Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 02:17:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038423.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_SRR5038423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038423_1.fastq.gz SRR5038423_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 02:17:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,047,880
Mapped reads	14,319,488 / 95.16%
Unmapped reads	728,392 / 4.84%
Mapped paired reads	14,319,488 / 95.16%
Mapped reads, first in pair	7,238,319 / 48.1%
Mapped reads, second in pair	7,081,169 / 47.06%
Mapped reads, both in pair	14,140,600 / 93.97%
Mapped reads, singletons	178,888 / 1.19%
Secondary alignments	0
Supplementary alignments	250,607 / 1.67%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	2,192,116 / 14.57%
Duplication rate	9.79%
Clipped reads	3,076,179 / 20.44%

2.2. ACGT Content

Number/percentage of A's	598,206,377 / 29.03%
Number/percentage of C's	428,883,358 / 20.81%
Number/percentage of T's	594,703,329 / 28.86%
Number/percentage of G's	438,645,826 / 21.29%
Number/percentage of N's	46,157 / 0%

GC Percentage	42.1%

2.3. Coverage

Mean	0.6661
Standard Deviation	9.7902

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	73,647.51
Standard Deviation	2,591,726.99
P25/Median/P75	203 / 247 / 301

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	29,688,573
Insertions	394,732
Mapped reads with at least one insertion	2.58%
Deletions	739,769
Mapped reads with at least one deletion	4.94%
Homopolymer indels	46.4%

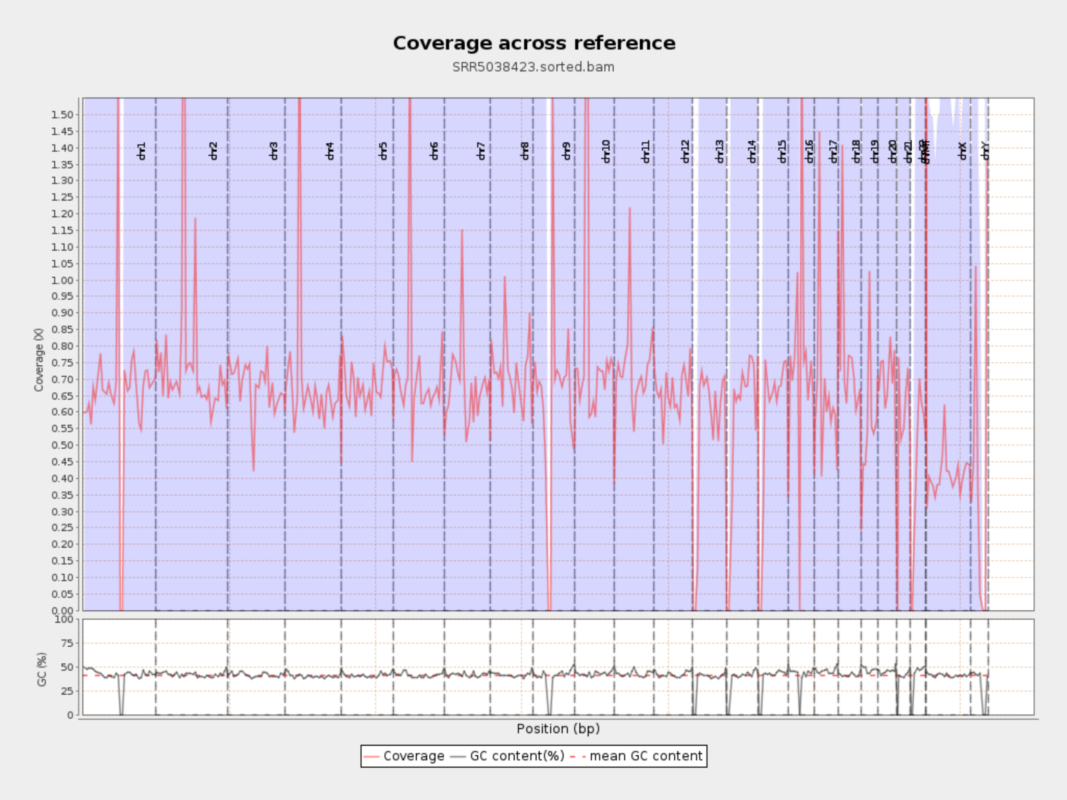
2.7. Chromosome stats

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

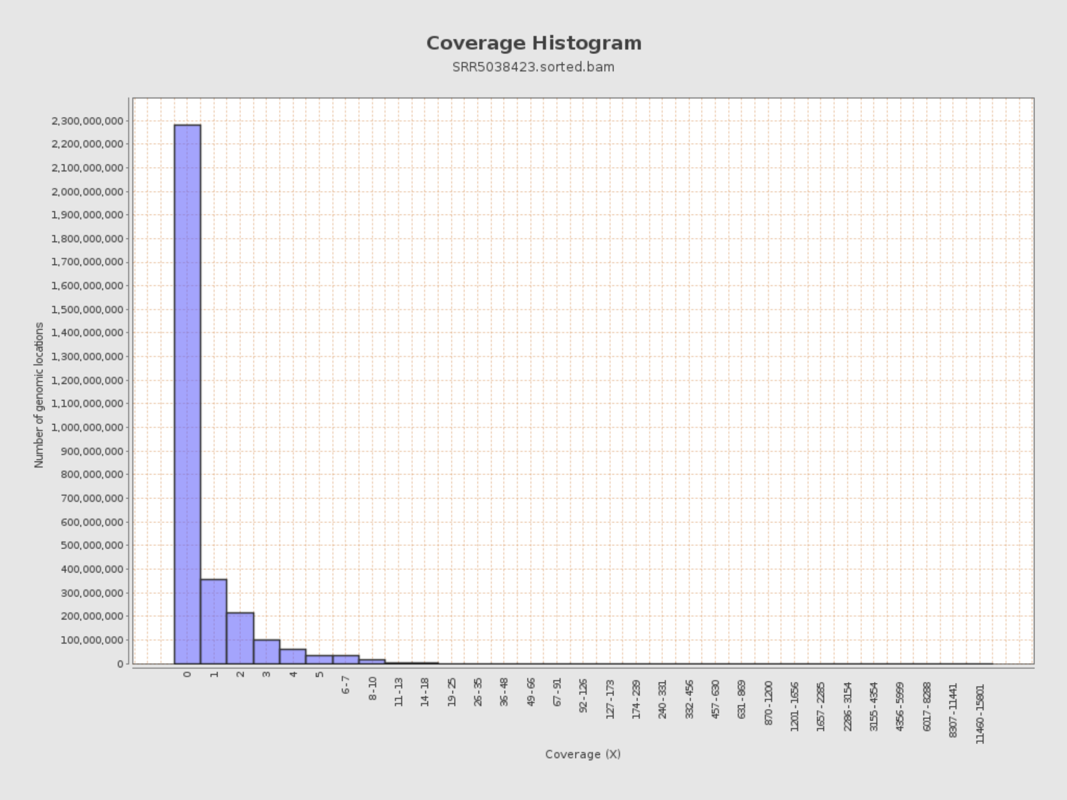
		bases	coverage	deviation
chr1	249250621	163995826	0.658	16.2566
chr2	243199373	186789907	0.7681	10.9614
chr3	198022430	134594764	0.6797	1.5217
chr4	191154276	134461016	0.7034	8.3036
chr5	180915260	124649773	0.689	1.6479
chr6	171115067	123915962	0.7242	13.3245
chr7	159138663	108744685	0.6833	8.4841
chr8	146364022	105217303	0.7189	2.8611
chr9	141213431	90804100	0.643	18.41
chr10	135534747	108236960	0.7986	13.9961
chr11	135006516	98745354	0.7314	8.4829
chr12	133851895	88546648	0.6615	1.5516
chr13	115169878	62008228	0.5384	1.3333
chr14	107349540	61218680	0.5703	1.5474
chr15	102531392	57981378	0.5655	1.3882
chr16	90354753	68462612	0.7577	8.5339
chr17	81195210	54695683	0.6736	12.1356
chr18	78077248	61017015	0.7815	16.0373
chr19	59128983	34103628	0.5768	8.4717
chr20	63025520	44493250	0.706	2.8191
chr21	48129895	27627079	0.574	3.7358
chr22	51304566	21940551	0.4277	1.3147
chrMT	16571	9032061	545.0523	383.4961
chrX	155270560	63628196	0.4098	2.3746

chrY	59373566	27109635	0.4566	10.8426

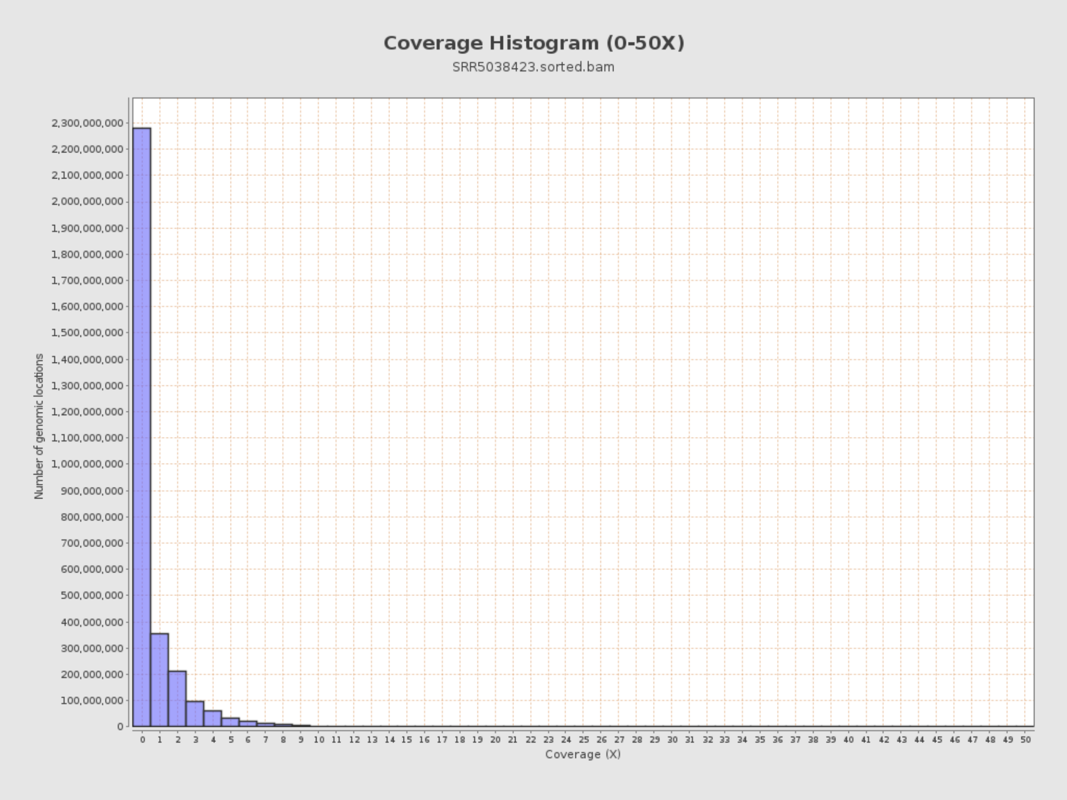
3. Results : Coverage across reference



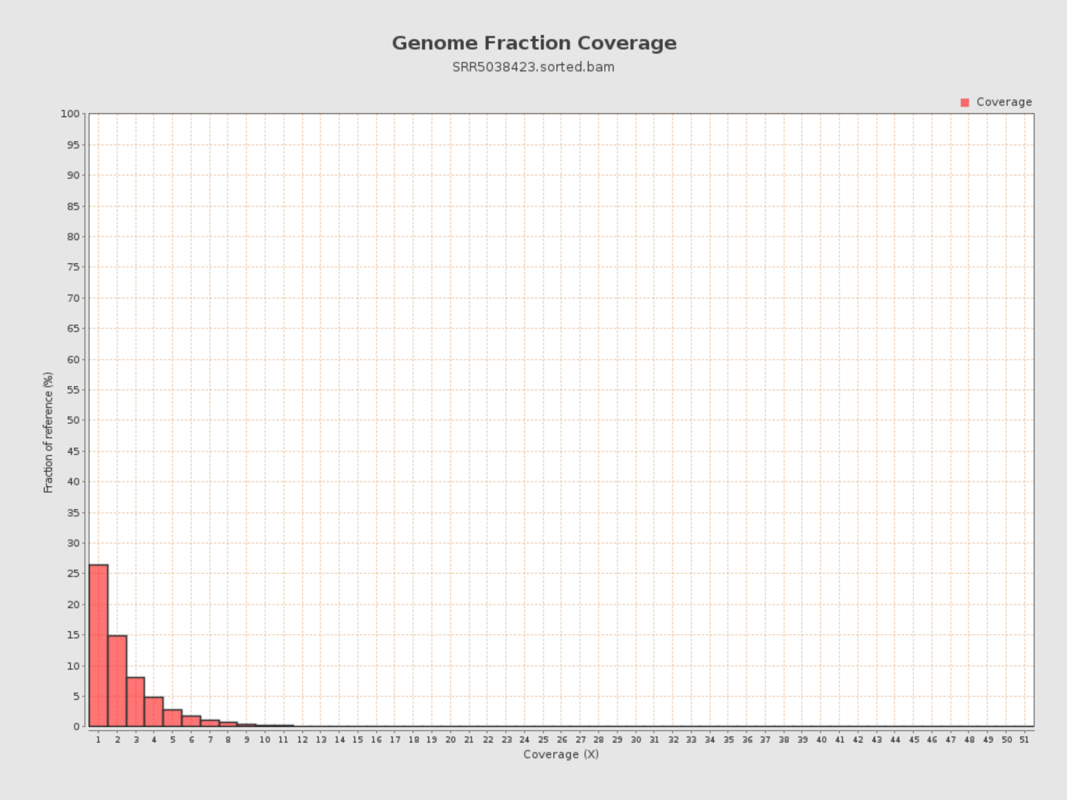
4. Results : Coverage Histogram



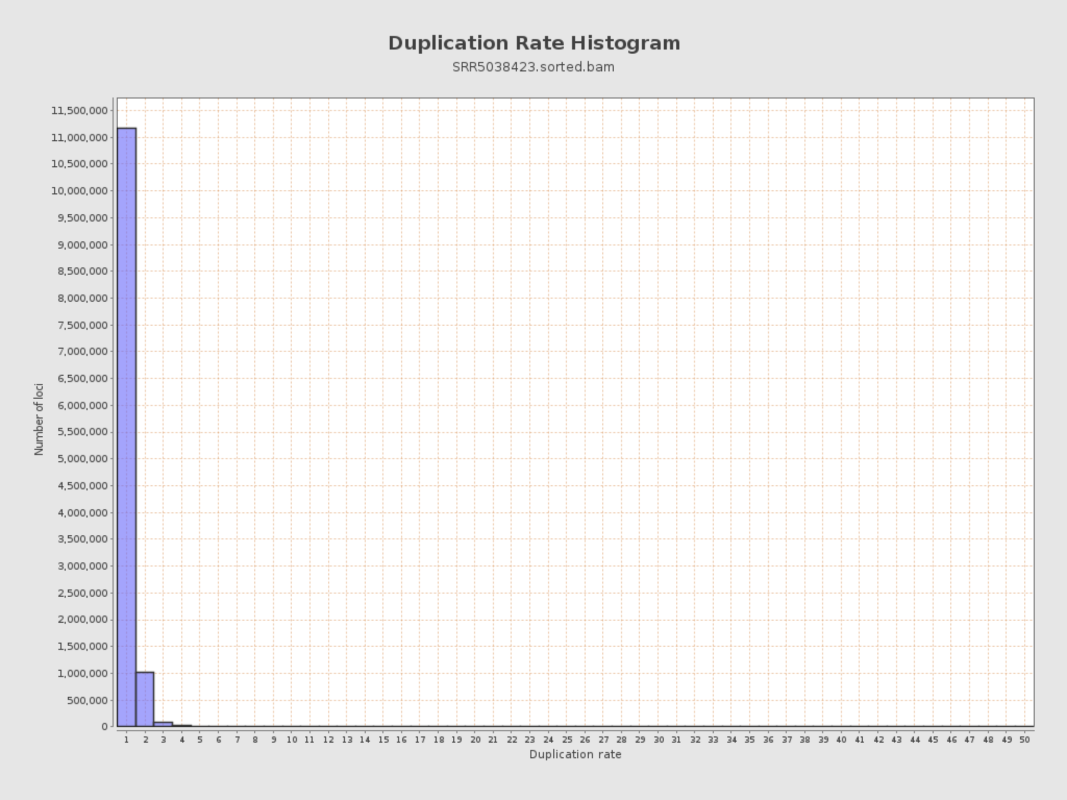
5. Results : Coverage Histogram (0-50X)



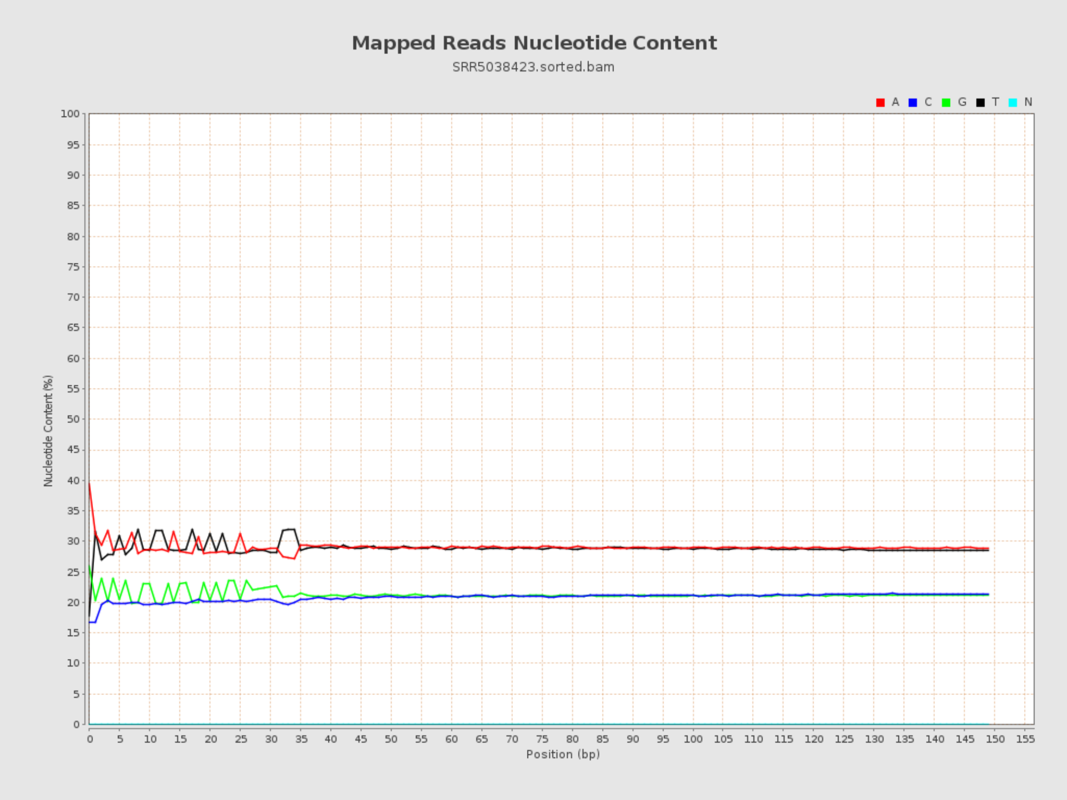
6. Results : Genome Fraction Coverage



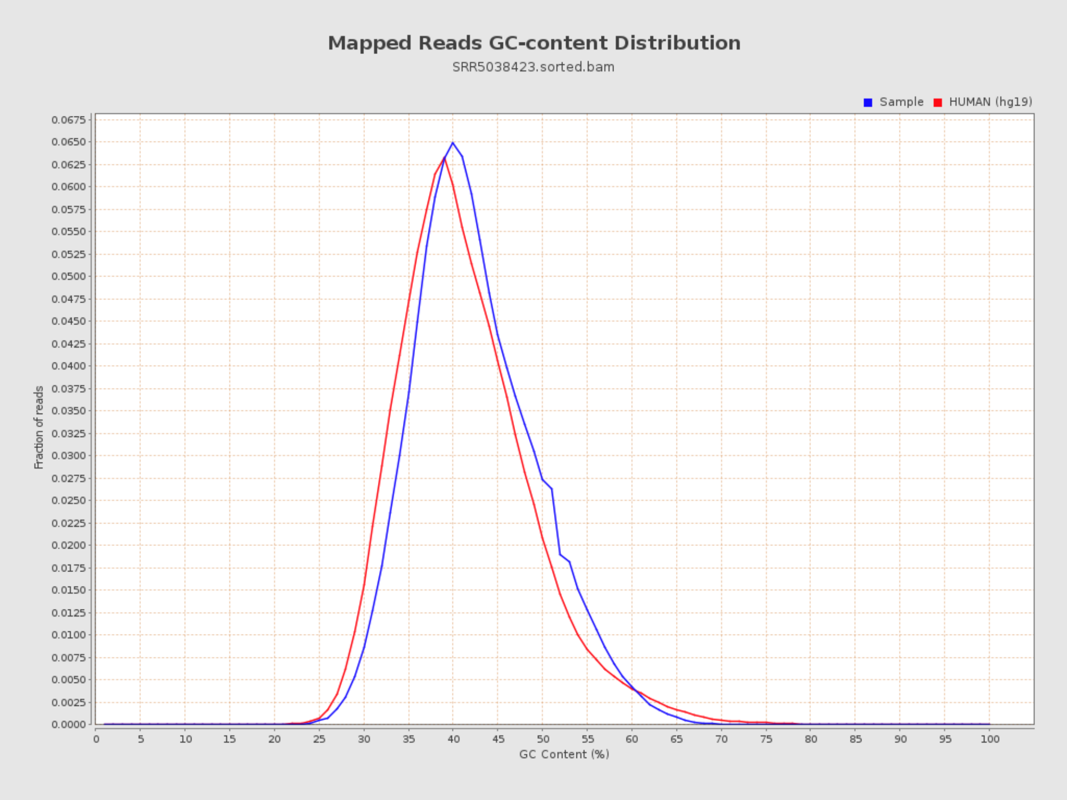
7. Results : Duplication Rate Histogram



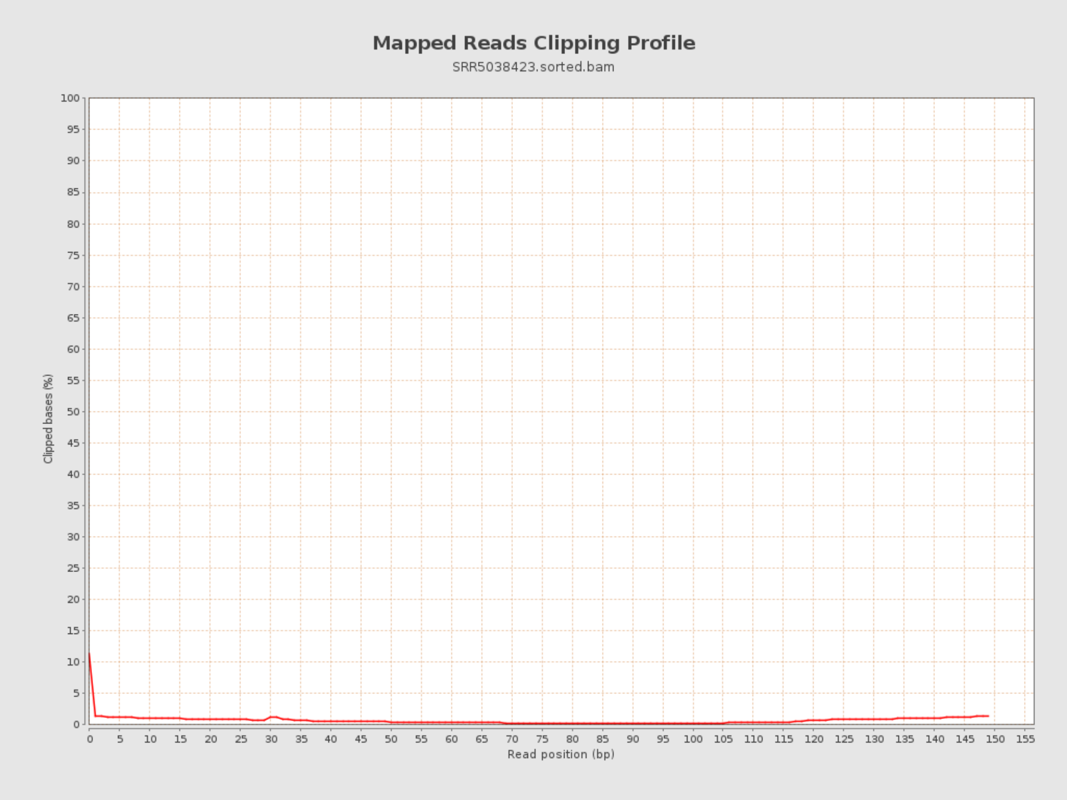
8. Results : Mapped Reads Nucleotide Content



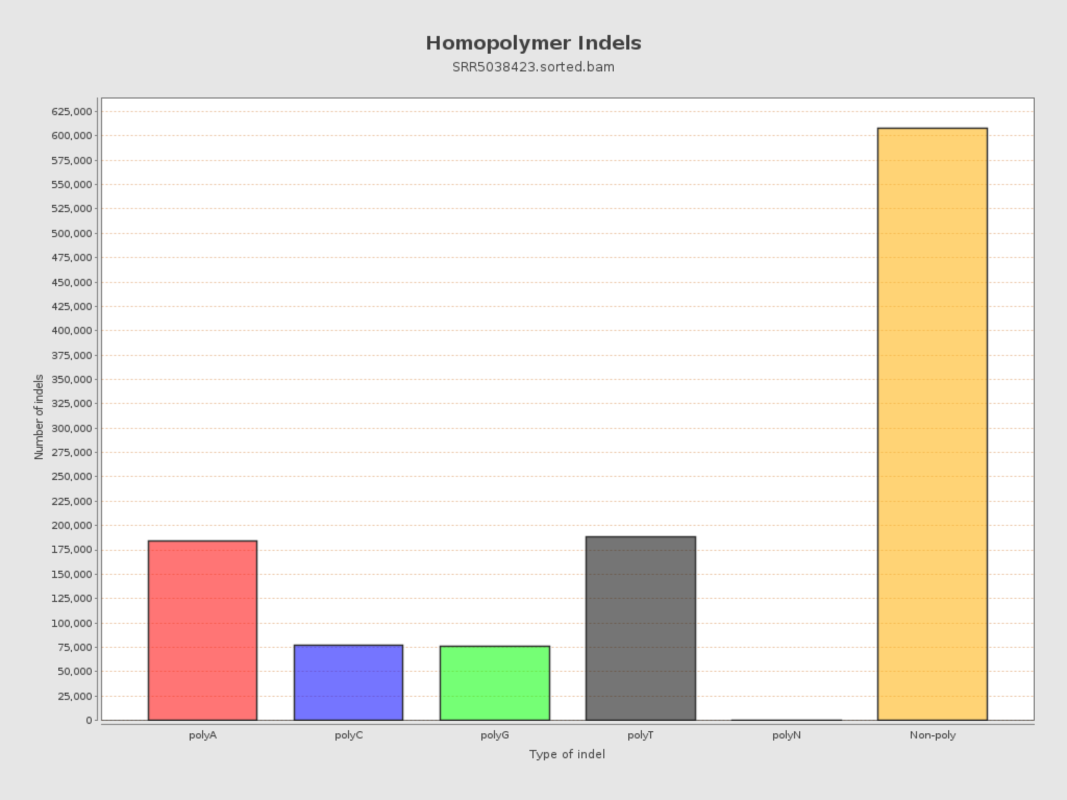
9. Results : Mapped Reads GC-content Distribution



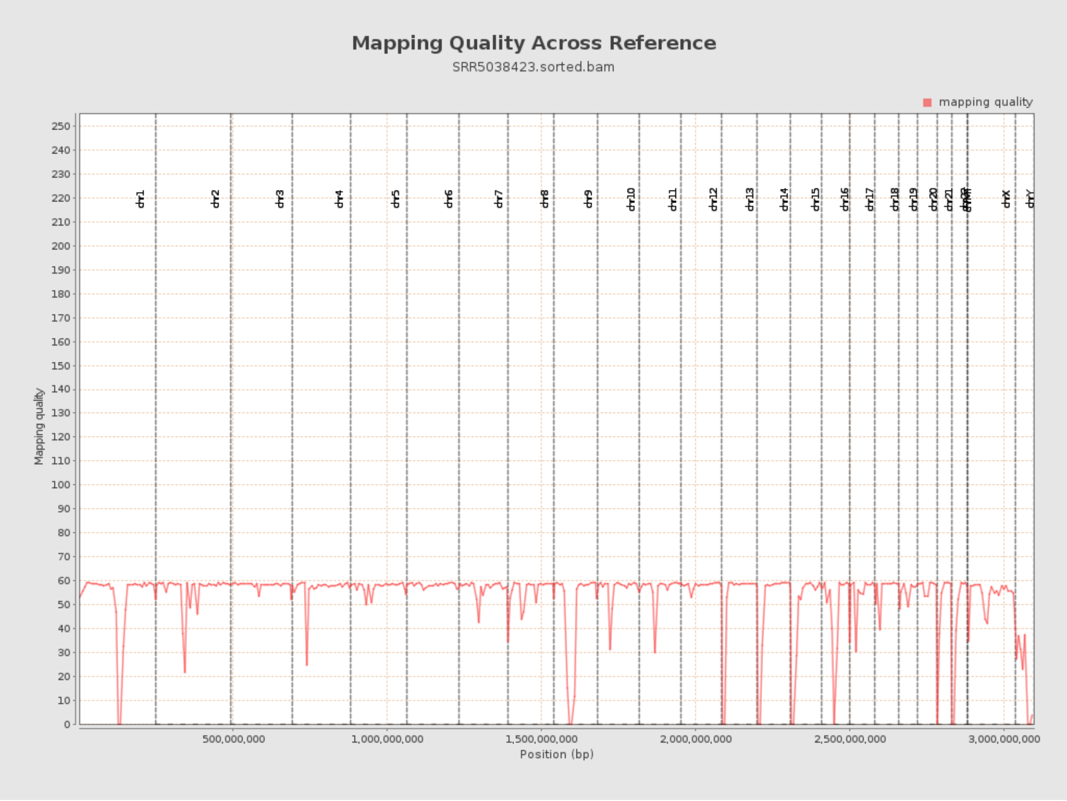
10. Results : Mapped Reads Clipping Profile



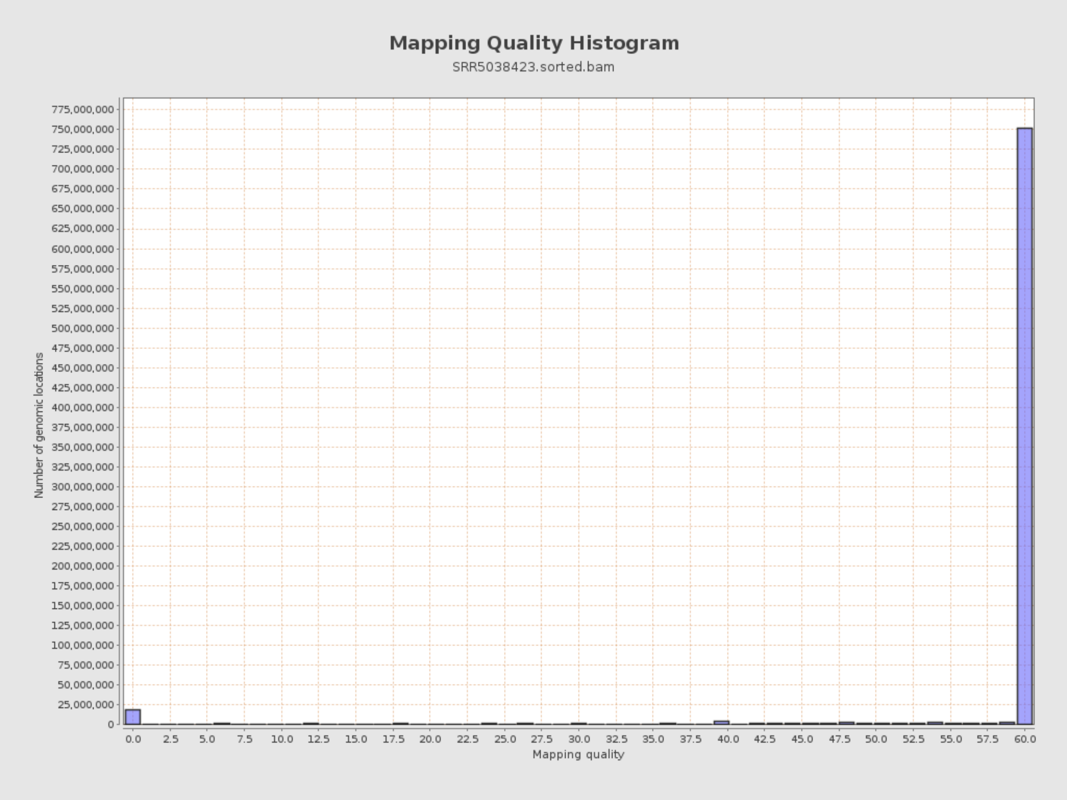
11. Results : Homopolymer Indels



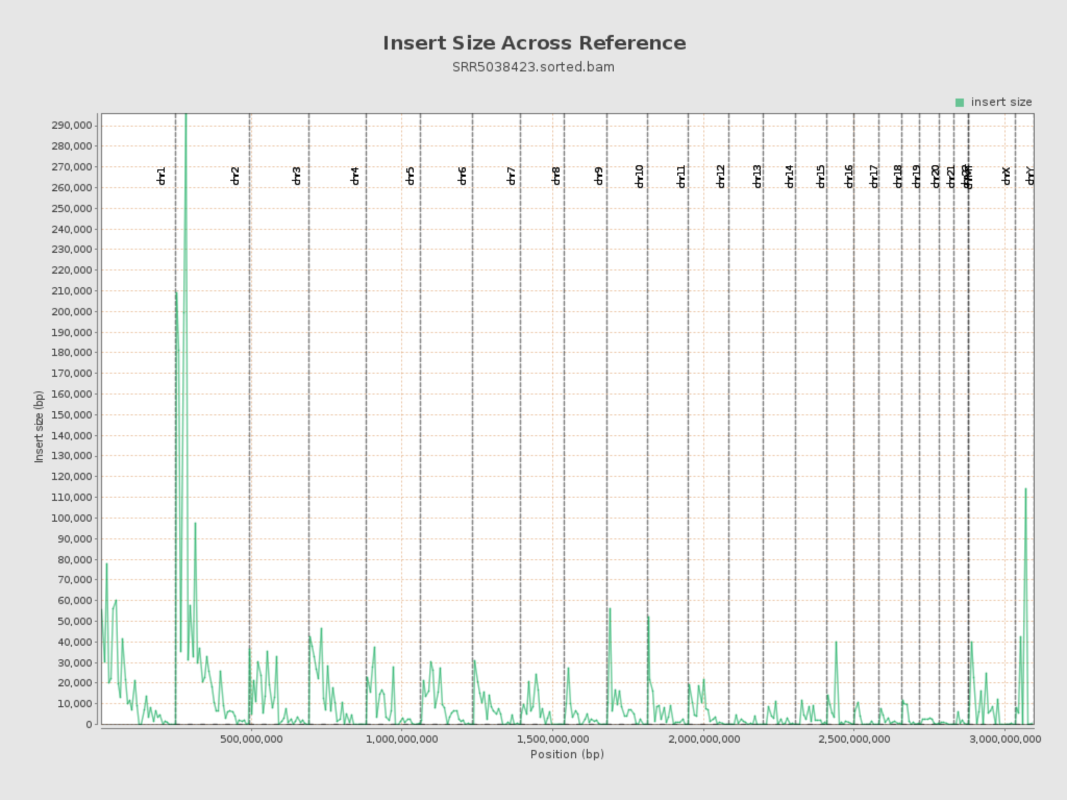
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram