Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/06 16:11:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124837.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_SRR3124837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124837_1.fastq.gz SRR3124837_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 06 16:11:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	830,295,530
Mapped reads	819,936,146 / 98.75%
Unmapped reads	10,359,384 / 1.25%
Mapped paired reads	819,936,146 / 98.75%
Mapped reads, first in pair	412,656,254 / 49.7%
Mapped reads, second in pair	407,279,892 / 49.05%
Mapped reads, both in pair	813,861,092 / 98.02%
Mapped reads, singletons	6,075,054 / 0.73%
Secondary alignments	0
Supplementary alignments	7,063,399 / 0.85%
Read min/max/mean length	30 / 150 / 150.39
Duplicated reads (estimated)	213,405,605 / 25.7%
Duplication rate	22.82%
Clipped reads	89,467,115 / 10.78%

2.2. ACGT Content

Number/percentage of A's	35,499,371,323 / 29.51%
Number/percentage of C's	24,604,111,849 / 20.45%
Number/percentage of T's	35,559,821,241 / 29.56%
Number/percentage of G's	24,630,299,627 / 20.47%
Number/percentage of N's	3,278,066 / 0%

GC Percentage	40.93%

2.3. Coverage

Mean	38.8725
Standard Deviation	280.6769

2.4. Mapping Quality

Mean Mapping Quality	54.51

2.5. Insert size

Mean	54,249.18
Standard Deviation	2,269,239.77
P25/Median/P75	233 / 295 / 368

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	865,428,280
Insertions	12,172,971
Mapped reads with at least one insertion	1.4%
Deletions	13,600,850
Mapped reads with at least one deletion	1.58%
Homopolymer indels	41.66%

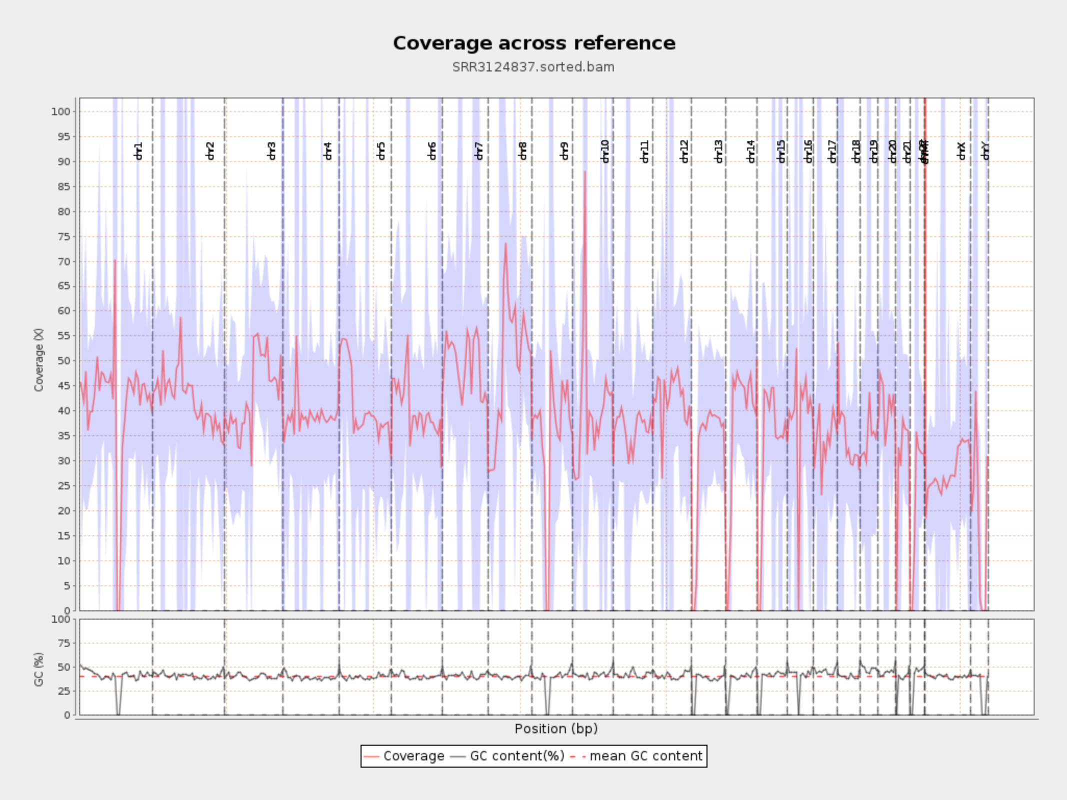
2.7. Chromosome stats

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

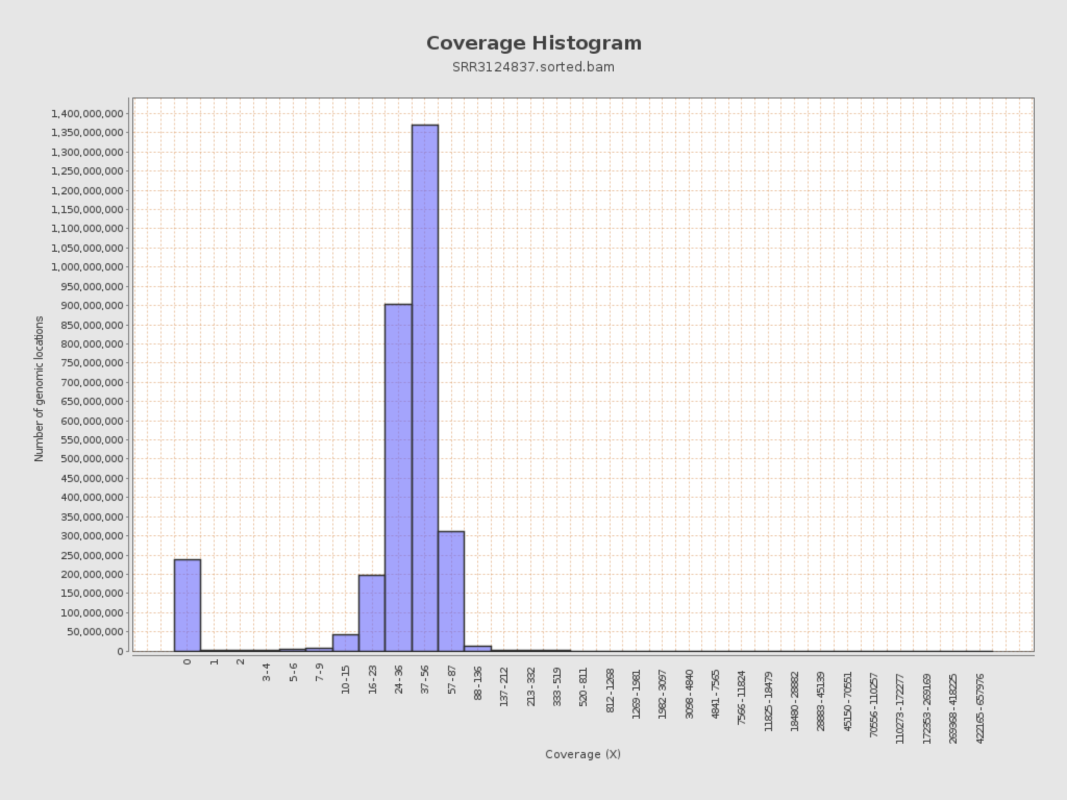
		bases	coverage	deviation
chr1	249250621	10413318560	41.7785	681.6566
chr2	243199373	10334538725	42.4941	270.5948
chr3	198022430	8632773086	43.5949	21.0508
chr4	191154276	7433902732	38.8895	186.6813
chr5	180915260	7456100824	41.2132	35.678
chr6	171115067	6943172004	40.576	110.4459
chr7	159138663	7831595933	49.2124	184.5144
chr8	146364022	7312616832	49.9618	298.4457
chr9	141213431	4928938720	34.9042	330.6606
chr10	135534747	5531064607	40.8092	455.3607
chr11	135006516	4920079912	36.4433	97.9754
chr12	133851895	5702371162	42.6021	190.0842
chr13	115169878	3613893949	31.3788	18.5789
chr14	107349540	3970030180	36.9823	24.7033
chr15	102531392	3304376491	32.2279	107.4523
chr16	90354753	3478007090	38.4928	113.8476
chr17	81195210	2758947016	33.9792	138.4117
chr18	78077248	2649694458	33.9368	306.8731
chr19	59128983	2038143507	34.4694	295.9016
chr20	63025520	2575522905	40.8648	67.5532
chr21	48129895	1491052177	30.9798	124.5963
chr22	51304566	1166020152	22.7274	101.1947
chrMT	16571	425837276	25,697.7416	2,821.8217
chrX	155270560	4333551700	27.9097	49.8404

chrY	59373566	1091887441	18.3901	239.1948

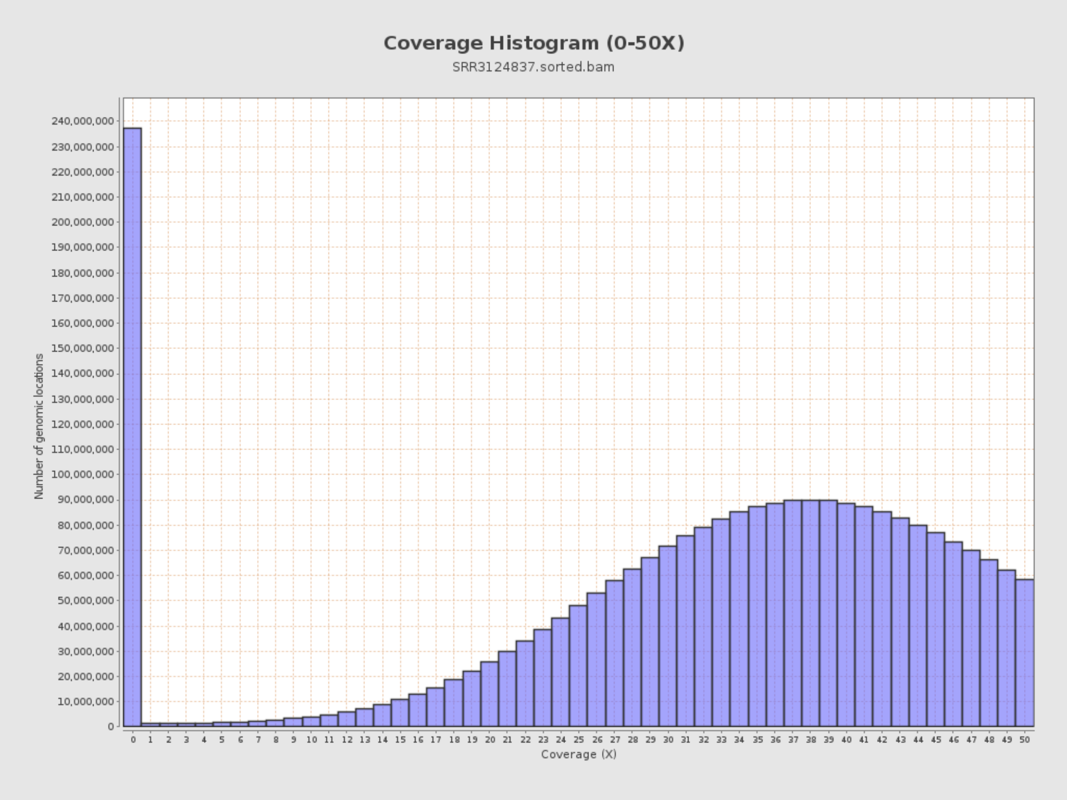
3. Results : Coverage across reference



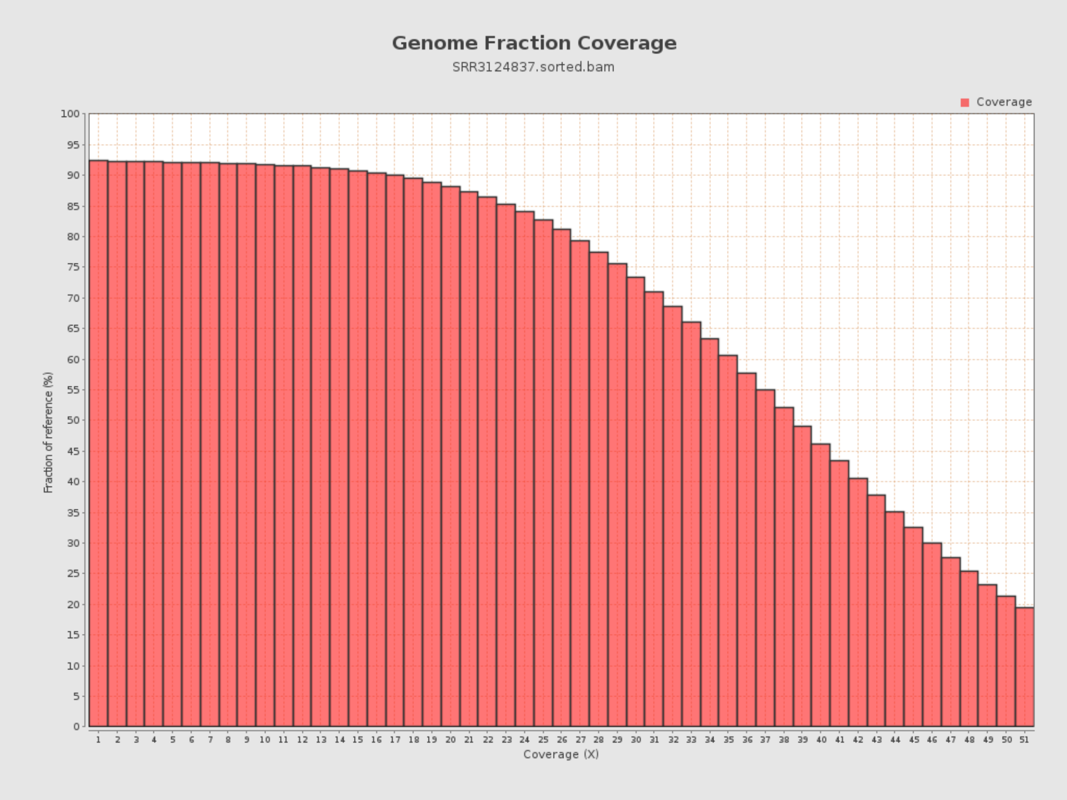
4. Results : Coverage Histogram



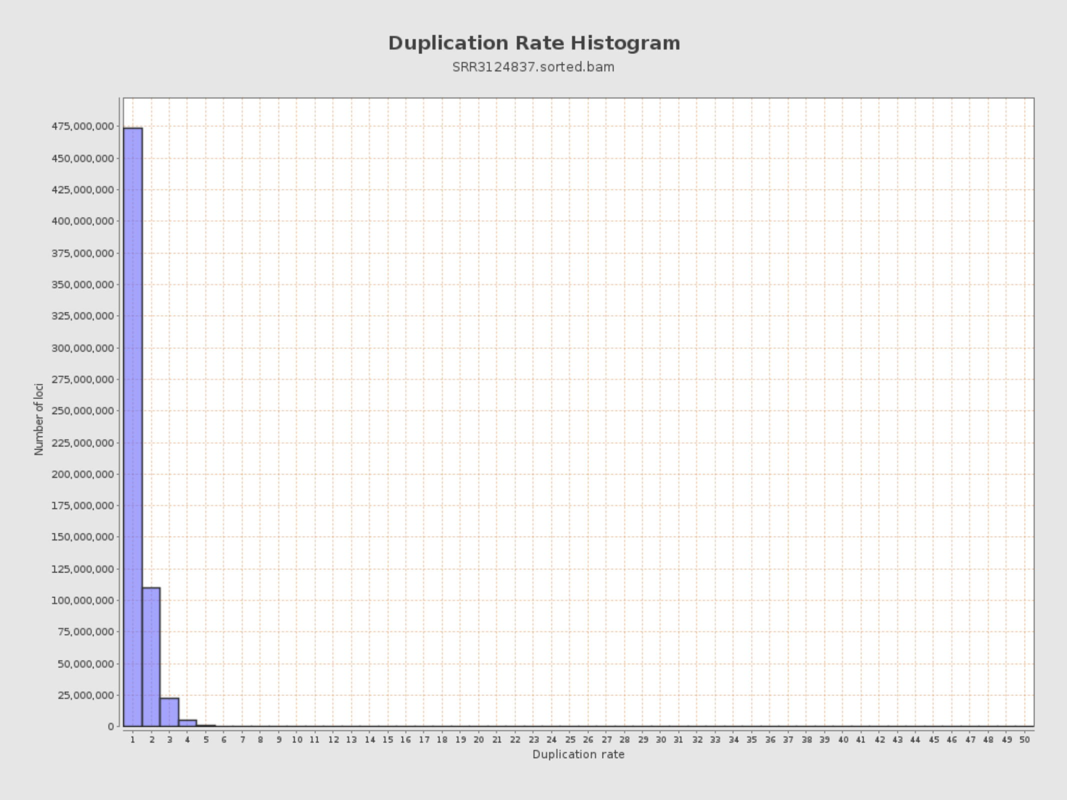
5. Results : Coverage Histogram (0-50X)



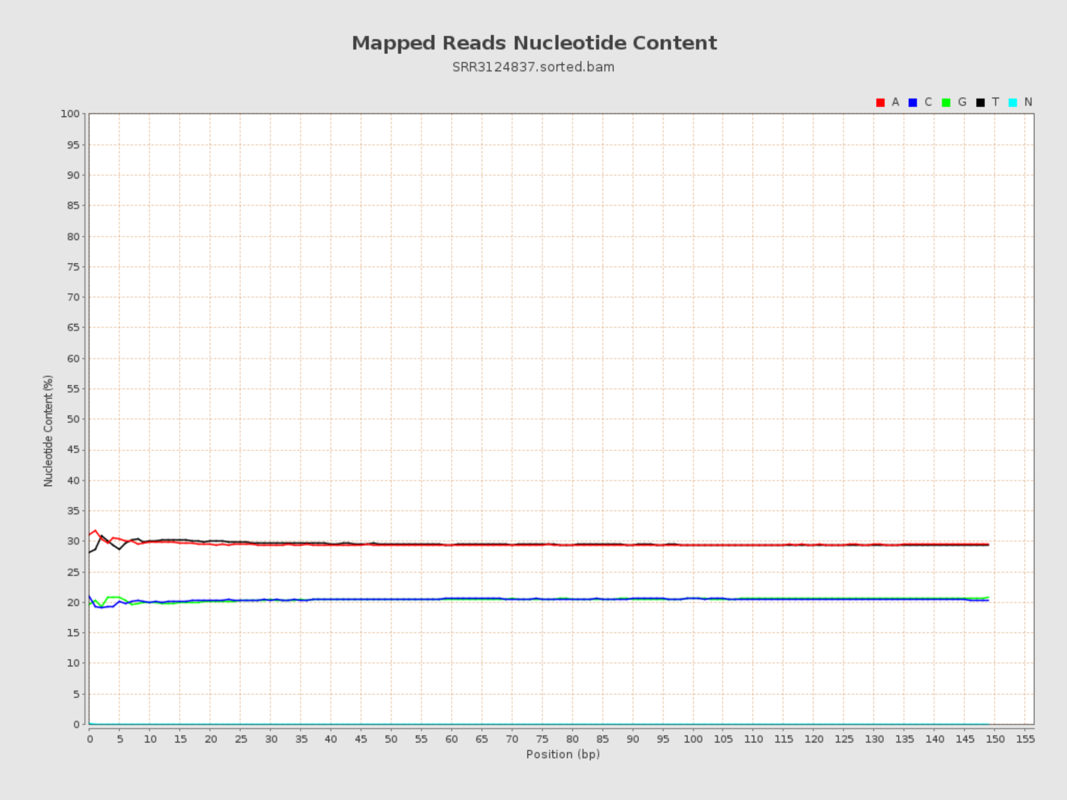
6. Results : Genome Fraction Coverage



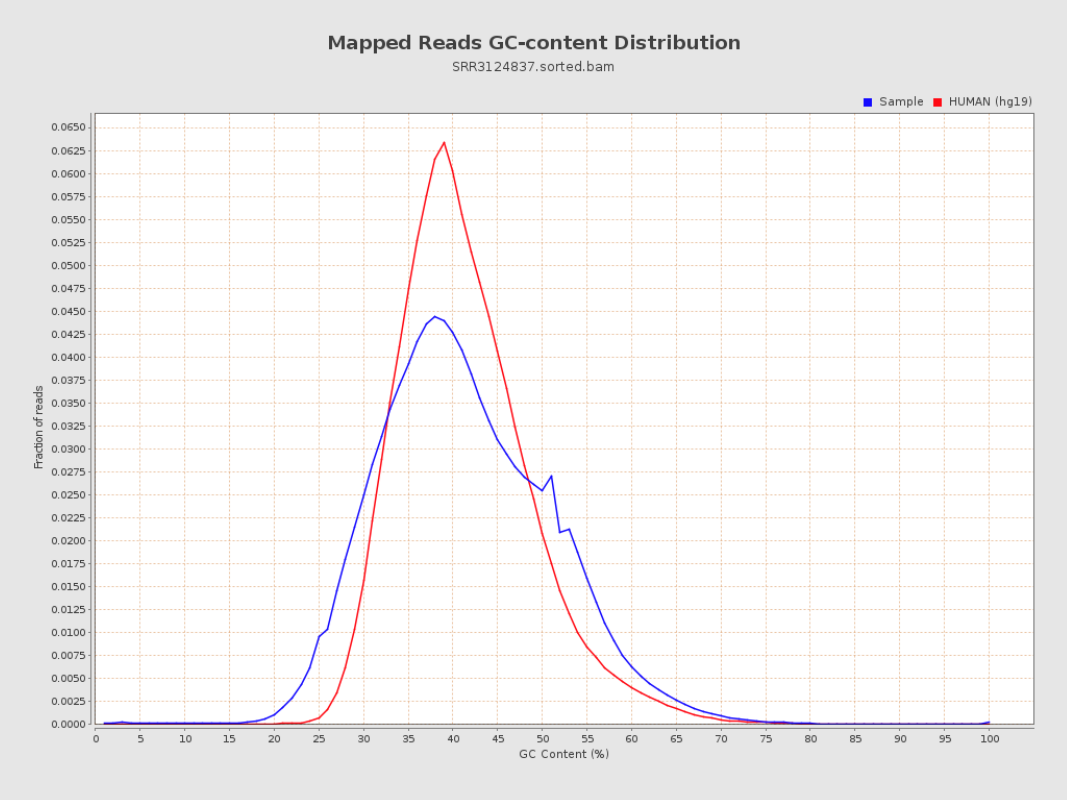
7. Results : Duplication Rate Histogram



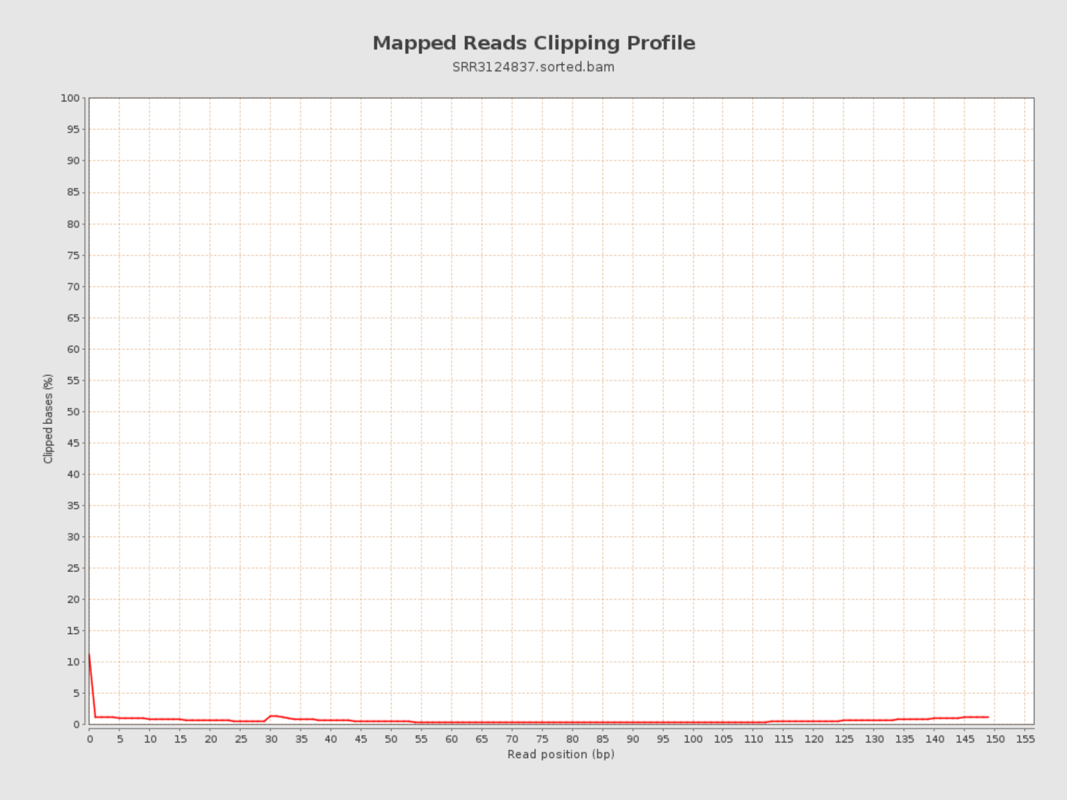
8. Results : Mapped Reads Nucleotide Content



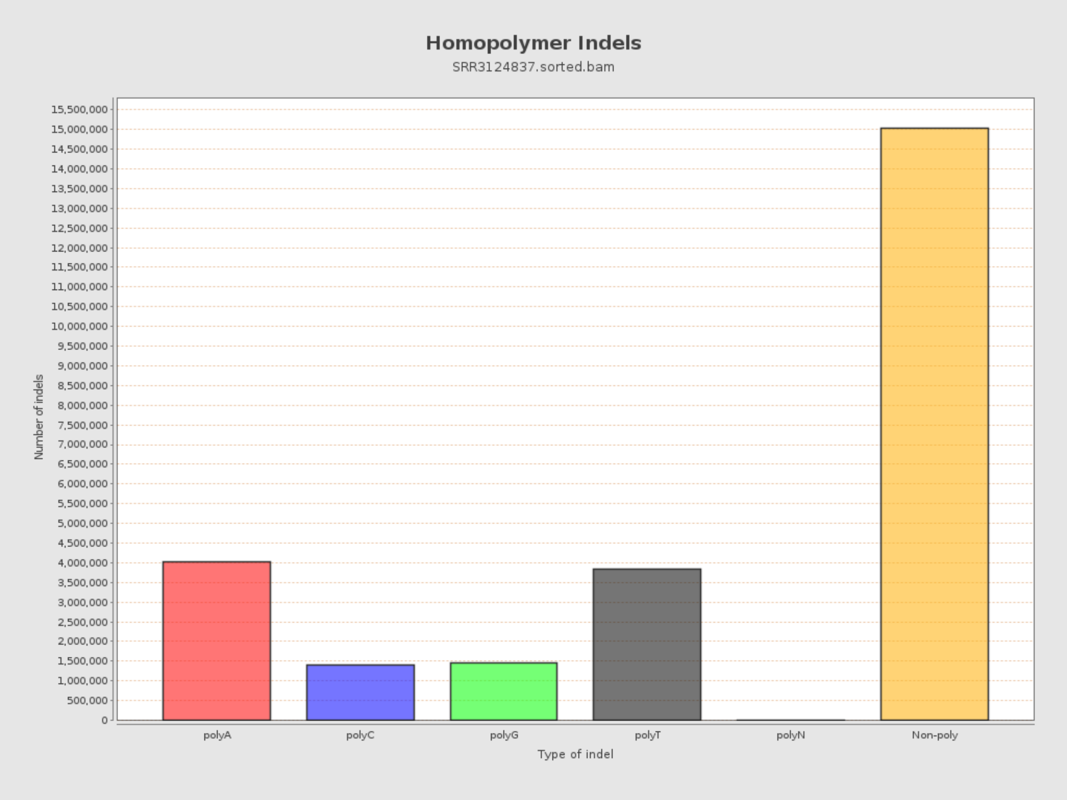
9. Results : Mapped Reads GC-content Distribution



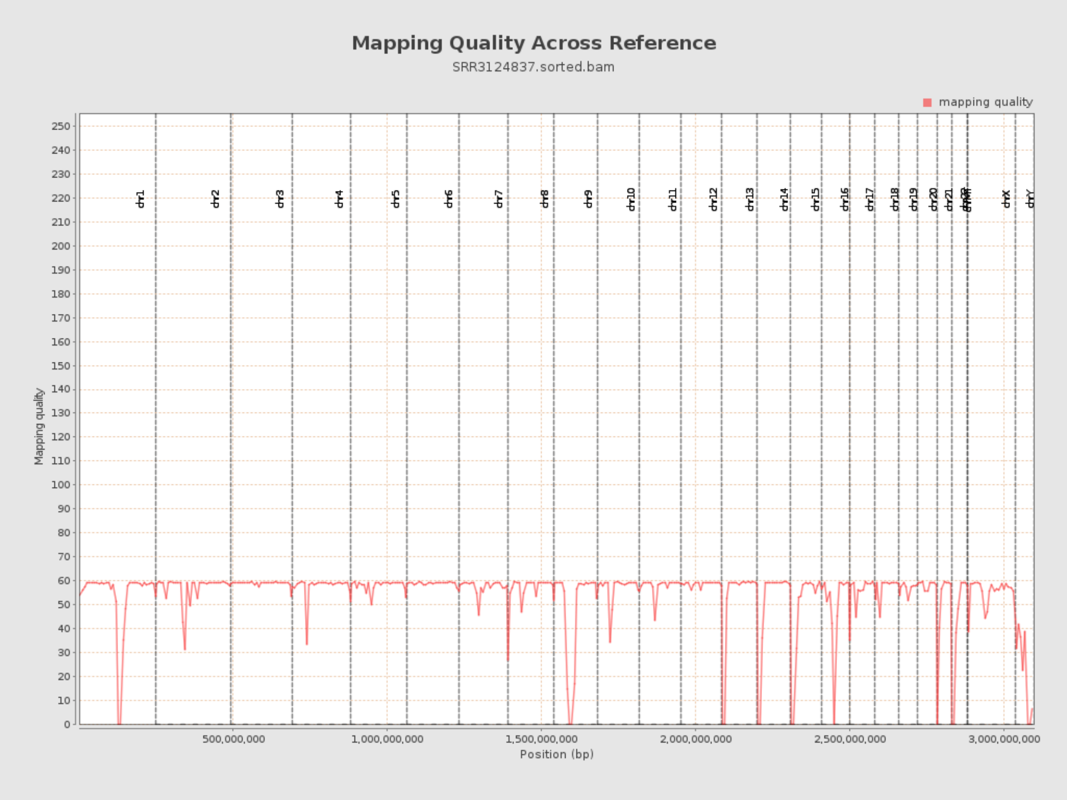
10. Results : Mapped Reads Clipping Profile



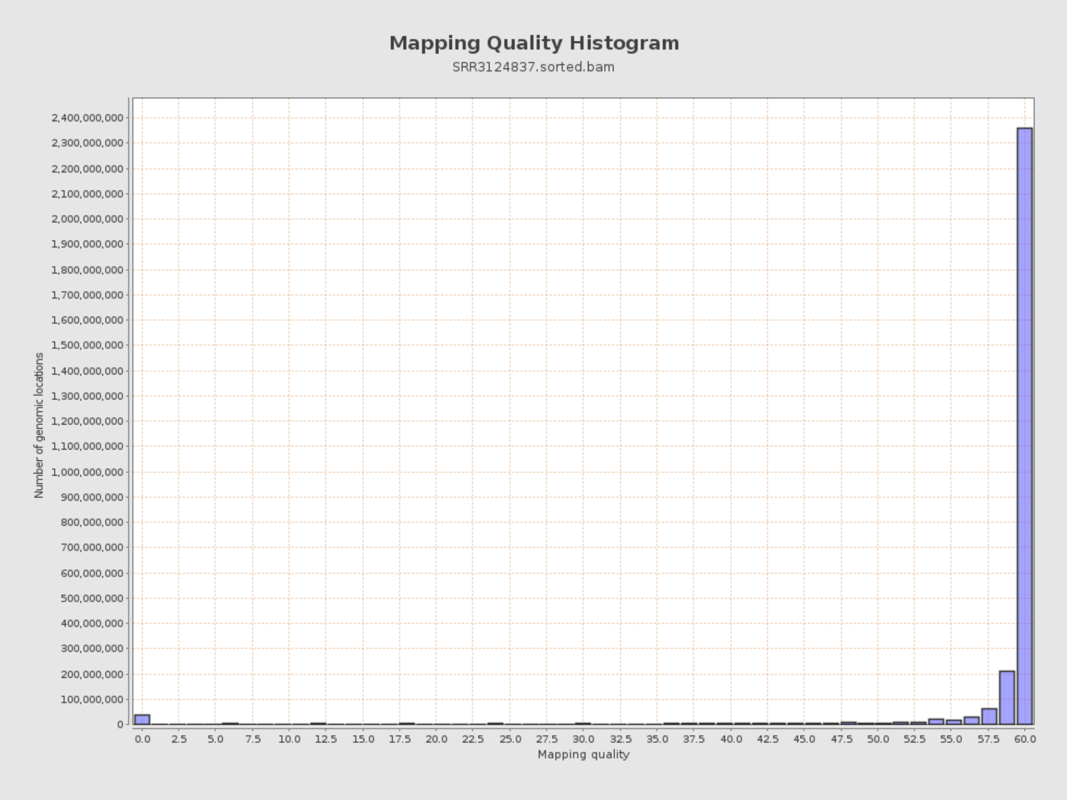
11. Results : Homopolymer Indels



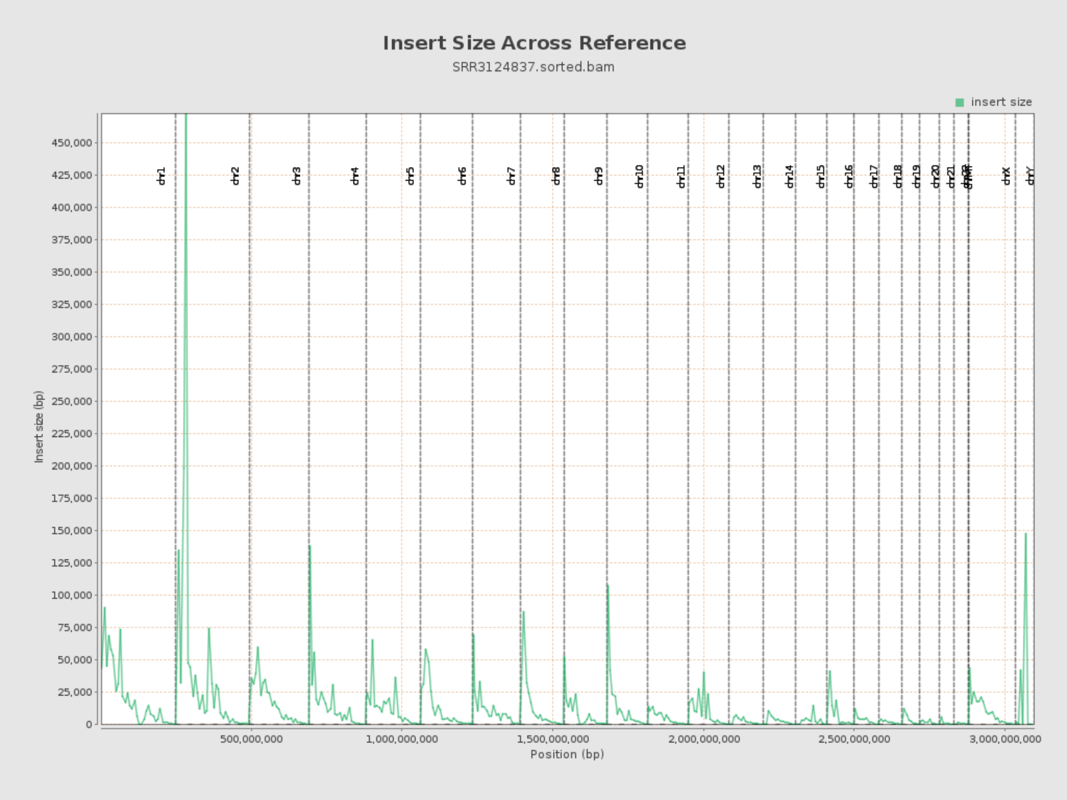
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram