Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 14:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038446.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_SRR5038446 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038446_1.fastq.gz SRR5038446_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 14:07:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038446.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,037,618
Mapped reads	15,369,506 / 95.83%
Unmapped reads	668,112 / 4.17%
Mapped paired reads	15,369,506 / 95.83%
Mapped reads, first in pair	7,804,748 / 48.67%
Mapped reads, second in pair	7,564,758 / 47.17%
Mapped reads, both in pair	15,071,536 / 93.98%
Mapped reads, singletons	297,970 / 1.86%
Secondary alignments	0
Supplementary alignments	264,696 / 1.65%
Read min/max/mean length	30 / 150 / 150.82
Duplicated reads (estimated)	3,085,637 / 19.24%
Duplication rate	13.29%
Clipped reads	7,273,837 / 45.35%

2.2. ACGT Content

Number/percentage of A's	591,899,655 / 28.62%
Number/percentage of C's	409,539,239 / 19.8%
Number/percentage of T's	604,761,342 / 29.25%
Number/percentage of G's	461,511,346 / 22.32%
Number/percentage of N's	158,479 / 0.01%

GC Percentage	42.12%

2.3. Coverage

Mean	0.6685
Standard Deviation	10.1267

2.4. Mapping Quality

Mean Mapping Quality	53.41

2.5. Insert size

Mean	105,147.75
Standard Deviation	3,124,567.48
P25/Median/P75	214 / 269 / 336

2.6. Mismatches and indels

General error rate	1.44%
Mismatches	28,684,692
Insertions	378,464
Mapped reads with at least one insertion	2.32%
Deletions	757,281
Mapped reads with at least one deletion	4.73%
Homopolymer indels	46.54%

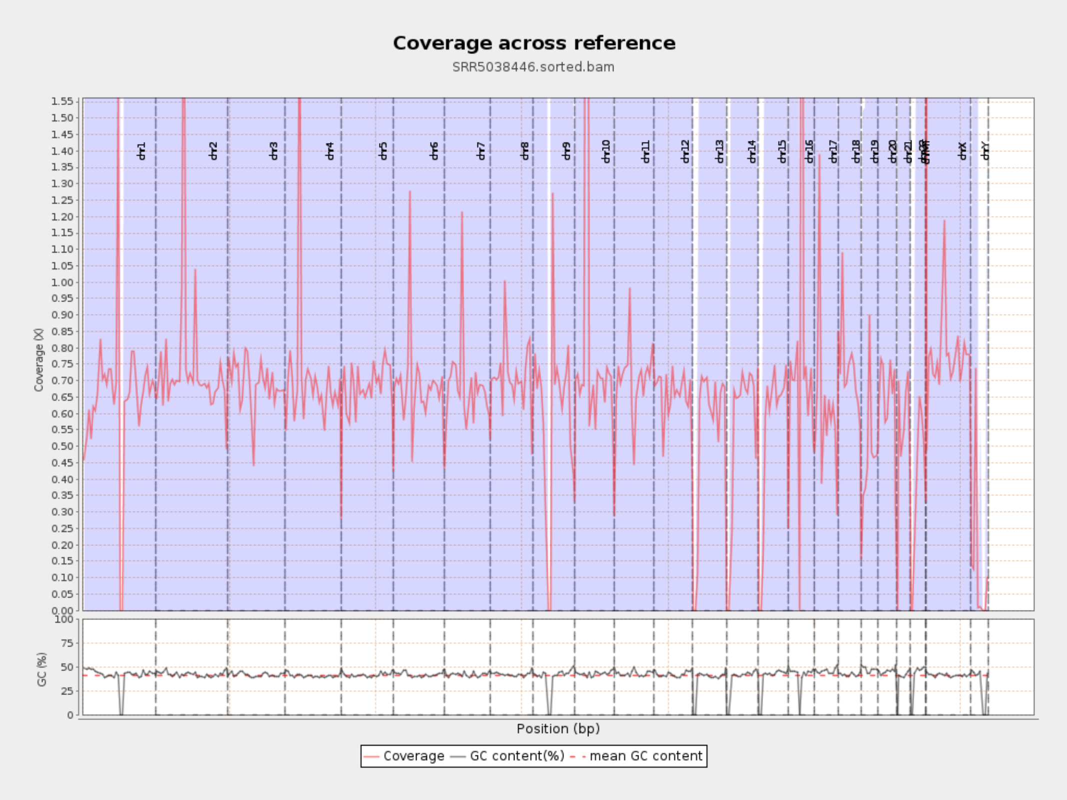
2.7. Chromosome stats

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

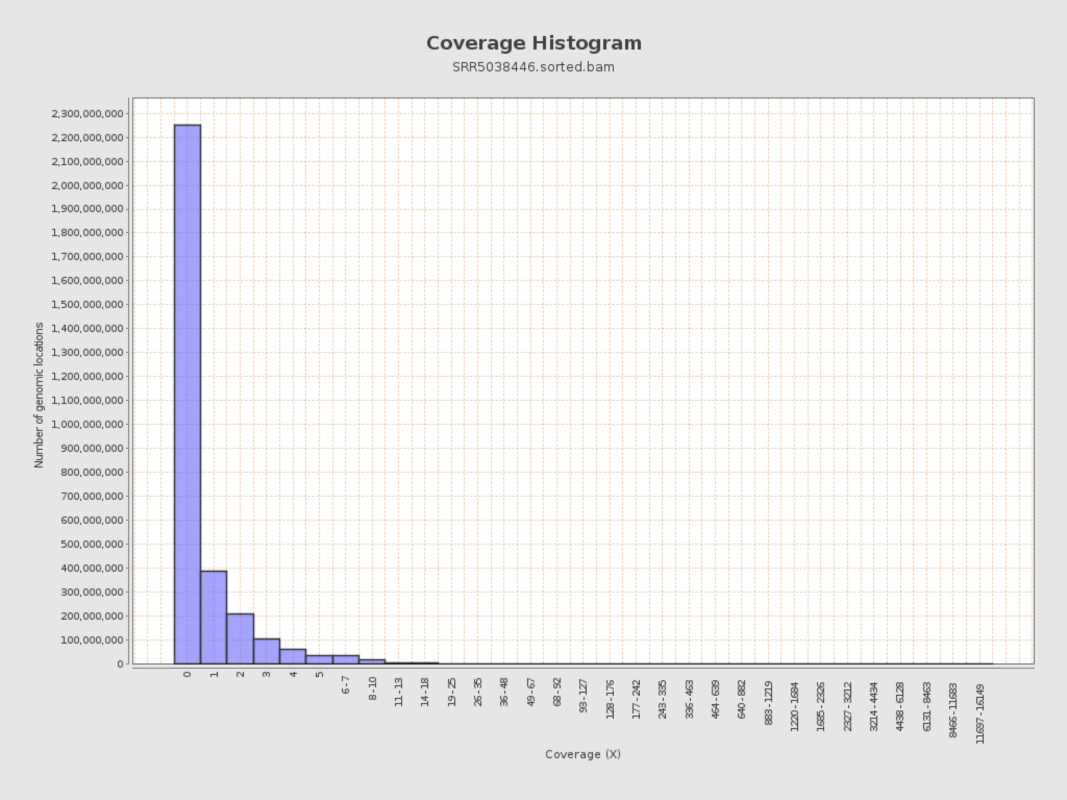
		bases	coverage	deviation
chr1	249250621	162743240	0.6529	15.882
chr2	243199373	184046270	0.7568	9.3445
chr3	198022430	136757342	0.6906	1.5876
chr4	191154276	138115084	0.7225	8.5654
chr5	180915260	123553201	0.6829	1.5182
chr6	171115067	118222961	0.6909	6.6666
chr7	159138663	108494976	0.6818	9.2941
chr8	146364022	104297967	0.7126	3.0791
chr9	141213431	85287978	0.604	15.0253
chr10	135534747	118167496	0.8719	27.1606
chr11	135006516	94636551	0.701	6.7364
chr12	133851895	88419555	0.6606	1.5889
chr13	115169878	62109409	0.5393	1.3047
chr14	107349540	58922737	0.5489	1.4943
chr15	102531392	55060395	0.537	1.3186
chr16	90354753	74523955	0.8248	16.0509
chr17	81195210	51939685	0.6397	11.4017
chr18	78077248	58105954	0.7442	11.3099
chr19	59128983	28400504	0.4803	7.173
chr20	63025520	41974544	0.666	2.6794
chr21	48129895	26092368	0.5421	4.0585
chr22	51304566	19606268	0.3822	1.2046
chrMT	16571	1082284	65.3119	35.5289
chrX	155270560	120474716	0.7759	3.5292

chrY	59373566	8353676	0.1407	10.4502

3. Results : Coverage across reference



4. Results : Coverage Histogram



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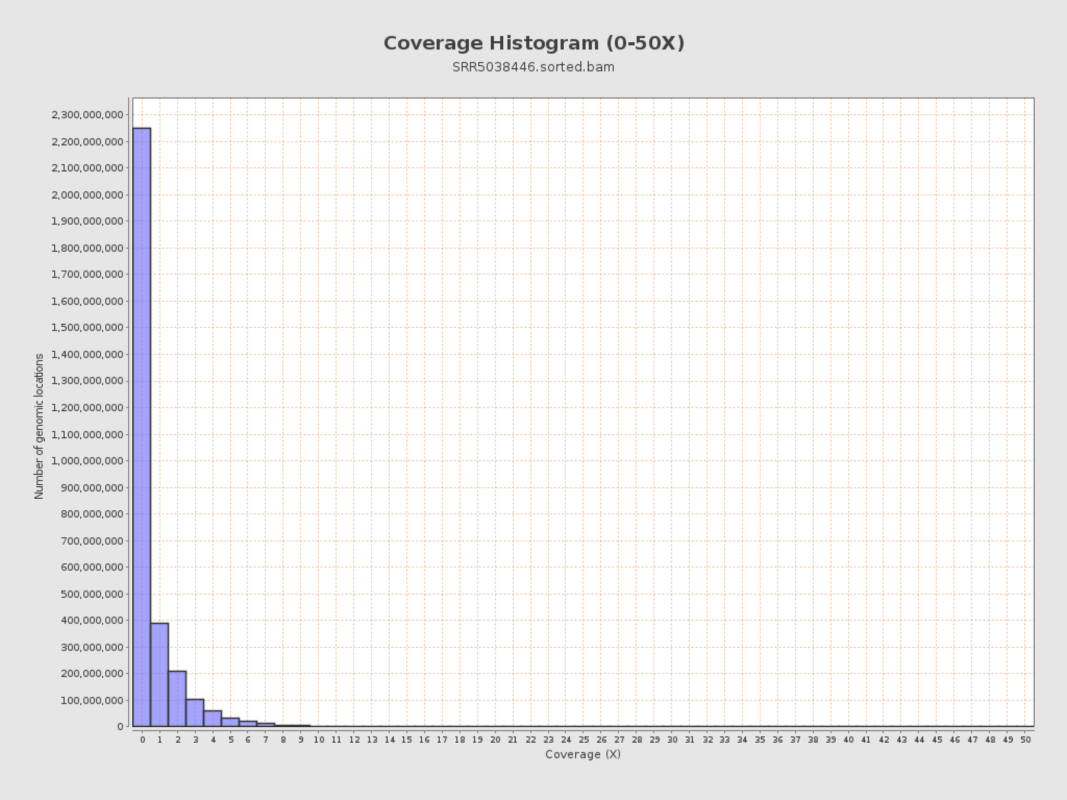
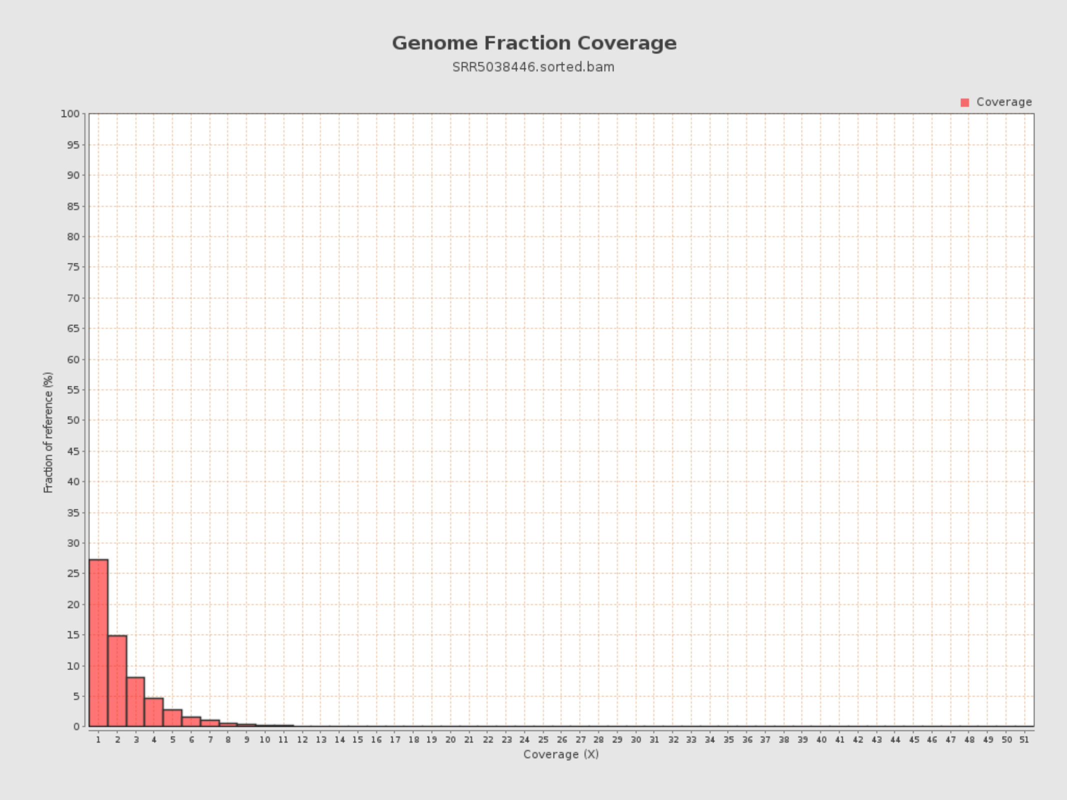
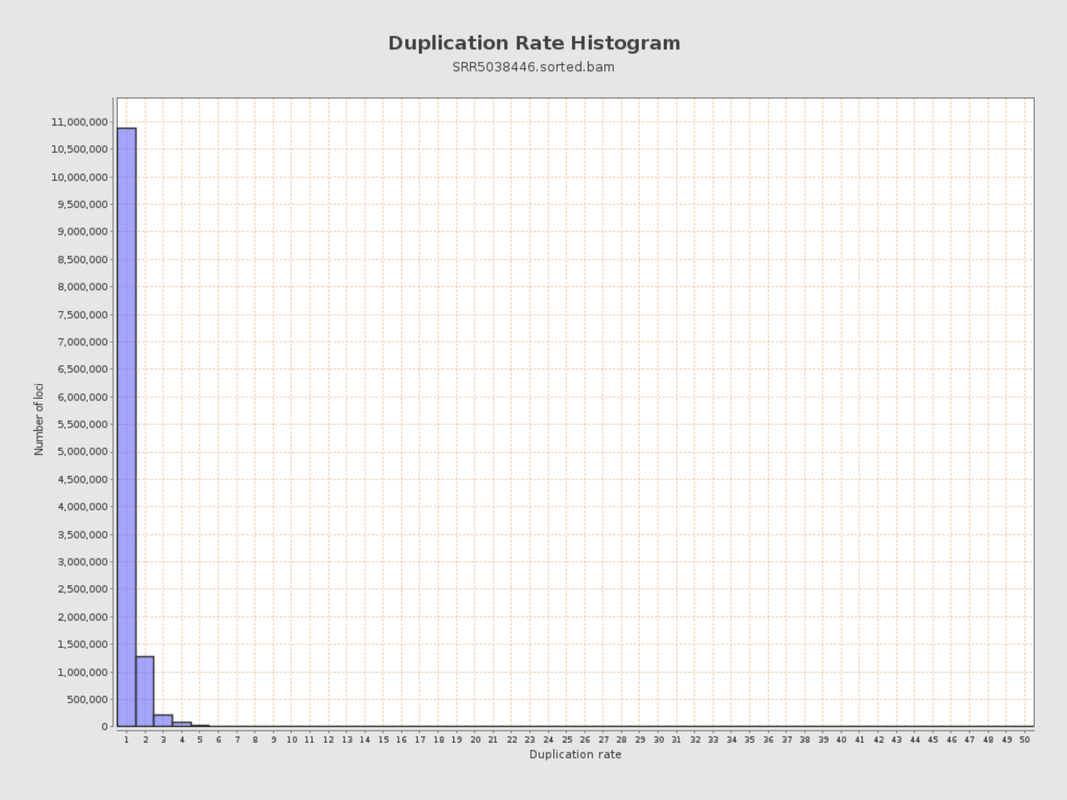
5. Results : Coverage Histogram (0-50X)



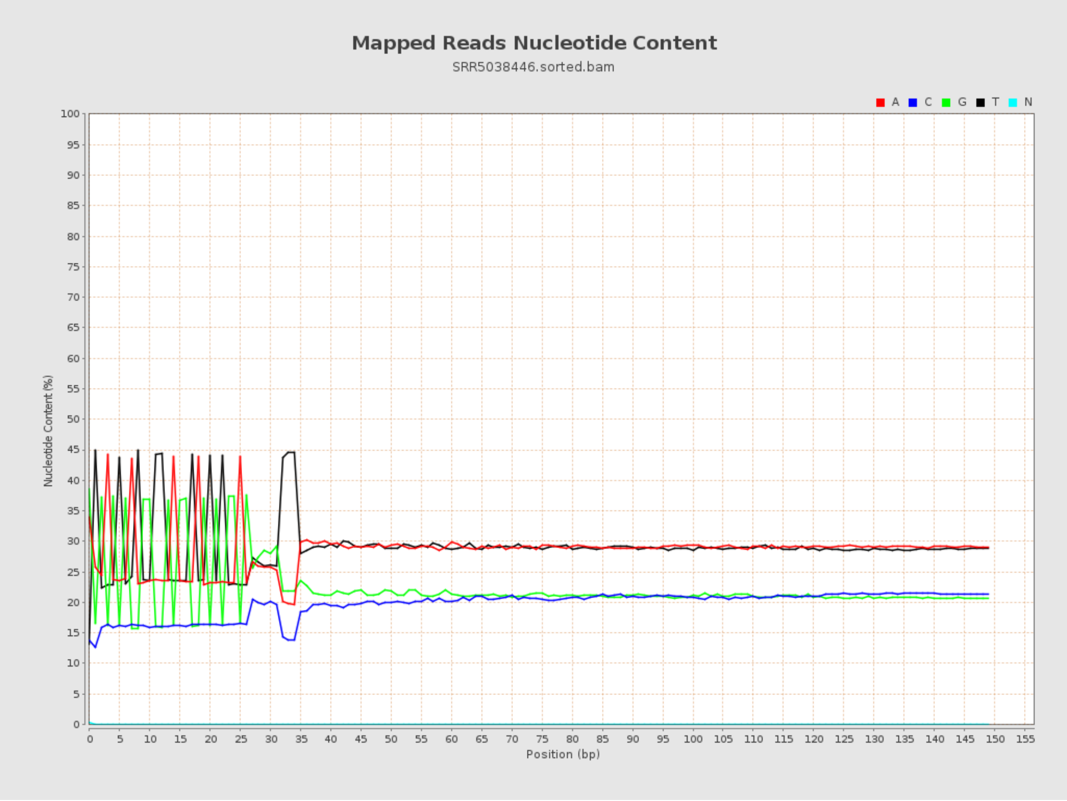
6. Results : Genome Fraction Coverage



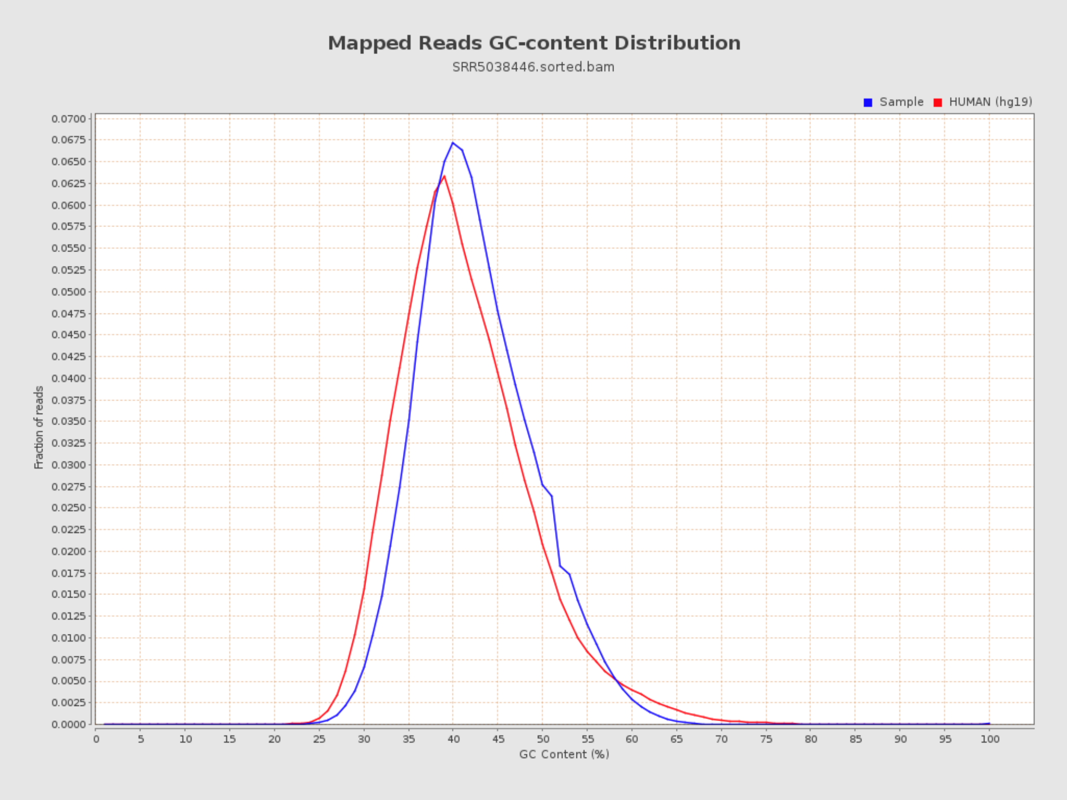
7. Results : Duplication Rate Histogram



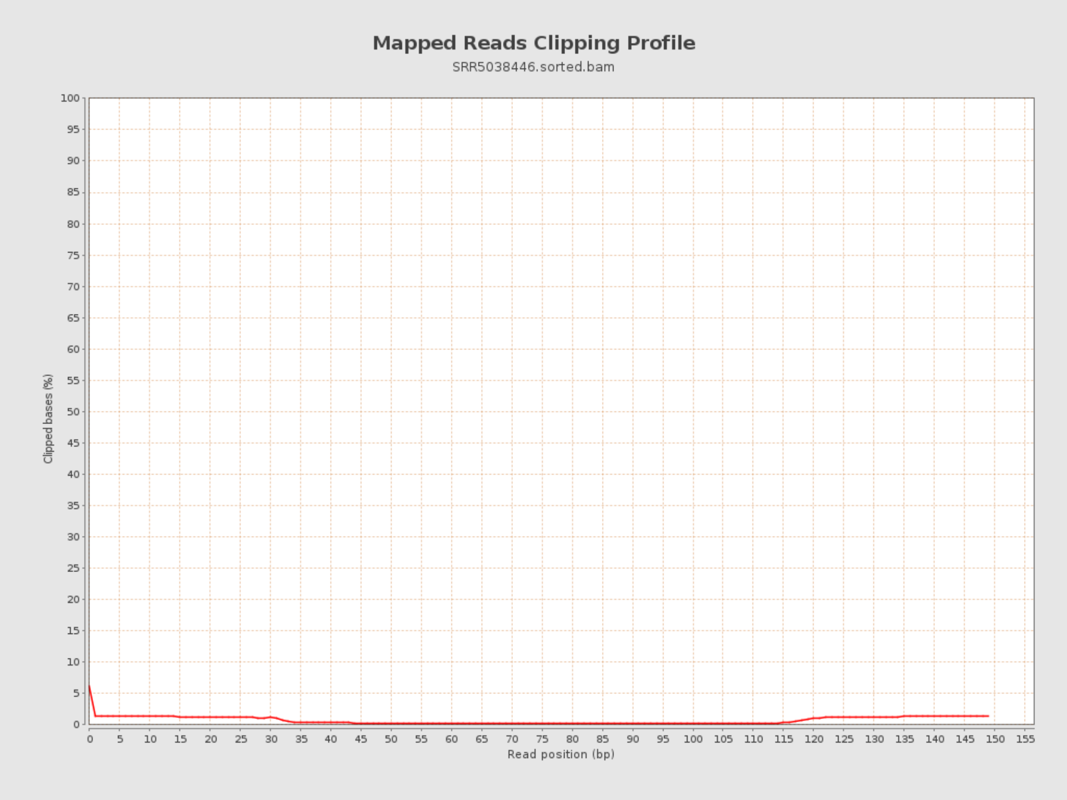
8. Results : Mapped Reads Nucleotide Content



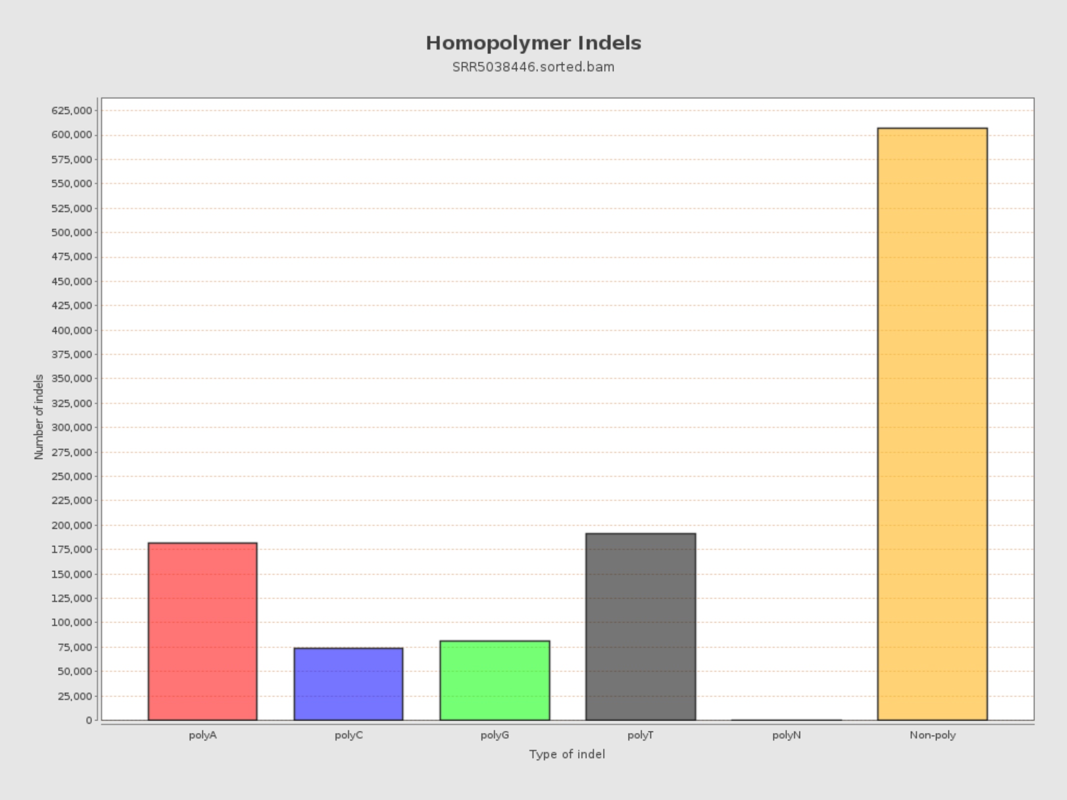
9. Results : Mapped Reads GC-content Distribution



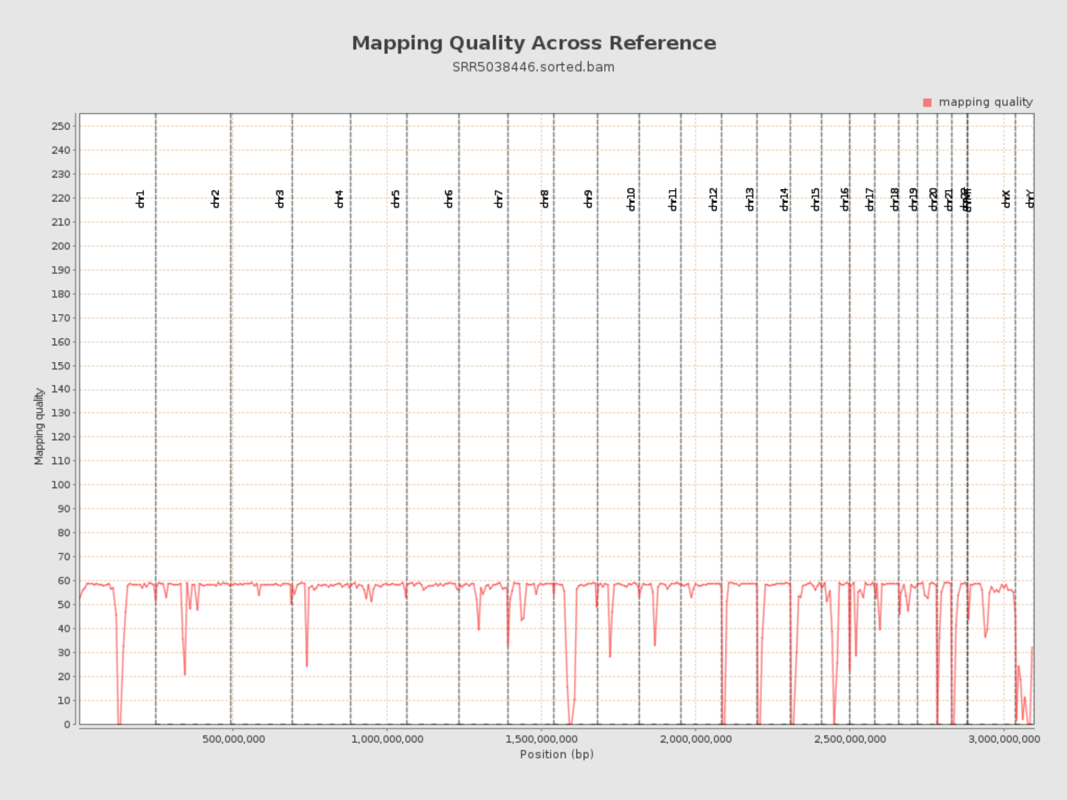
10. Results : Mapped Reads Clipping Profile



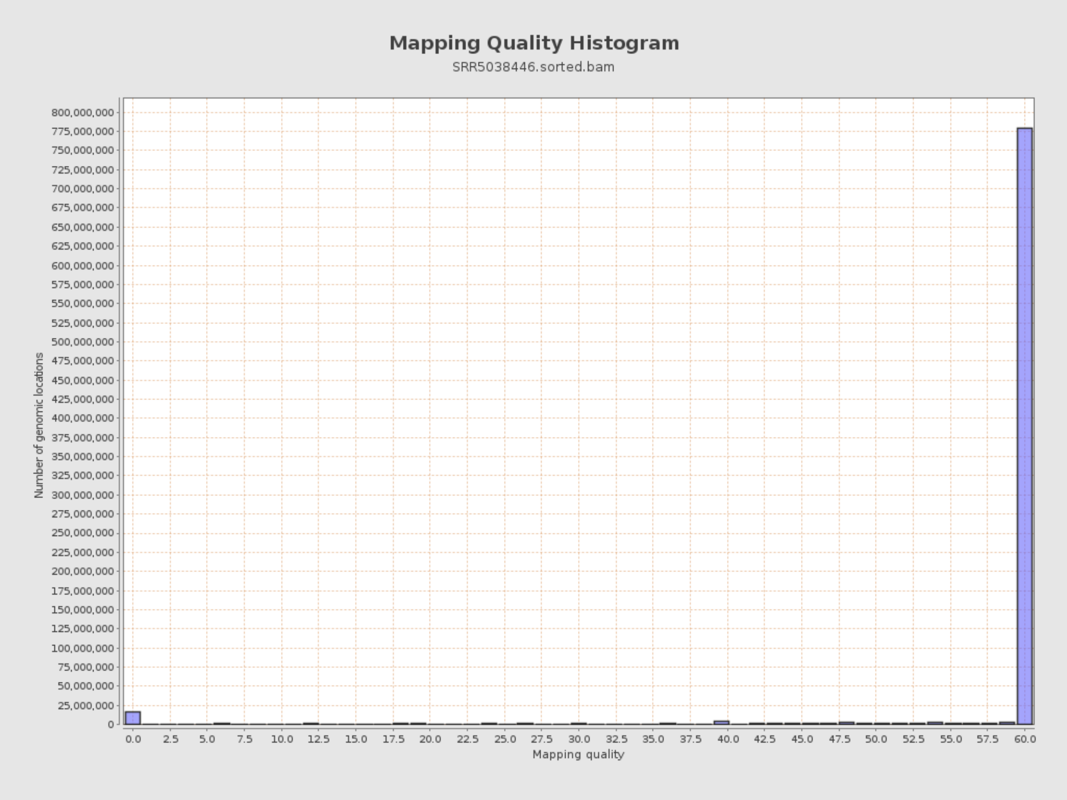
11. Results : Homopolymer Indels



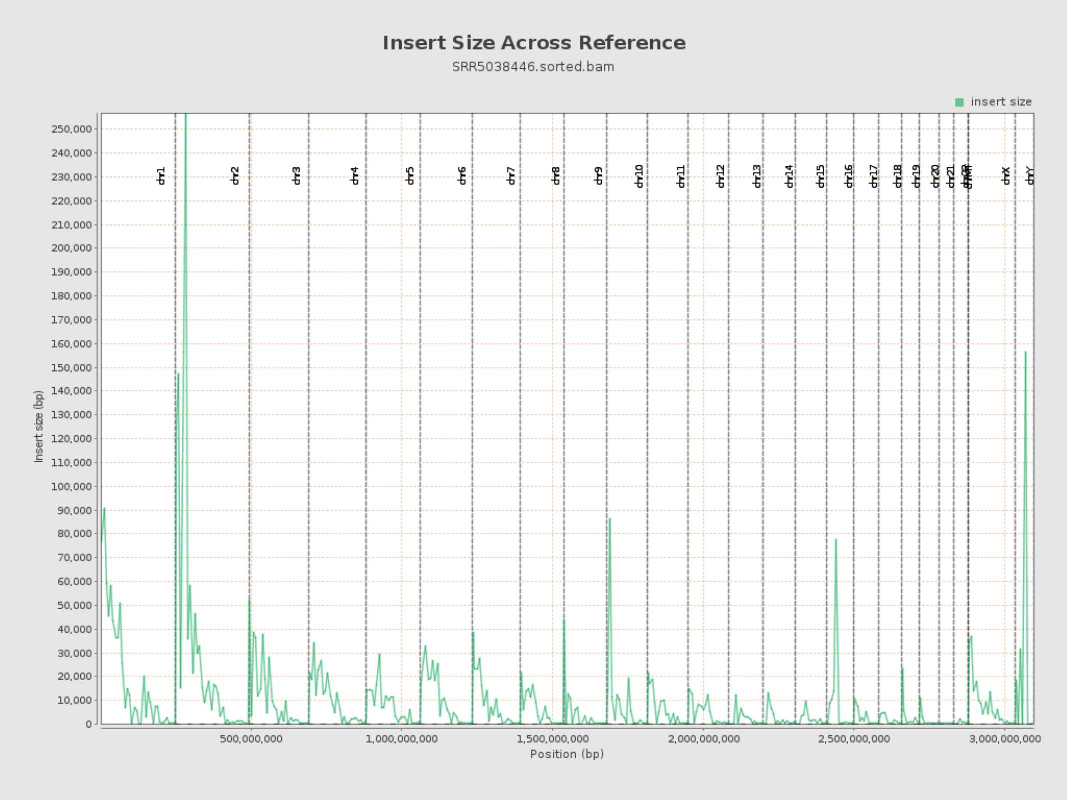
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram