Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 01:46:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038472.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_SRR5038472 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038472_1.fastq.gz SRR5038472_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 01:46:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038472.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,254,238
Mapped reads	12,895,791 / 97.3%
Unmapped reads	358,447 / 2.7%
Mapped paired reads	12,895,791 / 97.3%
Mapped reads, first in pair	6,535,928 / 49.31%
Mapped reads, second in pair	6,359,863 / 47.98%
Mapped reads, both in pair	12,701,528 / 95.83%
Mapped reads, singletons	194,263 / 1.47%
Secondary alignments	0
Supplementary alignments	257,101 / 1.94%
Read min/max/mean length	30 / 150 / 151
Duplicated reads (estimated)	2,168,965 / 16.36%
Duplication rate	9.46%
Clipped reads	3,187,343 / 24.05%

2.2. ACGT Content

Number/percentage of A's	546,607,887 / 29.7%
Number/percentage of C's	368,280,326 / 20.01%
Number/percentage of T's	546,545,249 / 29.7%
Number/percentage of G's	378,775,866 / 20.58%
Number/percentage of N's	38,447 / 0%

GC Percentage	40.6%

2.3. Coverage

Mean	0.5949
Standard Deviation	10.8643

2.4. Mapping Quality

Mean Mapping Quality	53.73

2.5. Insert size

Mean	73,207.6
Standard Deviation	2,528,433.75
P25/Median/P75	207 / 253 / 312

2.6. Mismatches and indels

General error rate	1.64%
Mismatches	28,964,981
Insertions	387,013
Mapped reads with at least one insertion	2.8%
Deletions	712,704
Mapped reads with at least one deletion	5.29%
Homopolymer indels	46.79%

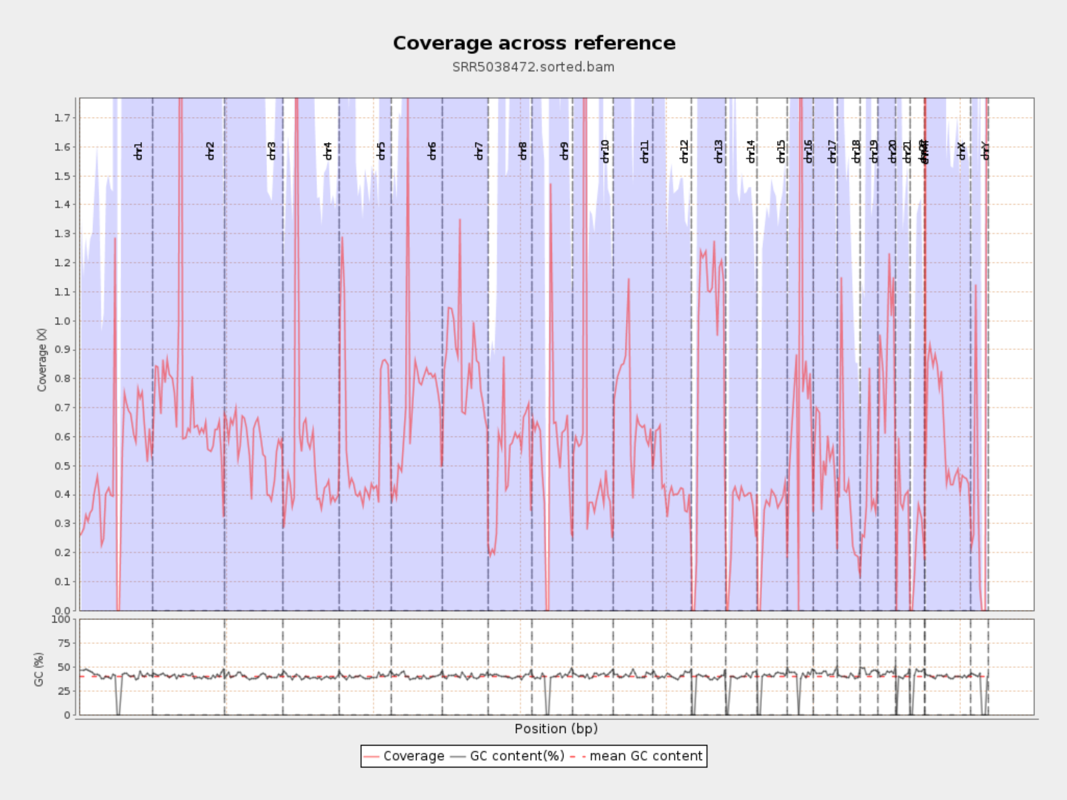
2.7. Chromosome stats

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

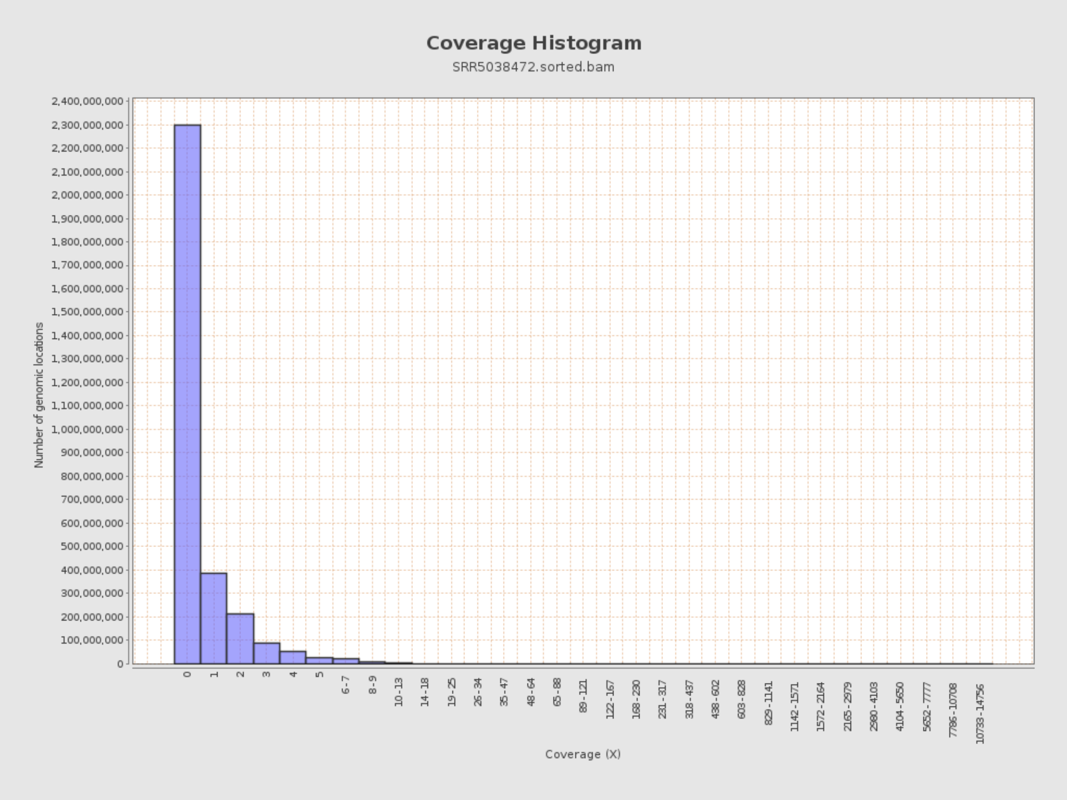
		bases	coverage	deviation
chr1	249250621	122098077	0.4899	14.9442
chr2	243199373	183516797	0.7546	13.3373
chr3	198022430	112593615	0.5686	1.349
chr4	191154276	103048272	0.5391	13.1675
chr5	180915260	107925301	0.5966	1.4791
chr6	171115067	125729822	0.7348	12.0635
chr7	159138663	135253877	0.8499	10.3189
chr8	146364022	74816728	0.5112	3.0185
chr9	141213431	76807459	0.5439	17.6474
chr10	135534747	82781107	0.6108	22.5654
chr11	135006516	93631492	0.6935	7.6282
chr12	133851895	58584113	0.4377	1.1497
chr13	115169878	108997756	0.9464	1.7552
chr14	107349540	34842859	0.3246	1.1729
chr15	102531392	32486201	0.3168	0.9019
chr16	90354753	74060933	0.8197	14.4706
chr17	81195210	42311982	0.5211	5.5369
chr18	78077248	31386919	0.402	14.5886
chr19	59128983	22770019	0.3851	8.1835
chr20	63025520	56892880	0.9027	4.1755
chr21	48129895	17528927	0.3642	5.7252
chr22	51304566	10259866	0.2	0.8289
chrMT	16571	4033820	243.4265	137.6895
chrX	155270560	93226290	0.6004	2.2509

chrY	59373566	36146393	0.6088	18.7697

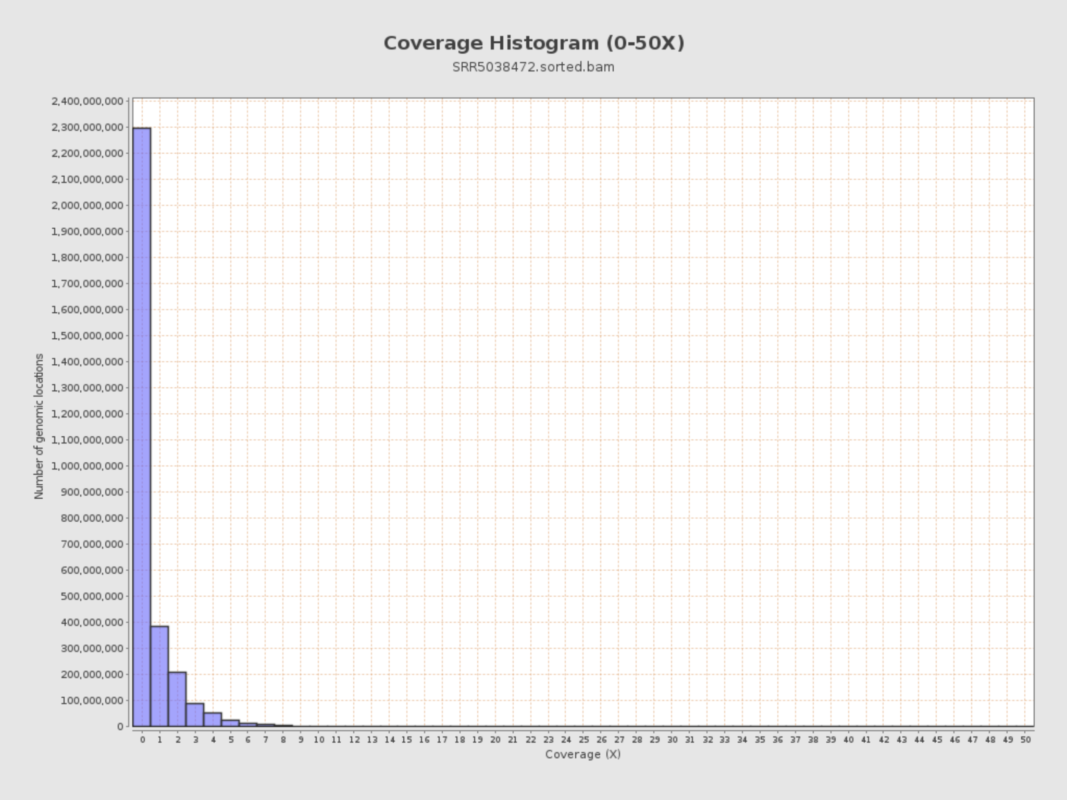
3. Results : Coverage across reference



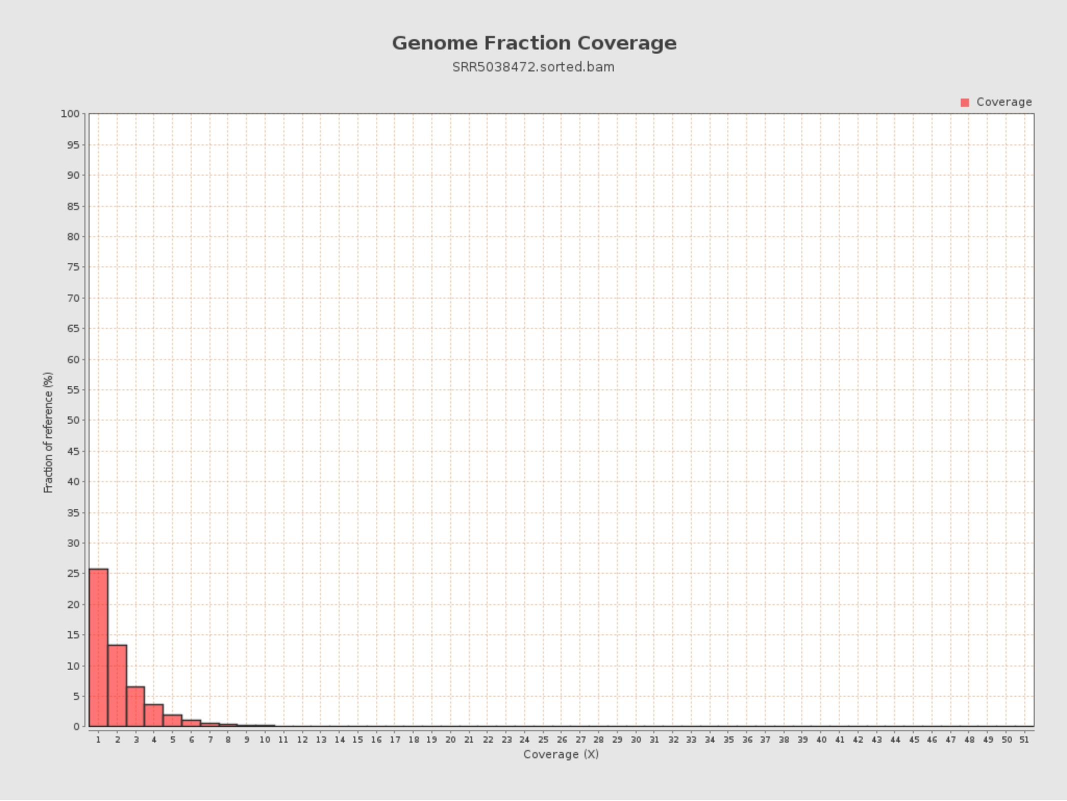
4. Results : Coverage Histogram



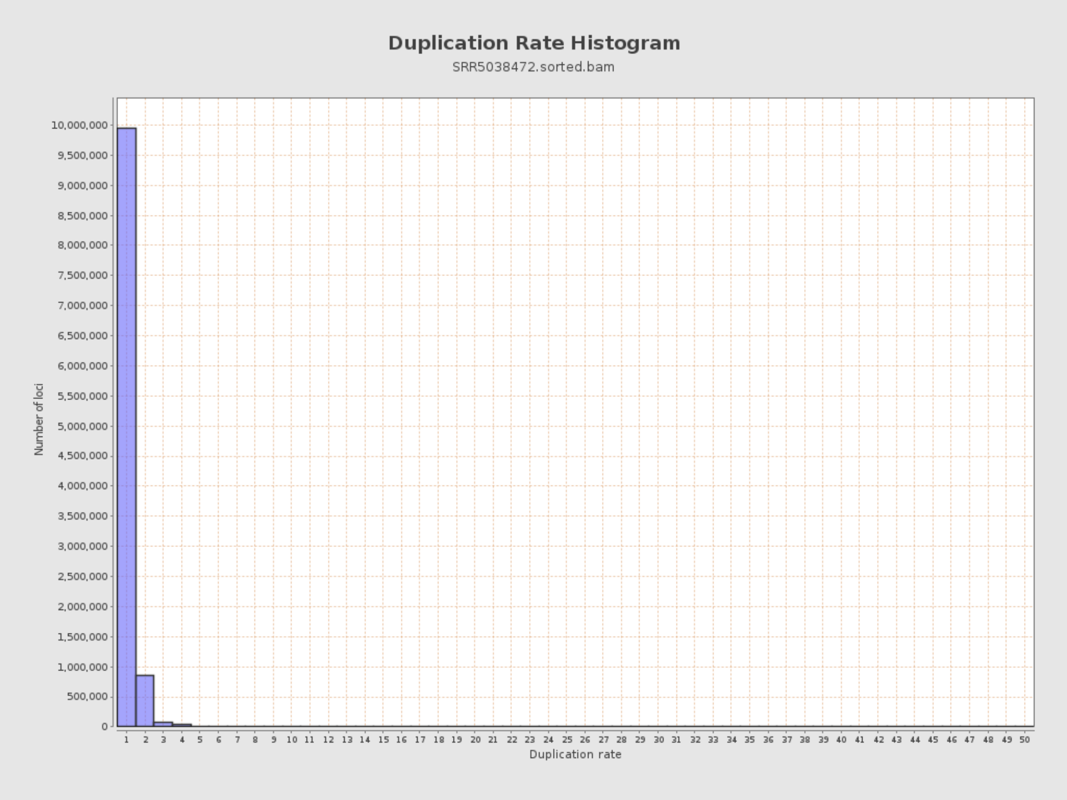
5. Results : Coverage Histogram (0-50X)



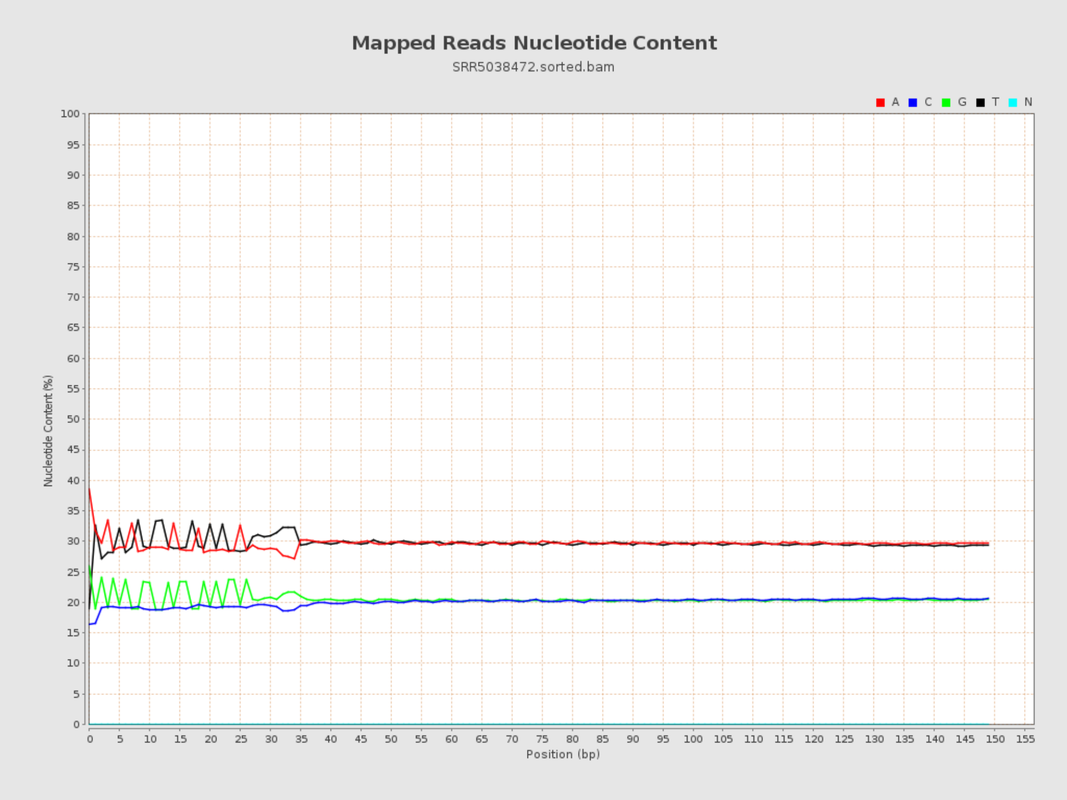
6. Results : Genome Fraction Coverage



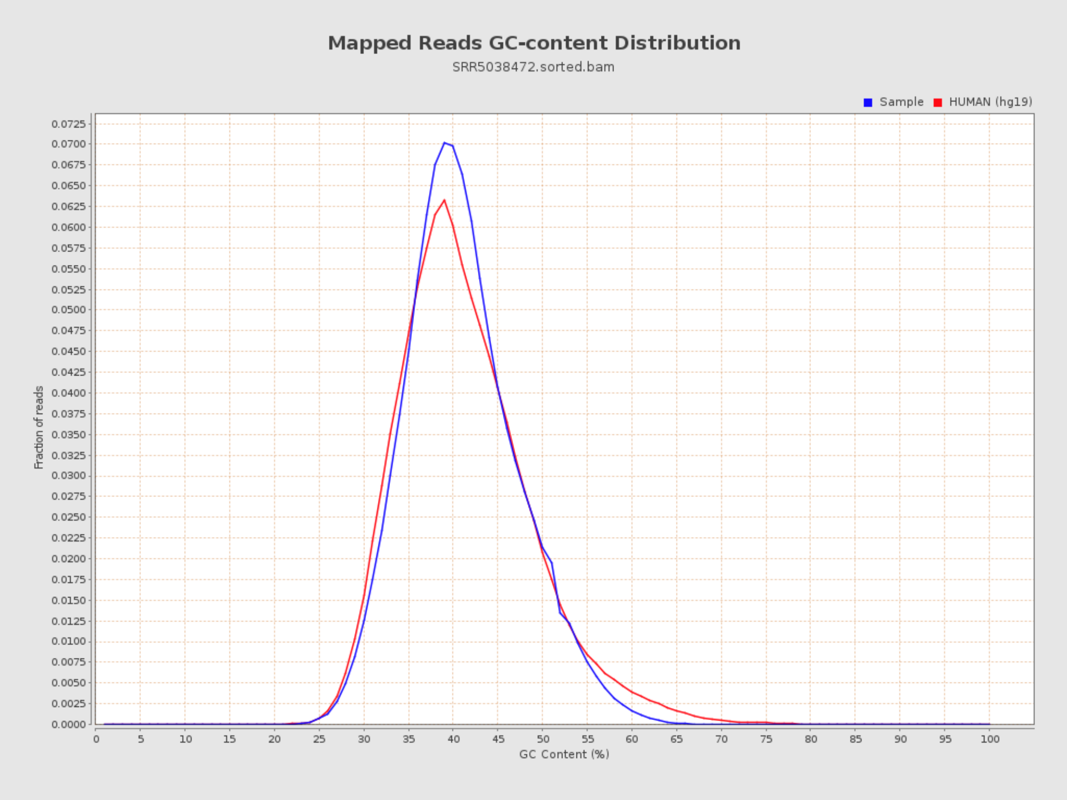
7. Results : Duplication Rate Histogram



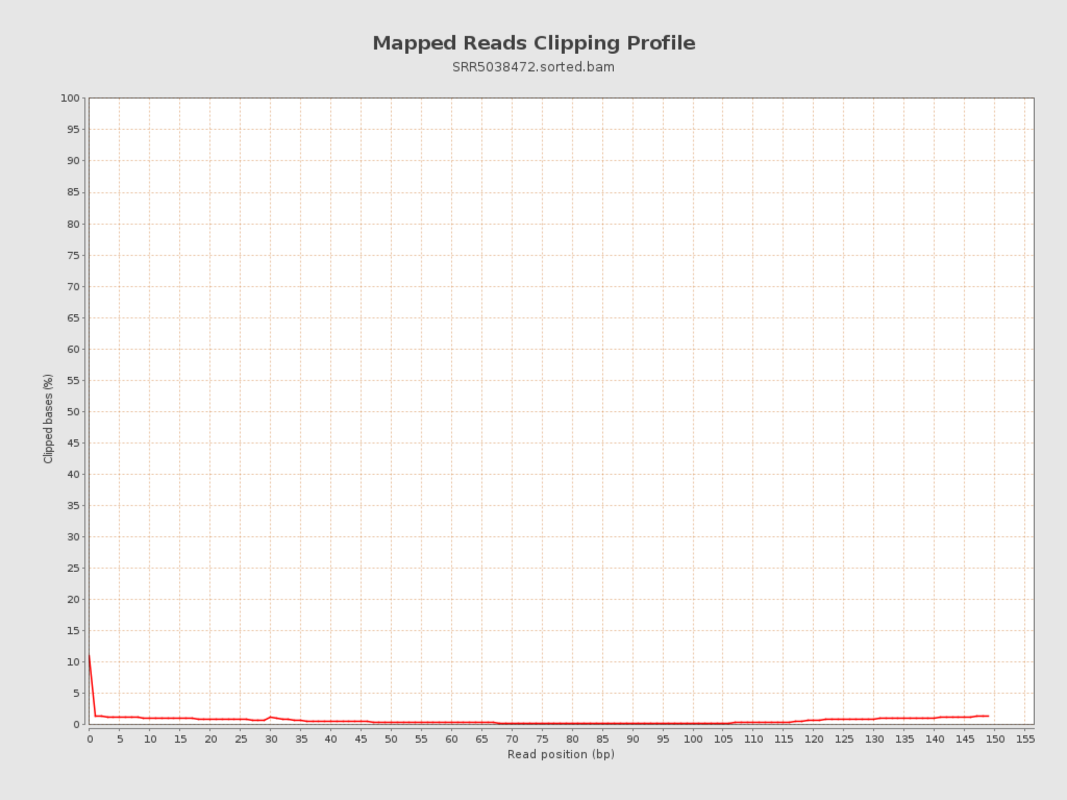
8. Results : Mapped Reads Nucleotide Content



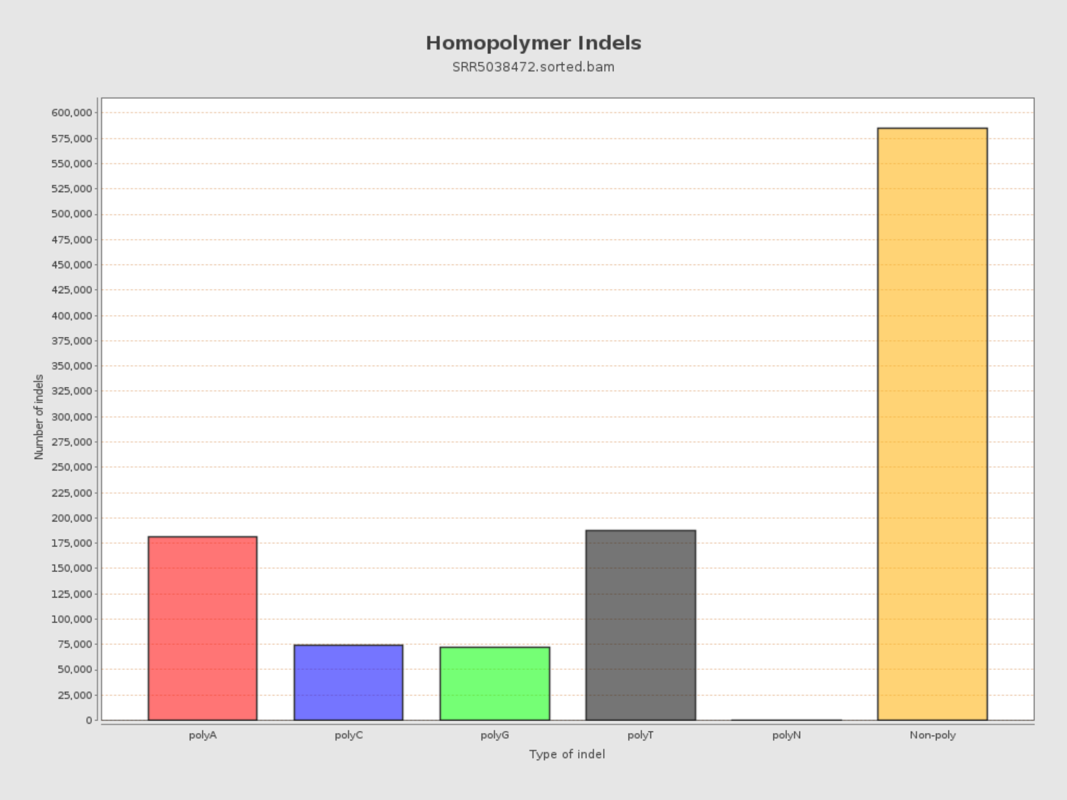
9. Results : Mapped Reads GC-content Distribution



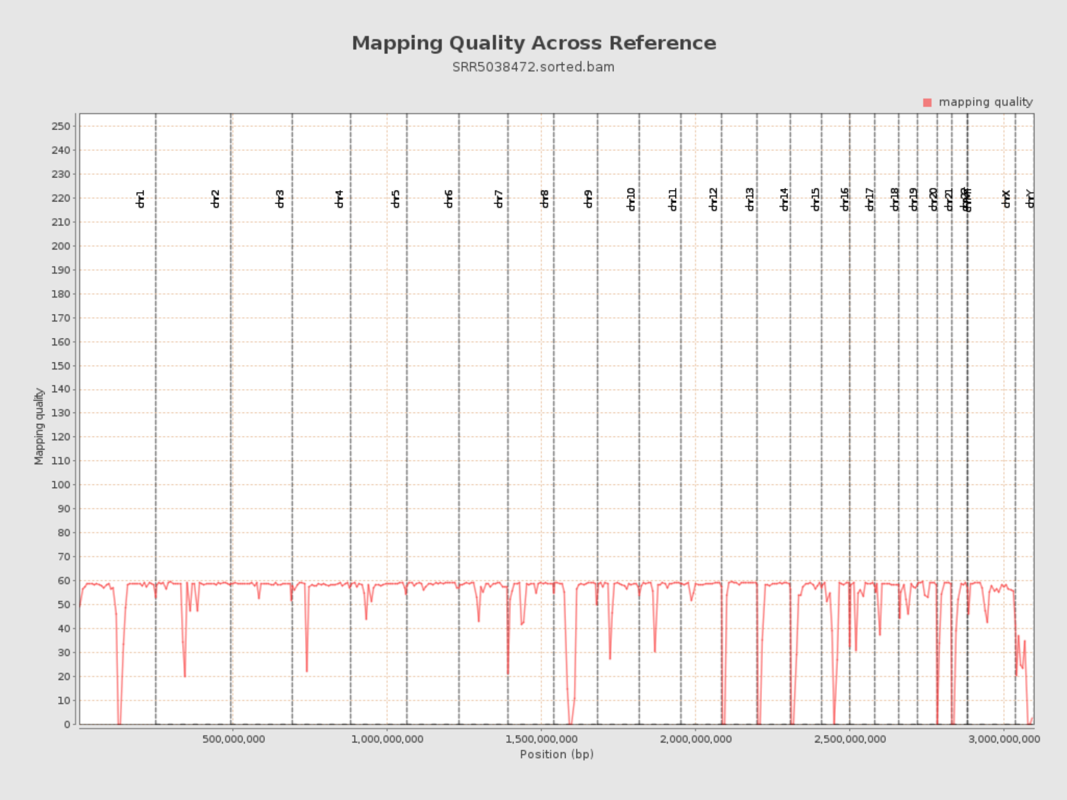
10. Results : Mapped Reads Clipping Profile



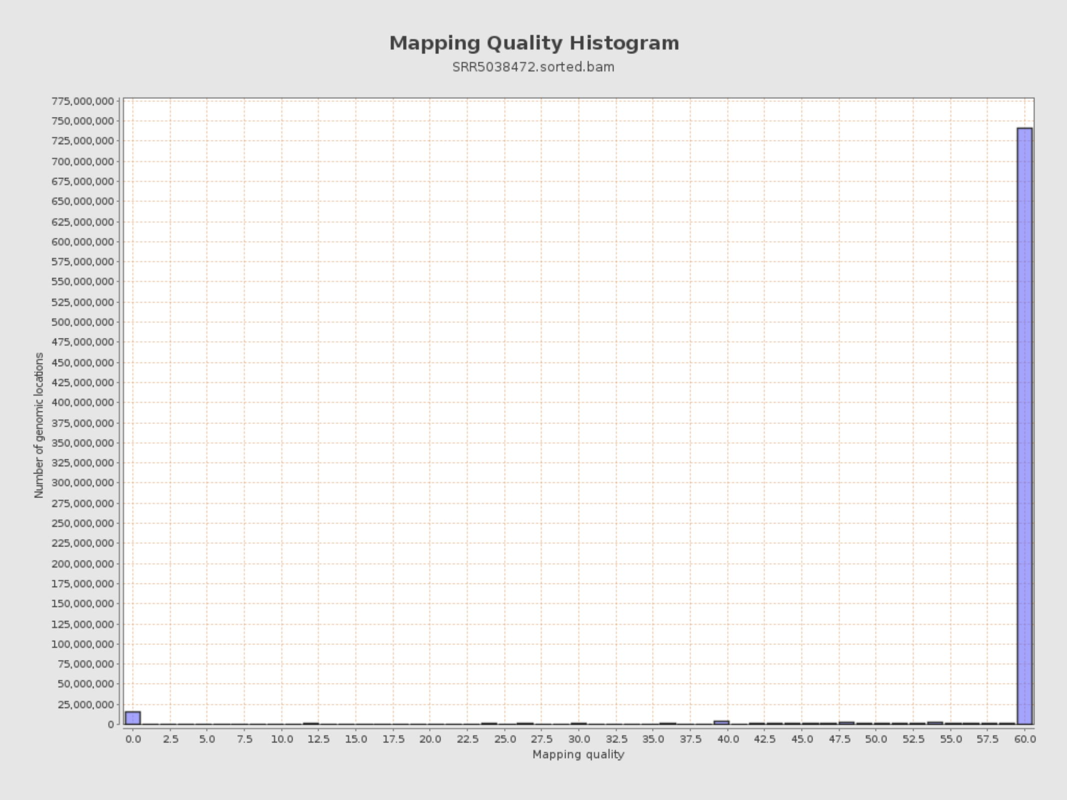
11. Results : Homopolymer Indels



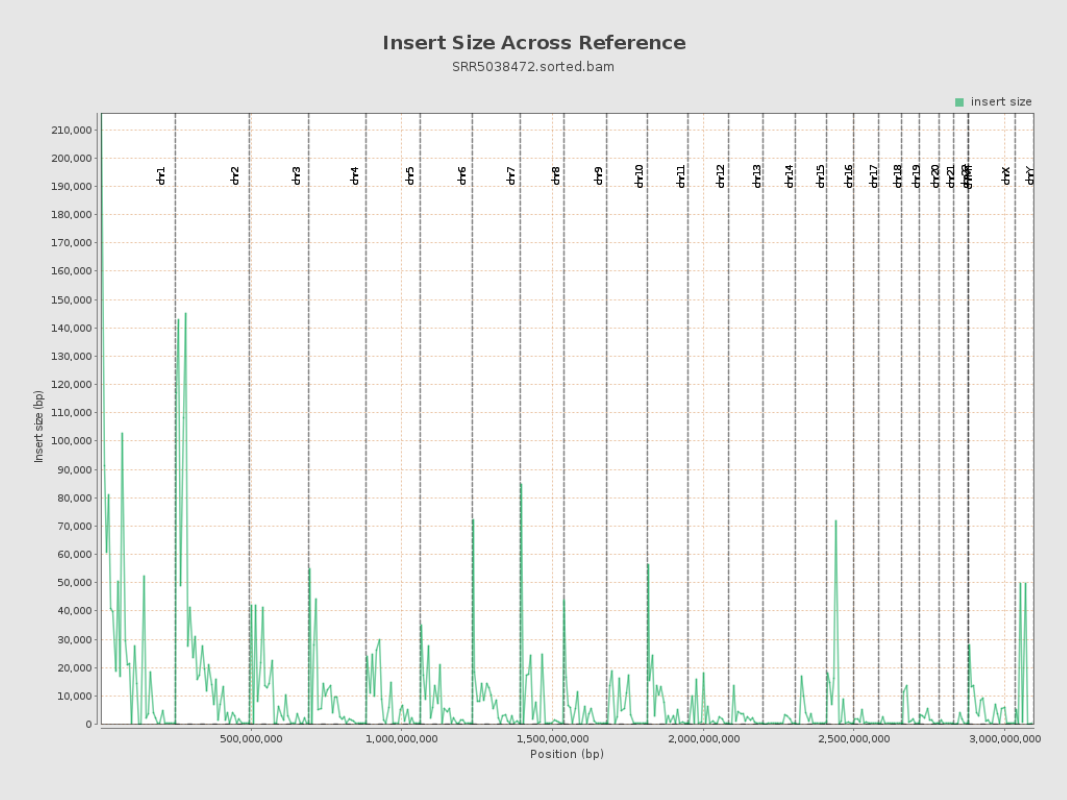
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram