Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 03:54:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038475.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_SRR5038475 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038475_1.fastq.gz SRR5038475_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 03:54:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038475.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,088,896
Mapped reads	14,718,047 / 97.54%
Unmapped reads	370,849 / 2.46%
Mapped paired reads	14,718,047 / 97.54%
Mapped reads, first in pair	7,433,003 / 49.26%
Mapped reads, second in pair	7,285,044 / 48.28%
Mapped reads, both in pair	14,552,902 / 96.45%
Mapped reads, singletons	165,145 / 1.09%
Secondary alignments	0
Supplementary alignments	166,307 / 1.1%
Read min/max/mean length	30 / 150 / 150.57
Duplicated reads (estimated)	1,557,322 / 10.32%
Duplication rate	7.67%
Clipped reads	1,726,055 / 11.44%

2.2. ACGT Content

Number/percentage of A's	630,143,534 / 29.16%
Number/percentage of C's	454,206,328 / 21.02%
Number/percentage of T's	623,703,729 / 28.86%
Number/percentage of G's	452,821,790 / 20.96%
Number/percentage of N's	48,334 / 0%

GC Percentage	41.97%

2.3. Coverage

Mean	0.6983
Standard Deviation	7.2285

2.4. Mapping Quality

Mean Mapping Quality	54.39

2.5. Insert size

Mean	102,426.9
Standard Deviation	3,204,894.22
P25/Median/P75	214 / 262 / 328

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	23,338,003
Insertions	281,216
Mapped reads with at least one insertion	1.79%
Deletions	292,750
Mapped reads with at least one deletion	1.9%
Homopolymer indels	44.35%

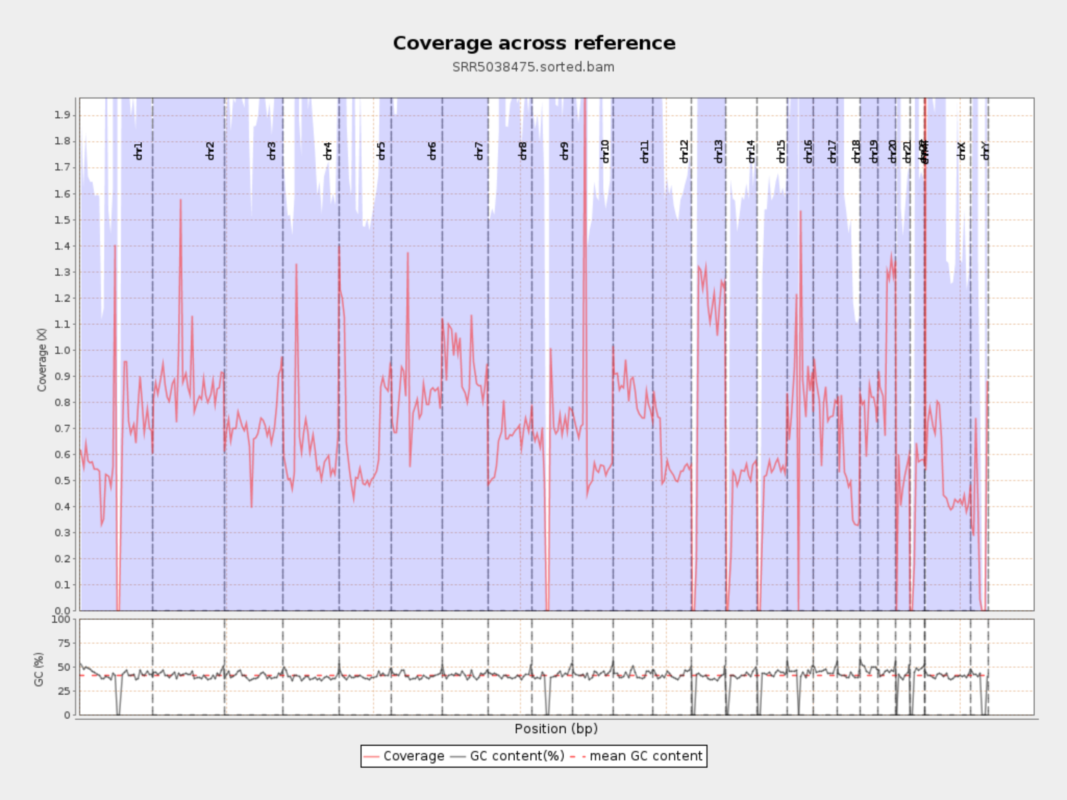
2.7. Chromosome stats

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

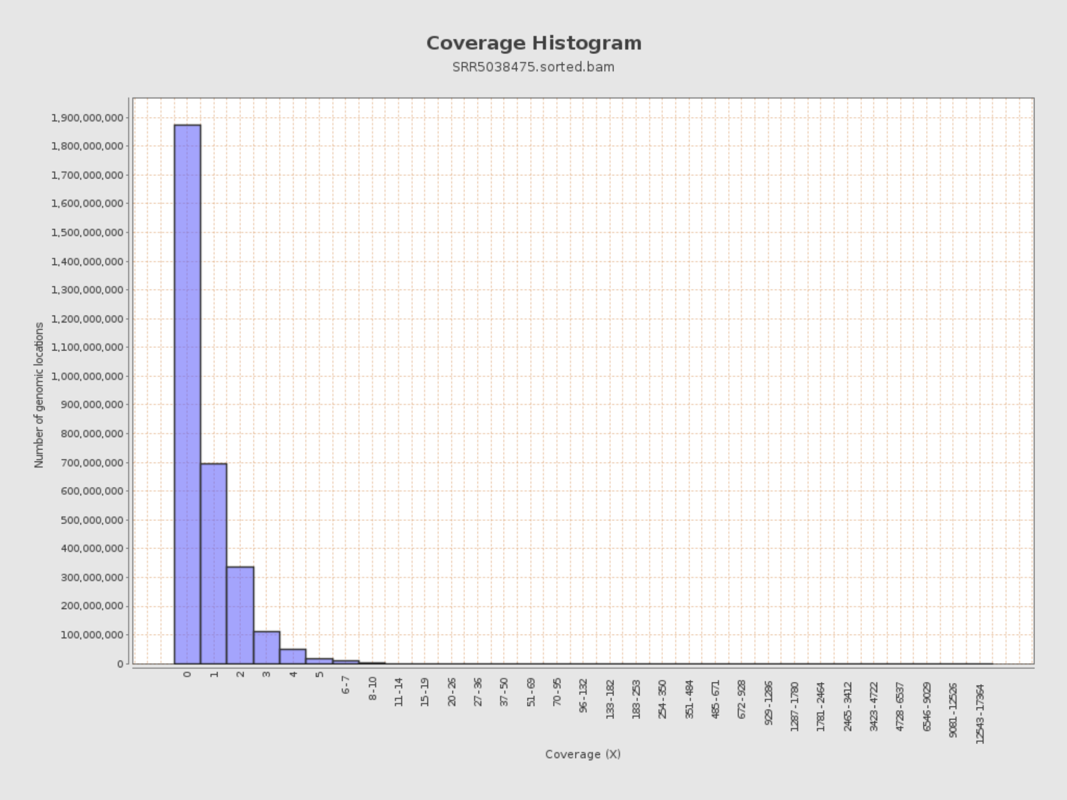
		bases	coverage	deviation
chr1	249250621	155288659	0.623	17.658
chr2	243199373	214664284	0.8827	5.7996
chr3	198022430	139760135	0.7058	1.0977
chr4	191154276	117256888	0.6134	6.1922
chr5	180915260	124404453	0.6876	1.1661
chr6	171115067	139895142	0.8176	6.3016
chr7	159138663	150557480	0.9461	5.6627
chr8	146364022	95739727	0.6541	4.7999
chr9	141213431	89122005	0.6311	8.1933
chr10	135534747	90604446	0.6685	12.6764
chr11	135006516	113091376	0.8377	4.3359
chr12	133851895	78329265	0.5852	1.0239
chr13	115169878	116732289	1.0136	1.3505
chr14	107349540	47145146	0.4392	0.9483
chr15	102531392	45925317	0.4479	0.8694
chr16	90354753	77086732	0.8532	5.6469
chr17	81195210	63911121	0.7871	3.3609
chr18	78077248	38393977	0.4917	8.0392
chr19	59128983	46186560	0.7811	7.9709
chr20	63025520	68013687	1.0791	2.4306
chr21	48129895	22746788	0.4726	3.2814
chr22	51304566	20834764	0.4061	2.1646
chrMT	16571	3479900	209.9994	26.3668
chrX	155270560	82496461	0.5313	1.3878

chrY	59373566	20073735	0.3381	7.7812

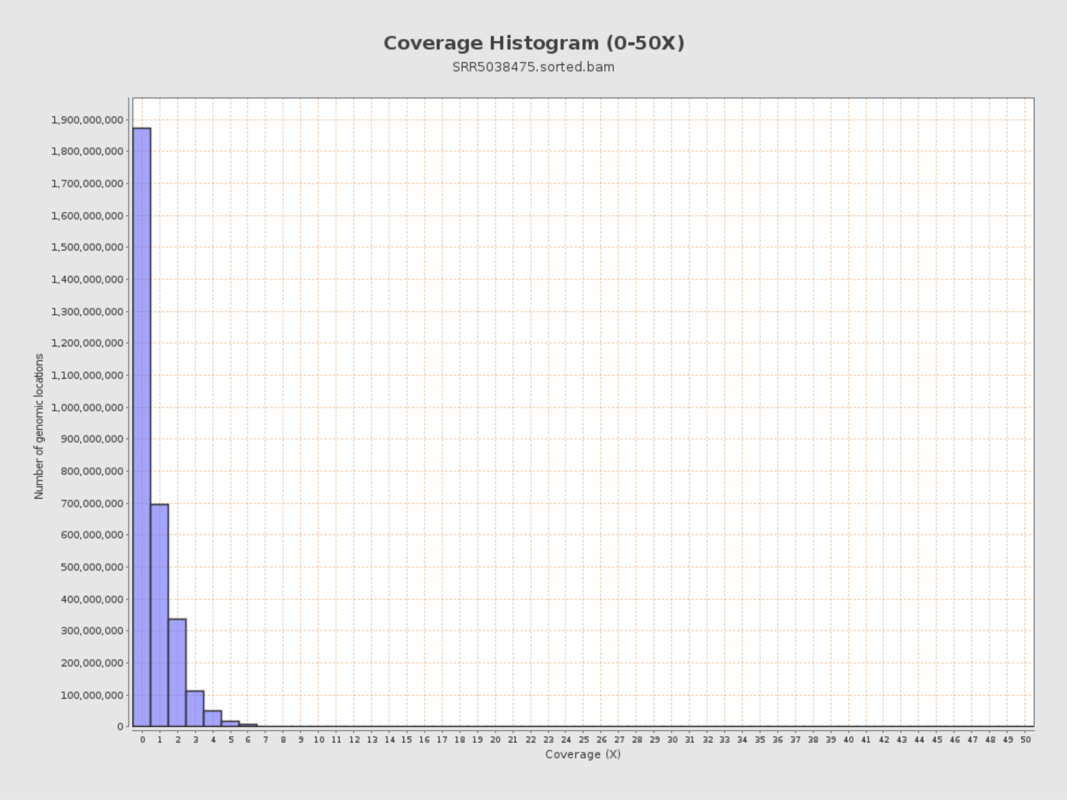
3. Results : Coverage across reference



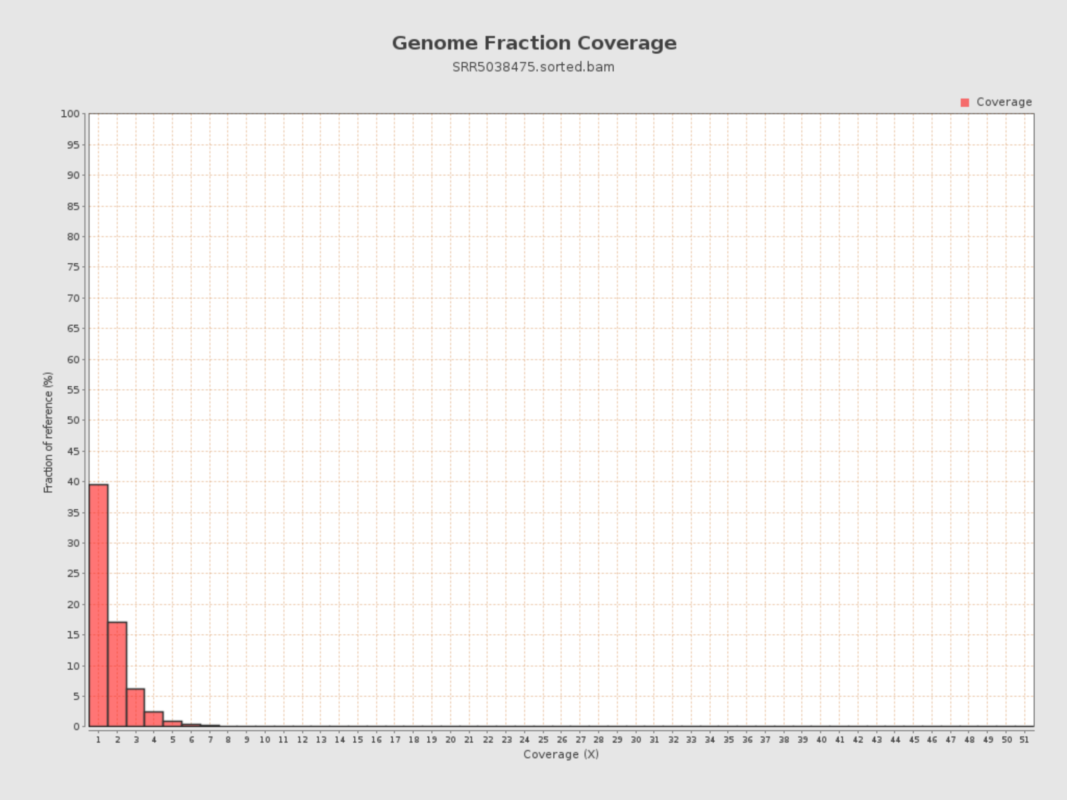
4. Results : Coverage Histogram



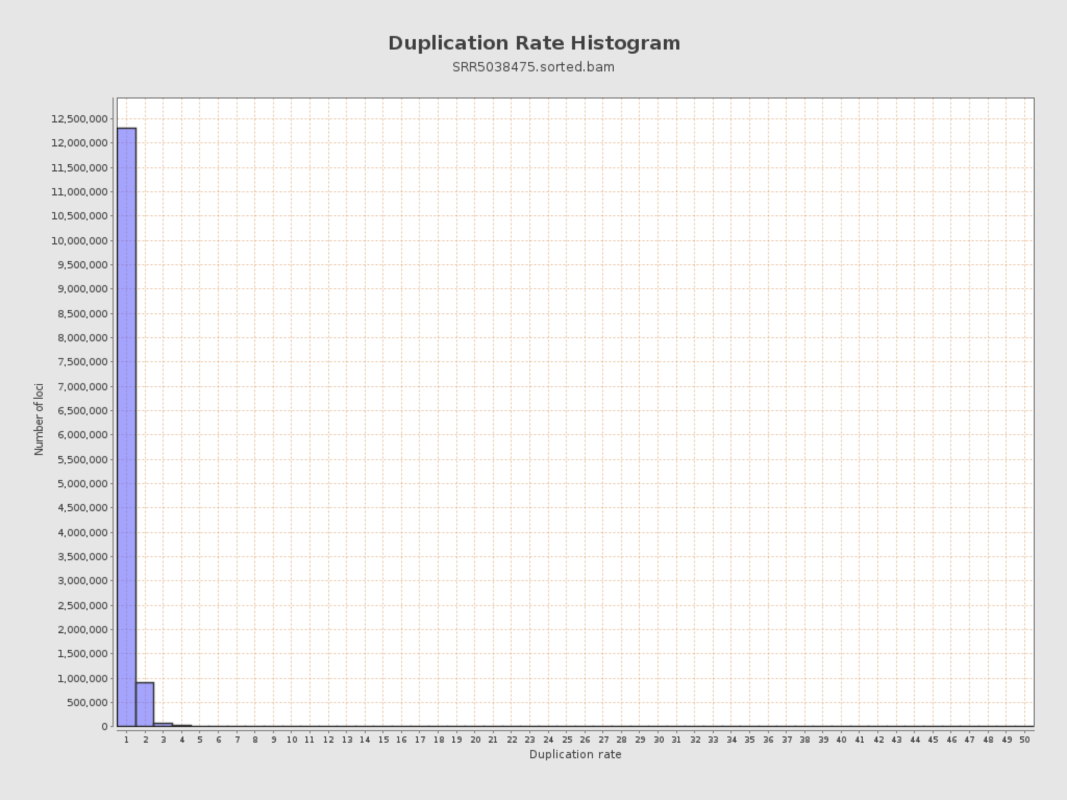
5. Results : Coverage Histogram (0-50X)



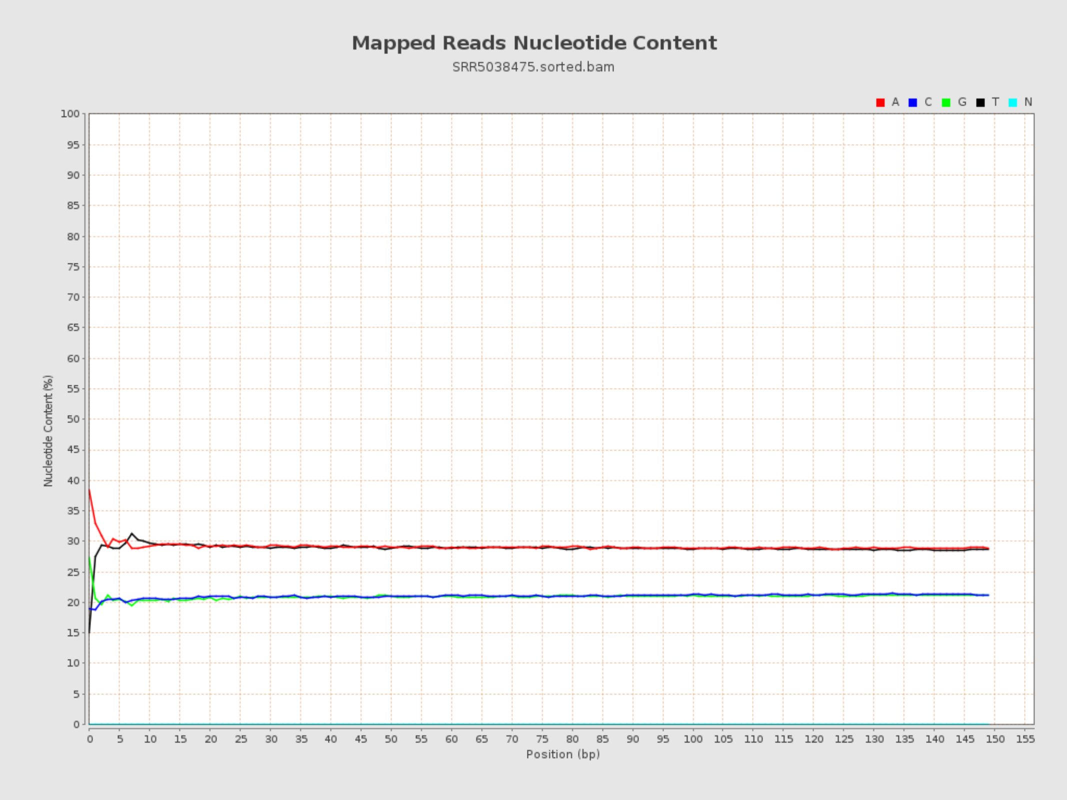
6. Results : Genome Fraction Coverage



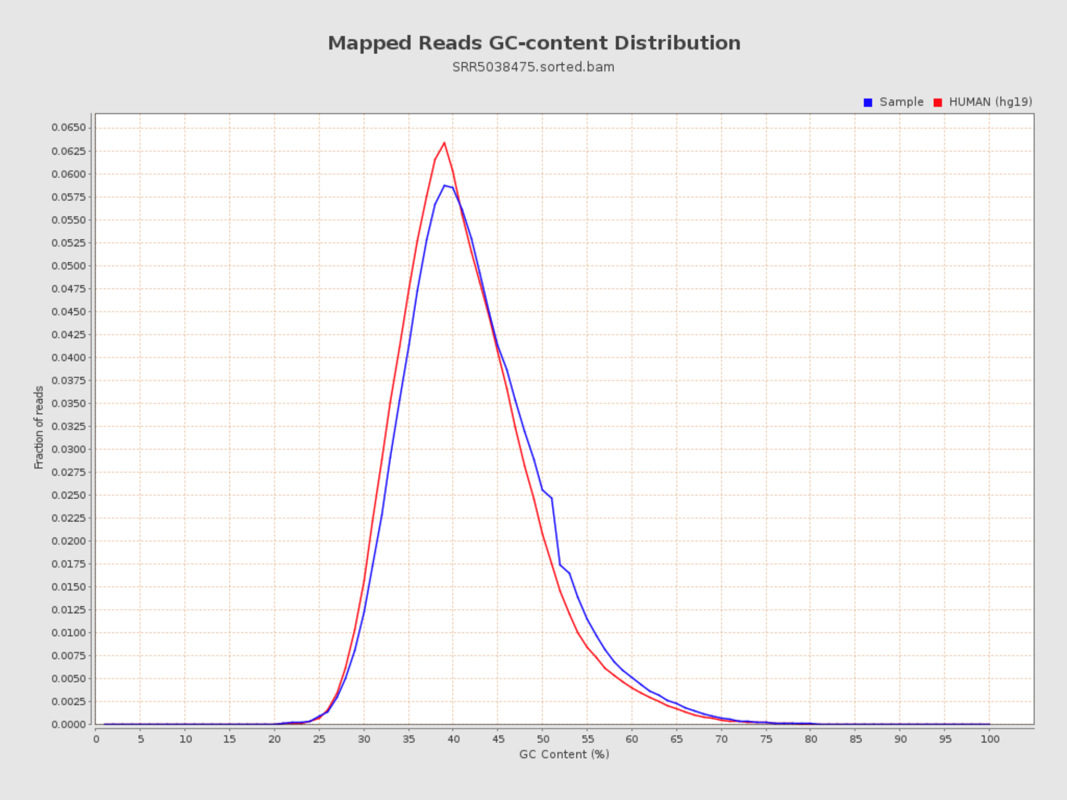
7. Results : Duplication Rate Histogram



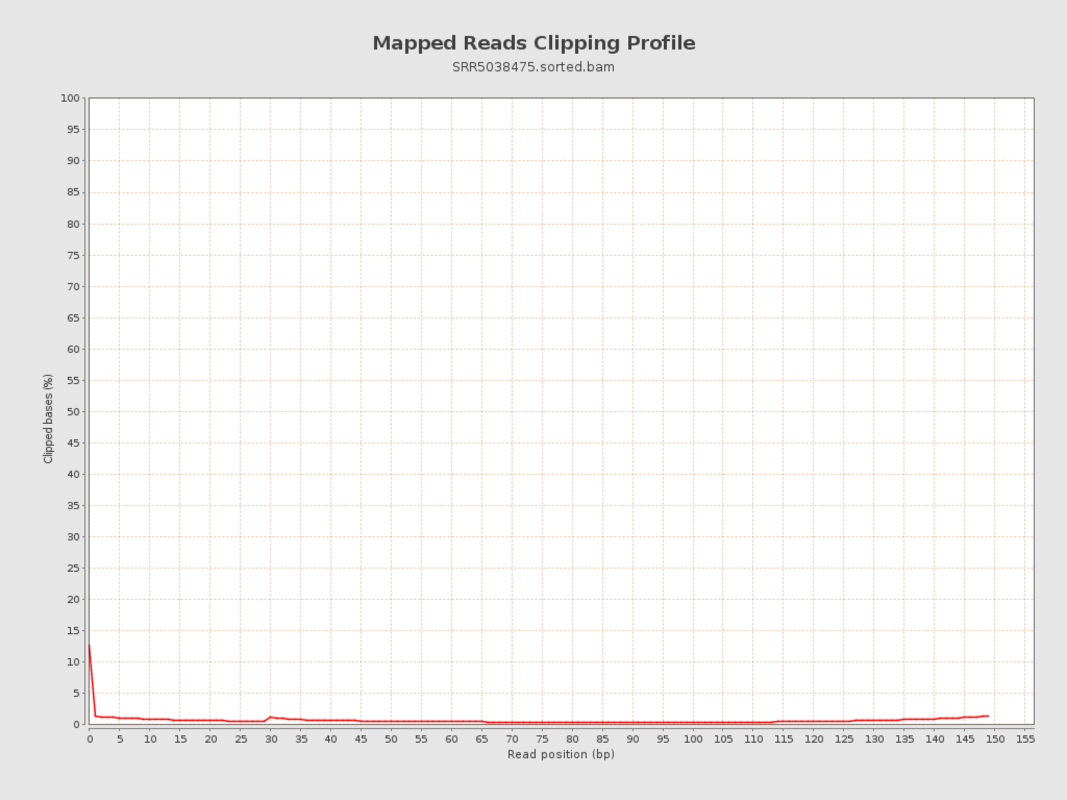
8. Results : Mapped Reads Nucleotide Content



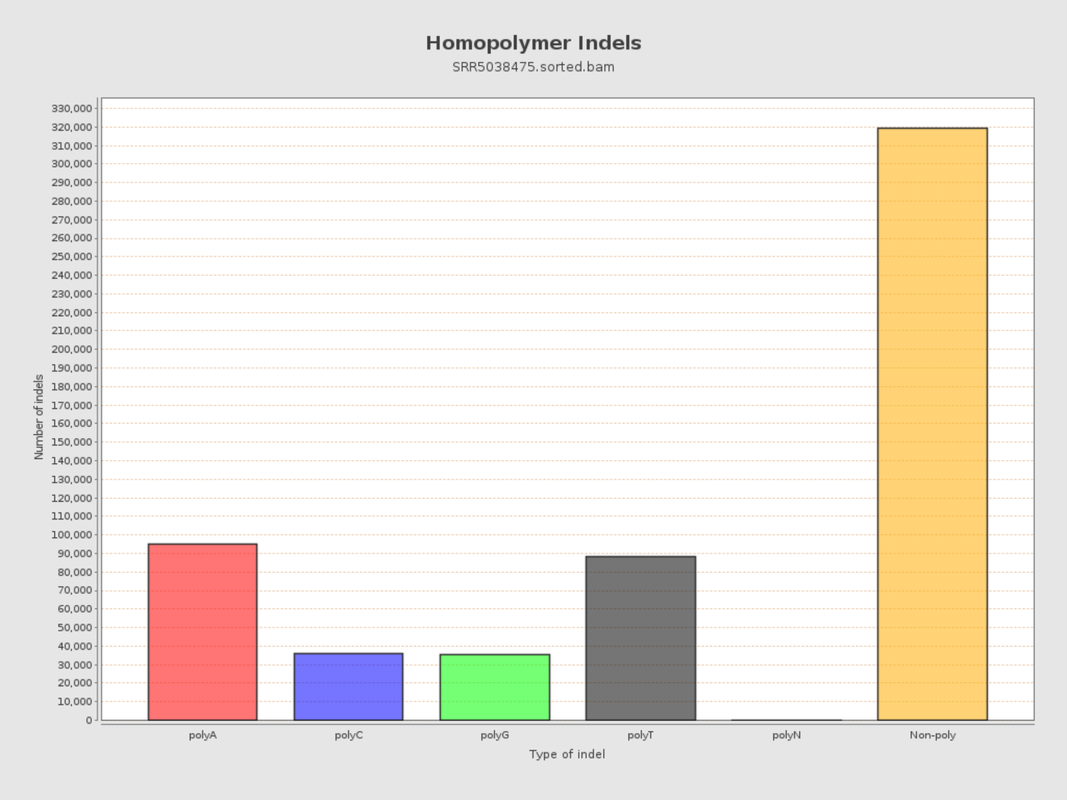
9. Results : Mapped Reads GC-content Distribution



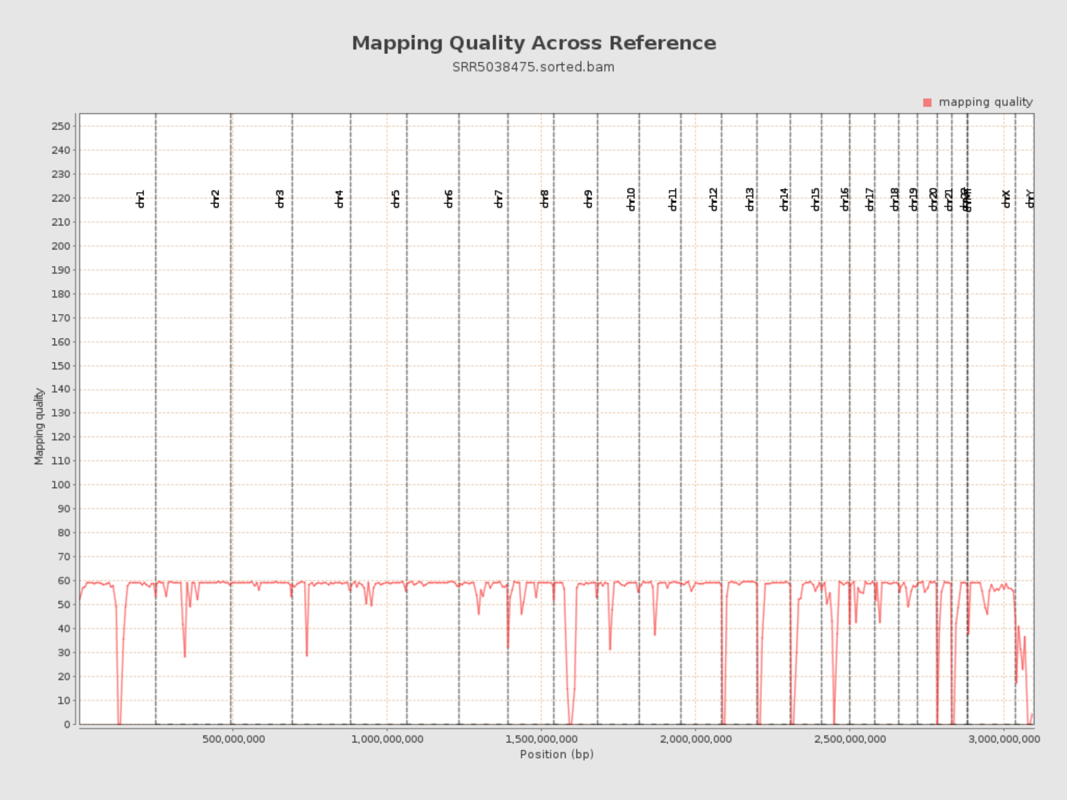
10. Results : Mapped Reads Clipping Profile



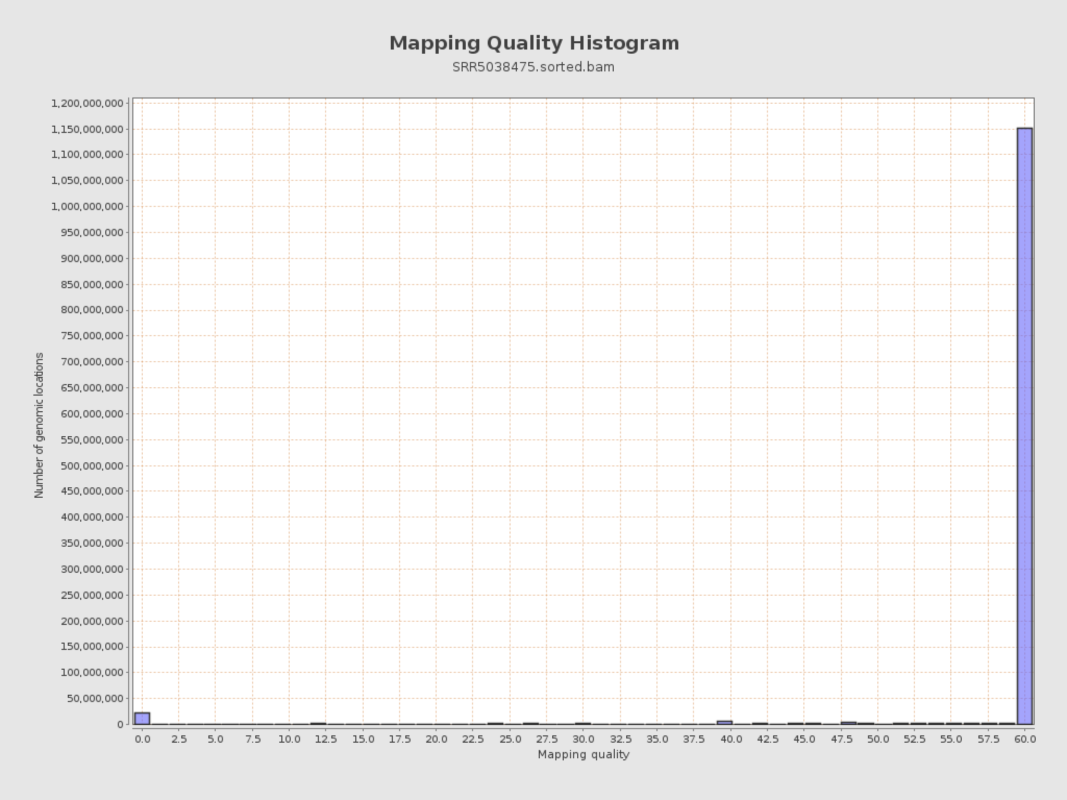
11. Results : Homopolymer Indels



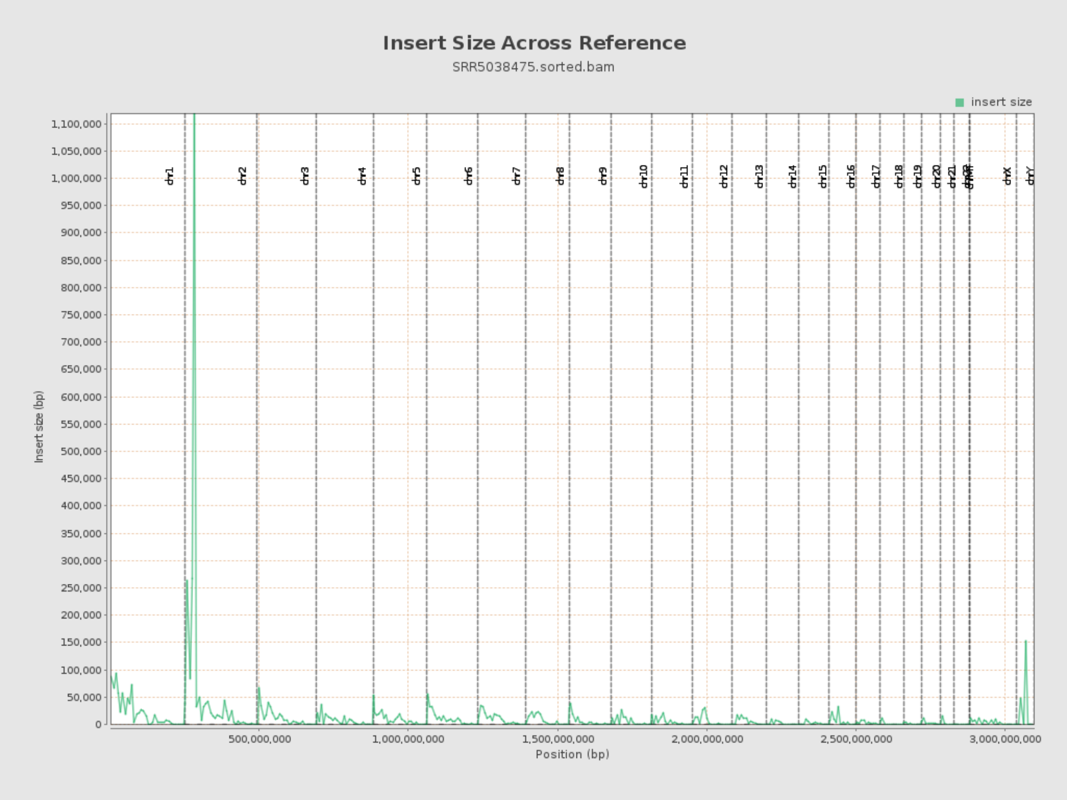
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram