Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 09:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038490.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_SRR5038490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038490_1.fastq.gz SRR5038490_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 09:42:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,187,652
Mapped reads	13,889,433 / 97.9%
Unmapped reads	298,219 / 2.1%
Mapped paired reads	13,889,433 / 97.9%
Mapped reads, first in pair	7,019,502 / 49.48%
Mapped reads, second in pair	6,869,931 / 48.42%
Mapped reads, both in pair	13,725,154 / 96.74%
Mapped reads, singletons	164,279 / 1.16%
Secondary alignments	0
Supplementary alignments	250,700 / 1.77%
Read min/max/mean length	30 / 150 / 150.91
Duplicated reads (estimated)	1,709,979 / 12.05%
Duplication rate	8.22%
Clipped reads	3,238,420 / 22.83%

2.2. ACGT Content

Number/percentage of A's	577,639,000 / 29.04%
Number/percentage of C's	407,713,849 / 20.5%
Number/percentage of T's	579,428,383 / 29.13%
Number/percentage of G's	424,219,102 / 21.33%
Number/percentage of N's	43,231 / 0%

GC Percentage	41.83%

2.3. Coverage

Mean	0.643
Standard Deviation	7.0435

2.4. Mapping Quality

Mean Mapping Quality	53.9

2.5. Insert size

Mean	86,784
Standard Deviation	2,793,740.52
P25/Median/P75	223 / 264 / 316

2.6. Mismatches and indels

General error rate	1.33%
Mismatches	25,520,438
Insertions	331,462
Mapped reads with at least one insertion	2.25%
Deletions	658,570
Mapped reads with at least one deletion	4.56%
Homopolymer indels	47.65%

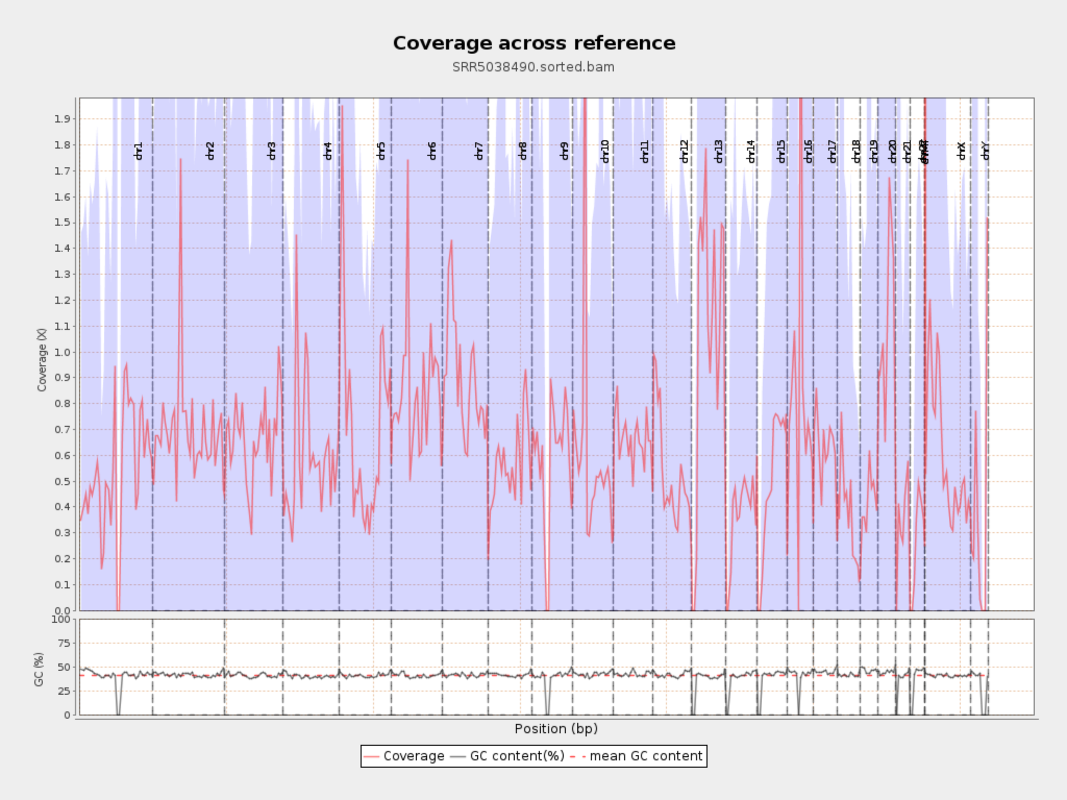
2.7. Chromosome stats

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

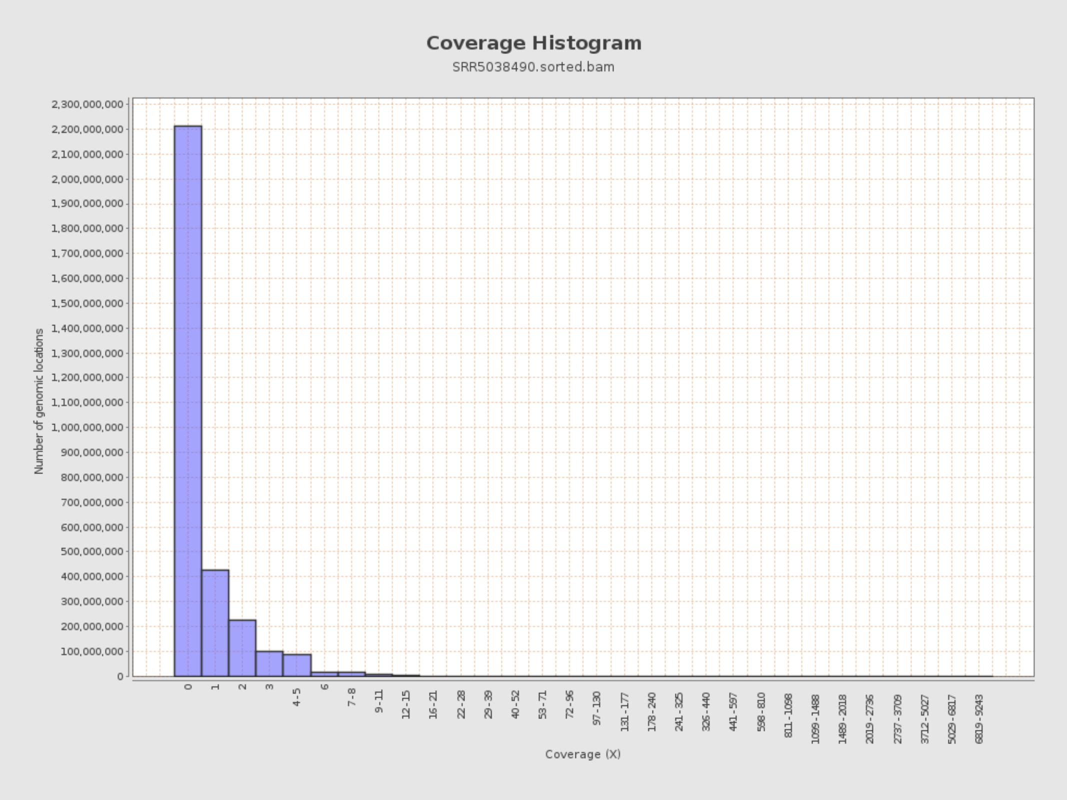
		bases	coverage	deviation
chr1	249250621	133601811	0.536	7.6343
chr2	243199373	171774254	0.7063	7.1812
chr3	198022430	132314852	0.6682	1.3925
chr4	191154276	113090376	0.5916	6.8624
chr5	180915260	129527531	0.716	1.5596
chr6	171115067	145603592	0.8509	8.6679
chr7	159138663	141873218	0.8915	7.4514
chr8	146364022	83819113	0.5727	1.829
chr9	141213431	80938891	0.5732	9.6873
chr10	135534747	85807986	0.6331	18.5752
chr11	135006516	88816566	0.6579	3.1801
chr12	133851895	72160515	0.5391	1.244
chr13	115169878	123128267	1.0691	1.9793
chr14	107349540	38385557	0.3576	1.0361
chr15	102531392	49904629	0.4867	1.1561
chr16	90354753	76357431	0.8451	12.983
chr17	81195210	50680425	0.6242	3.5813
chr18	78077248	28607860	0.3664	8.1114
chr19	59128983	24709296	0.4179	4.2446
chr20	63025520	70743662	1.1225	2.8265
chr21	48129895	16783096	0.3487	3.0758
chr22	51304566	13792381	0.2688	0.9213
chrMT	16571	1314019	79.2963	34.4996
chrX	155270560	93346536	0.6012	1.5718

chrY	59373566	23323764	0.3928	11.7

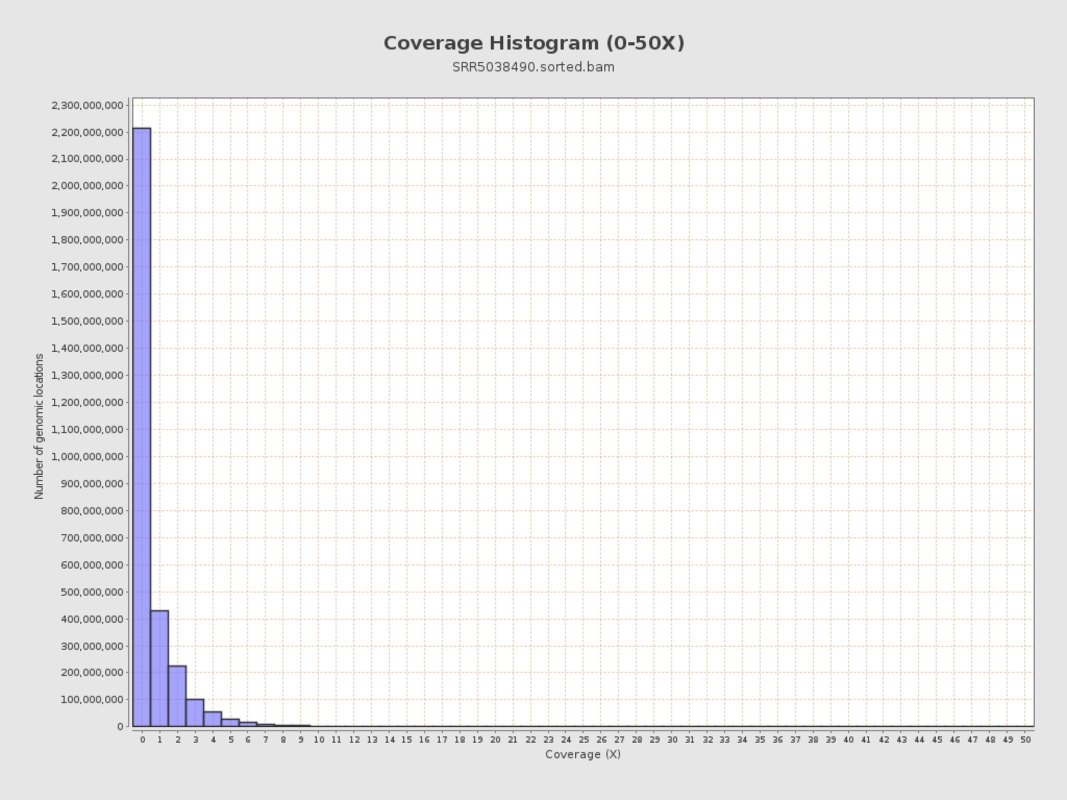
3. Results : Coverage across reference



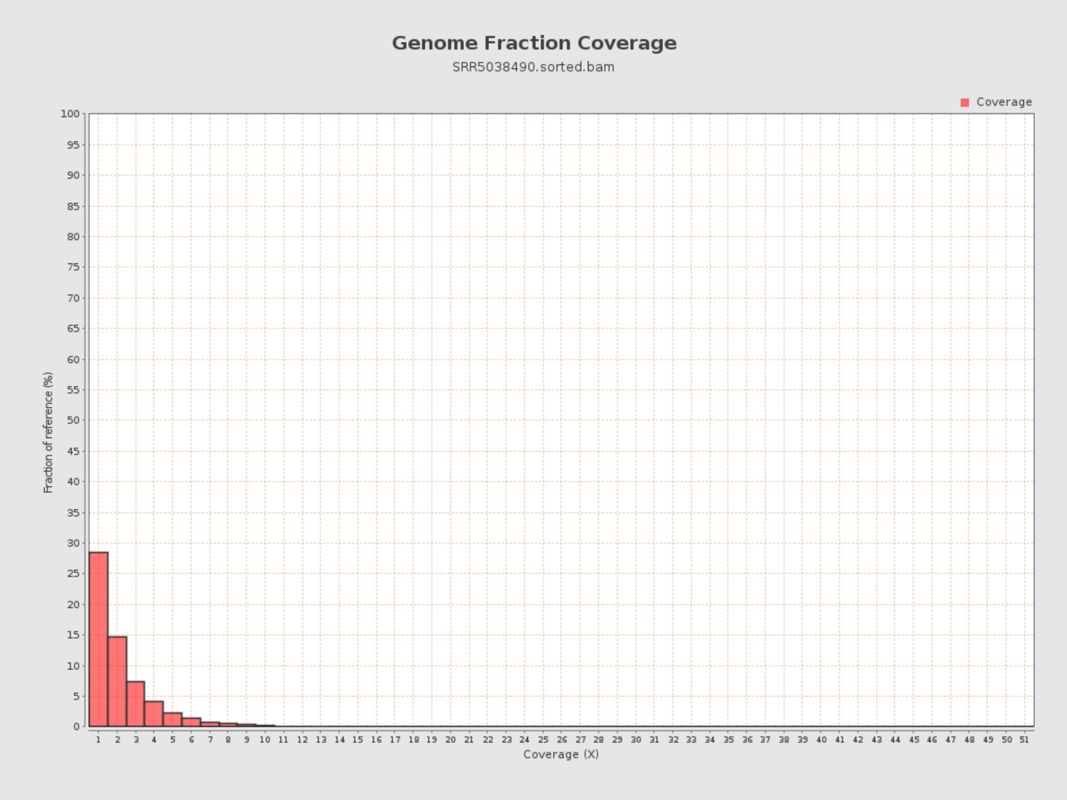
4. Results : Coverage Histogram



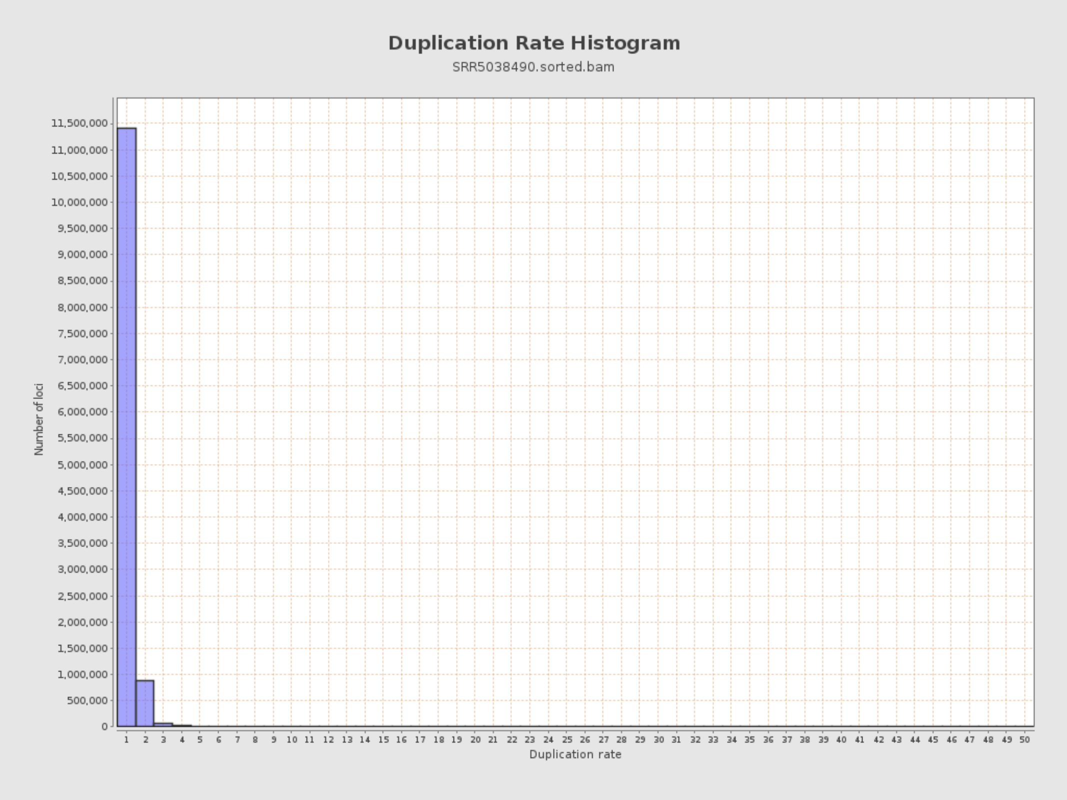
5. Results : Coverage Histogram (0-50X)



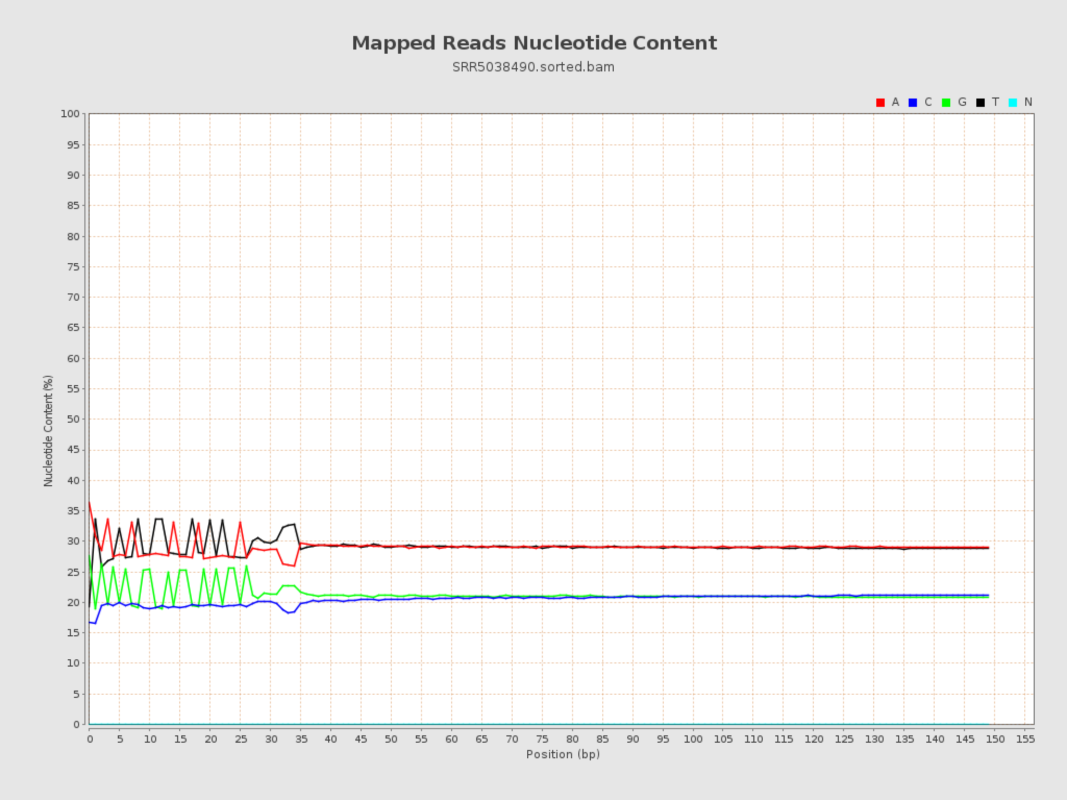
6. Results : Genome Fraction Coverage



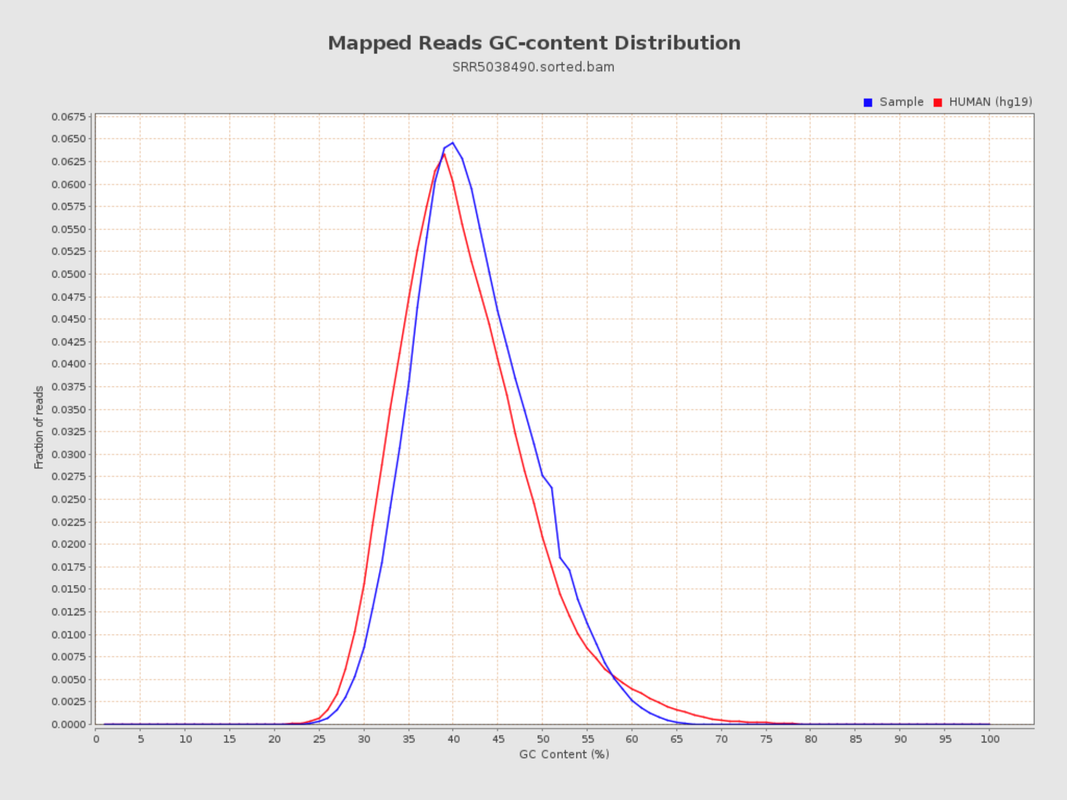
7. Results : Duplication Rate Histogram



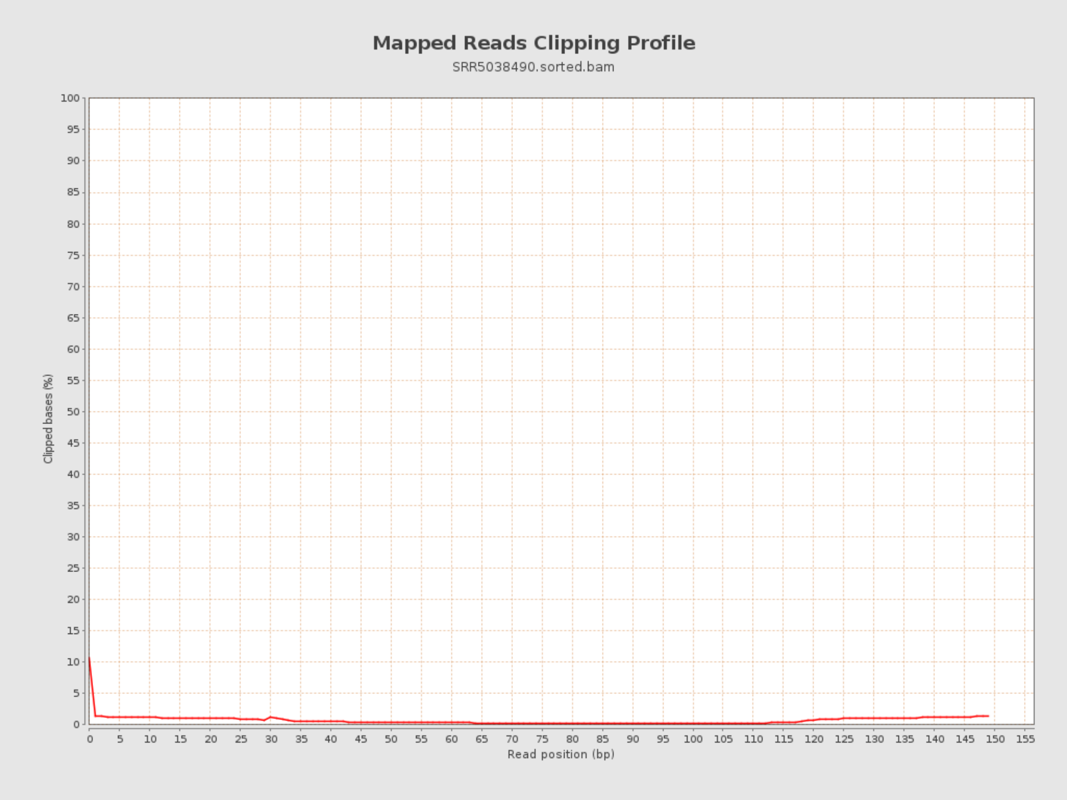
8. Results : Mapped Reads Nucleotide Content



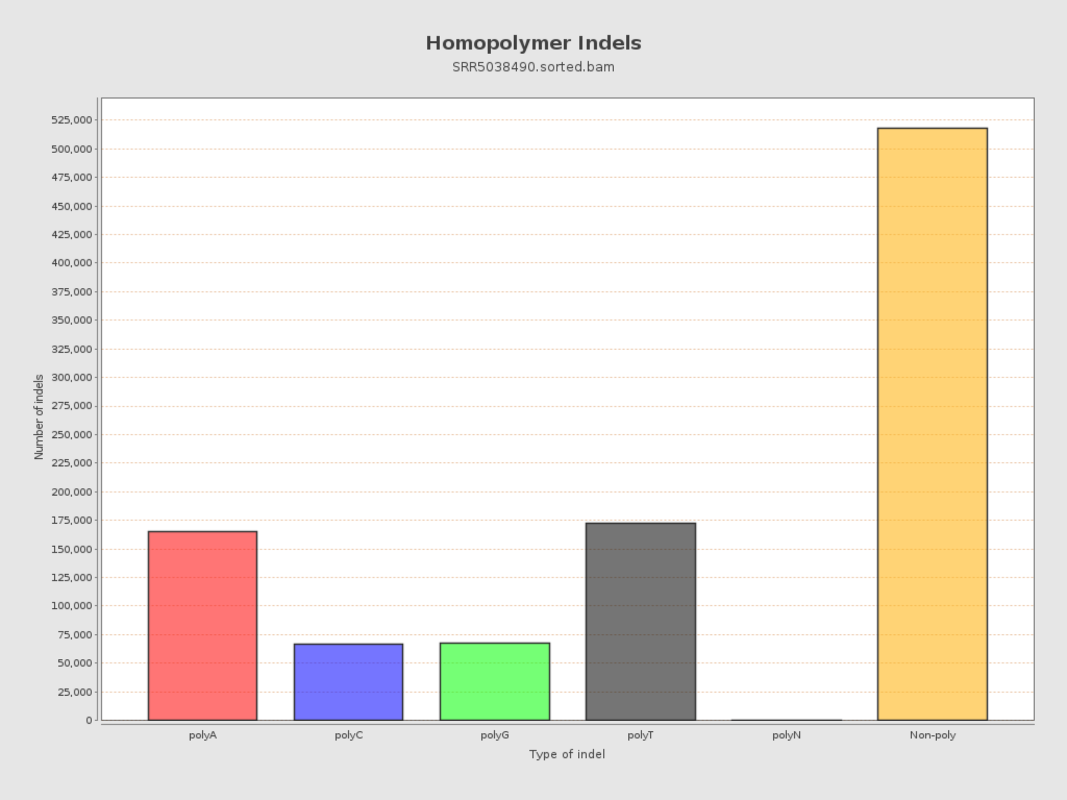
9. Results : Mapped Reads GC-content Distribution



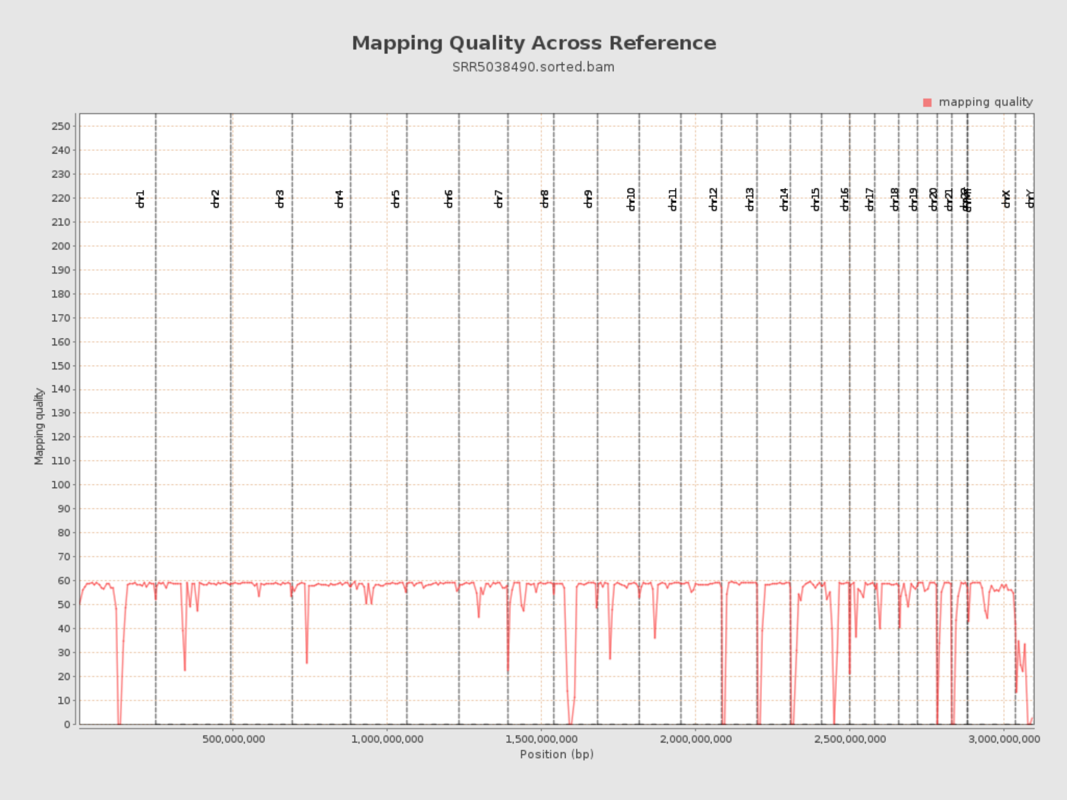
10. Results : Mapped Reads Clipping Profile



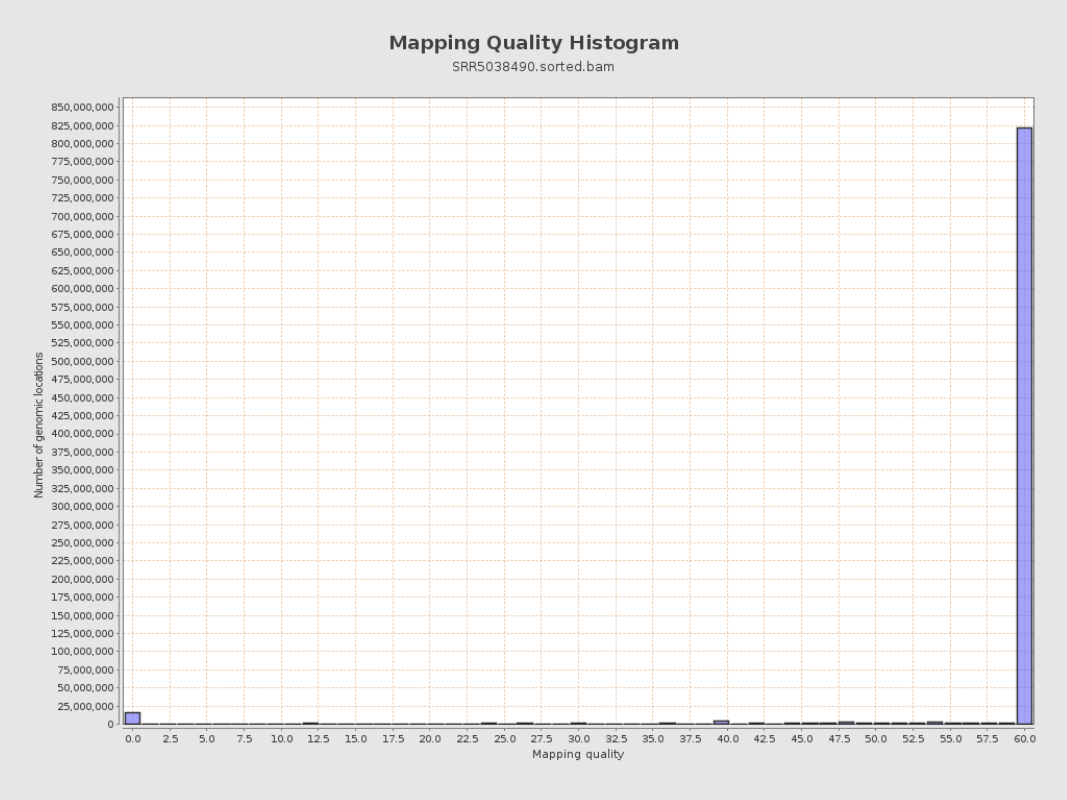
11. Results : Homopolymer Indels



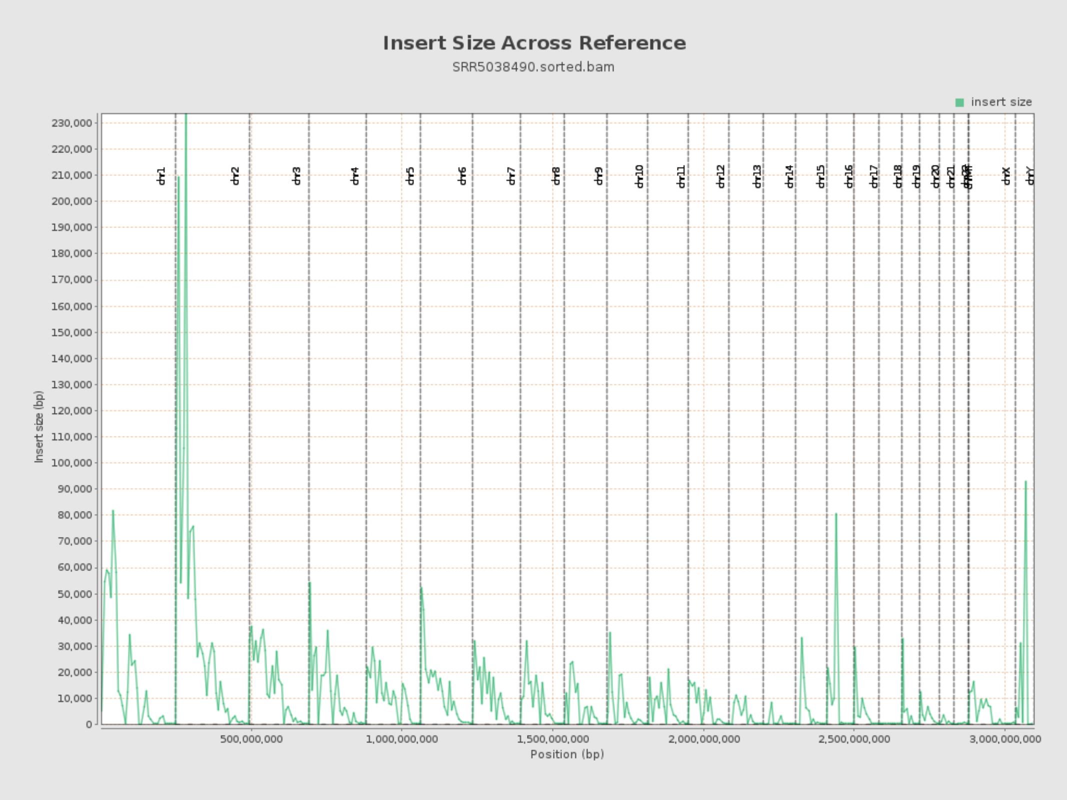
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram