Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/16 14:29:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038497.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_SRR5038497 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038497_1.fastq.gz SRR5038497_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 16 14:29:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038497.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,526,106
Mapped reads	12,211,315 / 97.49%
Unmapped reads	314,791 / 2.51%
Mapped paired reads	12,211,315 / 97.49%
Mapped reads, first in pair	6,178,630 / 49.33%
Mapped reads, second in pair	6,032,685 / 48.16%
Mapped reads, both in pair	12,051,740 / 96.21%
Mapped reads, singletons	159,575 / 1.27%
Secondary alignments	0
Supplementary alignments	185,663 / 1.48%
Read min/max/mean length	30 / 150 / 150.76
Duplicated reads (estimated)	1,523,941 / 12.17%
Duplication rate	8.22%
Clipped reads	2,607,347 / 20.82%

2.2. ACGT Content

Number/percentage of A's	509,692,283 / 29.05%
Number/percentage of C's	360,814,466 / 20.57%
Number/percentage of T's	510,191,885 / 29.08%
Number/percentage of G's	373,721,600 / 21.3%
Number/percentage of N's	36,731 / 0%

GC Percentage	41.87%

2.3. Coverage

Mean	0.5671
Standard Deviation	6.5607

2.4. Mapping Quality

Mean Mapping Quality	53.89

2.5. Insert size

Mean	84,765.6
Standard Deviation	2,764,674.53
P25/Median/P75	221 / 263 / 316

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	23,778,262
Insertions	290,704
Mapped reads with at least one insertion	2.24%
Deletions	597,004
Mapped reads with at least one deletion	4.7%
Homopolymer indels	47.54%

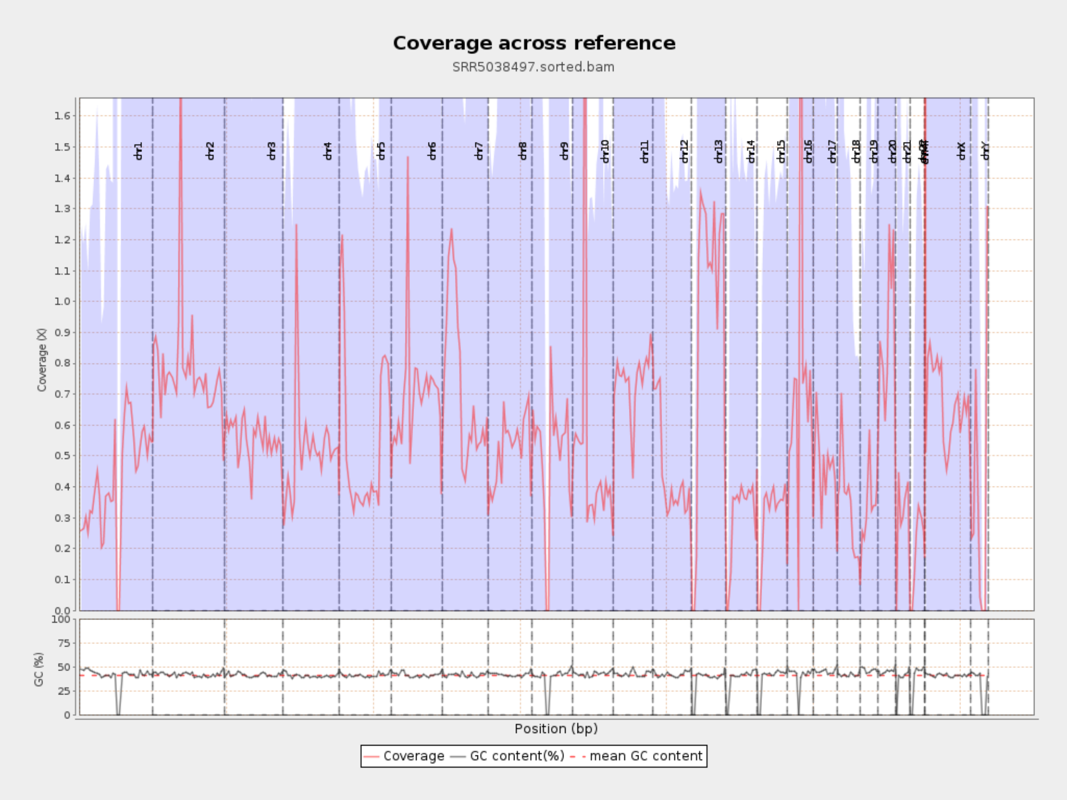
2.7. Chromosome stats

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

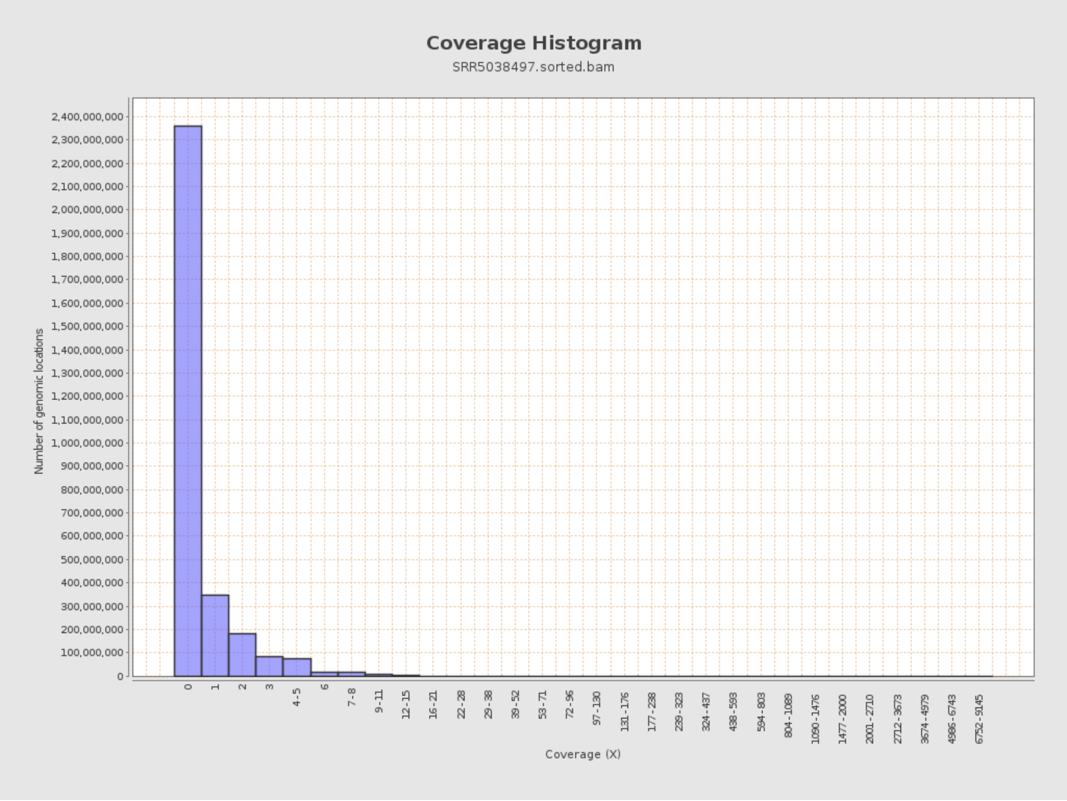
		bases	coverage	deviation
chr1	249250621	104715822	0.4201	4.0766
chr2	243199373	192209361	0.7903	7.4152
chr3	198022430	110258108	0.5568	1.3474
chr4	191154276	98878916	0.5173	5.5726
chr5	180915260	100151516	0.5536	1.415
chr6	171115067	120326061	0.7032	8.2556
chr7	159138663	115175182	0.7237	5.9607
chr8	146364022	76659900	0.5238	1.8128
chr9	141213431	68787286	0.4871	8.7454
chr10	135534747	72652162	0.536	18.2353
chr11	135006516	98775138	0.7316	3.7638
chr12	133851895	59521900	0.4447	1.2061
chr13	115169878	114272779	0.9922	2.0682
chr14	107349540	32217733	0.3001	1.0222
chr15	102531392	30544248	0.2979	0.9192
chr16	90354753	69275400	0.7667	14.249
chr17	81195210	37089352	0.4568	3.5698
chr18	78077248	26616324	0.3409	7.8769
chr19	59128983	19409518	0.3283	2.3535
chr20	63025520	55784443	0.8851	2.4439
chr21	48129895	14882269	0.3092	2.758
chr22	51304566	10064926	0.1962	0.8378
chrMT	16571	656283	39.6043	18.9242
chrX	155270560	104008546	0.6699	1.7336

chrY	59373566	22711175	0.3825	10.6088

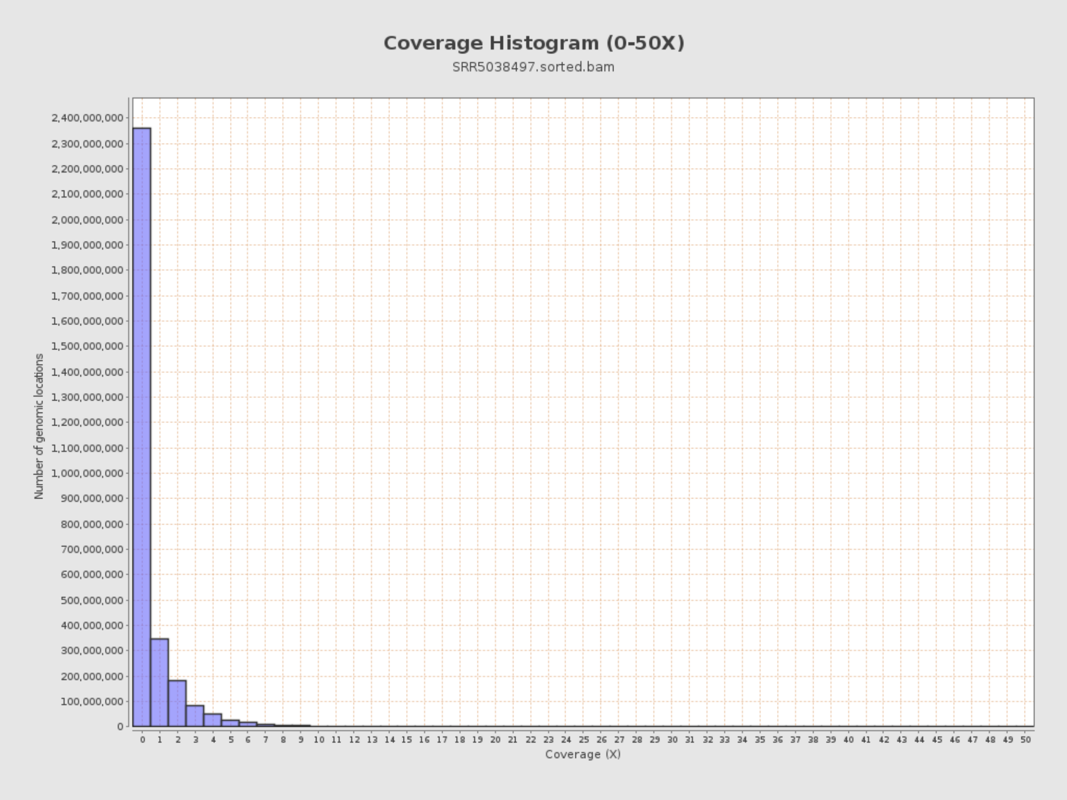
3. Results : Coverage across reference



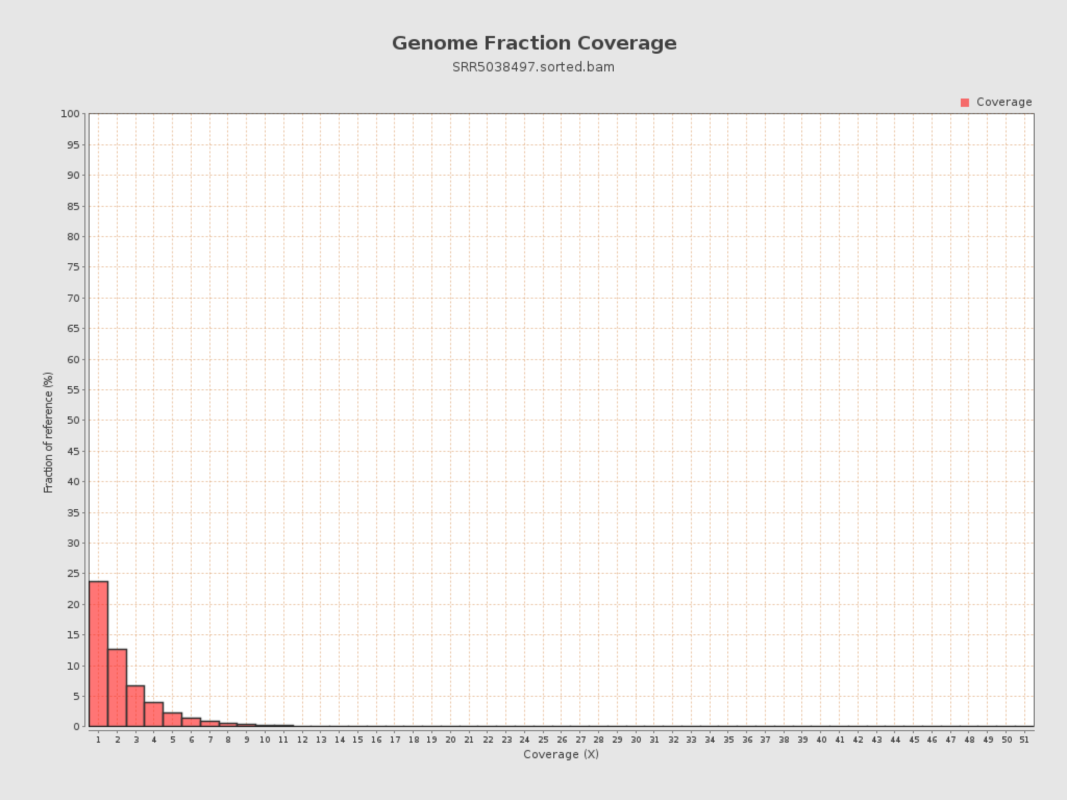
4. Results : Coverage Histogram



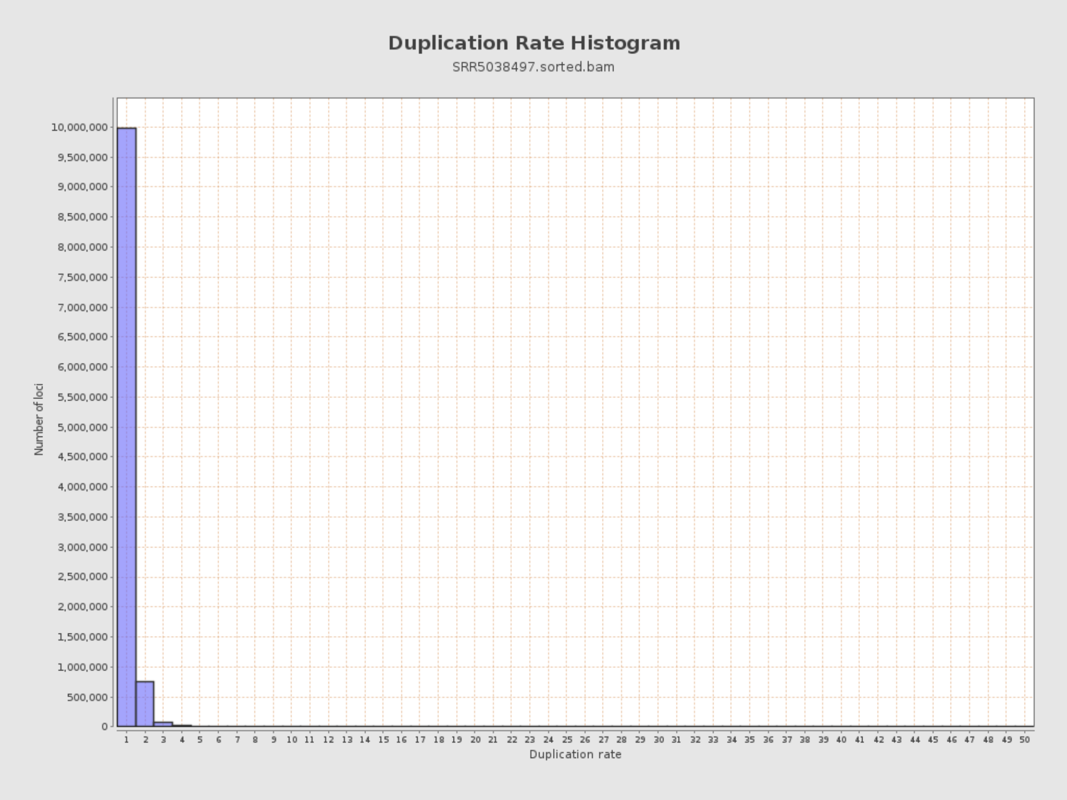
5. Results : Coverage Histogram (0-50X)



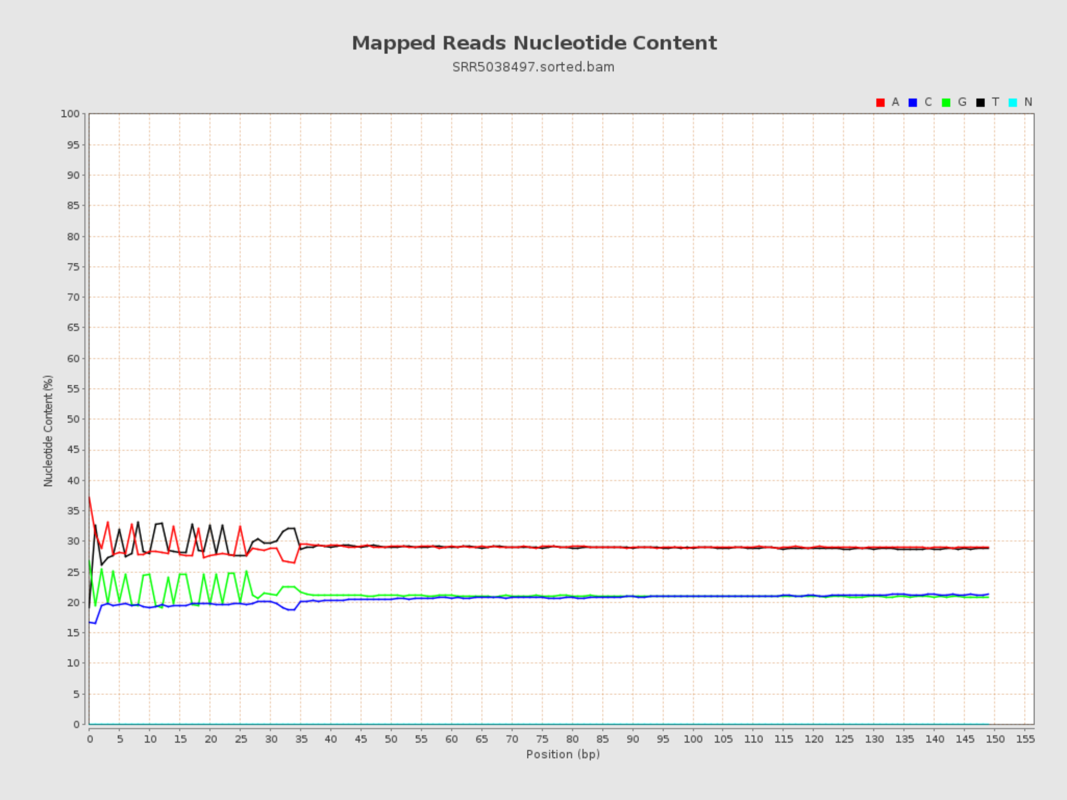
6. Results : Genome Fraction Coverage



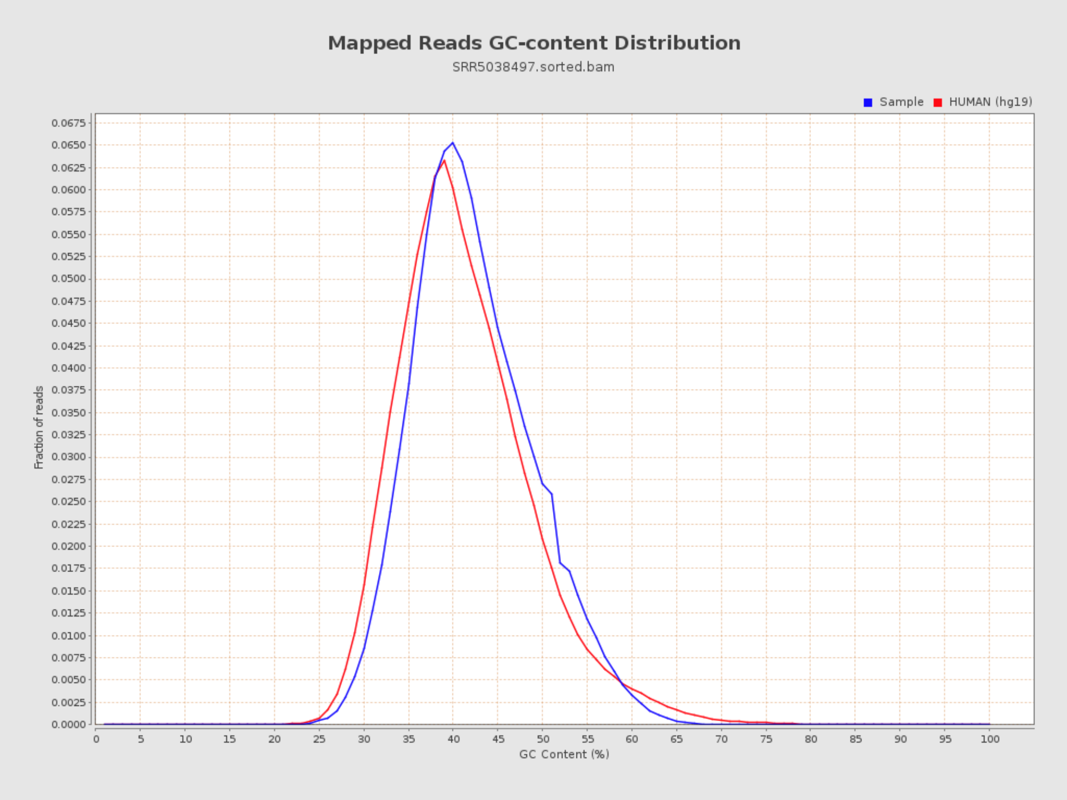
7. Results : Duplication Rate Histogram



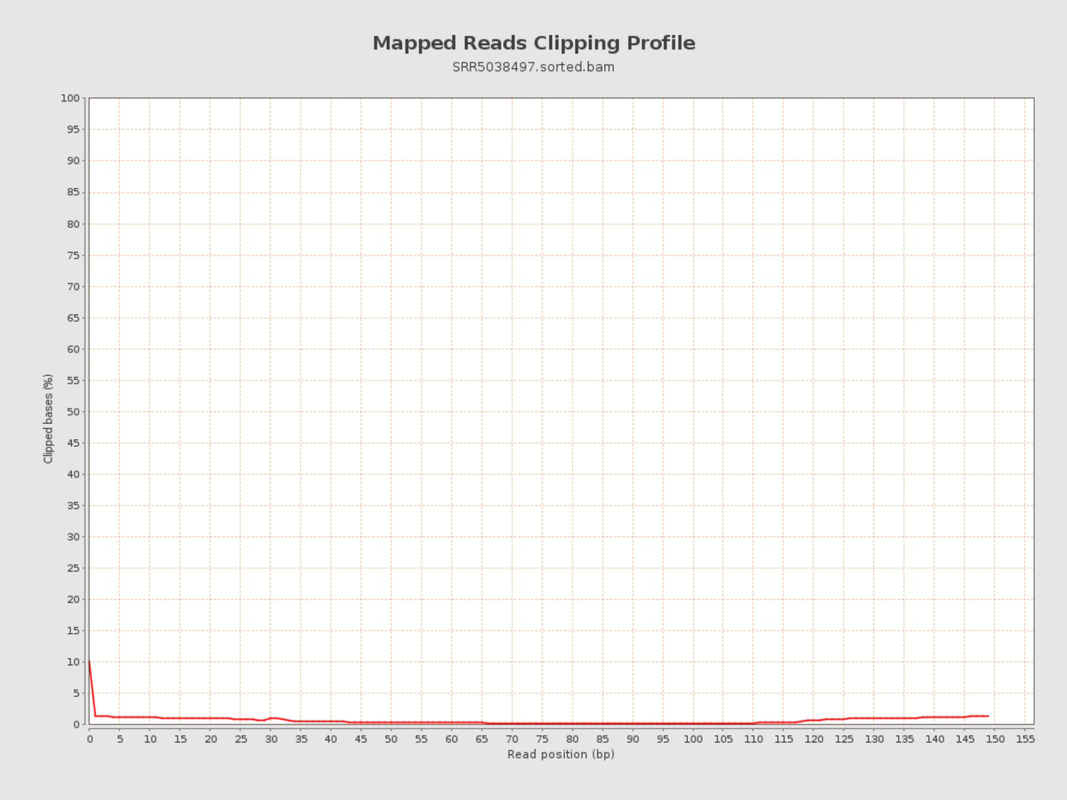
8. Results : Mapped Reads Nucleotide Content



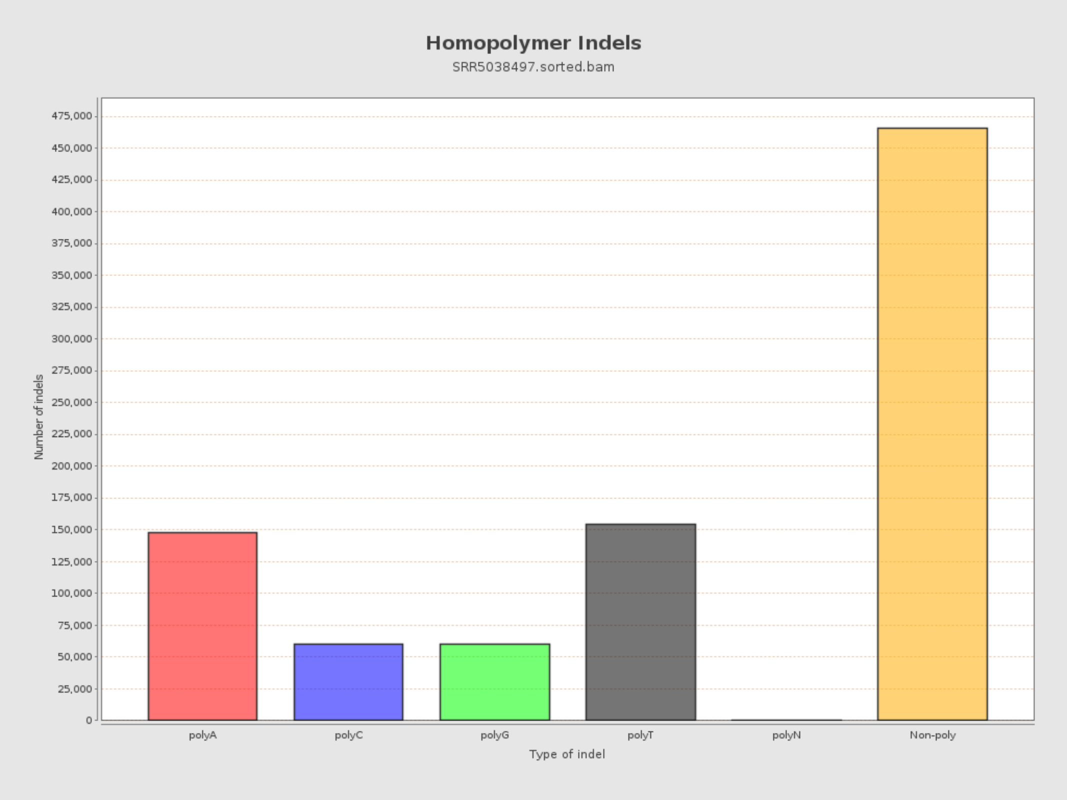
9. Results : Mapped Reads GC-content Distribution



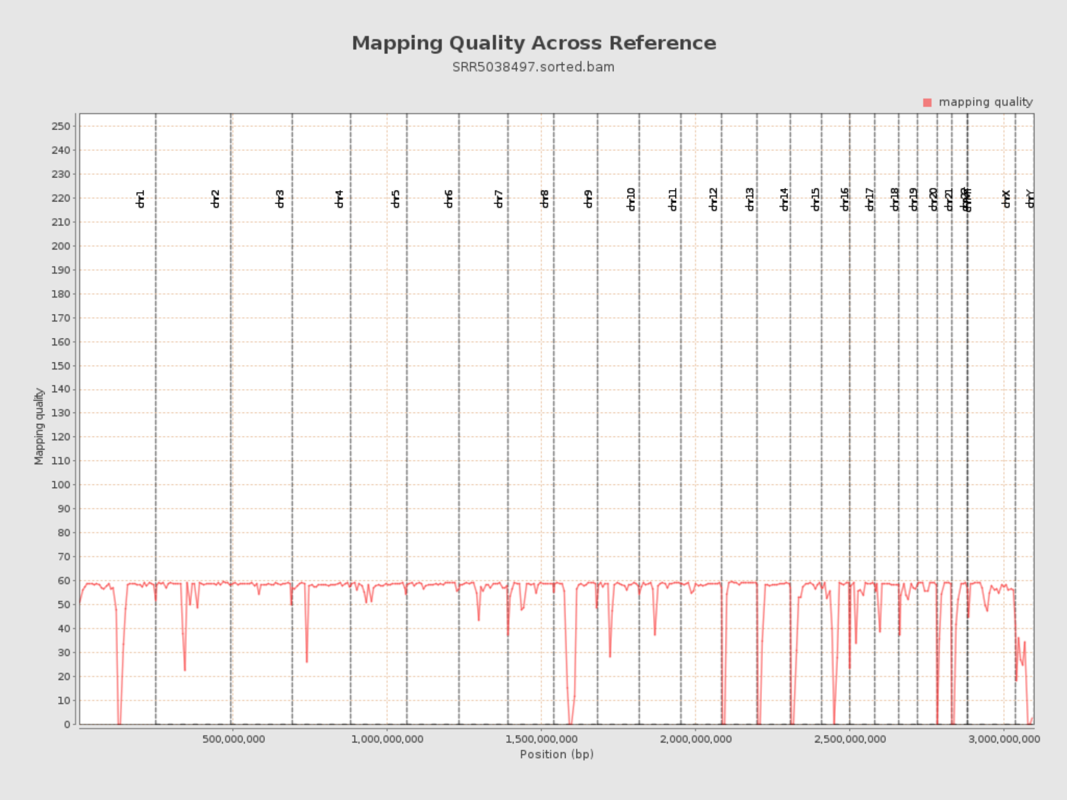
10. Results : Mapped Reads Clipping Profile



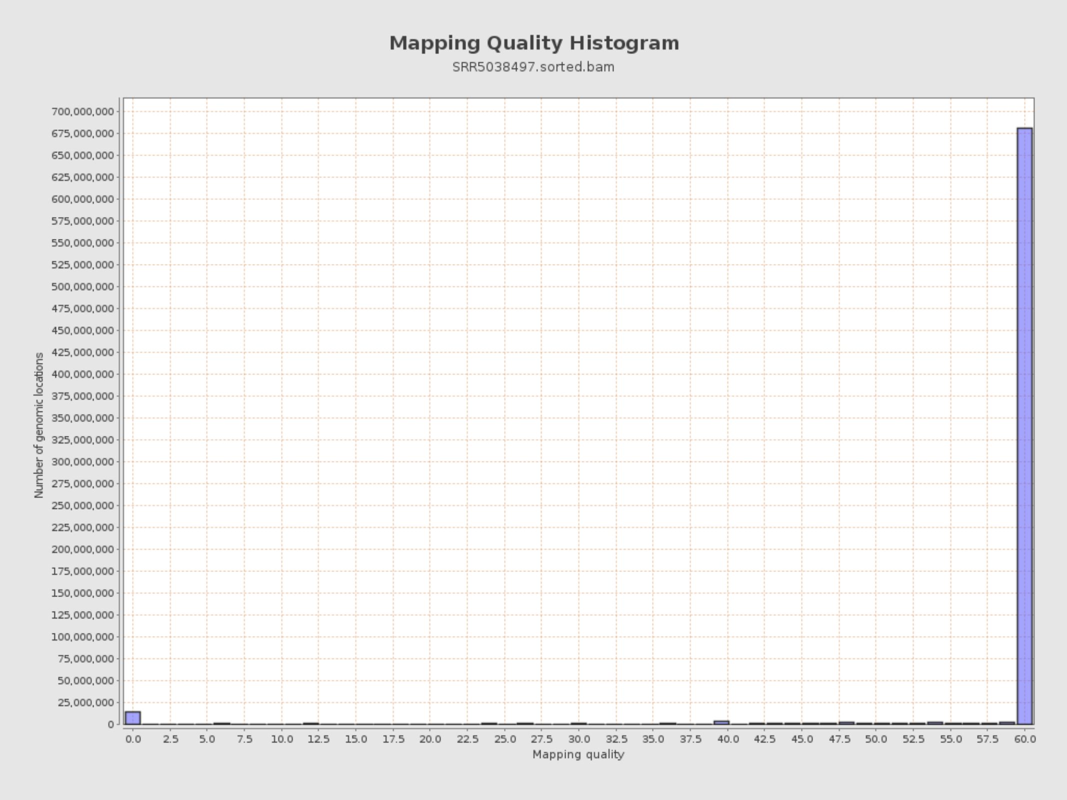
11. Results : Homopolymer Indels



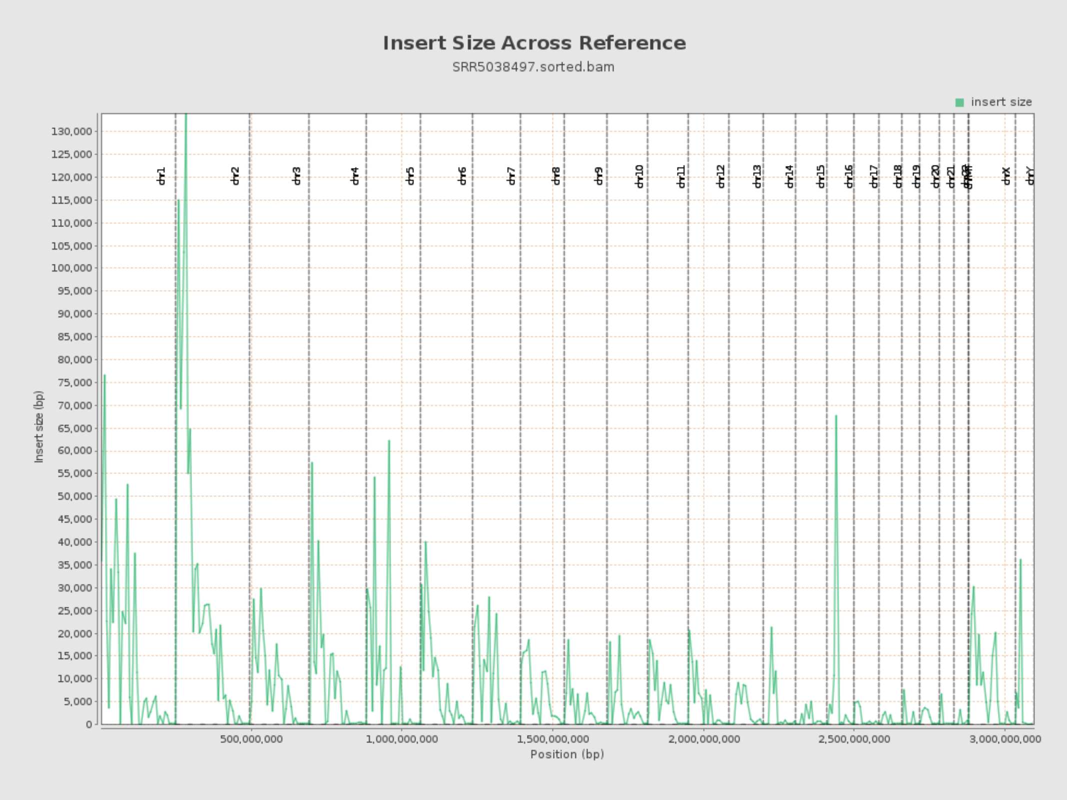
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram