Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/14 17:53:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038408.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_SRR5038408 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038408_1.fastq.gz SRR5038408_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 14 17:53:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038408.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,407,710
Mapped reads	18,772,648 / 96.73%
Unmapped reads	635,062 / 3.27%
Mapped paired reads	18,772,648 / 96.73%
Mapped reads, first in pair	9,481,565 / 48.85%
Mapped reads, second in pair	9,291,083 / 47.87%
Mapped reads, both in pair	18,535,020 / 95.5%
Mapped reads, singletons	237,628 / 1.22%
Secondary alignments	0
Supplementary alignments	276,452 / 1.42%
Read min/max/mean length	30 / 150 / 150.72
Duplicated reads (estimated)	4,097,266 / 21.11%
Duplication rate	15.36%
Clipped reads	8,853,975 / 45.62%

2.2. ACGT Content

Number/percentage of A's	725,134,748 / 28.62%
Number/percentage of C's	502,763,510 / 19.84%
Number/percentage of T's	739,068,623 / 29.17%
Number/percentage of G's	566,890,816 / 22.37%
Number/percentage of N's	201,167 / 0.01%

GC Percentage	42.21%

2.3. Coverage

Mean	0.8191
Standard Deviation	12.0671

2.4. Mapping Quality

Mean Mapping Quality	53.46

2.5. Insert size

Mean	66,757.15
Standard Deviation	2,484,024.93
P25/Median/P75	193 / 242 / 305

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	30,981,628
Insertions	438,833
Mapped reads with at least one insertion	2.22%
Deletions	883,068
Mapped reads with at least one deletion	4.53%
Homopolymer indels	47.2%

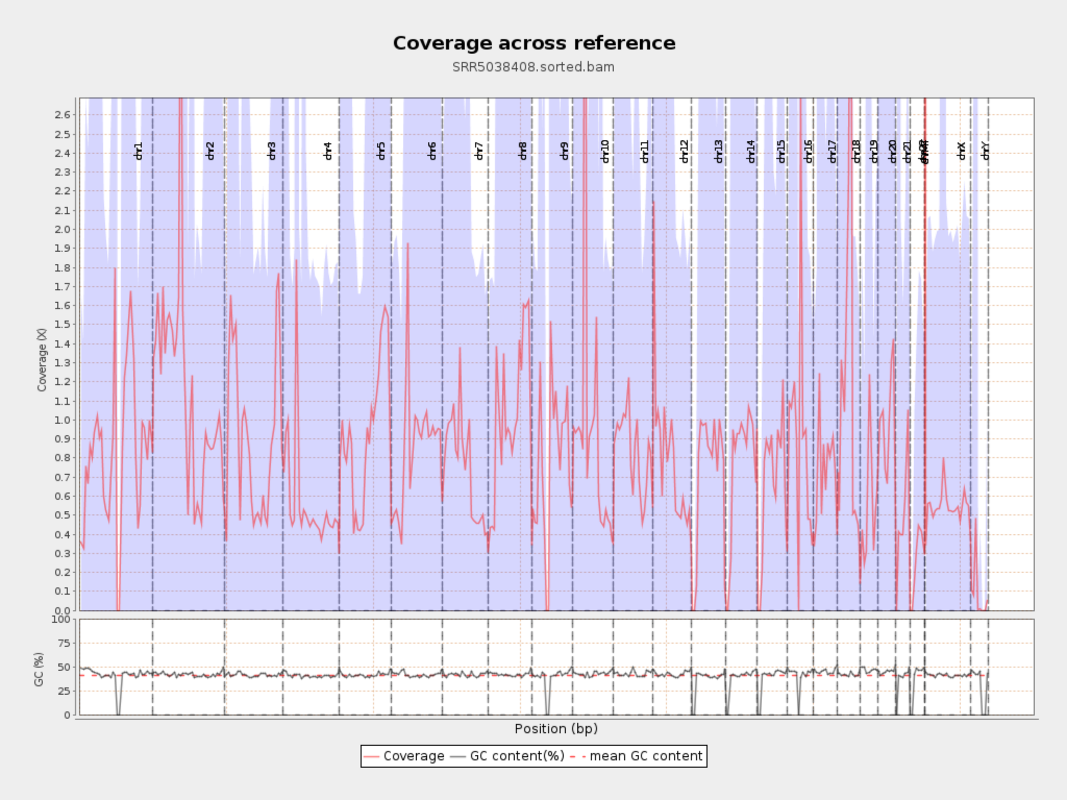
2.7. Chromosome stats

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

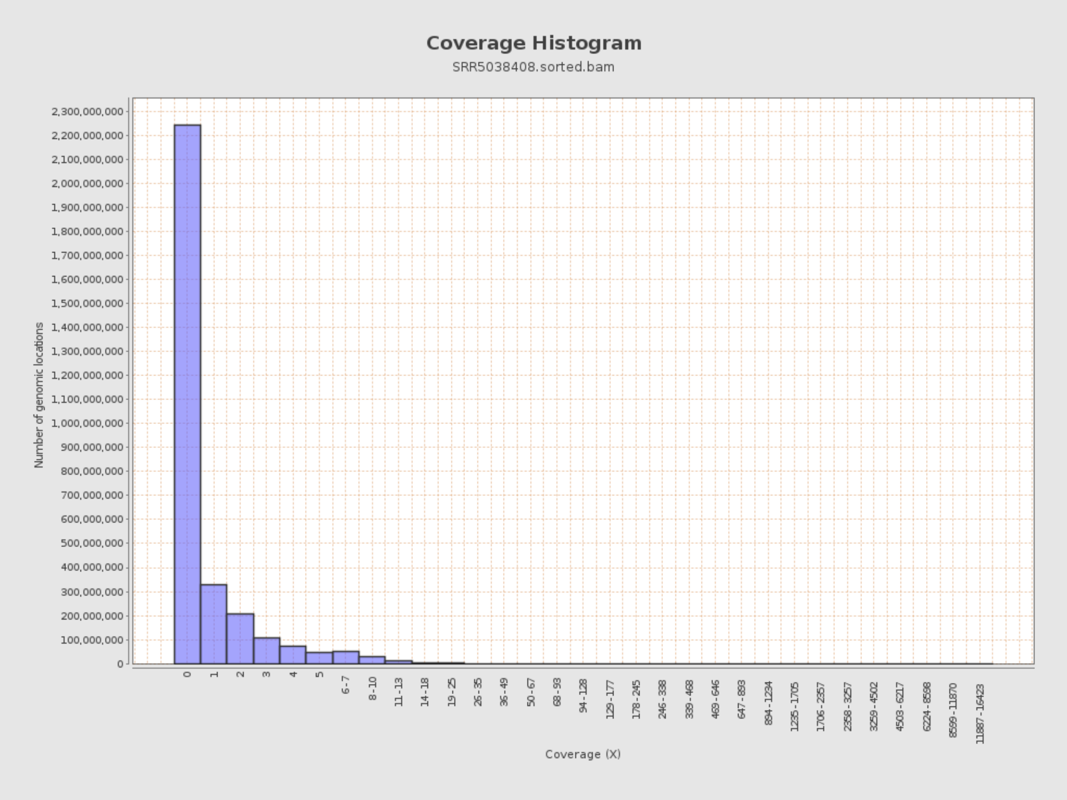
		bases	coverage	deviation
chr1	249250621	209793520	0.8417	15.9213
chr2	243199373	285113913	1.1723	15.1235
chr3	198022430	179837808	0.9082	2.1257
chr4	191154276	108825713	0.5693	11.2425
chr5	180915260	167882623	0.928	2.0005
chr6	171115067	149422038	0.8732	10.7053
chr7	159138663	118476972	0.7445	11.2071
chr8	146364022	153136875	1.0463	4.4394
chr9	141213431	106268549	0.7525	18.6918
chr10	135534747	136729699	1.0088	32.7979
chr11	135006516	112315283	0.8319	8.3159
chr12	133851895	107035405	0.7997	2.0135
chr13	115169878	84313036	0.7321	1.7237
chr14	107349540	81848533	0.7624	1.8812
chr15	102531392	67165507	0.6551	1.6553
chr16	90354753	80121806	0.8867	12.4737
chr17	81195210	58854934	0.7249	13.3248
chr18	78077248	102140770	1.3082	13.4473
chr19	59128983	31608576	0.5346	6.5657
chr20	63025520	62167285	0.9864	4.0143
chr21	48129895	24241594	0.5037	5.0732
chr22	51304566	13410862	0.2614	1.0141
chrMT	16571	4778784	288.3824	151.5315
chrX	155270560	84870946	0.5466	2.5091

chrY	59373566	5447054	0.0917	11.1378

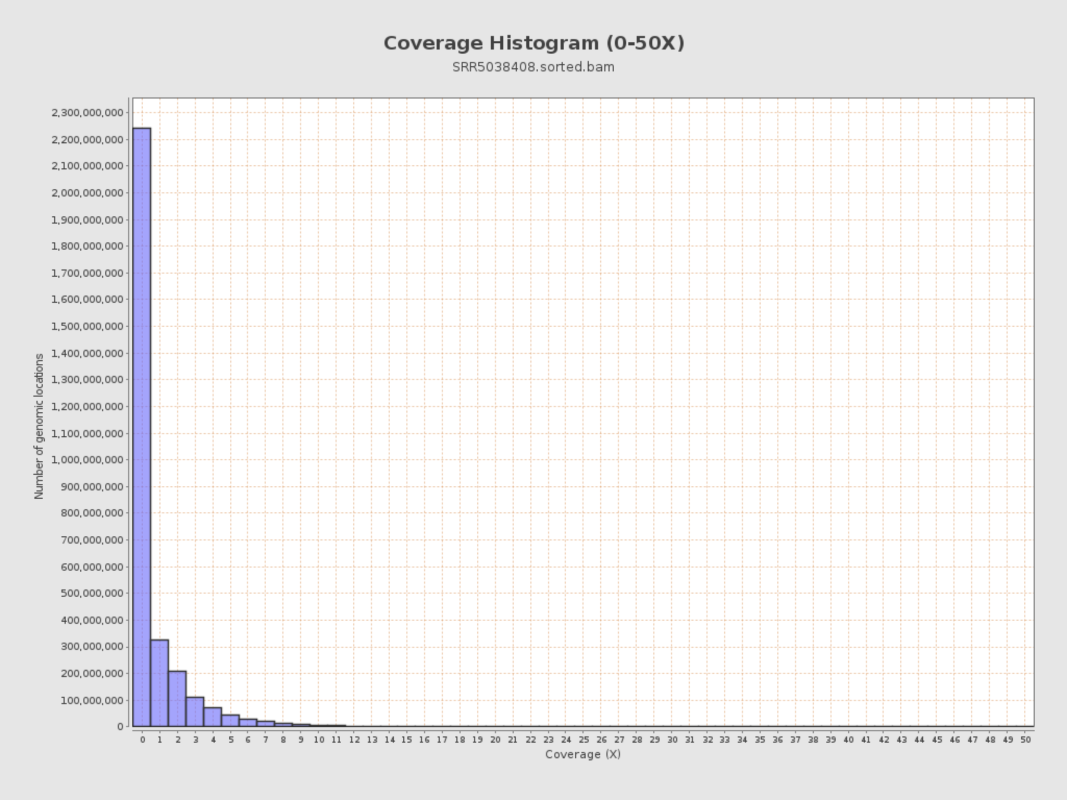
3. Results : Coverage across reference



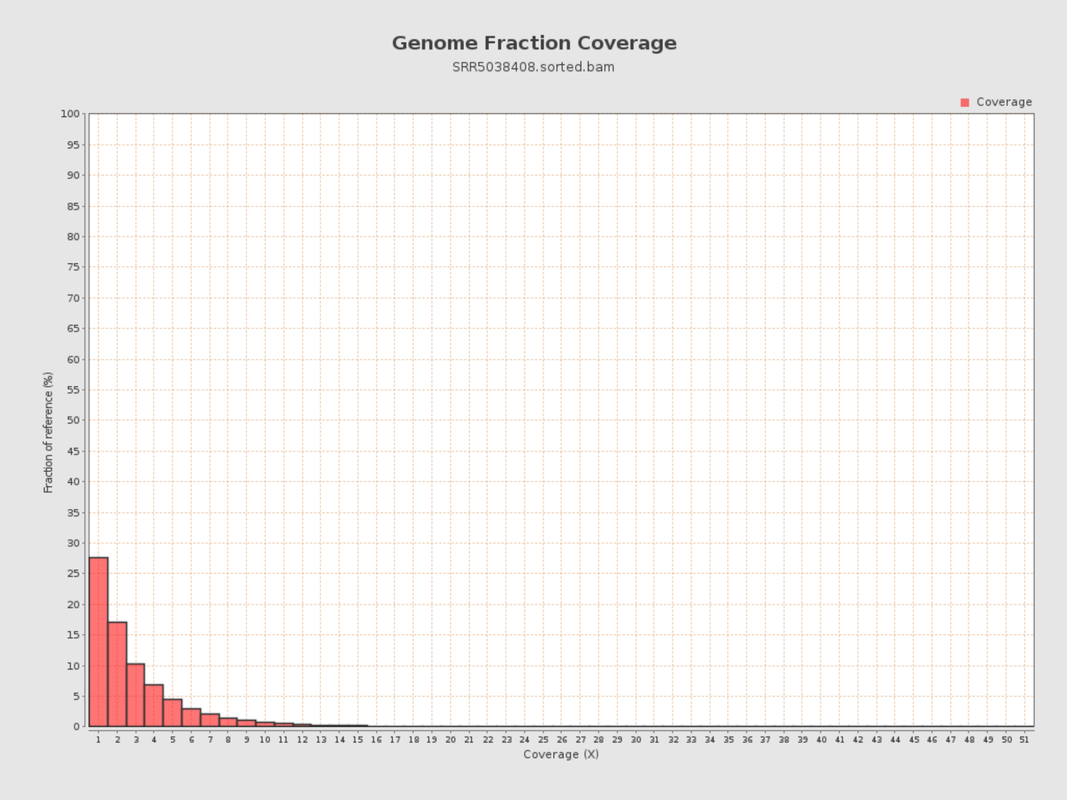
4. Results : Coverage Histogram



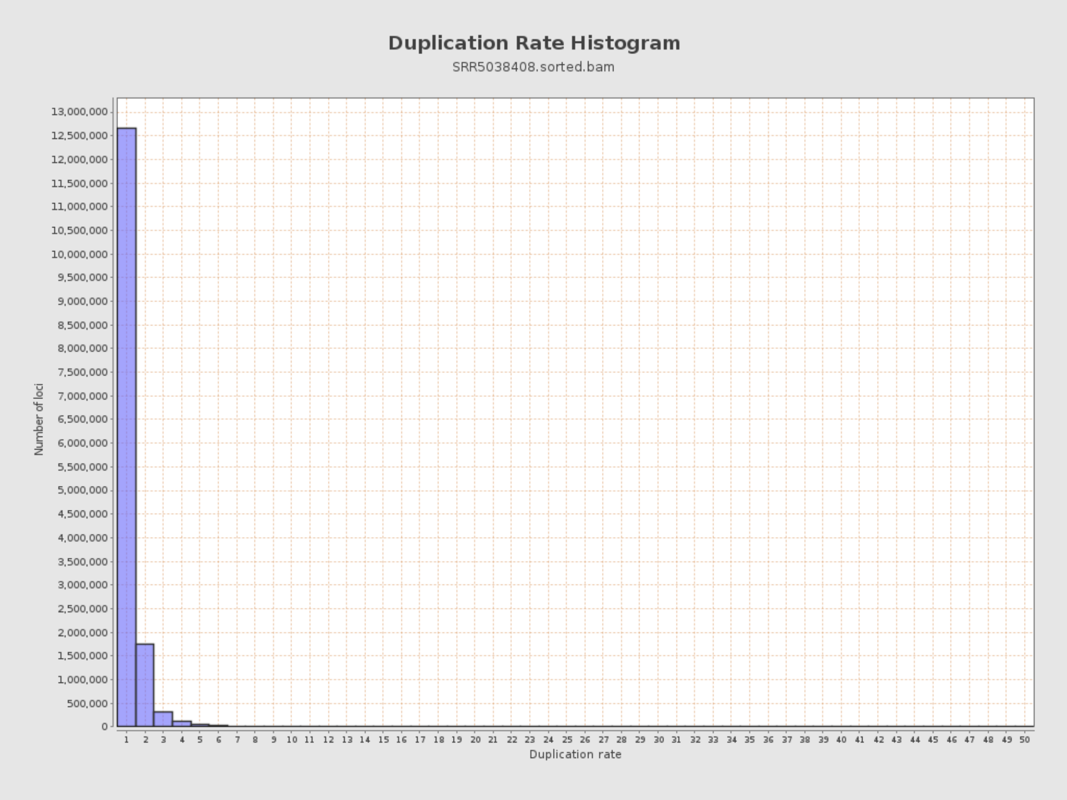
5. Results : Coverage Histogram (0-50X)



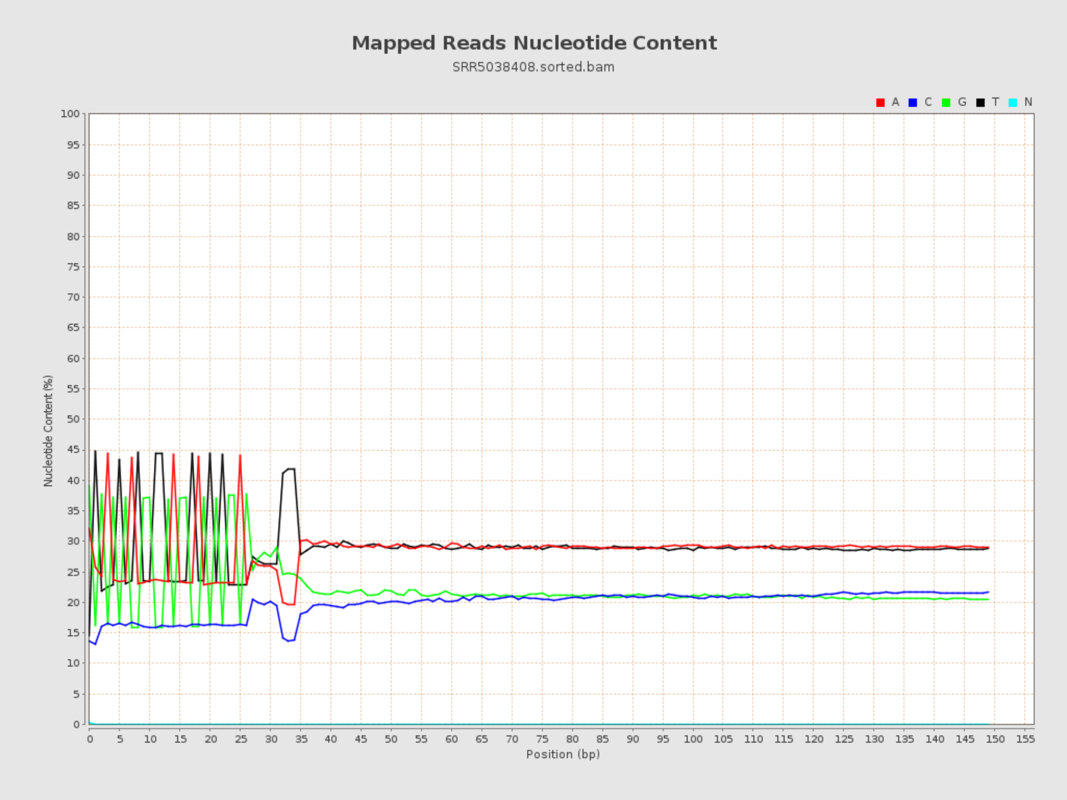
6. Results : Genome Fraction Coverage



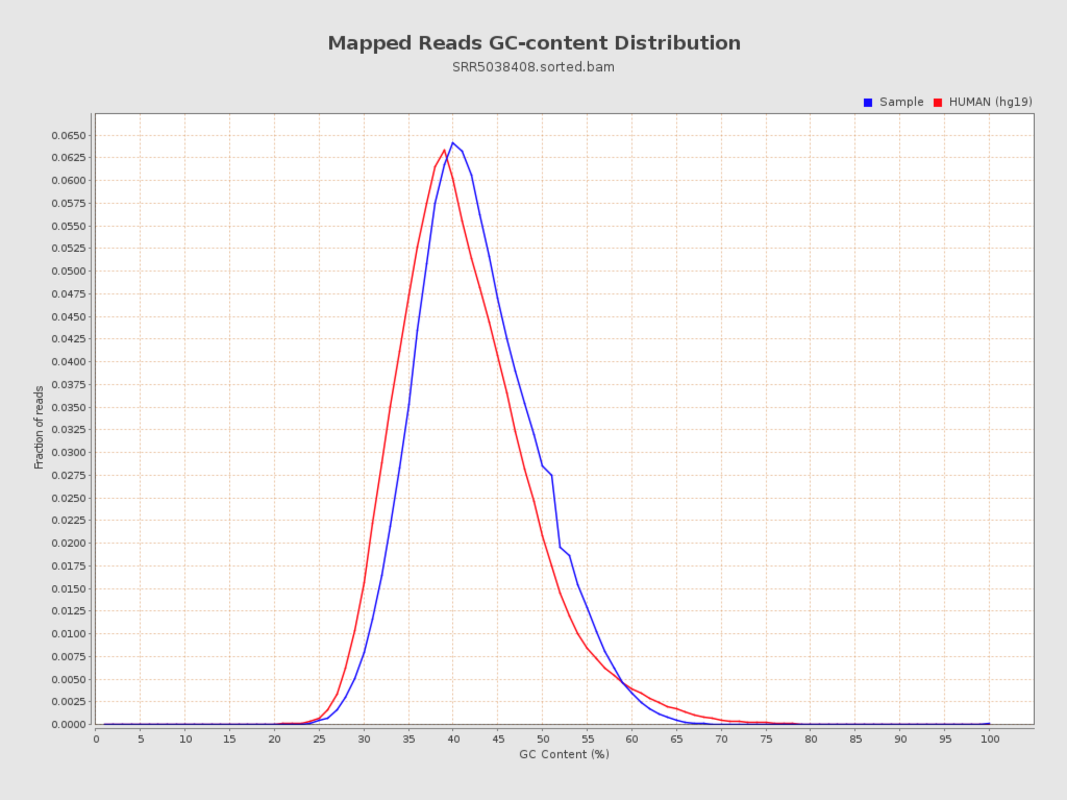
7. Results : Duplication Rate Histogram



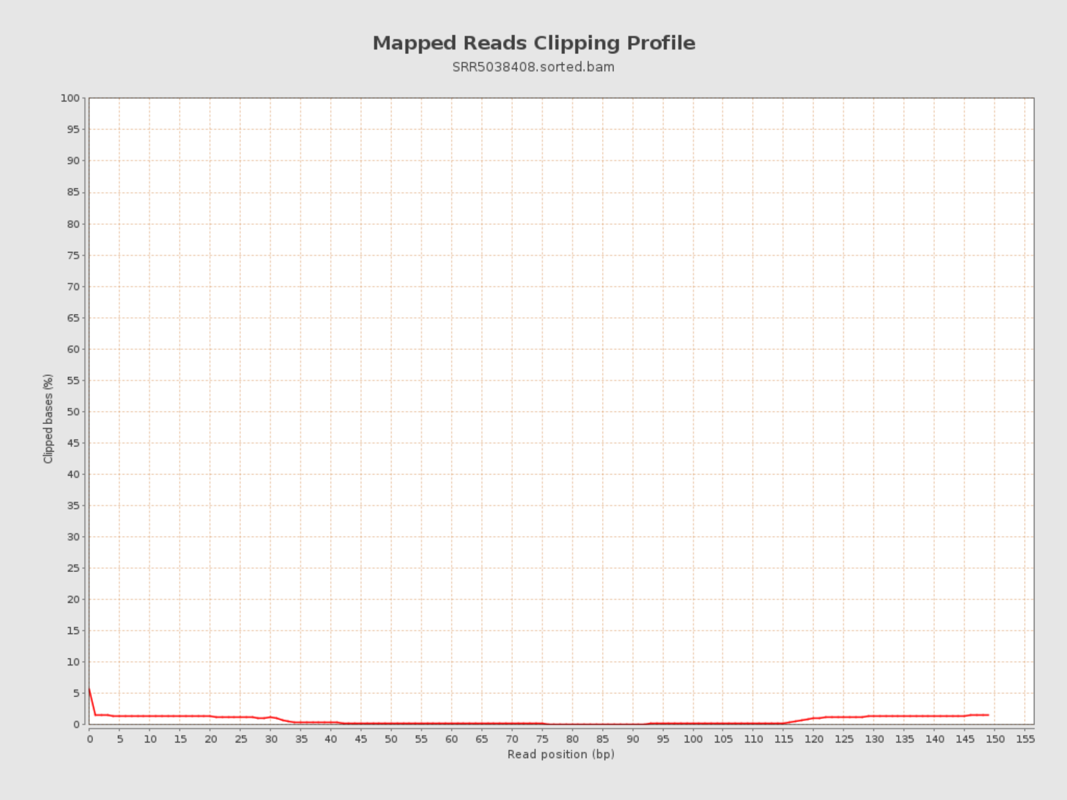
8. Results : Mapped Reads Nucleotide Content



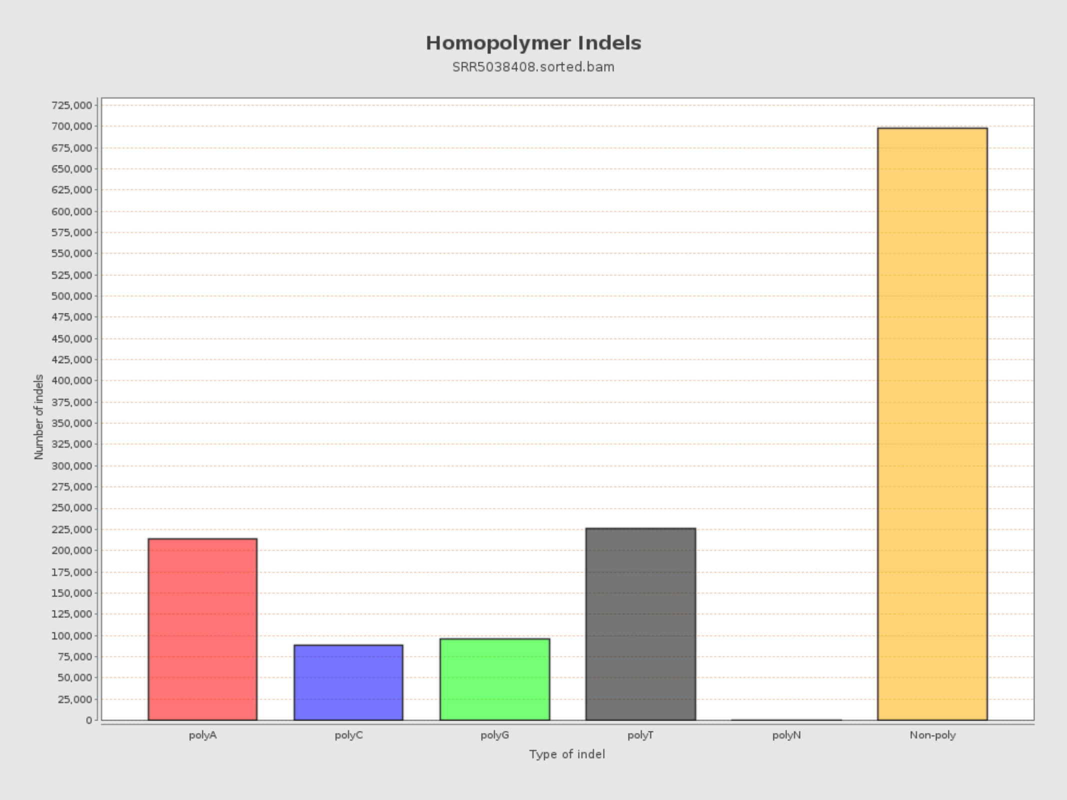
9. Results : Mapped Reads GC-content Distribution



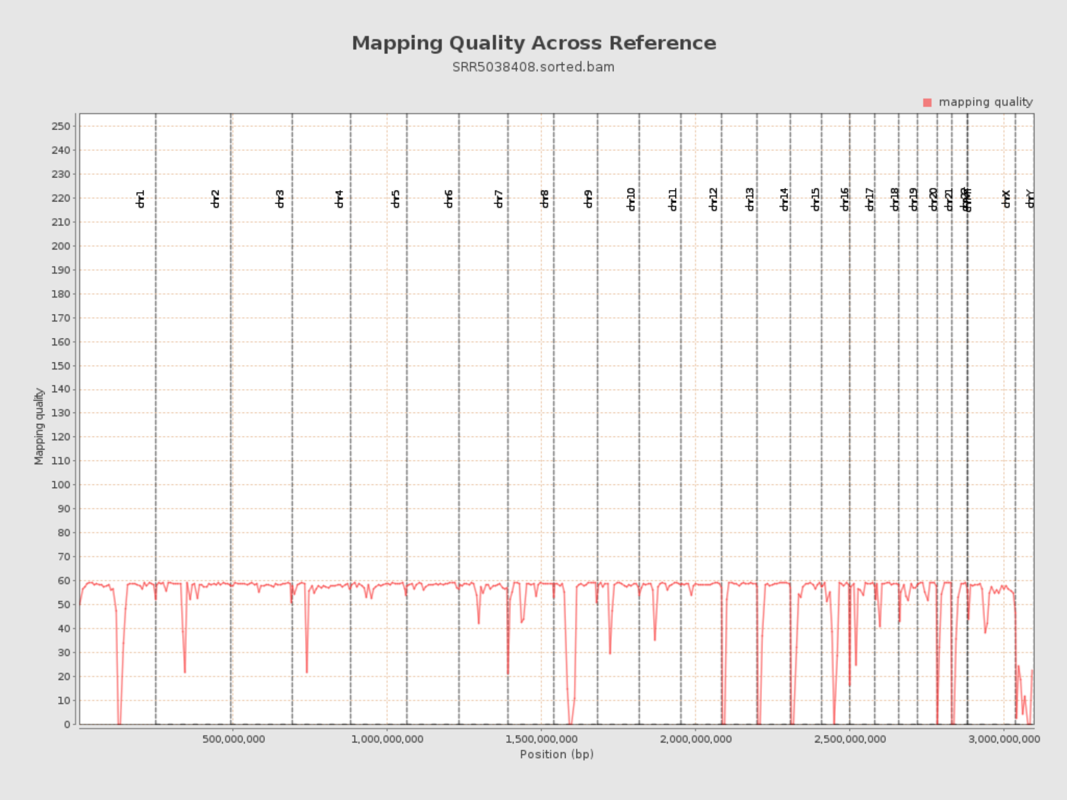
10. Results : Mapped Reads Clipping Profile



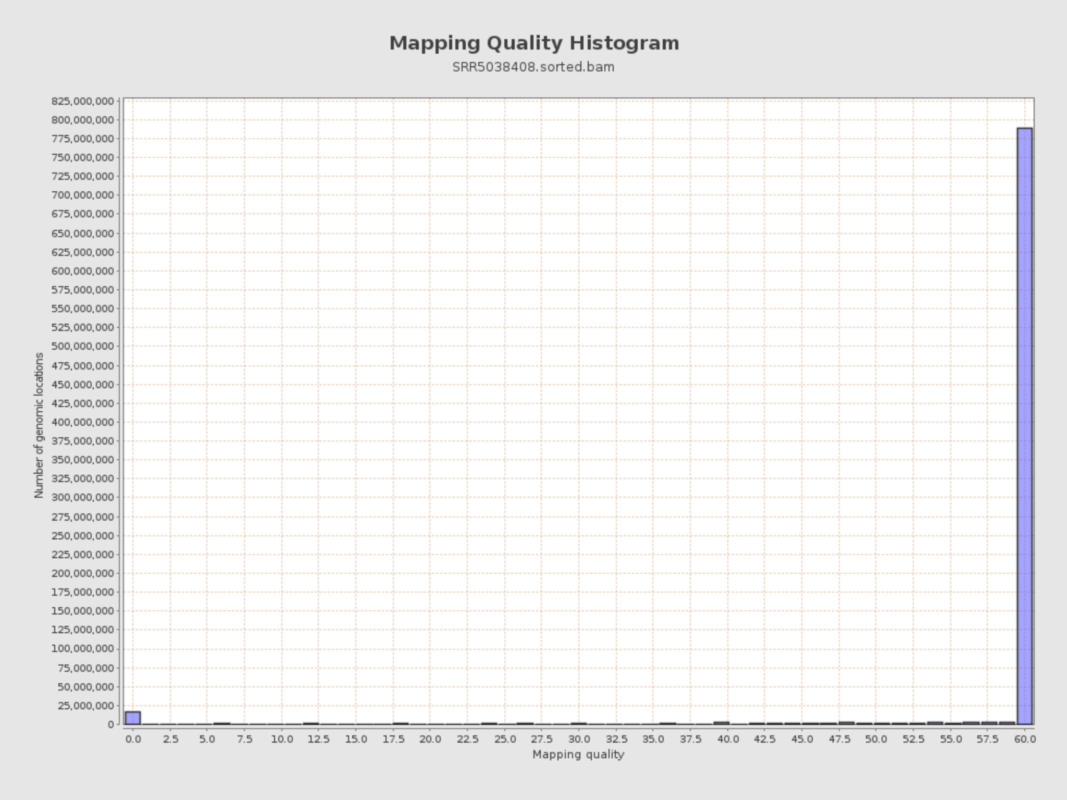
11. Results : Homopolymer Indels



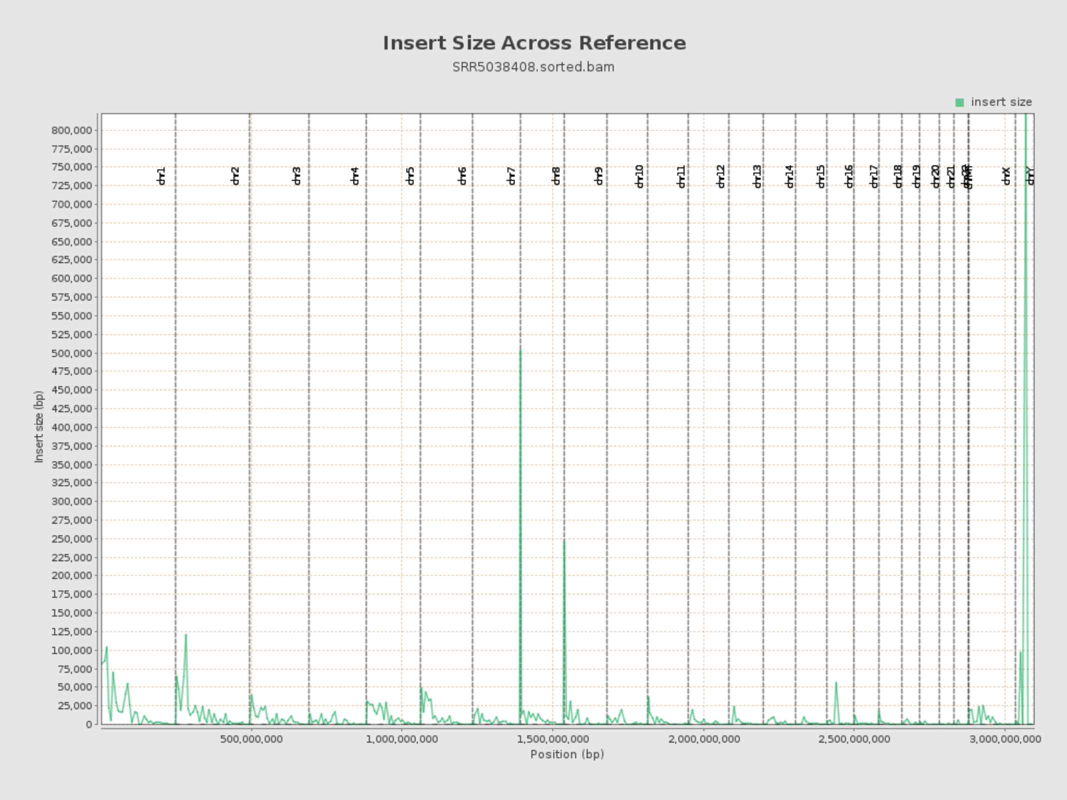
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram