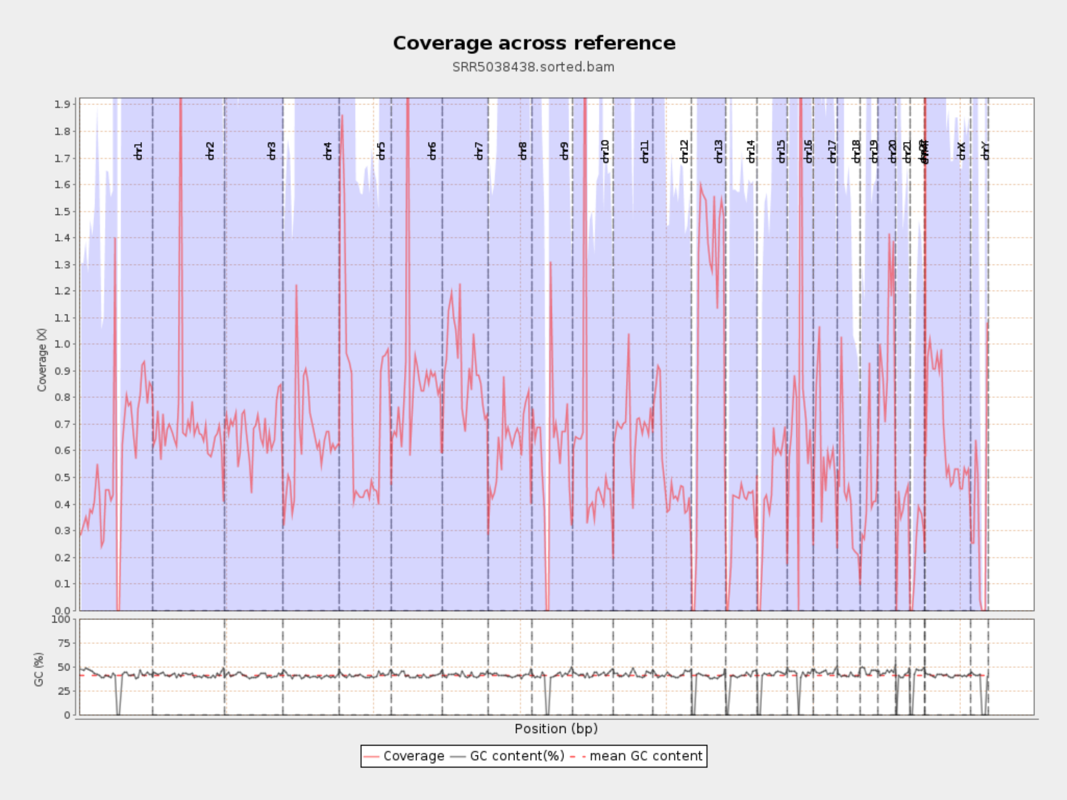
2.7. Chromosome stats

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

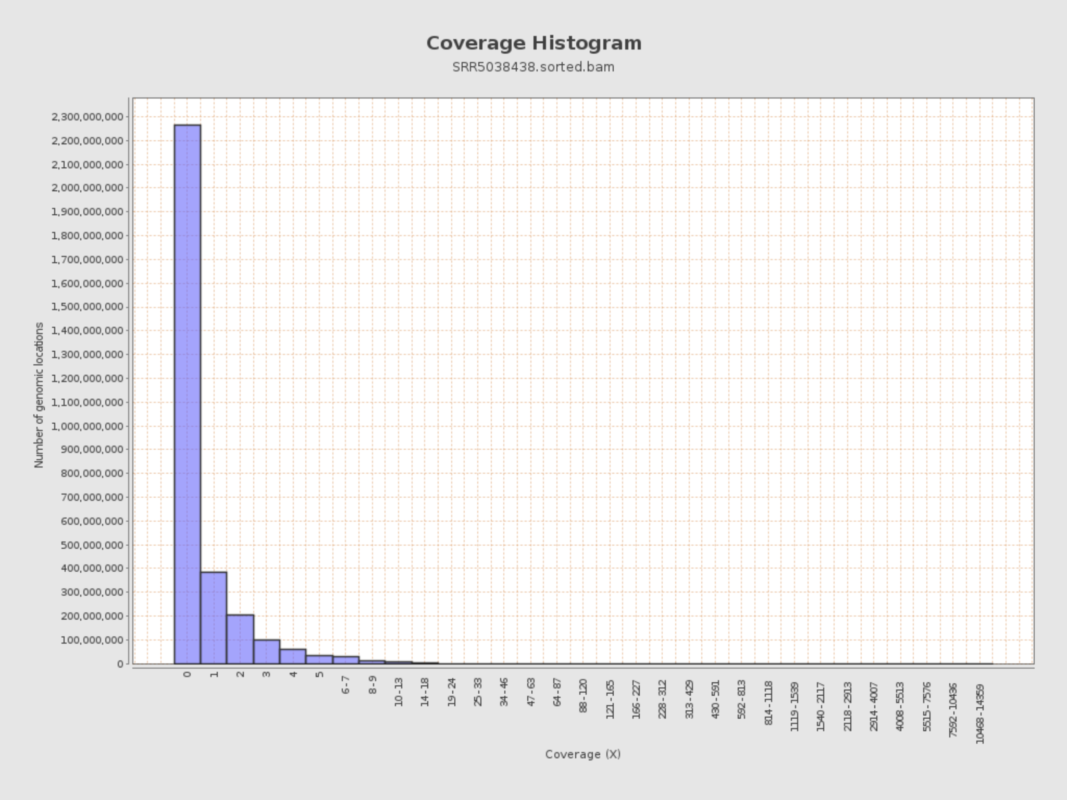
		bases	coverage	deviation
chr1	249250621	139774209	0.5608	15.0523
chr2	243199373	173240771	0.7123	9.2914
chr3	198022430	134114341	0.6773	1.4868
chr4	191154276	122728823	0.642	5.158
chr5	180915260	138521866	0.7657	1.7636
chr6	171115067	150639193	0.8803	17.7534
chr7	159138663	144442755	0.9077	9.2224
chr8	146364022	91235044	0.6233	2.4647
chr9	141213431	81578833	0.5777	15.2618
chr10	135534747	81836667	0.6038	17.1028
chr11	135006516	91100640	0.6748	7.0202
chr12	133851895	70484371	0.5266	1.3303
chr13	115169878	135939904	1.1803	2.252
chr14	107349540	37646495	0.3507	1.1329
chr15	102531392	45325122	0.4421	1.1553
chr16	90354753	69556060	0.7698	12.5911
chr17	81195210	47563113	0.5858	10.5644
chr18	78077248	32911364	0.4215	12.4103
chr19	59128983	24863776	0.4205	8.5334
chr20	63025520	63091612	1.001	2.5203
chr21	48129895	16987922	0.353	2.4738
chr22	51304566	11585638	0.2258	0.8207
chrMT	16571	2302385	138.9406	104.4802
chrX	155270560	103803575	0.6685	2.2324

chrY	59373566	20862056	0.3514	7.7149

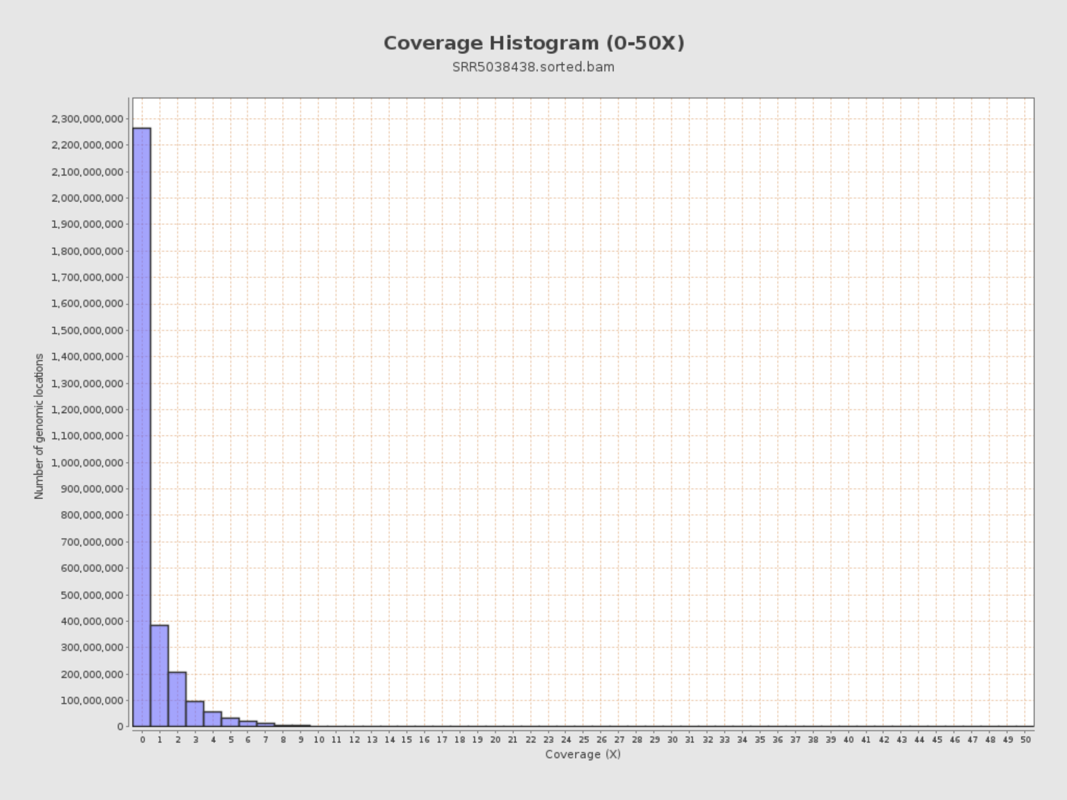
3. Results : Coverage across reference



