Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 22:17:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038415.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_SRR5038415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038415_1.fastq.gz SRR5038415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 22:17:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,115,950
Mapped reads	11,739,187 / 96.89%
Unmapped reads	376,763 / 3.11%
Mapped paired reads	11,739,187 / 96.89%
Mapped reads, first in pair	5,959,185 / 49.18%
Mapped reads, second in pair	5,780,002 / 47.71%
Mapped reads, both in pair	11,545,630 / 95.29%
Mapped reads, singletons	193,557 / 1.6%
Secondary alignments	0
Supplementary alignments	184,645 / 1.52%
Read min/max/mean length	30 / 150 / 150.79
Duplicated reads (estimated)	1,630,783 / 13.46%
Duplication rate	8.64%
Clipped reads	2,580,684 / 21.3%

2.2. ACGT Content

Number/percentage of A's	504,218,834 / 29.91%
Number/percentage of C's	334,871,691 / 19.86%
Number/percentage of T's	504,112,661 / 29.9%
Number/percentage of G's	342,750,477 / 20.33%
Number/percentage of N's	35,417 / 0%

GC Percentage	40.19%

2.3. Coverage

Mean	0.545
Standard Deviation	8.2137

2.4. Mapping Quality

Mean Mapping Quality	53.89

2.5. Insert size

Mean	76,720
Standard Deviation	2,628,346.18
P25/Median/P75	209 / 255 / 315

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	25,452,968
Insertions	298,420
Mapped reads with at least one insertion	2.41%
Deletions	590,420
Mapped reads with at least one deletion	4.84%
Homopolymer indels	47.6%

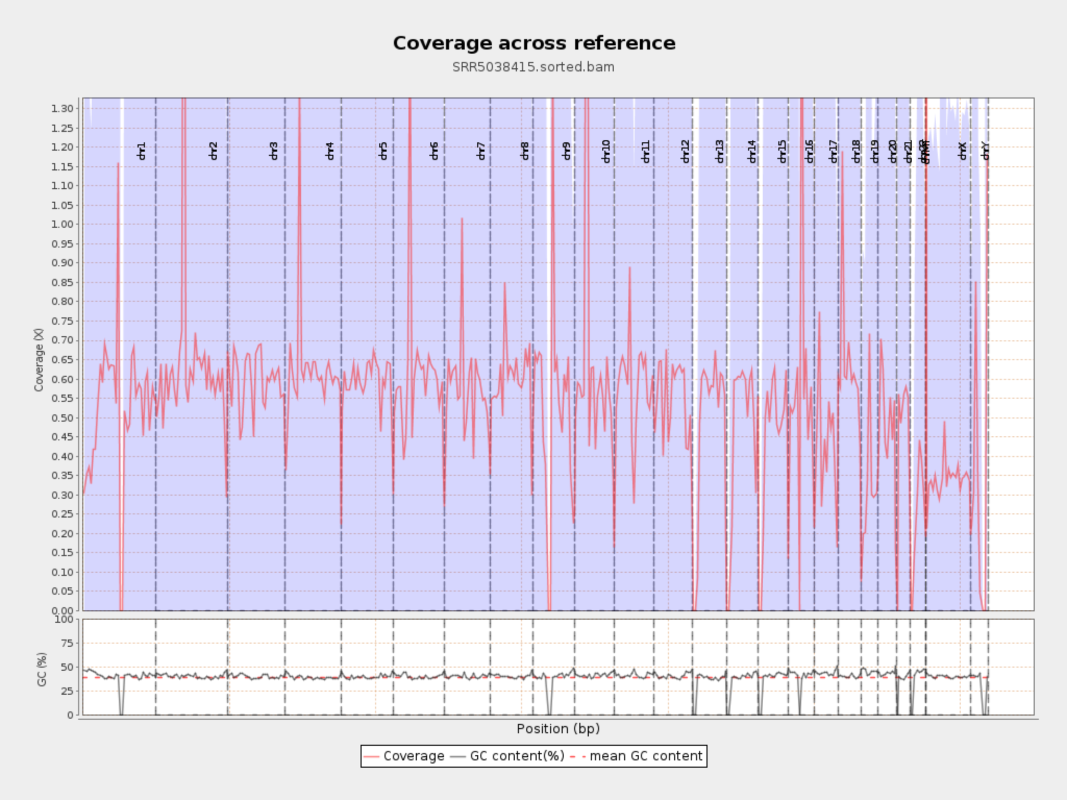
2.7. Chromosome stats

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

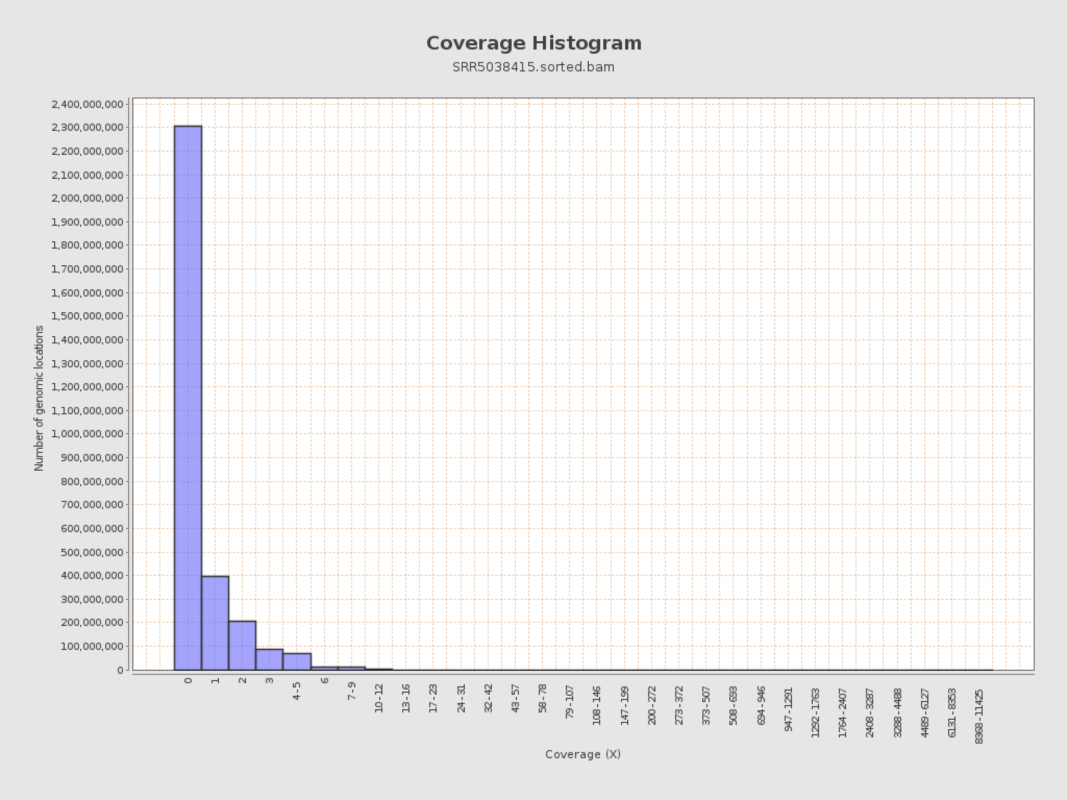
		bases	coverage	deviation
chr1	249250621	129864494	0.521	10.5799
chr2	243199373	159830163	0.6572	10.9595
chr3	198022430	118319853	0.5975	1.2827
chr4	191154276	120605203	0.6309	5.6601
chr5	180915260	106534384	0.5889	1.3886
chr6	171115067	106654543	0.6233	10.6177
chr7	159138663	91206976	0.5731	8.1172
chr8	146364022	88050996	0.6016	2.7082
chr9	141213431	75061311	0.5315	18.4741
chr10	135534747	88372562	0.652	13.9029
chr11	135006516	78255000	0.5796	5.3005
chr12	133851895	73178995	0.5467	1.2464
chr13	115169878	55368007	0.4808	1.1136
chr14	107349540	49874251	0.4646	1.2216
chr15	102531392	44341214	0.4325	1.0727
chr16	90354753	52902326	0.5855	9.5761
chr17	81195210	35847904	0.4415	5.6772
chr18	78077248	51025697	0.6535	14.3992
chr19	59128983	19146458	0.3238	5.7282
chr20	63025520	31512486	0.5	1.9081
chr21	48129895	22338995	0.4641	2.9083
chr22	51304566	12648435	0.2465	0.8396
chrMT	16571	1494810	90.2064	56.5972
chrX	155270560	52504503	0.3381	1.6946

chrY	59373566	22182745	0.3736	9.0952

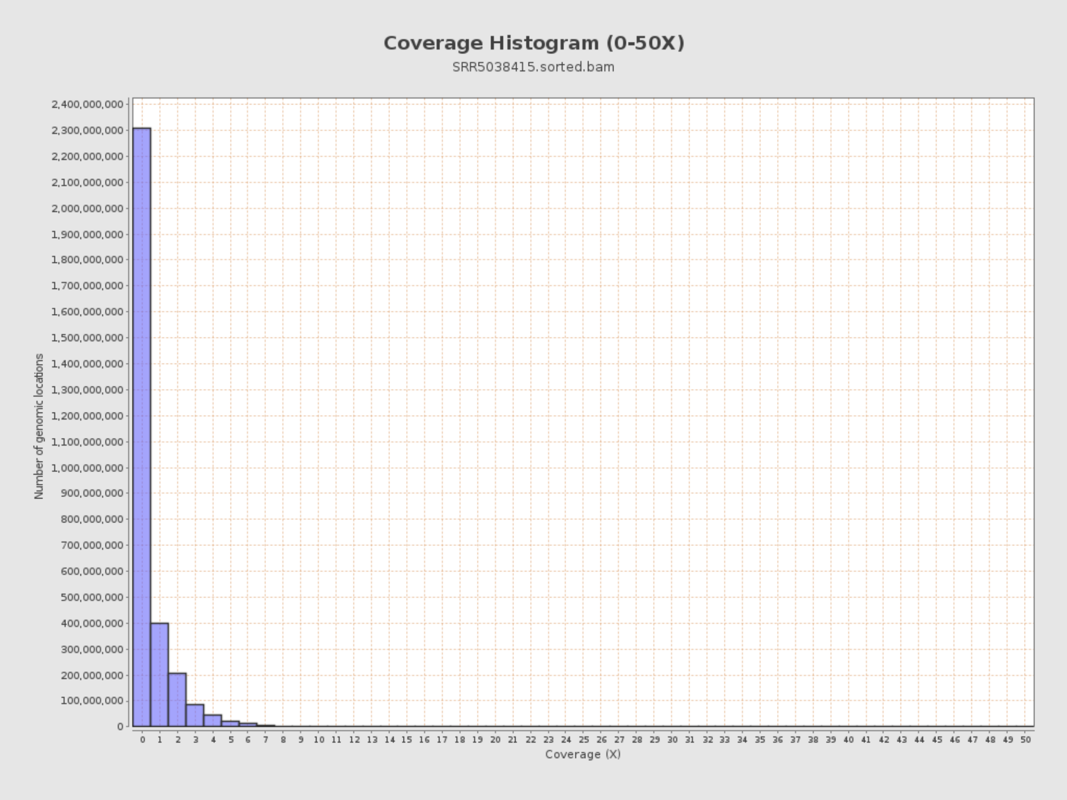
3. Results : Coverage across reference



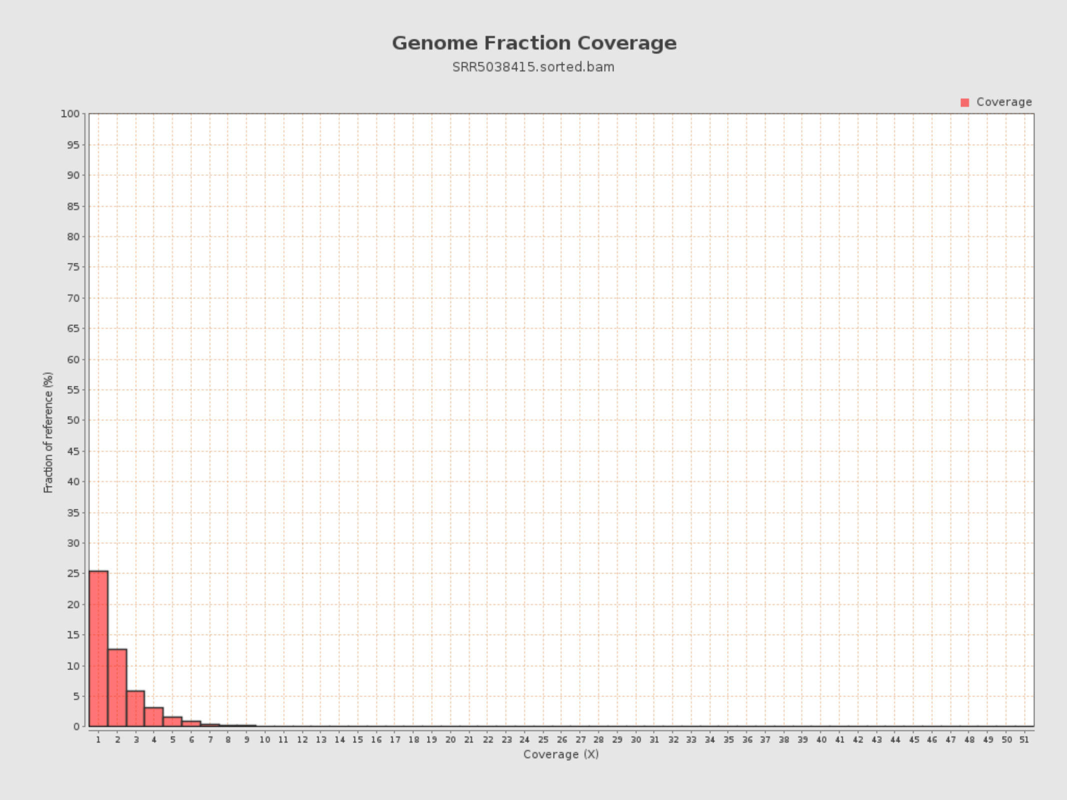
4. Results : Coverage Histogram



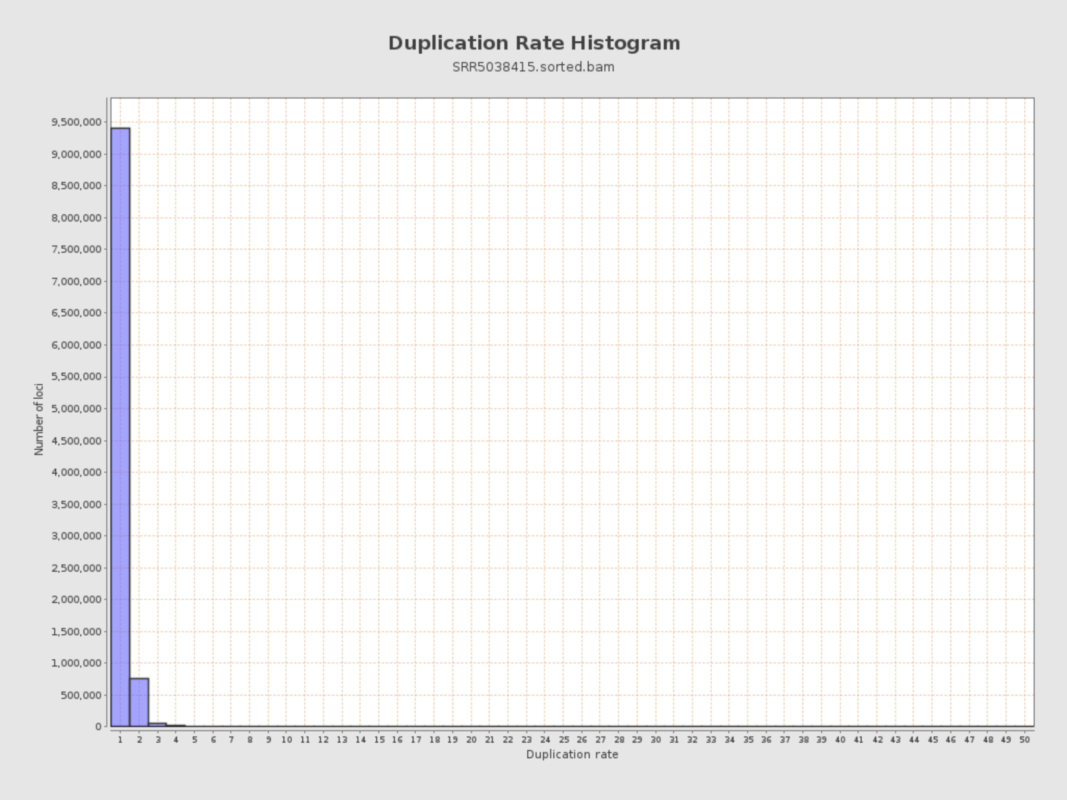
5. Results : Coverage Histogram (0-50X)



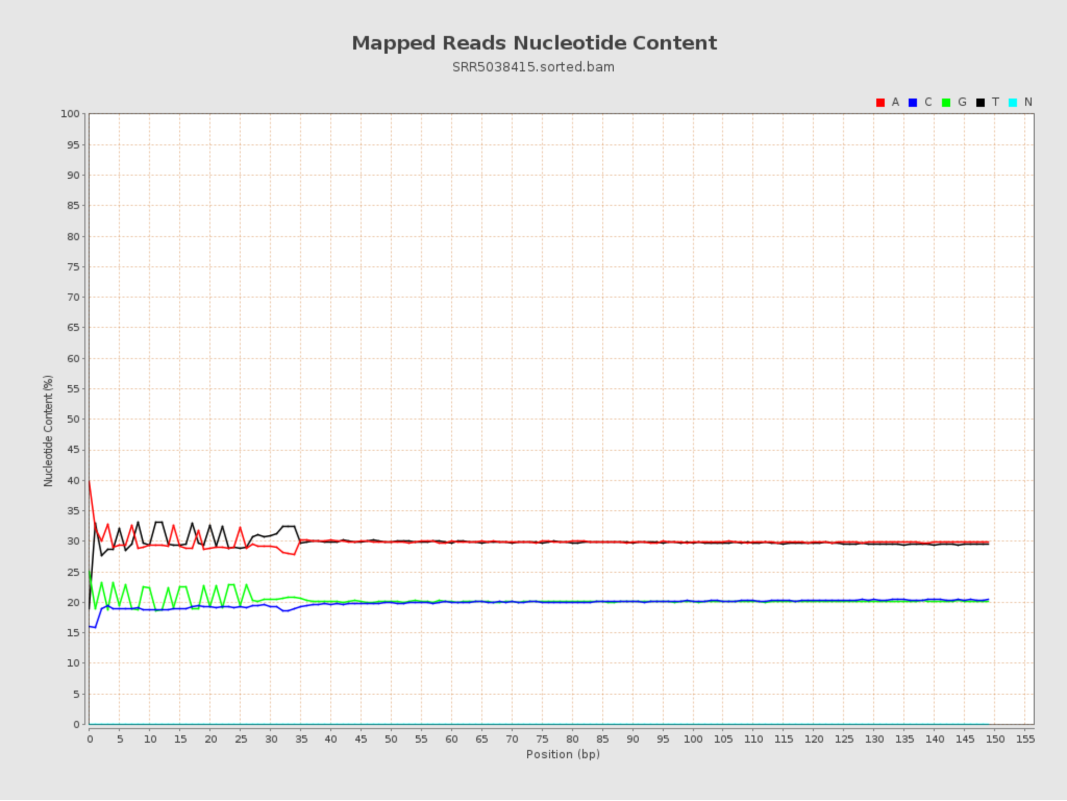
6. Results : Genome Fraction Coverage



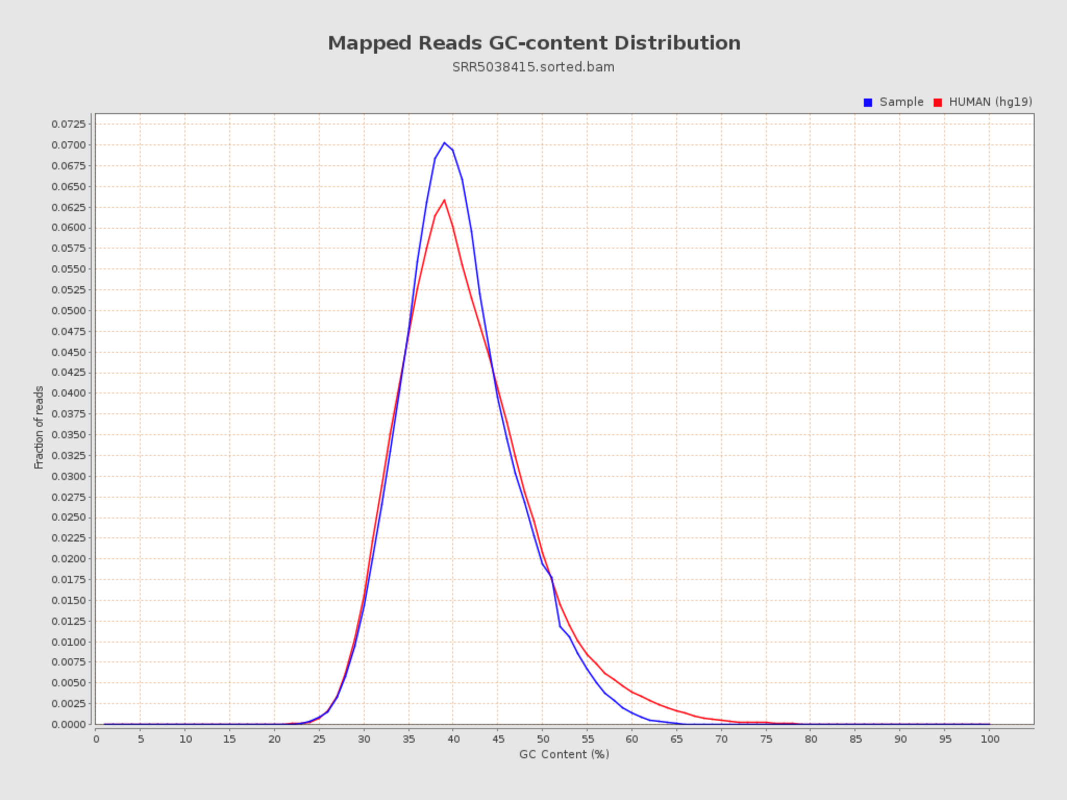
7. Results : Duplication Rate Histogram



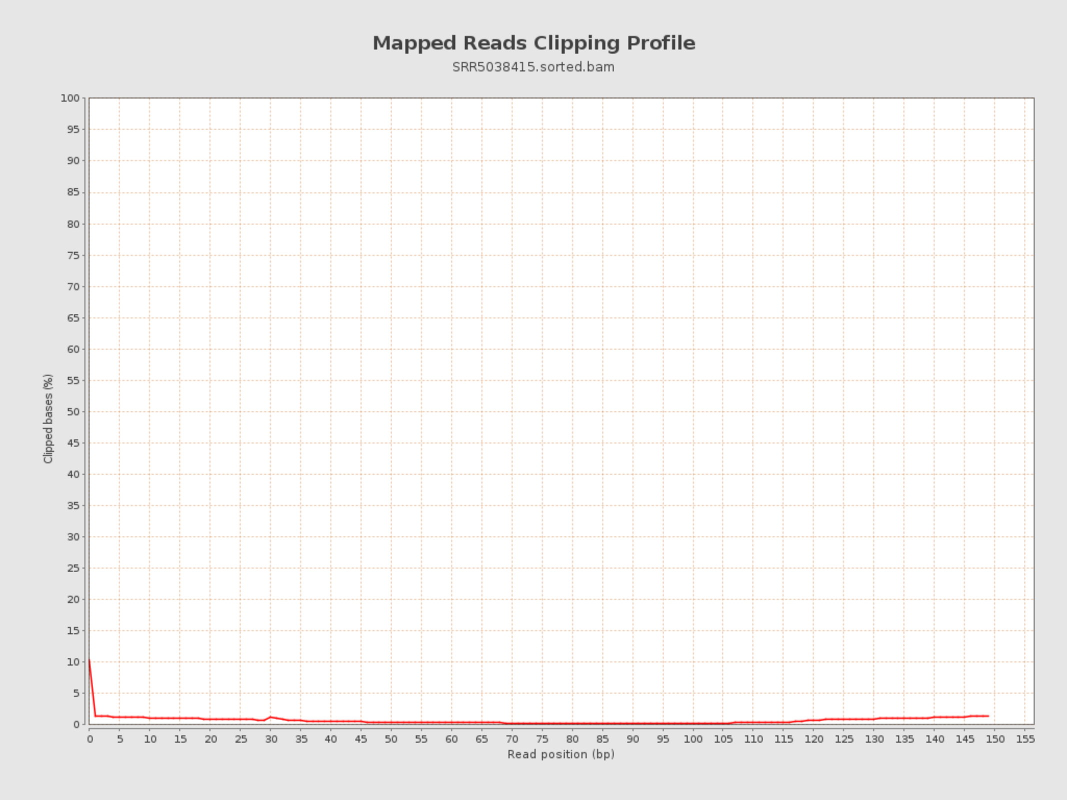
8. Results : Mapped Reads Nucleotide Content



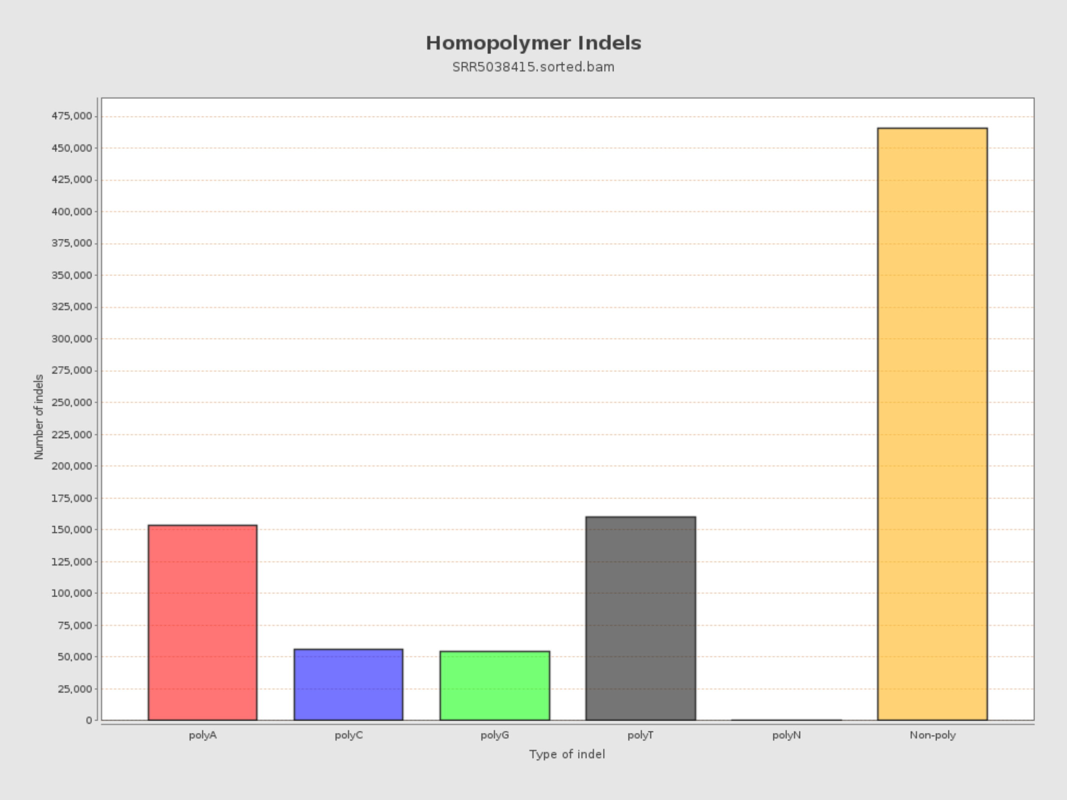
9. Results : Mapped Reads GC-content Distribution



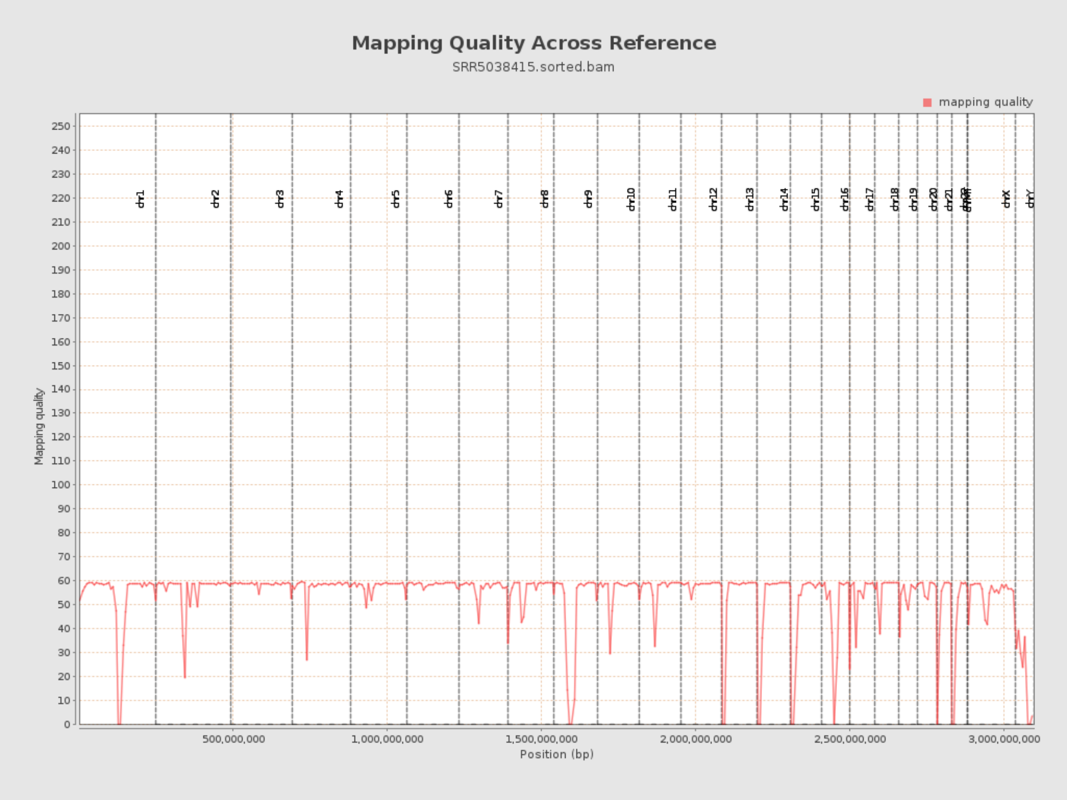
10. Results : Mapped Reads Clipping Profile



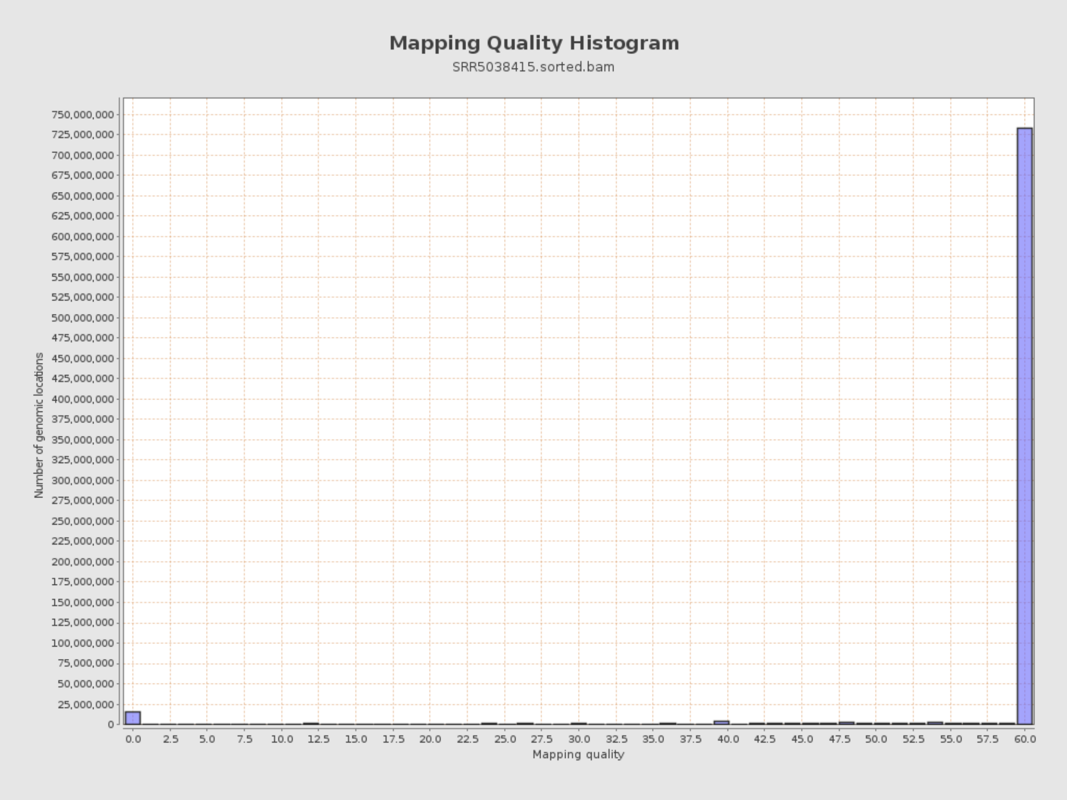
11. Results : Homopolymer Indels



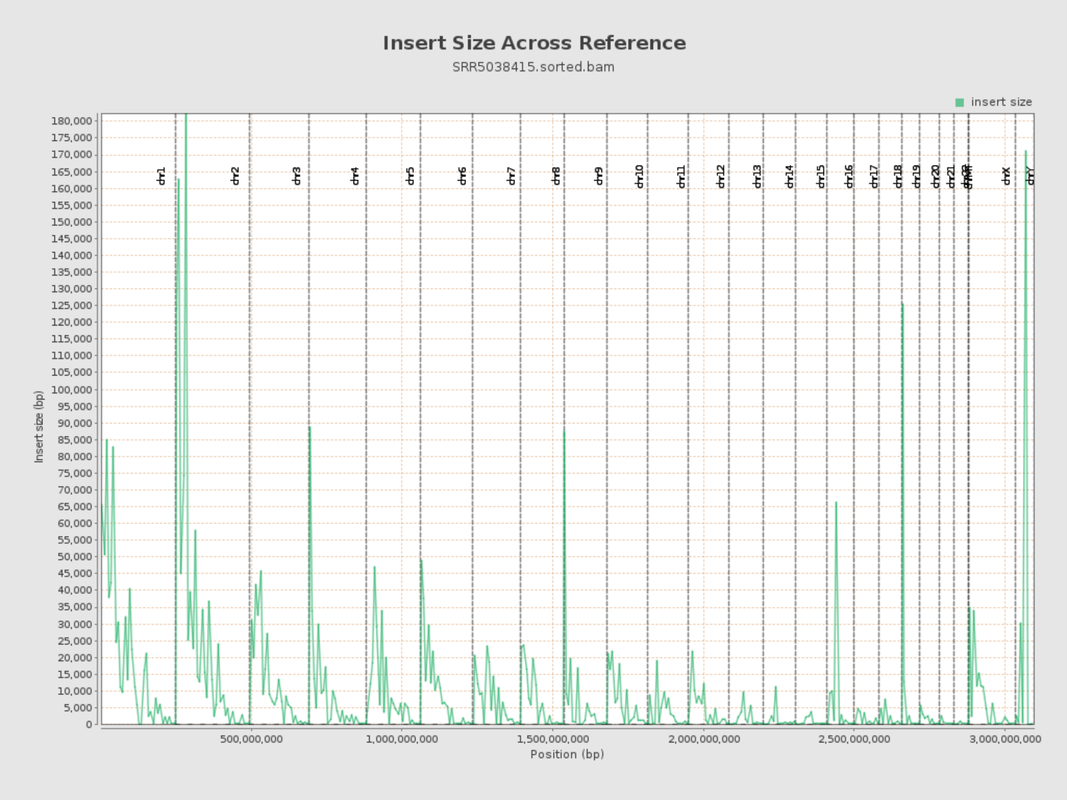
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram