

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/04/19 11:30:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam Vehicle_Rep_2.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/Vehicle_Rep_2_1_val_1.fq /athena/angsd/scratch/sah4030/angsd_homework/Project/MSIV/TrimGalore/Vehicle_Rep_2_2_val_2.fq -- outFileNamePrefix /athena/angsd/scratch/sah4030/angsd_homework/Project/Final/AlignReads/Vehicle_Rep_2. --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 11:30:26 EDT 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	Vehicle_Rep_2.Aligned.sortedByCoord.out.bam

2. Summary

2.1. Globals

Reference size	3,099,750,718
Number of reads	80,587,211
Mapped reads	80,587,211 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	80,587,211 / 100%
Mapped reads, first in pair	40,296,011 / 50%
Mapped reads, second in pair	40,291,200 / 50%
Mapped reads, both in pair	80,580,876 / 99.99%
Mapped reads, singletons	6,335 / 0.01%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 149.17
Duplicated reads (estimated)	62,491,521 / 77.55%
Duplication rate	54.1%
Clipped reads	6,027,253 / 7.48%

2.2. ACGT Content

Number/percentage of A's	2,903,139,670 / 24.28%
Number/percentage of C's	3,065,361,400 / 25.64%
Number/percentage of T's	2,915,962,272 / 24.39%
Number/percentage of G's	3,070,788,527 / 25.69%
Number/percentage of N's	104,286 / 0%
GC Percentage	51.33%

2.3. Coverage

Mean	58.9342
Standard Deviation	166.1706

2.4. Mapping Quality

Mean Mapping Quality	20.48
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2.5. Insert size

Mean	3,823.71
Standard Deviation	12,477.26
P25/Median/P75	252 / 614 / 2,837

2.6. Mismatches and indels

General error rate	0.02%
Mismatches	36,956,275
Insertions	1,160,586
Mapped reads with at least one insertion	1.42%
Deletions	584,023
Mapped reads with at least one deletion	0.72%
Homopolymer indels	51.79%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

1	248956422	18556256030	74.5362	151.4817
10	133797422	8016497623	59.9152	89.2398
11	135086622	10806490133	79.9967	223.2216
12	133275309	9545324044	71.6211	175.9985
13	114364328	4128013419	36.0953	131.7383
14	107043718	4275938498	39.9457	205.455
15	101991189	5476427514	53.6951	165.312
16	90338345	3952654787	43.7539	119.1498
17	83257441	9359432858	112.4156	238.9148
18	80373285	3217019939	40.026	68.6673
19	58617616	9494295764	161.97	442.1807
2	242193529	14802490823	61.1184	151.6753
20	64444167	6807602102	105.6357	166.4714
21	46709983	4036467255	86.4155	121.3568
22	50818468	3373548453	66.3843	128.0159
3	198295559	11474365146	57.865	130.1393
4	190214555	8114120891	42.6577	87.4196
5	181538259	7625302544	42.0038	93.6642
6	170805979	10508958657	61.5257	235.9541
7	159345973	10724797630	67.3051	114.2881
8	145138636	6882936064	47.4232	119.317
9	138394717	7523673348	54.3639	127.2907
MT	16569	286705773	17,303.7463	16,754.6545
X	156040895	3596058145	23.0456	97.5912

Y	57227415	5087287	0.0889	0.1896
KI270728.1	1872759	10010	0.0053	0.1204
KI270727.1	448248	0	0	0
KI270442.1	392061	4982	0.0127	0.0517
KI270729.1	280839	0	0	0
GL000225.1	211173	57274	0.2712	0.2739
KI270743.1	210658	4742	0.0225	0.3877
GL000008.2	209709	2892140	13.7912	13.5745
GL000009.2	201709	298	0.0015	0.0384
KI270747.1	198735	0	0	0
KI270722.1	194050	300	0.0015	0.05
GL000194.1	191469	5500446	28.7276	28.622
KI270742.1	186739	482134	2.5819	2.5672
GL000205.2	185591	1158655	6.2431	8.3699
GL000195.1	182896	1697319	9.2802	9.6389
KI270736.1	181920	0	0	0
KI270733.1	179772	40531853	225.4625	701.0437
GL000224.1	179693	8057	0.0448	0.8634
GL000219.1	179198	3866270	21.5754	24.8765
KI270719.1	176845	216	0.0012	0.0349
GL000216.2	176608	0	0	0
KI270712.1	176043	300	0.0017	0.0418
KI270706.1	175055	1792329	10.2387	10.0991
KI270725.1	172810	0	0	0

KI270744.1	168472	1494	0.0089	0.1388
KI270734.1	165050	75594	0.458	1.8441
GL000213.1	164239	0	0	0
GL000220.1	161802	29796468	184.1539	184.9252
KI270715.1	161471	0	0	0
GL000218.1	161147	348355	2.1617	3.5278
KI270749.1	158759	0	0	0
KI270741.1	157432	246214	1.5639	1.5637
GL000221.1	155397	732617	4.7145	4.6863
KI270716.1	153799	0	0	0
KI270731.1	150754	277	0.0018	0.0485
KI270751.1	150742	0	0	0
KI270750.1	148850	0	0	0
KI270519.1	138126	0	0	0
GL000214.1	137718	280	0.002	0.0557
KI270708.1	127682	0	0	0
KI270730.1	112551	0	0	0
KI270438.1	112505	271	0.0024	0.0645
KI270737.1	103838	0	0	0
KI270721.1	100316	15864	0.1581	0.3287
KI270738.1	99375	0	0	0
KI270748.1	93321	300	0.0032	0.0713
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	1398626	33.1349	36.9592
KI270745.1	41891	1543	0.0368	0.3618
KI270714.1	41717	42080	1.0087	2.7234
KI270732.1	41543	0	0	0
KI270713.1	40745	18330	0.4499	1.4447
KI270754.1	40191	0	0	0
KI270710.1	40176	0	0	0
KI270717.1	40062	2987	0.0746	0.1967
KI270724.1	39555	0	0	0
KI270720.1	39050	856	0.0219	0.1713
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	2376	0.0742	0.4338
KI270579.1	31033	0	0	0
KI270752.1	27745	56979	2.0537	2.2788
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

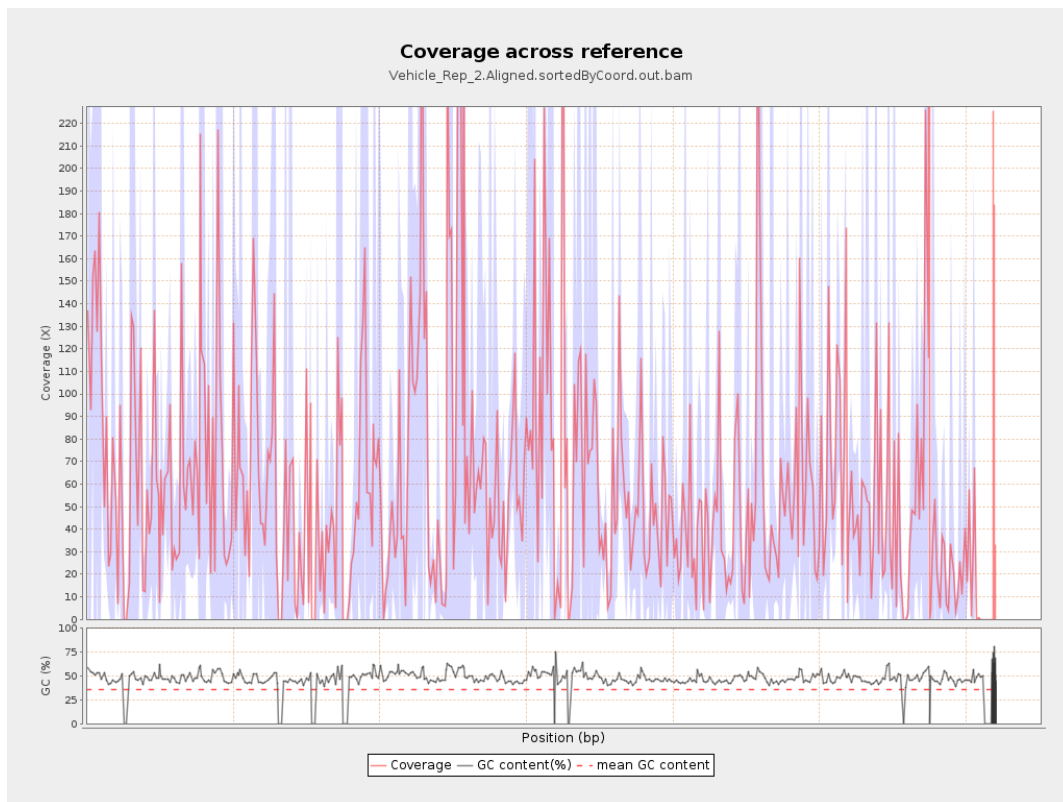
KI270467.1	3920	0	0	0
KI270362.1	3530	0	0	0
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KI270593.1	3041	0	0	0
KI270528.1	2983	0	0	0
KI270587.1	2969	0	0	0
KI270364.1	2855	0	0	0
KI270371.1	2805	0	0	0
KI270333.1	2699	0	0	0
KI270374.1	2656	0	0	0
KI270411.1	2646	0	0	0
KI270414.1	2489	0	0	0
KI270510.1	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

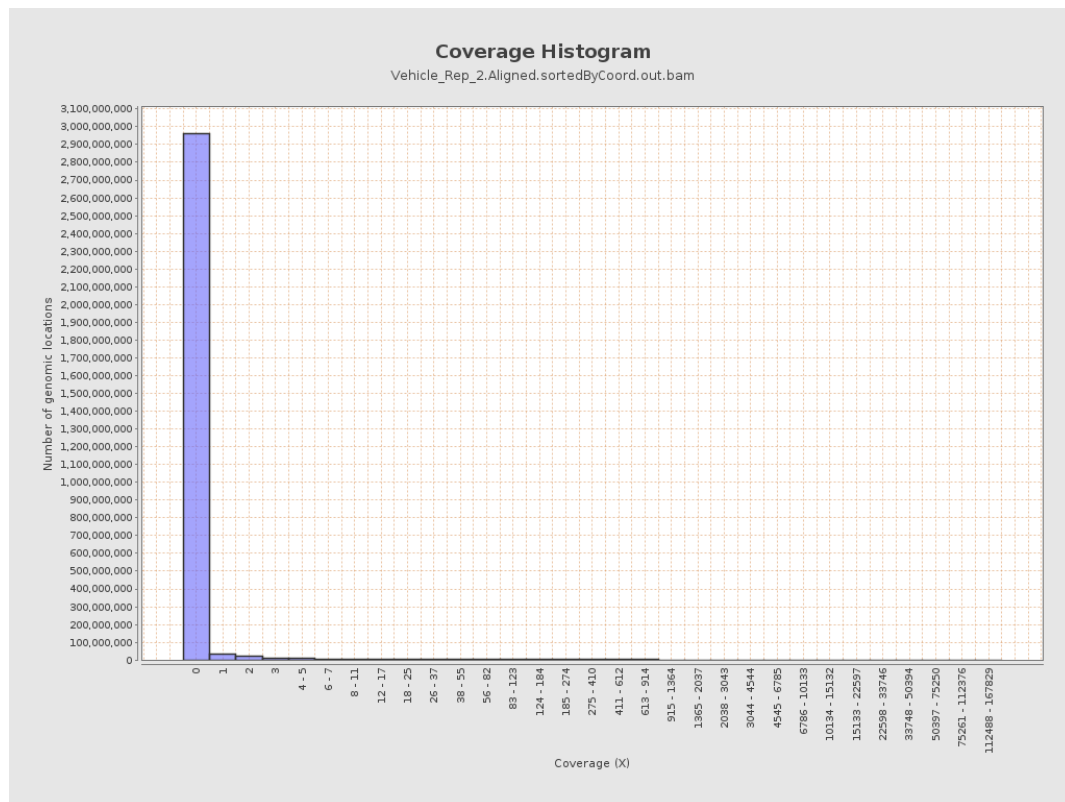
KI270583.1	1400	0	0	0
KI270334.1	1368	0	0	0
KI270429.1	1361	0	0	0
KI270393.1	1308	0	0	0
KI270516.1	1300	0	0	0
KI270389.1	1298	0	0	0
KI270466.1	1233	0	0	0
KI270388.1	1216	0	0	0
KI270544.1	1202	0	0	0
KI270310.1	1201	0	0	0
KI270412.1	1179	0	0	0
KI270395.1	1143	0	0	0
KI270376.1	1136	0	0	0
KI270337.1	1121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

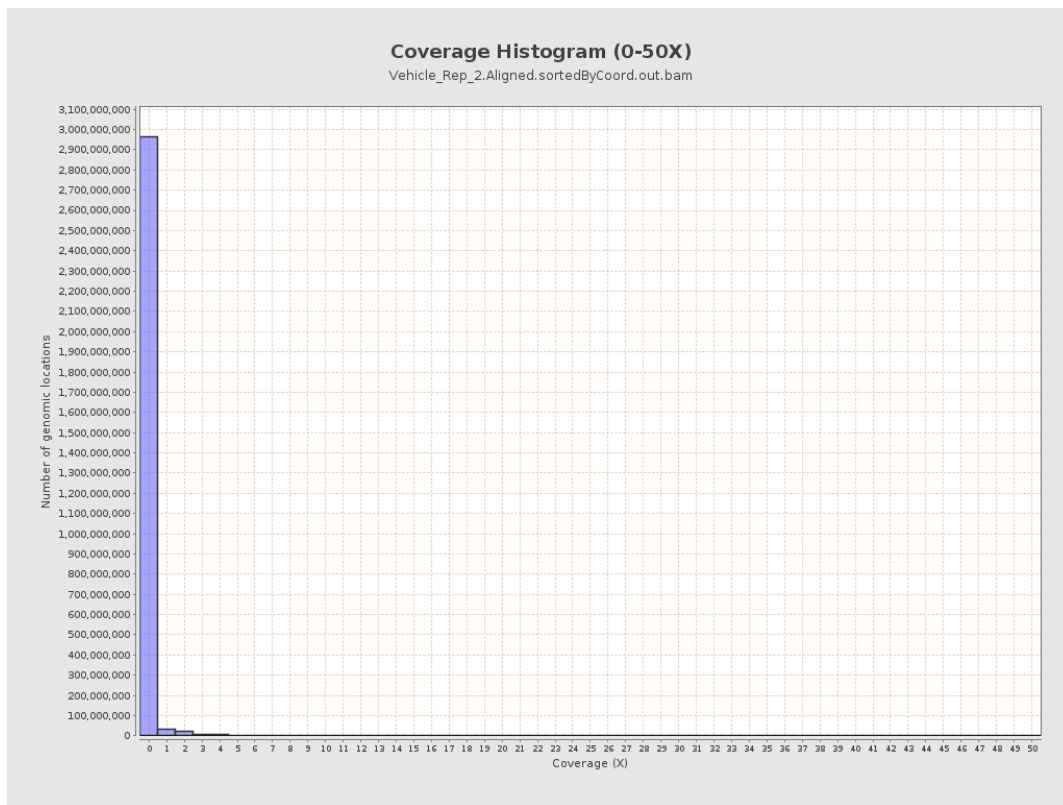
3. Results : Coverage across reference



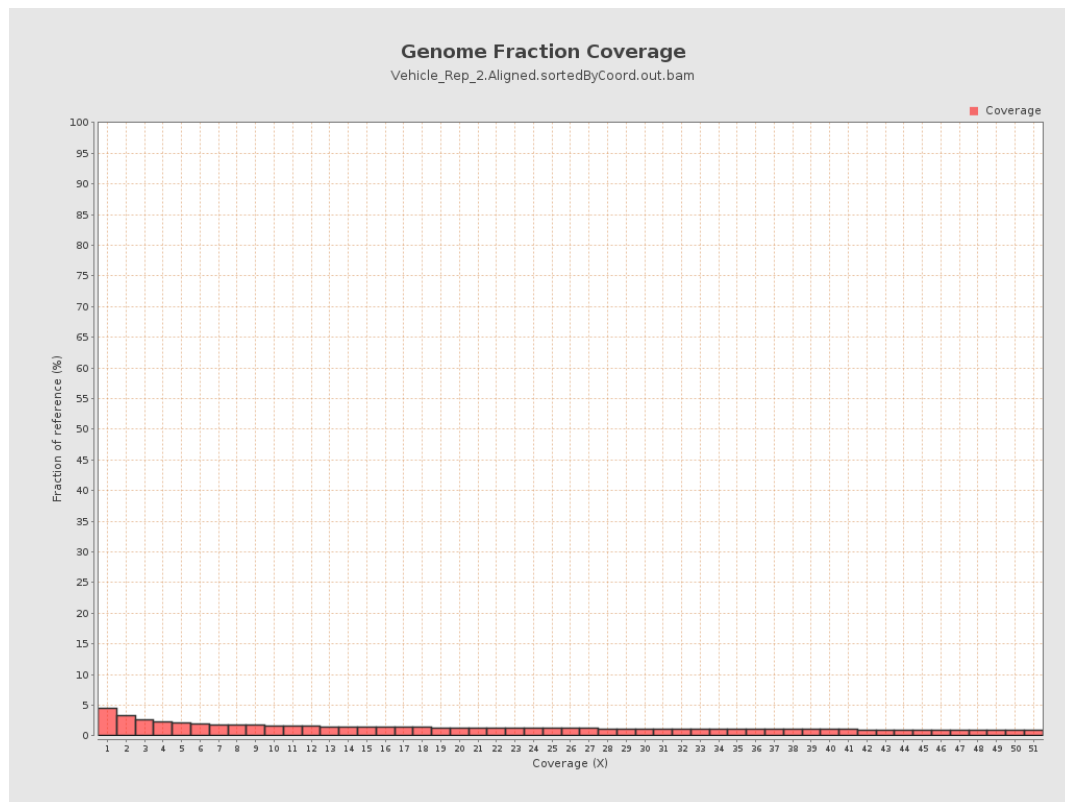
4. Results : Coverage Histogram



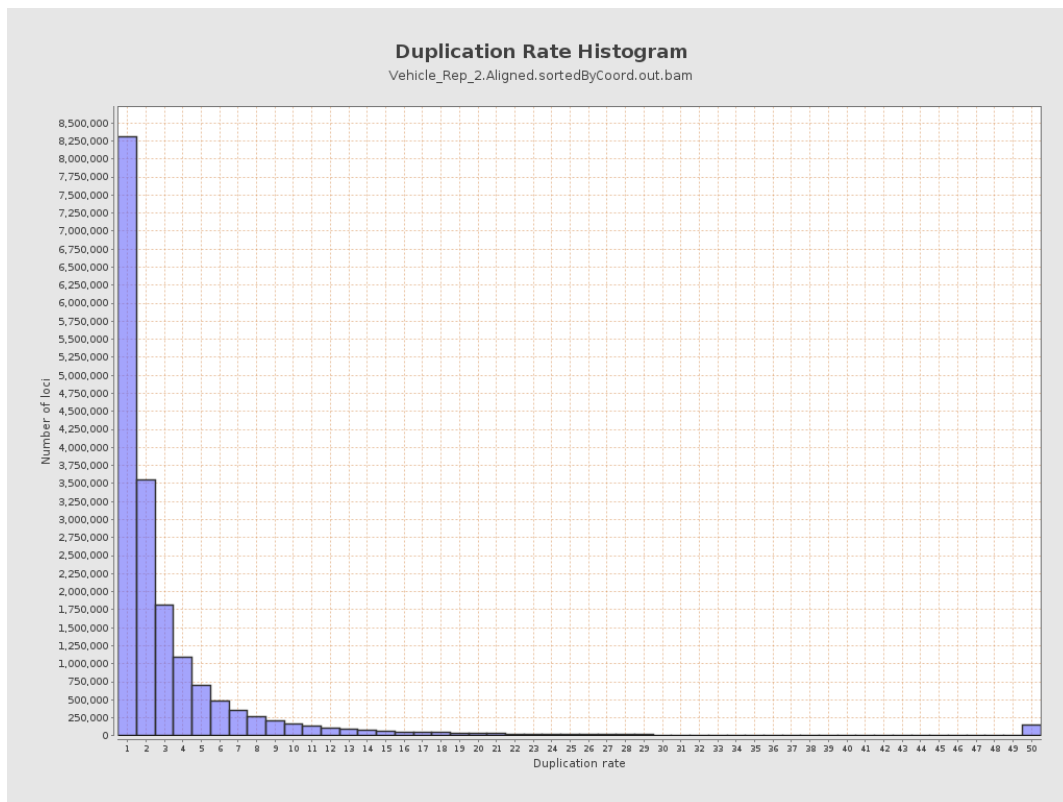
5. Results : Coverage Histogram (0-50X)



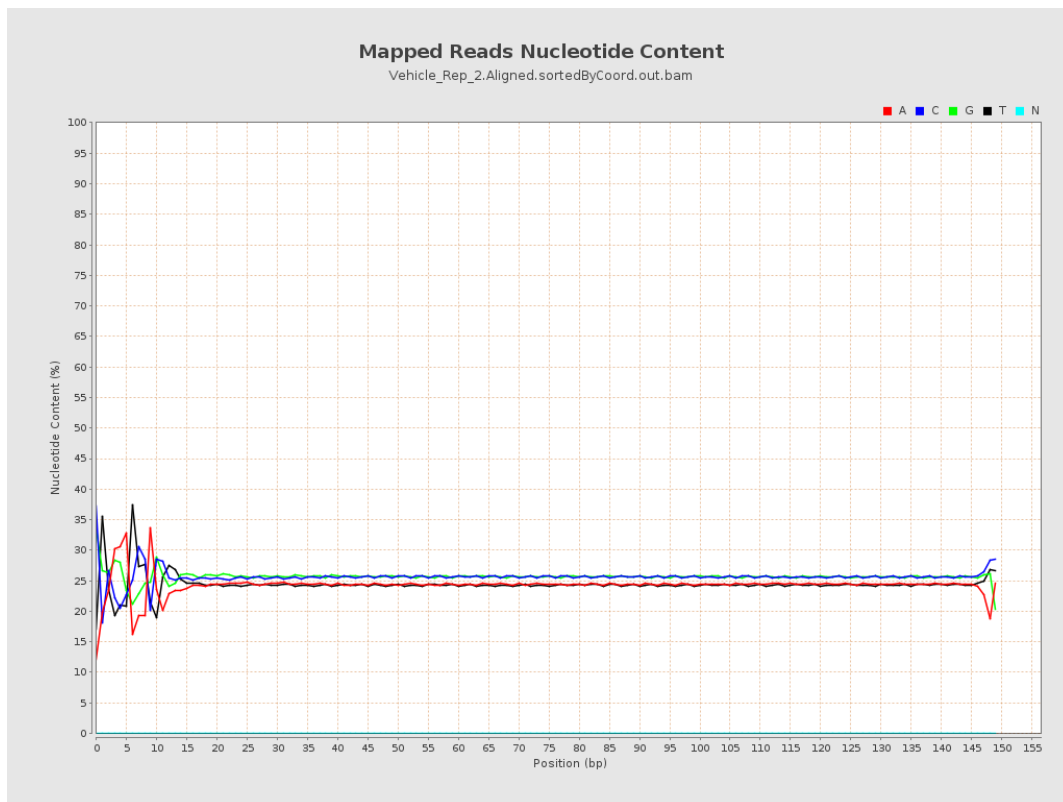
6. Results : Genome Fraction Coverage



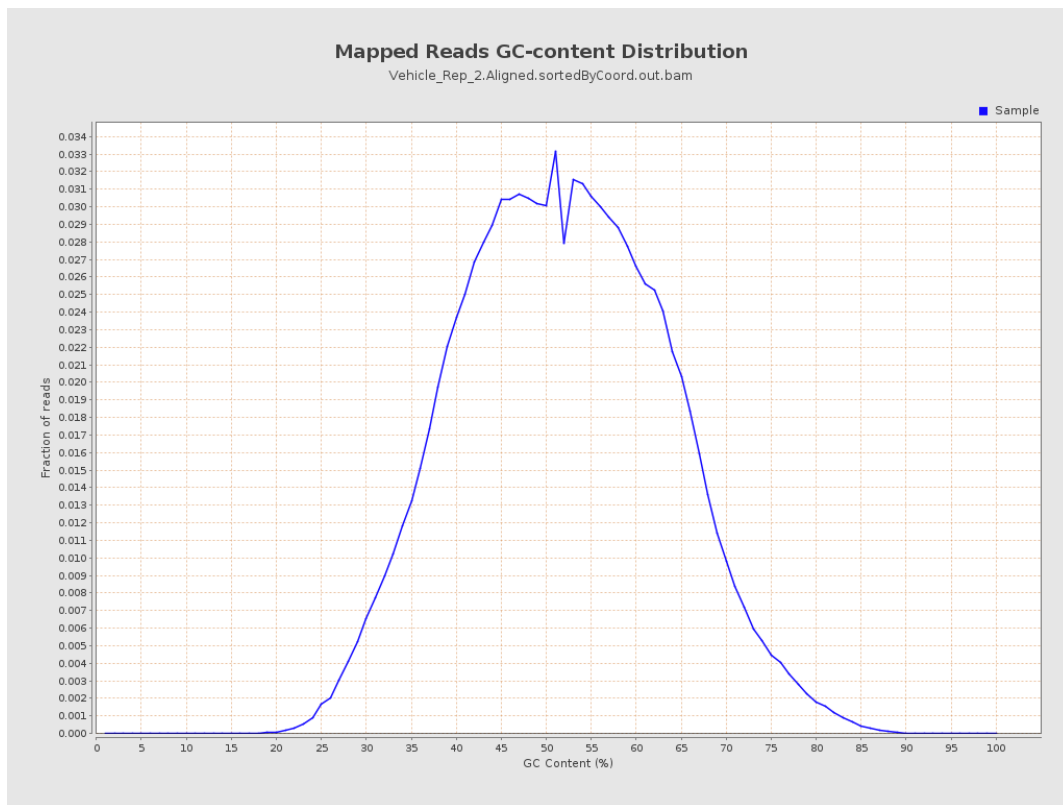
7. Results : Duplication Rate Histogram



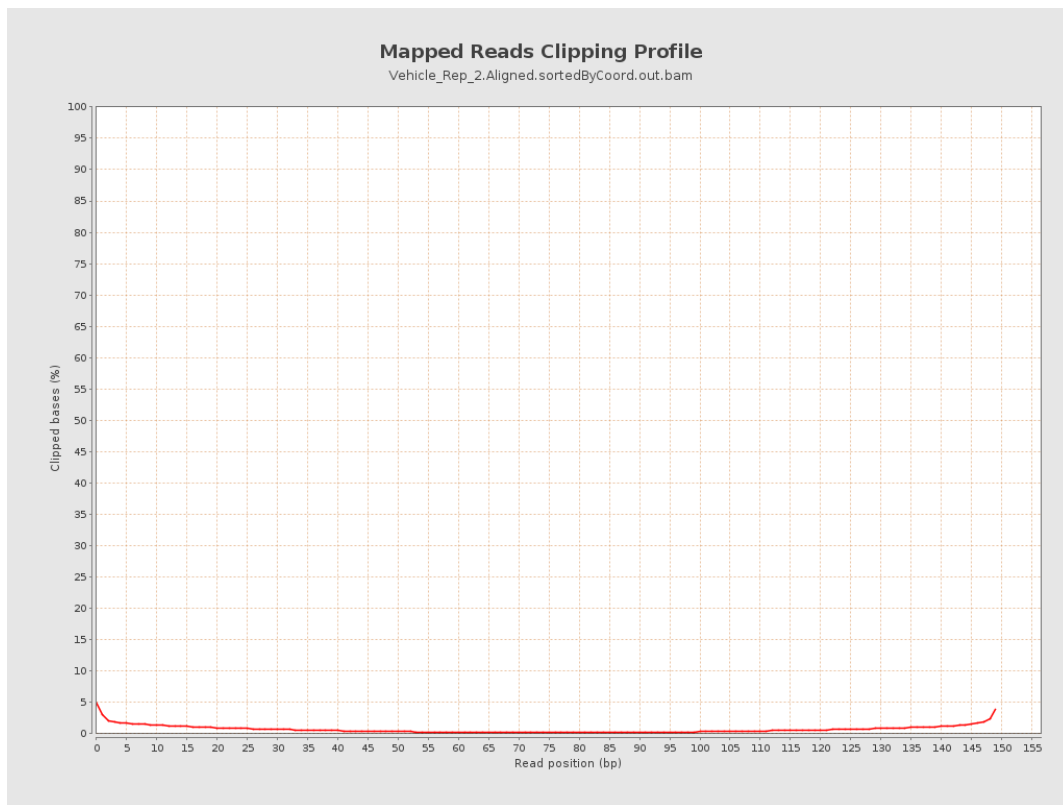
8. Results : Mapped Reads Nucleotide Content



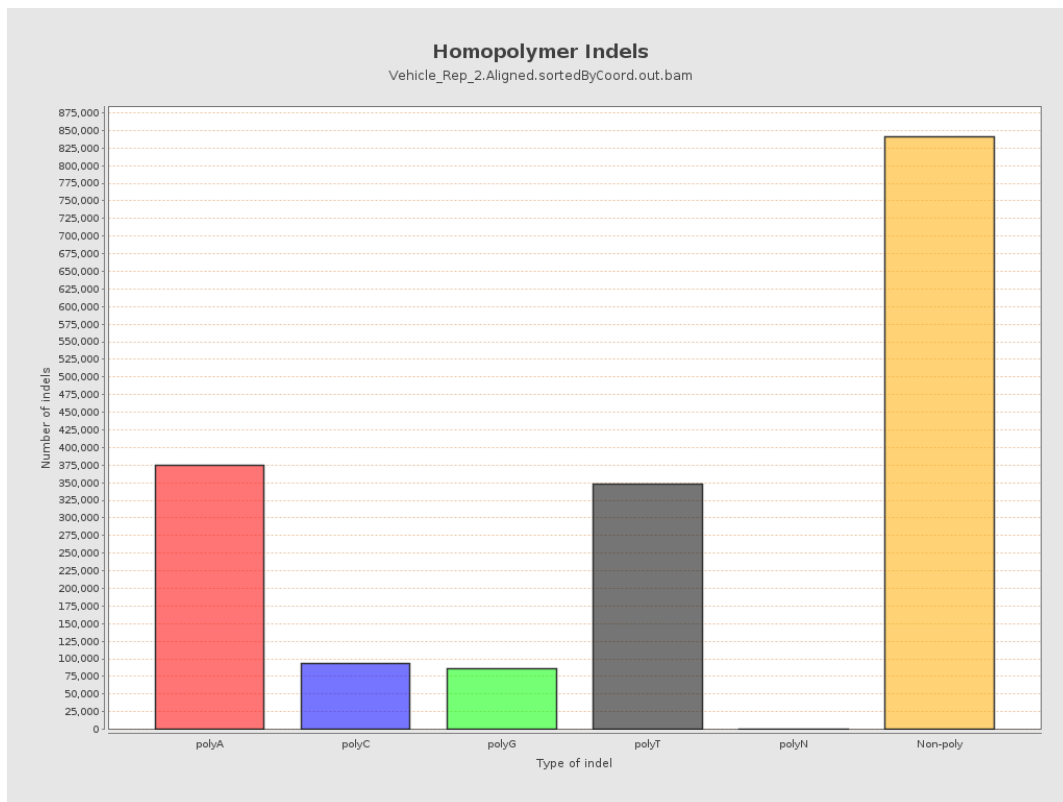
9. Results : Mapped Reads GC-content Distribution



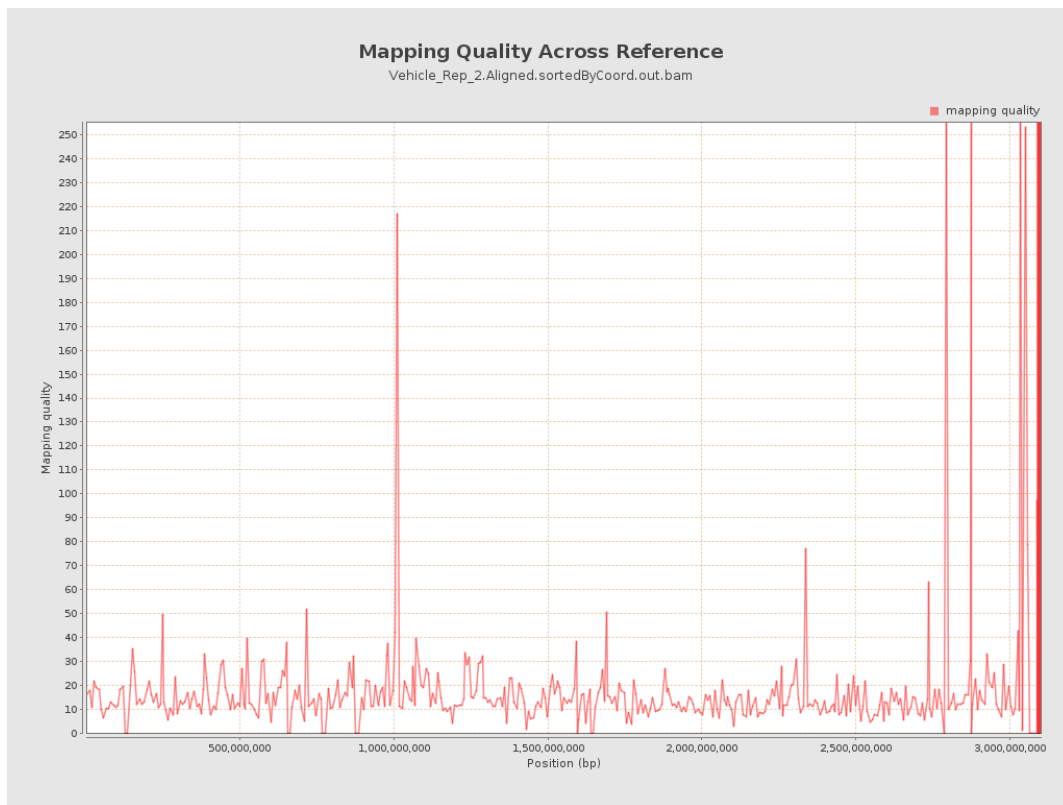
10. Results : Mapped Reads Clipping Profile



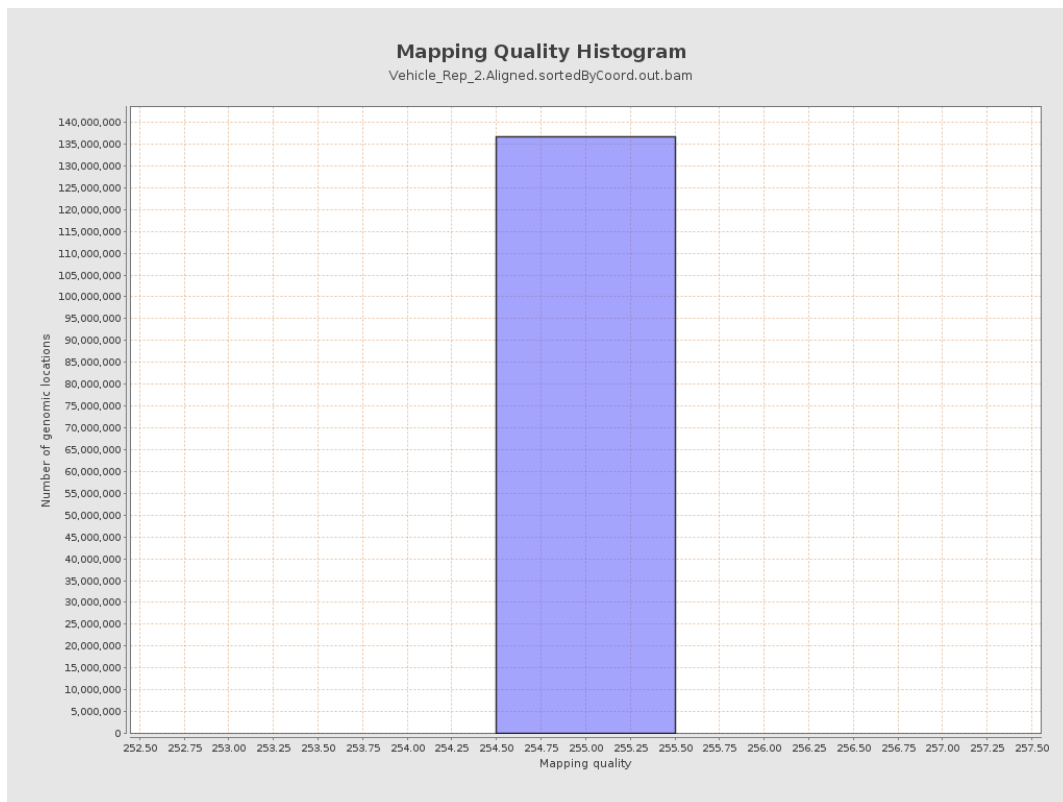
11. Results : Homopolymer Indels



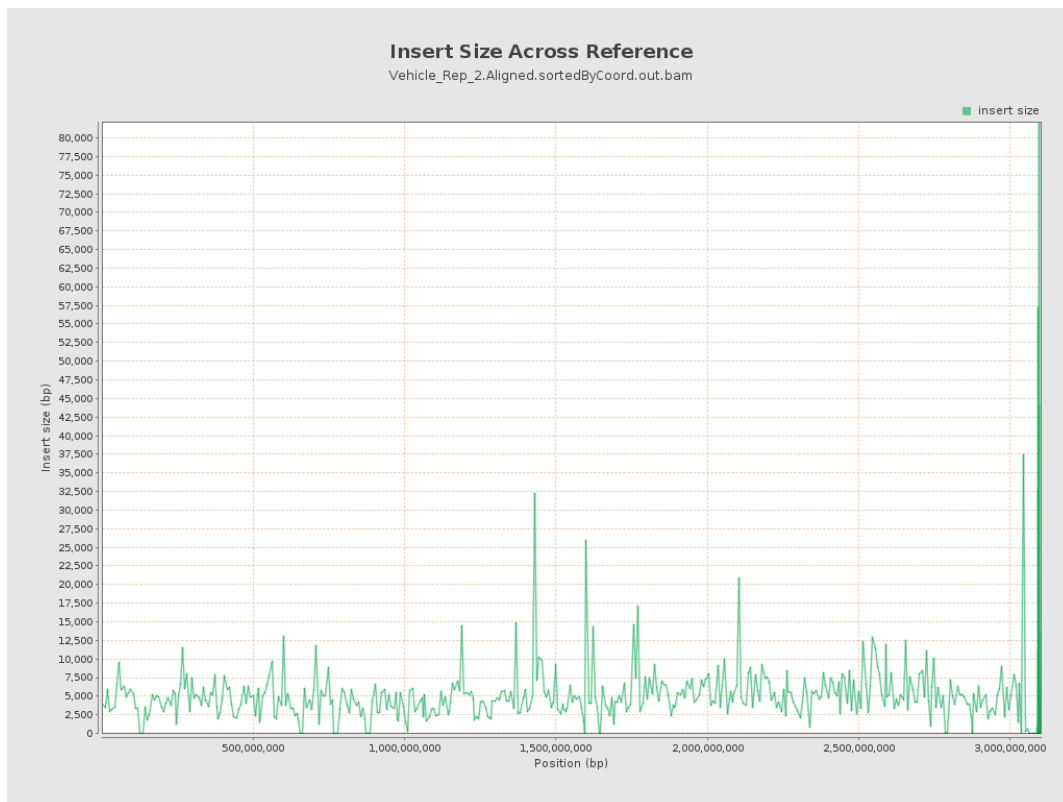
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