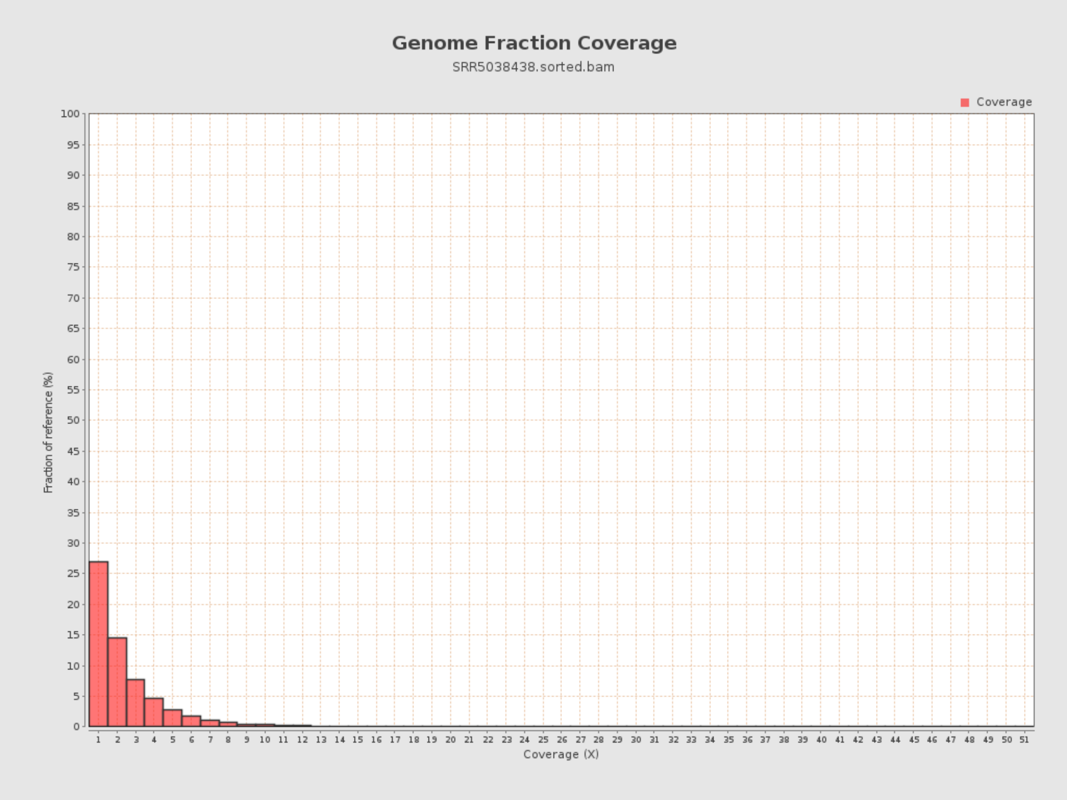
4. Results : Coverage Histogram



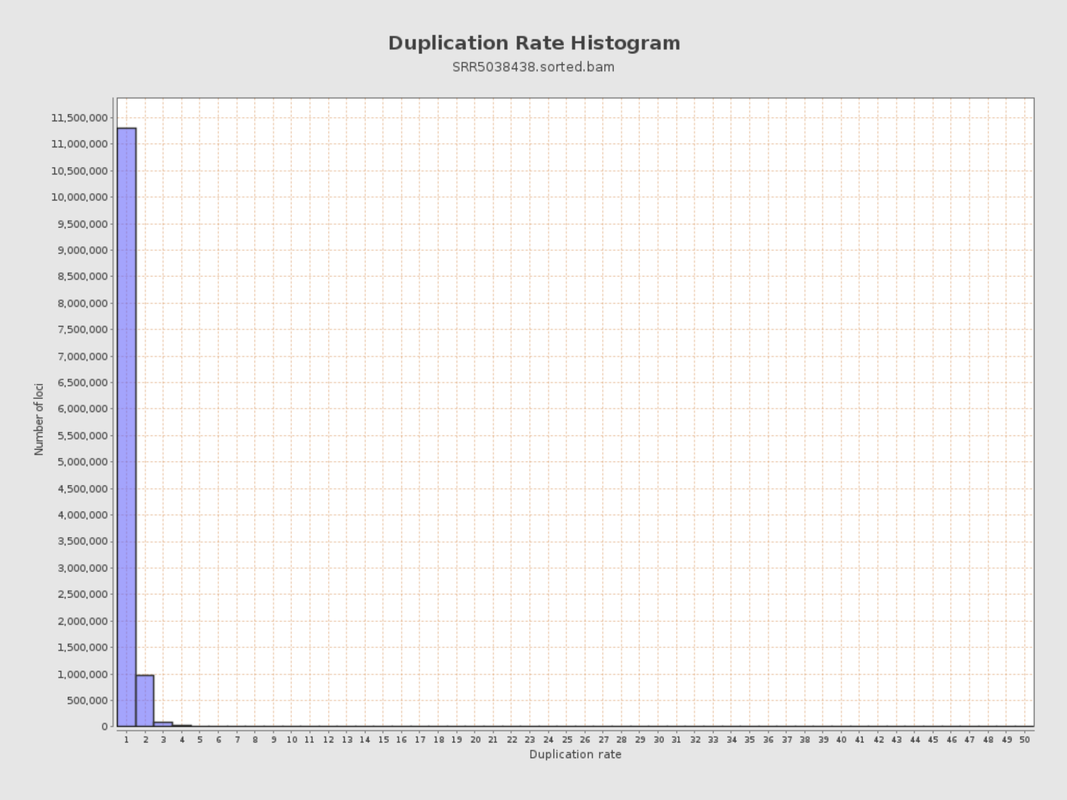
5. Results : Coverage Histogram (0-50X)



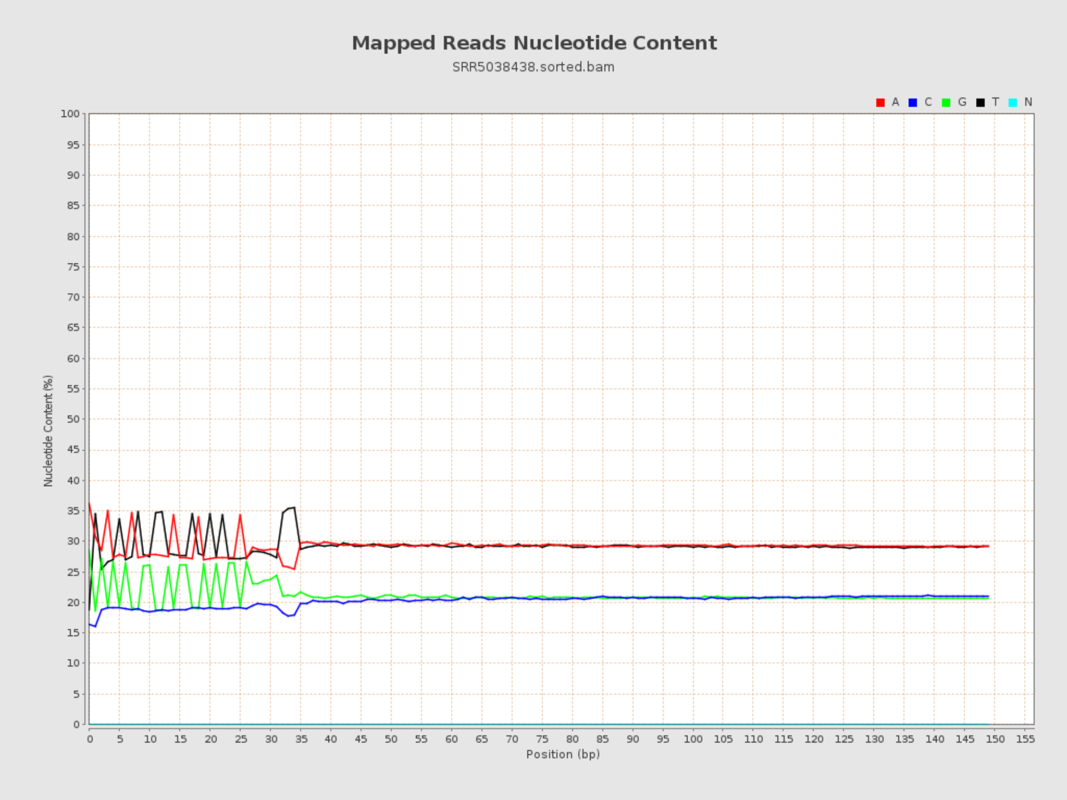
6. Results : Genome Fraction Coverage



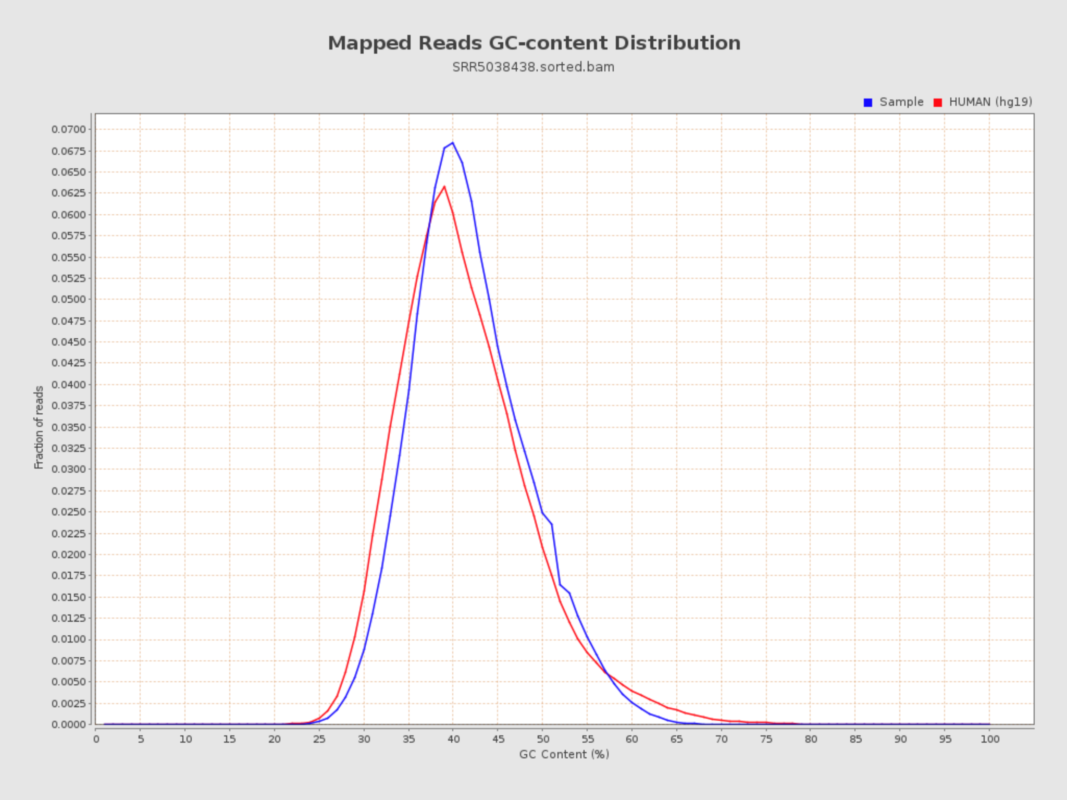
7. Results : Duplication Rate Histogram



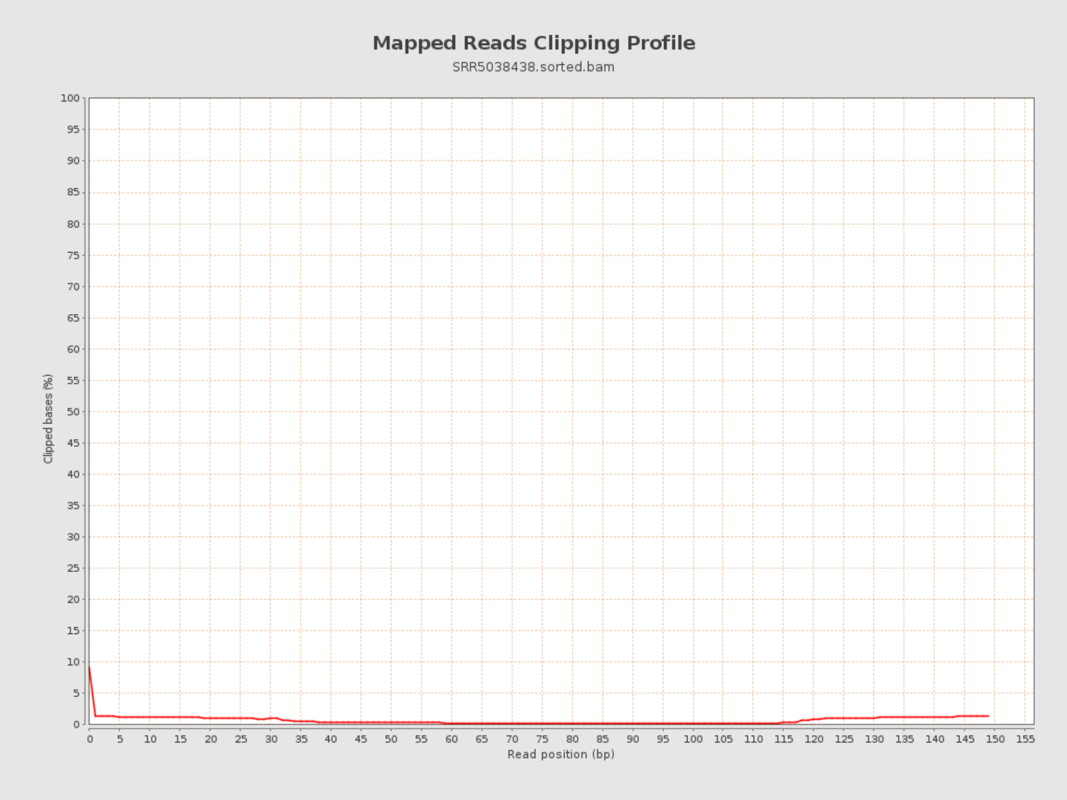
8. Results : Mapped Reads Nucleotide Content



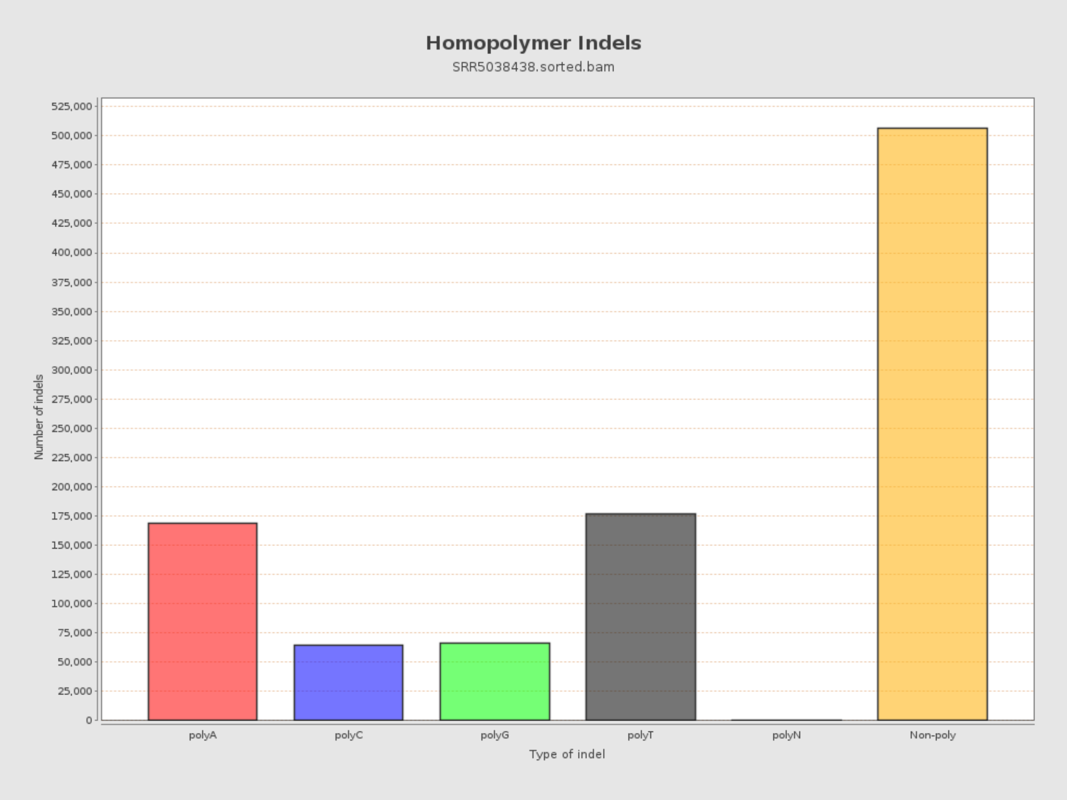
9. Results : Mapped Reads GC-content Distribution



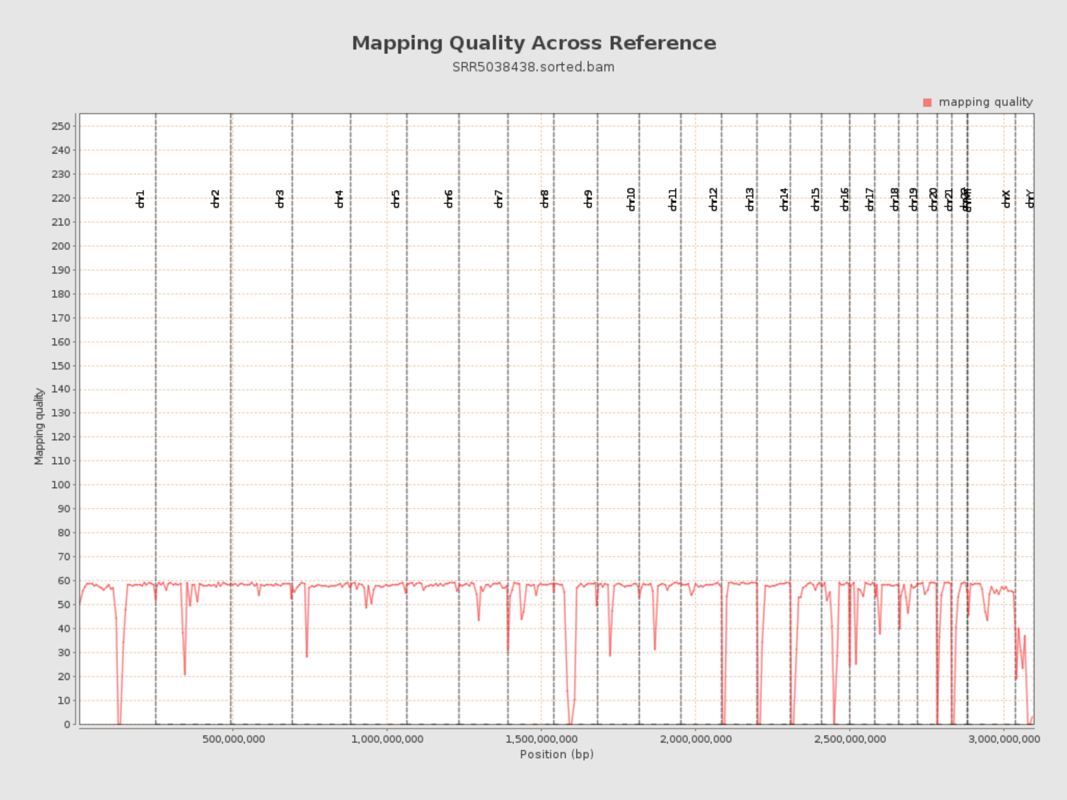
10. Results : Mapped Reads Clipping Profile



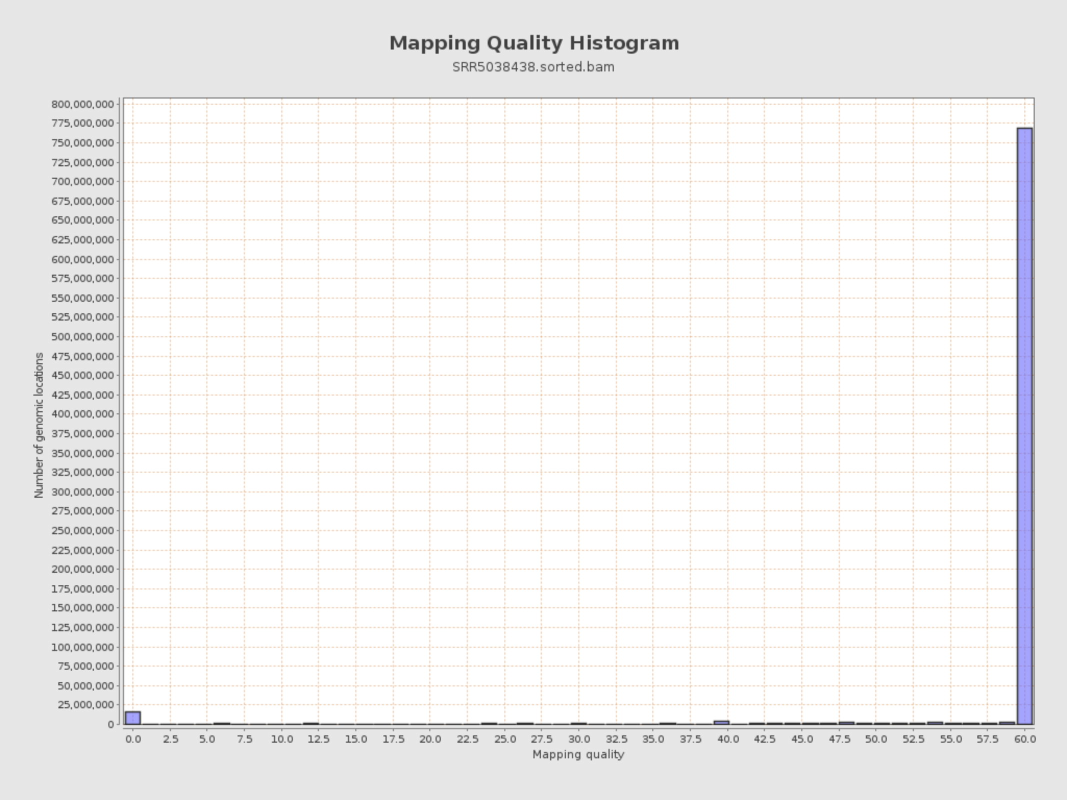
11. Results : Homopolymer Indels



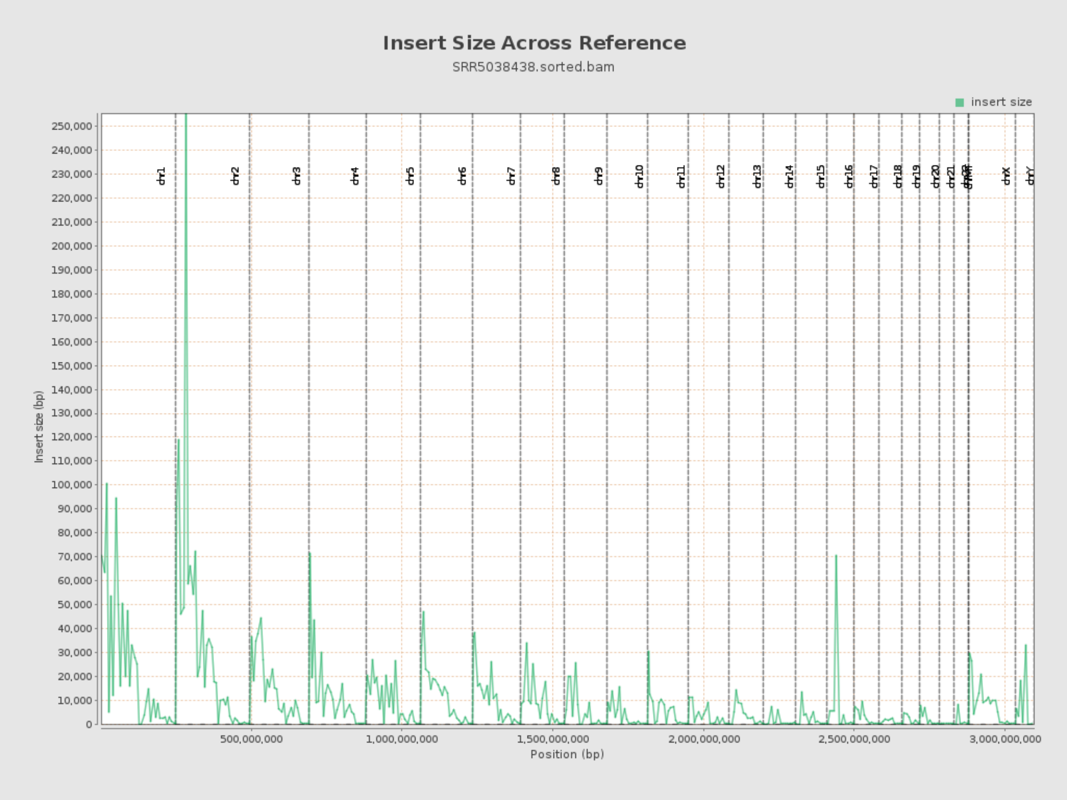
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram