Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 04:20:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038476.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_SRR5038476 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038476_1.fastq.gz SRR5038476_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 04:20:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038476.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,376,334
Mapped reads	18,306,452 / 89.84%
Unmapped reads	2,069,882 / 10.16%
Mapped paired reads	18,306,452 / 89.84%
Mapped reads, first in pair	9,282,077 / 45.55%
Mapped reads, second in pair	9,024,375 / 44.29%
Mapped reads, both in pair	17,980,078 / 88.24%
Mapped reads, singletons	326,374 / 1.6%
Secondary alignments	0
Supplementary alignments	329,820 / 1.62%
Read min/max/mean length	30 / 150 / 150.81
Duplicated reads (estimated)	4,416,686 / 21.68%
Duplication rate	17.13%
Clipped reads	9,625,753 / 47.24%

2.2. ACGT Content

Number/percentage of A's	686,957,362 / 28.34%
Number/percentage of C's	489,811,364 / 20.21%
Number/percentage of T's	696,179,446 / 28.72%
Number/percentage of G's	550,607,188 / 22.72%
Number/percentage of N's	186,631 / 0.01%

GC Percentage	42.93%

2.3. Coverage

Mean	0.7835
Standard Deviation	12.7022

2.4. Mapping Quality

Mean Mapping Quality	53.32

2.5. Insert size

Mean	88,041.5
Standard Deviation	2,877,376.58
P25/Median/P75	175 / 225 / 287

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	31,857,912
Insertions	445,209
Mapped reads with at least one insertion	2.3%
Deletions	874,791
Mapped reads with at least one deletion	4.6%
Homopolymer indels	46.54%

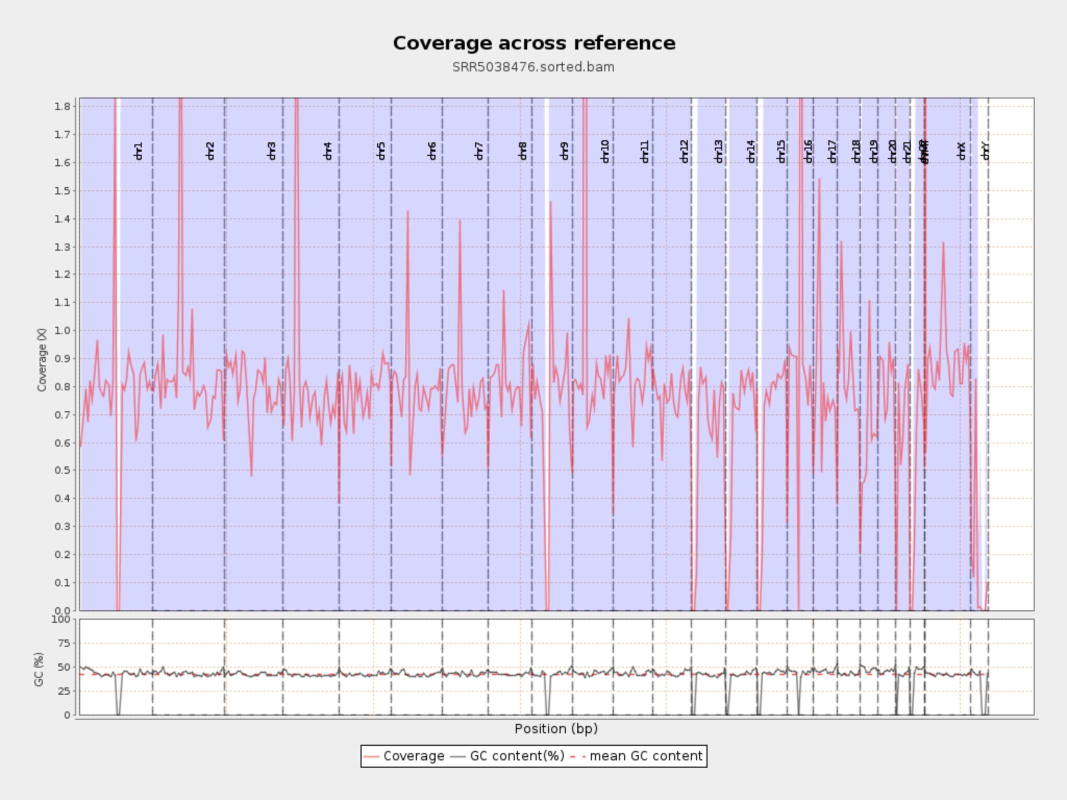
2.7. Chromosome stats

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

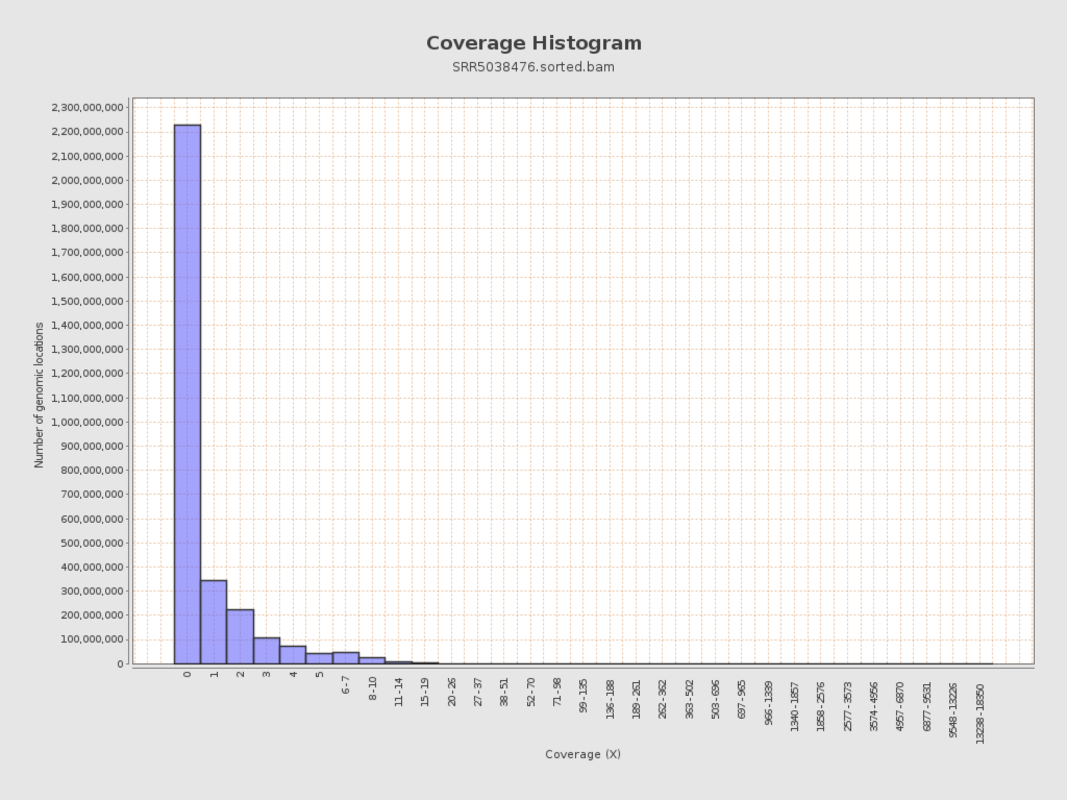
		bases	coverage	deviation
chr1	249250621	193181110	0.775	17.8004
chr2	243199373	213390303	0.8774	11.745
chr3	198022430	158502543	0.8004	2.0445
chr4	191154276	157367118	0.8232	11.4934
chr5	180915260	141919939	0.7845	1.7531
chr6	171115067	136827402	0.7996	7.522
chr7	159138663	125623730	0.7894	10.8086
chr8	146364022	121828685	0.8324	3.6401
chr9	141213431	100549427	0.712	17.0092
chr10	135534747	143917790	1.0619	38.7156
chr11	135006516	111479993	0.8257	7.2838
chr12	133851895	102286260	0.7642	1.874
chr13	115169878	70555815	0.6126	1.5247
chr14	107349540	69219274	0.6448	1.8054
chr15	102531392	66439609	0.648	1.6094
chr16	90354753	87695416	0.9706	17.0313
chr17	81195210	62934663	0.7751	13.1698
chr18	78077248	67192354	0.8606	14.5771
chr19	59128983	35805272	0.6055	8.312
chr20	63025520	51547380	0.8179	3.7096
chr21	48129895	30588253	0.6355	5.8337
chr22	51304566	25487226	0.4968	1.5156
chrMT	16571	4301566	259.584	172.4089
chrX	155270560	137613720	0.8863	3.7531

chrY	59373566	9260059	0.156	13.0714

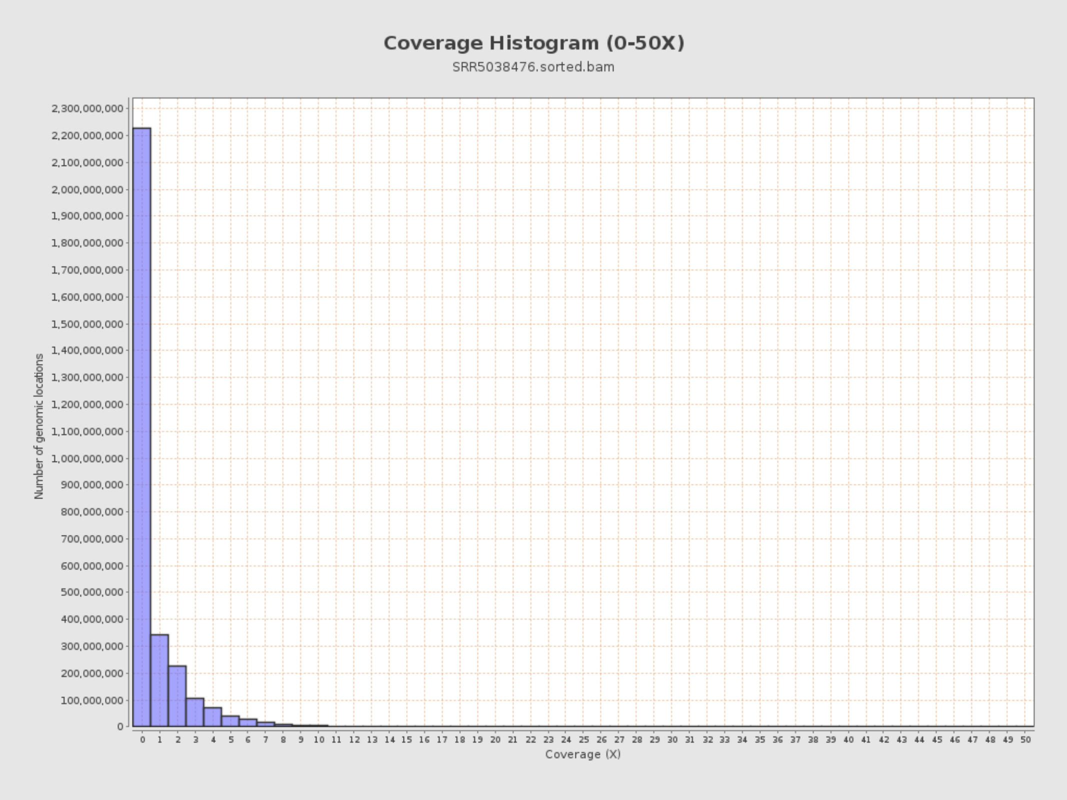
3. Results : Coverage across reference



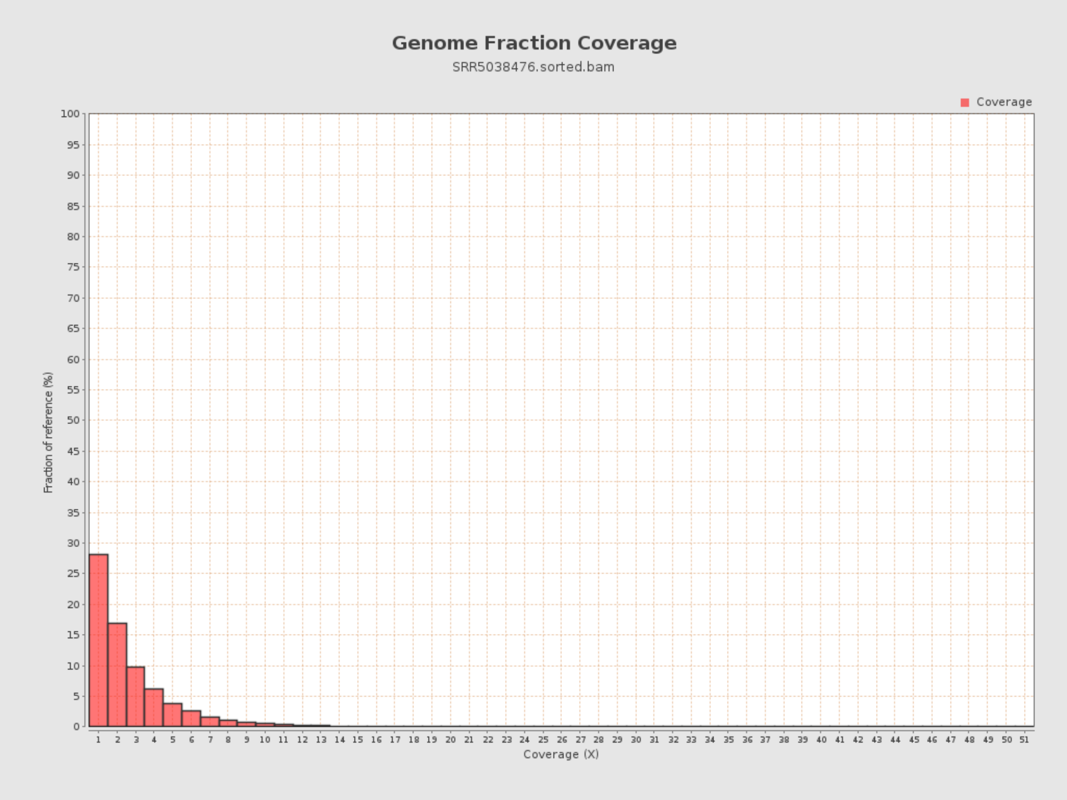
4. Results : Coverage Histogram



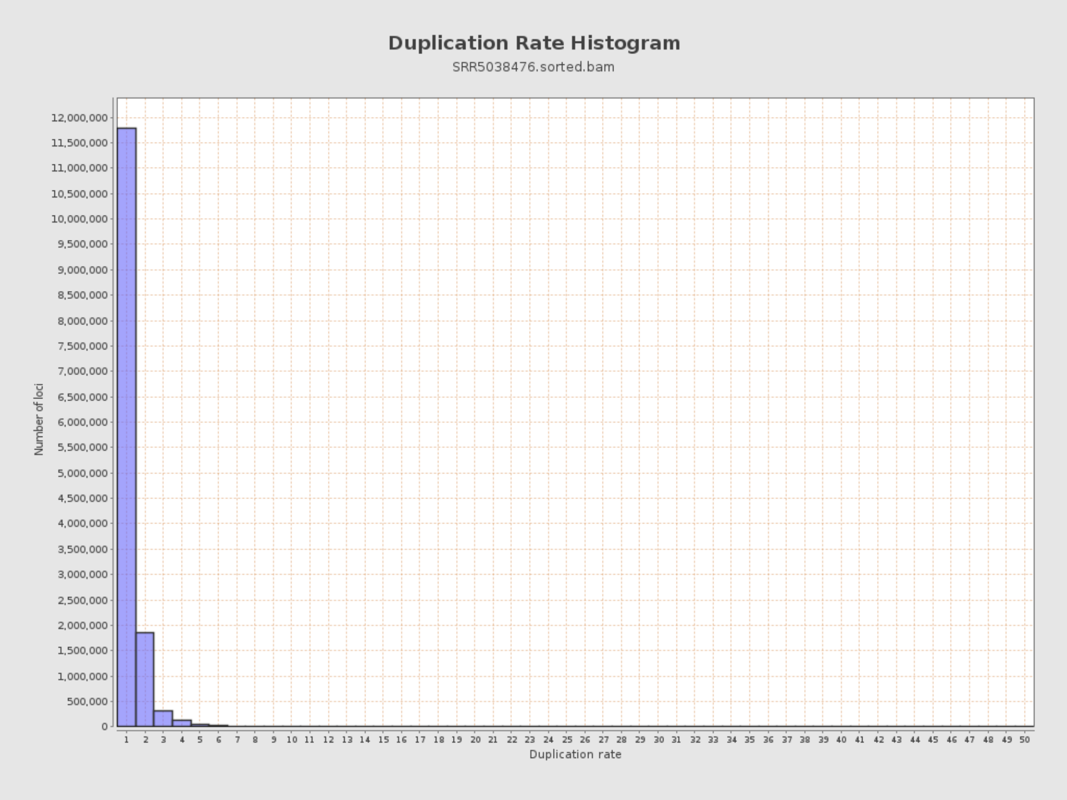
5. Results : Coverage Histogram (0-50X)



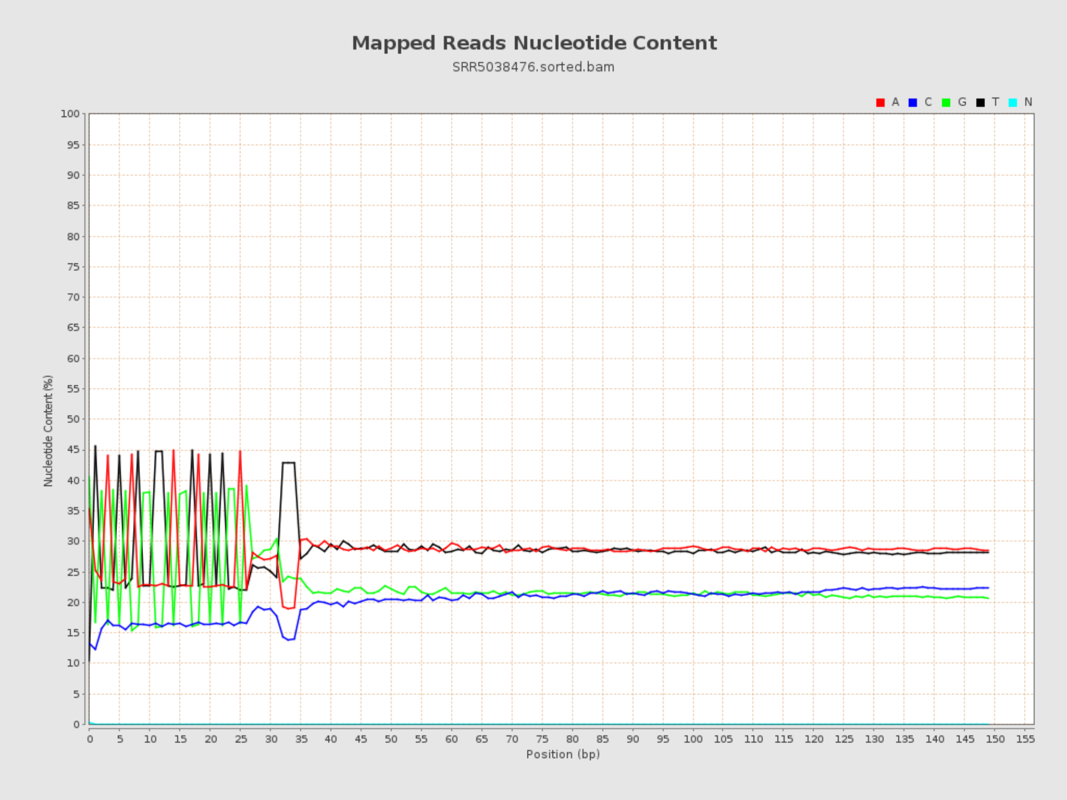
6. Results : Genome Fraction Coverage



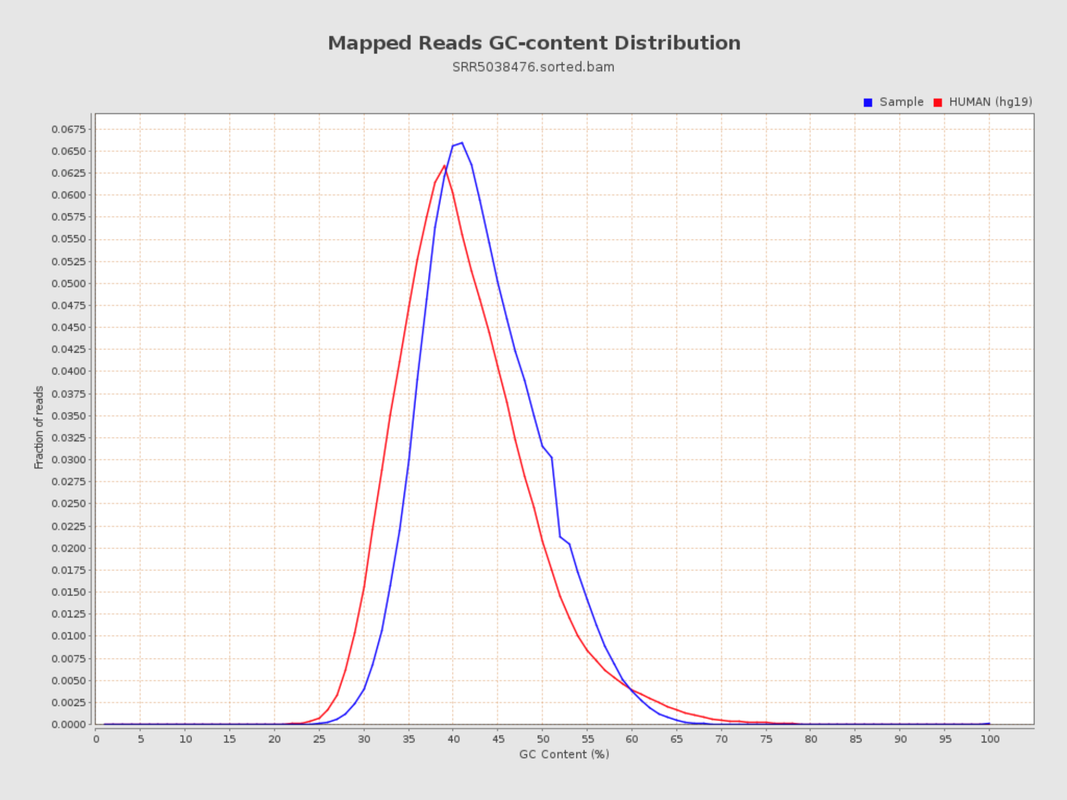
7. Results : Duplication Rate Histogram



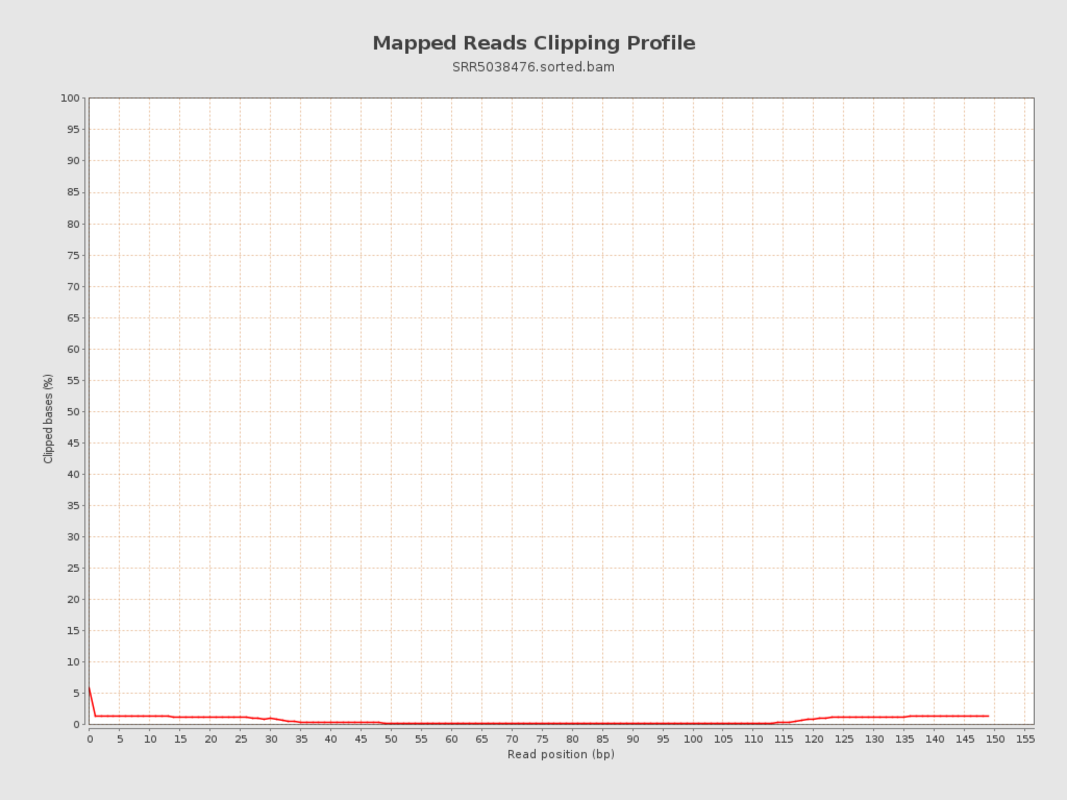
8. Results : Mapped Reads Nucleotide Content



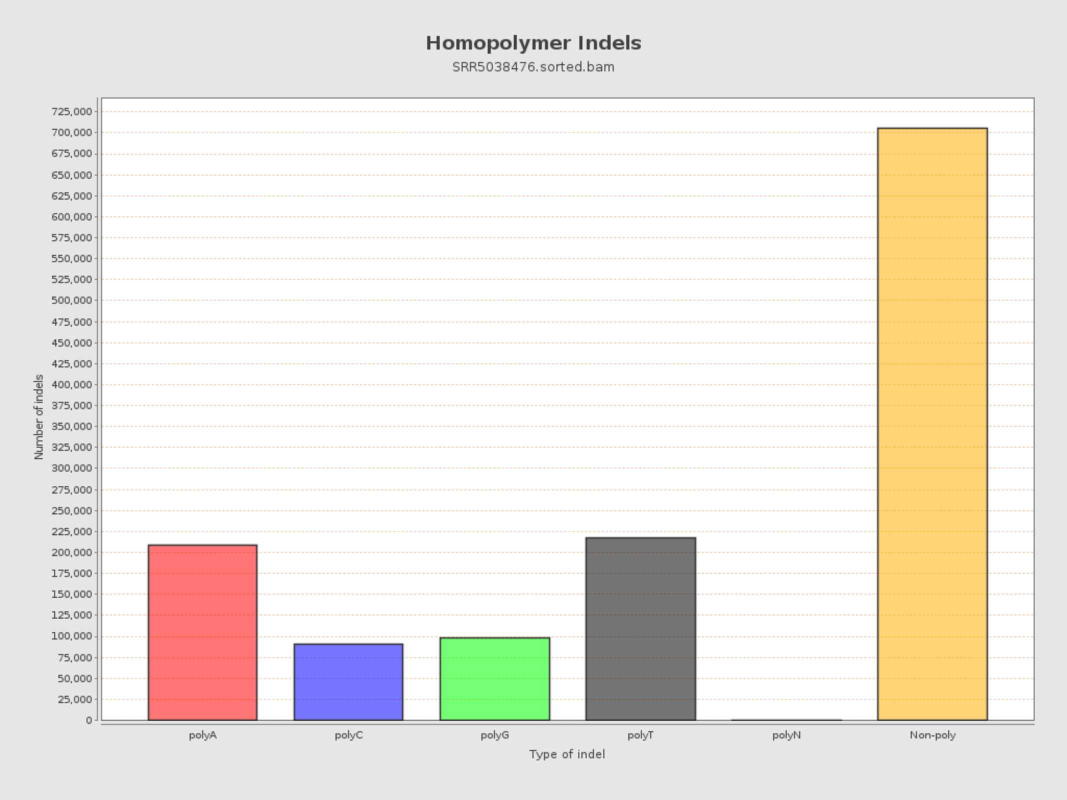
9. Results : Mapped Reads GC-content Distribution



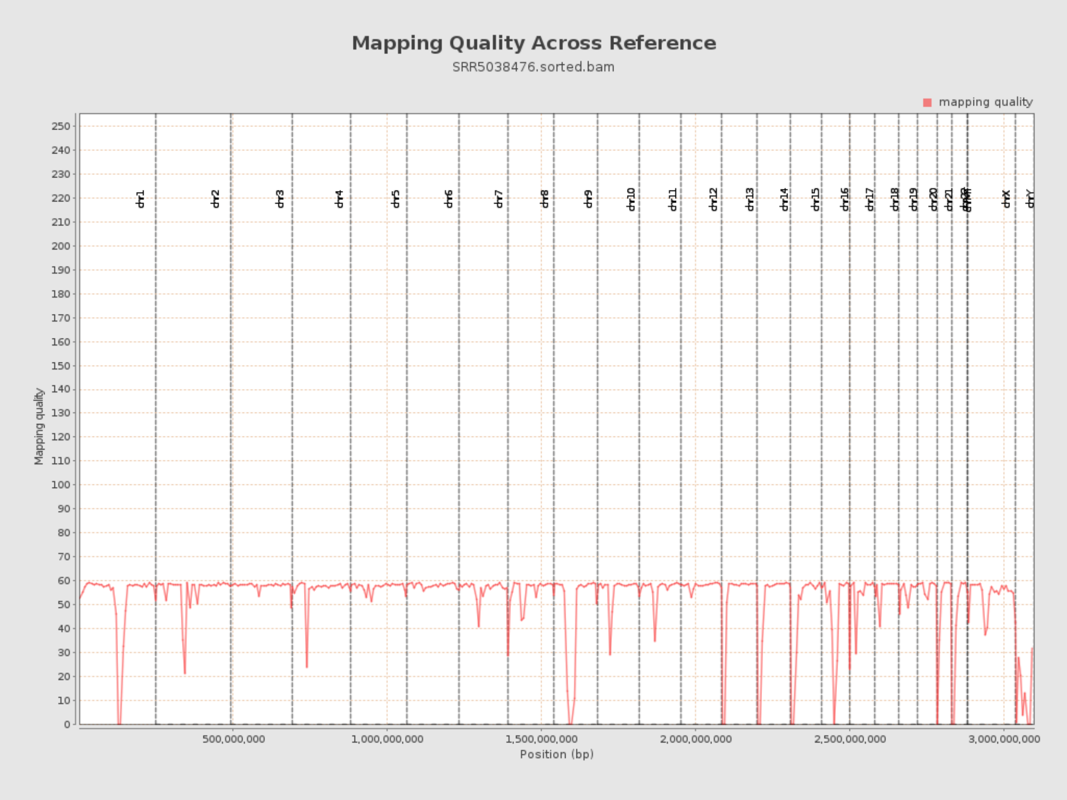
10. Results : Mapped Reads Clipping Profile



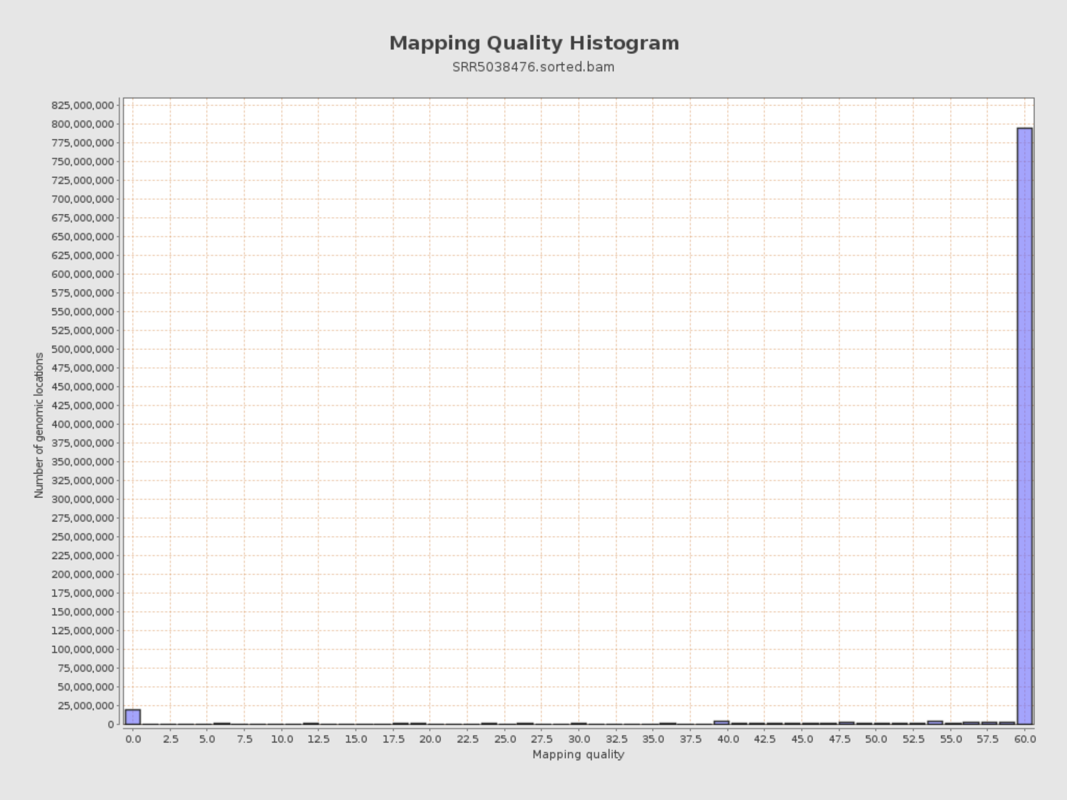
11. Results : Homopolymer Indels



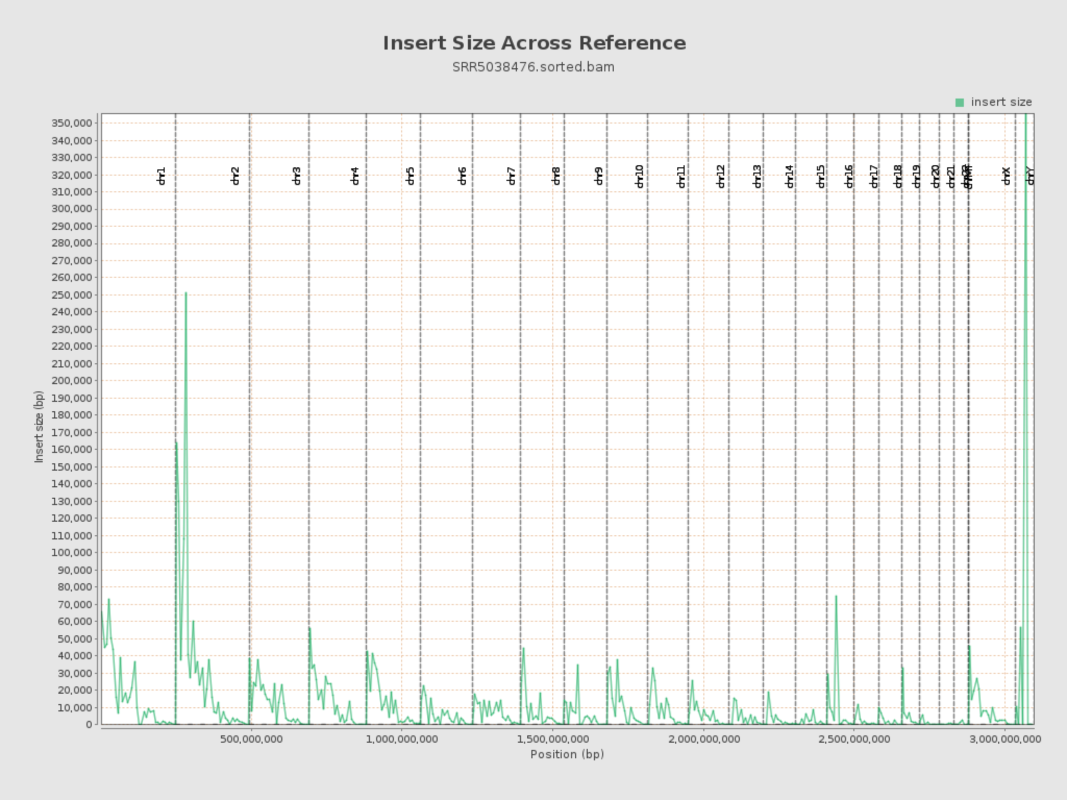
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram