Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 18:07:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038456.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_SRR5038456 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038456_1.fastq.gz SRR5038456_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 18:07:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038456.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,120,310
Mapped reads	13,668,611 / 90.4%
Unmapped reads	1,451,699 / 9.6%
Mapped paired reads	13,668,611 / 90.4%
Mapped reads, first in pair	6,950,891 / 45.97%
Mapped reads, second in pair	6,717,720 / 44.43%
Mapped reads, both in pair	13,392,864 / 88.58%
Mapped reads, singletons	275,747 / 1.82%
Secondary alignments	0
Supplementary alignments	154,716 / 1.02%
Read min/max/mean length	30 / 150 / 150.51
Duplicated reads (estimated)	2,602,012 / 17.21%
Duplication rate	14.19%
Clipped reads	6,052,415 / 40.03%

2.2. ACGT Content

Number/percentage of A's	517,477,738 / 27.89%
Number/percentage of C's	383,374,804 / 20.67%
Number/percentage of T's	523,629,410 / 28.23%
Number/percentage of G's	430,517,609 / 23.21%
Number/percentage of N's	147,314 / 0.01%

GC Percentage	43.87%

2.3. Coverage

Mean	0.5997
Standard Deviation	5.4284

2.4. Mapping Quality

Mean Mapping Quality	53.39

2.5. Insert size

Mean	96,162.74
Standard Deviation	3,065,437.76
P25/Median/P75	203 / 256 / 323

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	23,624,739
Insertions	292,176
Mapped reads with at least one insertion	2.03%
Deletions	653,571
Mapped reads with at least one deletion	4.62%
Homopolymer indels	48.19%

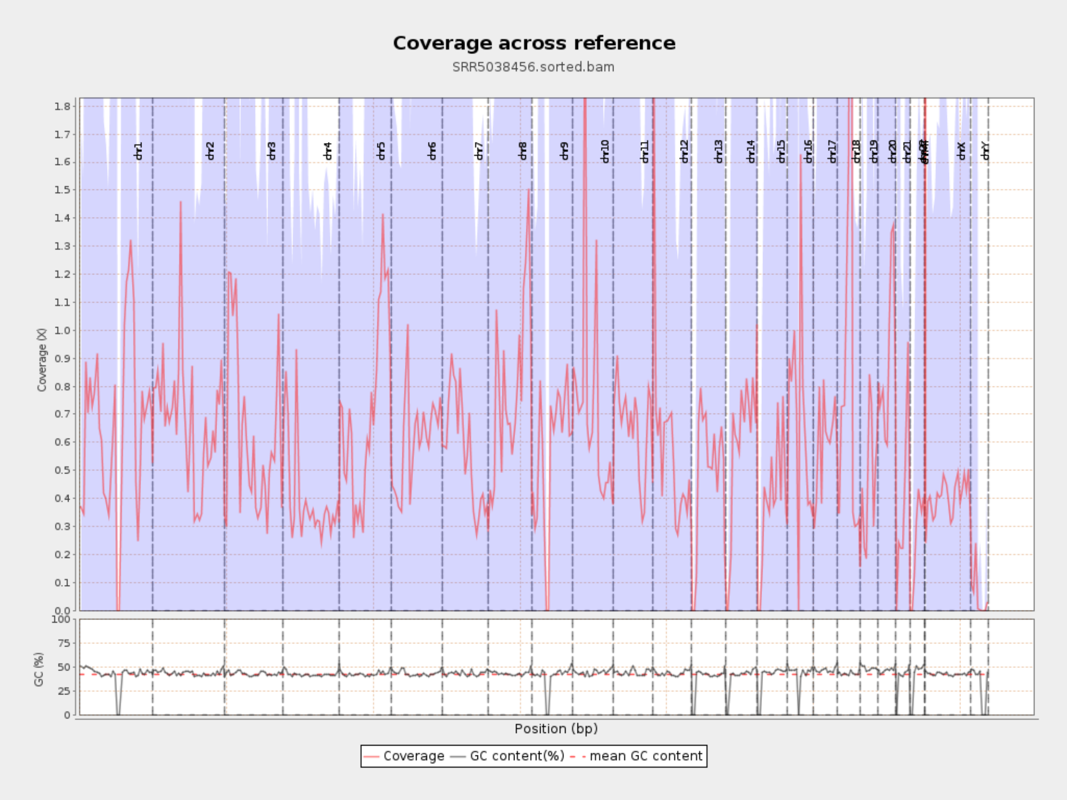
2.7. Chromosome stats

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

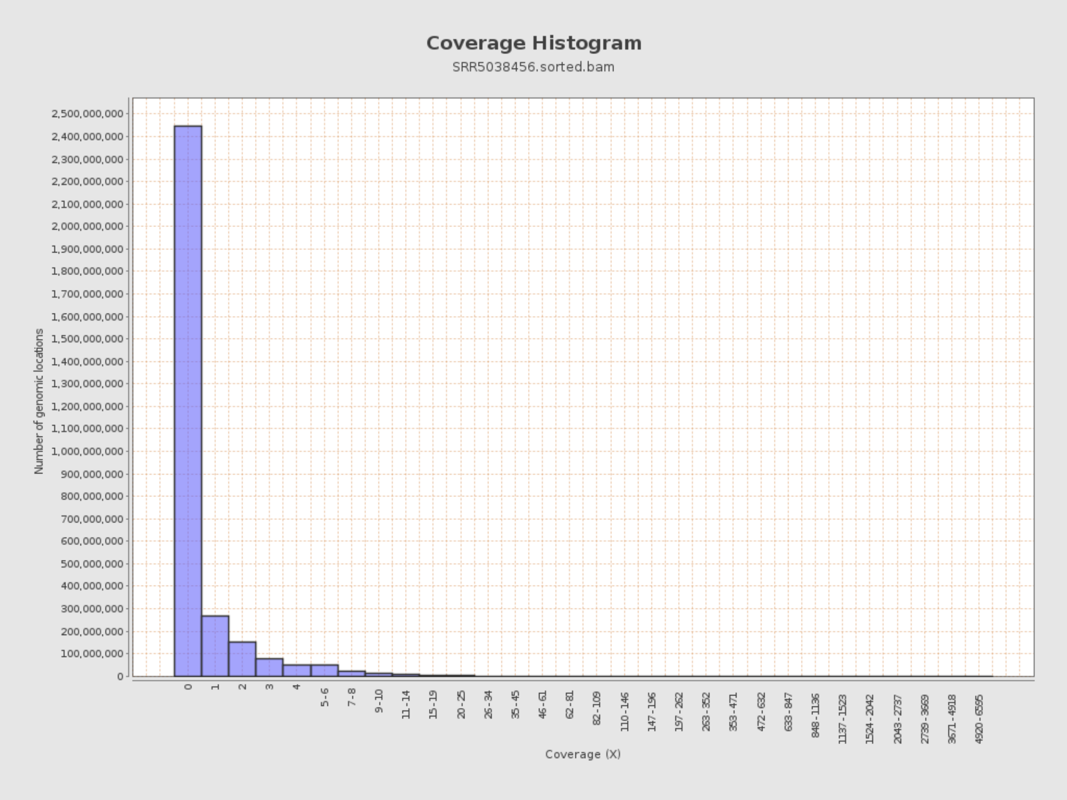
		bases	coverage	deviation
chr1	249250621	165073005	0.6623	4.0112
chr2	243199373	167097915	0.6871	6.552
chr3	198022430	125434986	0.6334	1.7616
chr4	191154276	76899779	0.4023	5.2434
chr5	180915260	127855577	0.7067	1.8667
chr6	171115067	105687848	0.6176	3.6819
chr7	159138663	91037981	0.5721	6.7619
chr8	146364022	117552338	0.8032	2.846
chr9	141213431	77887467	0.5516	8.2723
chr10	135534747	102852888	0.7589	15.1405
chr11	135006516	88288818	0.654	3.2703
chr12	133851895	79778964	0.596	1.8144
chr13	115169878	57273417	0.4973	1.4744
chr14	107349540	61896060	0.5766	1.66
chr15	102531392	40039895	0.3905	1.3209
chr16	90354753	60125822	0.6654	7.2927
chr17	81195210	48496289	0.5973	7.1141
chr18	78077248	79177082	1.0141	7.1277
chr19	59128983	26936683	0.4556	2.2551
chr20	63025520	57132881	0.9065	2.6911
chr21	48129895	19341312	0.4019	2.7276
chr22	51304566	13261585	0.2585	1.0876
chrMT	16571	1277666	77.1025	42.735
chrX	155270560	62794623	0.4044	1.5703

chrY	59373566	3152225	0.0531	5.0241

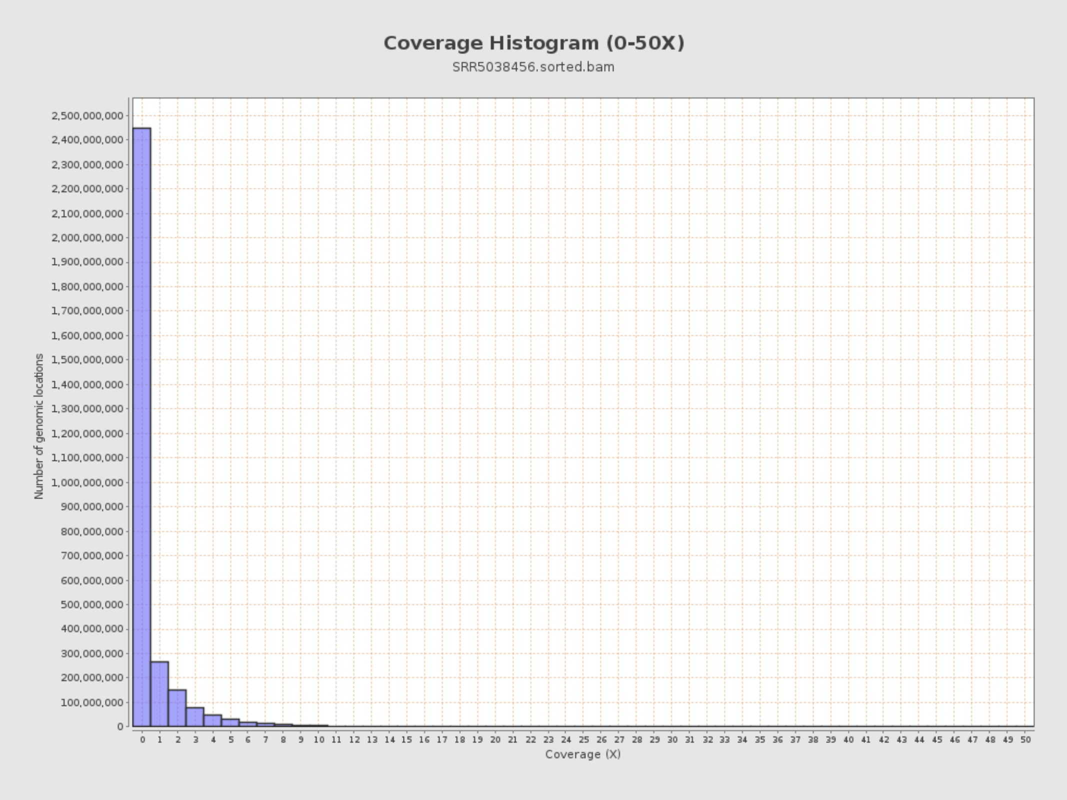
3. Results : Coverage across reference



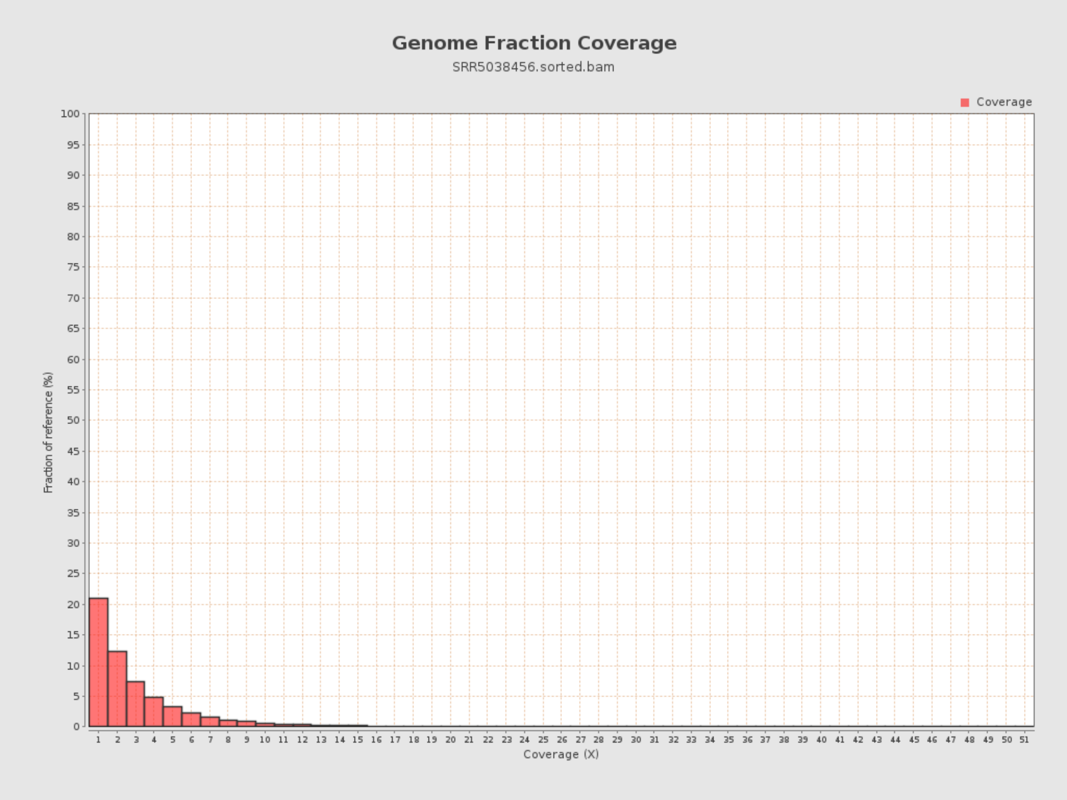
4. Results : Coverage Histogram



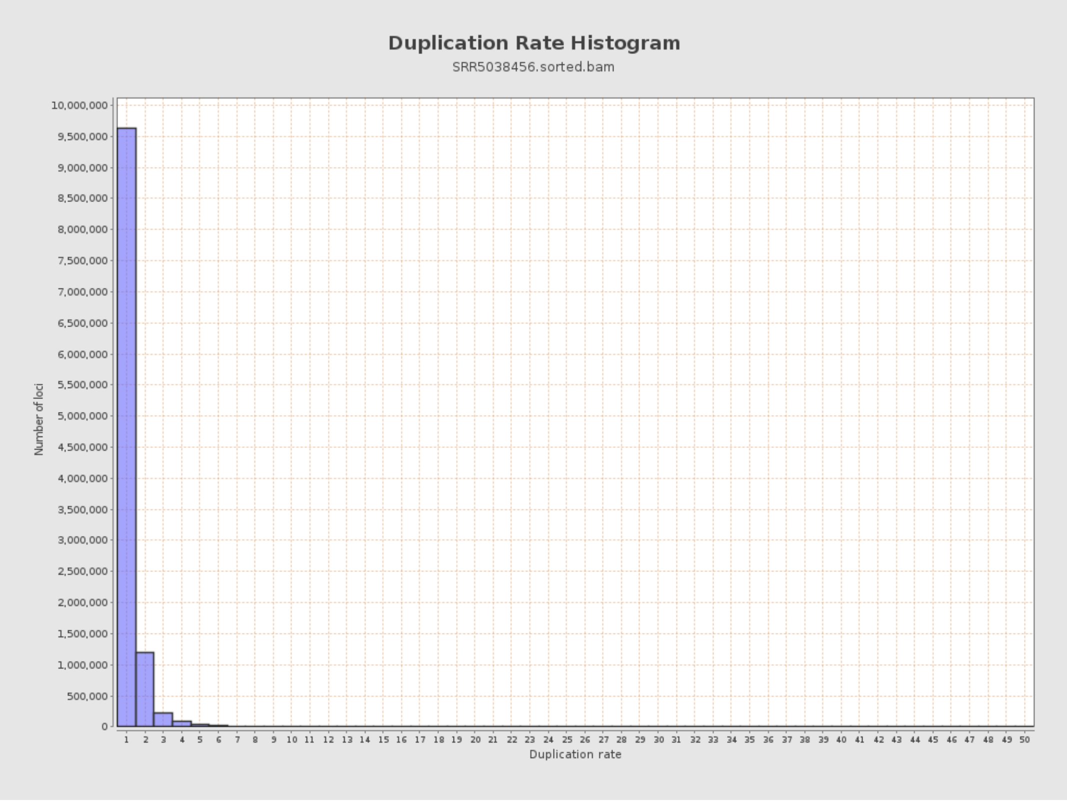
5. Results : Coverage Histogram (0-50X)



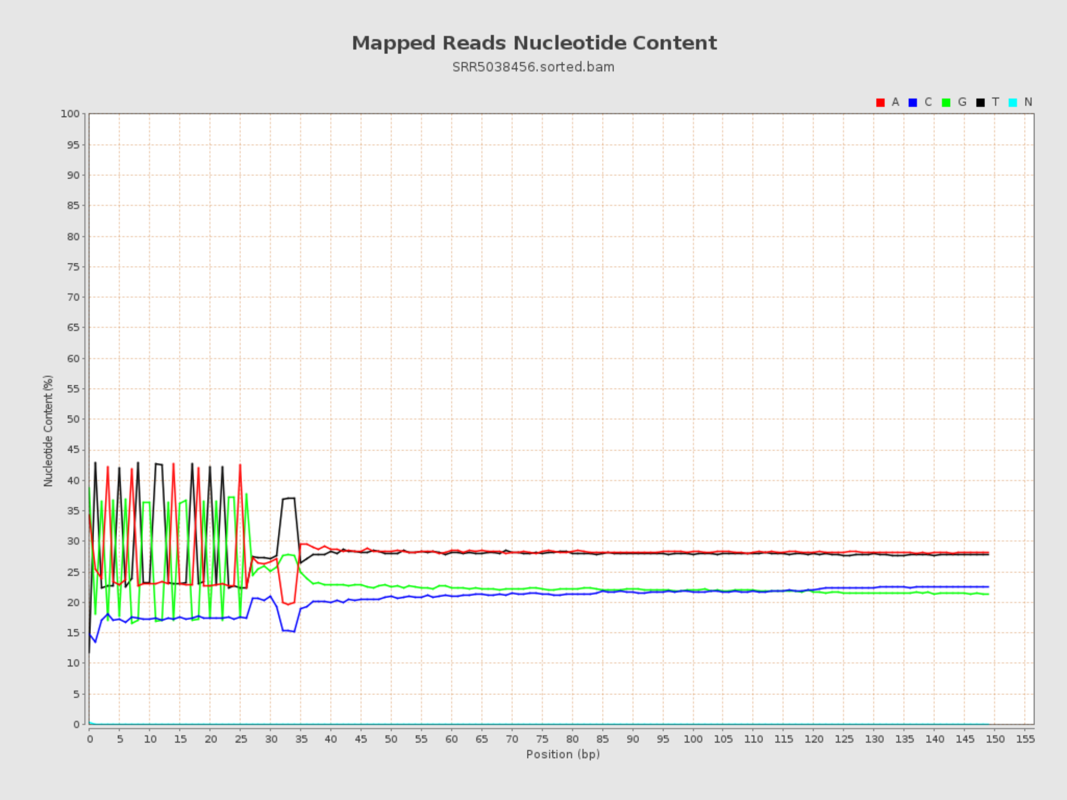
6. Results : Genome Fraction Coverage



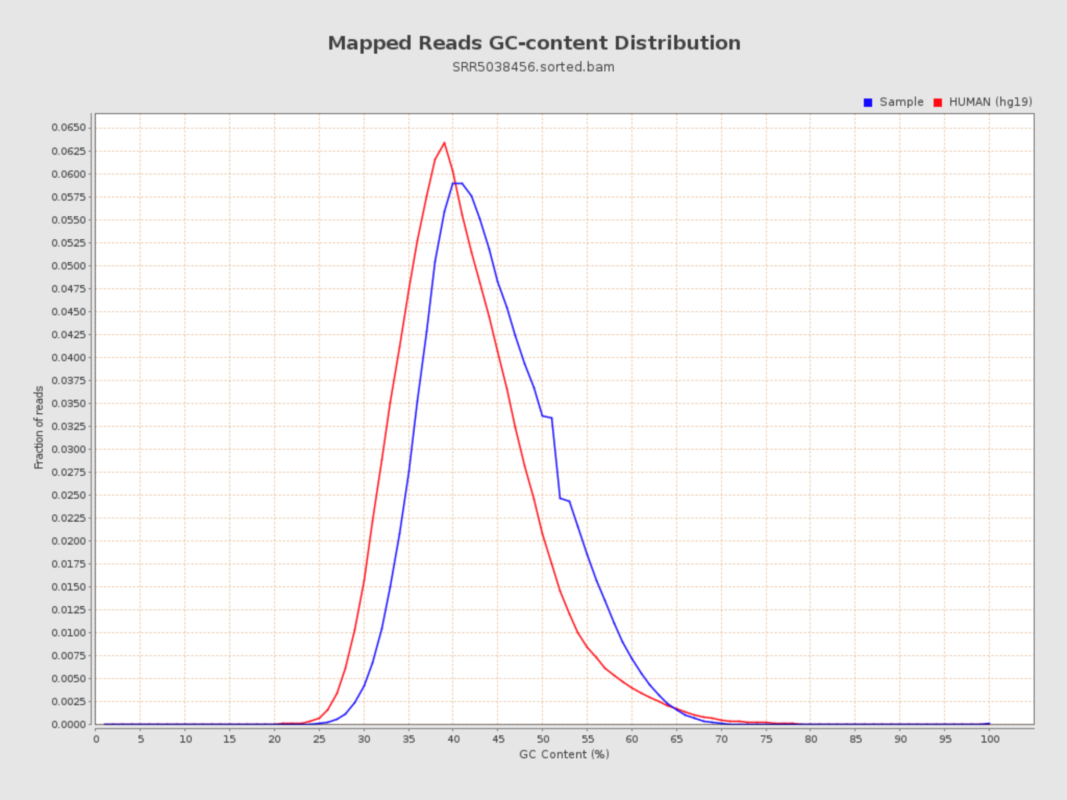
7. Results : Duplication Rate Histogram



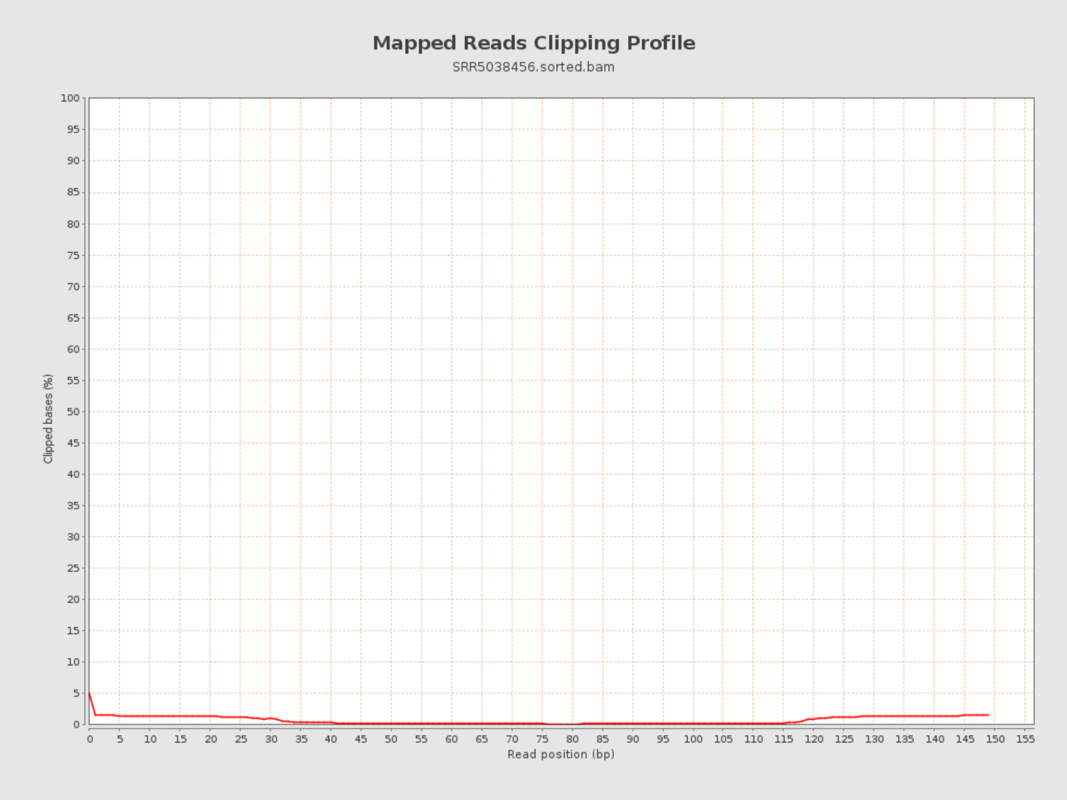
8. Results : Mapped Reads Nucleotide Content



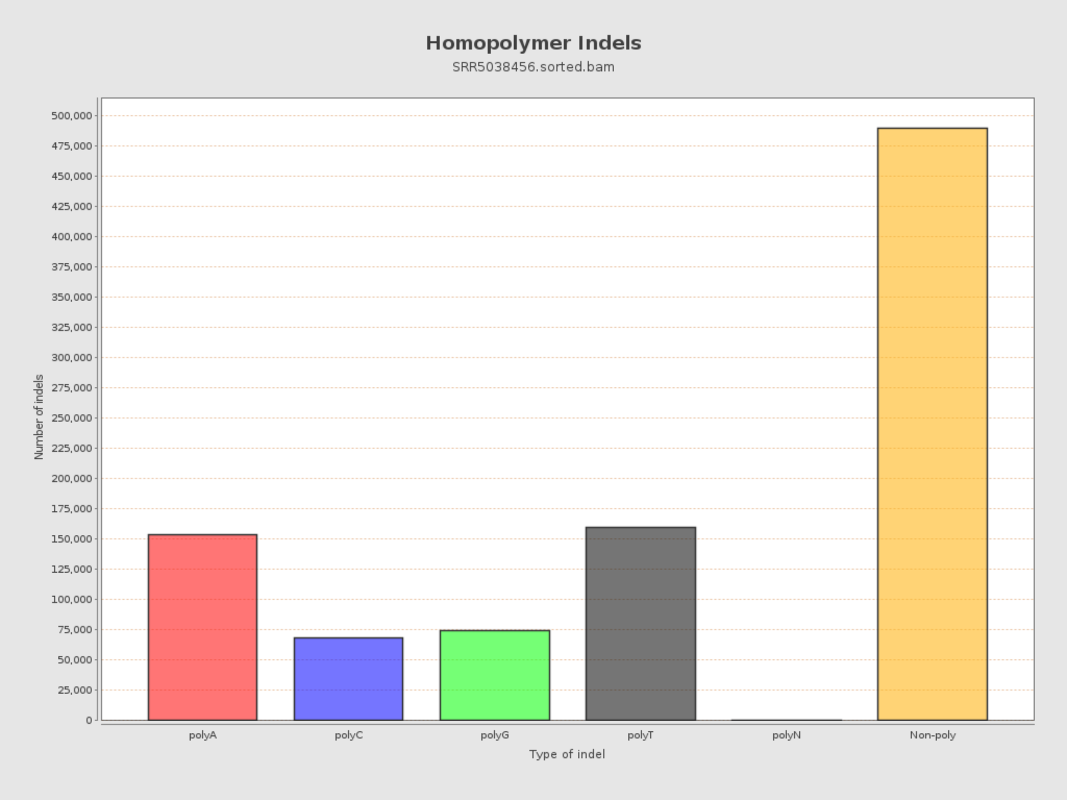
9. Results : Mapped Reads GC-content Distribution



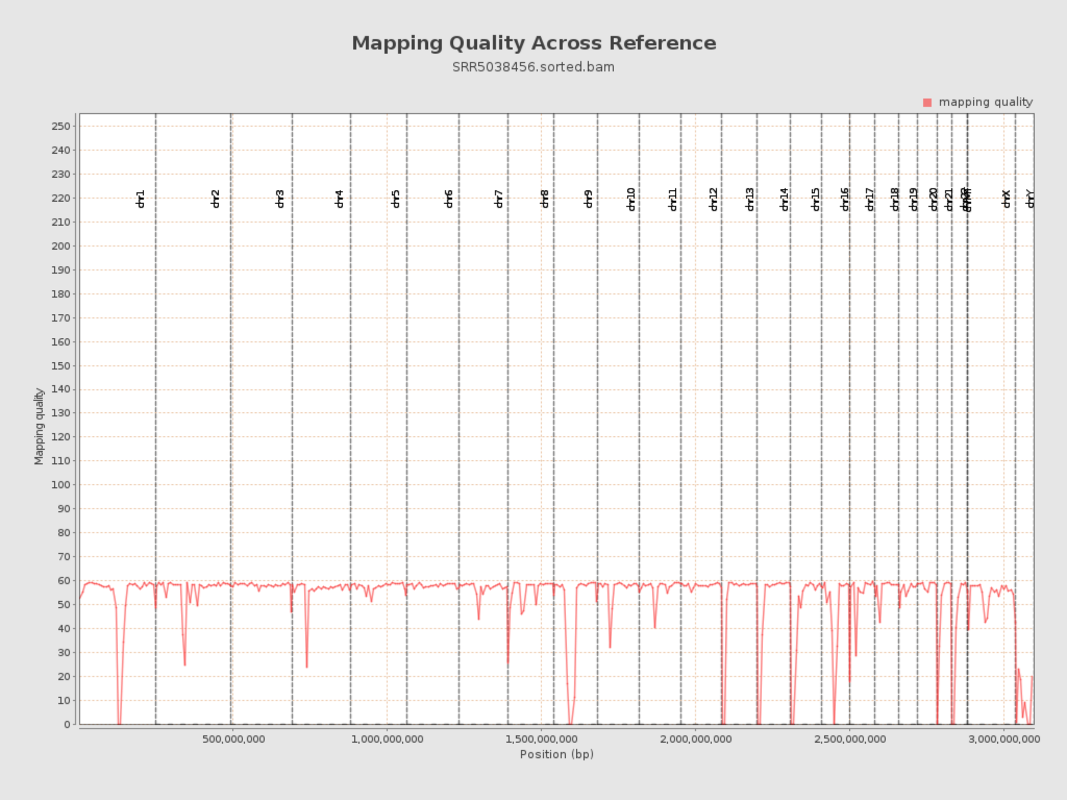
10. Results : Mapped Reads Clipping Profile



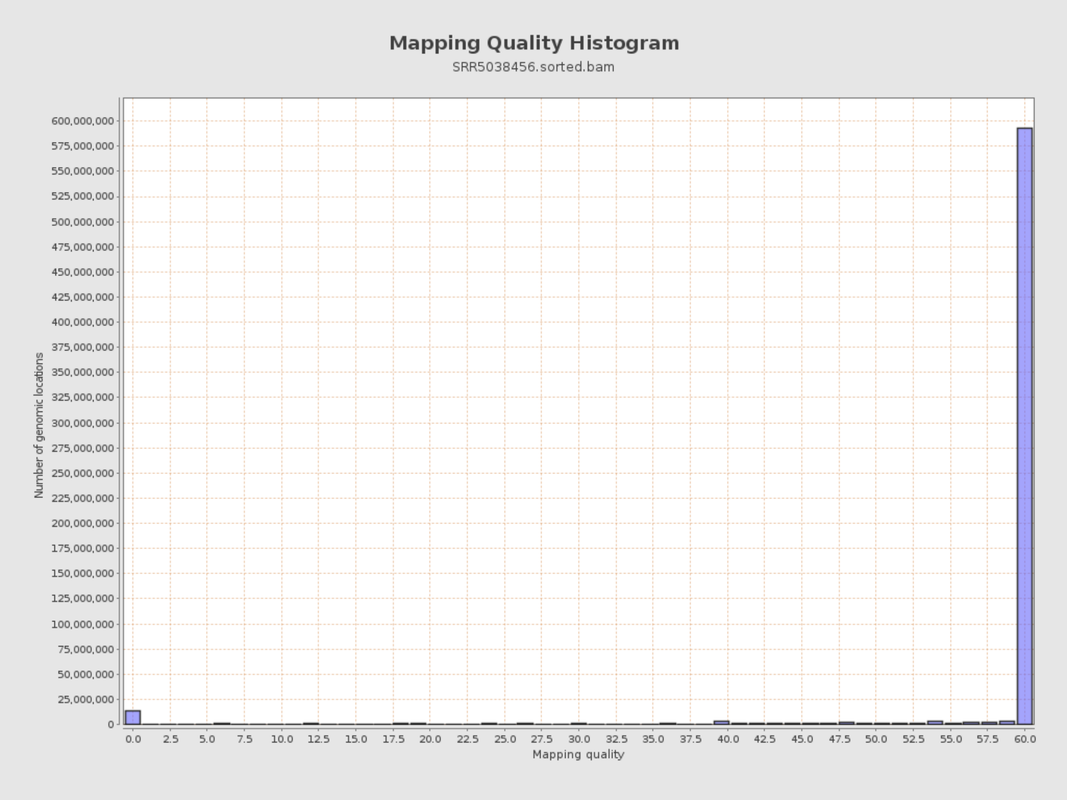
11. Results : Homopolymer Indels



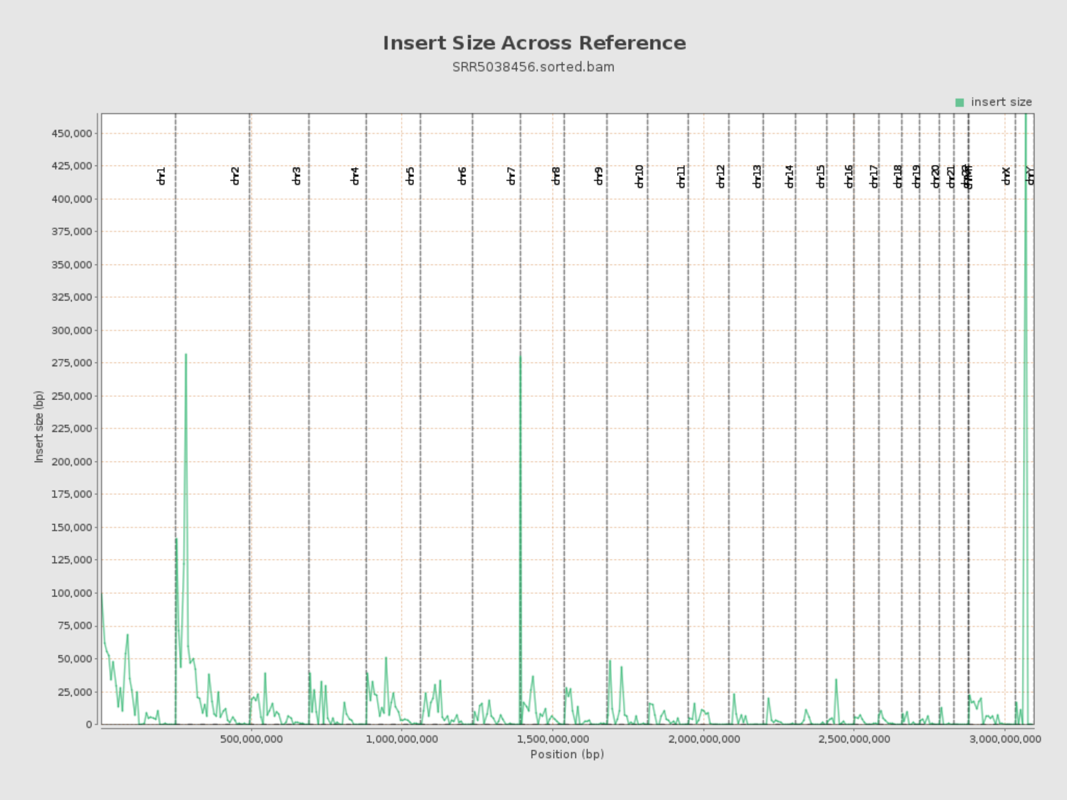
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram