Additional file 2.

Gene expression level

Genes with no insertion events - None
Genes with insertion events - Present

Data	Mean	Standard Deviation	Median	Upper Quartile	Lower Quartile	n
None	68.175	233.987	7.720	28.653	2.580	1913
Present	125.032	243.122	48.887	131.983	10.350	1913

Jarque-Bera Test:

	JB	Skewness	Kurtosis
None	459095.188	8.393	99.133
Present	119579.022	5.299	40.254

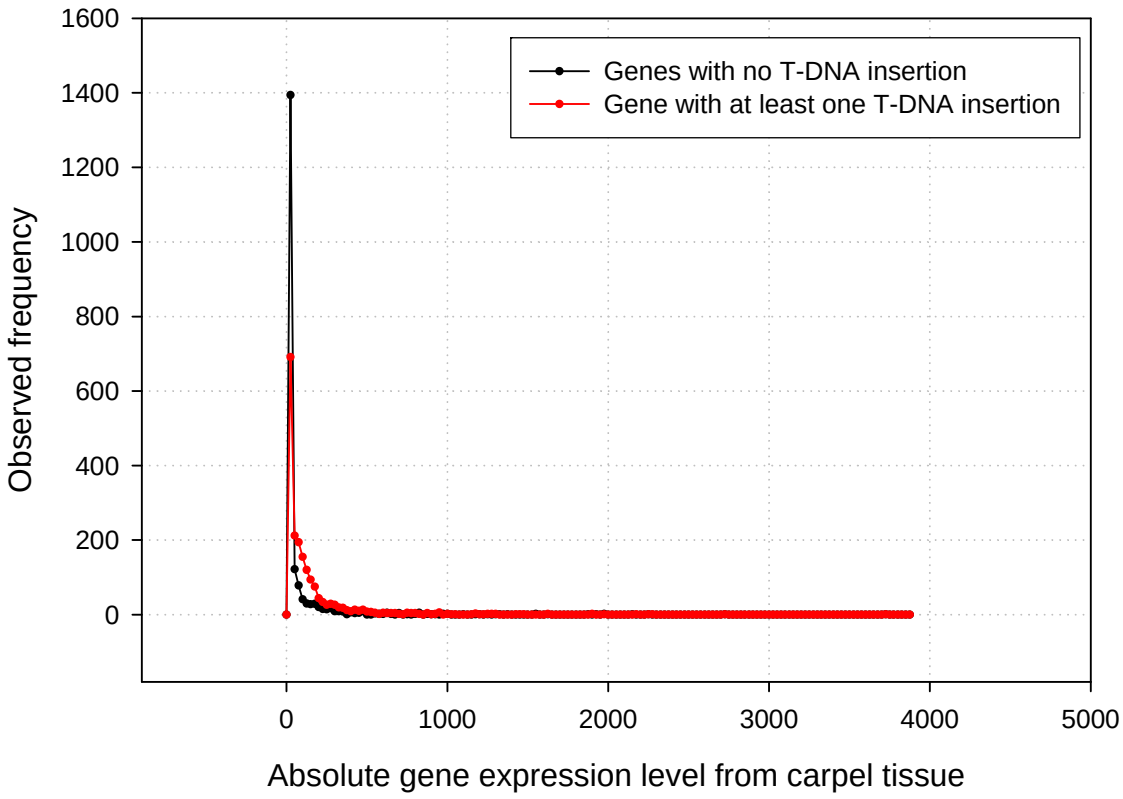
Probability: < 0.0001

Mann-Whitney-Wilcoxon Test:

Dataset	n	Rank sum: observed / expected
1	1913	2909214 /3659569
2	1913	4411836 /3659569

N (size of both datasets): 3826
z: -21.992058
Probability: <0.000001
Ranks of genes with no insertions are lower than expected

Plot of the distributions:


Genes with no T-DNA insertion
Gene with at least one T-DNA insertion
Observed frequency
1600
1400
1200
1000
800
600
400
200
0
0
1000
2000
3000
4000
5000
Absolute gene expression level from carpel tissue

Gene length – transcript (bp)

Genes with no insertion events - None
Genes with insertion events - Present

Data	Mean	Standard Deviation	Median	Upper Quartile	Lower Quartile	n
None	1131.756	911.020	841.000	1467.500	505.000	4806
Present	2418.472	1614.947	2081.500	3037.000	1358.000	4806

Jarque-Bera Test:

	JB	Skewness	Kurtosis
None	11244.068	2.438	8.690
Present	248262.798	4.008	37.285

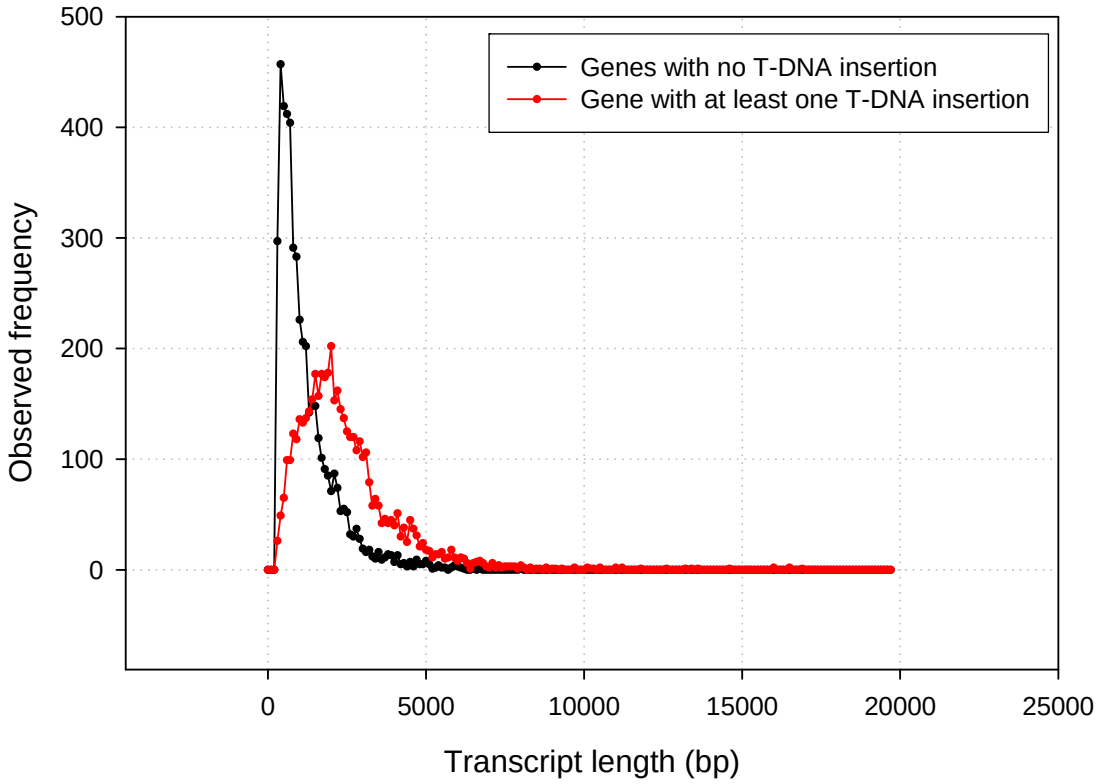
Probability: < 0.0001

Mann-Whitney-Wilcoxon Test:

Dataset	n	rank sum: observed / expected
1	4806	16145421 /23097636
2	4806	30054657 /23097636

N (size of both datasets): 9612
z: -1048041.30282
Probability: <0.000001
Ranks of genes with no insertions are lower than expected

Plot of the distributions:


Genes with no T-DNA insertion
Gene with at least one T-DNA insertion
Observed frequency
Transcript length (bp)
500
400
300
200
100
0
0
5000
10000
15000
20000
25000

Position relative to the centromere (Kbp)

Genes with no insertion events - None
Genes with insertion events - Present

Data	Mean	Standard Deviation	Median	Upper Quartile	Lower Quartile	n
None	5069.832	4279.960	3631.0	8115.5	1406127.5	4806
Present	7714.580	4173.393	7803.0	11109.0	4142395.0	4806

Jarque-Bera Test:

	JB	Skewness	Kurtosis
None	1723.144	1.434	2.380
Present	1657.428	1.331	1.910

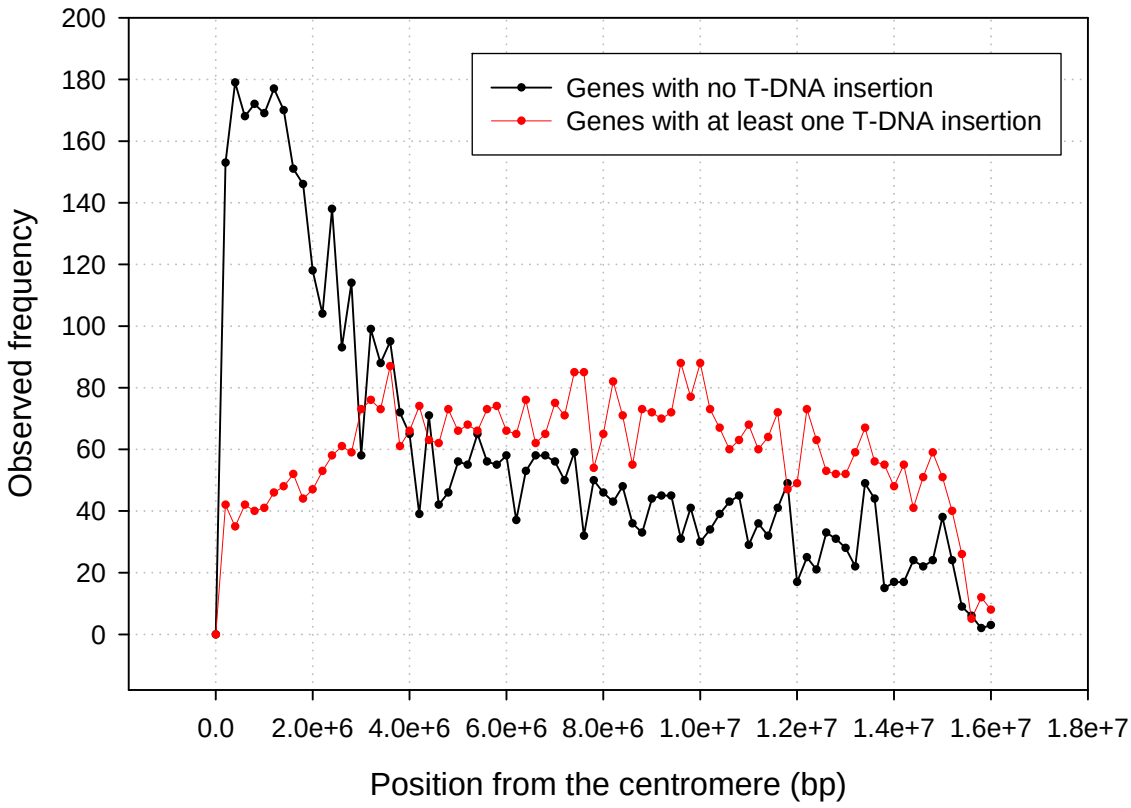
Probability: < 0.0001

Mann-Whitney-Wilcoxon Test:

Dataset	n	Rank sum: observed / expected
1	4806	18915972 /23097636
2	4806	27284105 /23097636

N (size of both datasets): 9612
z: -30.759262
Probability: <0.000001
Ranks of genes with no insertion are lower than expected

Plot of the distributions:


Genes with no T-DNA insertion
Genes with at least one T-DNA insertion
Observed frequency
Position from the centromere (bp)
0
20
40
60
80
100
120
140
160
180
200
0.0
2.0e+6
4.0e+6
6.0e+6
8.0e+6
1.0e+7
1.2e+7
1.4e+7
1.6e+7
1.8e+7

A) χ^2 contingency tables for basic gene characteristics:

i) Intron sequences:

	Genes with T-DNA hit	Genes with no T-DNA hit
Genes with intron	22,940	2,496
Gene without intron	4,338	3,508
X^2 1d.f.	4,941	P < 0.0001

ii) Annotated pseudogenes:

	Genes with T-DNA hit	Genes with no T-DNA hit
Genes	26,293	5,250
Pseudogenes	985	754
X^2 1d.f.	794	P < 0.0001

ii) Annotated single copy genes:

	Genes with T-DNA hit	Genes with no T-DNA hit
Gene family	24,140	5,509
Single copy genes	3,138	495
X^2 1d.f.	53.8	P < 0.0001

B) Proportional analysis of the 6,004 genes without a T-DNA integration

i) Genes lacking intron sequences (23.5% of the total):

	Genes with no introns	Genes with introns
Observed:	2,919	3,085
Expected:	4,593	1,411
X^2 1d.f.	2,596.1	P < 0.0001

ii) Genes annotated as pseudogenes (5.2% of the total):

	Annotated Genes	Annotated pseudogenes
Observed:	5,250	754
Expected:	5,692	312
X^2 1d.f.	660.5	P < 0.0001

iii) Genes present as a single copy (11.2% of the total):

	Duplicated Genes	Single Copy Genes
Observed:	5,508	496
Expected:	5,344	660
X^2 1d.f.	45.8	P < 0.0001