Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 15:22:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038449.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_SRR5038449 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038449_1.fastq.gz SRR5038449_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 15:22:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038449.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,244,120
Mapped reads	16,693,240 / 91.5%
Unmapped reads	1,550,880 / 8.5%
Mapped paired reads	16,693,240 / 91.5%
Mapped reads, first in pair	8,482,298 / 46.49%
Mapped reads, second in pair	8,210,942 / 45.01%
Mapped reads, both in pair	16,361,428 / 89.68%
Mapped reads, singletons	331,812 / 1.82%
Secondary alignments	0
Supplementary alignments	230,653 / 1.26%
Read min/max/mean length	30 / 150 / 150.63
Duplicated reads (estimated)	3,297,967 / 18.08%
Duplication rate	14.12%
Clipped reads	7,973,572 / 43.7%

2.2. ACGT Content

Number/percentage of A's	640,989,769 / 28.58%
Number/percentage of C's	445,337,822 / 19.86%
Number/percentage of T's	653,158,158 / 29.12%
Number/percentage of G's	503,176,755 / 22.43%
Number/percentage of N's	175,720 / 0.01%

GC Percentage	42.29%

2.3. Coverage

Mean	0.725
Standard Deviation	9.3934

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	77,783.87
Standard Deviation	2,722,916.67
P25/Median/P75	198 / 249 / 315

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	28,534,818
Insertions	377,987
Mapped reads with at least one insertion	2.15%
Deletions	772,355
Mapped reads with at least one deletion	4.46%
Homopolymer indels	47.25%

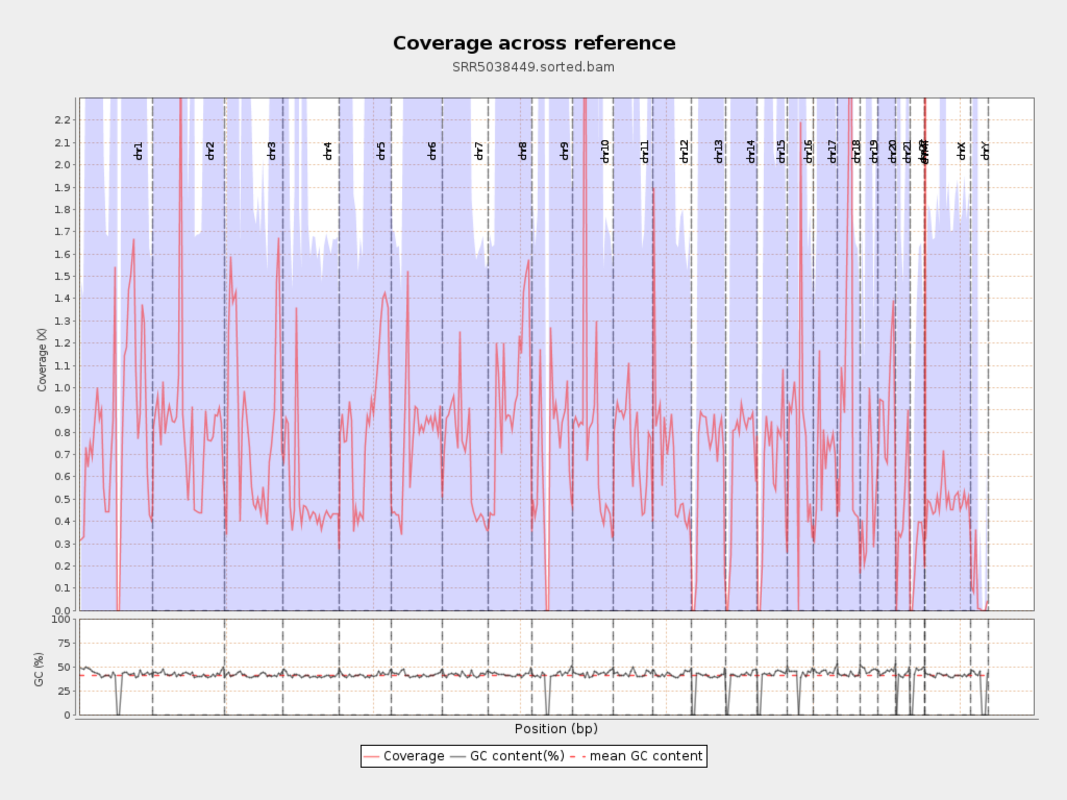
2.7. Chromosome stats

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

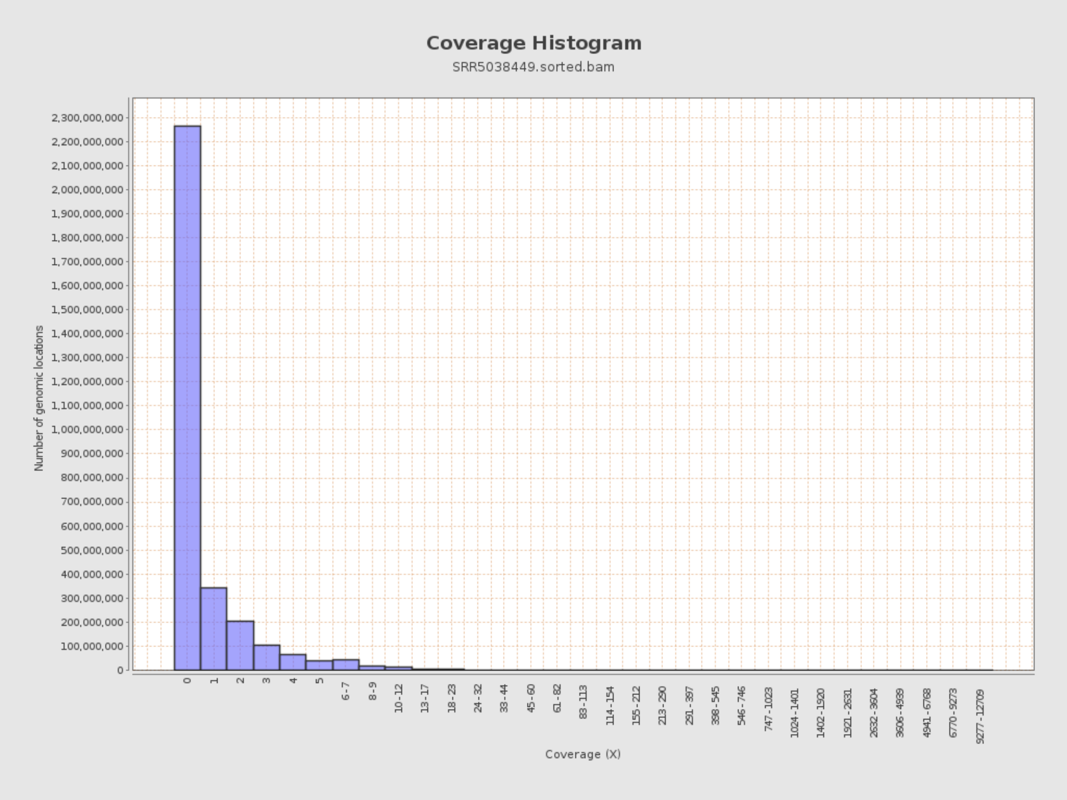
		bases	coverage	deviation
chr1	249250621	202652437	0.813	12.8264
chr2	243199373	203380640	0.8363	11.1786
chr3	198022430	167079686	0.8437	1.9287
chr4	191154276	97218160	0.5086	7.9836
chr5	180915260	154610326	0.8546	1.8297
chr6	171115067	131774811	0.7701	7.3497
chr7	159138663	108116561	0.6794	9.8975
chr8	146364022	142845175	0.976	3.8705
chr9	141213431	94803793	0.6714	15.396
chr10	135534747	118102193	0.8714	24.1361
chr11	135006516	102166974	0.7568	7.5507
chr12	133851895	92849895	0.6937	1.7736
chr13	115169878	76099124	0.6608	1.5623
chr14	107349540	72703040	0.6773	1.6701
chr15	102531392	60642815	0.5915	1.504
chr16	90354753	69682830	0.7712	10.115
chr17	81195210	54298354	0.6687	12.3475
chr18	78077248	89904167	1.1515	10.8135
chr19	59128983	27844971	0.4709	5.4547
chr20	63025520	59167330	0.9388	3.0601
chr21	48129895	21725980	0.4514	3.81
chr22	51304566	12172835	0.2373	0.9316
chrMT	16571	4046570	244.1959	130.422
chrX	155270560	76009984	0.4895	2.1915

chrY	59373566	4445545	0.0749	8.0851

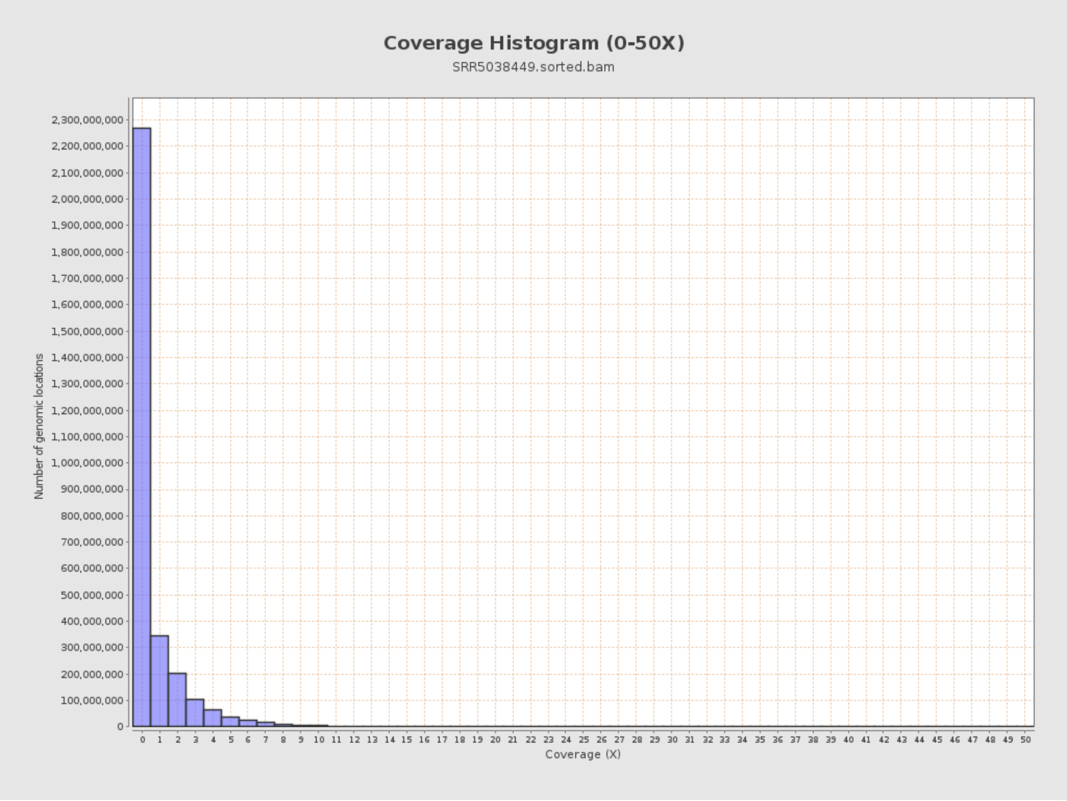
3. Results : Coverage across reference



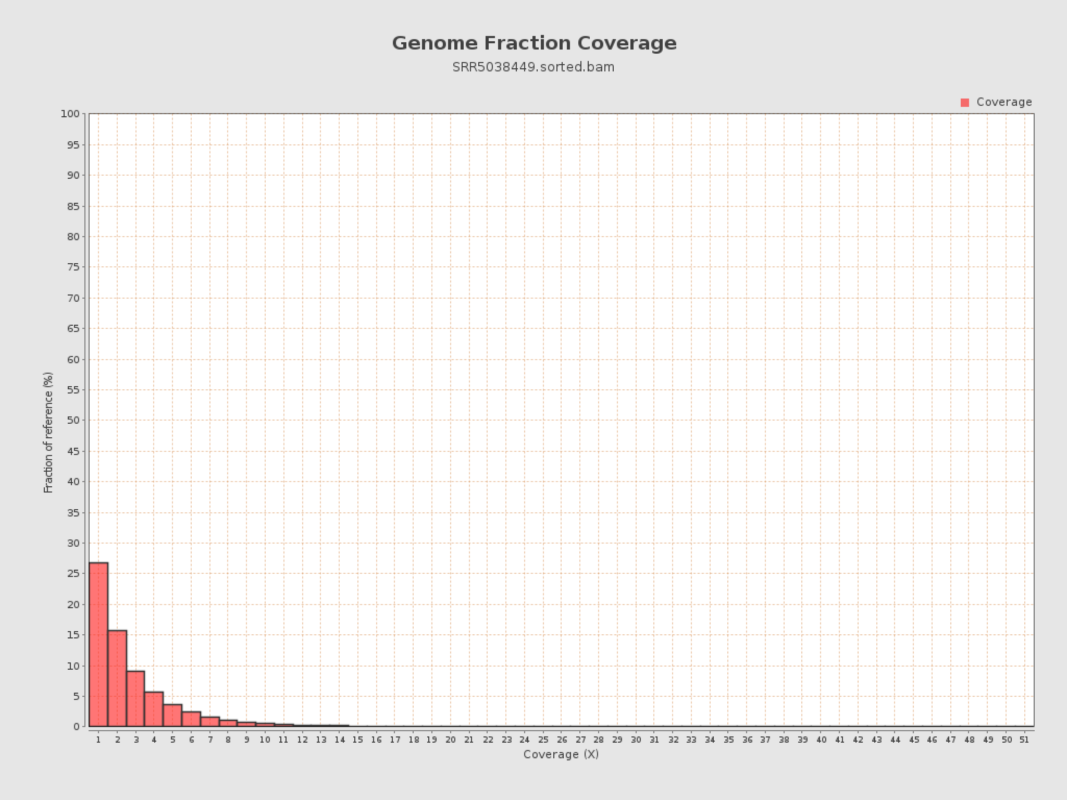
4. Results : Coverage Histogram



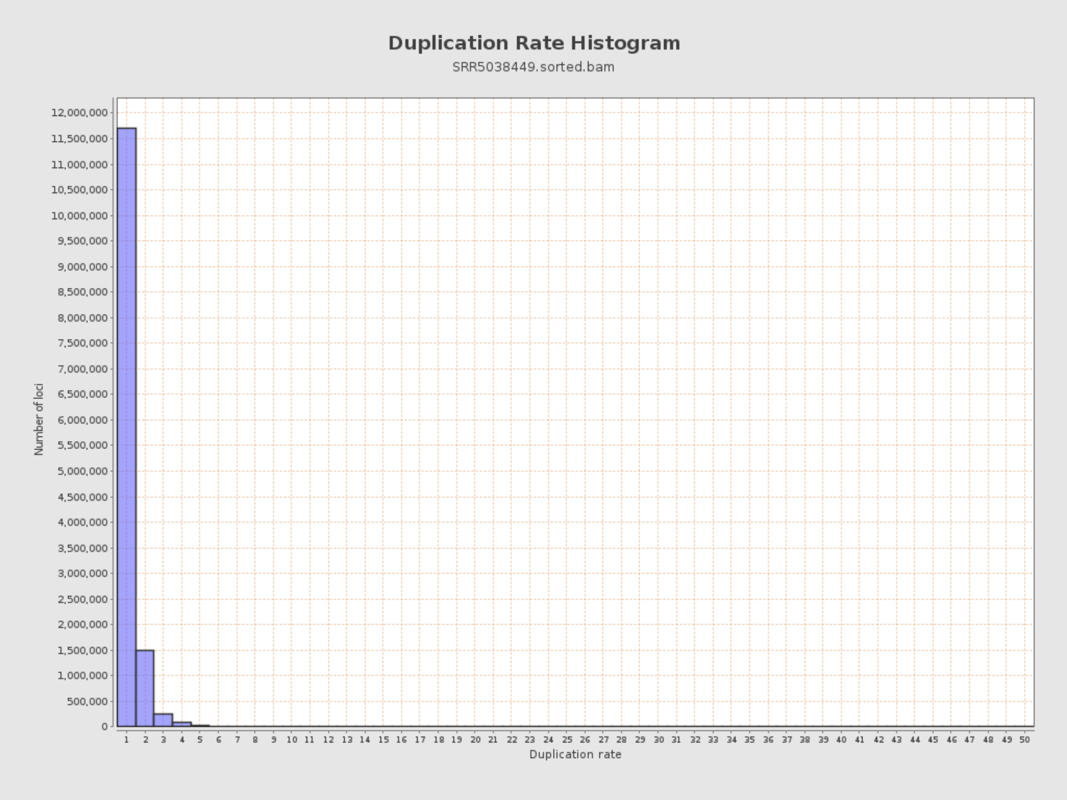
5. Results : Coverage Histogram (0-50X)



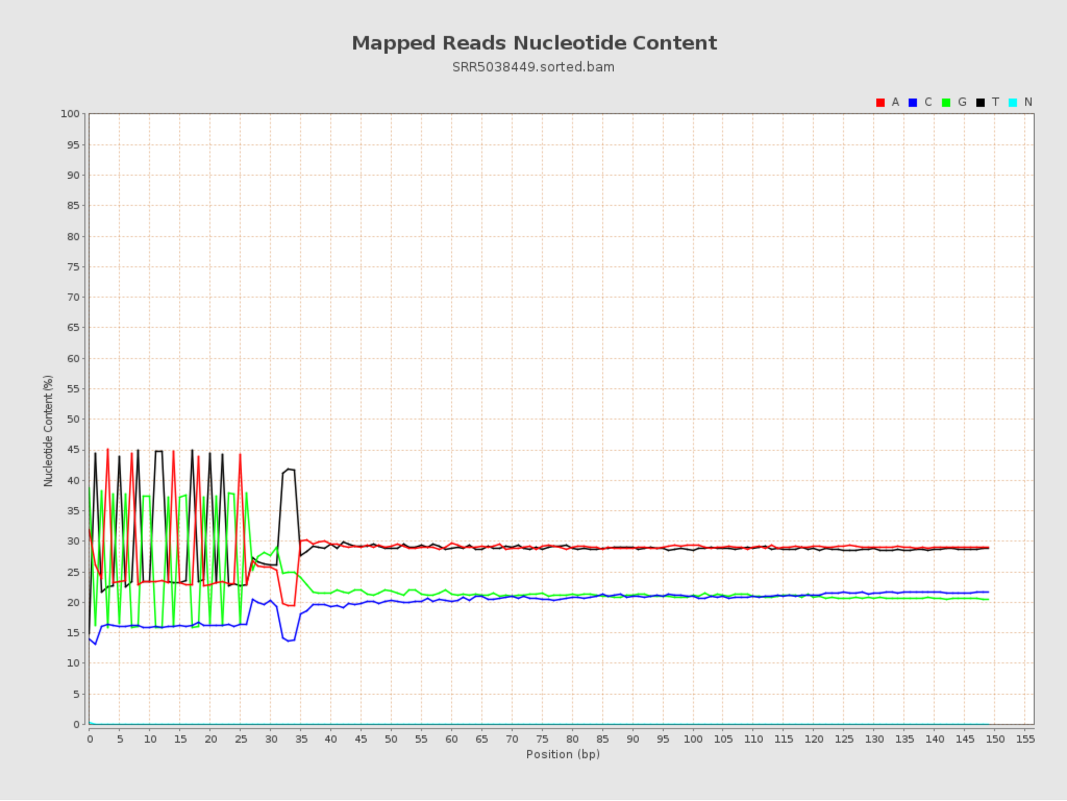
6. Results : Genome Fraction Coverage



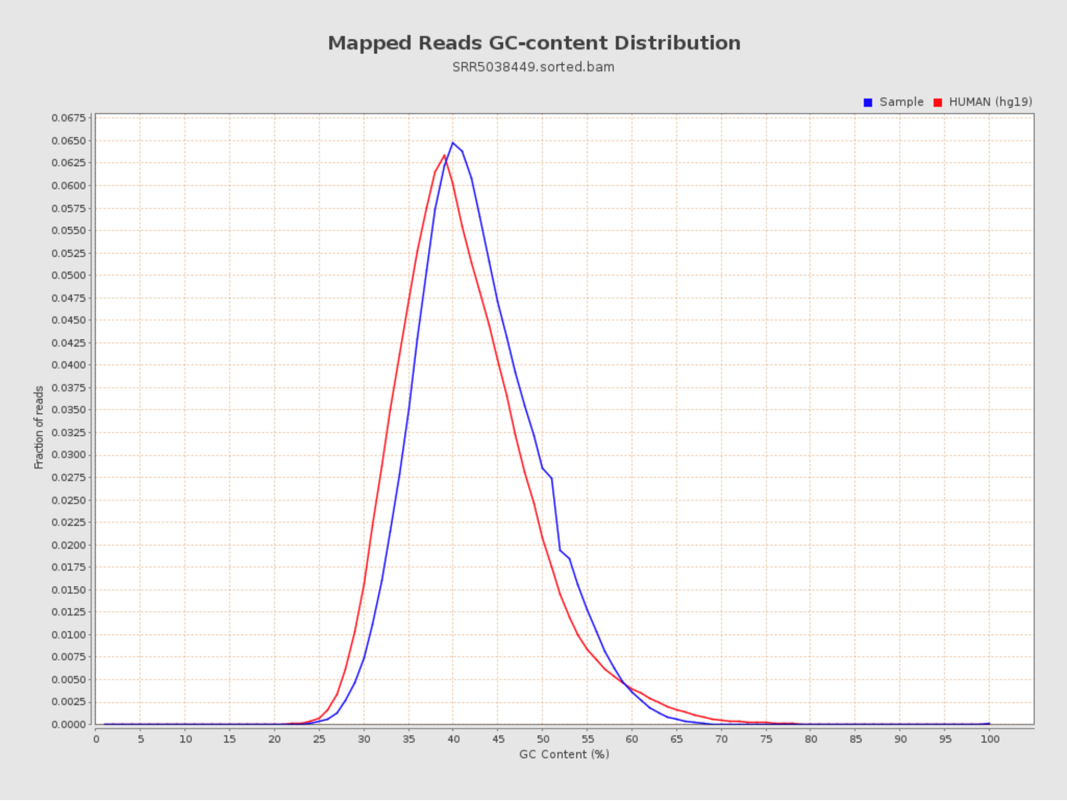
7. Results : Duplication Rate Histogram



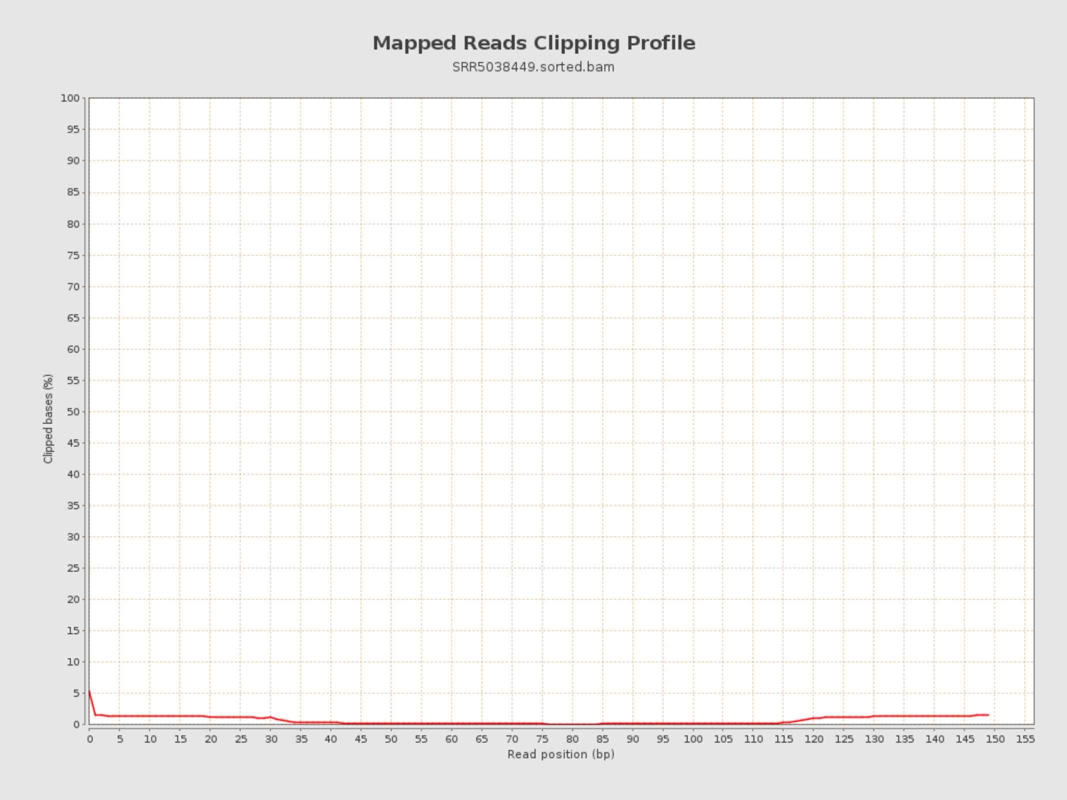
8. Results : Mapped Reads Nucleotide Content



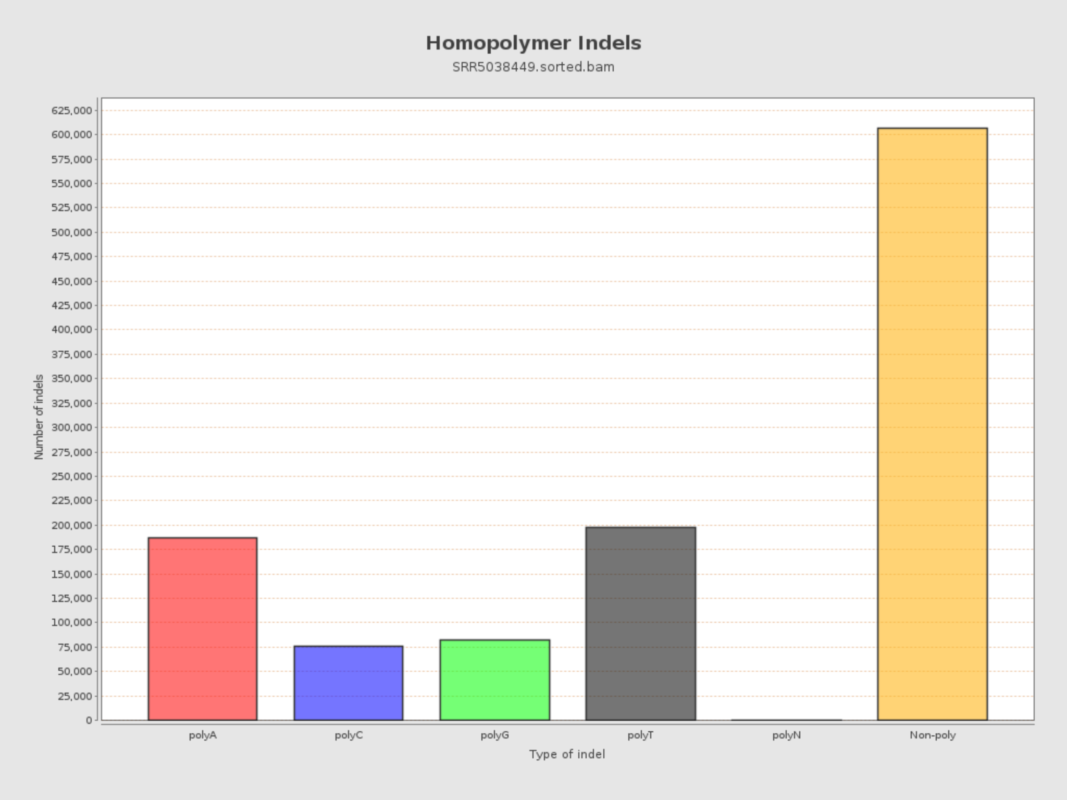
9. Results : Mapped Reads GC-content Distribution



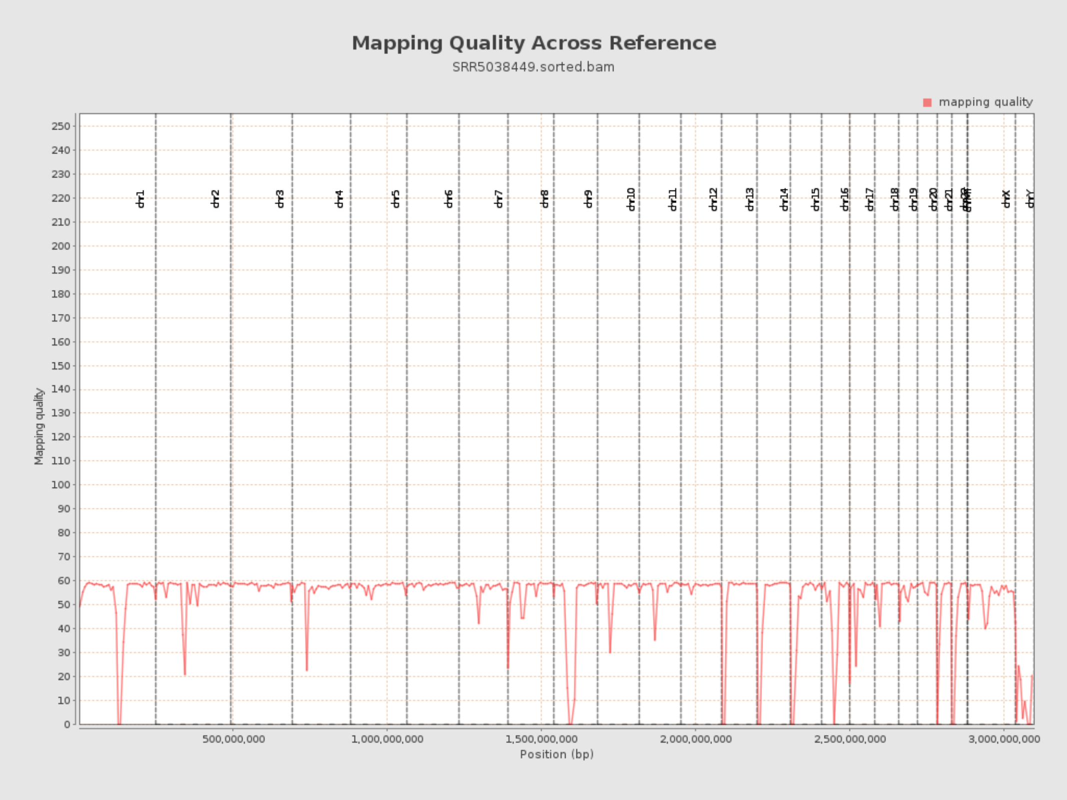
10. Results : Mapped Reads Clipping Profile



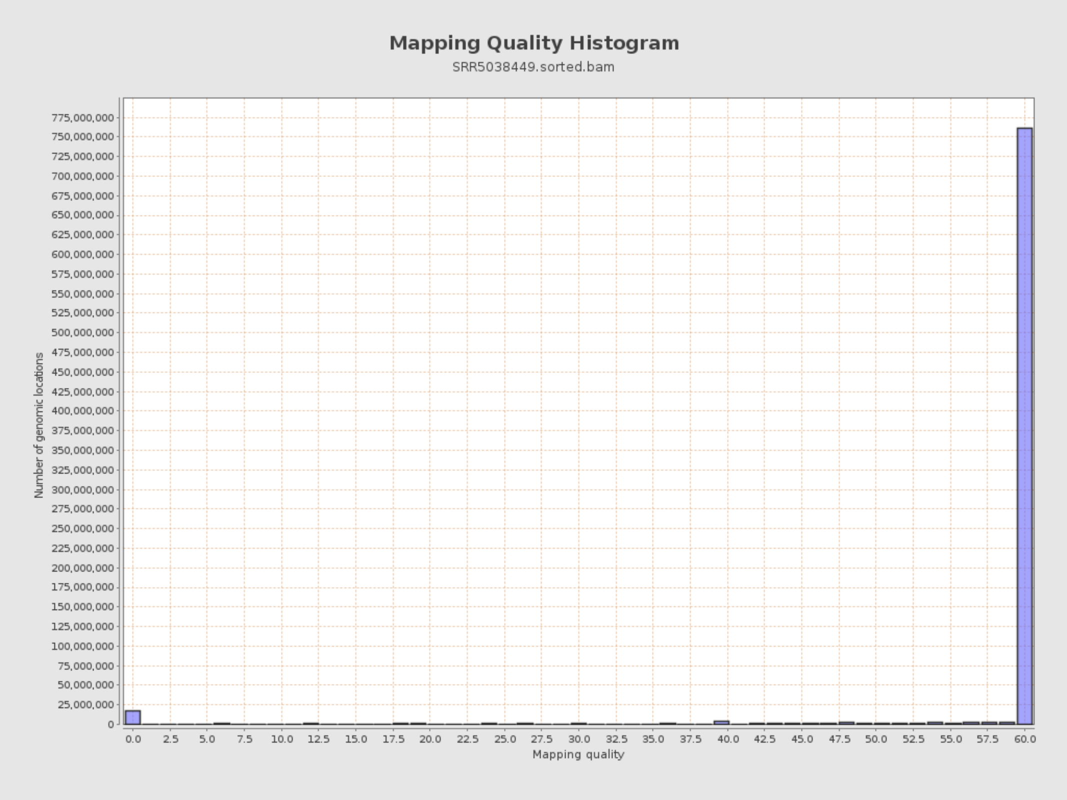
11. Results : Homopolymer Indels



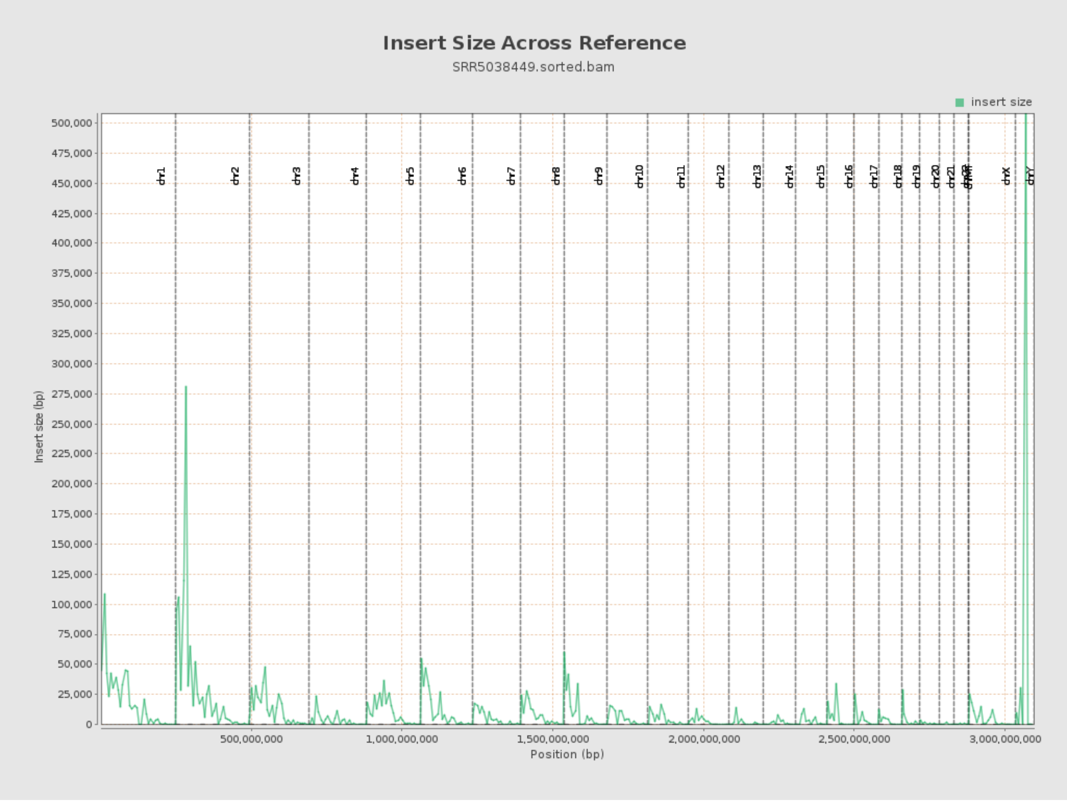
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram