

Gonzalez-Segovia et al. Supporting Information

List of Supplemental Tables provided in additional files

Table S1. Introgression events from the Top 1% outlying windows.

Table S2 Introgression events from the Top 10% outlying windows.

Table S3. Table of maize genes indicating their presence in introgression regions, local recombination rate, associated SNPs, SNP effect and Mexican highland-lowland Fst.

Table S4. Table of high and moderate effect SNPs fixed in Mexican highland samples

Table S5. Raw Fd output by window for highland test data set

Table S6. Raw Fd output by window South American lowland null data set

Table S7. Local recombination rate in the RV x PT cross, estimated every 500kb

Table S8. Local recombination rate in the RV x PT cross, estimated at every marker

Table S9. R/QTL cross object containing phenotypic and marker data for the RV x PT cross

Other Supplemental Tables (S10 - S17)

Table S10. Genome sequence data generated in this study

Identifier	Accession	Elevation (m)	Source	Coverage	Filtered SNPs
PT1	MEXI5	2,597	CIMMyT	41x	63,802,556
PT2	MEXI5	2,597	CIMMyT	42x	64,028,598
MM1	TC313	2,271	Carrera	70x	66,586,613

Table S11. Introgression events larger than 1 Mb identified from the top 10% outliers

Chromosome	Start (Mb)	End (Mb)	Size (Mb)	Gene count	RR (cM/Mb)
3	80.3	85.0	4.7	21	0.0
3	98.6	100.9	2.3	22	0.03
4	167.5	168.6	1.1	6	0.23
4	168.8	171.0	2.2	55	0.12
4	172.5	173.8	1.3	38	0.03
4	177.1	178.4	1.3	33	0.09
5	114.3	115.4	1.1	13	0.00
6	50.0	53.4	3.3	18	0.08
6	54.0	55.8	1.9	18	0.08

Table S12. Introgression events larger than 0.5 Mb located outside pericentromeric regions

chr	start	end	size	RR (cM/Mb)	RR NAM(cM/Mb)
1	178776090	179369070	592980	0.33	0.53
3	157784932	158395423	610491	0.58	0.81
4	8777068	9697246	920178	1.91	2.62
4	167471523	168578399	1106876	0.23	0.78
4	168782414	170998801	2216387	0.12	0.83
4	171586337	172138580	552243	0.05	1.08
4	172473846	173742820	1268974	0.03	1.2
4	173839003	174497224	658221	0.02	1.49
4	175801991	176531617	729626	0.04	1.61
4	177083713	178412600	1328887	0.09	1.53
4	178697931	179386468	688537	0.15	1.35

4	180085104	180656401	571297	0.23	1.22
4	180683844	181252546	568702	0.28	1.22
4	208214069	208771311	557242	0.02	0.16

Table S13. Contingency table for 21, 029 genes with Fst estimates

	In introgression	Not in introgression
Sig Fst	62	574
Non sig Fst	347	20, 046

Table S14. Contingency table for 18, 855 genes with Fst estimates outside chr 4

	In introgression	Not in introgression
Sig Fst	28	311
Non sig Fst	383	18, 133

Table S15. Contingency table for genes with fixed high effect SNPs

	In introgression	Not in introgression
High effects	40	422
Other SNPs	1, 340	37, 503

Table S16. Contingency table for genes with fixed moderate effect SNPs

	In introgression	Not in introgression
Moderate effects	502	7, 528
Other SNPs	878	30, 397

Table S17. Inbreeding coefficients

Sample	Inbreeding coefficient
RIMMA0703	0.22
RIMMA0733	0.30

TIL25	0.59
TIL08	0.66
TDD39103	0.64
BKN022	0.69
PT1	0.00084
PT2	0.00156
MM	0.00042
TIL10	0.49
TIL05	0.56
TIL01	0.48

