Table S10 List of joint outliers with respect to Tajima's *D* and Fay and Wu's *H* that were annotated with respect to putative gene products.

Amplicon	Putative gene product	Tajima's <i>D</i>	Fay and Wu's H
0_10631_01	HSP7NAT-2 (HEAT-SHOCK PROTEIN 7NAT-2); ATP	-1.84	-5.18
	binding		
0_10631_02	HSP7NAT-2 (HEAT-SHOCK PROTEIN 7NAT-2); ATP	-1.71	-3.42
	binding		
0_12117_01	universal stress protein (USP) family protein	-1.70	-5.25
0_3461_01	DIN1NA (DARK INDUCIBLE 1NA); hydrolase, hydrolyzing	-2.14	-8.18
	O-glycosyl compounds		
0_8408_01	glyoxal oxidase-related	-1.82	-3.22
0_8694_01	sodium:solute symporter family protein	-2.08	-8.60
0_9825_01	DIR1 (DEFECTIVE IN INDUCED RESISTANCE 1); lipid	-1.85	-5.23
	binding / lipid transporter		
2_4925_01	zinc finger (C3HC4-type RING finger) family protein	-1.72	-6.87
2_6183_01	CRK1NA (CYSTEINE-RICH RLK1NA); ATP binding /	-2.08	-4.85
	kinase/ protein kinase/ protein serine/threonine		
	kinase/ protein tyrosine kinase		
2_9466_01	membrane-associated zinc metalloprotease, putative	-1.85	-3.34
CL1344Contig1_03	PFK2 (PHOSPHOFRUCTOKINASE 2); 6-	-1.71	-3.45
	phosphofructokinase		
CL162Contig1_01	pectinesterase family protein	-1.82	-5.08
CL2463Contig1_03	TMKL1 (transmembrane kinase-like 1); ATP binding /	-1.69	-3.34
	kinase/ protein serine/threonine kinase		
CL4663Contig1_02	FTSZ1-1; protein binding / structural molecule	-1.85	-3.34
UMN_3361_01	DNA-binding protein, putative	-1.82	-5.08
UMN_5367_02	chaperonin, putative	-1.69	-5.20