Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.3
2024/04/19 10:18:39

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam Vehicle_Rep_1.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/Vehicle_Rep_1_1_val_1.fq /athena/angsd/scratch/sah4030/angsd_homework/Project/MSIV/TrimGalore/Vehicle_Rep_1_2_val_2.fq --outFileNamePrefix /athena/angsd/scratch/sah4030/angsd_homework/Project/Final/AlignReads/Vehicle_Rep_1. --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)

PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Analysis date:	Fri Apr 19 10:18:39 EDT 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	Vehicle_Rep_1.Aligned.sortedByCoord.out.bam

2. Summary

2.1. Globals

Reference size	3,099,750,718
Number of reads	63,613,215
Mapped reads	63,613,215 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	63,613,215 / 100%
Mapped reads, first in pair	31,808,126 / 50%
Mapped reads, second in pair	31,805,089 / 50%
Mapped reads, both in pair	63,608,556 / 99.99%
Mapped reads, singletons	4,659 / 0.01%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 149.28
Duplicated reads (estimated)	47,964,945 / 75.4%
Duplication rate	51.16%
Clipped reads	4,953,979 / 7.79%

2.2. ACGT Content

Number/percentage of A's	2,312,724,554 / 24.49%
Number/percentage of C's	2,401,645,414 / 25.43%
Number/percentage of T's	2,321,955,421 / 24.59%
Number/percentage of G's	2,405,899,293 / 25.48%
Number/percentage of N's	82,679 / 0%
GC Percentage	50.91%

2.3. Coverage

Mean	45.7483
Standard Deviation	147.2632

2.4. Mapping Quality

Mean Mapping Quality	20.35

2.5. Insert size

Mean	3,926.38
Standard Deviation	12,440.35
P25/Median/P75	266 / 732 / 3,038

2.6. Mismatches and indels

General error rate	0.02%
Mismatches	33,132,431
Insertions	923,138
Mapped reads with at least one insertion	1.43%
Deletions	450,521
Mapped reads with at least one deletion	0.7%
Homopolymer indels	51.68%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

1	248956422	14414977549	57.9016	126.2479
10	133797422	6120084432	45.7414	71.6606
11	135086622	8172322639	60.4969	198.377
12	133275309	7332024190	55.0141	146.1792
13	114364328	3258482138	28.4921	138.1313
14	107043718	3287983677	30.7163	123.511
15	101991189	4314783083	42.3054	153.0284
16	90338345	3007855929	33.2955	100.3736
17	83257441	7030428386	84.442	193.0369
18	80373285	2644163877	32.8985	59.8956
19	58617616	7750272836	132.2175	456.6889
2	242193529	11461517981	47.3238	128.9813
20	64444167	5449056959	84.5547	153.0576
21	46709983	2929521811	62.7173	89.9408
22	50818468	2538796997	49.9582	102.2428
3	198295559	8989482327	45.3338	128.4468
4	190214555	6336812652	33.314	89.6851
5	181538259	6072594862	33.4508	91.8543
6	170805979	8225182366	48.1551	220.416
7	159345973	8165872937	51.2462	86.1175
8	145138636	5442808534	37.5008	107.5154
9	138394717	5811600016	41.9929	122.4139
MT	16569	209783547	12,661.2075	12,242.9471
X	156040895	2757611928	17.6724	95.7241

Y	57227415	3590747	0.0627	0.1417
KI270728.1	1872759	4474	0.0024	0.0867
KI270727.1	448248	0	0	0
KI270442.1	392061	0	0	0
KI270729.1	280839	0	0	0
GL000225.1	211173	0	0	0
KI270743.1	210658	101111	0.48	0.5315
GL000008.2	209709	2992206	14.2684	14.0644
GL000009.2	201709	1198	0.0059	0.1081
KI270747.1	198735	0	0	0
KI270722.1	194050	297	0.0015	0.0481
GL000194.1	191469	5755064	30.0574	29.954
KI270742.1	186739	134567	0.7206	0.7718
GL000205.2	185591	1087170	5.8579	7.715
GL000195.1	182896	1726698	9.4409	9.9049
KI270736.1	181920	0	0	0
KI270733.1	179772	34626172	192.6116	580.293
GL000224.1	179693	9208	0.0512	1.0506
GL000219.1	179198	3874511	21.6214	24.9579
KI270719.1	176845	297	0.0017	0.0466
GL000216.2	176608	0	0	0
KI270712.1	176043	600	0.0034	0.098
KI270706.1	175055	1371239	7.8332	7.7252
KI270725.1	172810	0	0	0

