Supplementary File 05: Summary of outlier pairwise comparisons detected in the boxplot analyses.

Genus	Analysed COI sequences			Pairwise Comparisons			Intraspecific outliers		Interspecific outliers	
	Total	Involved in at least one outlier	% from total	Total of possible comparisons *	Observed outliers	% from total	Observed outliers	N sequences involved	Observed outliers	N sequences involved
Aeolothrips	313	225	71.88	48,828	2,546	5.21	2,256	204	290	211
Anaphothrips	80	80	100	3,160	458	14.49	417	80	41	24
Bactrothrips	20	5	25	190	6	3.16	0	0	6	5
Dendrothrips	27	5	18.52	351	4	1.14	0	0	4	5
Frankliniella	1,781	1,495	83.94	1,585,090	17,063	1.08	346	122	16,717	1,384
Franklinothrips	22	17	77.28	231	15	6.49	15	17	0	0
Gynaikothrips	26	25	96.15	325	46	14.15	13	14	33	14
Haplothrips	415	393	94.70	85,905	7,160	8.33	3,816	348	3,344	320
Hydatothrips	7	3	42.86	21	2	9.52	2	3	0	0
Kladothrips	16	10	62.50	120	12	10	0	0	12	10
Megalurothrips	192	147	76.56	18,336	1,242	6.77	1,125	134	117	22
Mycterothrips	36	36	100	630	122	19.36	23	21	99	34
Neohydatothrips	47	10	21.28	1,081	10	0.92	10	10	0	0
Odontothrips	152	80	52.63	11,476	156	1.36	156	80	0	0
Orothrips	10	3	30	45	2	4.44	1	2	1	2
Oxythrips	19	3	15.79	171	2	1.17	0	0	2	3
Scirtothrips	644	390	60.56	207,046	3,176	1.53	0	0	3,176	390
Taeniothrips	3,629	3,626	99.92	6,583,006	140,578	2.14	119,904	3,626	20,674	2,623
Thrips	1,933	1,899	98.24	1,867,278	55,564	2.98	42,316	1,419	13,248	1,104

* The total of possible comparisons for each genus was calculated as the total number of sequences analysed (Nseq) multiplied by Nseq-1, then divided by two to remove repeated comparisons that just invert the order the sequences are listed.