Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 21:45:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038463.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_SRR5038463 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038463_1.fastq.gz SRR5038463_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 21:45:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038463.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,017,356
Mapped reads	10,374,098 / 94.16%
Unmapped reads	643,258 / 5.84%
Mapped paired reads	10,374,098 / 94.16%
Mapped reads, first in pair	5,250,219 / 47.65%
Mapped reads, second in pair	5,123,879 / 46.51%
Mapped reads, both in pair	10,231,914 / 92.87%
Mapped reads, singletons	142,184 / 1.29%
Secondary alignments	0
Supplementary alignments	163,436 / 1.48%
Read min/max/mean length	30 / 150 / 150.76
Duplicated reads (estimated)	1,268,463 / 11.51%
Duplication rate	8.09%
Clipped reads	2,500,728 / 22.7%

2.2. ACGT Content

Number/percentage of A's	428,123,591 / 28.92%
Number/percentage of C's	304,134,752 / 20.55%
Number/percentage of T's	429,651,434 / 29.03%
Number/percentage of G's	318,227,946 / 21.5%
Number/percentage of N's	30,840 / 0%

GC Percentage	42.05%

2.3. Coverage

Mean	0.4785
Standard Deviation	5.5594

2.4. Mapping Quality

Mean Mapping Quality	53.87

2.5. Insert size

Mean	85,763.33
Standard Deviation	2,787,449.99
P25/Median/P75	225 / 266 / 318

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	19,590,786
Insertions	249,257
Mapped reads with at least one insertion	2.27%
Deletions	516,413
Mapped reads with at least one deletion	4.79%
Homopolymer indels	47.98%

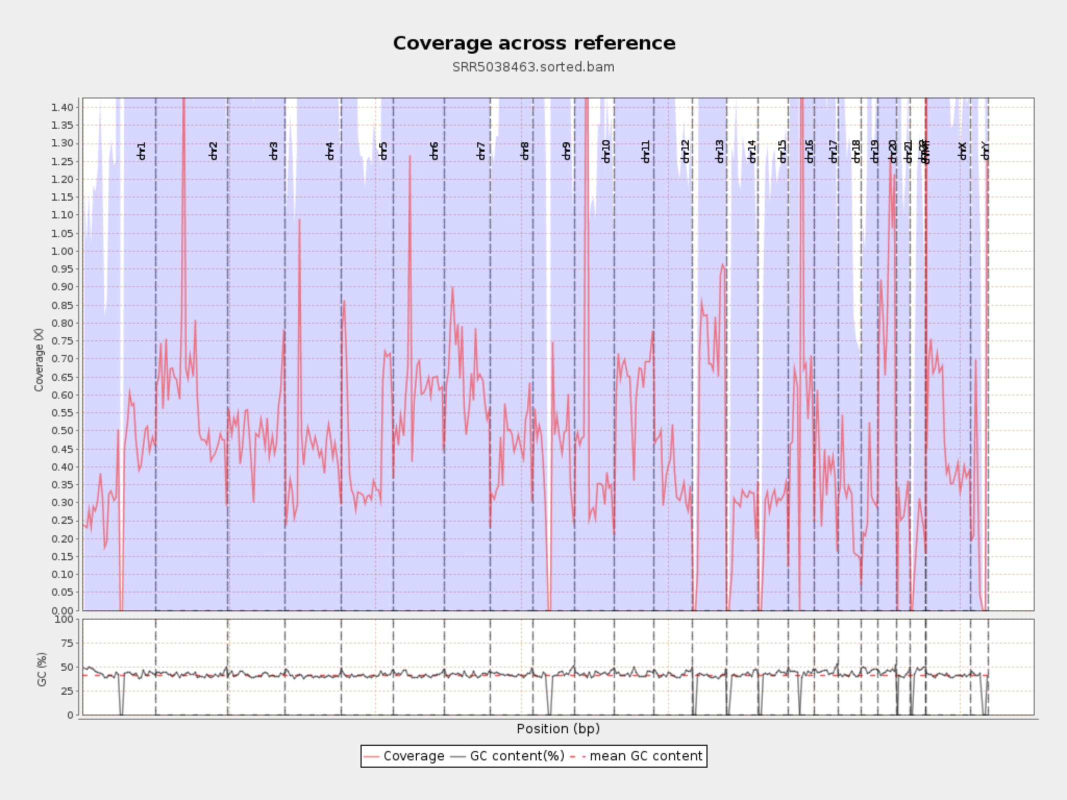
2.7. Chromosome stats

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

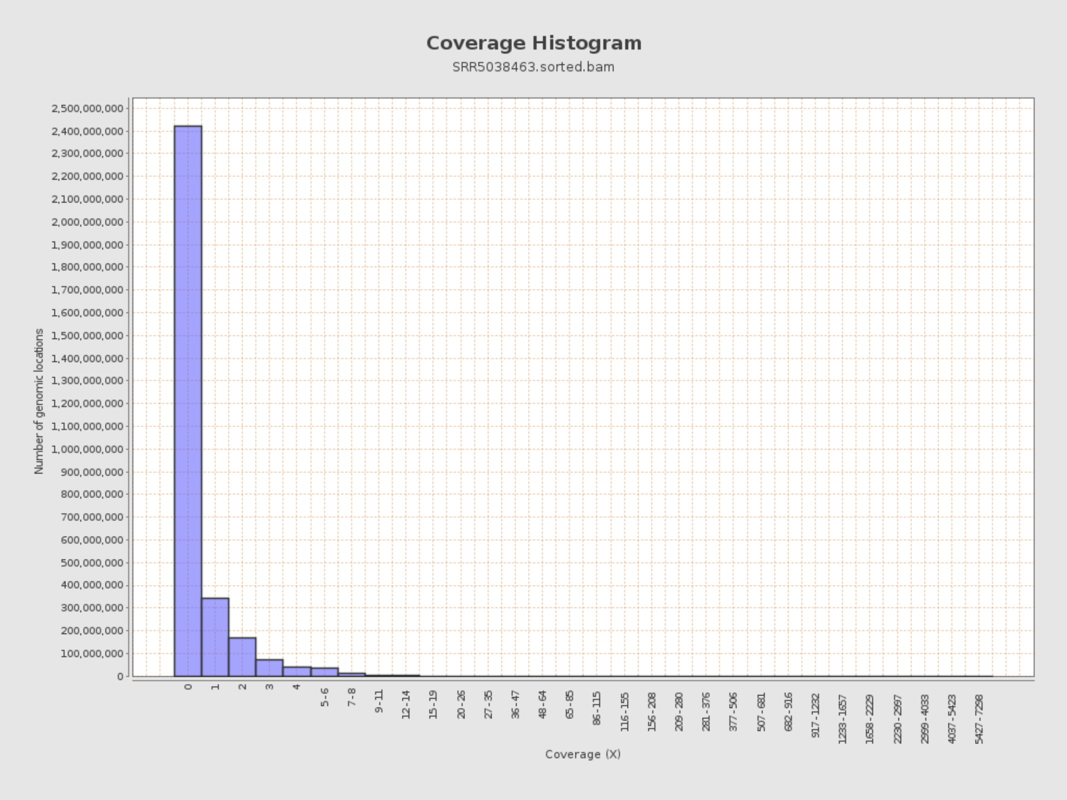
		bases	coverage	deviation
chr1	249250621	90122752	0.3616	3.4012
chr2	243199373	149589530	0.6151	6.5829
chr3	198022430	99772204	0.5038	1.2157
chr4	191154276	84205792	0.4405	5.1434
chr5	180915260	83110394	0.4594	1.1926
chr6	171115067	106027271	0.6196	6.9073
chr7	159138663	104429855	0.6562	5.7227
chr8	146364022	65590908	0.4481	1.5387
chr9	141213431	59815128	0.4236	7.535
chr10	135534747	63106231	0.4656	14.8249
chr11	135006516	85753729	0.6352	3.3312
chr12	133851895	50972461	0.3808	1.034
chr13	115169878	75636288	0.6567	1.4889
chr14	107349540	27154174	0.253	0.8709
chr15	102531392	26465926	0.2581	0.8121
chr16	90354753	59988039	0.6639	11.6713
chr17	81195210	32283833	0.3976	3.1274
chr18	78077248	22562160	0.289	5.9739
chr19	59128983	17141085	0.2899	2.0796
chr20	63025520	57741393	0.9162	2.4109
chr21	48129895	12613873	0.2621	2.6142
chr22	51304566	9056411	0.1765	0.7629
chrMT	16571	881119	53.1723	26.4984
chrX	155270560	76433251	0.4923	1.4136

chrY	59373566	20735389	0.3492	9.8607

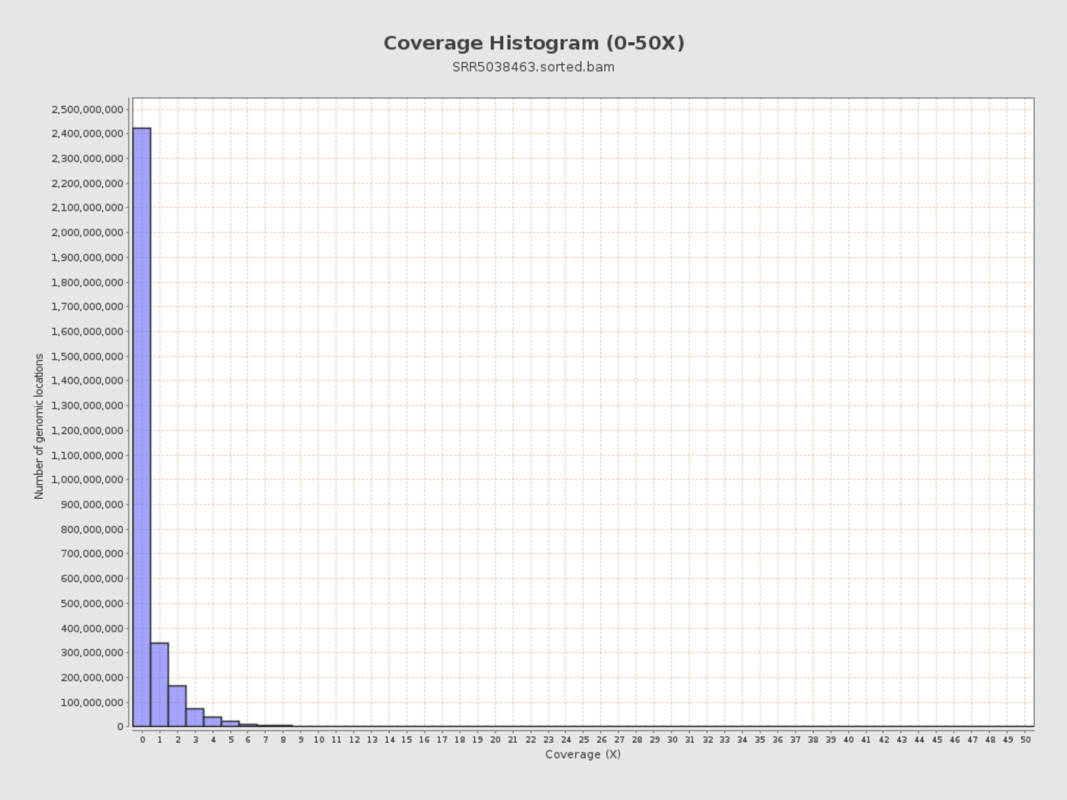
3. Results : Coverage across reference



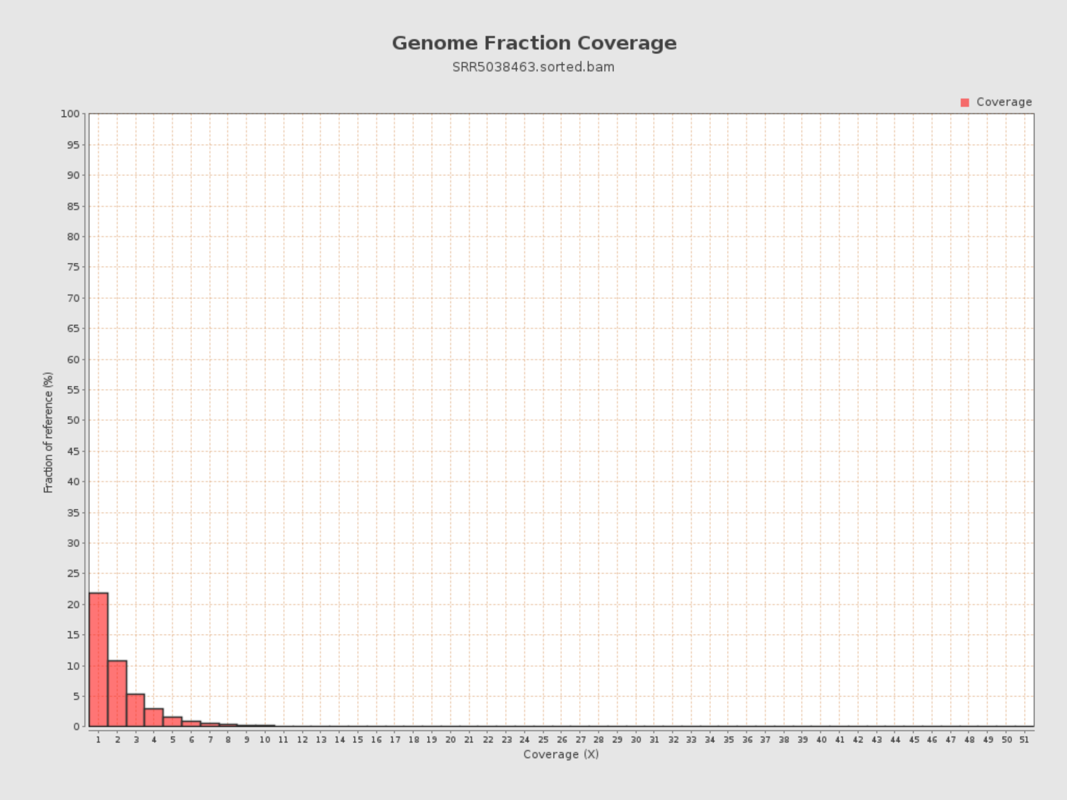
4. Results : Coverage Histogram



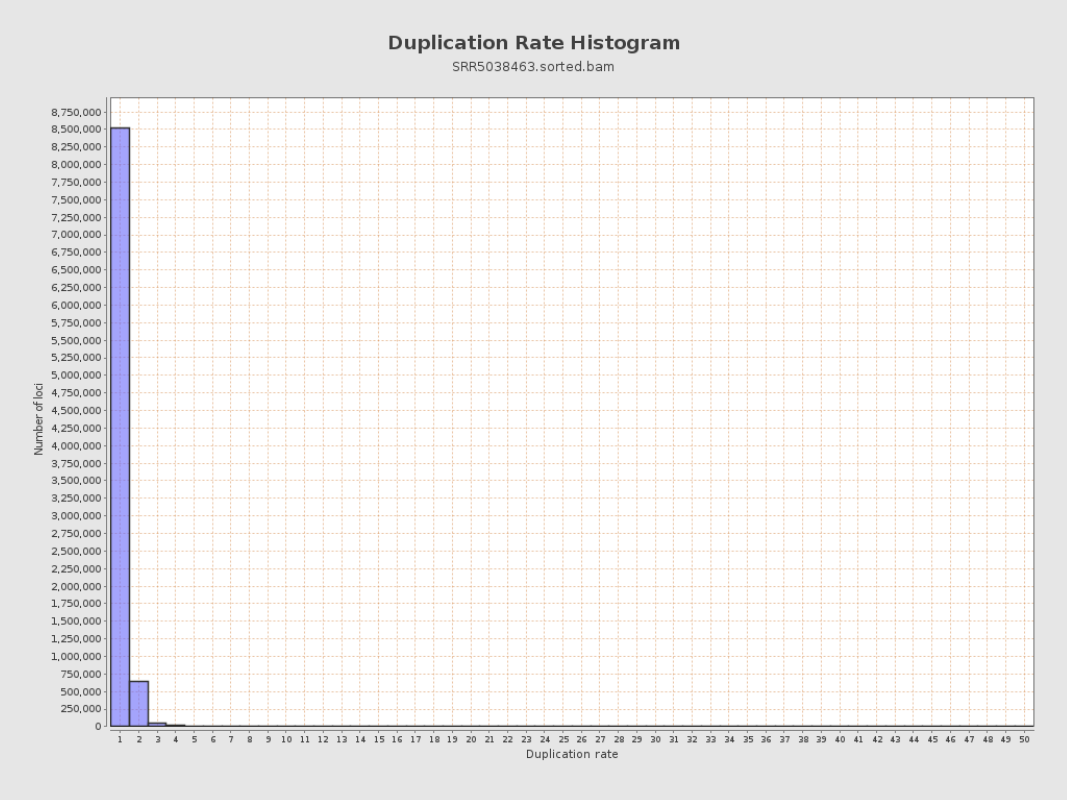
5. Results : Coverage Histogram (0-50X)



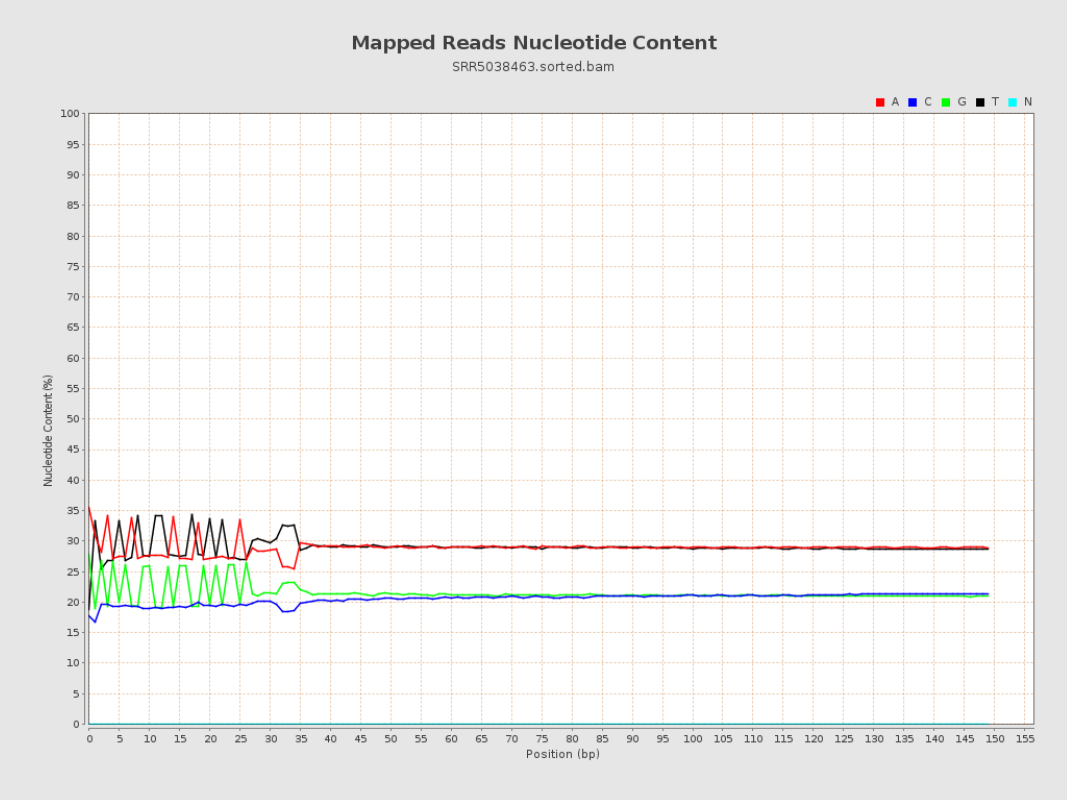
6. Results : Genome Fraction Coverage



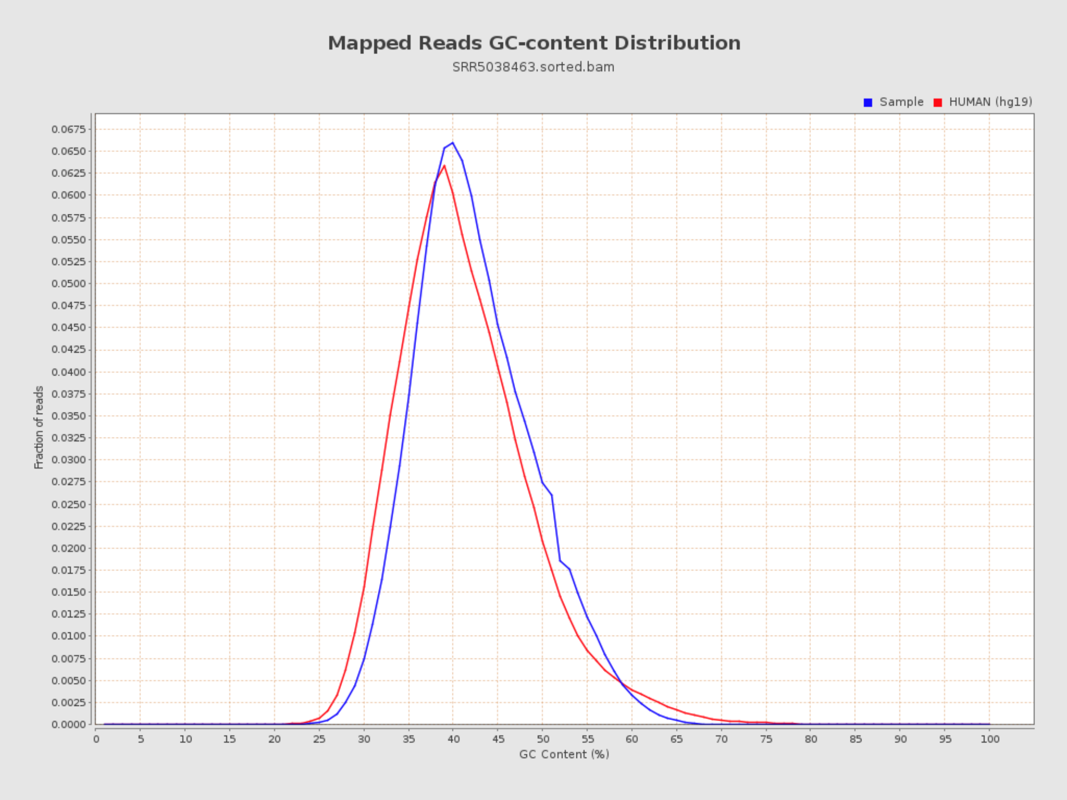
7. Results : Duplication Rate Histogram



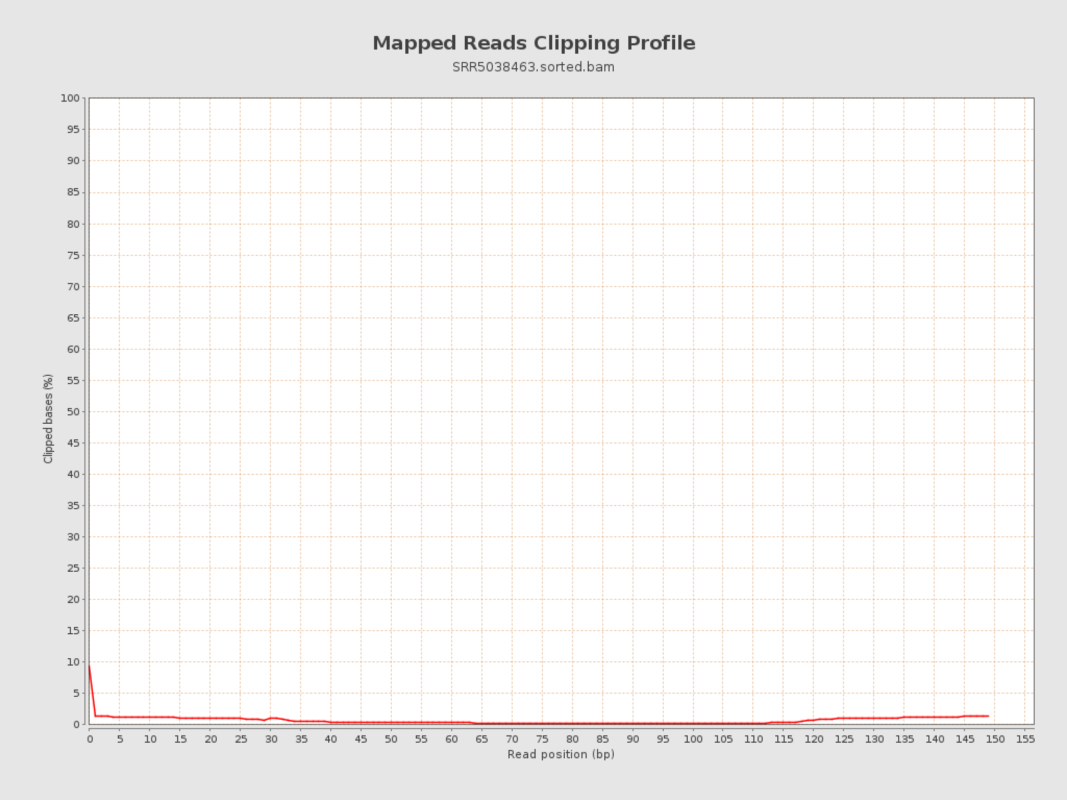
8. Results : Mapped Reads Nucleotide Content



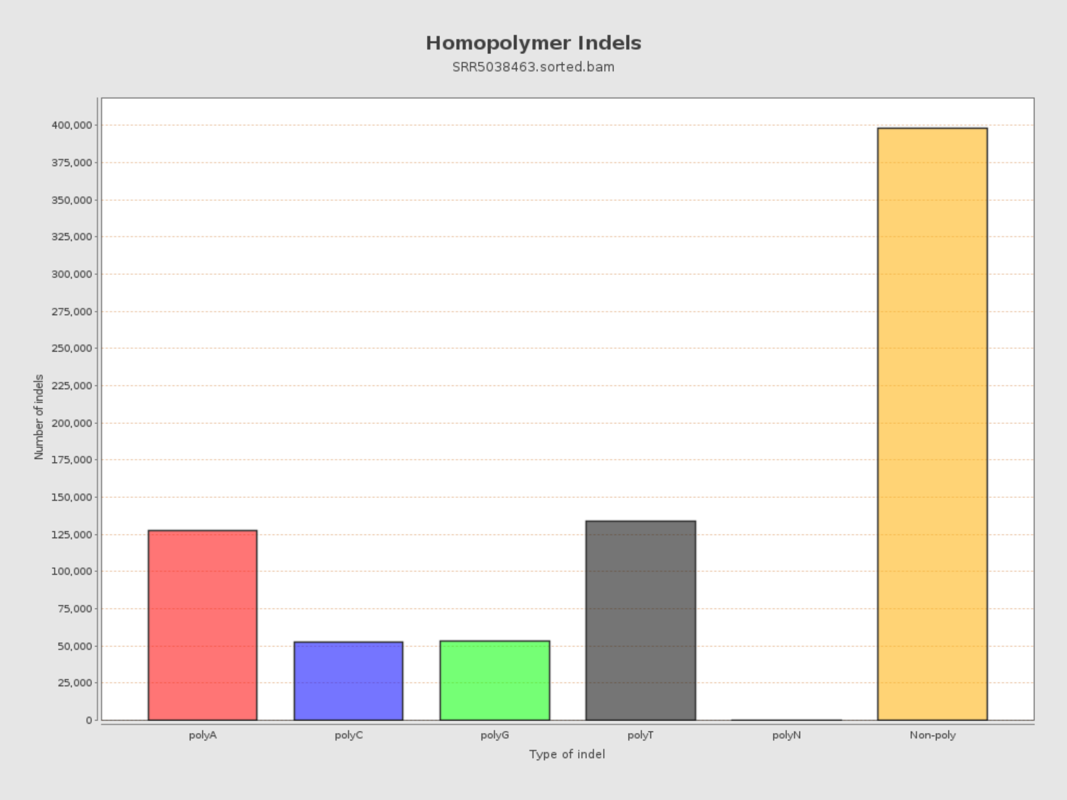
9. Results : Mapped Reads GC-content Distribution



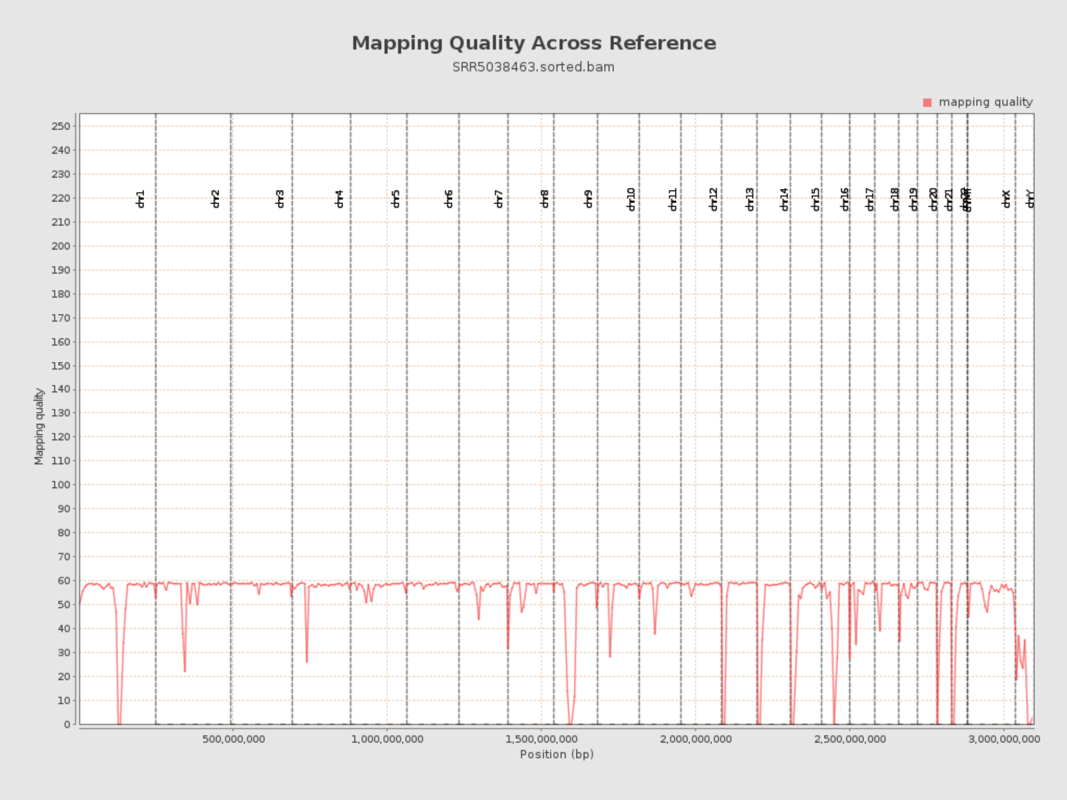
10. Results : Mapped Reads Clipping Profile



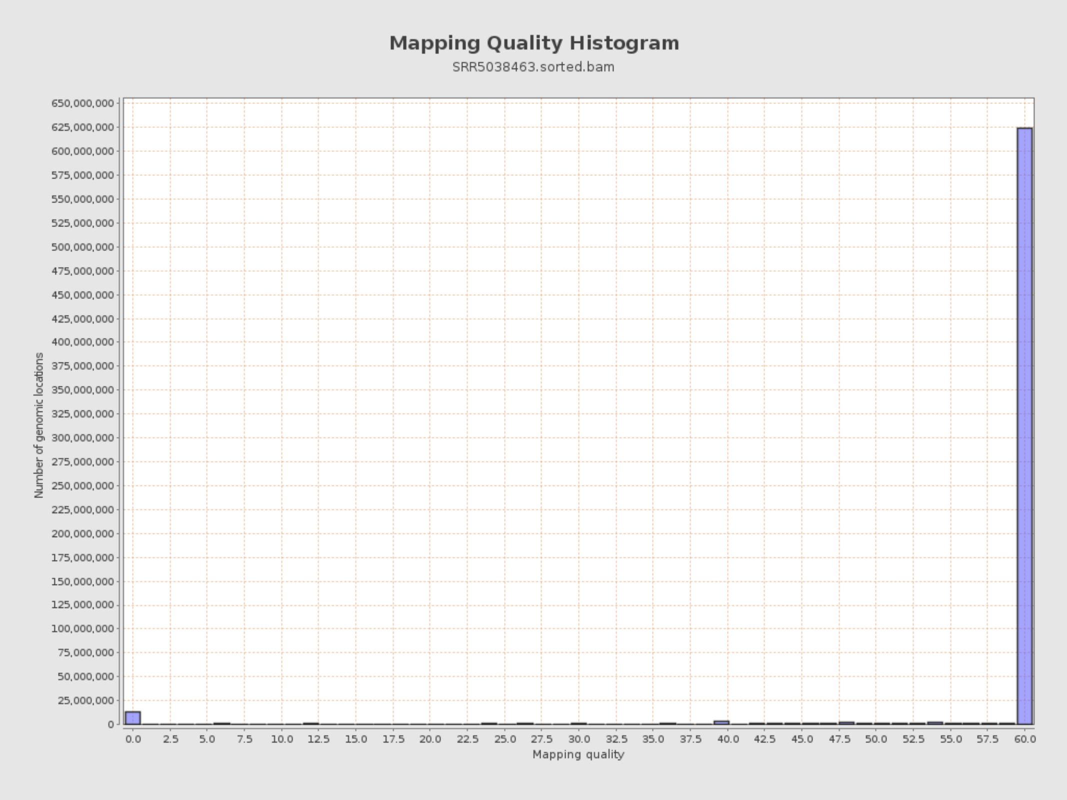
11. Results : Homopolymer Indels



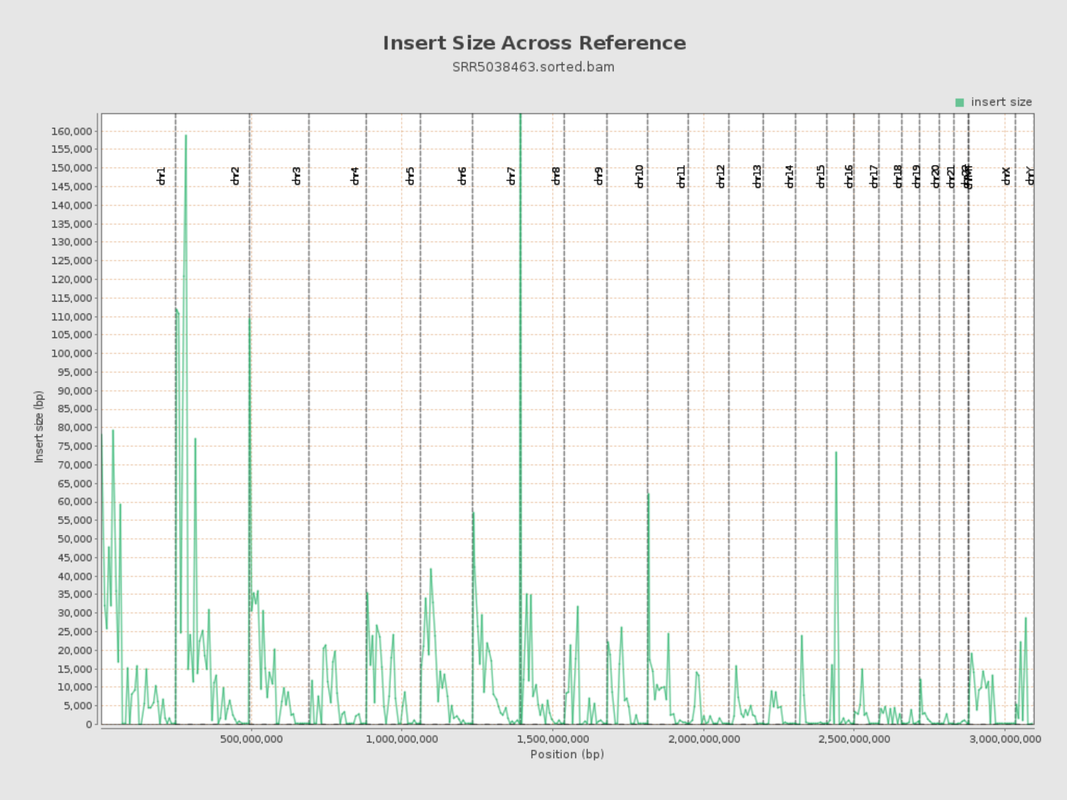
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram