Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 15:29:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038402.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_SRR5038402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038402_1.fastq.gz SRR5038402_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 15:29:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,226,912
Mapped reads	19,288,447 / 90.87%
Unmapped reads	1,938,465 / 9.13%
Mapped paired reads	19,288,447 / 90.87%
Mapped reads, first in pair	9,783,638 / 46.09%
Mapped reads, second in pair	9,504,809 / 44.78%
Mapped reads, both in pair	18,893,858 / 89.01%
Mapped reads, singletons	394,589 / 1.86%
Secondary alignments	0
Supplementary alignments	391,739 / 1.85%
Read min/max/mean length	30 / 150 / 150.89
Duplicated reads (estimated)	5,541,731 / 26.11%
Duplication rate	20.34%
Clipped reads	11,394,996 / 53.68%

2.2. ACGT Content

Number/percentage of A's	728,255,161 / 28.92%
Number/percentage of C's	480,799,021 / 19.09%
Number/percentage of T's	748,825,119 / 29.73%
Number/percentage of G's	560,326,009 / 22.25%
Number/percentage of N's	191,648 / 0.01%

GC Percentage	41.34%

2.3. Coverage

Mean	0.8141
Standard Deviation	10.984

2.4. Mapping Quality

Mean Mapping Quality	53.15

2.5. Insert size

Mean	87,554.13
Standard Deviation	2,847,649.26
P25/Median/P75	176 / 220 / 272

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	30,978,892
Insertions	503,713
Mapped reads with at least one insertion	2.46%
Deletions	899,390
Mapped reads with at least one deletion	4.47%
Homopolymer indels	46.9%

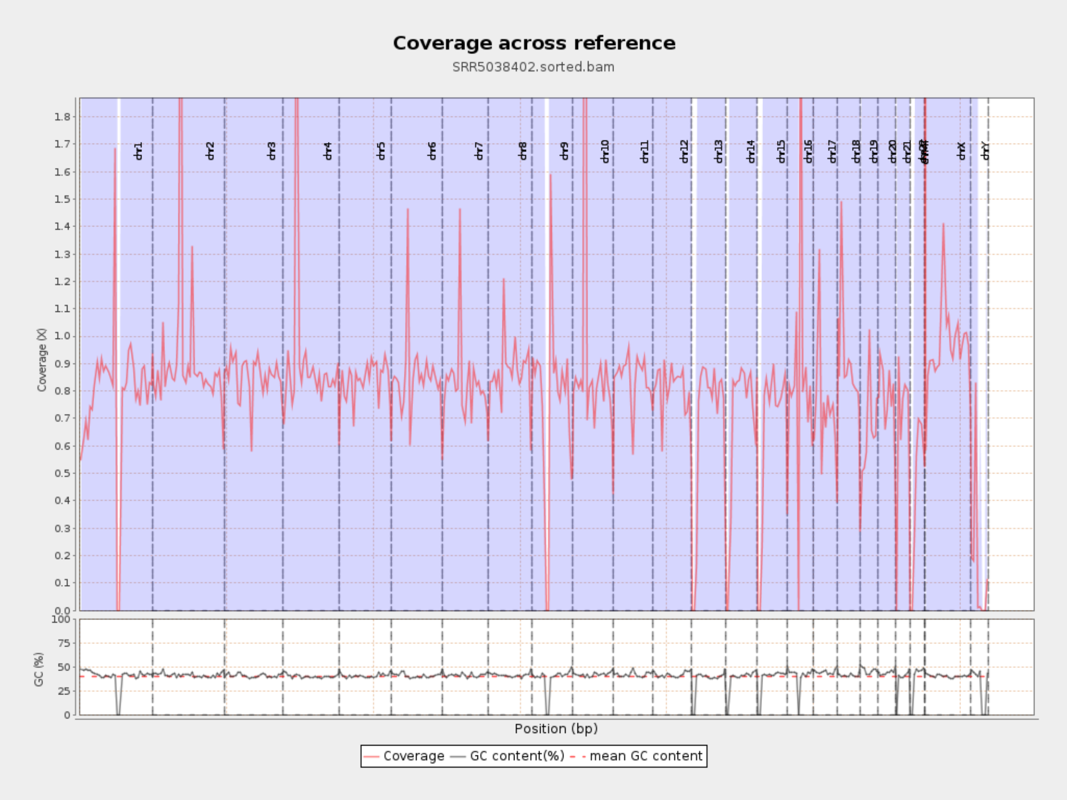
2.7. Chromosome stats

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

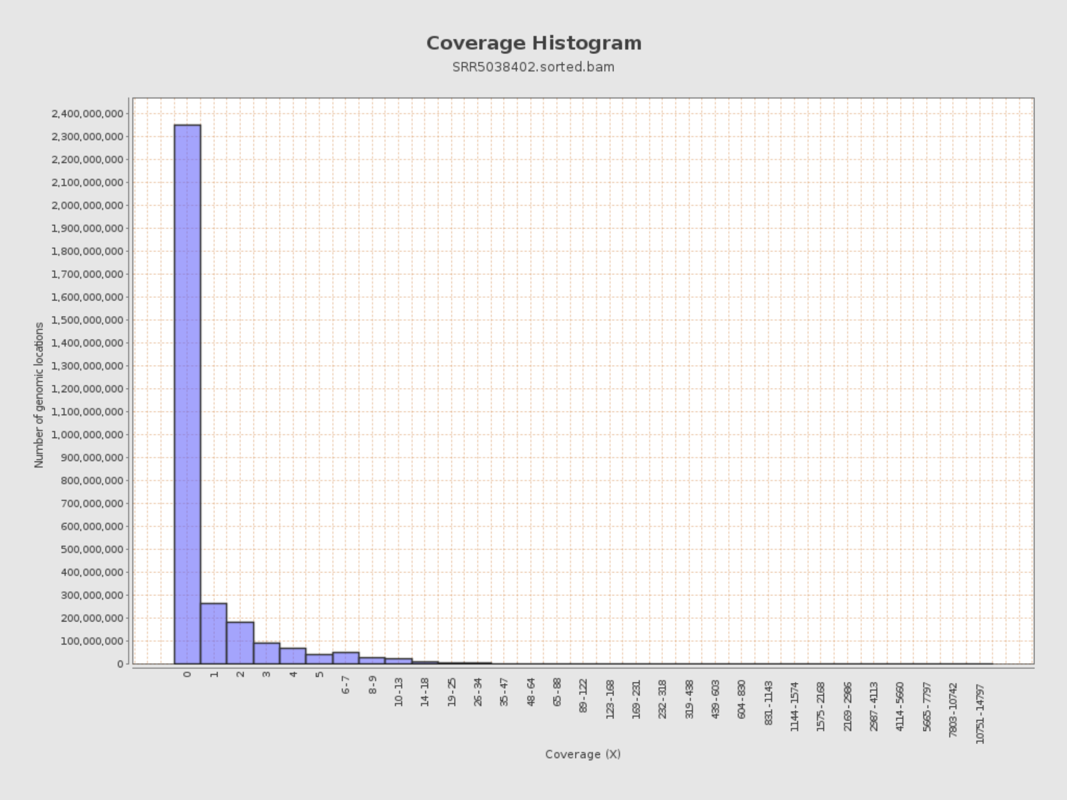
		bases	coverage	deviation
chr1	249250621	196481777	0.7883	14.8541
chr2	243199373	227132313	0.9339	14.3074
chr3	198022430	169192298	0.8544	2.2364
chr4	191154276	174452090	0.9126	11.4236
chr5	180915260	151271010	0.8361	2.2899
chr6	171115067	147394802	0.8614	7.397
chr7	159138663	132116940	0.8302	11.2666
chr8	146364022	127906734	0.8739	4.1826
chr9	141213431	104997153	0.7435	17.4418
chr10	135534747	133873946	0.9877	25.9731
chr11	135006516	113218019	0.8386	6.349
chr12	133851895	108300594	0.8091	2.3168
chr13	115169878	78286983	0.6798	1.9588
chr14	107349540	72383402	0.6743	2.2213
chr15	102531392	66564407	0.6492	1.8817
chr16	90354753	77319122	0.8557	12.8367
chr17	81195210	59830005	0.7369	10.8039
chr18	78077248	71597454	0.917	16.3868
chr19	59128983	37656875	0.6369	7.8144
chr20	63025520	49409496	0.784	3.9276
chr21	48129895	33234289	0.6905	5.6069
chr22	51304566	22499988	0.4386	2.0568
chrMT	16571	4697888	283.5006	244.5335
chrX	155270560	150594496	0.9699	4.1675

chrY	59373566	9877580	0.1664	13.6757

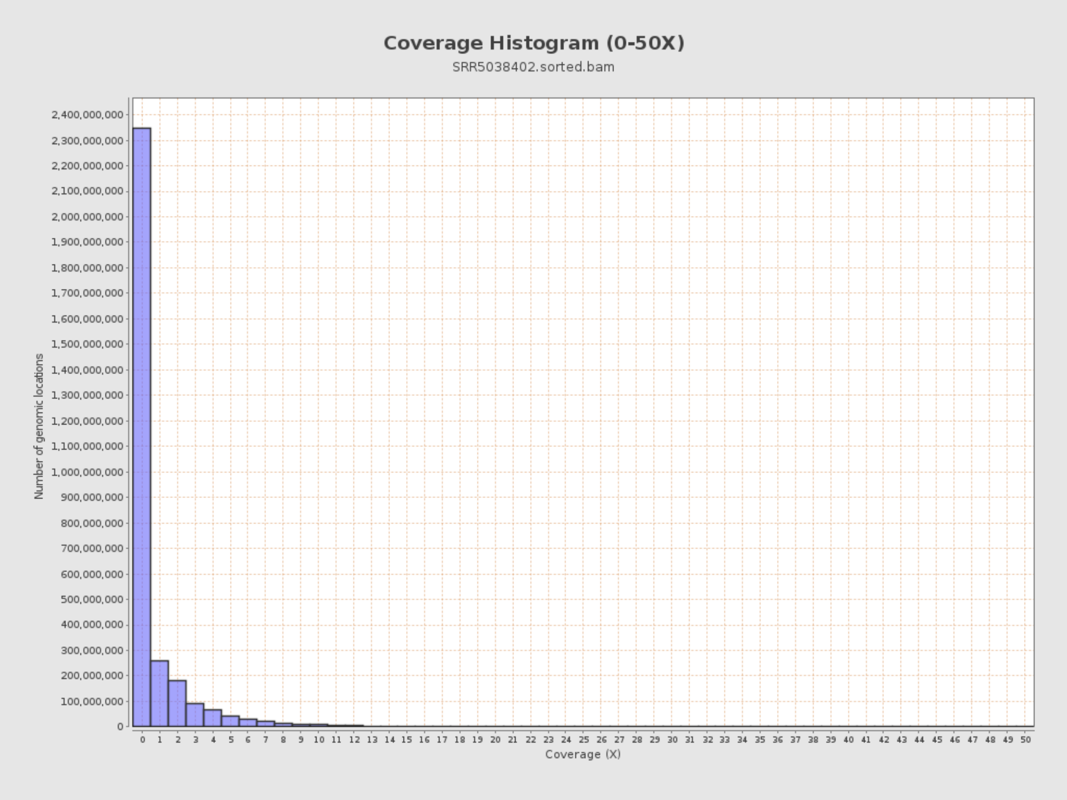
3. Results : Coverage across reference



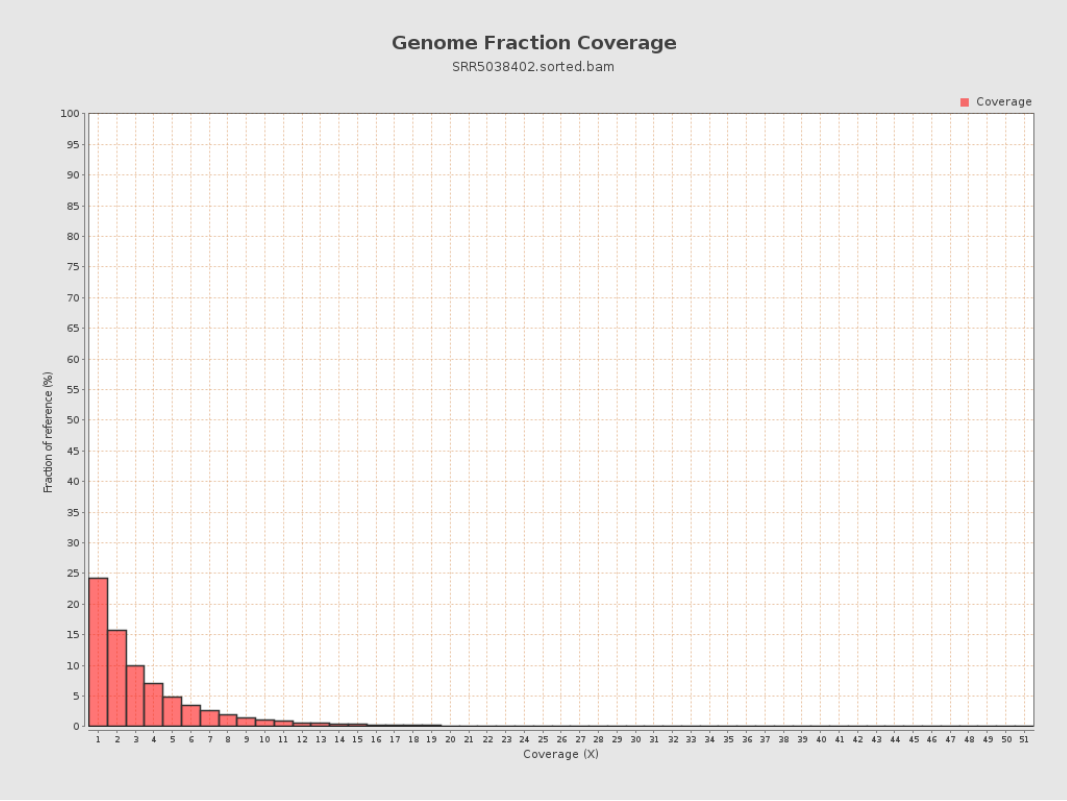
4. Results : Coverage Histogram



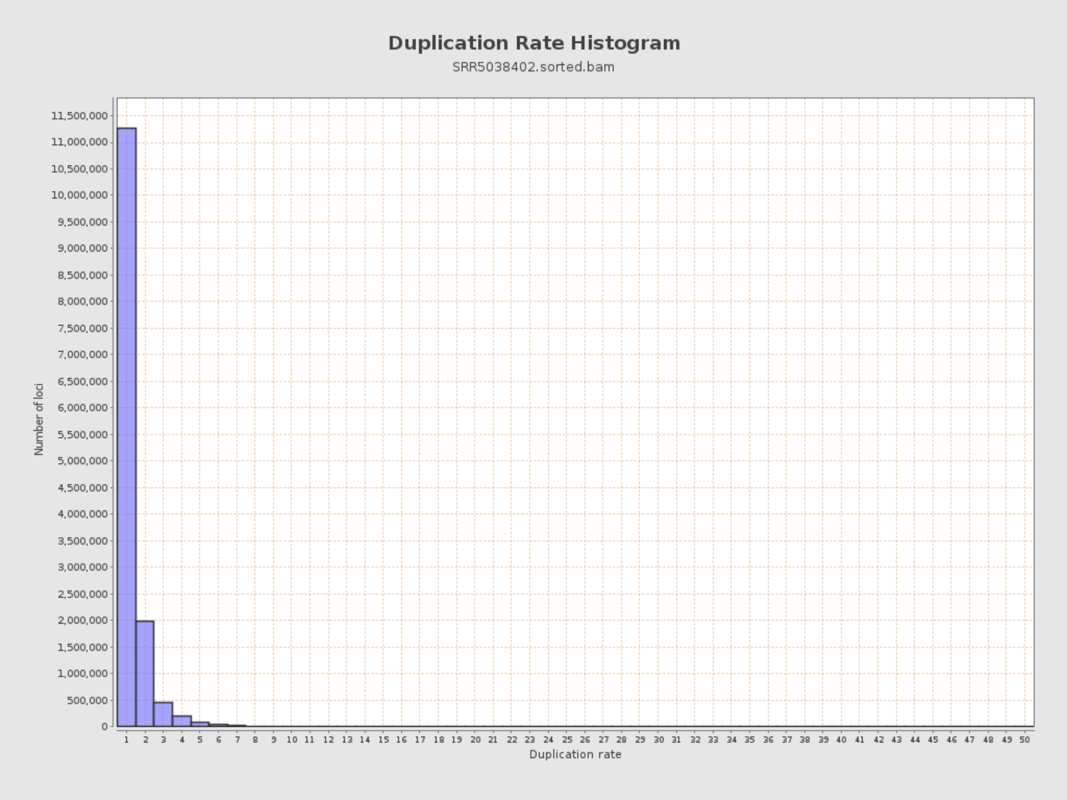
5. Results : Coverage Histogram (0-50X)



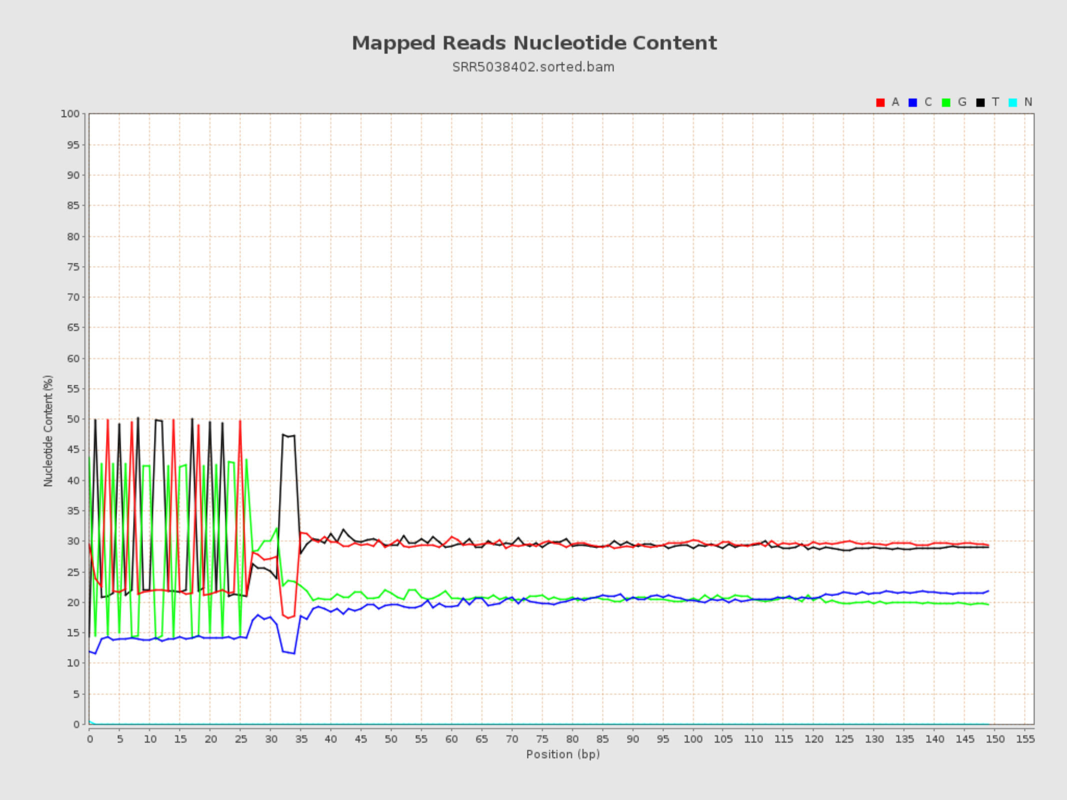
6. Results : Genome Fraction Coverage



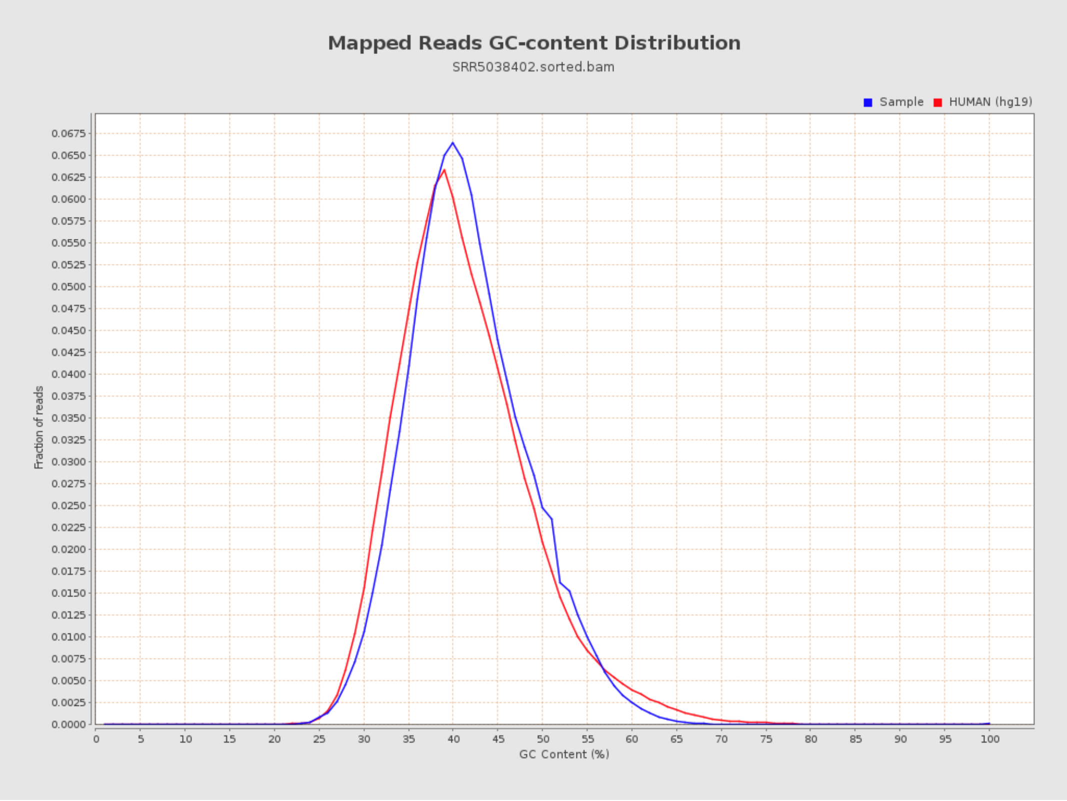
7. Results : Duplication Rate Histogram



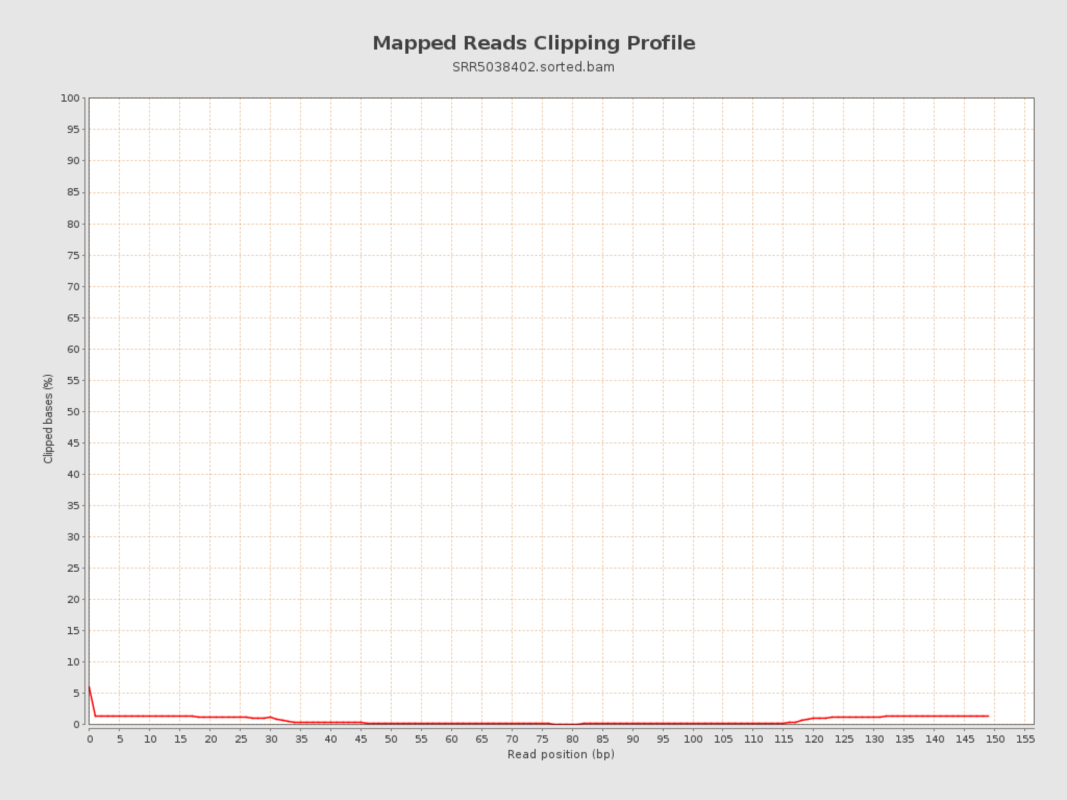
8. Results : Mapped Reads Nucleotide Content



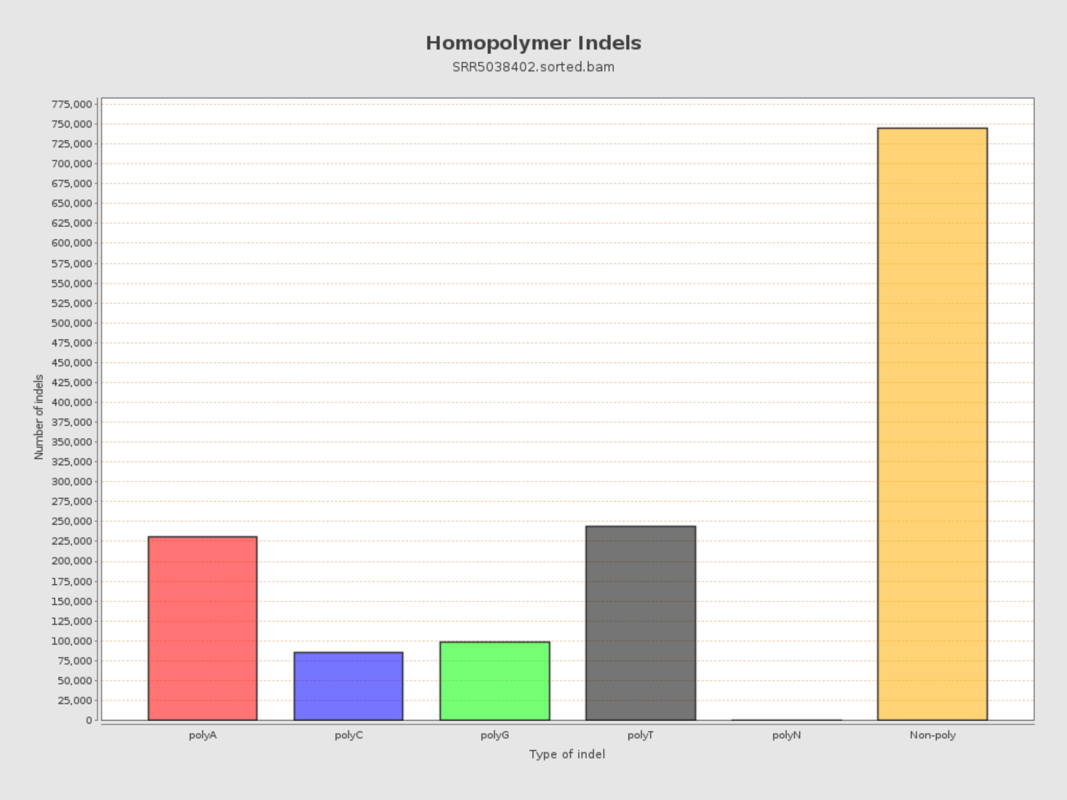
9. Results : Mapped Reads GC-content Distribution



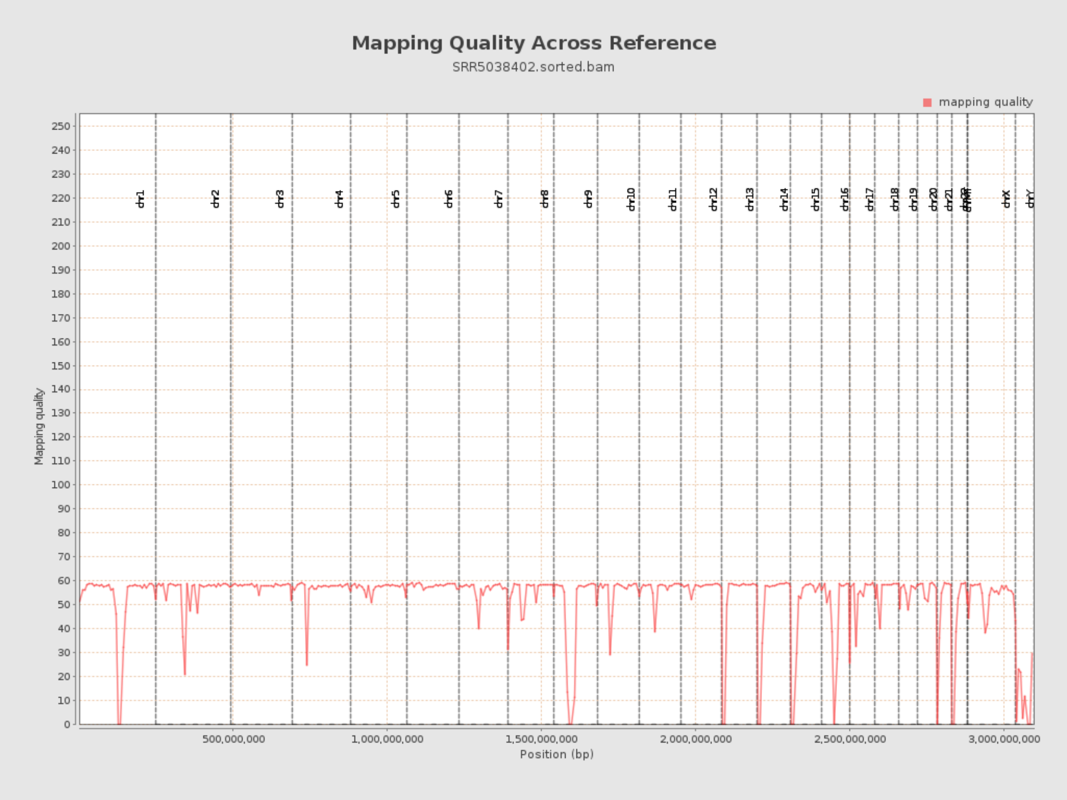
10. Results : Mapped Reads Clipping Profile



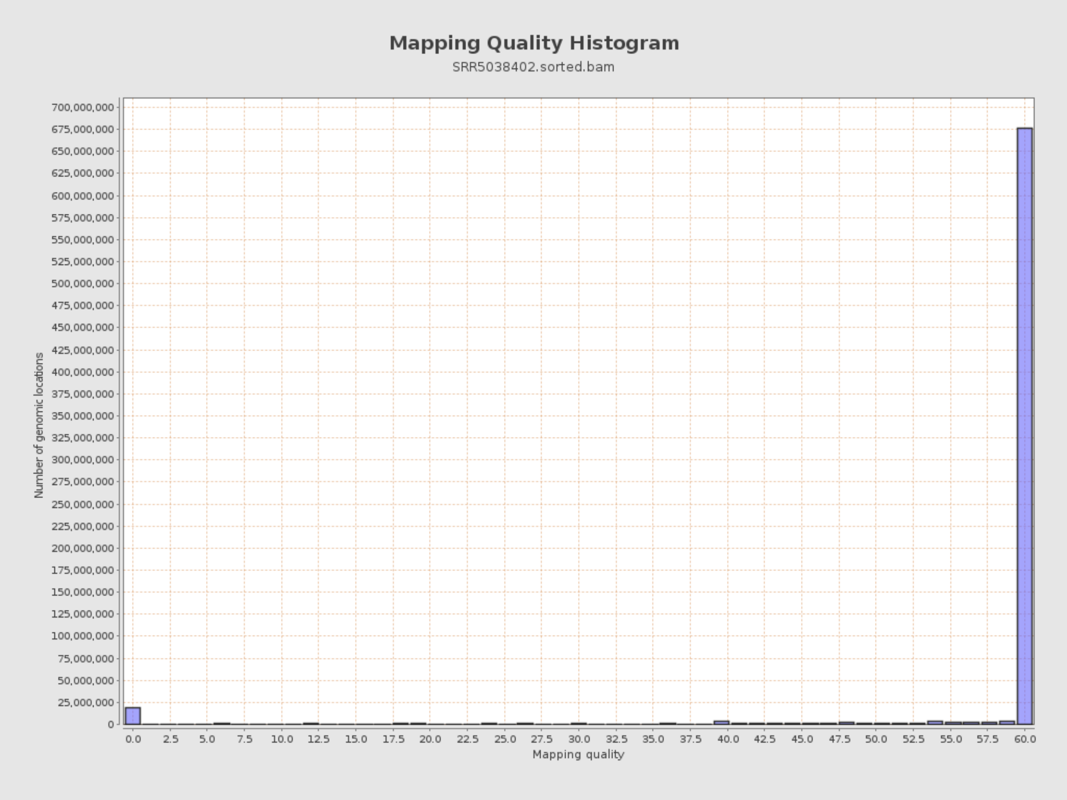
11. Results : Homopolymer Indels



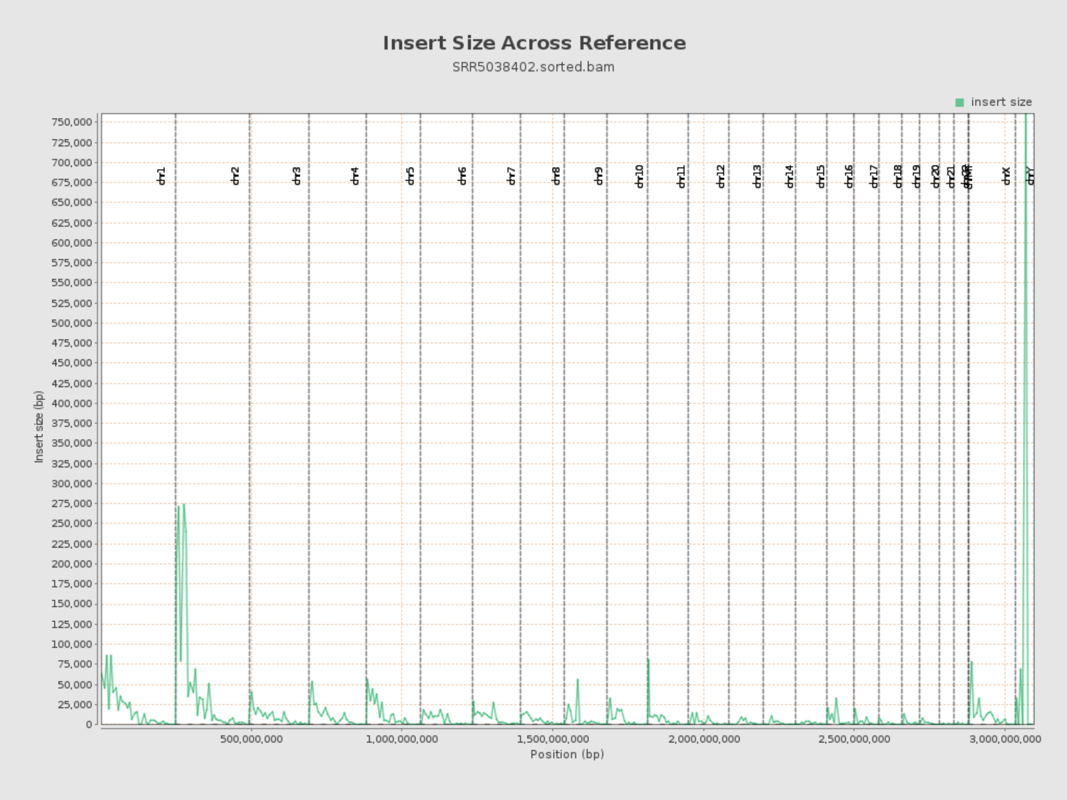
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram