S12 Table. Genes displaying a minimum F_{ST} z-score of 2.5 in both the introgression and the F2 mapping experiments

Contig ID	Gene ID		F_{ST} z-score Introgression mapping	IVM F2 mapping	Minimum score
Cont209	TELCIR_02985	Triacylglycerol lipase	3.4	4.5	3.4
Cont209	TELCIR_02988	Triacylglycerol lipase	3.3	4.5	3.3
Cont228	TELCIR_03131	ABC transporter (*Tci-mrp-6*)	4.2	3.0	3.0
Cont228	TELCIR_03132	Hypothetical protein	3.7	3.0	3.0
Cont133	TELCIR_02272	Conserved domain protein	2.8	4.0	2.8
Cont133	TELCIR_02271	6-phosphofructo-2-kinase	2.8	4.0	2.8
Cont6655	TELCIR_15612	Conserved domain protein	2.8	4.5	2.8
Cont6655	TELCIR_15613	Putative lipoyl synthase	2.7	4.5	2.7
Cont209	TELCIR_02984	Conserved domain protein	2.6	4.5	2.6
Cont228	TELCIR_03125	Hypothetical protein	2.6	3.0	2.6
Cont6655	TELCIR_15611	Ground-like domain protein	2.6	4.5	2.6
Cont228	TELCIR_03126	Hypothetical protein	2.6	3.0	2.6
Cont133	TELCIR_02273	Hypothetical protein	2.5	4.0	2.5
Cont5	TELCIR_00170	Ligand-gated anion channel (*Tci-lgc-54*)	5.0	2.5	2.5
Cont5	TELCIR_00169	Conserved domain protein	4.7	2.5	2.5
Cont5	TELCIR_00168	PHD-finger	4.4	2.5	2.5
Cont5	TELCIR_00174	Conserved hypothetical protein	3.8	2.5	2.5
Cont5	TELCIR_00167	Protein-tyrosine phosphatase	3.7	2.5	2.5