Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 13:23:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038444.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_SRR5038444 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038444_1.fastq.gz SRR5038444_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 13:23:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038444.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,137,270
Mapped reads	19,449,225 / 96.58%
Unmapped reads	688,045 / 3.42%
Mapped paired reads	19,449,225 / 96.58%
Mapped reads, first in pair	9,851,097 / 48.92%
Mapped reads, second in pair	9,598,128 / 47.66%
Mapped reads, both in pair	19,151,432 / 95.1%
Mapped reads, singletons	297,793 / 1.48%
Secondary alignments	0
Supplementary alignments	272,526 / 1.35%
Read min/max/mean length	30 / 150 / 150.69
Duplicated reads (estimated)	3,999,833 / 19.86%
Duplication rate	14.41%
Clipped reads	8,409,547 / 41.76%

2.2. ACGT Content

Number/percentage of A's	751,019,330 / 28.32%
Number/percentage of C's	541,135,639 / 20.41%
Number/percentage of T's	761,459,313 / 28.71%
Number/percentage of G's	598,144,564 / 22.55%
Number/percentage of N's	213,072 / 0.01%

GC Percentage	42.96%

2.3. Coverage

Mean	0.8572
Standard Deviation	12.3232

2.4. Mapping Quality

Mean Mapping Quality	53.55

2.5. Insert size

Mean	78,937.26
Standard Deviation	2,737,205.69
P25/Median/P75	191 / 241 / 306

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	33,958,660
Insertions	434,964
Mapped reads with at least one insertion	2.13%
Deletions	925,749
Mapped reads with at least one deletion	4.59%
Homopolymer indels	47.58%

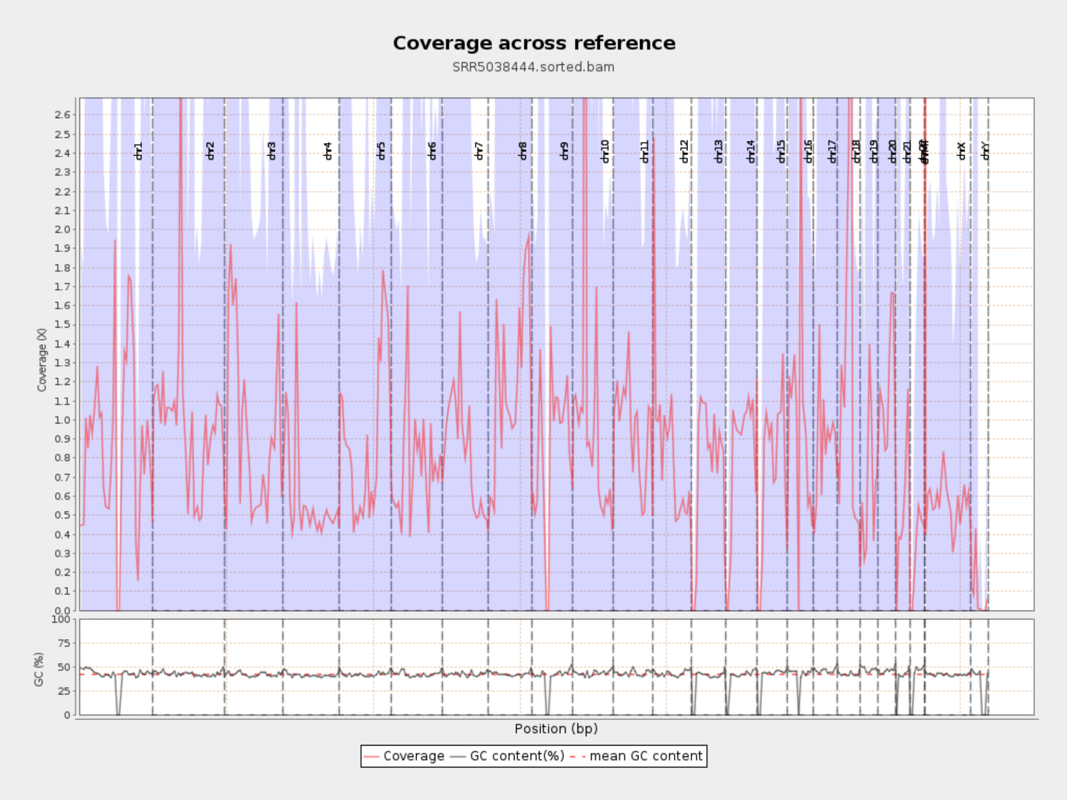
2.7. Chromosome stats

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

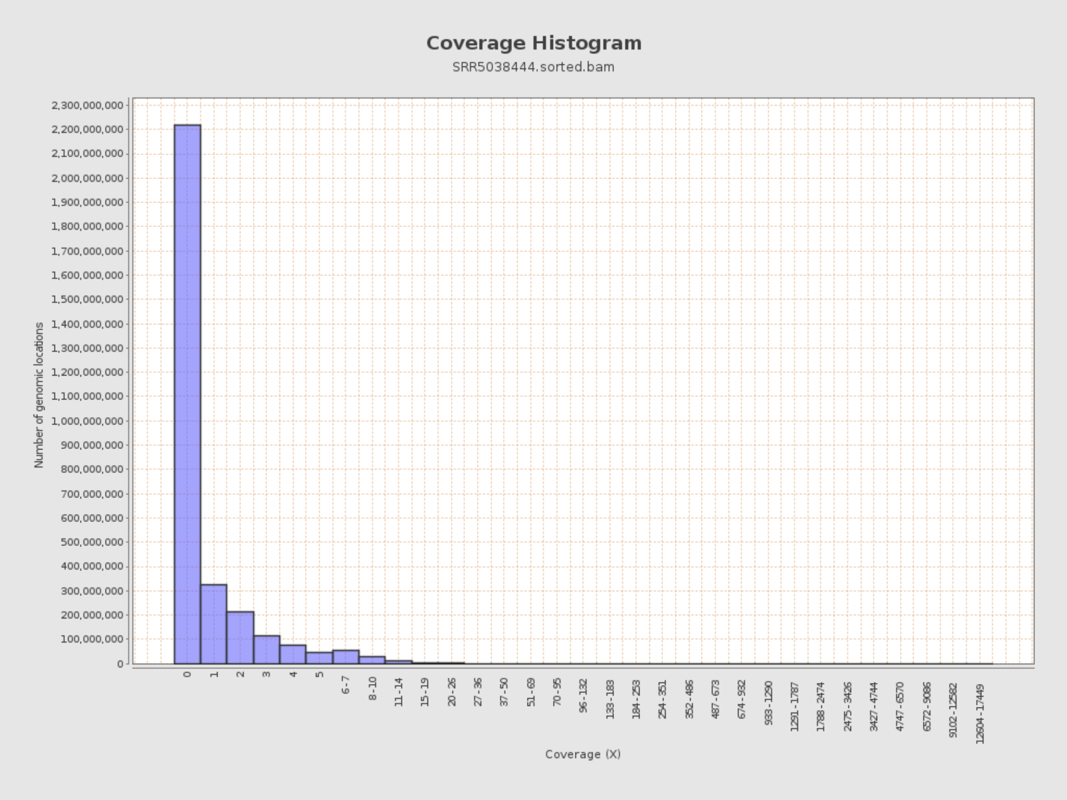
		bases	coverage	deviation
chr1	249250621	219994525	0.8826	17.3412
chr2	243199373	245009891	1.0074	12.8362
chr3	198022430	187606372	0.9474	2.2025
chr4	191154276	113185940	0.5921	9.2405
chr5	180915260	162547077	0.8985	1.969
chr6	171115067	132941333	0.7769	10.0173
chr7	159138663	132707039	0.8339	13.2864
chr8	146364022	176906656	1.2087	4.8313
chr9	141213431	117102918	0.8293	17.9414
chr10	135534747	148201428	1.0935	34.8048
chr11	135006516	128914991	0.9549	10.8926
chr12	133851895	113939755	0.8512	2.0748
chr13	115169878	88001710	0.7641	1.7611
chr14	107349540	86972827	0.8102	1.9327
chr15	102531392	75260216	0.734	1.7778
chr16	90354753	89858670	0.9945	13.6225
chr17	81195210	70553900	0.8689	15.3937
chr18	78077248	109957771	1.4083	12.3075
chr19	59128983	37741334	0.6383	7.1849
chr20	63025520	74504500	1.1821	3.6322
chr21	48129895	26750523	0.5558	4.2802
chr22	51304566	16684219	0.3252	1.158
chrMT	16571	5666363	341.9445	174.4757
chrX	155270560	87526864	0.5637	2.7526

chrY	59373566	5207290	0.0877	8.8758

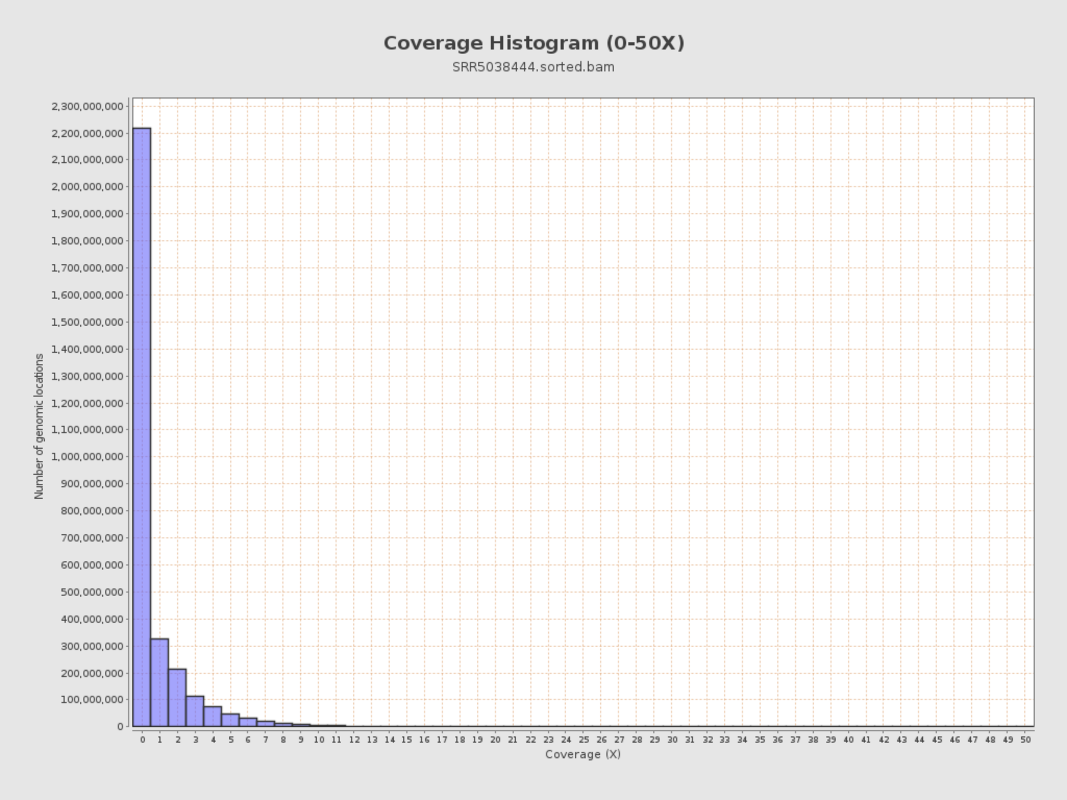
3. Results : Coverage across reference



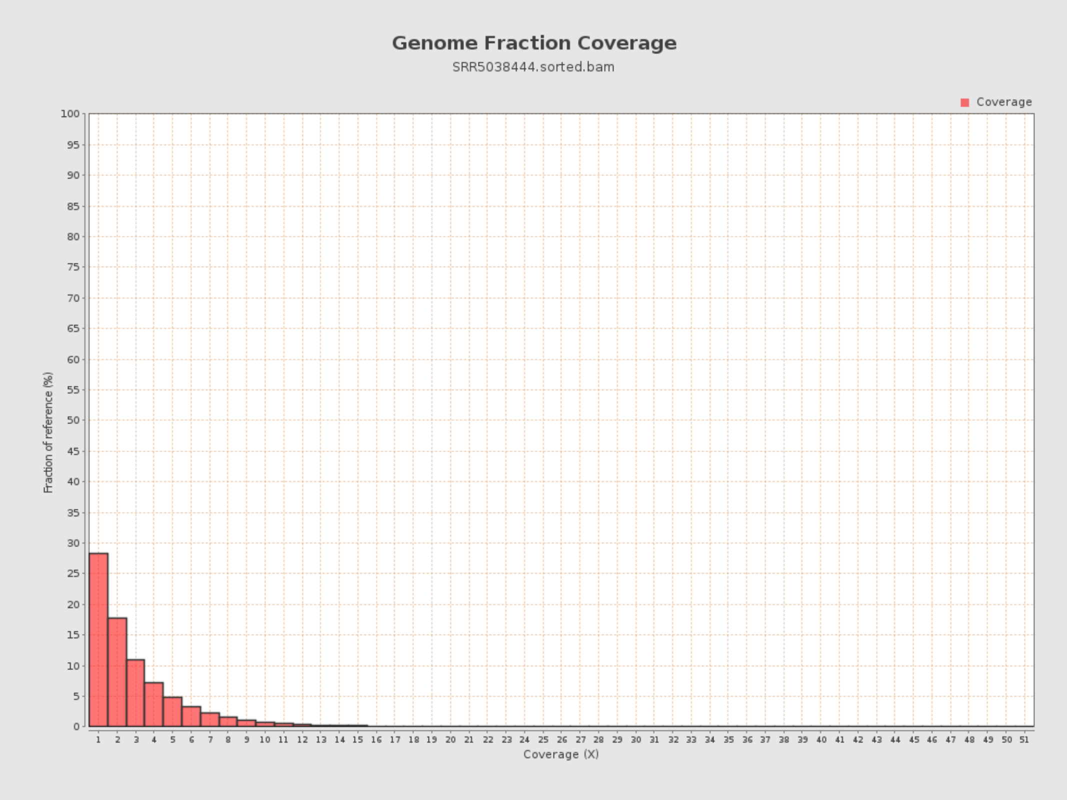
4. Results : Coverage Histogram



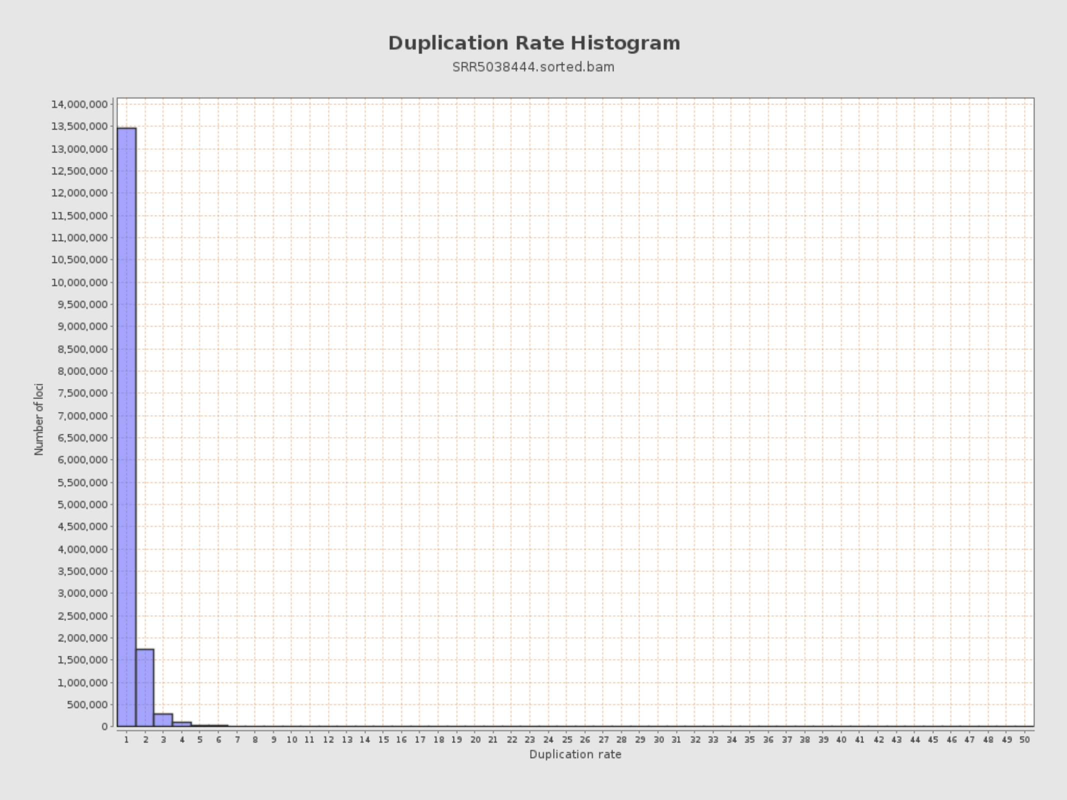
5. Results : Coverage Histogram (0-50X)



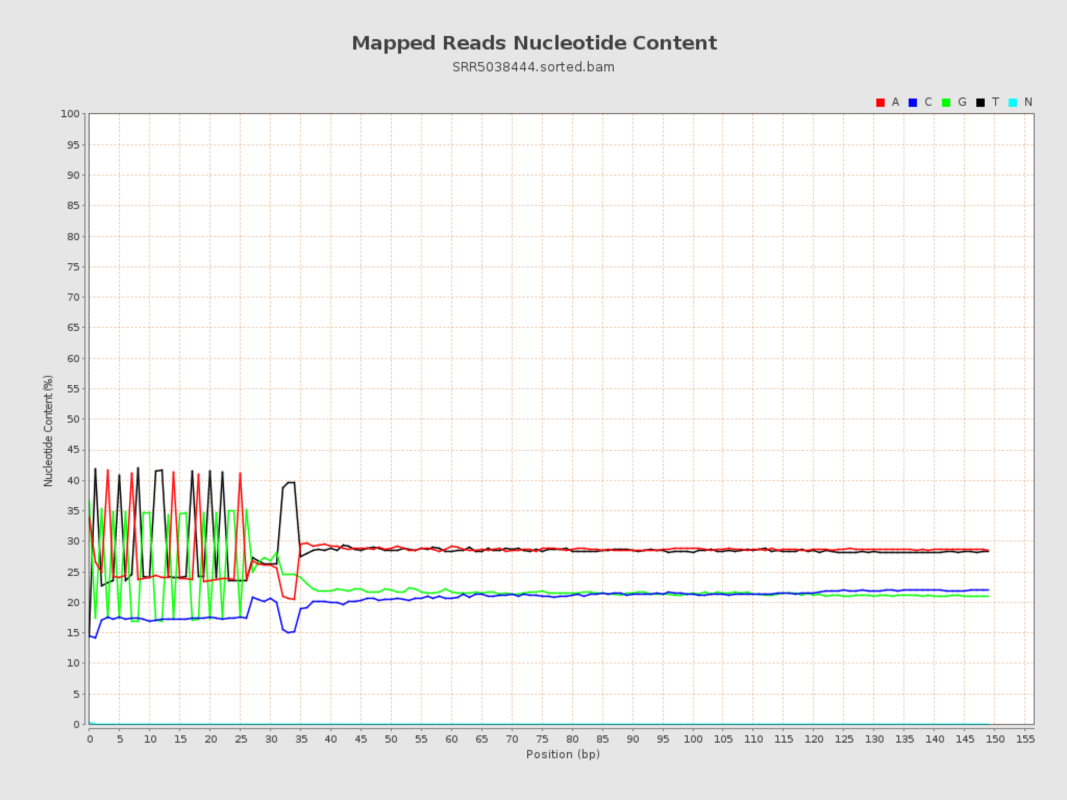
6. Results : Genome Fraction Coverage



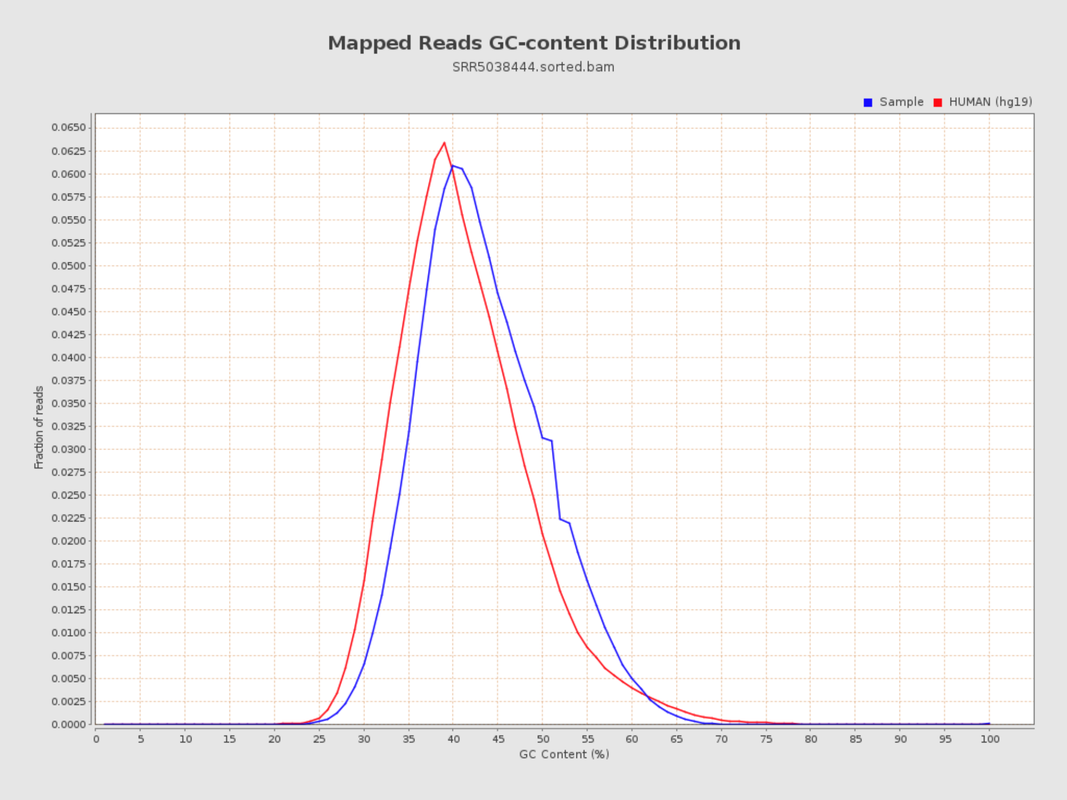
7. Results : Duplication Rate Histogram



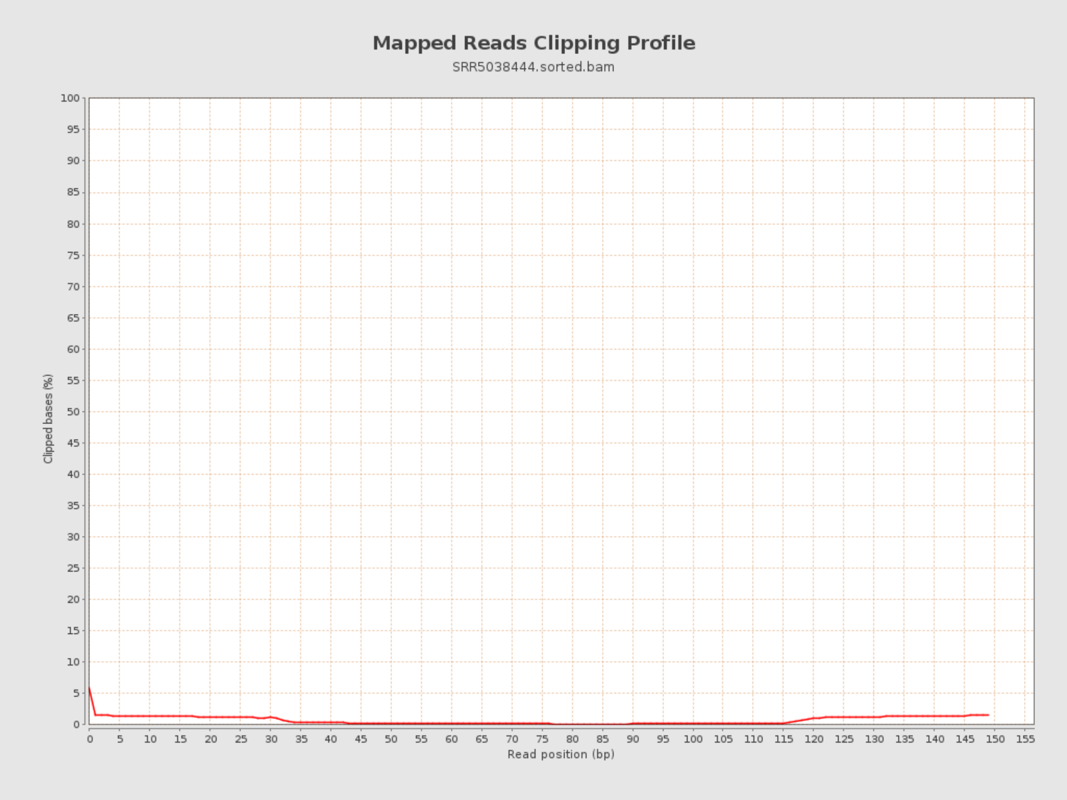
8. Results : Mapped Reads Nucleotide Content



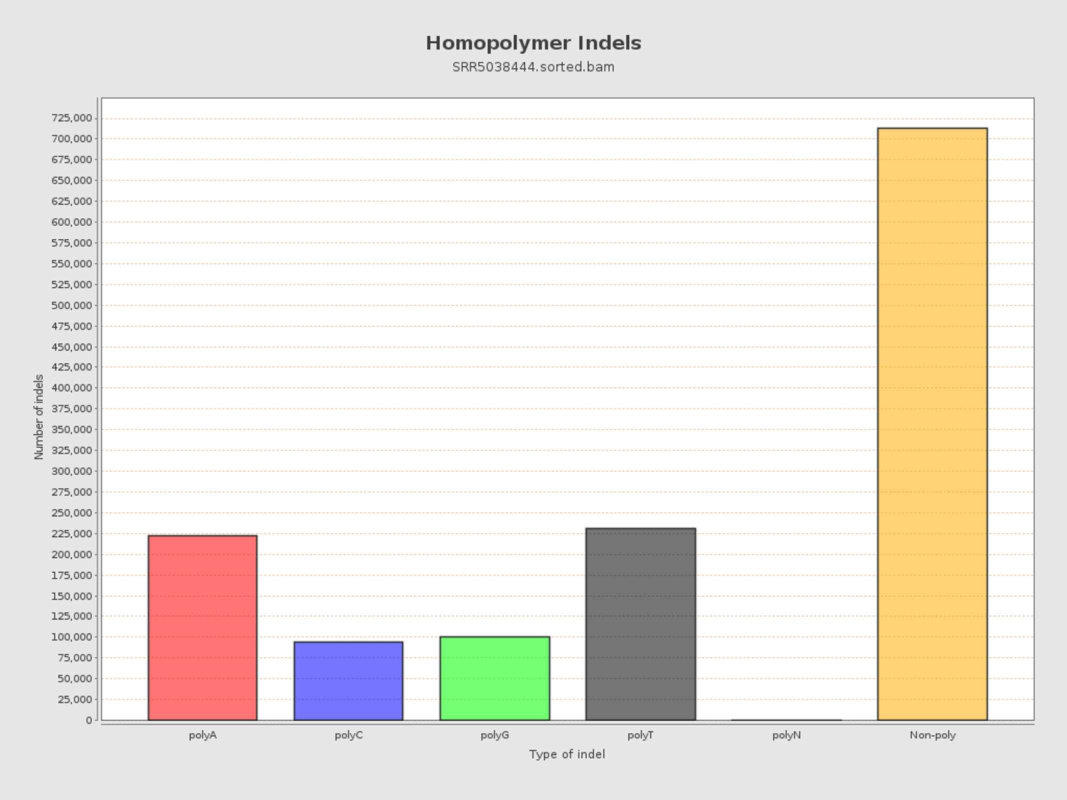
9. Results : Mapped Reads GC-content Distribution



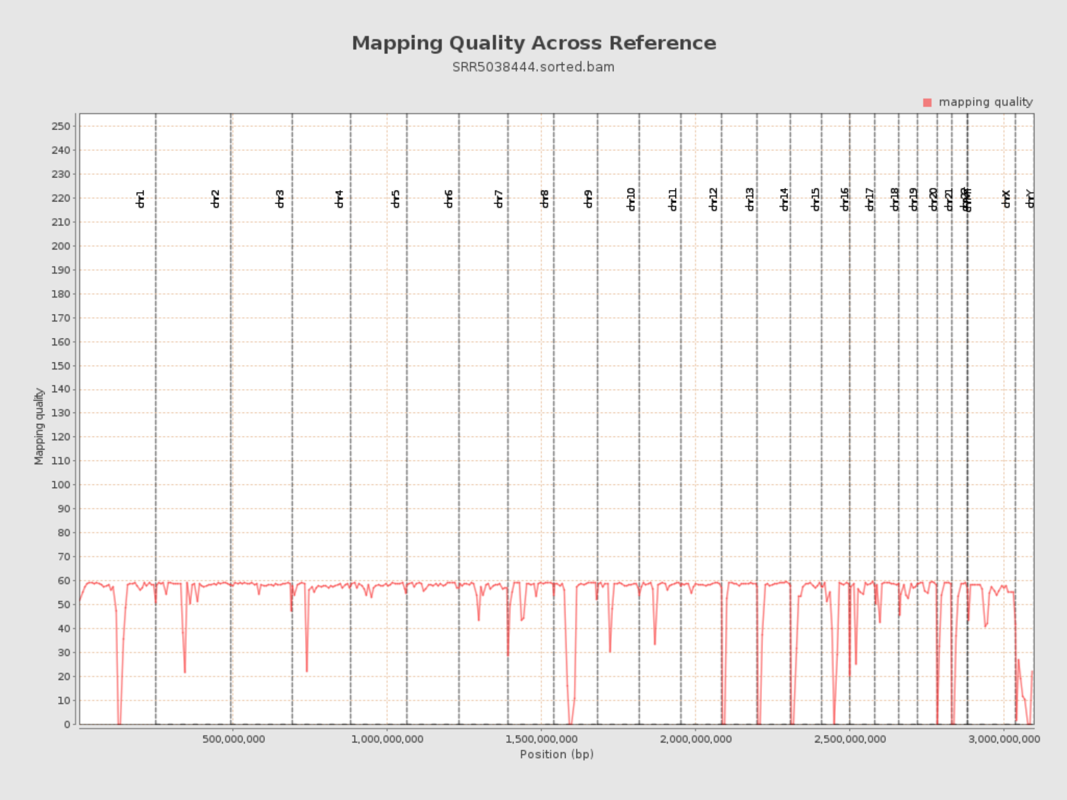
10. Results : Mapped Reads Clipping Profile



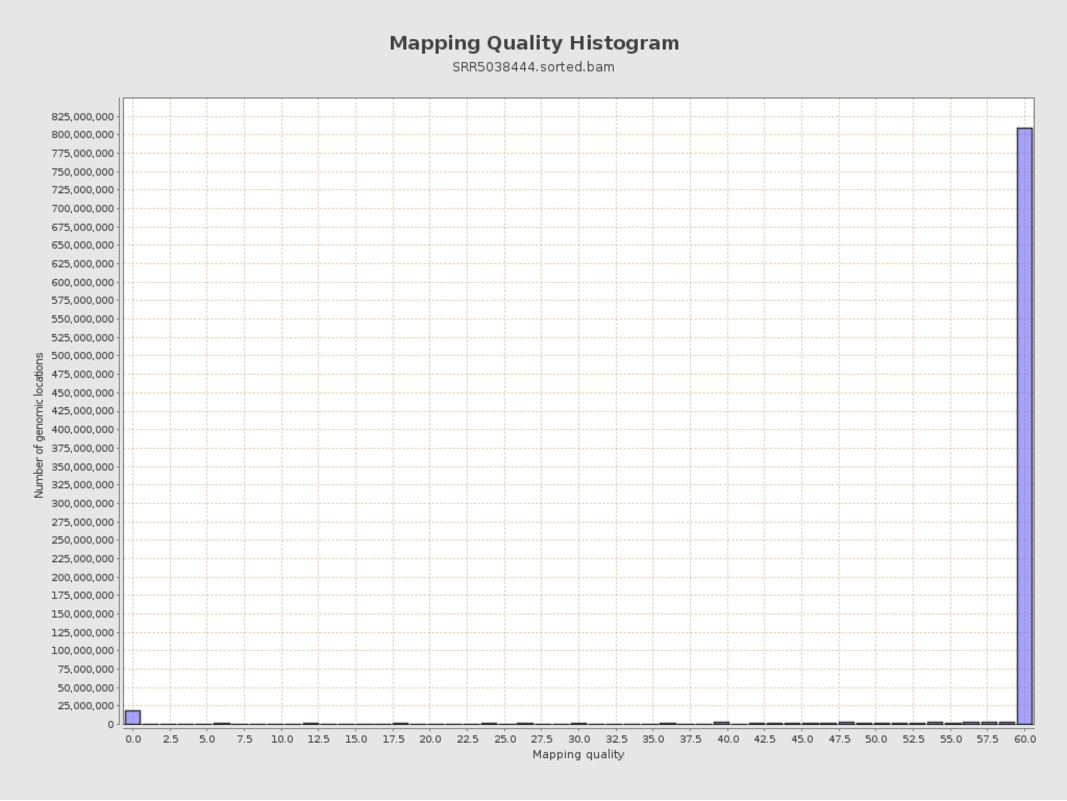
11. Results : Homopolymer Indels



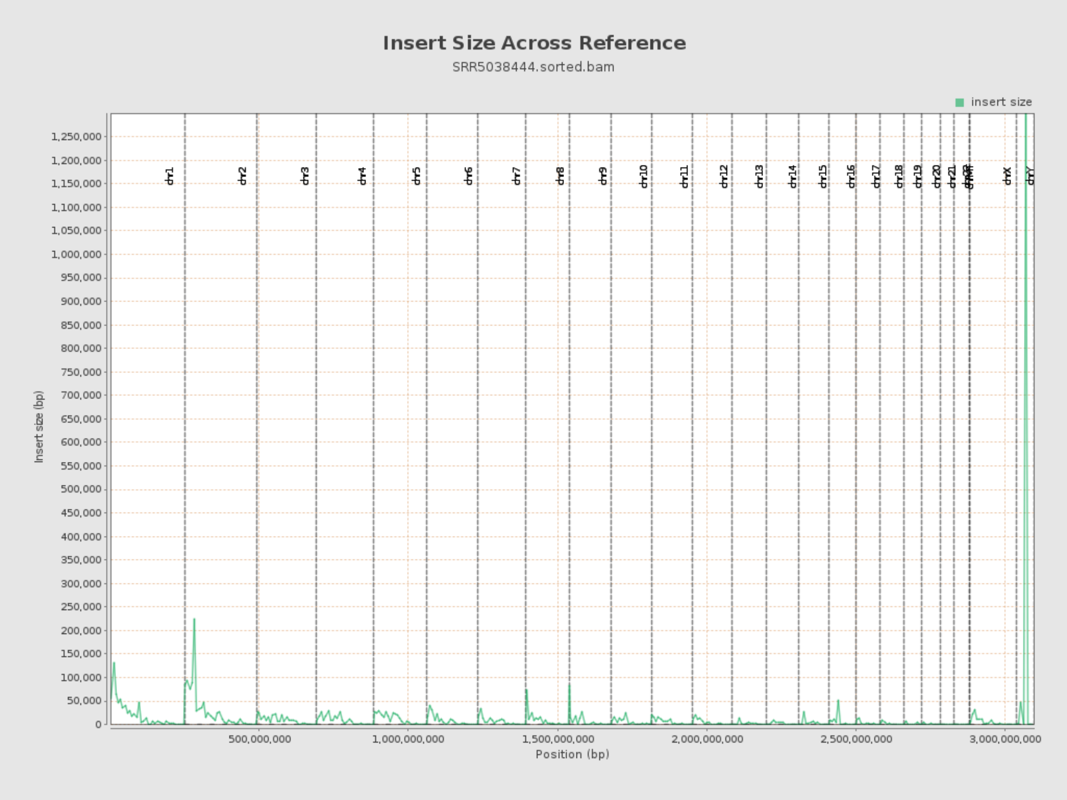
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram