Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.3
2024/04/19 09:31:22

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam -nw 400 -hm 3

1.2. Alignment

Command line:	/athena/angsd/scratch/mef3005/share/envs/angsd/bin/STAR-avx2 --runMode alignReads --runThreadN 4 --genomeDir /athena/angsd/scratch/sah4030/angsd_homework/Project/Final/hg38_STARindex --readFilesIn /athena/angsd/scratch/sah4030/angsd_homework/Project/MSIV/TrimGalore/Irinotecan_Rep_2_1_val_1.fq /athena/angsd/scratch/sah4030/angsd_homework/Project/MSIV/TrimGalore/Irinotecan_Rep_2_2_val_2.fq --outFileNamePrefix /athena/angsd/scratch/sah4030/angsd_homework/Project/Final/AlignReads/Irinotecan_Rep_2. --outSAMtype BAM SortedByCoordinate --outSAMattributes NH HI NM MD AS nM --outFilterMultimapNmax 1 --alignIntronMin 20 --alignIntronMax 200000
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (2.7.11a)

Analysis date:	Fri Apr 19 09:31:22 EDT 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam

2. Summary

2.1. Globals

Reference size	3,099,750,718
Number of reads	62,485,371
Mapped reads	62,485,371 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	62,485,371 / 100%
Mapped reads, first in pair	31,244,886 / 50%
Mapped reads, second in pair	31,240,485 / 50%
Mapped reads, both in pair	62,479,492 / 99.99%
Mapped reads, singletons	5,879 / 0.01%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 148.87
Duplicated reads (estimated)	46,524,204 / 74.46%
Duplication rate	53.32%
Clipped reads	5,343,691 / 8.55%

2.2. ACGT Content

Number/percentage of A's	2,256,537,424 / 24.44%
Number/percentage of C's	2,354,692,498 / 25.5%
Number/percentage of T's	2,263,009,791 / 24.51%
Number/percentage of G's	2,359,394,448 / 25.55%
Number/percentage of N's	79,283 / 0%
GC Percentage	51.05%

2.3. Coverage

Mean	44.7108
Standard Deviation	110.1925

2.4. Mapping Quality

Mean Mapping Quality	19.9

2.5. Insert size

Mean	3,653.04
Standard Deviation	11,775.83
P25/Median/P75	242 / 531 / 2,771

2.6. Mismatches and indels

General error rate	0.03%
Mismatches	38,038,389
Insertions	878,719
Mapped reads with at least one insertion	1.39%
Deletions	430,589
Mapped reads with at least one deletion	0.68%
Homopolymer indels	51.51%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

1	248956422	14359960170	57.6806	118.8799
10	133797422	5950222415	44.4719	63.452
11	135086622	8085718414	59.8558	139.1187
12	133275309	7141370848	53.5836	128.727
13	114364328	3087383863	26.996	69.9694
14	107043718	3348298272	31.2797	179.4021
15	101991189	4208972967	41.268	102.782
16	90338345	2922900740	32.355	68.3415
17	83257441	7046594188	84.6362	154.516
18	80373285	2544761542	31.6618	53.6203
19	58617616	7062867907	120.4905	237.0542
2	242193529	11405558205	47.0927	107.0187
20	64444167	5274203230	81.8414	122.8829
21	46709983	2590689743	55.4633	79.419
22	50818468	2589266005	50.9513	79.2799
3	198295559	8694422737	43.8458	75.3208
4	190214555	6344796365	33.356	57.1502
5	181538259	5746778058	31.656	54.4559
6	170805979	8804405559	51.5462	158.7601
7	159345973	7909876128	49.6396	86.9922
8	145138636	4967371930	34.225	69.7211
9	138394717	5575180003	40.2846	77.9423
MT	16569	194011085	11,709.2815	11,087.0709
X	156040895	2683511701	17.1975	61.4329

Y	57227415	3006407	0.0525	0.1336
KI270728.1	1872759	5345	0.0029	0.0794
KI270727.1	448248	0	0	0
KI270442.1	392061	234	0.0006	0.0244
KI270729.1	280839	0	0	0
GL000225.1	211173	420	0.002	0.0517
KI270743.1	210658	4166	0.0198	0.4032
GL000008.2	209709	1677270	7.9981	7.9386
GL000009.2	201709	98472	0.4882	0.4895
KI270747.1	198735	0	0	0
KI270722.1	194050	0	0	0
GL000194.1	191469	3651287	19.0699	19.0629
KI270742.1	186739	231015	1.2371	1.2452
GL000205.2	185591	822072	4.4295	5.7262
GL000195.1	182896	1385487	7.5753	7.7413
KI270736.1	181920	0	0	0
KI270733.1	179772	22727092	126.4218	428.1787
GL000224.1	179693	20125	0.112	1.0849
GL000219.1	179198	2171475	12.1177	14.1077
KI270719.1	176845	300	0.0017	0.0479
GL000216.2	176608	0	0	0
KI270712.1	176043	1198	0.0068	0.1293
KI270706.1	175055	974465	5.5666	5.4883
KI270725.1	172810	0	0	0

KI270744.1	168472	1491	0.0089	0.122
KI270734.1	165050	137185	0.8312	2.1166
GL000213.1	164239	513	0.0031	0.0995
GL000220.1	161802	14164059	87.5395	87.9157
KI270715.1	161471	0	0	0
GL000218.1	161147	404015	2.5071	3.6087
KI270749.1	158759	0	0	0
KI270741.1	157432	475207	3.0185	3.0141
GL000221.1	155397	126883	0.8165	0.8381
KI270716.1	153799	0	0	0
KI270731.1	150754	306	0.002	0.052
KI270751.1	150742	0	0	0
KI270750.1	148850	0	0	0
KI270519.1	138126	0	0	0
GL000214.1	137718	0	0	0
KI270708.1	127682	0	0	0
KI270730.1	112551	0	0	0
KI270438.1	112505	0	0	0
KI270737.1	103838	0	0	0
KI270721.1	100316	35714	0.356	0.3913
KI270738.1	99375	0	0	0
KI270748.1	93321	0	0	0
KI270435.1	92983	226	0.0024	0.0542
GL000208.1	92689	0	0	0

KI270538.1	91309	300	0.0033	0.081
KI270756.1	79590	0	0	0
KI270739.1	73985	0	0	0
KI270757.1	71251	0	0	0
KI270709.1	66860	0	0	0
KI270746.1	66486	0	0	0
KI270753.1	62944	0	0	0
KI270589.1	44474	0	0	0
KI270726.1	43739	0	0	0
KI270735.1	42811	0	0	0
KI270711.1	42210	1110427	26.3072	30.3571
KI270745.1	41891	1786	0.0426	0.44
KI270714.1	41717	38443	0.9215	1.6856
KI270732.1	41543	0	0	0
KI270713.1	40745	19298	0.4736	1.6488
KI270754.1	40191	0	0	0
KI270710.1	40176	0	0	0
KI270717.1	40062	894	0.0223	0.2519
KI270724.1	39555	0	0	0
KI270720.1	39050	3904	0.1	0.2636
KI270723.1	38115	0	0	0
KI270718.1	38054	0	0	0
KI270317.1	37690	0	0	0
KI270740.1	37240	0	0	0

KI270755.1	36723	0	0	0
KI270707.1	32032	1117	0.0349	0.2082
KI270579.1	31033	0	0	0
KI270752.1	27745	60537	2.1819	2.4234
KI270512.1	22689	0	0	0
KI270322.1	21476	0	0	0
GL000226.1	15008	0	0	0
KI270311.1	12399	0	0	0
KI270366.1	8320	0	0	0
KI270511.1	8127	0	0	0
KI270448.1	7992	0	0	0
KI270521.1	7642	0	0	0
KI270581.1	7046	0	0	0
KI270582.1	6504	0	0	0
KI270515.1	6361	0	0	0
KI270588.1	6158	0	0	0
KI270591.1	5796	0	0	0
KI270522.1	5674	0	0	0
KI270507.1	5353	0	0	0
KI270590.1	4685	0	0	0
KI270584.1	4513	0	0	0
KI270320.1	4416	0	0	0
KI270382.1	4215	0	0	0
KI270468.1	4055	0	0	0

KI270467.1	3920	0	0	0
KI270362.1	3530	0	0	0
KI270517.1	3253	0	0	0
KI270593.1	3041	0	0	0
KI270528.1	2983	0	0	0
KI270587.1	2969	0	0	0
KI270364.1	2855	0	0	0
KI270371.1	2805	0	0	0
KI270333.1	2699	0	0	0
KI270374.1	2656	0	0	0
KI270411.1	2646	0	0	0
KI270414.1	2489	0	0	0
KI270510.1	2415	0	0	0
KI270390.1	2387	0	0	0
KI270375.1	2378	0	0	0
KI270420.1	2321	0	0	0
KI270509.1	2318	0	0	0
KI270315.1	2276	0	0	0
KI270302.1	2274	0	0	0
KI270518.1	2186	0	0	0
KI270530.1	2168	0	0	0
KI270304.1	2165	0	0	0
KI270418.1	2145	0	0	0
KI270424.1	2140	0	0	0

KI270417.1	2043	0	0	0
KI270508.1	1951	0	0	0
KI270303.1	1942	0	0	0
KI270381.1	1930	0	0	0
KI270529.1	1899	0	0	0
KI270425.1	1884	0	0	0
KI270396.1	1880	0	0	0
KI270363.1	1803	0	0	0
KI270386.1	1788	0	0	0
KI270465.1	1774	0	0	0
KI270383.1	1750	0	0	0
KI270384.1	1658	0	0	0
KI270330.1	1652	0	0	0
KI270372.1	1650	0	0	0
KI270548.1	1599	0	0	0
KI270580.1	1553	0	0	0
KI270387.1	1537	0	0	0
KI270391.1	1484	0	0	0
KI270305.1	1472	0	0	0
KI270373.1	1451	0	0	0
KI270422.1	1445	0	0	0
KI270316.1	1444	0	0	0
KI270340.1	1428	0	0	0
KI270338.1	1428	0	0	0

KI270583.1	1400	0	0	0
KI270334.1	1368	0	0	0
KI270429.1	1361	0	0	0
KI270393.1	1308	0	0	0
KI270516.1	1300	0	0	0
KI270389.1	1298	0	0	0
KI270466.1	1233	0	0	0
KI270388.1	1216	0	0	0
KI270544.1	1202	0	0	0
KI270310.1	1201	0	0	0
KI270412.1	1179	0	0	0
KI270395.1	1143	0	0	0
KI270376.1	1136	0	0	0
KI270337.1	1121	0	0	0
KI270335.1	1048	0	0	0
KI270378.1	1048	0	0	0
KI270379.1	1045	0	0	0
KI270329.1	1040	0	0	0
KI270419.1	1029	0	0	0
KI270336.1	1026	0	0	0
KI270312.1	998	0	0	0
KI270539.1	993	0	0	0
KI270385.1	990	0	0	0
KI270423.1	981	0	0	0

KI270392.1	971	0	0	0
KI270394.1	970	0	0	0

3. Results : Coverage across reference

Coverage across reference
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
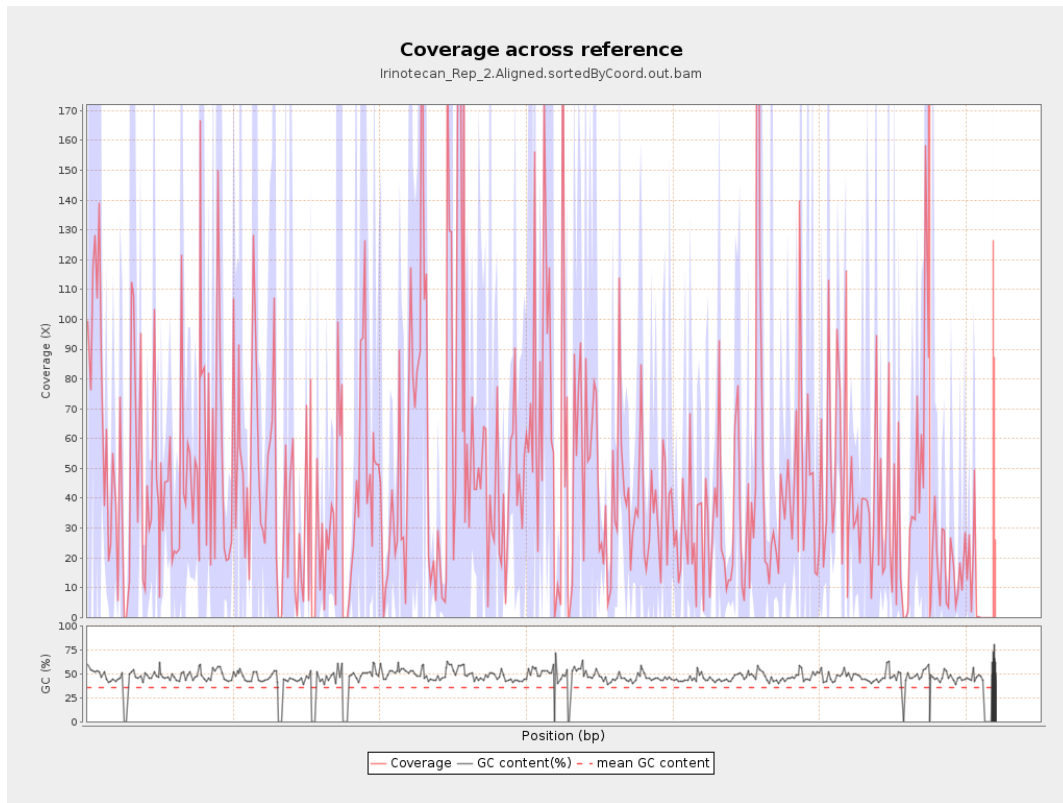
4. Results : Coverage Histogram
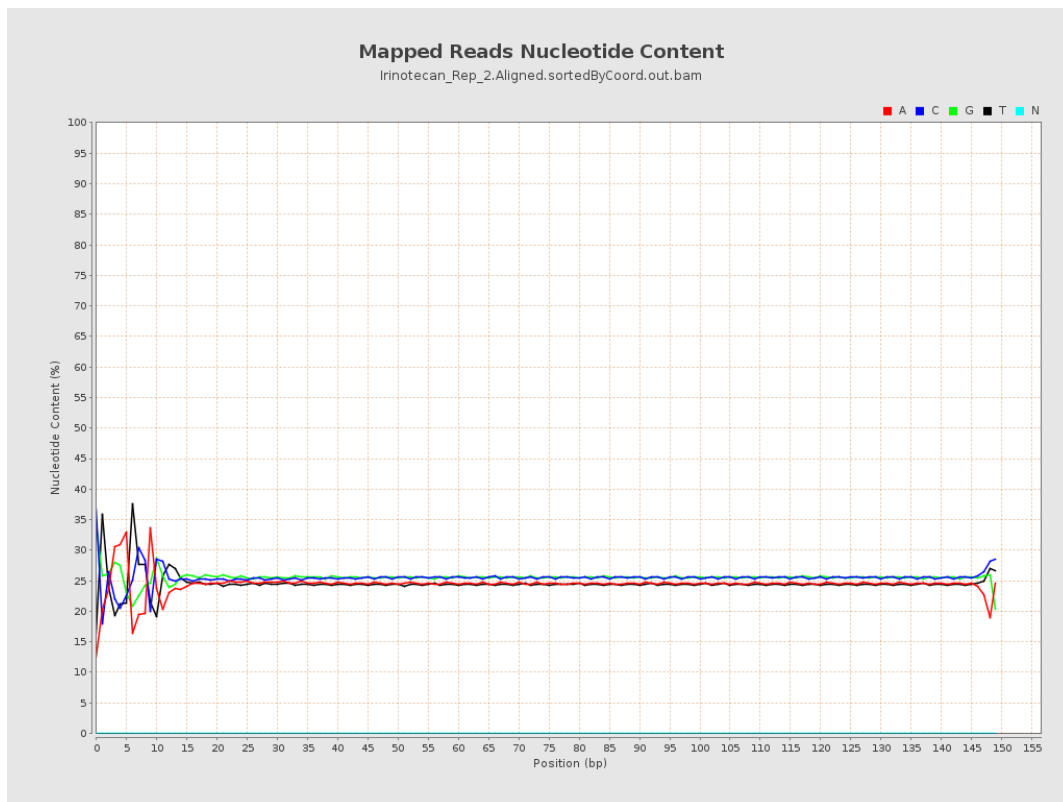
5. Results : Coverage Histogram (0-50X)

Coverage Histogram (0-50X)
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
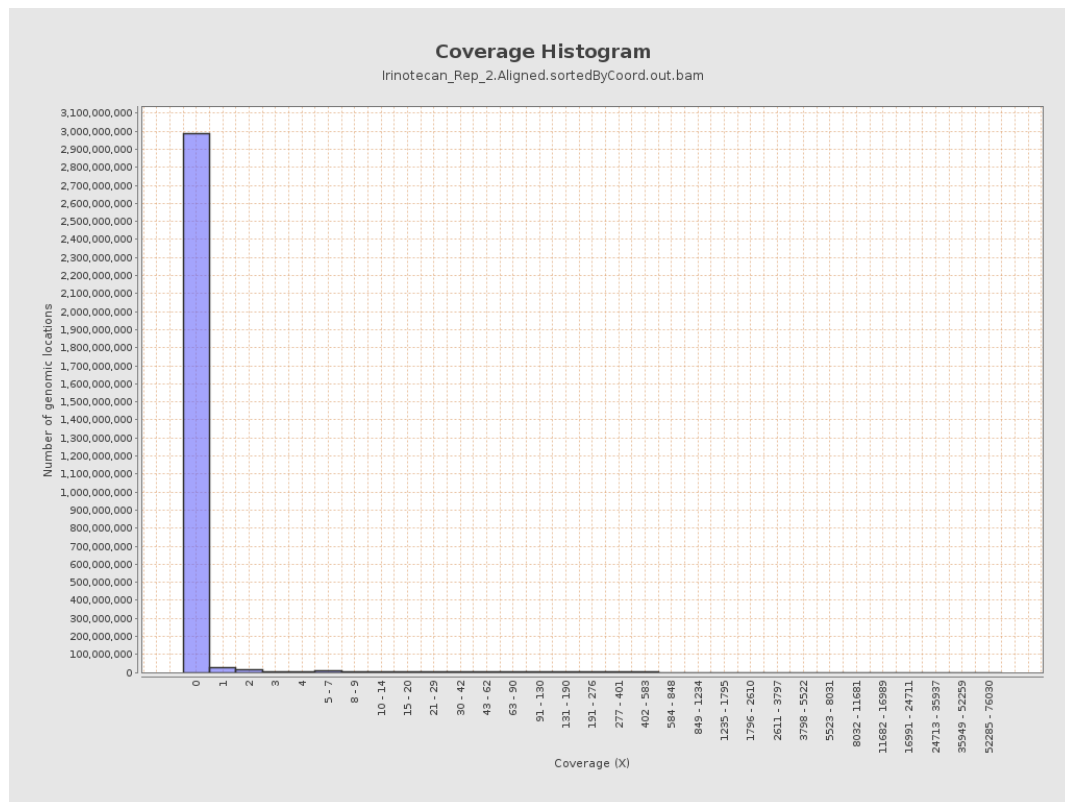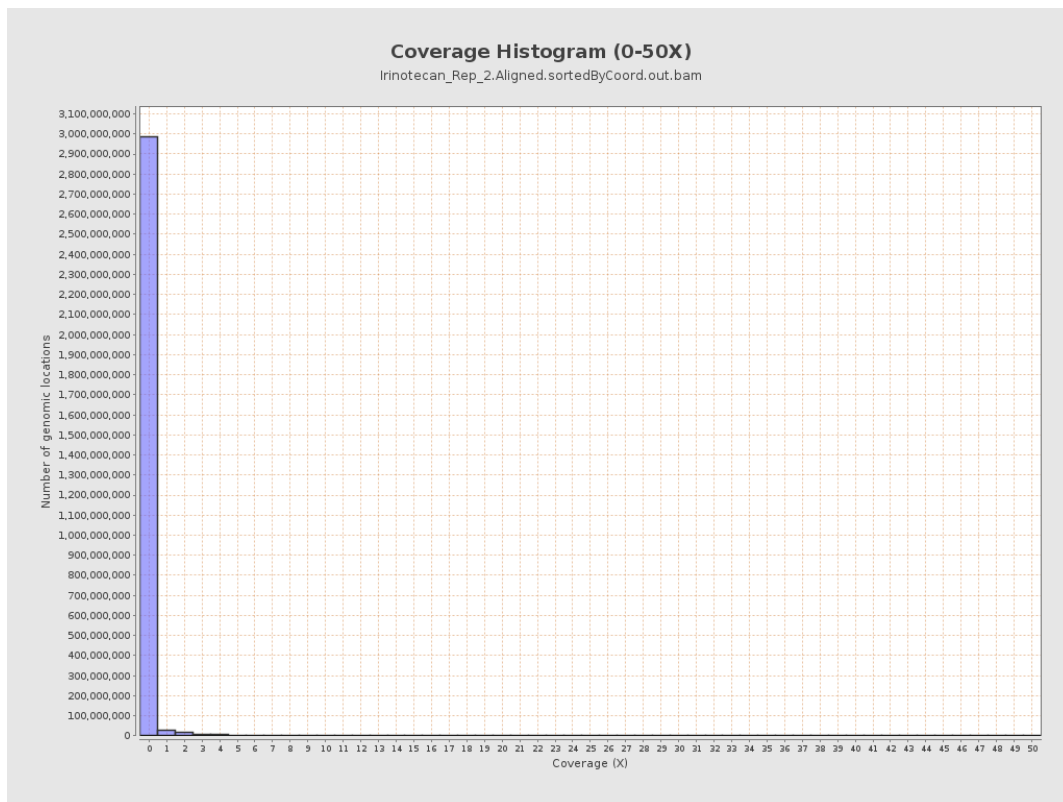
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
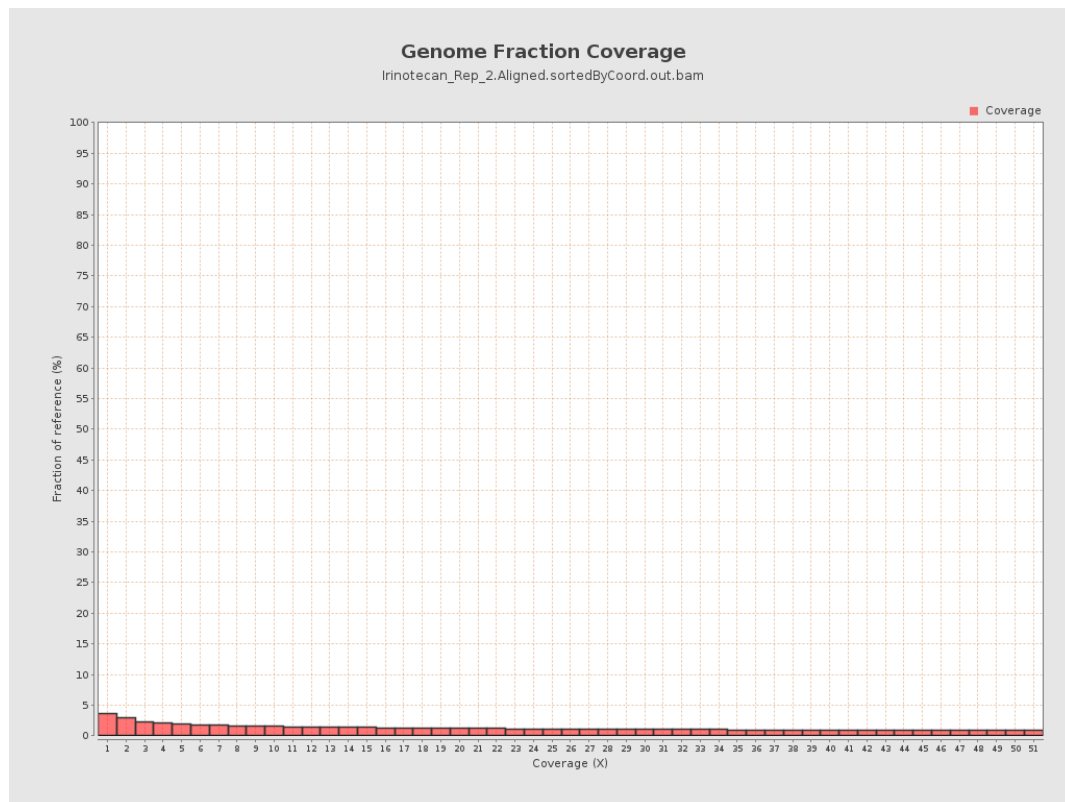
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
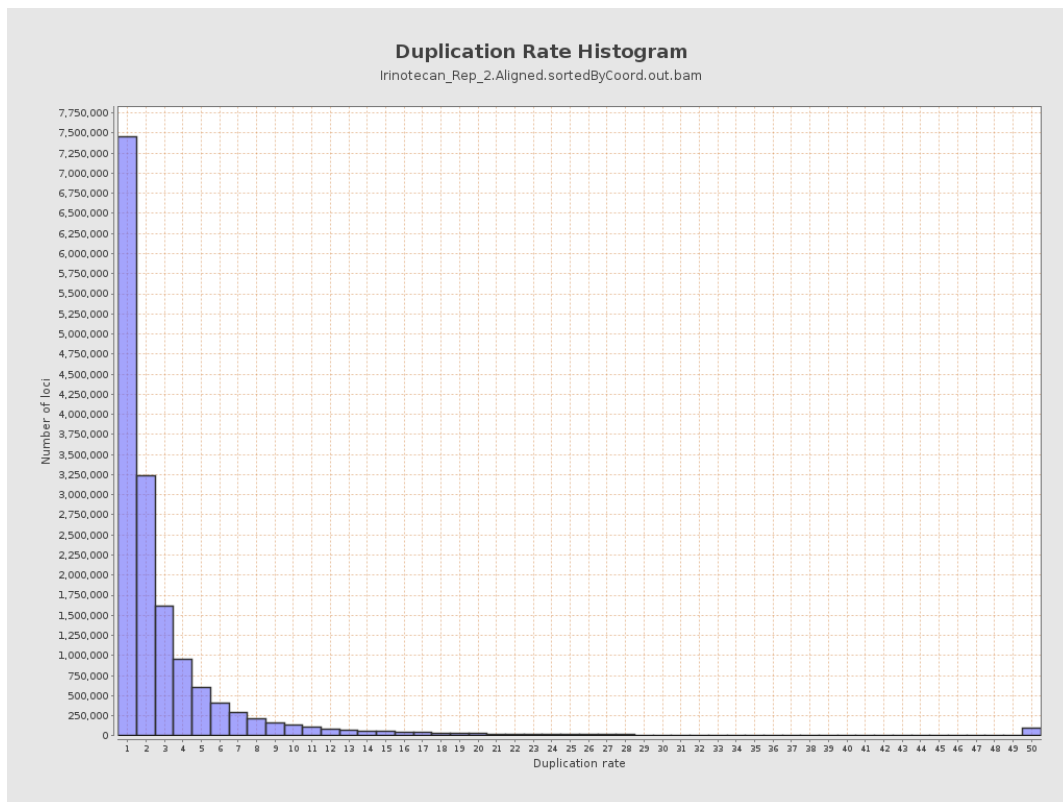
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
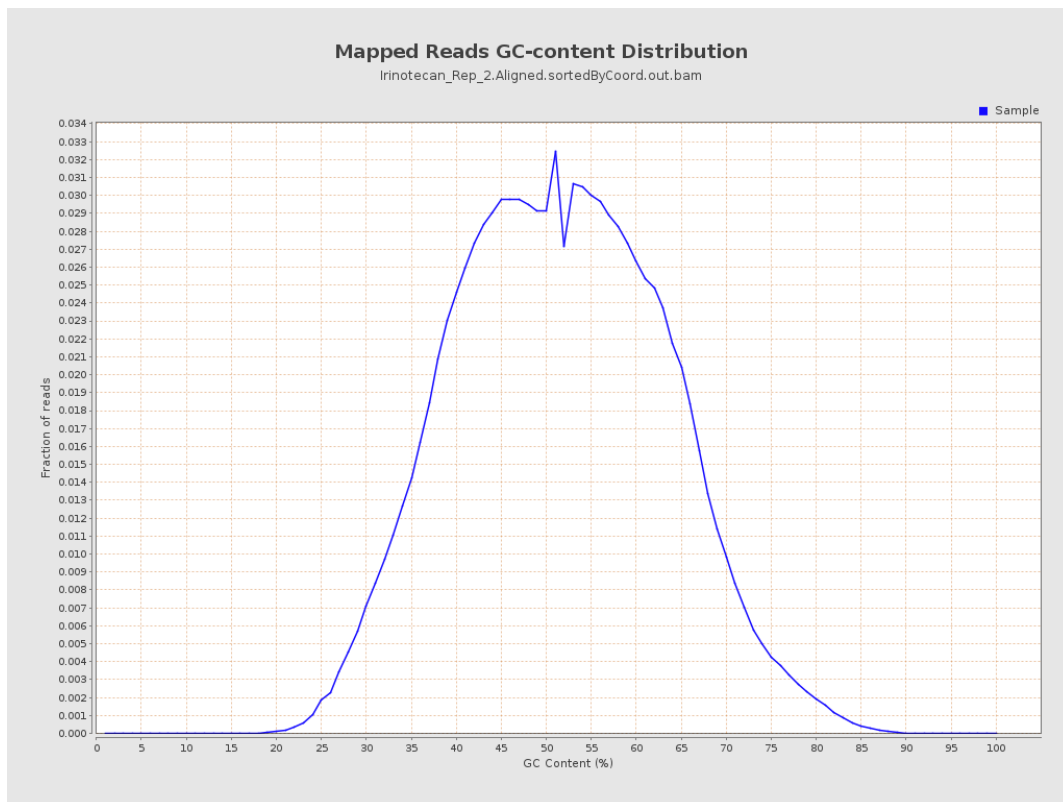
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
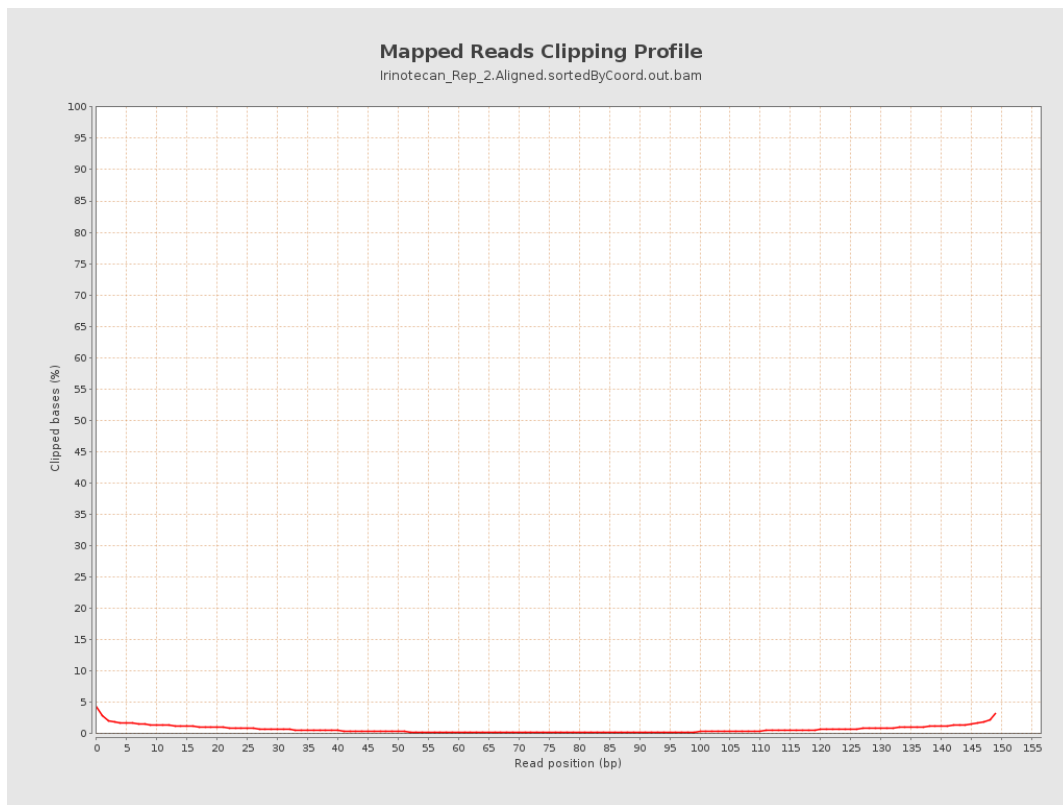
11. Results : Homopolymer Indels
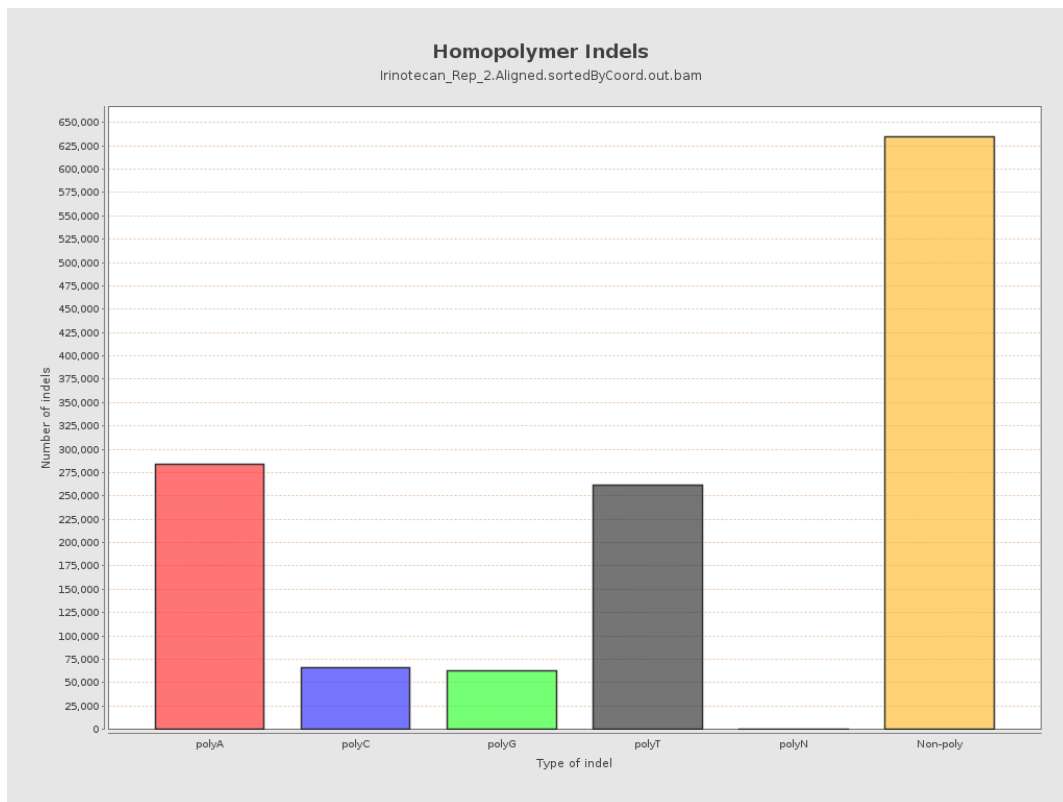
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
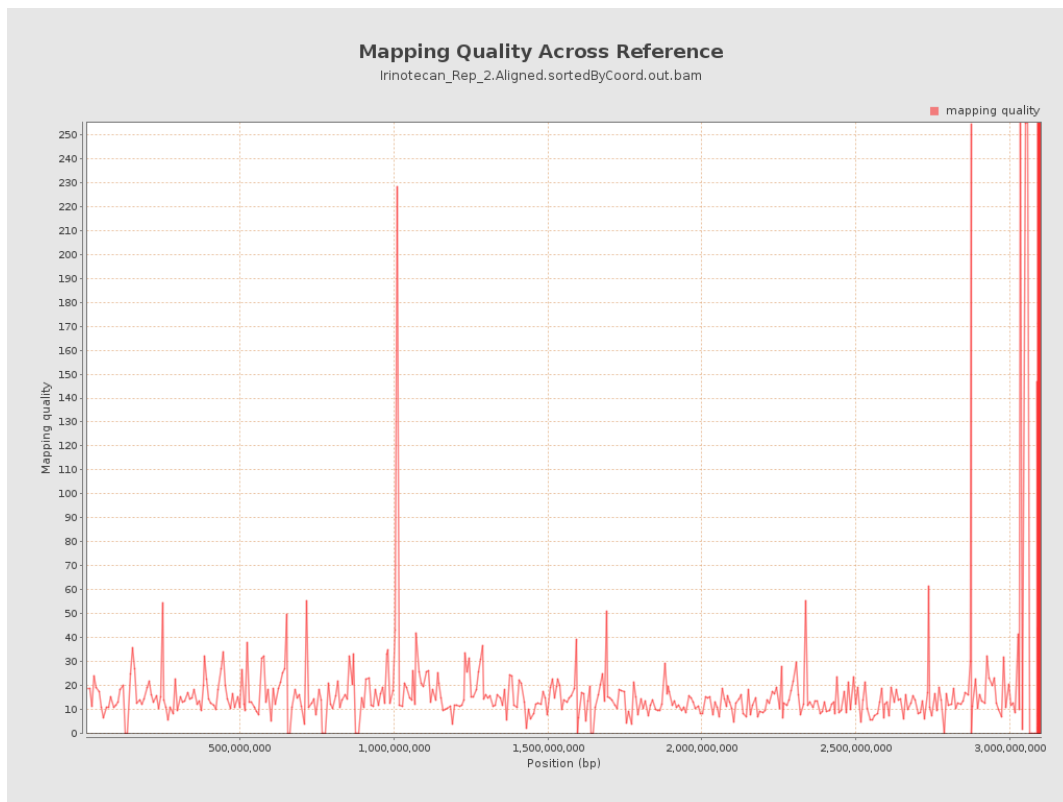
Mapping Quality Histogram
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
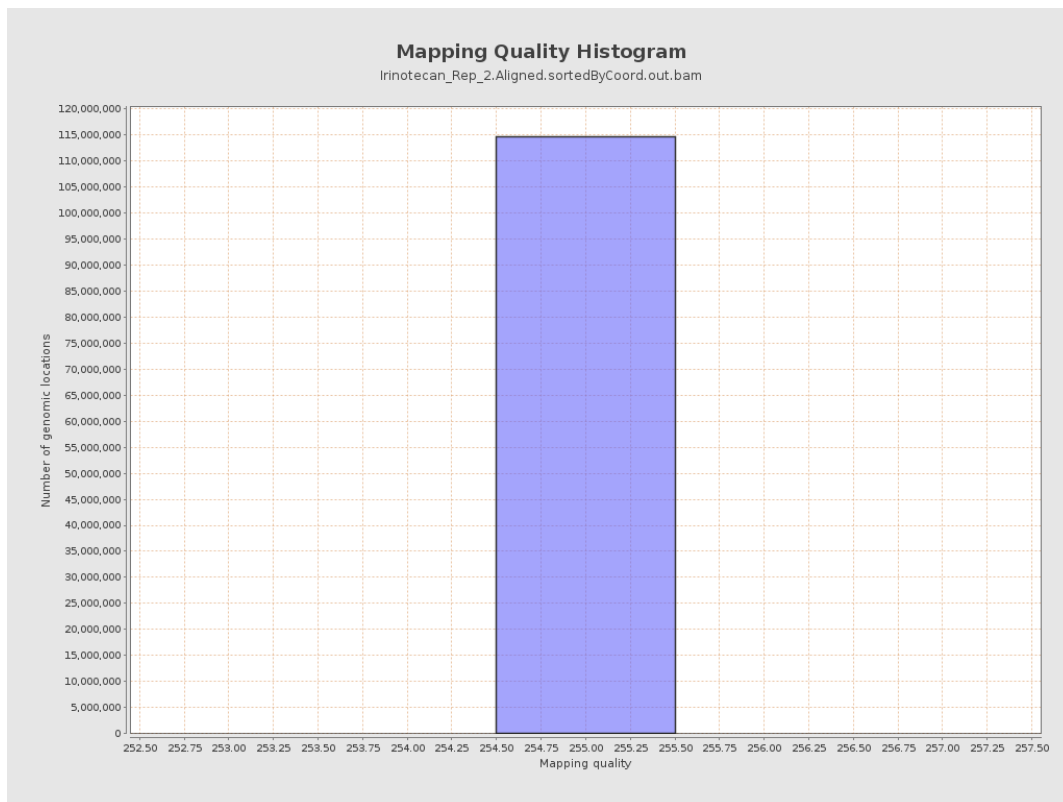
14. Results : Insert Size Across Reference

Insert Size Across Reference
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam
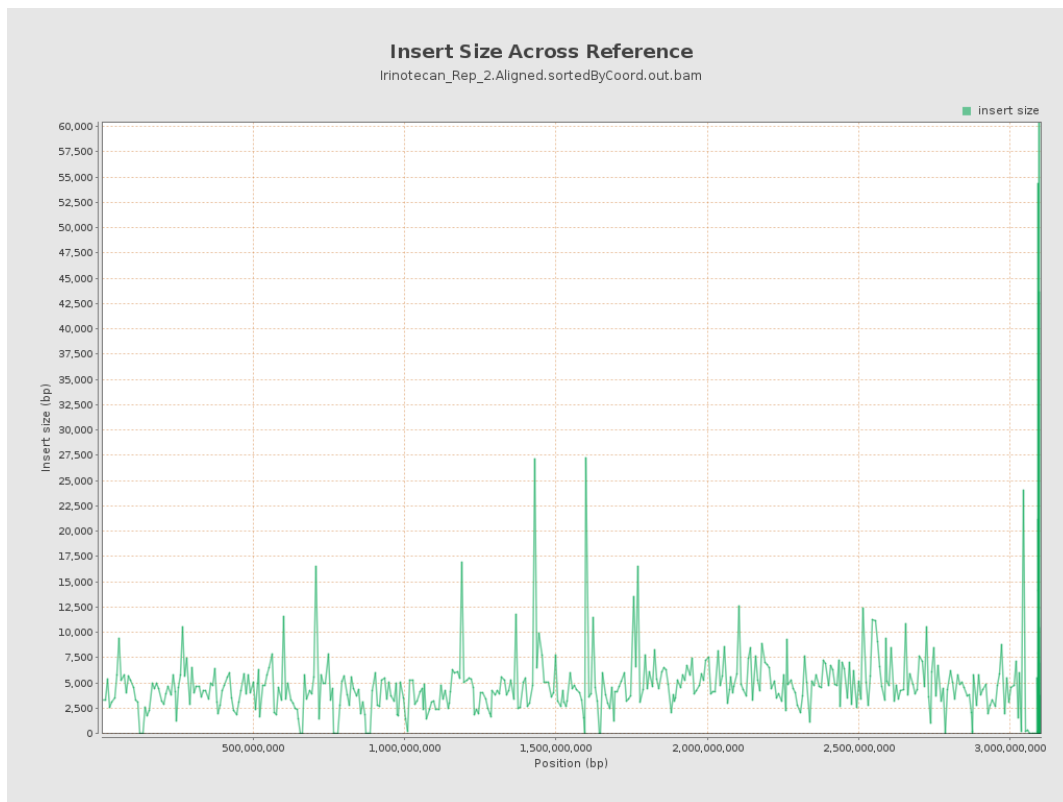
15. Results : Insert Size Histogram

Insert Size Histogram
Irinotecan_Rep_2.Aligned.sortedByCoord.out.bam