

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/04/19 08:43:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam Irinotecan_Rep_1.Aligned.sortedByCoord.out.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	<pre>/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_1_1_val_1.fq /athena/angsd/scratch/sah4030/angsd_homework/Project/MSIV/TrimGalore/Irinotecan_Rep_1_2_val_2.fq --outFileNamePrefix /athena/angsd/scratch/sah4030/angsd_homework/Project/Final/AlignReads/Irinotecan_Rep_1. --outSAMtype BAM SortedByCoordinate --outSAMattributes NH HI NM MD AS nM --outFilterMultimapNmax 1 --alignIntronMin 20 --alignIntronMax 200000</pre>
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (2.7.11a)

Analysis date:	Fri Apr 19 08:43:02 EDT 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	Irinotecan_Rep_1.Aligned.sortedByC oord.out.bam

2. Summary

2.1. Globals

Reference size	3,099,750,718
Number of reads	77,476,095
Mapped reads	77,476,095 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	77,476,095 / 100%
Mapped reads, first in pair	38,739,758 / 50%
Mapped reads, second in pair	38,736,337 / 50%
Mapped reads, both in pair	77,471,146 / 99.99%
Mapped reads, singletons	4,949 / 0.01%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 149.09
Duplicated reads (estimated)	59,712,961 / 77.07%
Duplication rate	55.06%
Clipped reads	5,664,810 / 7.31%

2.2. ACGT Content

Number/percentage of A's	2,766,654,812 / 24.08%
Number/percentage of C's	2,968,664,836 / 25.84%
Number/percentage of T's	2,778,416,296 / 24.19%
Number/percentage of G's	2,973,383,621 / 25.88%
Number/percentage of N's	99,178 / 0%
GC Percentage	51.73%

2.3. Coverage

Mean	54.9866
Standard Deviation	147.571

2.4. Mapping Quality

Mean Mapping Quality	20.31
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2.5. Insert size

Mean	3,658.23
Standard Deviation	11,889.87
P25/Median/P75	245 / 533 / 2,721

2.6. Mismatches and indels

General error rate	0.02%
Mismatches	32,569,955
Insertions	1,092,722
Mapped reads with at least one insertion	1.39%
Deletions	562,004
Mapped reads with at least one deletion	0.72%
Homopolymer indels	51.57%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

1	248956422	17641533821	70.8619	140.2438
10	133797422	7278287955	54.3978	77.187
11	135086622	10085959147	74.6629	172.2055
12	133275309	8653386787	64.9287	163.0554
13	114364328	3713809068	32.4735	86.9342
14	107043718	4124641558	38.5323	272.8605
15	101991189	5059135893	49.6037	122.4767
16	90338345	3743948591	41.4436	92.0512
17	83257441	9045075769	108.6398	201.5919
18	80373285	3026462588	37.6551	63.2081
19	58617616	9472586618	161.5997	321.584
2	242193529	13722092345	56.6576	130.1116
20	64444167	6692642996	103.8518	154.5186
21	46709983	3425938680	73.3449	102.1795
22	50818468	3338680489	65.6982	103.8886
3	198295559	10450077636	52.6995	92.5798
4	190214555	7316703220	38.4655	63.8556
5	181538259	6955055281	38.3118	68.0173
6	170805979	9991568845	58.4966	180.0491
7	159345973	10015944577	62.8566	114.1555
8	145138636	6025684165	41.5167	87.3272
9	138394717	6915404696	49.9687	97.7647
MT	16569	342703848	20,683.4358	20,262.5208
X	156040895	3324570860	21.3058	77.7088

Y	57227415	2722616	0.0476	0.102
KI270728.1	1872759	4227	0.0023	0.0768
KI270727.1	448248	294	0.0007	0.0291
KI270442.1	392061	0	0	0
KI270729.1	280839	0	0	0
GL000225.1	211173	0	0	0
KI270743.1	210658	5393	0.0256	0.4728
GL000008.2	209709	2989813	14.257	14.0772
GL000009.2	201709	1195	0.0059	0.1173
KI270747.1	198735	0	0	0
KI270722.1	194050	0	0	0
GL000194.1	191469	4706176	24.5793	24.5023
KI270742.1	186739	430213	2.3038	2.3007
GL000205.2	185591	858803	4.6274	6.3234
GL000195.1	182896	2063049	11.2799	11.3897
KI270736.1	181920	0	0	0
KI270733.1	179772	35143687	195.4903	611.651
GL000224.1	179693	7484	0.0416	0.7708
GL000219.1	179198	2014668	11.2427	13.7123
KI270719.1	176845	300	0.0017	0.0521
GL000216.2	176608	0	0	0
KI270712.1	176043	528	0.003	0.1095
KI270706.1	175055	1553436	8.874	8.7547
KI270725.1	172810	0	0	0

KI270744.1	168472	2097	0.0124	0.2753
KI270734.1	165050	148980	0.9026	2.3019
GL000213.1	164239	596	0.0036	0.1204
GL000220.1	161802	27537733	170.194	170.9324
KI270715.1	161471	0	0	0
GL000218.1	161147	244740	1.5187	3.0449
KI270749.1	158759	253	0.0016	0.0399
KI270741.1	157432	434462	2.7597	2.7567
GL000221.1	155397	381780	2.4568	2.4505
KI270716.1	153799	0	0	0
KI270731.1	150754	0	0	0
KI270751.1	150742	0	0	0
KI270750.1	148850	0	0	0
KI270519.1	138126	0	0	0
GL000214.1	137718	539	0.0039	0.0747
KI270708.1	127682	0	0	0
KI270730.1	112551	0	0	0
KI270438.1	112505	300	0.0027	0.0722
KI270737.1	103838	0	0	0
KI270721.1	100316	80409	0.8016	0.8714
KI270738.1	99375	0	0	0
KI270748.1	93321	0	0	0
KI270435.1	92983	0	0	0
GL000208.1	92689	0	0	0

KI270538.1	91309	0	0	0
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	1202590	28.4906	31.9021
KI270745.1	41891	1689	0.0403	0.2689
KI270714.1	41717	35351	0.8474	2.676
KI270732.1	41543	0	0	0
KI270713.1	40745	34243	0.8404	2.2038
KI270754.1	40191	0	0	0
KI270710.1	40176	0	0	0
KI270717.1	40062	0	0	0
KI270724.1	39555	0	0	0
KI270720.1	39050	900	0.023	0.203
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	1495	0.0467	0.3101
KI270579.1	31033	0	0	0
KI270752.1	27745	233272	8.4077	8.6376
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

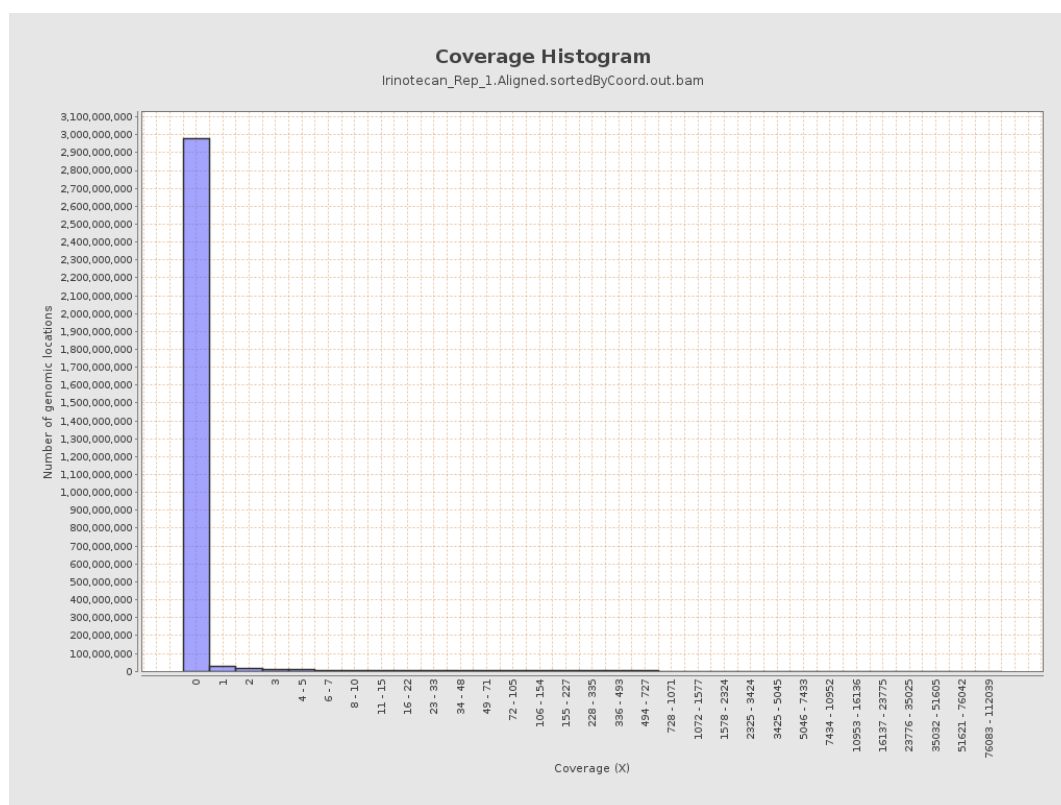
KI270583.1	1400	0	0	0
KI270334.1	1368	0	0	0
KI270429.1	1361	0	0	0
KI270393.1	1308	0	0	0
KI270516.1	1300	0	0	0
KI270389.1	1298	0	0	0
KI270466.1	1233	0	0	0
KI270388.1	1216	0	0	0
KI270544.1	1202	0	0	0
KI270310.1	1201	0	0	0
KI270412.1	1179	0	0	0
KI270395.1	1143	0	0	0
KI270376.1	1136	0	0	0
KI270337.1	1121	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

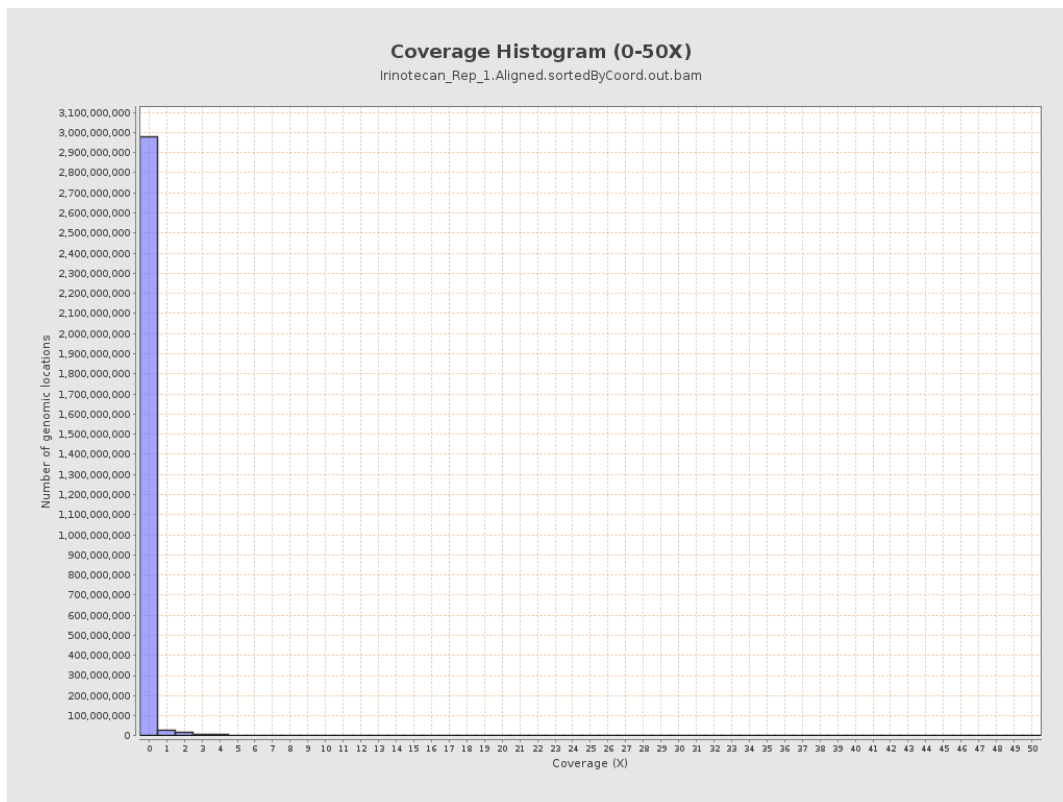
3. Results : Coverage across reference



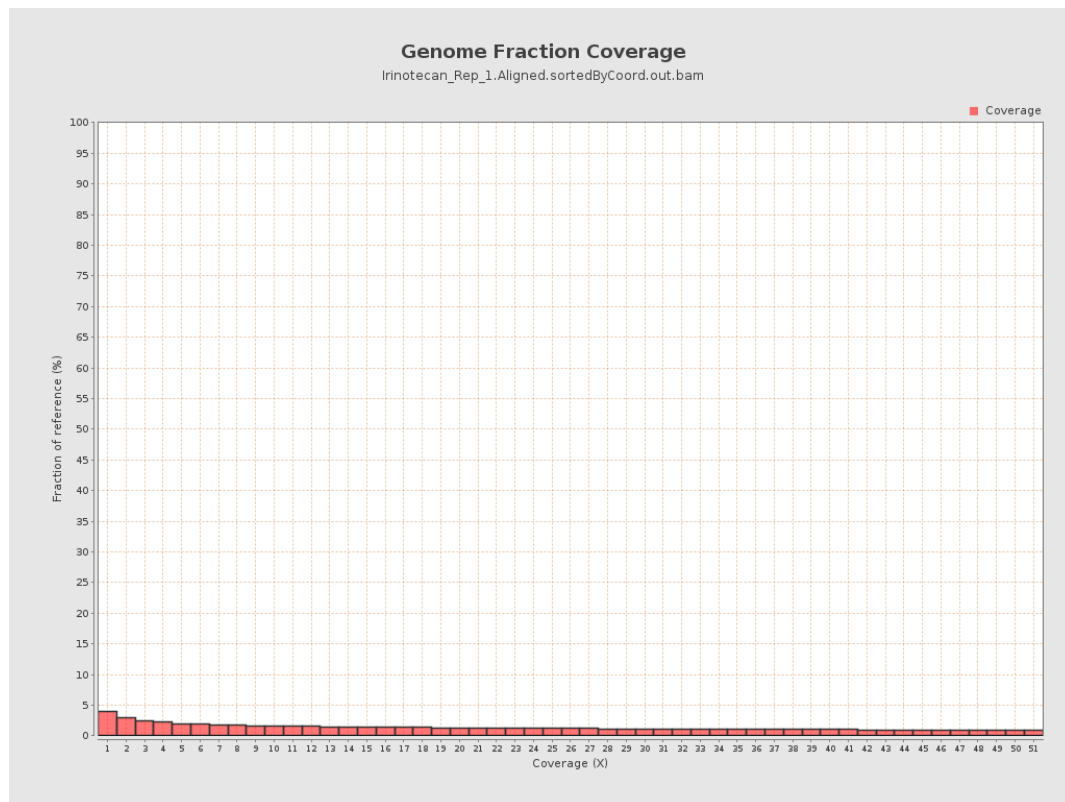
4. Results : Coverage Histogram



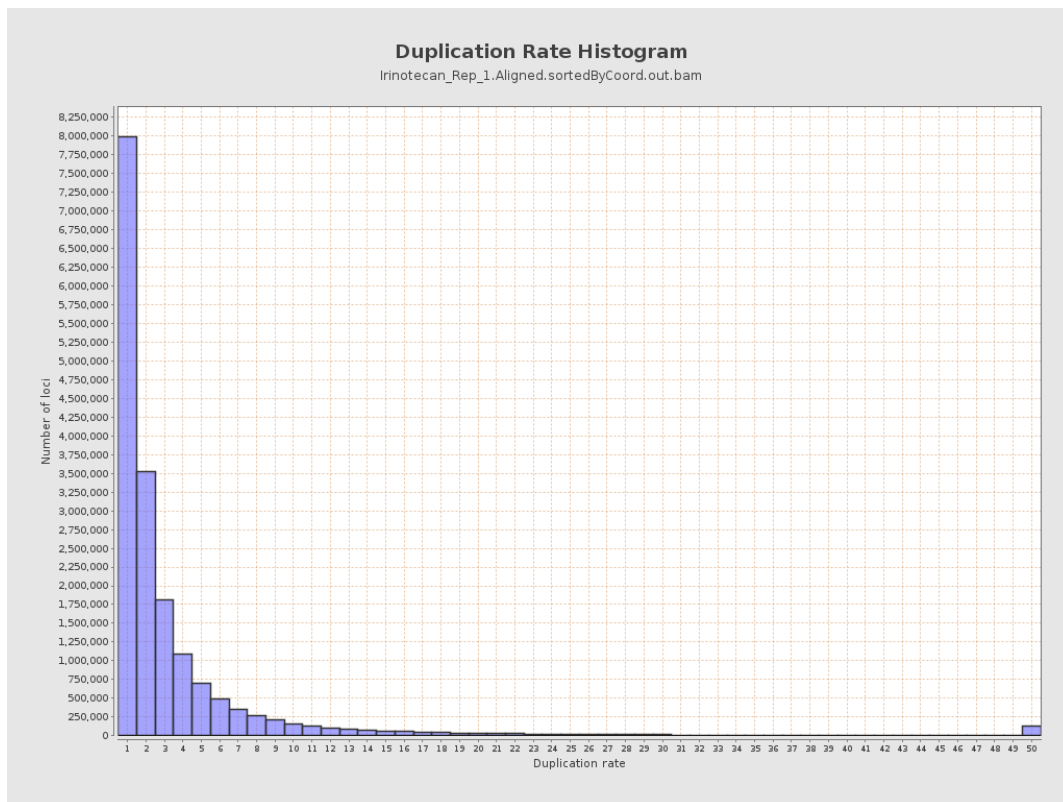
5. Results : Coverage Histogram (0-50X)



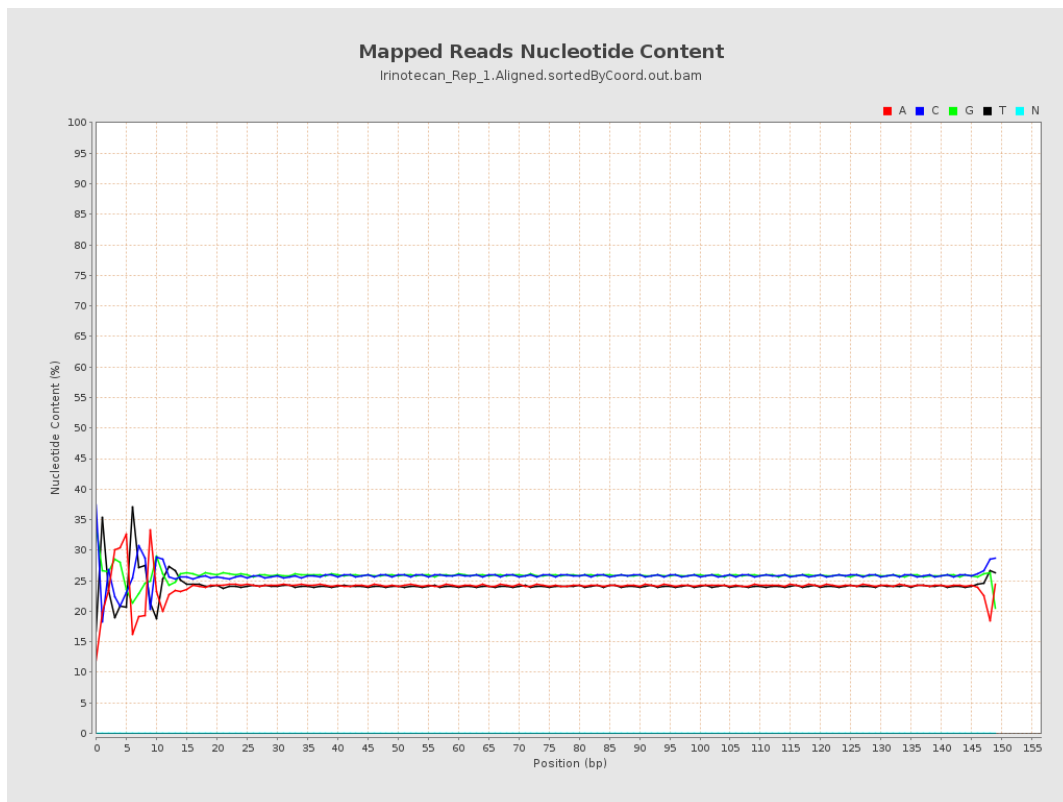
6. Results : Genome Fraction Coverage



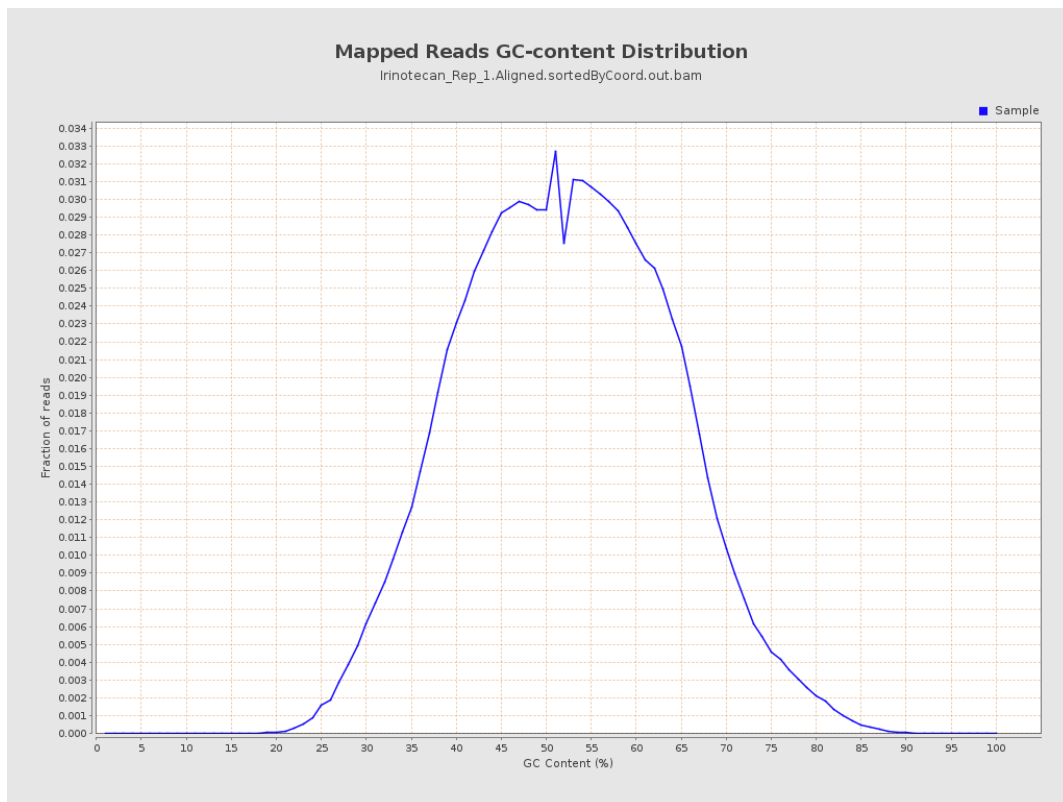
7. Results : Duplication Rate Histogram



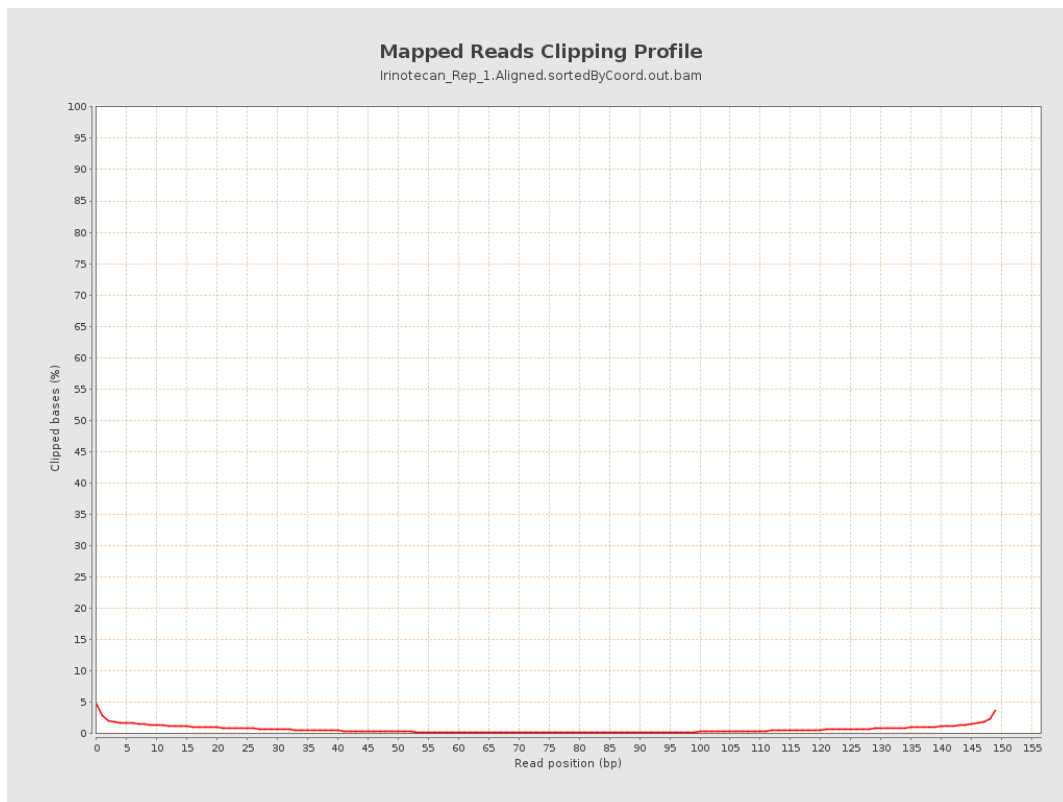
8. Results : Mapped Reads Nucleotide Content



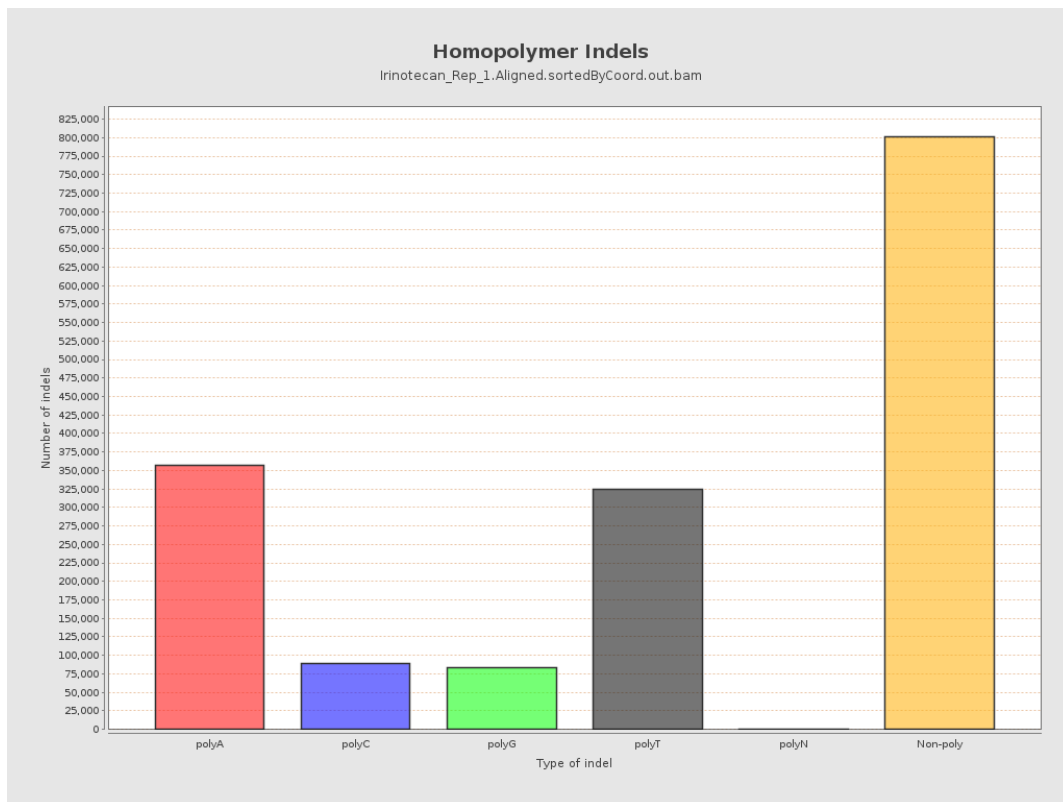
9. Results : Mapped Reads GC-content Distribution



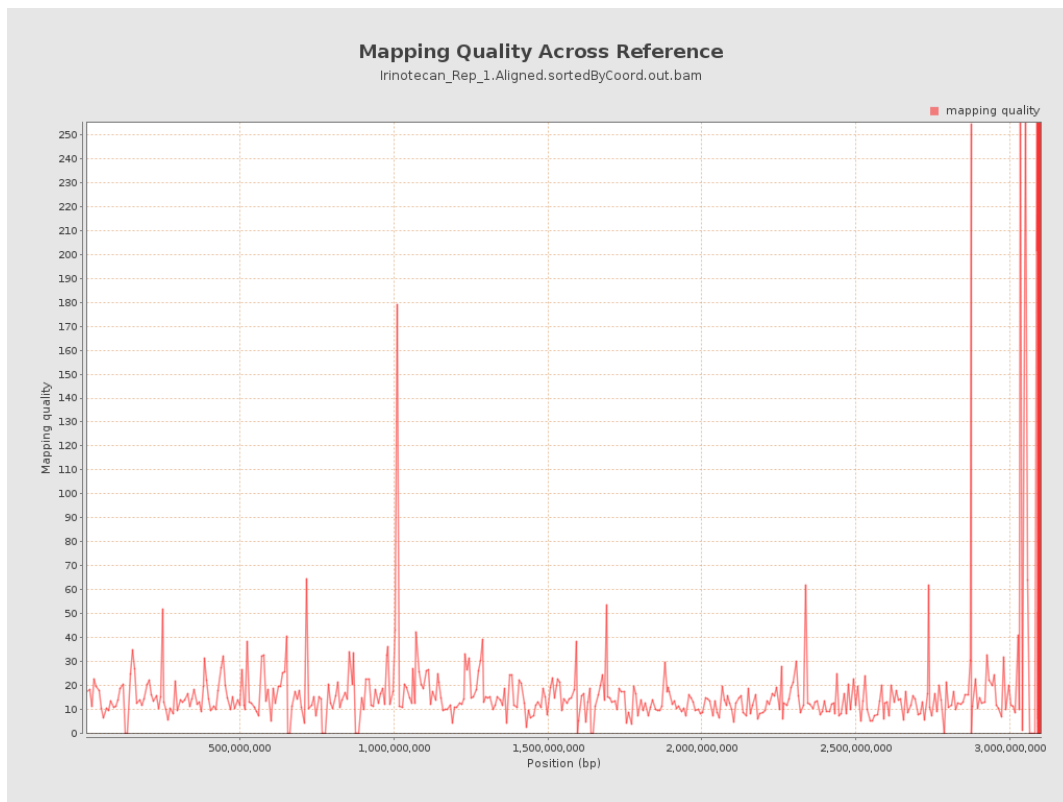
10. Results : Mapped Reads Clipping Profile



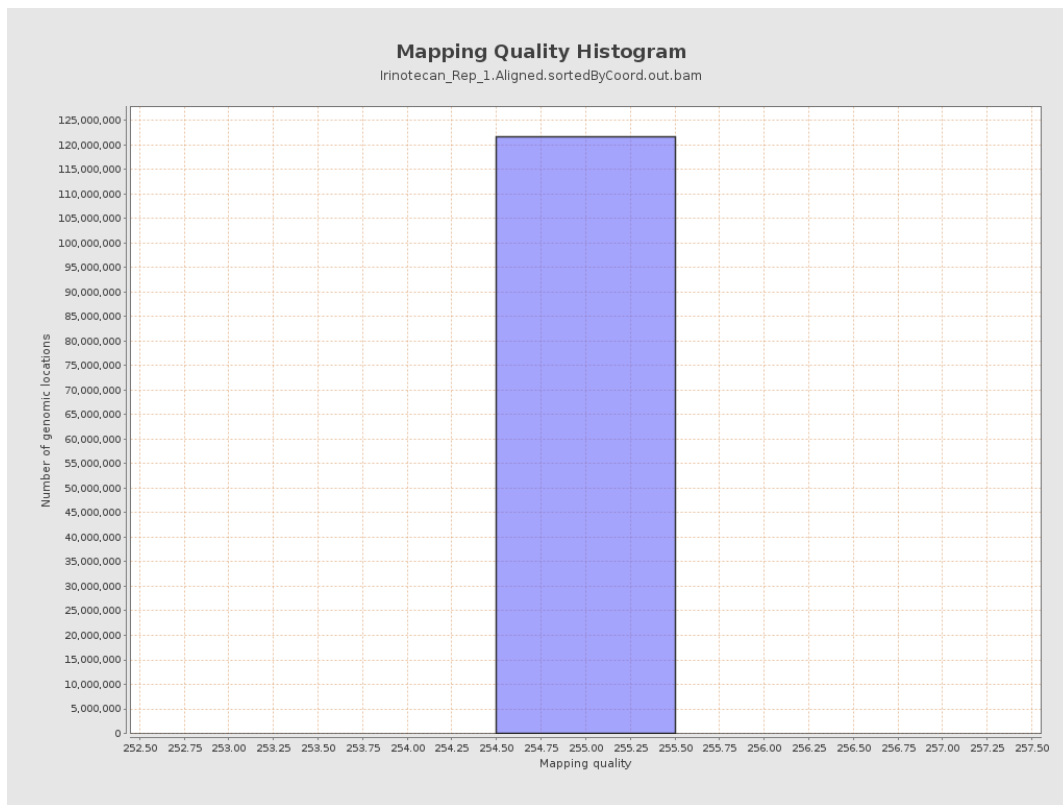
11. Results : Homopolymer Indels



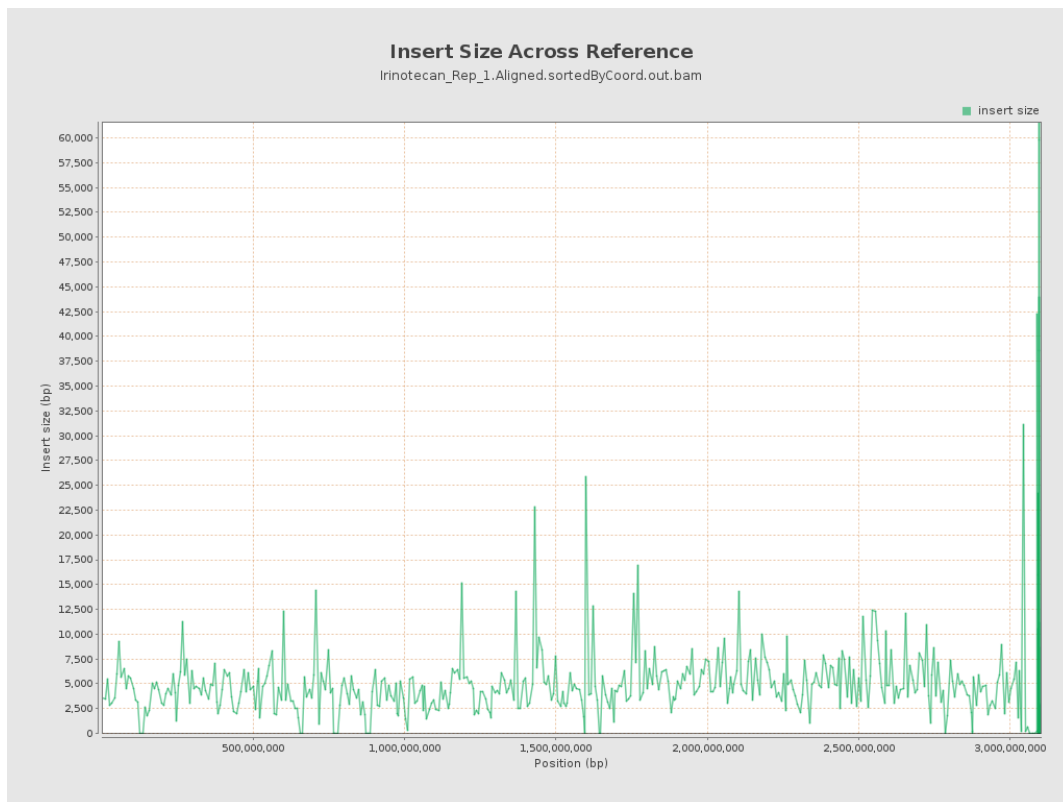
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

