Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 04:46:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038477.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_SRR5038477 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038477_1.fastq.gz SRR5038477_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 04:46:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038477.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,955,116
Mapped reads	15,583,051 / 91.91%
Unmapped reads	1,372,065 / 8.09%
Mapped paired reads	15,583,051 / 91.91%
Mapped reads, first in pair	7,903,490 / 46.61%
Mapped reads, second in pair	7,679,561 / 45.29%
Mapped reads, both in pair	15,311,380 / 90.31%
Mapped reads, singletons	271,671 / 1.6%
Secondary alignments	0
Supplementary alignments	219,687 / 1.3%
Read min/max/mean length	30 / 150 / 150.65
Duplicated reads (estimated)	3,091,620 / 18.23%
Duplication rate	14.53%
Clipped reads	7,371,715 / 43.48%

2.2. ACGT Content

Number/percentage of A's	597,688,213 / 28.51%
Number/percentage of C's	418,032,492 / 19.94%
Number/percentage of T's	607,135,721 / 28.96%
Number/percentage of G's	473,581,925 / 22.59%
Number/percentage of N's	163,142 / 0.01%

GC Percentage	42.53%

2.3. Coverage

Mean	0.6777
Standard Deviation	8.2494

2.4. Mapping Quality

Mean Mapping Quality	53.43

2.5. Insert size

Mean	79,902.38
Standard Deviation	2,757,019.78
P25/Median/P75	203 / 258 / 325

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	26,215,510
Insertions	360,192
Mapped reads with at least one insertion	2.2%
Deletions	756,458
Mapped reads with at least one deletion	4.68%
Homopolymer indels	48.27%

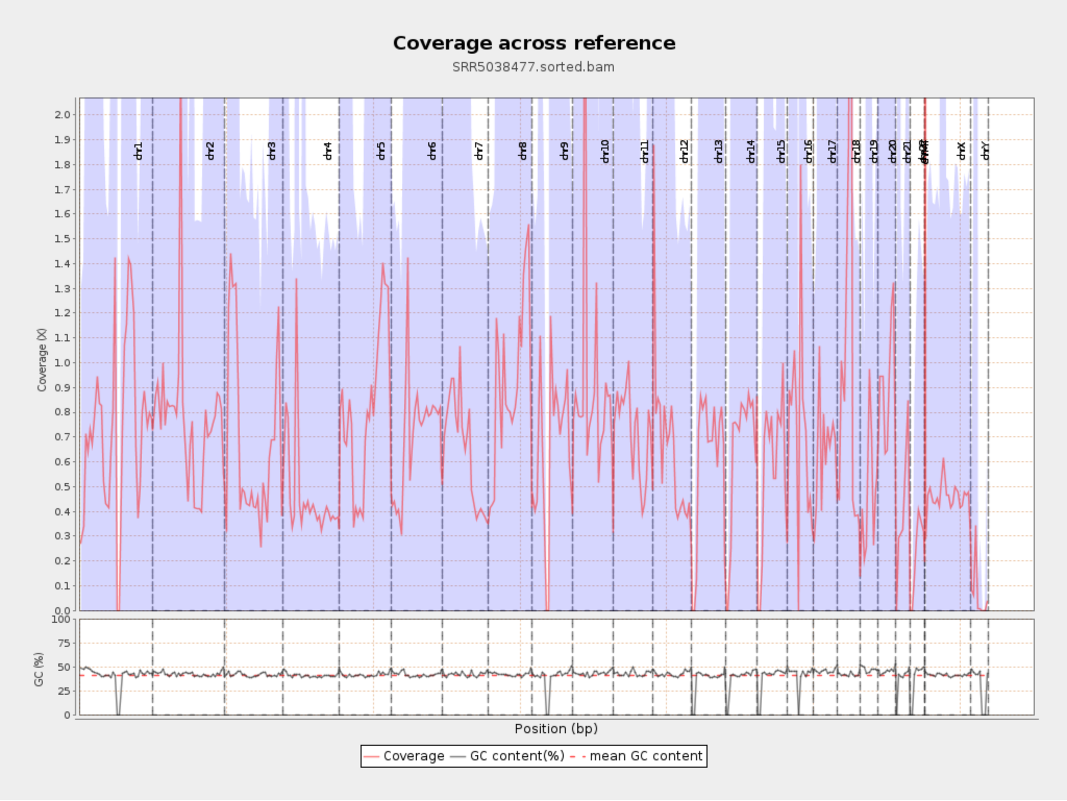
2.7. Chromosome stats

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

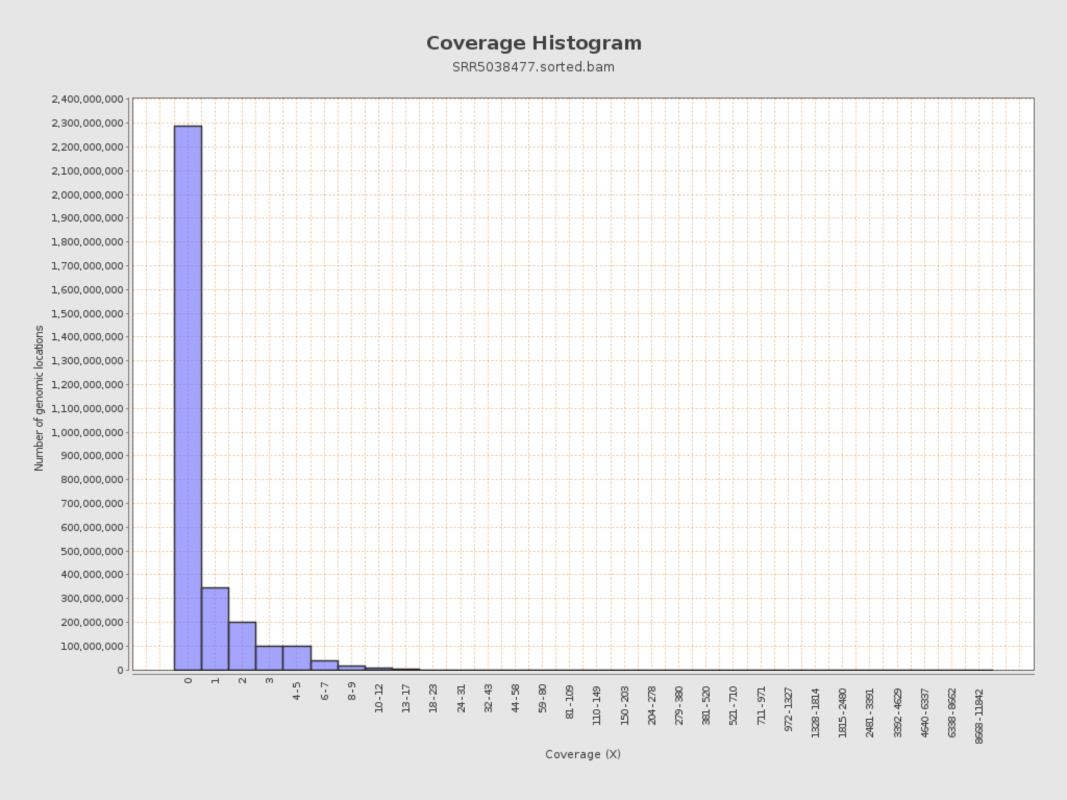
		bases	coverage	deviation
chr1	249250621	183110067	0.7346	12.0245
chr2	243199373	189756896	0.7803	9.5756
chr3	198022430	133926490	0.6763	1.6358
chr4	191154276	89814542	0.4699	8.2121
chr5	180915260	146415567	0.8093	1.7298
chr6	171115067	123345733	0.7208	6.9603
chr7	159138663	102228745	0.6424	8.375
chr8	146364022	136152539	0.9302	3.4707
chr9	141213431	89829070	0.6361	14.4624
chr10	135534747	126473141	0.9331	19.2047
chr11	135006516	96387172	0.7139	6.7023
chr12	133851895	88385890	0.6603	1.6975
chr13	115169878	70960301	0.6161	1.4641
chr14	107349540	68956200	0.6424	1.5726
chr15	102531392	57554583	0.5613	1.4271
chr16	90354753	64288204	0.7115	7.7427
chr17	81195210	51489202	0.6341	10.7255
chr18	78077248	85168542	1.0908	9.7907
chr19	59128983	27197072	0.46	5.0932
chr20	63025520	57657263	0.9148	2.9958
chr21	48129895	20156134	0.4188	3.7347
chr22	51304566	11957607	0.2331	0.8883
chrMT	16571	1986283	119.865	72.3266
chrX	155270560	70915754	0.4567	1.8821

chrY	59373566	3922635	0.0661	8.6414

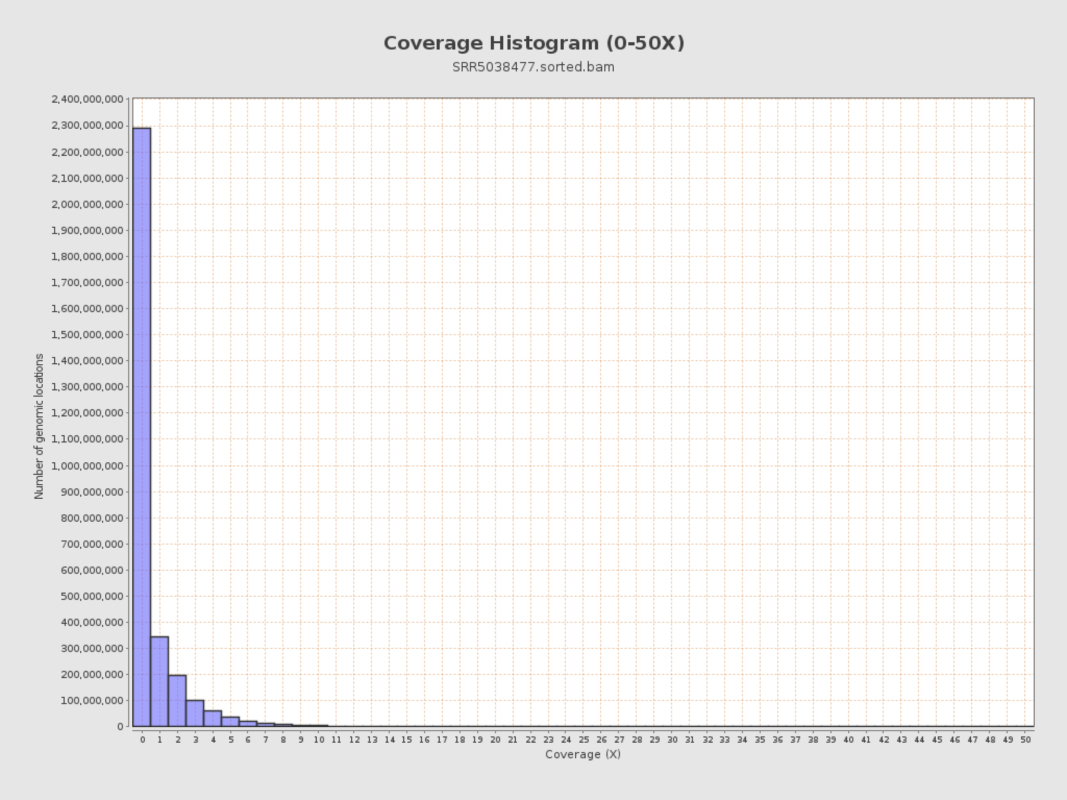
3. Results : Coverage across reference



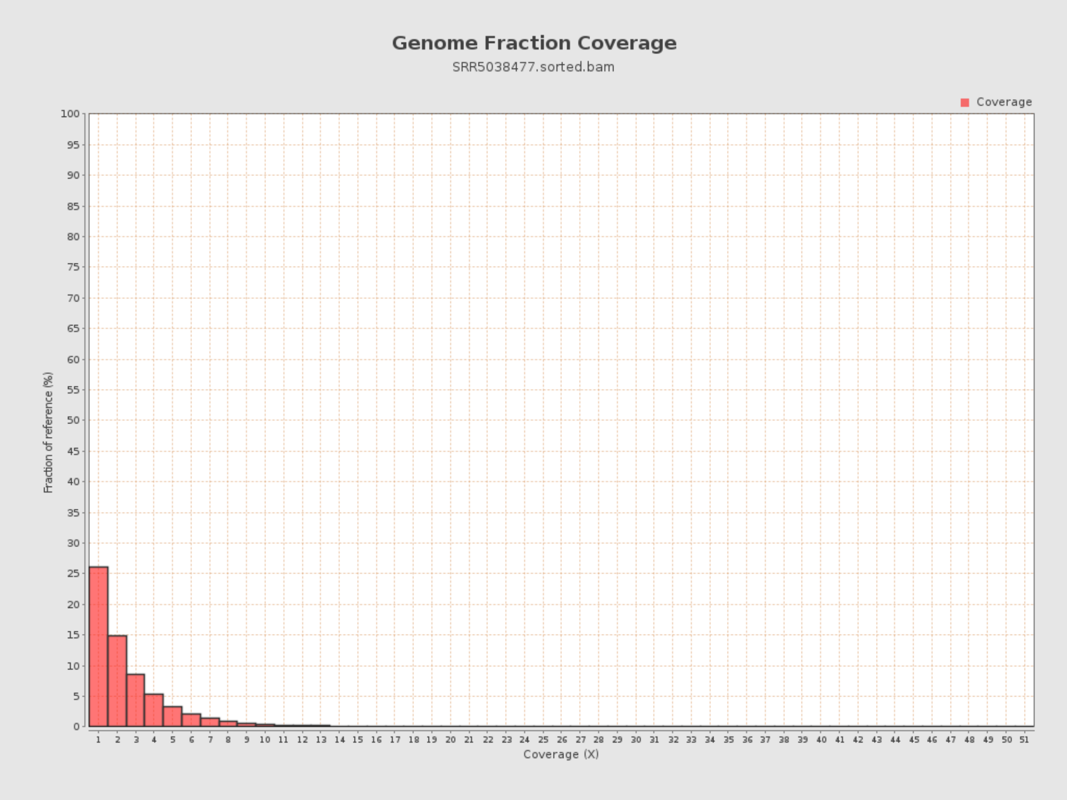
4. Results : Coverage Histogram



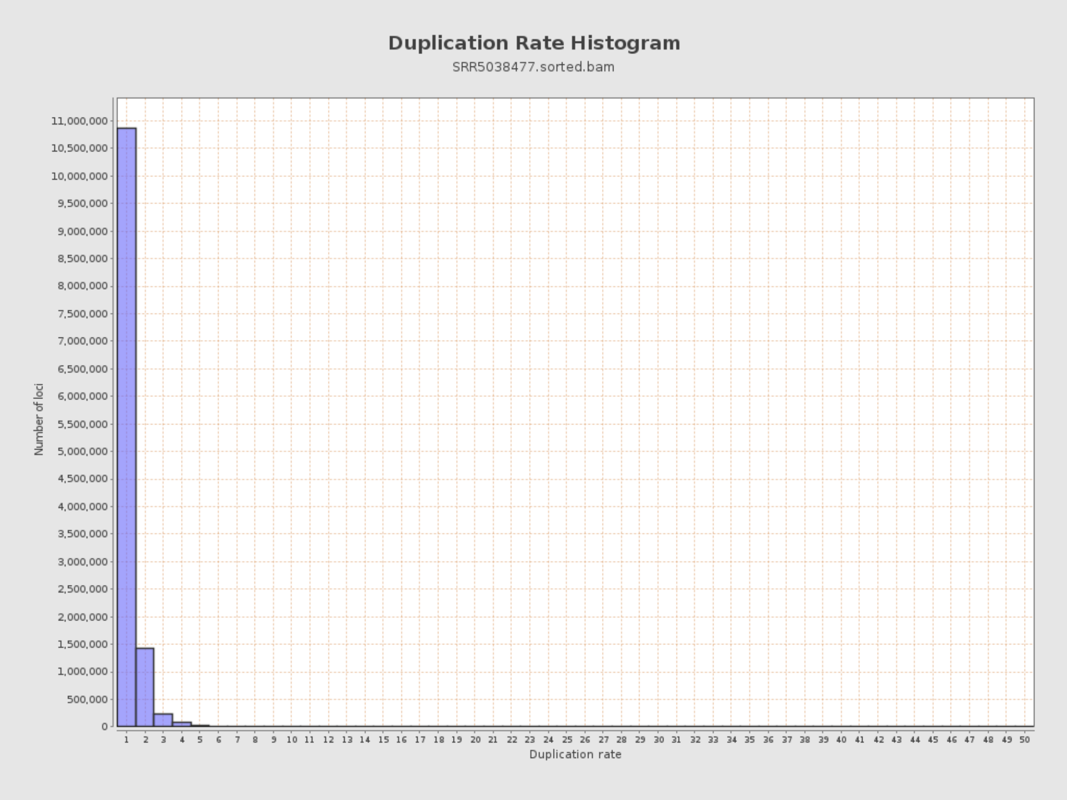
5. Results : Coverage Histogram (0-50X)



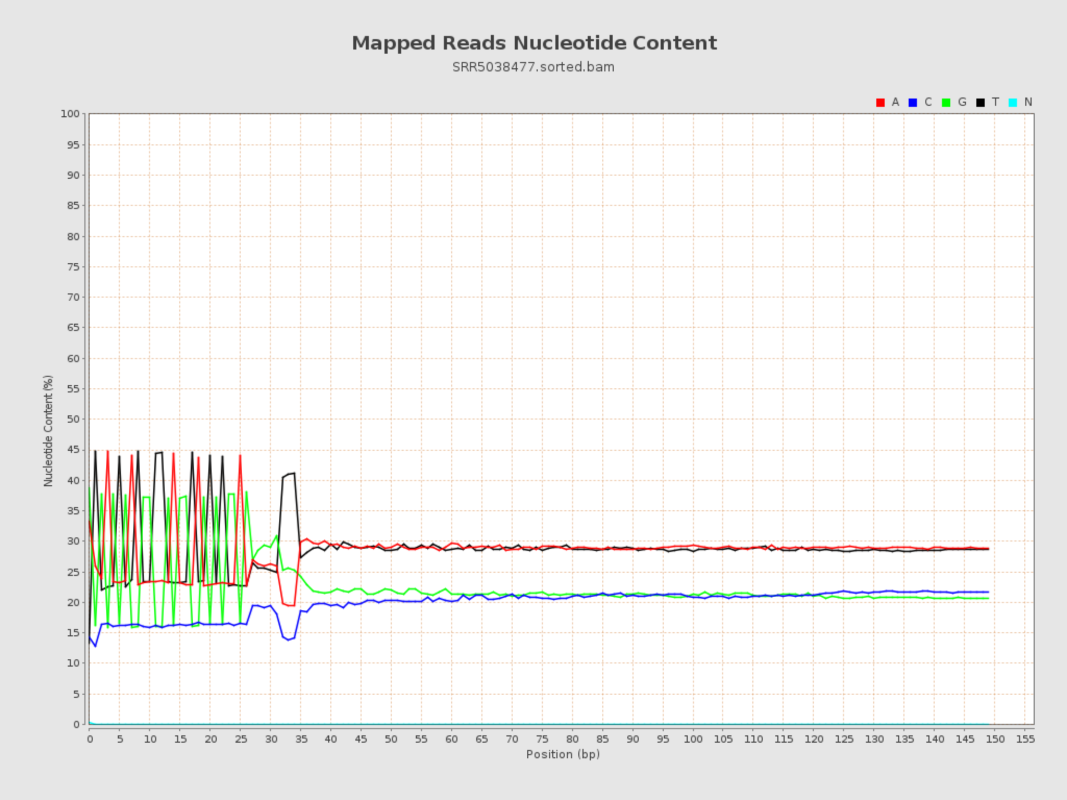
6. Results : Genome Fraction Coverage



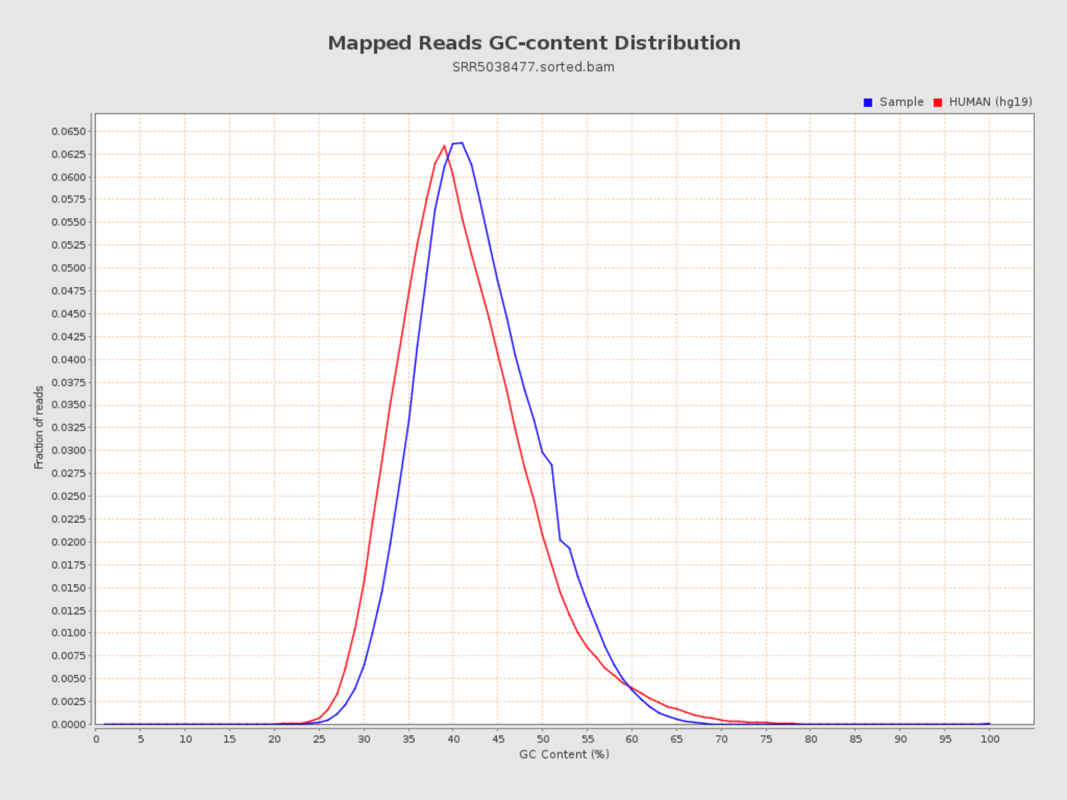
7. Results : Duplication Rate Histogram



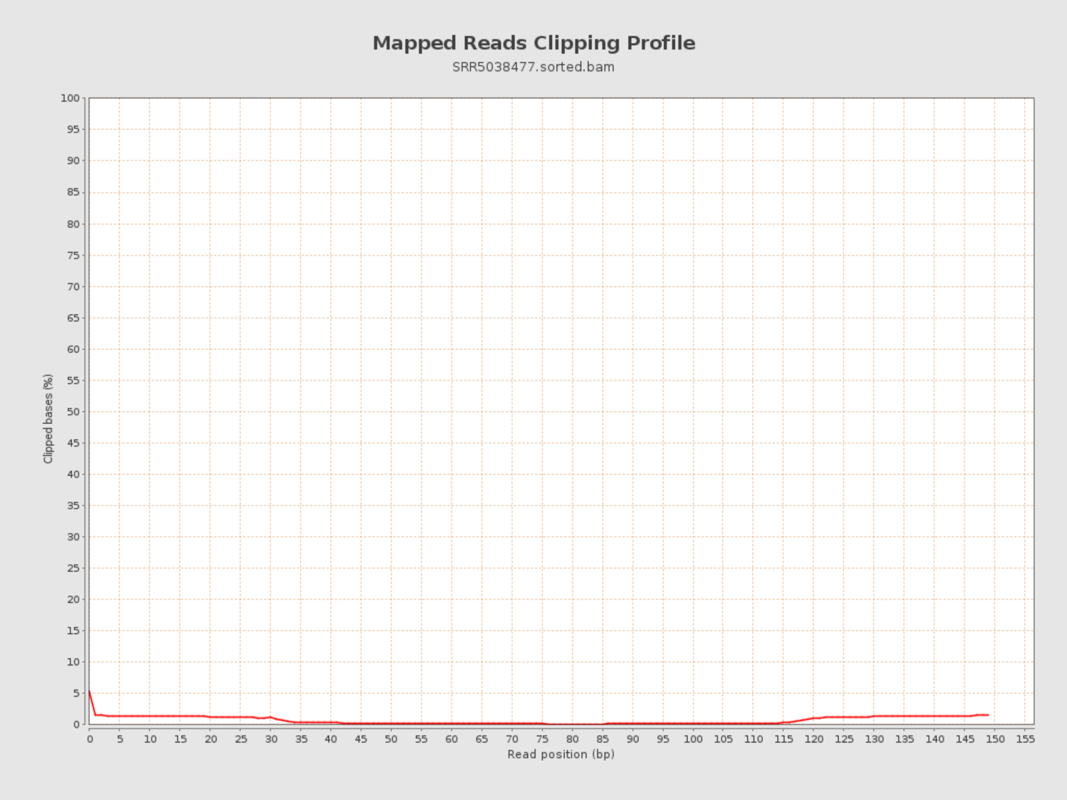
8. Results : Mapped Reads Nucleotide Content



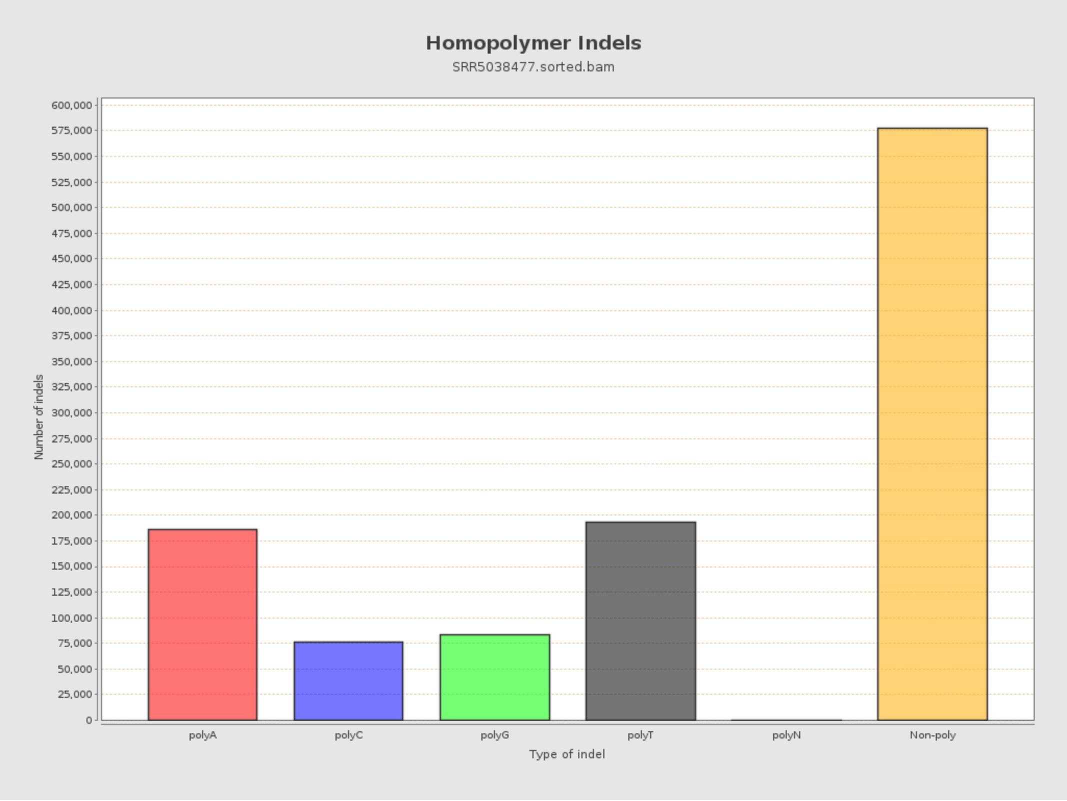
9. Results : Mapped Reads GC-content Distribution



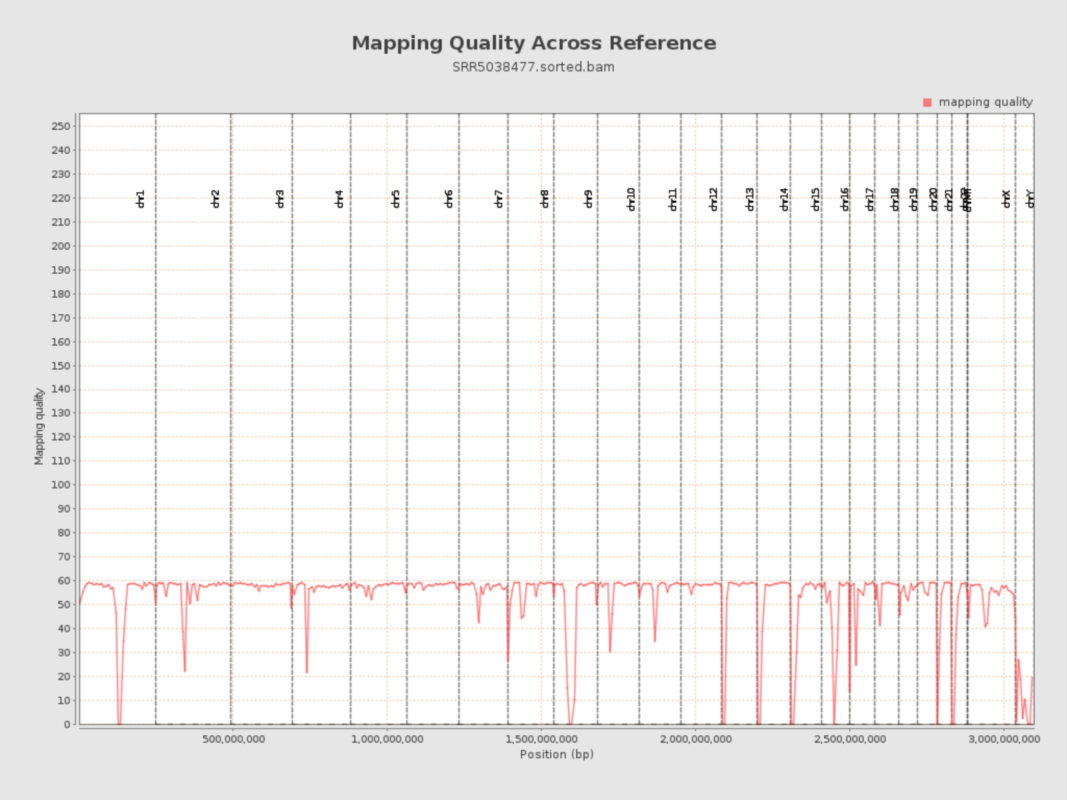
10. Results : Mapped Reads Clipping Profile



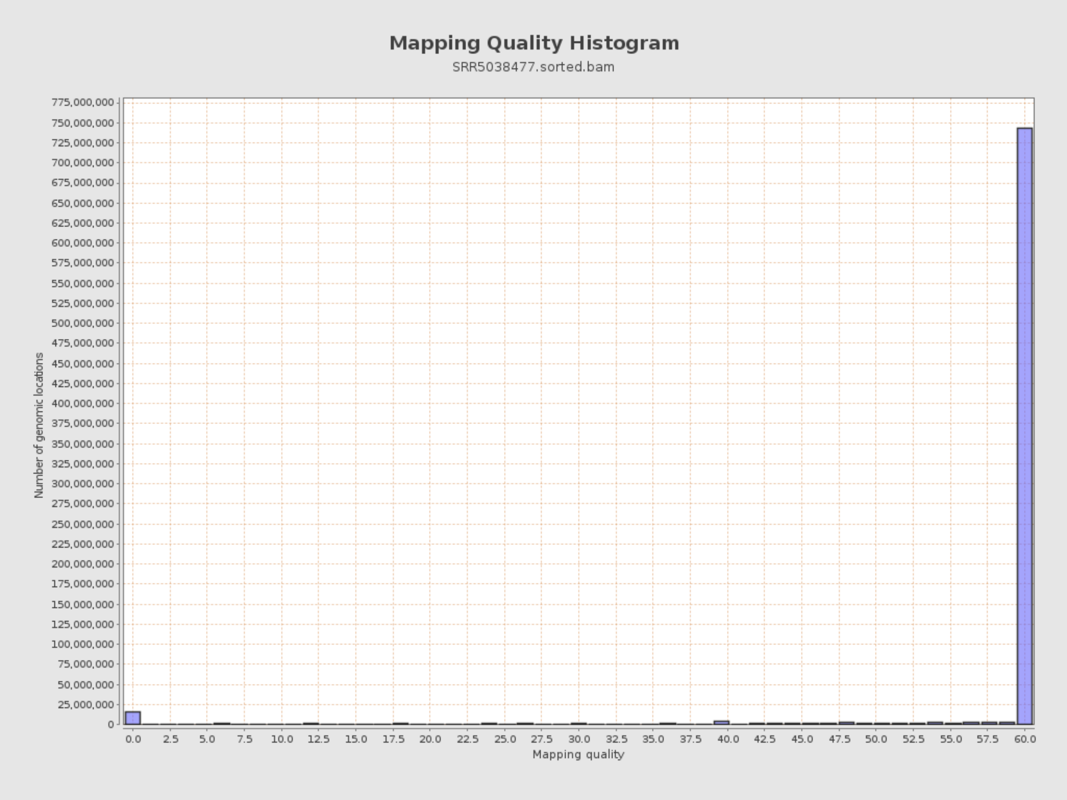
11. Results : Homopolymer Indels



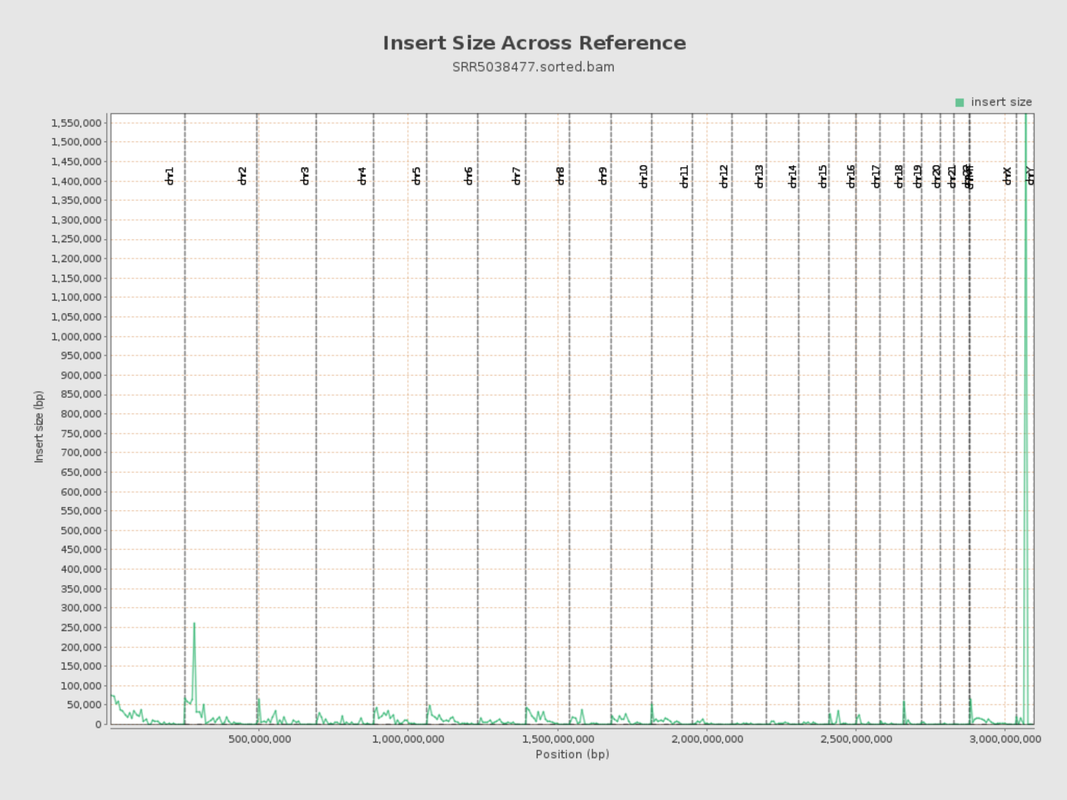
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram