

Fig. S1. Three cases illustrating the comparison of HGTs identified by Vogel et al (2018)¹ and this study.

Case 1: HGT identified by both Vogel et al (2018)¹ and this study (example)

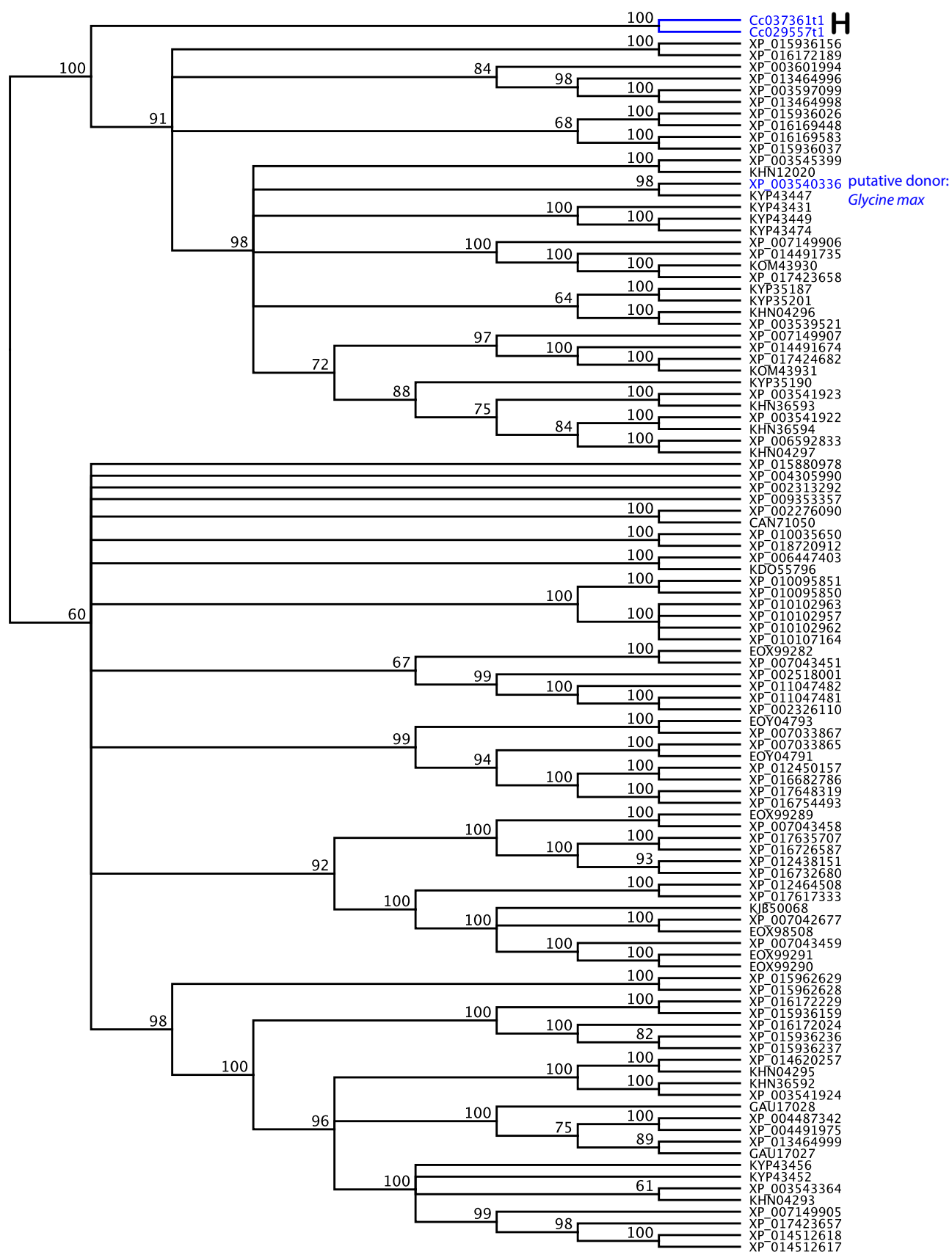
Figure A shows the maximum likelihood tree from this study, with HGT sequences indicated by red arrows. Figure B shows the cladogram from Vogel et al (2018)¹ generated by FastTree.

- 1 Vogel, A. *et al.* Footprints of parasitism in the genome of the parasitic flowering plant *Cuscuta campestris*. *Nat Commun* **9**, 2515, doi:10.1038/s41467-018-04344-z (2018).



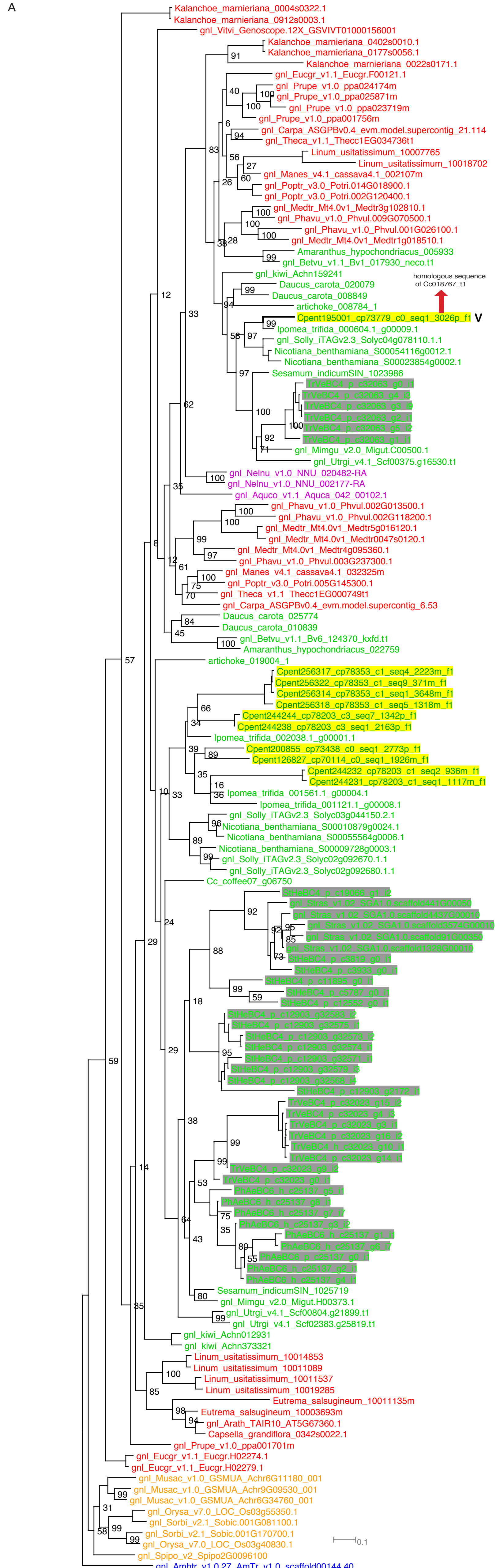
B

Putative donor sequences: XP_003540336.1



Case 2: HGT identified by Vogel et al (2018)¹ but not in this study

An example showing one putative HGT identified by Vogel but not with the expanded taxon set used by the current study. Figure A shows the phylogenetic tree for the corresponding sequence annotated in this study. The red arrow points out the sequence “Cpent195001_cp73779_c0_seq1_3026p_f1”, which is the same sequence as Cc018767_t1 from Vogel et al (2018)¹. The tree rejects this gene as a well-supported HGT, but instead shows strong support for it being a vertically transmitted sequence (“V” on the right of the sequence), as the closest sequence of Cpent195001_cp73779_c0_seq1_3026p_f1 on the tree is from *Ipomoea trifida*. Both *Cuscuta* and *Ipomoea* are members of the same family (Convolvulaceae). Panel B shows the evidence from HGTpropor – the proportion of this sequence from the distal rosid group is only 0.26, which also fails to meet the criteria of HGT in this study. Figure C shows the FastTree analysis of Vogel et al (2018)¹, which lacks taxon labels. Panel D and panel E show evidence from a BLAST search the peptide sequence Cc018767_t1 against the NR database using BLASTP. The top blast hits from the NR database are from *Gossypium*, suggesting HGT, but sequence identity with *Gossypium* sequences is very low (40%). Panel F shows BLAST results using our customized HGT database, which includes NR and manually selected close taxa from other sources. As can be seen from our BLAST output, sequences from *Ipomea* have much higher identity (80%) than *Gossypium*, which is consistent with the tree presented here, thus rejecting HGT and supporting vertical transmission.

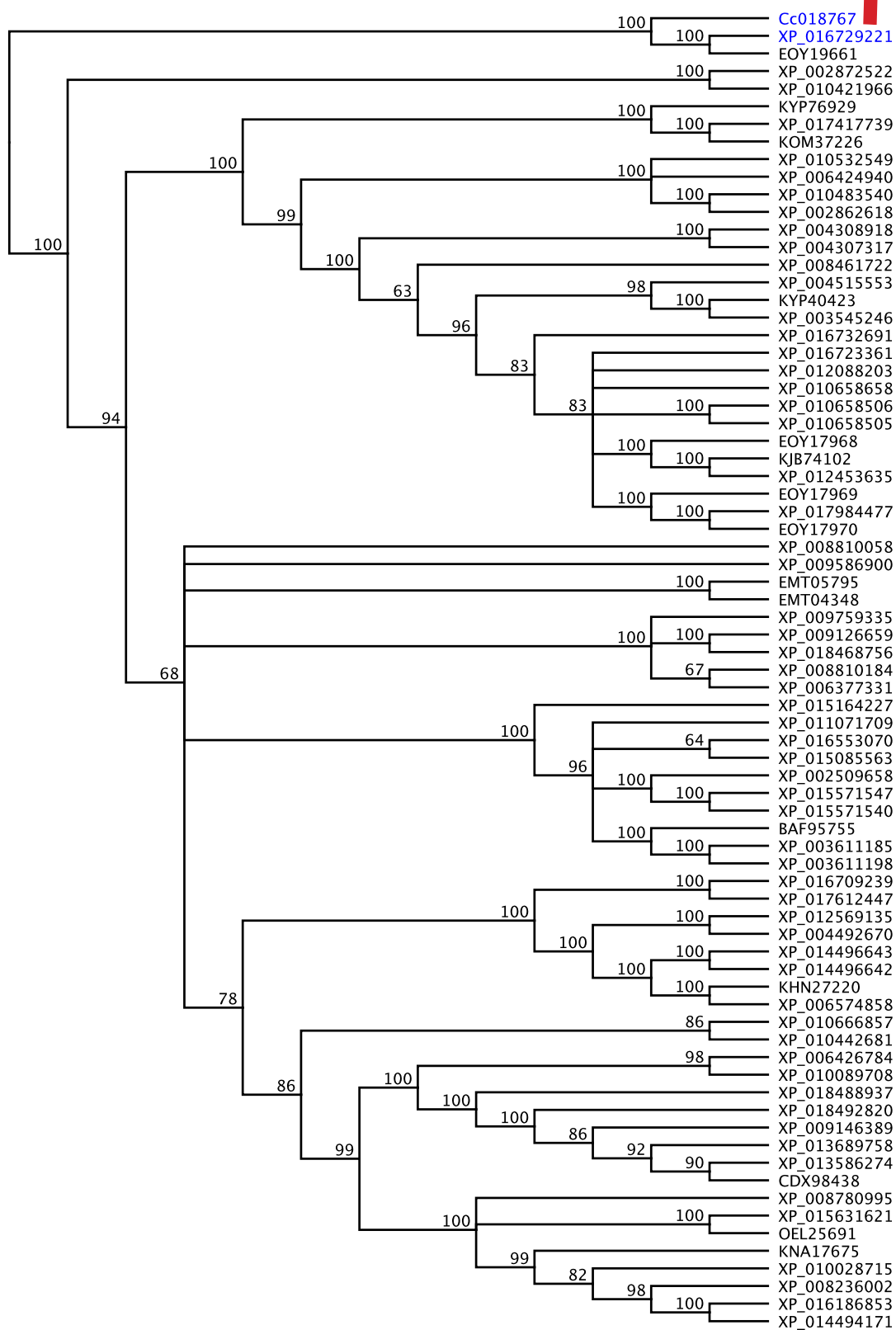


B

sequence	self propor	close propor	distal rosid propor	distal monocot propor	distal basal asterid propor
Cpent195001_cp73779_c0_seq1_3026p_f1	0.06	0.66	0.26	0	0.02

C

Putative donor sequences: XP_016729221.1

PREDICTED: subtilisin-like protease
SBT4.9 [Gossypium hirsutum]

D

Description					Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	PREDICTED: subtilisin-like protease SBT4.9 (Gossypium hirsutum)				412	412	71%	3e-127	40%	XP_016729221.1
<input type="checkbox"/>	Uncharacterized protein TCM_044828 (Theobroma cacao)				385	385	70%	3e-118	35%	EQY18661.1
<input type="checkbox"/>	hypothetical protein B456_013G257400 (Gossypium raimondii)				324	324	61%	3e-99	39%	KJB83667.1
<input type="checkbox"/>	hypothetical protein GOBAR_DD13641 (Gossypium barbadense)				327	327	72%	9e-98	35%	PPD89413.1
<input type="checkbox"/>	hypothetical protein GOBAR_AA33036 (Gossypium barbadense)				225	367	63%	5e-58	43%	PPR87645.1
<input type="checkbox"/>	cucumisin (Artemisia annua)				212	212	74%	6e-55	29%	PWA71293.1
<input type="checkbox"/>	cucumisin (Artemisia annua)				211	211	74%	1e-54	29%	PWA95098.1
<input type="checkbox"/>	PREDICTED: cucumisin-like (Gossypium hirsutum)				208	208	74%	1e-53	30%	XP_016723361.1
<input type="checkbox"/>	hypothetical protein GOBAR_AA31525 (Gossypium barbadense)				210	405	78%	5e-53	30%	PPR89157.1
<input type="checkbox"/>	hypothetical protein GOBAR_DD01946 (Gossypium barbadense)				207	453	68%	3e-52	38%	PPE00983.1
<input type="checkbox"/>	Cucumisin (Cajanus cajan)				202	202	74%	5e-52	30%	KYP40423.1
<input type="checkbox"/>	hypothetical protein LR48_Vigan712a000400 (Vigna angularis)				202	202	74%	7e-52	29%	KOM29508.1
<input type="checkbox"/>	PREDICTED: cucumisin-like (Vigna angularis)				202	202	74%	1e-51	29%	XP_017410255.1
<input type="checkbox"/>	PREDICTED: LOW QUALITY PROTEIN: cucumisin (Nicotiana tabacum)				201	201	74%	2e-51	28%	XP_016507803.1
<input type="checkbox"/>	PREDICTED: cucumisin-like (Gossypium arboreum)				201	201	74%	2e-51	28%	XP_017644647.1
<input type="checkbox"/>	cucumisin-like (Cajanus cajan)				202	202	74%	3e-51	30%	XP_020202280.1
<input type="checkbox"/>	cucumisin-like isoform X1 (Amborella trichopoda)				201	201	74%	5e-51	30%	XP_020526608.1
<input type="checkbox"/>	cucumisin-like (Herrania umbratica)				201	201	76%	6e-51	29%	XP_021295311.1
<input type="checkbox"/>	cucumisin-like isoform X2 (Amborella trichopoda)				200	200	74%	9e-51	30%	XP_020526609.1
<input type="checkbox"/>	cucumisin-like (Vigna radiata var. radiata)				199	199	74%	1e-50	28%	XP_014502996.2
<input type="checkbox"/>	PREDICTED: cucumisin-like (Cicer arietinum)				200	200	78%	1e-50	29%	XP_004515553.1
<input type="checkbox"/>	Chain A: Crystal Structure Of Cucumisin, A Subtilisin-like Endoprotease From Cucumis Melo L.				197	197	74%	1e-50	29%	3VTA_A
<input type="checkbox"/>	cucumisin (Artemisia annua)				201	201	74%	2e-50	30%	PWA60075.1
<input type="checkbox"/>	cucumisin-like (Helianthus annuus)				199	199	74%	2e-50	29%	XP_022007129.1
<input type="checkbox"/>	PREDICTED: cucumisin-like (Glycine max)				199	199	74%	2e-50	29%	XP_008590070.1

Low identity



E PREDICTED: subtilisin-like protease SBT4.9 [Gossypium hirsutum]

Sequence ID: [XP_016729221.1](#) Length: 952 Number of Matches: 1

► [See 3 more title\(s\)](#)

Range 1: 344 to 940 [GenPept](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score		Expect	Method	Identities	Positives	Gaps
412 bits(1059)		3e-127	Compositional matrix adjust.	242/610(40%)	354/610(58%)	75/610(12%)
Query	25	SQSVYEDHEVVIVEQSMFRSQEFMNDKGALMSTEREDSSVD-NFRPVIAIVDTGVNPNH				83
		S ++Y +E++ V MF+ Q F+ D+ E +++ SV+ + +IAI+D+G+N NH				
Sbjct	344	STNIY-GNEMISVTPCMFKFQNFIMDEEEKYRFEDKEKISVEEKSKSIIAIIIDSGINVNH				402
Query	84	ECFKDNHIPPIDDRWSGGTISVPYKRKILALRNYYADKPRTSAVEDACLHDVNFDPEDLK				143
		ECF+D HIP + + +++P KRKI+A+ NY K T A A D NFPEDL				
Sbjct	403	ECFEDKHIPILESNH-----LNIPLKRKIVAIENYTKGKVLTKA---AGFVDFNFPEDLN				454
Query	144	GHGTACASIAAAASTGVELL-----ERVFAFRTL----				172
		GHGTACASIAA A T ++ L +RV R++				
Sbjct	455	GHGTACASIAAGALTELKWLKDISGISDSKIQGANPFARIASYKVSQDRVTVDRSVEVLK				514
Query	173	-----IKGLRTFFDDPLNYGSLAFKNNILVCKSAGNDG				206
		+ + ++ DP+N G YLA K N++VC S+GN G				
Sbjct	515	NSLLDAMKKATLDKVDVIMVSLNTDDLSNISSYLCDPVNMGGYLAMKENVIVCTSSGNHG				574
Query	207	PWMLSLTGGLAPWTMVVGACGSGGHFITNVELGSSVTLEGFNAFLDKDWDYSELVHQTEC				266
		+L+GGLAPW + VG+C SGG FIT VELG ++GF +F+DKD DY EL+H ++				
Sbjct	575	DSYYTLSGGLAPWVIEVGSCNSGGRFITQVELGGGTQIKGFGSFMDKQVDVYELIHWSDA				634
Query	267	YKEKLKIEPKKEKGKKSREEAPEPKQEINYETVKGKILVW-EHGKCPRKILDQAARGILR				325
		K + KE K+ + K+ E VKGKI+ E K K++L+A GIL				
Sbjct	635	IKAVGTSKGKEVESKAETSQQLQKKKMEIREDVKGKIIYGDEEIKGRIKELNLNAVAGILY				694
Query	326	VGVLKNEFSSSHNLQESIVYVTMEDGKKIYDYIAQSRASKKKPTARLLRSIYKEKE-DTNI				384
		+ + + S+L ++YVT +DG KI YI S +KK A++ ++Y+E++ D				
Sbjct	695	LSQIYDS-RSYELHRPVIYVTRKDGIKIQKYIDNSNRREKK--AKIYQTVYEEQDGDLCN				751
Query	385	LCLKSSRGPNNMLDEYICKPDICAPVENIFCATRWNEVNMNGGYRMLSGTSMNAMVAGMI				444
		+ L S +GPN D Y+ KPDICAP E+I CA++++ NM Y+++SGTSM+NA+VAGM+				
Sbjct	752	VSLISGKGPNPYDPYVLKPDICAPGEDILCASKYDAQNMYAHYQVMSGTSMANAVVAGML				811
Query	445	SRIKSIKKDWGPGRIRSAIITTATPM--NKSFLSMGCGSGRINPTRALDPGLVYDVSWDE				502
		S IK+ KDWG RI+SAI+T+A P+ S + GSG INP +A++PGLVYD+S +E				
Sbjct	812	SYIKTFHKDWGIARIKSAIMTSANPVINFSSAAVLAMGSGCINPLKAMNPGLVYDISPEE				871
Query	503	FRRYLLGRPADMRFLAEIGENTNGEVIPSNALNLPFSFLAGKERTSEIFRRTLTVNGPKP				562
		+RRYLL R ++++LA + EN GE + LNLP+FSL + + IF RTLTVNG P				
Sbjct	872	YRRYLLSREGELKYLALMEENIEGEKLLGMDLNLNPNFSLVLDKASEYIFNRTLTVNGC-P				930
Query	563	ICSYRAQLHL 572				
		C+Y+A++ L				
Sbjct	931	KCTYKAEIRL 940				

F

Higher identity than with *Gossypium hirsutum* sequences

query	hit	identity	aln_length	eval	bitscore	hit_order	hit_family	hit_group	hit_species
Cpent195001_cp73779_c0_seq1_3026p_f1	Cpent195001_cp73779_c0_seq1_3026p_f1	100	775	0	1594	Solanales	Convolvulaceae	asterids	Cuscuta pentagona
Cpent195001_cp73779_c0_seq1_3026p_f1	Cuscuta_pentagona_Ranjan_122822	99.35	775	0	1575	Solanales	Convolvulaceae	asterids	Cuscuta pentagona
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-ERWT-2045874-Ipomoea_coccinea	78.89	777	0	1263	Solanales	Convolvulaceae	asterids	Ipomoea coccinea
Cpent195001_cp73779_c0_seq1_3026p_f1	Ipomea_trifida_000604.1_g00009.1	80.91	749	0	1260	Solanales	Convolvulaceae	asterids	Ipomea trifida
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-EMBR-2059929-Ipomoea_pubescens	80.64	749	0	1254	Solanales	Convolvulaceae	asterids	Ipomoea pubescens
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-VXKB-2064733-Ipomoea_purpurea-leaf_stem_flower	80.37	749	0	1253	Solanales	Convolvulaceae	asterids	Ipomoea purpurea
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-QSLH-2057052-Ipomoea_hederacea	80.51	749	0	1251	Solanales	Convolvulaceae	asterids	Ipomoea hederacea
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-NAUM-2056069-Ipomoea_lindheimeri	80.51	749	0	1250	Solanales	Convolvulaceae	asterids	Ipomoea lindheimeri
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-IZNU-2045896-Ipomoea_lobata	79.97	749	0	1250	Solanales	Convolvulaceae	asterids	Ipomoea lobata
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-OQBM-2059420-Ipomoea_indica	80.11	749	0	1248	Solanales	Convolvulaceae	asterids	Ipomoea indica
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-ALUC-2000515-Ipomoea_quamoclit	79.21	755	0	1233	Solanales	Convolvulaceae	asterids	Ipomoea quamoclit
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 697122313 ref XP_009615143.1	70.78	770	0	1125	Solanales	Solanaceae	asterids	Nicotiana tomentosiformis
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 723604057 gb AIK97848.1	70.65	770	0	1124	Solanales	Solanaceae	asterids	Nicotiana tabacum
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 698518080 ref XP_009803919.1	69.87	770	0	1117	Solanales	Solanaceae	asterids	Nicotiana sylvestris
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Soltu.3.4 PGSC0003DMP400037294	69.22	770	0	1105	Solanales	Solanaceae	asterids	Solanum tuberosum
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 565392774 ref XP_006362066.1	69.22	770	0	1105	Solanales	Solanaceae	asterids	Solanum tuberosum
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-DLJZ-2012111-Solanum_ptychanthum	69	771	0	1104	Solanales	Solanaceae	asterids	Solanum ptychanthum
Cpent195001_cp73779_c0_seq1_3026p_f1	Nicotiana_benthamiana_S00054116g0012.1	70.13	770	0	1104	Solanales	Solanaceae	asterids	Nicotiana benthamiana
Cpent195001_cp73779_c0_seq1_3026p_f1	Cuscuta_pentagona_science_CuPeSoLyGFBC_65495	98.72	545	0	1103	Solanales	Convolvulaceae	asterids	Cuscuta pentagona
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-GHLP-2006137-Solanum_dulcamara	68.57	770	0	1100	Solanales	Solanaceae	asterids	Solanum dulcamara
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Solly_ITAGv2.3 Solyc04g078110.1.1	69.1	767	0	1098	Solanales	Solanaceae	asterids	Solanum lycopersicum
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-LQJY-2083383-Solanum_xanthocarpum	68.74	771	0	1098	Solanales	Solanaceae	asterids	Solanum xanthocarpum
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 350537151 ref NP_001234282.1	69.1	767	0	1096	Solanales	Solanaceae	asterids	Solanum lycopersicum
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-LWCK-2003232-Lycium_barbarum	71.14	745	0	1095	Solanales	Solanaceae	asterids	Lycium barbarum
Cpent195001_cp73779_c0_seq1_3026p_f1	Verbenaceae-GCFE-2057282-Verbena_hastata	66.24	773	0	1067	Lamiales	Verbenaceae	asterids	Verbena hastata
Cpent195001_cp73779_c0_seq1_3026p_f1	Paulownia_fargesii_c32189_g1_1	66.93	774	0	1065	Lamiales	Paulowniaceae	asterids	Paulownia fargesii
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-BOLZ-2171762-Atropa_belladonna	69.2	737	0	1056	Solanales	Solanaceae	asterids	Atropa belladonna
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 747047611 ref XP_011069783.1	66.8	774	0	1054	Lamiales	Pedaliaceae	asterids	Sesamum indicum
Cpent195001_cp73779_c0_seq1_3026p_f1	asteridSolanaceae-DMLT-2103231-Vitex_agnus_castus	66.54	777	0	1047	Solanales	Solanaceae	asterids	Vitex agnus-castus
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 568836489 ref XP_006472275.1	67.55	752	0	1038	Sapindales	Rutaceae	rosids	Citrus sinensis
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 255538108 ref XP_002510119.1	65.28	769	0	1038	Malpighiales	Euphorbiaceae	rosids	Ricinus communis
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-BFJL-2196080-Cornus_floridana	66.62	776	0	1038	Cornales	Cornaceae	asterids	Cornus florida
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 743803501 ref XP_011017137.1	65.23	768	0	1032	Malpighiales	Salicaceae	rosids	Populus euphratica
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 566157587 ref XP_002301156.2	64.23	780	0	1032	Malpighiales	Salicaceae	rosids	Populus trichocarpa
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Poptr_v3.0 Potri.002G120400.1	64.23	780	0	1031	Malpighiales	Salicaceae	rosids	Populus trichocarpa
Cpent195001_cp73779_c0_seq1_3026p_f1	Daucus_carota_008849	66.85	742	0	1031	Apiales	Apiaceae	asterids	Daucus carota
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Poptr_v3.0 Potri.014G018900.1	64.57	779	0	1030	Malpighiales	Salicaceae	rosids	Populus trichocarpa
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 566201913 ref XP_006374838.1	64.57	779	0	1030	Malpighiales	Salicaceae	rosids	Populus trichocarpa
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Manes_v4.1 cassava4.1_002107m	66.36	764	0	1029	Malpighiales	Euphorbiaceae	rosids	Manihot esculenta
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 743786710 ref XP_011028928.1	64.77	772	0	1029	Malpighiales	Salicaceae	rosids	Populus euphratica
Cpent195001_cp73779_c0_seq1_3026p_f1	asterid-TQKZ-2016132-Angelica_archangelica	64.55	773	0	1029	Apiales	Apiaceae	asterids	Angelica archangelica
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Carpa_ASGPBv0.4 evm.model.supercontig_21.114	64.63	769	0	1027	Brassicales	Caricaceae	rosids	Carica papaya
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 848903857 ref XP_012851663.1	66.28	777	0	1026	Lamiales	Phrymaceae	asterids	Erythranthe guttata
Cpent195001_cp73779_c0_seq1_3026p_f1	Fraxinus_excelsior_ash_000391730.1	66.24	773	0	1024	Lamiales	Oleaceae	asterids	Fraxinus excelsior
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Mimgu_v2.0 Migut.C00500.1	66.32	775	0	1023	Lamiales	Phrymaceae	asterids	Mimulus guttatus
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 802570688 ref XP_012068251.1	65.69	749	0	1023	Malpighiales	Euphorbiaceae	rosids	Jatropha curcas
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 643734974 gb KDP41644.1	65.69	749	0	1023	Malpighiales	Euphorbiaceae	rosids	Jatropha curcas
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 604306704 gb EYU25500.1	66.32	775	0	1023	Lamiales	Phrymaceae	asterids	Erythranthe guttata
Cpent195001_cp73779_c0_seq1_3026p_f1	gi 659087673 ref XP_008444575.1	66.35	746	0	1019	Cucurbitales	Cucurbitaceae	rosids	Cucumis melo
Cpent195001_cp73779_c0_seq1_3026p_f1	gnl Nelnu_v1.0 NNU_020482-RA	66.17	739	0	1018	Proteales	Nelumbonaceae	Basal eudico	Nelumbo nucifera

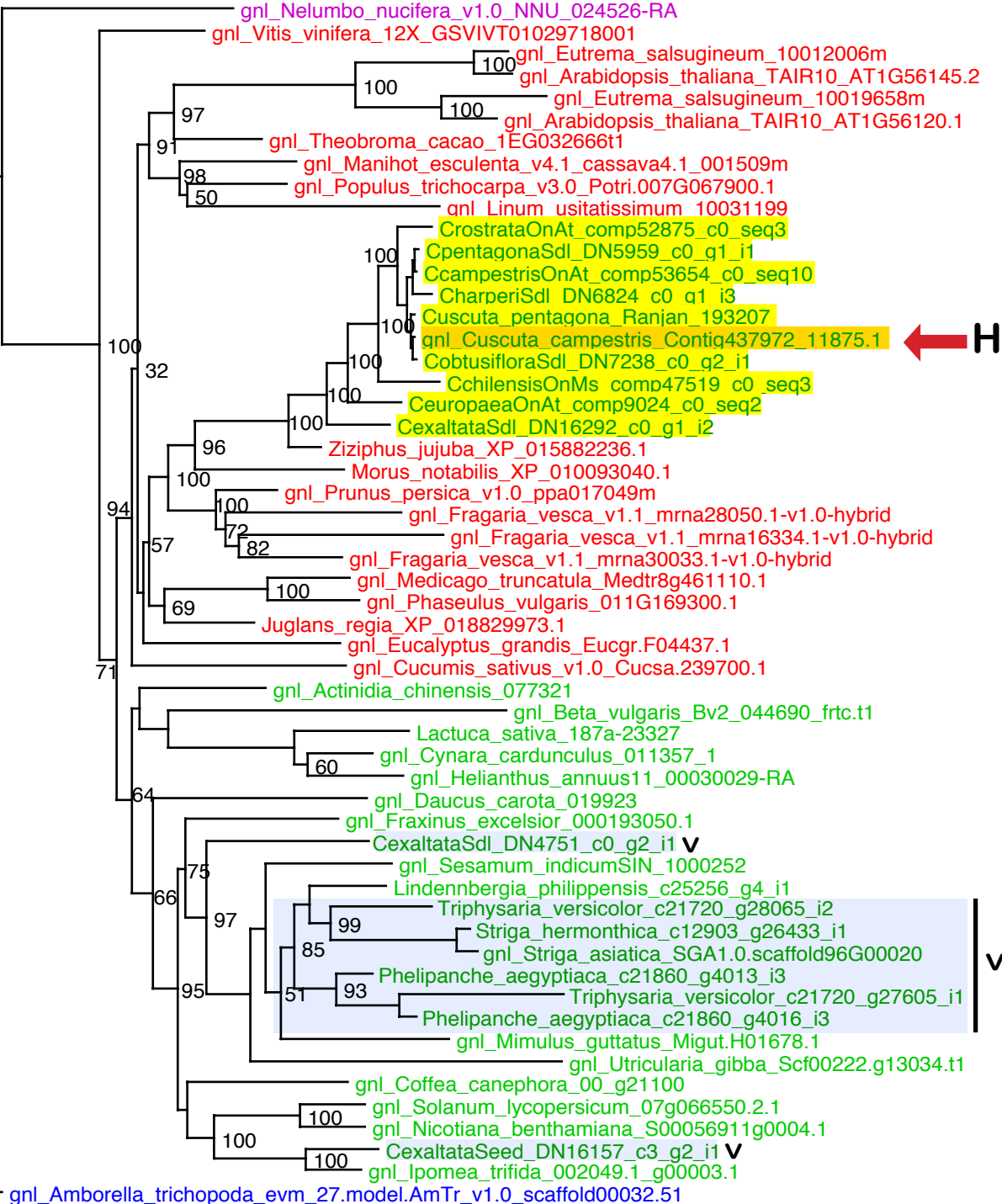
Case 3: HGT detected in this study but not by Vogel et al (2018)¹

Many of the HGT sequences identified in this study were not identified by Vogel et al. (2018)¹. Figure A shows a well-supported phylogenetic tree from this study (also part of Fig. 3), with the HGT sequence indicated by a red arrow. The following table compares the HGT sequences from the two studies using a tabular BLASTN output with coding sequences (CDS). Only alignments with length greater than 250 bp and identity greater than 95% are shown. The HGT sequences shown in the first column contain only high-confidence HGT sequences (selected from Table S2) identified by a phylogenomic screen with support from phylogenetic trees. The first (yellow highlighted row²) is an example showing a HGT sequence, Cc_v0.1_Contig437972_11875.1, identified by this study but not detected by Vogel et al. (2018)¹. The green highlighted rows 3 to 8 show the common sequences identified in both studies.

- 1 Vogel, A. *et al.* Footprints of parasitism in the genome of the parasitic flowering plant *Cuscuta campestris*. *Nat Commun* **9**, 2515, doi:10.1038/s41467-018-04344-z (2018).

A

| 0.1



HGT_seq_by_Yang	Cc_gene_by_Vogel	iden	aln_len	evaluate	bitscore
Cc_v0.1_Contig437972_11875.1	Cc028484_t1	100	913	0	1681
Cc_v0.1_Contig2689_08538.1	Cc029557_t1	96	1494	0	2423
Cc_v0.1_Contig5000_22158.1	Cc038461_t1	99	1491	0	2667
Cc_v0.1_Contig91890_17675.1	Cc013727_t1	100	1446	0	2665
Cc_v0.1_Contig47755_16800.1	Cc026087_t1	100	1065	0	1967
Cc_v0.1_Contig48442_04378.1	Cc002477_t1	100	529	0	977
Cc_v0.1_Contig2739_00034.1	Cc016559_t1	100	345	0	638
Cc_v0.1_Contig33532_12039.1	Cc024215_t1	100	3135	0	5790
Cc_v0.1_Contig48381_13172.1	Cc024749_t1	100	3016	0	5570
Cc_v0.1_Contig8323_05250.1	Cc021701_t1	100	2951	0	5450
Cuscuta_pentagona_Neelima_178617	Cc030785_t1	100	2931	0	5413
Cc_v0.1_Contig34187_07057.1	Cc024766_t1	100	2781	0	5136
Cpent15302_cp77311_c2_seq2_2853p_f1	Cc044734_t1	99	2682	0	4870
Cc_v0.1_Contig257269_37298.1	Cc029734_t1	92	2477	0	3434
Cuscuta_pentagona_Neelima_178617	Cc030785_t1	100	2469	0	4560
Cc_v0.1_Contig45736_HGT_part_rm_intron_coding	Cc030682_t1	99	2409	0	4331
Cc_v0.1_Contig11782_02795.1	Cc017355_t1	98	2337	0	4052
Cc_v0.1_Contig375838_40633.1	Cc027040_t1	99	2271	0	4096
Cc_v0.1_Contig55076_23326.1	Cc015288_t1	100	2205	0	4054
Cc_v0.1_Contig638733_16193.1	Cc044810_t1	100	2055	0	3736
Cc_v0.1_Contig236330_23287.1	Cc019421_t2	100	2048	0	3783
Cc_v0.1_Contig33036_03694.1	Cc015991_t1	100	1995	0	3685
Cc_v0.1_Contig34187_07060.1	Cc024763_t1	99	1945	0	3439
Cc_v0.1_Contig97344_12070.1	Cc026162_t1	100	1821	0	3363
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	1809	0	3336
Cc_v0.1_Contig228851_08157.1	Cc045885_t2	100	1789	0	3304
Cc_v0.1_Contig2855_01303.1	Cc038673_t1	100	1692	0	3125
Cc_v0.1_Contig2855_01304.1	Cc038674_t1	100	1662	0	3070
Cc_v0.1_Contig2855_01305.1	Cc038662_t1	100	1662	0	3070
Cpent218016_cp73155_c0_seq4_2296p_f1	Cc000100_t1	100	1659	0	3064
Cc_v0.1_Contig49980_00612.3	Cc008444_t1	100	1611	0	2976
Cc_v0.1_Contig371501_32727.1	Cc016994_t1	100	1604	0	2957
Cc_v0.1_Contig547062_33180.1	Cc018235_t1	100	1581	0	2920
Cc_v0.1_Contig6533_03415.1	Cc037719_t1	100	1501	0	2765
Cc_v0.1_Contig130847_28444.1	Cc035306_t1	95	1478	0	2313
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	1470	0	2715
Cc_v0.1_Contig609812_RC_HGT_part_coding	Cc034685_t1	99	1443	0	2562

Cc_v0.1_Contig46474_03904.1	Cc030739_t1	100	1398	0	2577
Cc_v0.1_Contig79974_20104.1	Cc000903_t1	100	1388	0	2545
Cc_v0.1_Contig119953_26915.1	Cc013817_t1	100	1383	0	2555
Cc_v0.1_Contig609812_41947.1	Cc034685_t1	99	1383	0	2451
Cc_v0.1_Contig51717_28510.1	Cc033842_t1	100	1352	0	2492
Cc_v0.1_Contig26409_18930.1	Cc002499_t1	95	1348	0	2104
Cc_v0.1_Contig19261_04969.6	Cc004753_t1	98	1339	0	2335
Cc_v0.1_Contig64993_18356.1	Cc044968_t1	100	1324	0	2446
Cc_v0.1_Contig50709_05360.2	Cc045157_t1	98	1323	0	2305
Cc_v0.1_Contig39005_40801.1	Cc016843_t1	100	1314	0	2427
Cc_v0.1_Contig145090_05749.5	Cc045256_t1	99	1308	0	2372
Cc_v0.1_Contig47324_14699.1	Cc001511_t1	98	1307	0	2239
Cc_v0.1_Contig302218_27975.1	Cc029731_t1	91	1306	0	1736
Cc_v0.1_Contig14454_05663.1	Cc031432_t1	100	1299	0	2394
Cc_v0.1_Contig139462_09696.5	Cc012076_t1	100	1286	0	2359
Cc_v0.1_Contig2855_01306.1	Cc038661_t1	100	1284	0	2364
Cc_v0.1_Contig207174_30759.1	Cc008877_t1	100	1279	0	2351
Cc_v0.1_Contig269614_27751.1	Cc034800_t1	100	1268	0	2331
Cc_v0.1_Contig213121_06326.1	Cc012016_t1	100	1267	0	2329
Cc_v0.1_Contig418041_HGT_part_part ial_coding	Cc035966_t1	92	1242	0	1773
Cc_v0.1_Contig368077_29884.1	Cc035637_t1	100	1240	0	2285
Cc_v0.1_Contig149425_03103.4	Cc012076_t1	95	1239	0	1945
Cc_v0.1_Contig46639_04257.1	Cc041569_t1	100	1223	0	2259
Cc_v0.1_Contig56908_15264.1	Cc031432_t1	91	1222	0	1628
Cc_v0.1_Contig29594_24374.1	Cc034802_t1	100	1221	0	2255
Cc_v0.1_Contig295652_23759.1	Cc023348_t1	100	1206	0	2228
Cc_v0.1_Contig13759_20150.1	Cc021845_t2	100	1203	0	2222
Cc_v0.1_Contig97344_12070.1	Cc026162_t1	99	1194	0	2128
Cc_v0.1_Contig272365_18177.1	Cc018957_t1	98	1189	0	2097
Cc_v0.1_Contig34187_07058.2	Cc024764_t1	100	1186	0	2180
Cc_v0.1_Contig21876_08250.1	Cc023348_t1	97	1186	0	1965
Cpent216098_cp72185_c0_seq1_1757 m_f1	Cc001028_t1	99	1182	0	2146
Cc_v0.1_Contig29209_08614.1	Cc031432_t1	96	1159	0	1869
Cc_v0.1_Contig79516_04901.1	Cc033905_t1	100	1153	0	2124
Cc_v0.1_Contig88066_42001.1	Cc046017_t1	100	1131	0	2089
Cc_v0.1_Contig619590_37437.1	Cc046421_t1	100	1131	0	2073
Cc_v0.1_Contig93927_HGT_part_codin g	Cc045882_t1	100	1120	0	2063
Cc_v0.1_Contig56848_07146.1	Cc036645_t1	98	1114	0	1903
CpentagonaSdl_DN6186_c0_g2_i1	Cc001220_t1	99	1106	0	1975

Cc_v0.1_Contig477093_39356.1	Cc022688_t1	100	1092	0	2017
Cc_v0.1_Contig165911_15534.1	Cc044496_t1	100	1088	0	2010
Cc_v0.1_Contig11940_11014.1	Cc000985_t1	100	1083	0	2001
Cc_v0.1_Contig6720_15639.1	Cc046005_t1	99	1083	0	1941
Cc_v0.1_Contig154672_40622.1	Cc022688_t1	98	1077	0	1875
Cc_v0.1_Contig91525_20482.1	Cc024743_t1	100	1076	0	1988
Cc_v0.1_Contig310616_41078.1	Cc037001_t1	100	1076	0	1977
Cc_v0.1_Contig14892_41551.1	Cc029557_t1	100	1074	0	1967
Cc_v0.1_Contig35060_25340.1	Cc007871_t2	98	1056	0	1812
Cc_v0.1_Contig25325_36268.1	Cc045355_t1	100	1053	0	1945
Cc_v0.1_Contig2422_11221.1	Cc007971_t1	100	1053	0	1934
Cc_v0.1_Contig46295_17574.1	Cc032677_t1	95	1035	0	1648
Cc_v0.1_Contig133187_21507.1	Cc017927_t1	96	1028	0	1661
Cc_v0.1_Contig97116_09030.1	Cc021458_t1	100	1026	0	1895
Cc_v0.1_Contig91525_20482.1	Cc024743_t1	100	1014	0	1873
Cc_v0.1_Contig208748_HGT_part_part ial_coding	Cc019473_t1	100	1014	0	1862
Cc_v0.1_Contig14575_01846.1	Cc005546_t1	98	1014	0	1731
Cc_v0.1_Contig208748_39840.1	Cc019473_t1	100	1008	0	1851
Cc_v0.1_Contig726833_28878.1	Cc018082_t2	99	986	0	1788
Cc_v0.1_Contig56848_07145.1	Cc036646_t1	98	955	0	1628
Cc_v0.1_Contig42337_06229.1	Cc016395_t1	100	946	0	1736
Cc_v0.1_Contig117172_15135.2	Cc006530_t1	92	930	0	1306
Cc_v0.1_Contig46474_03905.1	Cc030738_t1	100	928	0	1714
Cc_v0.1_Contig395697_31101.1	Cc001913_t1	97	926	0	1561
Cc_v0.1_Contig48661_01712.1	Cc006530_t1	100	918	0	1670
Cc_v0.1_Contig6963_13485.1	Cc003207_t1	100	918	0	1674
Cc_v0.1_Contig70751_10696.3	Cc007145_t1	100	911	0	1683
Cc_v0.1_Contig81485_11959.1	Cc018869_t1	100	904	0	1664
Cc_v0.1_Contig24936_RC_HGT_part_p artial_coding	Cc018585_t1	100	902	0	1666
Cc_v0.1_Contig515125_36101.1	Cc024746_t1	96	895	0	1448
Cc_v0.1_Contig119012_28186.2	Cc019239_t1	100	891	0	1640
Cc_v0.1_Contig180818_22923.1	Cc035199_t1	95	877	0	1369
Cc_v0.1_Contig169540_00720.1	Cc000793_t1	100	848	0	1561
Cc_v0.1_Contig56848_07146.1	Cc036645_t1	100	846	0	1563
Cc_v0.1_Contig162346_07709.1	Cc046417_t1	100	845	0	1555
Cc_v0.1_Contig272365_18177.1	Cc018957_t1	95	844	0	1277
Cc_v0.1_Contig56848_07145.1	Cc036646_t1	100	841	0	1554
Cc_v0.1_Contig56848_07145.1	Cc036646_t1	100	841	0	1554
Cuscuta_pentagona_Neelima_178617	Cc030785_t1	100	834	0	1541
Cc_v0.1_Contig26549_00464.1	Cc030840_t1	93	819	0	1192

Cc_v0.1_Contig41987_00663.1	Cc014430_t2	100	814	0	1496
Cc_v0.1_Contig108693_37940.1	Cc030663_t1	97	808	0	1356
Cpent255306_cp78071_c0_seq7_2075 m_f1	Cc024218_t1	97	806	0	1328
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	802	0	1482
Cc_v0.1_Contig217765_24560.1	Cc046583_t1	98	777	0	1330
Cc_v0.1_Contig13522_14848.1	Cc045798_t1	100	775	0	1426
Cc_v0.1_Contig267673_18003.1	Cc016936_t1	98	774	0	1358
Cc_v0.1_Contig116600_33567.1	Cc028831_t1	99	751	0	1349
Cc_v0.1_Contig27628_38000.1	Cc018614_t1	97	745	0	1238
Cc_v0.1_Contig113598_06738.1	Cc018614_t1	100	741	0	1363
Cc_v0.1_Contig73234_20115.1	Cc037001_t1	100	732	0	1352
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	727	0	1343
Cc_v0.1_Contig228851_08156.3	Cc045884_t1	99	721	0	1282
Cc_v0.1_Contig209294_29296.1	Cc037593_t1	100	719	0	1317
Cc_v0.1_Contig172885_23445.1	Cc017393_t1	100	719	0	1310
CobtusifloraSdl_DN8470_c0_g1_i9	Cc037017_t1	95	719	0	1127
Cc_v0.1_Contig21455_19725.1	Cc018957_t1	100	716	0	1323
Cc_v0.1_Contig79158_24158.1	Cc032347_t2	97	708	0	1181
Cc_v0.1_Contig237682_26308.1	Cc003329_t1	100	699	0	1271
Cc_v0.1_Contig2879_03744.1	Cc038661_t1	97	686	0	1134
Cc_v0.1_Contig172885_23445.1	Cc017393_t1	100	684	0	1264
Cc_v0.1_Contig228851_08156.3	Cc045884_t1	100	676	0	1243
Cc_v0.1_Contig228851_08157.1	Cc045885_t2	100	673	0	1243
Cc_v0.1_Contig401560_28136.2	Cc029038_t1	100	667	0	1227
Cc_v0.1_Contig15373_39227.1	Cc023947_t1	100	663	0	1219
Cc_v0.1_Contig56848_07146.1	Cc036645_t1	94	655	0	1000
Cc_v0.1_Contig370794_05529.1	Cc023680_t1	100	653	0	1206
Cc_v0.1_Contig286807_34360.1	Cc013907_t1	100	644	0	1184
Cc_v0.1_Contig11014_20286.1	Cc046583_t1	100	638	0	1179
Cc_v0.1_Contig26956_34057.1	Cc013907_t1	97	637	0	1053
Cc_v0.1_Contig76675_23922.1	Cc007429_t1	100	624	0	1153
Cc_v0.1_Contig3196_00098.1	Cc006607_t1	97	620	0	1009
Cc_v0.1_Contig632722_HGT_part_part ial_coding	Cc018957_t1	100	617	0	1129
Cc_v0.1_Contig214261_RC_HGT_part_ partial_coding	Cc006818_t1	100	612	0	1114
Cc_v0.1_Contig221438_40726.1	Cc007870_t1	100	603	0	1103
Cc_v0.1_Contig14575_01846.1	Cc005546_t1	100	602	0	1112
Cc_v0.1_Contig4422_08271.1	Cc012276_t1	100	595	0	1099
Cc_v0.1_Contig21930_00944.1	Cc029954_t1	99	595	0	1066
Cc_v0.1_Contig357450_41831.1	Cc024834_t1	100	590	0	1090

Cc_v0.1_Contig48381_13176.1	Cc024745_t1	100	577	0	1066
Cc_v0.1_Contig162520_27911.1	Cc034948_t1	100	576	0	1064
Cc_v0.1_Contig172431_16373.1	Cc046327_t2	100	572	0	1057
Cc_v0.1_Contig172431_16373.1	Cc046327_t2	100	571	0	1055
Cc_v0.1_Contig357250_38603.1	Cc002148_t1	100	571	0	1050
Cc_v0.1_Contig56848_07145.1	Cc036646_t1	100	570	0	1053
Cc_v0.1_Contig368077_29884.1	Cc035637_t1	100	546	0	1003
Cc_v0.1_Contig116111_25250.1	Cc016720_t1	100	531	0	976
Cc_v0.1_Contig116111_25250.1	Cc016720_t1	99	528	0	959
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	515	0	946
Cc_v0.1_Contig430128_RC_HGT_part_ partial_coding	Cc006818_t1	97	504	0	833
Cc_v0.1_Contig21455_19725.1	Cc018957_t1	100	501	0	913
Cc_v0.1_Contig2765_13249.1	Cc000300_t1	100	498	0	909
Cc_v0.1_Contig79516_04901.1	Cc033905_t1	100	492	0	909
Cc_v0.1_Contig145090_05749.5	Cc045256_t1	100	489	0	904
Cc_v0.1_Contig172431_16373.1	Cc046327_t2	100	486	0	898
Cc_v0.1_Contig22571_10667.1	Cc032677_t1	100	471	0	870
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	465	0	854
Cc_v0.1_Contig48442_04378.1	Cc002477_t1	97	464	0	760
Cc_v0.1_Contig431685_39178.1	Cc021847_t1	100	463	0	843
Cc_v0.1_Contig267673_18003.1	Cc016936_t1	97	451	0	750
Cc_v0.1_Contig172431_16373.1	Cc046327_t2	100	445	0	822
Cc_v0.1_Contig51308_16880.1	Cc023632_t1	100	444	0	821
Cpent130069_cp70761_c0_seq4_1514 x_f1	Cc014533_t2	100	444	0	821
Cc_v0.1_Contig449938_15237.1	Cc030662_t1	100	442	0	811
Cc_v0.1_Contig608570_15700.1	Cc030662_t1	99	442	0	789
Cc_v0.1_Contig49454_08202.1	Cc021373_t1	100	441	0	809
Cc_v0.1_Contig3609_06616.1	Cc017573_t1	97	432	0	715
Cc_v0.1_Contig272365_18178.1	Cc000525_t1	100	430	0	795
Cc_v0.1_Contig271957_30274.1	Cc011893_t1	100	426	0	782
Cc_v0.1_Contig114799_30807.1	Cc002681_t1	99	425	0	756
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	100	424	0	784
Cc_v0.1_Contig113598_06738.1	Cc018614_t1	99	424	0	767
Cc_v0.1_Contig27628_38000.1	Cc018614_t1	97	424	0	708
Cc_v0.1_Contig21779_15717.1	Cc015805_t1	99	417	0	750
Cc_v0.1_Contig605226_36241.1	Cc016720_t1	97	415	0	697
Cpent191365_cp74144_c0_seq3_1782 p_f1	Cc032765_t1	98	411	0	706
CpentagonaSdl_DN6186_c0_g2_i1	Cc001220_t1	100	408	0	743
Cc_v0.1_Contig46474_03905.1	Cc030738_t1	100	407	0	747

Cc_v0.1_Contig605226_36241.1	Cc016720_t1	100	406	0	750
Cc_v0.1_Contig116111_25250.1	Cc016720_t1	100	402	0	737
Cc_v0.1_Contig213121_06326.1	Cc012016_t1	100	398	0	736
Cc_v0.1_Contig185284_16257.1	Cc027377_t1	100	393	0	719
Cc_v0.1_Contig39025_01970.1	Cc028325_t1	100	390	0	721
Cc_v0.1_Contig48733_23939.1	Cc030738_t1	99	386	0	697
Cc_v0.1_Contig416076_32258.1	Cc000525_t1	100	384	0	710
Cc_v0.1_Contig437972_11875.1	Cc028484_t1	100	384	0	704
Cc_v0.1_Contig21455_19725.1	Cc018957_t1	99	382	0	695
Cc_v0.1_Contig35060_25340.1	Cc007871_t2	98	380	0	658
Cc_v0.1_Contig197214_28322.1	Cc034330_t1	100	378	0	693
Cc_v0.1_Contig79974_20104.1	Cc000903_t1	99	373	0	662
Cc_v0.1_Contig437972_11875.1	Cc028484_t1	100	369	0	676
Cc_v0.1_Contig225706_07960.1	Cc017990_t1	100	366	0	676
Cc_v0.1_Contig297485_22280.1	Cc019283_t1	100	366	0	676
Cc_v0.1_Contig72639_11102.1	Cc019193_t1	100	365	0	669
Cc_v0.1_Contig48733_23939.1	Cc030738_t1	96	359	9.03E-165	580
Cc_v0.1_Contig4422_08271.1	Cc012276_t1	100	355	0	656
Cc_v0.1_Contig77230_15397.1	Cc029731_t1	94	354	2.65E-148	527
Cc_v0.1_Contig50709_05360.2	Cc045157_t1	98	346	4.66E-172	606
Cc_v0.1_Contig2739_00009.1	Cc016534_t2	99	341	3.05E-175	617
Cc_v0.1_Contig79974_20104.1	Cc000903_t1	99	340	9.15E-174	612
Cc_v0.1_Contig51717_28510.1	Cc033842_t1	100	336	1.07E-176	621
Cc_v0.1_Contig39025_01970.1	Cc028325_t1	95	331	3.74E-141	503
Cc_v0.1_Contig14575_01846.1	Cc005546_t1	100	328	7.01E-172	606
Cc_v0.1_Contig169540_00720.1	Cc000793_t1	100	328	2.58E-172	606
Cc_v0.1_Contig437972_11875.1	Cc028484_t1	100	325	2.07E-170	601
Cc_v0.1_Contig21455_19725.1	Cc018957_t1	99	321	7.61E-165	582
Cc_v0.1_Contig22571_10667.1	Cc032677_t1	100	317	2.98E-164	579
Cc_v0.1_Contig202470_31088.1	Cc029954_t1	100	312	9.89E-164	577
Cpent130069_cp70761_c0_seq4_1514					
x_f1	Cc014533_t2	100	312	1.41E-163	577
Cc_v0.1_Contig202470_31088.1	Cc029954_t1	100	309	4.60E-162	571
Cc_v0.1_Contig236330_23287.1	Cc019421_t2	100	307	2.00E-160	568
Cc_v0.1_Contig4785_27415.1	Cc013099_t1	100	305	1.42E-159	564
Cc_v0.1_Contig39025_01970.1	Cc028325_t1	100	305	7.87E-158	558
Cc_v0.1_Contig77230_15397.1	Cc029731_t1	96	305	9.66E-138	492
Cc_v0.1_Contig124613_12691.2	Cc031501_t1	100	304	4.03E-159	562
Cc_v0.1_Contig39025_01970.1	Cc028325_t1	100	303	2.19E-158	560
Cc_v0.1_Contig49454_08202.1	Cc021373_t1	100	300	4.71E-155	549
Cc_v0.1_Contig149425_03103.4	Cc012076_t1	100	297	2.83E-153	544
Cc_v0.1_Contig13522_14848.1	Cc045798_t1	100	296	1.71E-154	547

Cc_v0.1_Contig2855_01306.1	Cc038661_t1	100	295	3.09E-152	540
Cc_v0.1_Contig174003_23034.1	Cc038448_t1	97	293	9.04E-137	486
Cc_v0.1_Contig21779_15717.1	Cc015805_t1	100	290	2.18E-151	536
Cc_v0.1_Contig205519_26719.1	Cc030386_t1	91	290	4.22E-101	370
Cc_v0.1_Contig3196_00098.1	Cc006607_t1	99	288	8.48E-147	521
Cc_v0.1_Contig77230_15397.1	Cc029731_t1	99	288	2.06E-144	514
Cc_v0.1_Contig127172_41391.1	Cc013099_t1	98	287	7.48E-137	486
Cc_v0.1_Contig176771_HGT_part_part ial_coding	Cc007206_t1	99	278	9.33E-142	503
Cc_v0.1_Contig21455_19725.1	Cc018957_t1	100	272	2.84E-139	497
Cc_v0.1_Contig370794_05529.1	Cc023680_t1	100	267	2.42E-138	494
Cc_v0.1_Contig225706_07960.1	Cc017990_t1	100	266	4.91E-138	492
Cc_v0.1_Contig29594_24374.1	Cc034802_t1	97	262	1.71E-119	431
Cc_v0.1_Contig130847_28444.1	Cc035306_t1	95	262	8.52E-114	412
Cc_v0.1_Contig49454_08202.1	Cc021373_t1	99	260	1.76E-129	464
Cc_v0.1_Contig257269_37298.1	Cc029734_t1	96	255	9.93E-115	416
Cc_v0.1_Contig39025_01970.1	Cc028325_t1	100	253	6.35E-129	462
Cc_v0.1_Contig77230_15397.1	Cc029731_t1	94	253	3.63E-107	390