KI270744.1	168472	1467	0.0087	0.1227
KI270734.1	165050	55289	0.335	1.328
GL000213.1	164239	239	0.0015	0.0424
GL000220.1	161802	26629637	164.5816	165.237
KI270715.1	161471	0	0	0
GL000218.1	161147	366406	2.2737	4.2689
KI270749.1	158759	0	0	0
KI270741.1	157432	323303	2.0536	2.0531
GL000221.1	155397	402168	2.588	2.5706
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	300	0.0022	0.0473
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	18833	0.1877	0.3268
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	21496	0.4915	0.4916
KI270735.1	42811	0	0	0
KI270711.1	42210	1168099	27.6735	31.444
KI270745.1	41891	3725	0.0889	0.397
KI270714.1	41717	52791	1.2655	3.2321
KI270732.1	41543	0	0	0
KI270713.1	40745	22074	0.5418	1.2906
KI270754.1	40191	300	0.0075	0.1022
KI270710.1	40176	0	0	0
KI270717.1	40062	300	0.0075	0.0999
KI270724.1	39555	0	0	0
KI270720.1	39050	1198	0.0307	0.4125
KI270723.1	38115	0	0	0
KI270718.1	38054	233	0.0061	0.078
KI270317.1	37690	0	0	0
KI270740.1	37240	0	0	0

KI270755.1	36723	0	0	0
KI270707.1	32032	2999	0.0936	0.5378
KI270579.1	31033	0	0	0
KI270752.1	27745	51691	1.8631	2.0178
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
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam
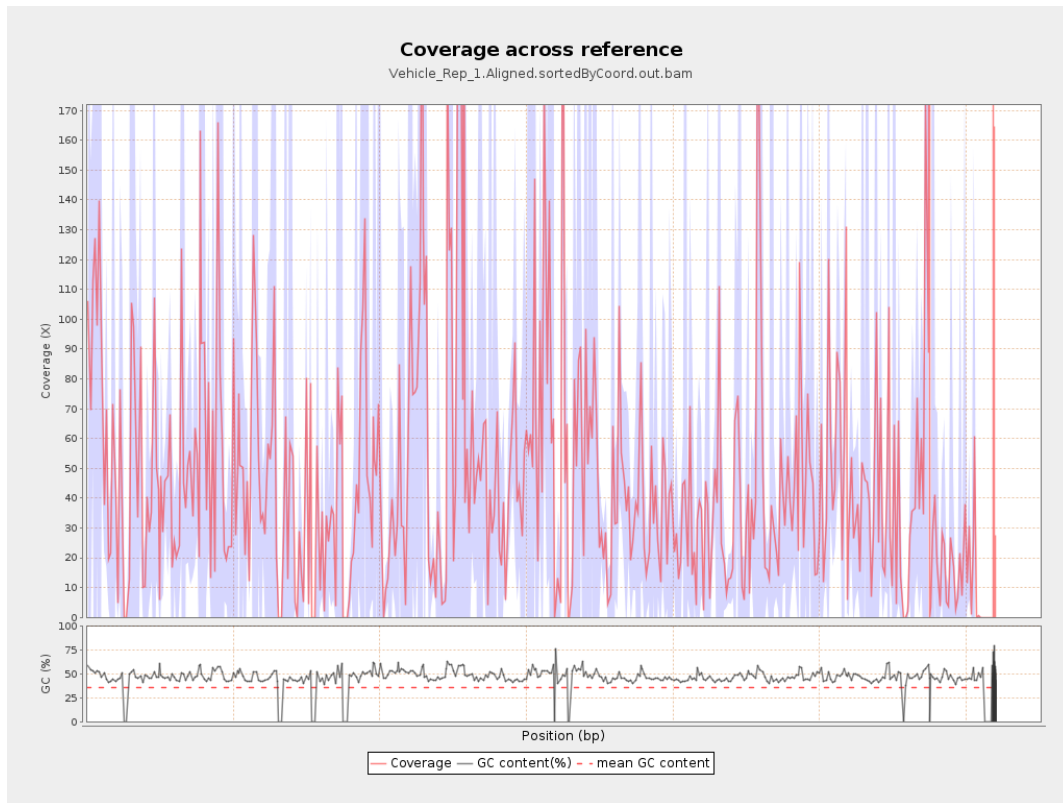
4. Results : Coverage Histogram

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

Coverage Histogram (0-50X)
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam
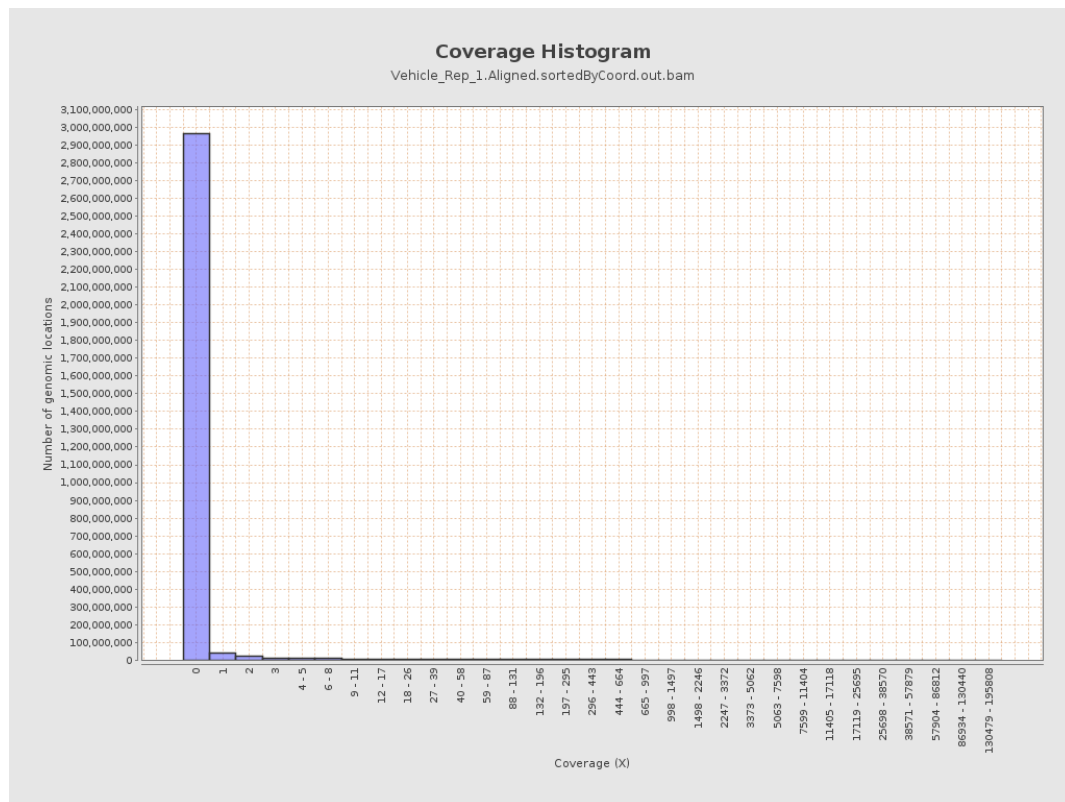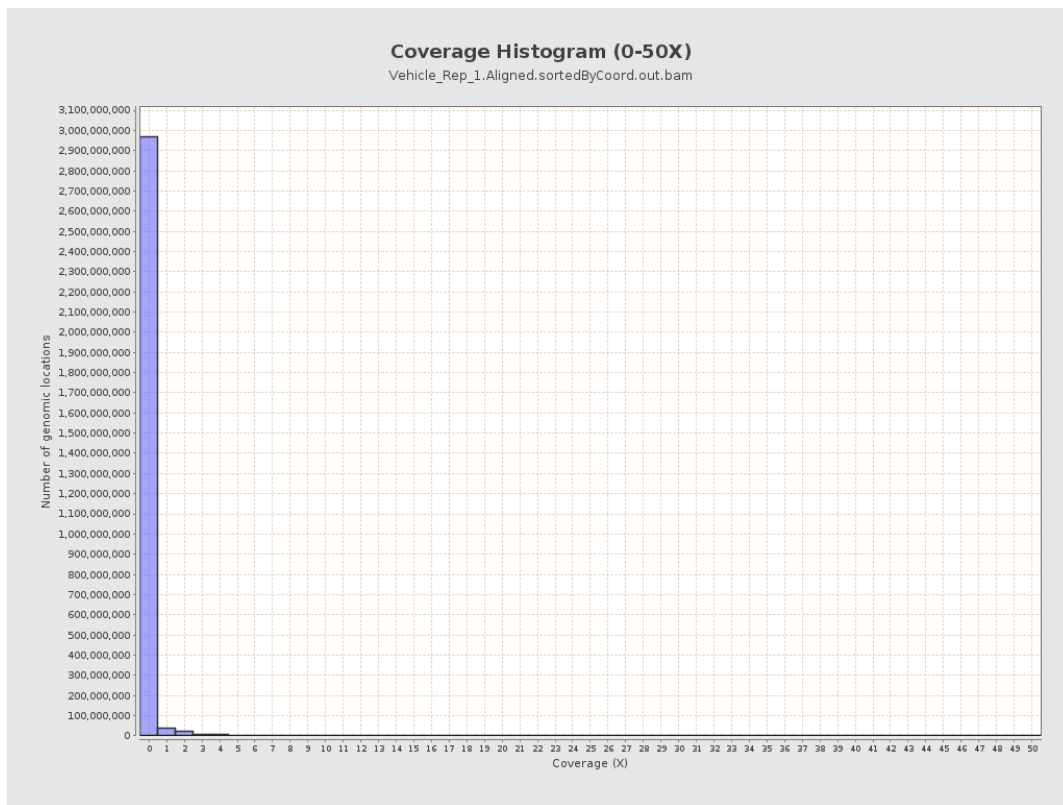
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam
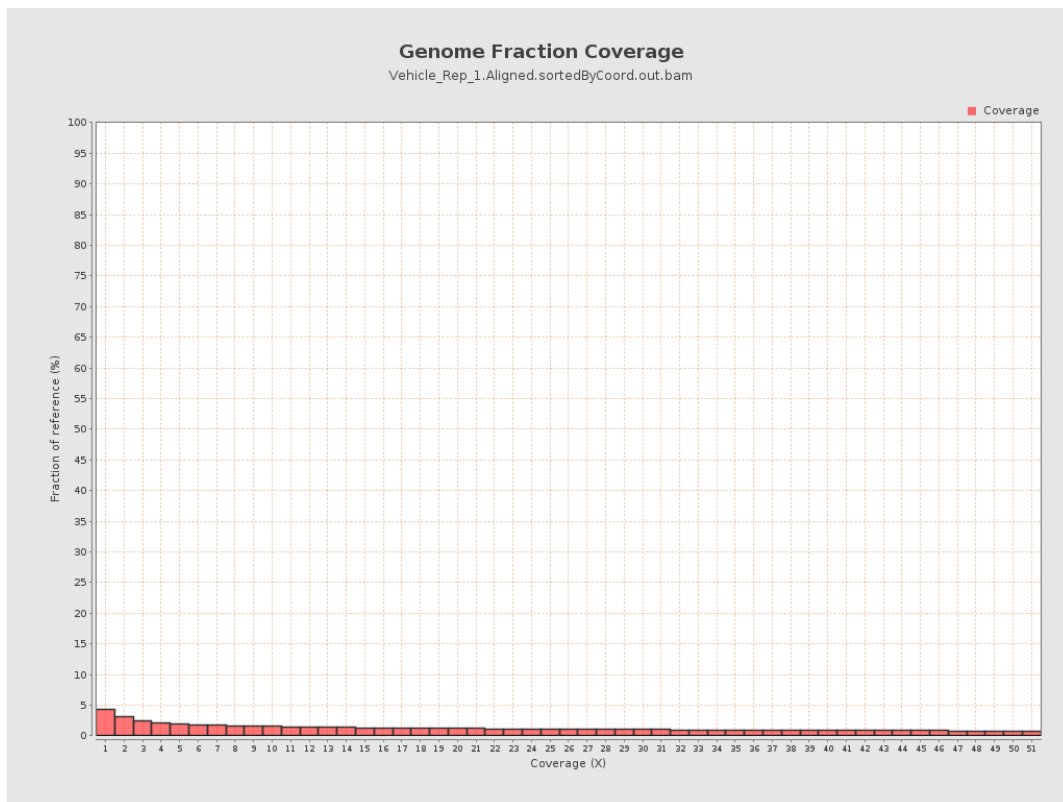
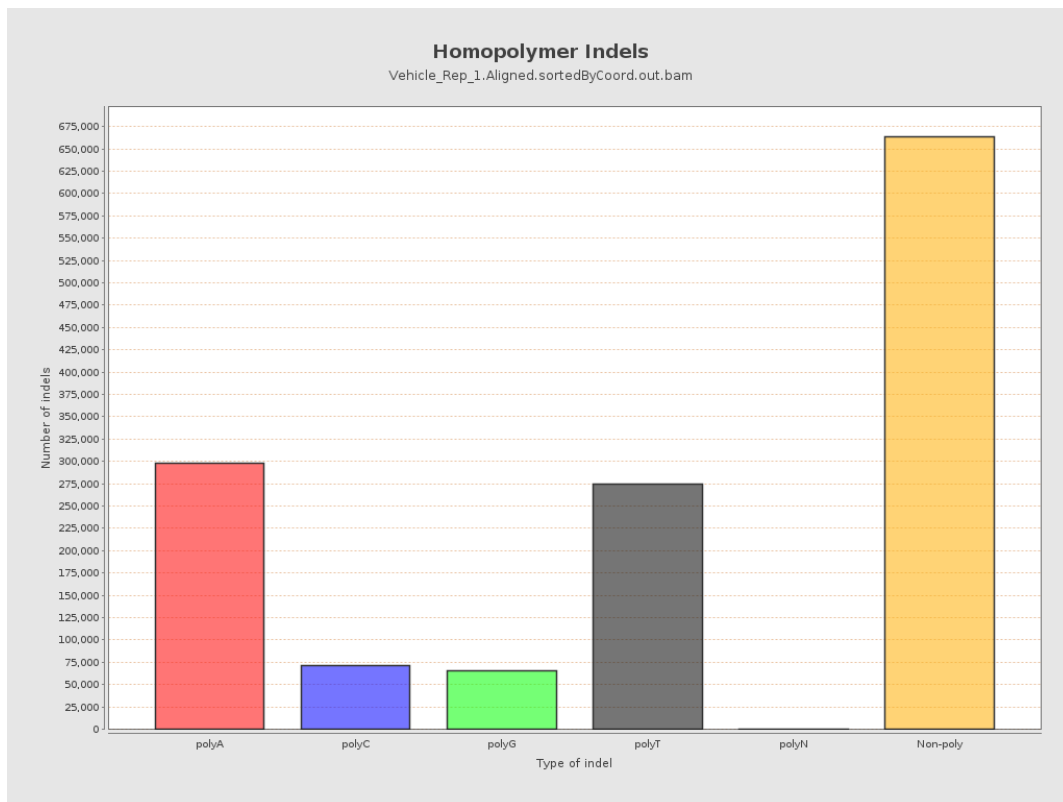# 7. Results : Duplication Rate Histogram
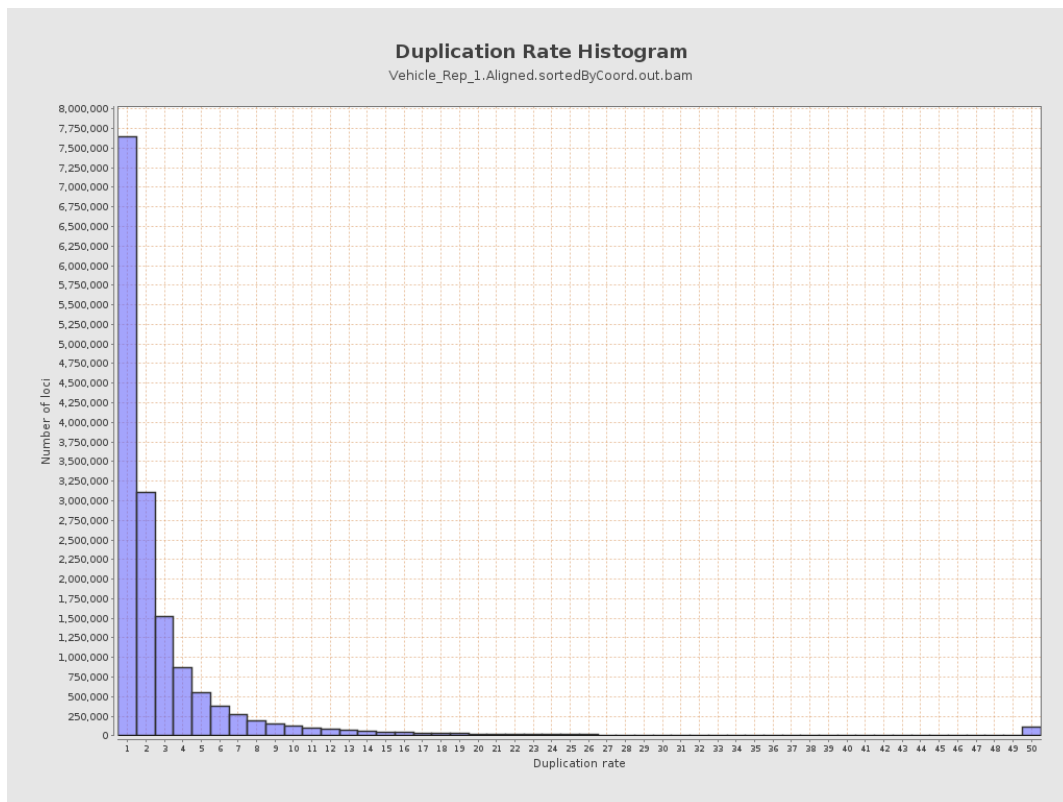
8. Results : Mapped Reads Nucleotide Content
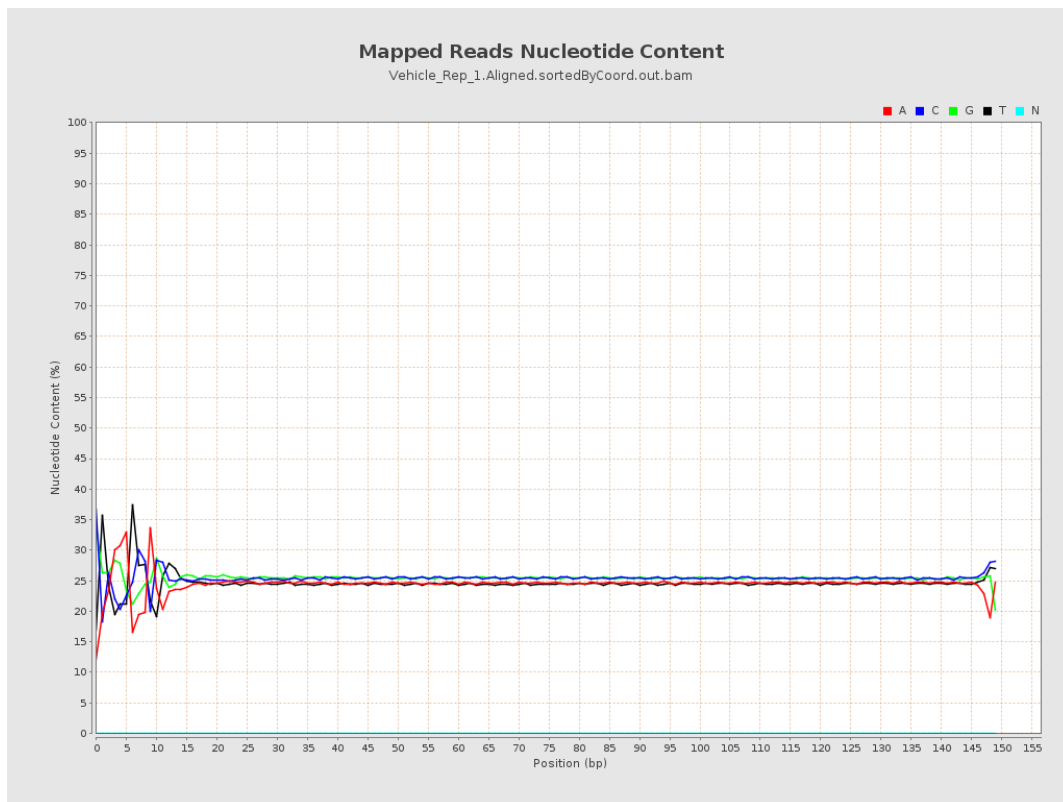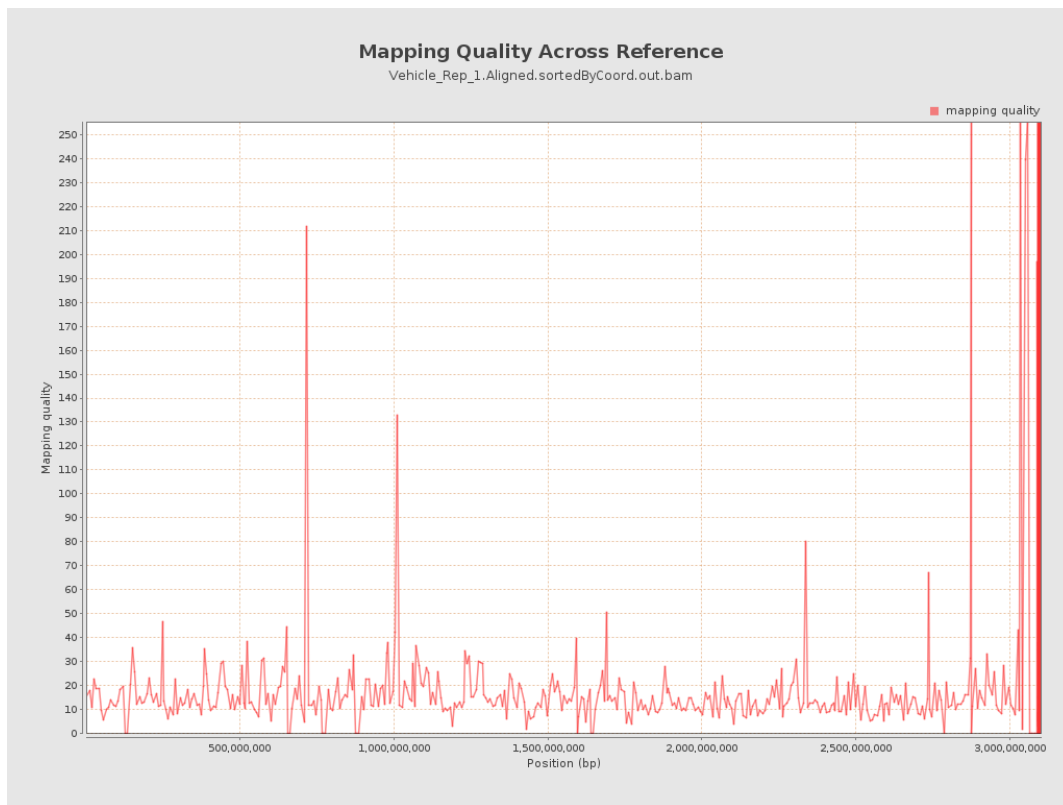
9. Results : Mapped Reads GC-content Distribution
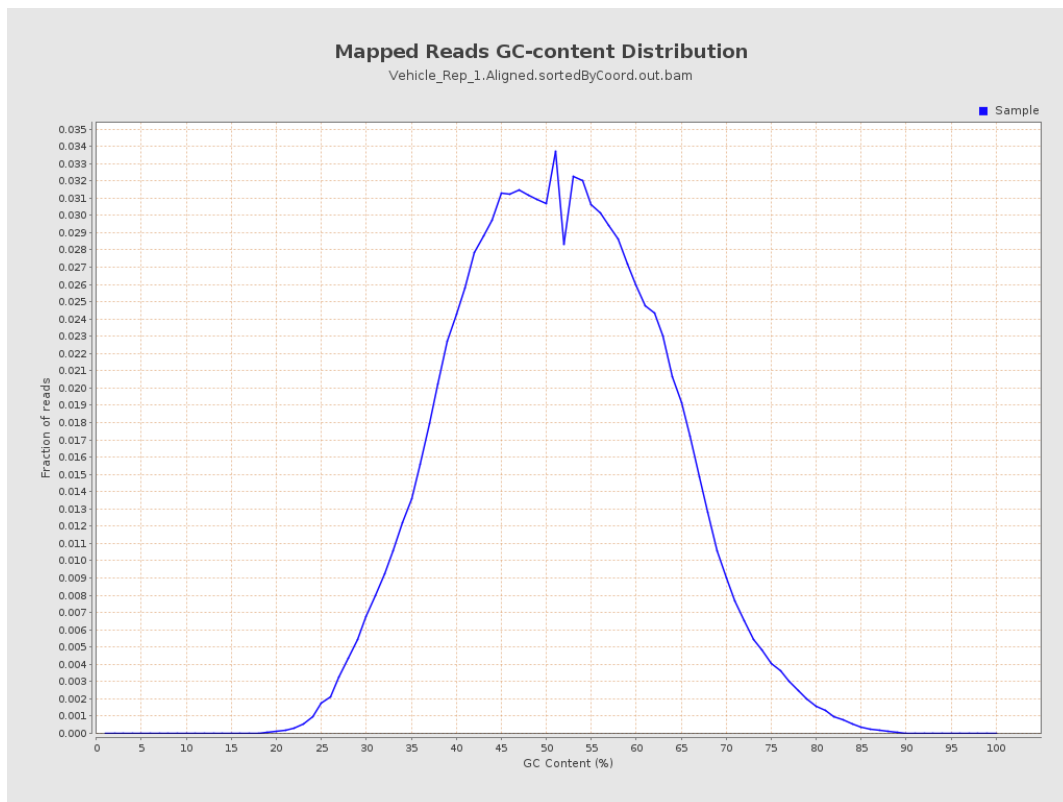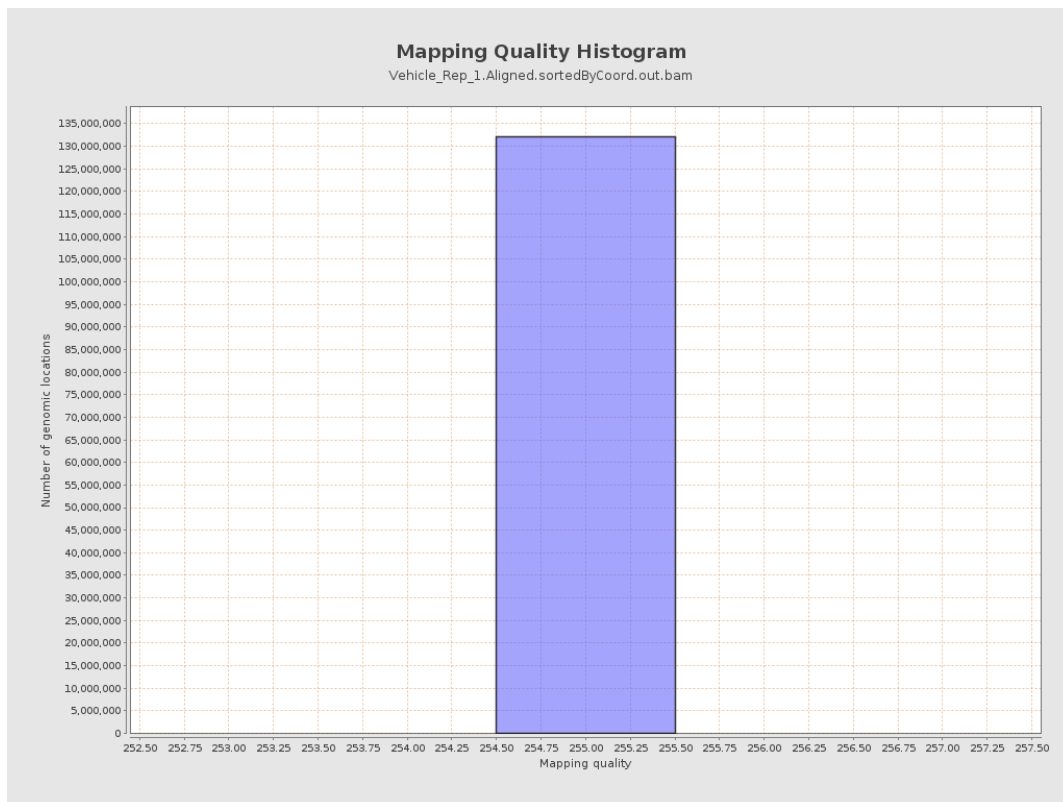
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam
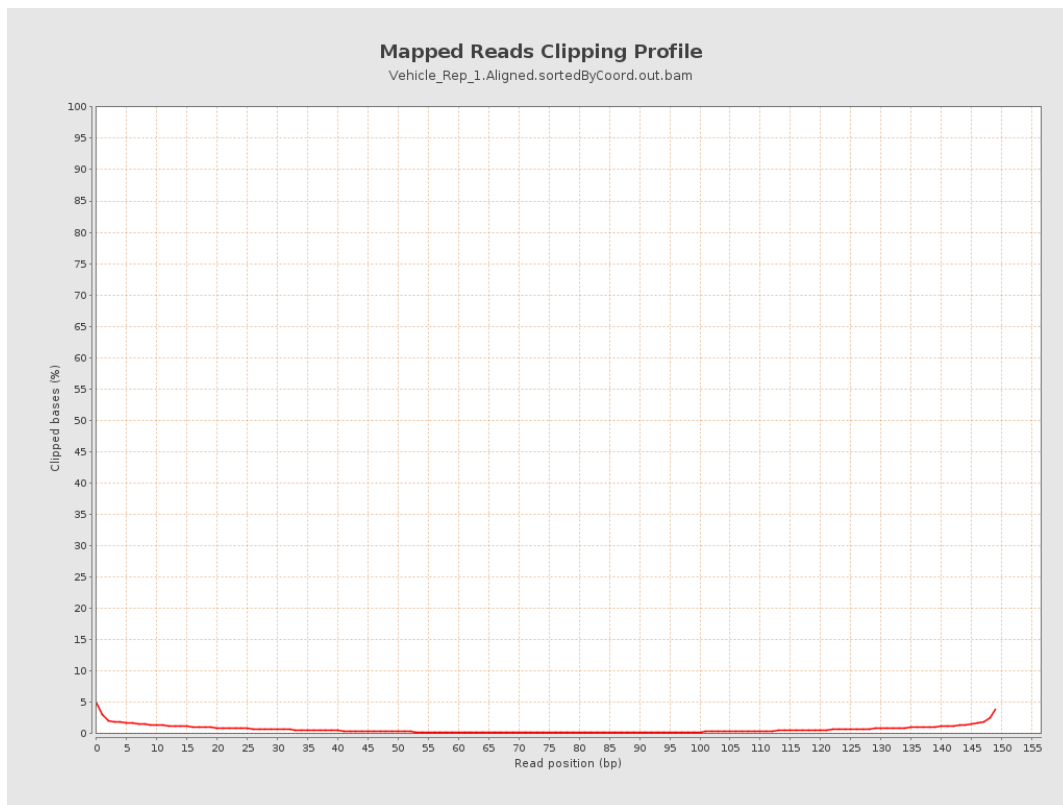
11. Results : Homopolymer Indels

Homopolymer Indels
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam

14. Results : Insert Size Across Reference
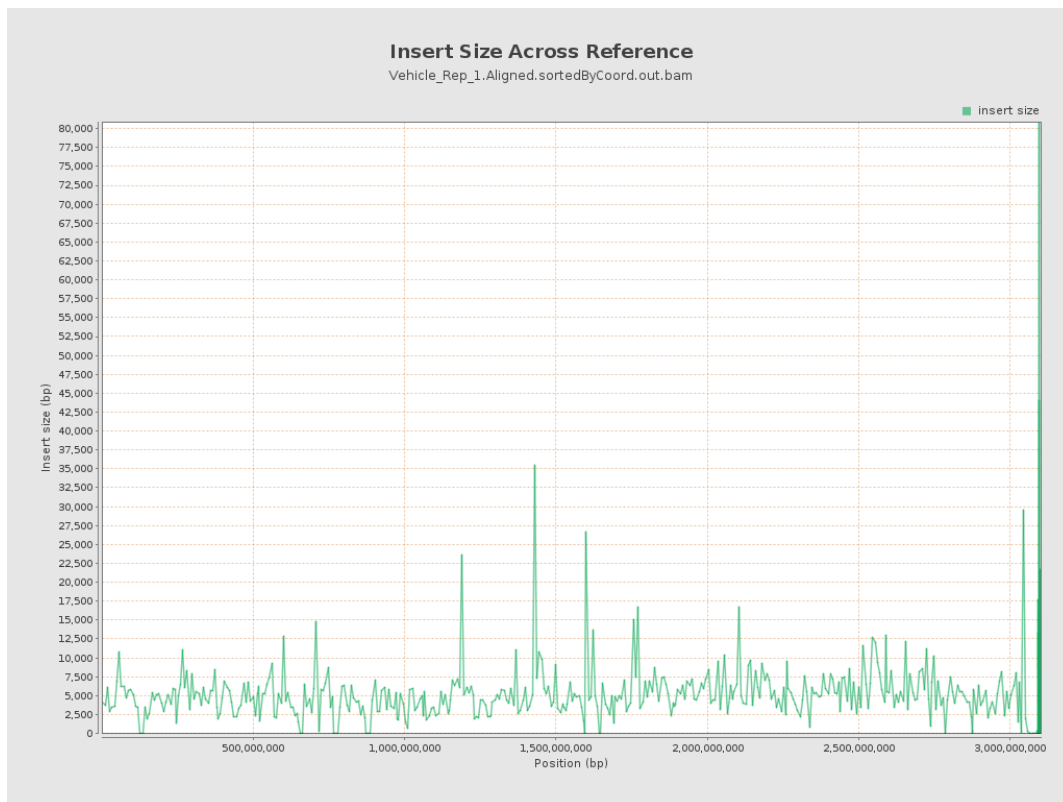
15. Results : Insert Size Histogram

Insert Size Histogram
Vehicle_Rep_1.Aligned.sortedByCoord.out.bam