Table S1: Characteristics of amplicons of candidate reference genes amplified using gene specific primers

Gene Symbol	Product Tm (°C)	Amplicon length	Efficiency	Amplification efficiency	Correlation coefficient
Actin	84	110	1.79	78.56	0.99
18s	82	100	1.85	84.58	0.97
28s	79	100	1.88	88.3	0.99
TUB	82	114	1.83	82.96	0.98
GADPH	82	120	1.73	72.57	0.94
EF	84	111	2.01	100.71	1
RPL17	83	103	1.95	94.97	0.95
Hist3	82	113	2.45	144.68	0.99
UbiCE	83	113	1.87	86.8	0.99
TATA	81	114	1.97	97.3	1
E2F	83	100	1.92	92.11	0.98
vATPase	81	103	2.75	175.1	0.79
SOD	84	102	1.96	95.94	0.99
GSTD2	80	100	1.86	86.38	0.99

Table S2. Detailed Bestkeeper analysis for all candidate reference genes

ADULT											
		18S	**28S**	**TUB**	**EF**	**RPL17**	**UBICE**	**TATA**	**E2F**	**SOD**	**GSTD2**
geo mean	**CP**	22.93	22.75	25.46	24.09	26.85	24.99	27.74	24.38	23.31	20.76
AR mean	**CP**	22.94	22.76	25.47	24.09	26.85	24.99	27.74	24.38	23.32	20.77
Min	**CP**	21.94	22.05	24.53	23.94	26.82	24.48	27.68	24.15	22.35	20.17
Max	**CP**	23.94	23.47	26.41	24.24	26.88	25.50	27.79	24.72	24.10	21.51
Stddev	**[± CP]**	0.67	0.47	0.63	0.10	0.02	0.34	0.04	0.23	0.65	0.49
Cv	**%CP**	2.91	2.08	2.46	0.42	0.07	1.36	0.13	0.93	2.77	2.38
Min	**x-fold**	-1.98	-1.63	-1.90	-1.11	-1.02	-1.42	-1.04	-1.17	-1.94	-1.51
Max	**x-fold**	2.02	1.64	1.93	1.11	1.02	1.43	1.04	1.27	1.73	1.68
Stddev	**[± x-fold]**	1.59	1.39	1.54	1.07	1.01	1.27	1.02	1.17	1.57	1.41
Pearson correlation coefficient											
BestKeeper vs.coeff. of correlation		0.997	0.997	0.997	0.001	0.997	0.997	0.997	0.001	0.994	0.969
p-value		0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.837	0.001	0.007
NYMPH											
		18S	**28S**	**TUB**	**EF**	**RPL17**	**UBICE**	**TATA**	**E2F**	**SOD**	**GSTD2**
geo Mean [CP]	**CP**	24.66	24.13	24.97	25.53	25.67	28.13	25.33	25.37	23.50	20.56
ar Mean [CP]	**CP**	24.69	24.18	25.00	25.65	25.71	28.13	25.34	25.39	23.52	20.58
min [CP]	**CP**	23.84	23.09	23.46	23.24	24.49	27.91	24.41	24.28	22.53	19.77
max [CP]	**CP**	26.36	26.30	26.54	29.00	27.87	28.24	26.27	26.64	25.00	22.00
stddev [± CP]	**[± CP]**	1.12	1.41	1.03	2.24	1.44	0.15	0.62	0.83	0.98	0.94
CV [% CP]	**%CP**	4.52	5.85	4.12	8.72	5.59	0.52	2.46	3.27	4.18	4.59
min [x-fold]	**x-fold**	-1.76	-2.06	-2.85	-4.90	-2.26	-1.16	-1.89	-2.14	-1.96	-1.73
max [x-fold]	**x-fold**	3.25	4.49	2.97	11.05	4.60	1.08	1.92	2.40	2.83	2.71
stddev [± x-fold]	**[± x-**	2.17	2.66	2.04	4.71	2.71	1.11	1.54	1.78	1.98	1.92

	fold]										
Pearson correlation coefficient (r)											
BestKeeper vs.coeff. of corr. [r]		0.912	0.933	0.924	0.96	0.976	0.001	0.956	0.971	0.999	0.969
p-value		0.031	0.021	0.025	0.01	0.004	0.028	0.011	0.006	0.001	0.006
STARVATION STRESS											
GENE		**18S**	**28S**	**TUB**	**EF**	**RPL17**	**UBICE**	**TATA**	**E2F**	**SOD**	**GSTD2**
geo mean	**CP**	24.57	24.90	25.33	26.16	26.41	25.72	29.21	27.59	25.24	22.64
AR mean	**CP**	24.57	24.92	25.33	26.16	26.43	25.72	29.21	27.59	25.27	22.65
Min	**CP**	24.00	23.77	25.03	25.92	25.00	25.40	28.87	27.28	24.00	22.06
Max	**CP**	24.97	26.06	25.63	26.59	27.39	26.34	29.69	28.00	27.18	23.76
Stddev	**[± CP]**	0.38	0.77	0.20	0.29	0.95	0.41	0.32	0.27	1.27	0.74
Cv	**%CP**	1.56	3.08	0.79	1.10	3.61	1.61	1.10	0.99	5.03	3.27
Min	**x-fold**	-1.48	-2.19	-1.23	-1.18	-2.66	-1.25	-1.26	-1.24	-2.36	-1.49
Max	**x-fold**	1.32	2.23	1.23	1.35	1.97	1.54	1.40	1.33	3.85	2.18
Stddev	**[± x-fold]**	1.30	1.70	1.15	1.22	1.94	1.33	1.25	1.21	2.41	1.67
Pearson correlation coefficient											
BestKeeper vs.coeff. of correlation		0.968	0.549	0.999	0.117	0.962	0.83	0.001	0.001	0.928	0.859
p-value		0.007	0.338	0.001	0.851	0.009	0.082	0.006	0.166	0.023	0.062

Table S3 : Normfinder based stability values of different candidate genes

GENES	**ADULT**	**NYMPH**	**Starvation Stress**
18s	0.164	0.083	0.007
28s	0.026	0.121	0.525
TUB	0.128	0.094	0.007
EF	0.210	1.451	0.162
RPL17	0.098	0.109	0.357
UbiCE	0.005	1.503	0.019
TATA	0.086	0.178	0.455
E2F	0.189	0.034	0.342
SOD	0.102	0.003	0.899
GSTD2	0.029	0.003	0.181

Table S4 : Geometric mean ranking of candidate reference genes using RefFinder

ADULT		**NYMPH**		**Starvation stress**	
GENES	**Geomean of ranking values**	**GENES**	**Geomean of ranking values**	**GENES**	**Geomean of ranking values**
UbiCE	2.34	*E2F*	2.06	*TUB*	1.19
28s	3.13	*SOD*	2.11	*18s*	1.78
TATA	3.87	*TATA*	2.51	*UbiCE*	3.57
RPL17	3.94	*GSTD2*	3.66	*EF*	3.72
GSTD2	4.21	*UbiCE*	5.62	*E2F*	4.36
TUB	4.45	*TUB*	5.63	*GSTD2*	5.92
18s	5.03	*EF*	5.63	*TATA*	6.05
SOD	5.33	*RPL17*	5.79	*RPL17*	7.97
EF	7.02	*28s*	8.18	*28s*	8.74
E2F	7.75	*18s*	9	*SOD*	10

Table S5 :Listof genes associated with RNAi mechanism identified in the *T. tabaci* assembled transcriptome at *E*-value < e^{-30}. *Similarity; $^{\#}$Alignment length

Gene	CDS/Transcript Number	Annotation	S-value	S*	AL$^{\#}$
DsRNA uptake					
SID-1	CDS_15961_transcript_14627	gi|646715429|gb|KDR19041.1|SID1 transmembrane family member 1 [*Zootermopsisnevadensis*]	5.09814E-49	77	178
	CDS_15962_transcript_14627		0	70	622
	CDS_15963_transcript_14628			72	798
Clathrin Heavy Chain	CDS_194_transcript_841	gi|646720852|gb|KDR22435.1|Clathrin heavy chain [*Zootermopsisnevadensis*]	0	97	1676
	CDS_24400_transcript_25704		1.13E-77	96	137
	CDS_25967_transcript_29416		1.1E-178	94	323
	CDS_25967_transcript_29416		1.1E-178	94	323
Innexin2	CDS_13894_transcript_12670	gi|242014052|ref|XP_002427712.1|Innexin inx2, putative [*Pediculushumanuscorporis*]	0	86	399
	CDS_4215_transcript_4271		0	91	358
	CDS_13893_transcript_12669		0	86	399
	CDS_13894_transcript_12670		0	86	399
dsRNA cleavage					
Dicer-1	CDS_24712_transcript_26352	gi|240247227|emb|CAX68236.1|dicer-1 [*Blattellagermanica*]	0	64	807
	CDS_25848_transcript_29057		5.3605E-161	78	415
	CDS_23342_transcript_23605		1.38053E-30	71	154
Dicer-2	CDS_20968_transcript_20034	gi|406034947|emb|CCF23094.1|Dicer 2 [*Blattellagermanica*]	3.9936E-157	47	1709
	CDS_21294_transcript_20494		0	56	1653
Drosha	CDS_20526_transcript_19507	gi|646694518|gb|KDR08017.1|Ribonuclease 3 [*Zootermopsisnevadensis*]	0	86	982
Endonuclease activity					
Argonaute 1	CDS_15926_transcript_14593	gi|516306731|gb|AGO85968.1|argonaute 1, partial [*Locustamigratoria*]	0	99	403
	CDS_15921_transcript_14590		0	97	855
	CDS_15922_transcript_14590		0	97	418
	CDS_15923_transcript_14591		0	97	855

Argonaute 2	CDS_6124_transcript_5961	gi|723784142|gb|AIY24303.1|Argonaute 2 [*Laodelphaxstriatella*]	0	98	433
	CDS_6122_transcript_5961		1.06074E-90	75	223
	CDS_6123_transcript_5961		6.0224E-160	64	583
	CDS_6125_transcript_5962		0	67	818
	CDS_6126_transcript_5962		0	67	818
	CDS_6128_transcript_5963		0	67	818
	CDS_6130_transcript_5965		0	67	818
	CDS_18274_transcript_16947				
	CDS_25525_transcript_28247				
PCDG 6 (ALG-6)	CDS_16858_transcript_15514	gi|646723721|gb|KDR24234.1|Programmed cell death protein 6 [*Zootermopsisnevadensis*]	5.7885E-114	97	175
	CDS_24257_transcript_25393		5.7885E-114	97	175
PIWI	CDS_11559_transcript_10537	gi|646703429|gb|KDR12118.1|Piwi-like protein 1 [*Zootermopsisnevadensis*]	0	74	782
	CDS_11560_transcript_10538		0	75	773
Aub	CDS_26052_transcript_29621	gi|817196653|ref|XP_012273923.1|PREDICTED: protein aubergine-like isoform X2 [*Orussusabietinus*]	8.02156E-39	64	148
	CDS_24257_transcript_25393		8.49505E-40	77	109
Asp Spindle E	CDS_828_transcript_1424	gi|646720534|gb|KDR22214.1|Protein abnormal spindle [*Zootermopsisnevadensis*]	3.87747E-39	50	558
	CDS_829_transcript_1425		9.26456E-68	73	232
Others					

Tudor	CDS_9987_transcript_9161	gi|646703152|gb|KDR11968.1|Tudor domain-containing protein 5 [*Zootermopsisnevadensis*]	2.95608E-80	58	139
	CDS_9990_transcript_9164		1.13593E-11	55	182
	CDS_10607_transcript_9637		1.2331E-12	52	182
	CDS_10608_transcript_9638		1.20765E-12	52	182
	CDS_11871_transcript_10813		1.20765E-12	52	435
	CDS_11872_transcript_10813		1.9006E-123	66	435
	CDS_11873_transcript_10813		1.9006E-123	66	90
	CDS_11874_transcript_10814		9.21698E-09	53	188
	CDS_11875_transcript_10815		5.36742E-16	54	622
	CDS_11876_transcript_10815		1.56031E-87	53	188
	CDS_11877_transcript_10815		5.36742E-16	54	90
	CDS_11878_transcript_10816		9.21698E-09	53	188
	CDS_11879_transcript_10816		5.36742E-16	54	622
	CDS_11880_transcript_10816		1.56031E-87	53	90
	CDS_12288_transcript_11176		9.21698E-09	53	622
	CDS_14189_transcript_12964		1.56031E-87	53	188
	CDS_14190_transcript_12965		5.36742E-16	54	39
	CDS_15383_transcript_14106		2.65212E-07	69	1183
	CDS_15384_transcript_14107		4.8541E-153	50	163
	CDS_15385_transcript_14108		4.9947E-14	53	85
	CDS_15386_transcript_14109		1.21319E-07	54	832
	CDS_15387_transcript_14109		8.90154E-90	50	827
	CDS_15388_transcript_14110		2.1975E-90	50	85
	CDS_15389_transcript_14111		1.08125E-07	54	827
	CDS_15390_transcript_14111		2.1975E-90	50	832
	CDS_17731_transcript_16404		7.85433E-90	50	181
	CDS_17732_transcript_16405		3.02975E-30	61	599
	CDS_22526_transcript_22311		7.68318E-60	49	569
	CDS_23795_transcript_24504		1.52443E-60	49	570
	CDS_24864_transcript_26674		2.4689E-61	49	513
	CDS_3219_transcript_3489		2.17002E-24	44	469
	CDS_3220_transcript_3489		1.08973E-30	46	285
	CDS_3221_transcript_3489		2.58141E-26	48	

Mut-7	CDS_3222_transcript_3490	gi|646704864|gb|KDR12833.1|putative exonuclease mut-7-like protein [*Zootermopsisnevadensis*]	5.4797E-153	63	579
	CDS_3223_transcript_3490		3.36557E-10	64	62
	CDS_3224_transcript_3490		6.96901E-13	61	98
	CDS_3225_transcript_3491		5.4797E-153	63	579
	CDS_3226_transcript_3491		6.96901E-13	61	98
	CDS_3227_transcript_3492		3.36557E-10	64	62
	CDS_3228_transcript_3492		2.61635E-30	54	222
	CDS_3229_transcript_3492		5.4797E-153	63	579
	CDS_3230_transcript_3493		3.36557E-10	64	62
	CDS_3231_transcript_3493		6.96901E-13	61	98
	CDS_3232_transcript_3494		5.4797E-153	63	579
	CDS_3233_transcript_3494		3.0543E-172	59	728
	CDS_3234_transcript_3494		3.36557E-10	64	62
HPS4	CDS_18050_transcript_16726	gi|646704291|gb|KDR12556.1|Hermansky-Pudlak syndrome 4 protein [*Zootermopsisnevadensis*]	0	57	929
	CDS_18051_transcript_16727		0	57	929
Belle	CDS_2216_transcript_2724	gi|805814300|ref|XP_012148170.1|PREDICTED: DEAD-box ATP-dependent RNA helicase 20 [*Megachilerotundata*]	4.07E-08	66	57
	CDS_3872_transcript_4046		0	87	481
Gawky	CDS_1202_transcript_1771	gi|572313755|ref|XP_006622570.1|PREDICTED: protein Gawky-like [*Apisdorsata*]	2.41E-51	68	187
	CDS_1203_transcript_1772		2.41E-51	68	187
	CDS_1204_transcript_1773		2.41E-51	68	187
	CDS_1199_transcript_1770		2.41E-51	68	187
	CDS_1207_transcript_1774		2.41E-51	68	187
	CDS_1209_transcript_1775		2.41E-51	68	187
CLP1	CDS_17314_transcript_15991	gi|646701253|gb|KDR11058.1|CLP1-like protein [*Zootermopsisnevadensis*]	0	88	414
V-type proton ATPase subunit H	CDS_9906_transcript_9079	gi|646704147|gb|KDR12485.1|V-type proton ATPase subunit H [Zootermopsisnevadensis]	0	80	558
	CDS_9907_transcript_9080		1.65118E-96	85	182
	CDS_9908_transcript_9080		8.4095E-179	92	289
	CDS_9909_transcript_9081		8.4095E-179	92	289
	CDS_9910_transcript_9082		0	88	484

Rab-7a	CDS_24868_transcript_26695 CDS_24869_transcript_26696 CDS_1706_transcript_2230 CDS_1707_transcript_2231 CDS_1708_transcript_2232 CDS_21319_transcript_20533 CDS_21320_transcript_20534	>gi|936578738|ref|XP_014204028.1|PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578741|ref|XP_014204029.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578744|ref|XP_014204030.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578747|ref|XP_014204031.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578750|ref|XP_014204032.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578753|ref|XP_014204033.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578756|ref|XP_014204034.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578759|ref|XP_014204035.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578762|ref|XP_014204037.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum] >gi|936578765|ref|XP_014204038.1| PREDICTED: ras-related protein Rab-7a [Copidosomafloridanum]	9.8E-128 1.1E-127 7E-133 7E-133 7E-133 4.5E-113 3.3E-115	93 93 93 93 93 87 72	208 208 206 206 206 207 287
RISC	CDS_2188_transcript_2700 CDS_4702_transcript_4696 CDS_2185_transcript_2699	gi|646700117|gb|KDR10415.1|putative RISC-loading complex subunit [Zootermopsisnevadensis]	6.2E-23 3E-149 6.2E-23	48 81 48	353 331 353

DEAD box protein	CDS_17843_transcript_16505	gi|242021722|ref|XP_002431292.1|DEAD box ATP-dependent RNA helicase, putative [Pediculushumanuscorporis] >gi|212516560|gb|EEB18554.1| DEAD box ATP-dependent RNA helicase, putative [Pediculushumanuscorporis]	5.8E-110	61	474
	CDS_3872_transcript_4046		0	87	481
	CDS_19922_transcript_18854		4.99E-06	65	84
	CDS_2216_transcript_2724		4.07E-08	66	57
dsRNAse 2	CDS_24848_transcript_26641	gi|599126388|gb|AHN55089.1|dsRNase 2, partial [Schistocercagregaria]	2.93687E-36	76	111
RDRP	CDS_2003_transcript_2493	gi|527355229|gb|AGS13094.1|RdRP [Cowpea mild mottle virus]	0	95	330
	CDS_2006_transcript_2493		2.3133E-06	44	198
	CDS_2007_transcript_2494		9.2932E-174	87	331
	CDS_2009_transcript_2494		0	95	330
	CDS_2010_transcript_2494		0	57	1027
	CDS_2012_transcript_2495		4.7604E-153	95	255
	CDS_2013_transcript_2495		9.2932E-174	87	331
	CDS_2017_transcript_2495		0	57	1027
	CDS_2018_transcript_2496		0	95	330
	CDS_2020_transcript_2496		9.2932E-174	87	331
	CDS_2021_transcript_2496		0	57	1027
	CDS_2023_transcript_2497		9.2932E-174	87	331
	CDS_2024_transcript_2497		2.3721E-156	56	833
	CDS_2026_transcript_2498		0	95	330
	CDS_2027_transcript_2498		0	74	512
	CDS_2028_transcript_2498		2.22675E-31	45	477
	CDS_2030_transcript_2498		9.2932E-174	87	331
	CDS_2032_transcript_2499		0	57	1027

Table S6: Primer sequences for dsRNA template of potential RNAi machinery

Genes	**dsRNA Primer Sequence**
Dicer-2	Fwd: 5'TAATACGACTCACTATAGGGCCATCACCTACTCATTC3' Rev: 5'TAATACGACTCACTATAGGGGTTAGTAGAGCCTTCAG3'
Staufen	Fwd: 5'TAATACGACTCACTATAGCAGGAGCCTCTTTATAC 3' Rev: 5'TAATACGACTCACTATAGCCTTAGGAAAGTCTGAG3'
Aubergine	Fwd: 5'TAATACGACTCACTATAGGGCTAAAGCTGAGAAGAGG3' Rev: 5'TAATACGACTCACTATAGGGCACCTCCGTATTTACTC3'