

Additional file 5. Annotation of HGTs that are transferred between Magnaporthales (using *M. incrustans* as a reference) and *Colletotrichum*

No.	Family	Genes*	Products	UFboot	Mag. Clade ¹	Donor ²	CAZyme	Transporter	Peptidase	Colleto. long_ctg ³	No. Colleto. ⁴
1	1	<i>M. incrustans.scf1_204.g77</i>	arabinan_endo-alpha-l-arabinosidase	100	Clade_C	Magnapo	GH43			1	>1
2	2	<i>M. incrustans.scf108_47.g25</i>	ligninase_h2	98	Clade_C	Magnapo	AA2			1	>1
3	3	<i>M. incrustans.scf11_109.g17</i>	sodium_symporter_family_protein	100	Clade_C	Colleto				1	>1
4	4	<i>M. incrustans.scf11_109.g75</i>	hypothetical_protein_GGTG_03148	92	Clade_ABC	unknown				1	>1
5	5	<i>M. incrustans.scf113_40.g13</i>	amino-acid_permease_inda1	100	Clade_A	Magnapo		TC-DB		1	>1
6	6	<i>M. incrustans.scf113_40.g27</i>	hypothetical_protein_MGG_02132	100	Clade_ABC	unknown				1	>1
7	7	<i>M. incrustans.scf114_41.g13</i>	hypothetical_protein_CFIO01_07988	100	Clade_C	Magnapo				1	1
8	8	<i>M. incrustans.scf115_49.g24</i>	tat_pathway_signal_sequence	100	Clade_C	unknown				1	>1
9	9	<i>M. incrustans.scf115_49.g27</i>	mfs_transporter	100	Clade_BC	unknown				1	>1
10	10	<i>M. incrustans.scf135_29.g14</i>	cation_diffusion_facilitator_1_protein	100	Clade_ABC	unknown				1	>1
11	11	<i>M. incrustans.scf15_119.g86</i>	chlorogenic_acid_esterase_precursor	100	Clade_C	Colleto	CE10,CE10		S09X	0	>1
12	12	<i>M. incrustans.scf163_39.g23</i>	exoglucanase_3	94	Clade_BC	Magnapo	GH6			1	>1
13	13	<i>M. incrustans.scf163_39.g5</i>	hypothetical_protein_GGTG_10533	96	Clade_BC	unknown				1	1
14	14	<i>M. incrustans.scf18_111.g63</i>	glycoside_hydrolase	95	Clade_B	Magnapo	CBM18			1	>1
15	15	<i>M. incrustans.scf18_111.g65</i>	domain-containing_protein	100	Clade_BC	unknown	CBM50			0	1
16	16	<i>M. incrustans.scf186_26.g5</i>	cyclohexanone_-monooxygenase	100	Clade_C	unknown				1	>1
17	17	<i>M. incrustans.scf19_115.g13</i>	carboxylesterase_family_protein	100	Clade_C	Magnapo	CE10		S09X	1	>1
18	18	<i>M. incrustans.scf19_115.g97</i>	choline_monooxygenase	100	Clade_BC	Colleto				1	>1
19	19	<i>M. incrustans.scf195_22.g10</i>	hypothetical_protein_GGTG_04880	100	Clade_C	Magnapo	GH131			1	>1
20	20	<i>M. incrustans.scf2_209.g41</i>	hypothetical_protein_GGTG_05571	99	Clade_C	Magnapo	GH115			1	>1
21	21	<i>M. incrustans.scf2_209.g43</i>	glycosyl_hydrolase_family_38_domain	100	Clade_BC	Colleto	GH38			1	>1
22	22	<i>M. incrustans.scf2_209.g60</i>	arylsulfatase_precursor	100	Clade_C	Magnapo	CBM20 GH15			1	1
23	23	<i>M. incrustans.scf206_28.g23</i>	amino_acid_permease	97	Clade_ABC	Colleto		TC-DB		1	>1
24	24	<i>M. incrustans.scf208_29.g19</i>	mfs_general_substrate_transporter	100	Clade_C	Magnapo		TC-DB		1	1
25	25	<i>M. incrustans.scf209_24.g8</i>	short_chain_dehydrogenase_reductase_family	99	Clade_C	unknown				1	>1
26	26	<i>M. incrustans.scf209_24.g9</i>	hypothetical_protein_GGTG_08358	100	Clade_ABC	Colleto				1	>1
27	27	<i>M. incrustans.scf21_75.g70</i>	hypothetical_protein_CGGC5_15363	93	Clade_BC	Magnapo				0	1
28	28	<i>M. incrustans.scf21_75.g71</i>	methyltransferase_type_partial	100	Clade_C	unknown				0	1
29	29	<i>M. incrustans.scf225_20.g1</i>	peptidase_family_m28	100	Clade_ABC	Magnapo	CBM12		M28A	1	>1
30	30	<i>M. incrustans.scf23_91.g22</i>	pectate_lyase	99	Clade_BC	Magnapo	PL1,PL1			1	>1
31	31	<i>M. incrustans.scf233_15.g10</i>	beta-ketoacyl_synthase_domain-containing	100	Clade_B	Magnapo				1	>1
32	32	<i>M. incrustans.scf233_15.g11</i>		100	Clade_B	Magnapo				1	>1
33	32	<i>M. incrustans.scf233_15.g12</i>	enoyl_reductase	100	Clade_B	Magnapo				1	1
34	33	<i>M. incrustans.scf24_104.g84</i>	arsenite_efflux_transporter	100	Clade_BC	unknown				1	>1
35	34	<i>M. incrustans.scf26_101.g7</i>	acidic_mammalian_chitinase	100	Clade_BC	Magnapo	GH18			1	>1

36	35	<i>M. incrustans.scf269_12.g7</i>	hypothetical_protein_GGTG_02130	100	Clade_ABC	unknown		1	>1
37	36	<i>M. incrustans.scf294_12.g12</i>	methyltransferase_domain-containing_protein	100	Clade_ABC	Colleto		1	>1
38	37	<i>M. incrustans.scf3_191.g103</i>	amino_acid_permease	100	Clade_C	Colleto	TC-DB	1	>1
39	38	<i>M. incrustans.scf3_191.g97</i>	nad_-binding_protein	98	Clade_C	unknown		1	>1
40	39	<i>M. incrustans.scf302_11.g7</i>	isochorismatase_hydrolase	85	Clade_BC	unknown		1	>1
41	40	<i>M. incrustans.scf307_9.g9</i>	mgt_family_glycosyltransferase	99	Clade_BC	Magnapo	GT1	1	>1
42	41	<i>M. incrustans.scf308_8.g1</i>	ligninase_1g6_precursor	100	Clade_BC	unknown	AA2	1	>1
43	42	<i>M. incrustans.scf309_10.g4</i>	methyltransferase_domain-containing_protein	100	Clade_BC	Colleto		1	>1
44	43	<i>M. incrustans.scf31_87.g11</i>	hexose_transporter	99	Clade_BC	Colleto		1	>1
45	44	<i>M. incrustans.scf31_87.g44</i>	extracellular_cellulase	95	Clade_ABC	unknown	CBM63	1	>1
46	45	<i>M. incrustans.scf32_89.g43</i>	tannase_and_feruloyl_esterase	100	Clade_C	Magnapo		1	>1
47	46	<i>M. incrustans.scf32_89.g81</i>	glycosyl_hydrolase_family_81	100	Clade_C	Magnapo	GH81	1	>1
48	46	<i>M. incrustans.scf75_46.g31</i>	glycosyl_hydrolase_family_81	100	Clade_C	Colleto	GH81	1	>1
49	47	<i>M. incrustans.scf321_10.g5</i>	hypothetical_protein_GGTG_13171	100	Clade_BC	Magnapo		1	>1
50	48	<i>M. incrustans.scf33_97.g79</i>	hypothetical_protein_GGTG_05928	100	Clade_ABC	unknown		1	1
51	49	<i>M. incrustans.scf33_97.g84</i>	monocarboxylate_permease-like_protein	100	Clade_ABC	Colleto	TC-DB	1	>1
52	50	<i>M. incrustans.scf34_78.g16</i>	cornichon_protein	94	Clade_ABC	unknown		1	>1
53	51	<i>M. incrustans.scf4_208.g109</i>	choline_transport	96	unclear	Magnapo	TC-DB	1	>1
54	52	<i>M. incrustans.scf4_208.g112</i>	dimethylaniline_monooxygenase	100	Clade_C	Magnapo		1	>1
55	53	<i>M. incrustans.scf4_208.g135</i>	mannitol_1-phosphate_dehydrogenase	100	Clade_ABC	Magnapo		1	>1
56	54	<i>M. incrustans.scf4_208.g23</i>	heterokaryon_incompatibility_protein	100	Clade_C	Colleto		1	>1
57	55	<i>M. incrustans.scf4_208.g53</i>	major_facilitator_superfamily_transporter	100	Clade_C	Magnapo		1	>1
58	56	<i>M. incrustans.scf4_208.g57</i>	glyoxalase_bleomycin_resistance_protein	100	Clade_C	Colleto		1	>1
59	56	<i>M. incrustans.scf46_67.g47</i>	dioxygenase_superfamily	100	Clade_BC	unknown		1	>1
60	57	<i>M. incrustans.scf4_208.g79</i>	asparagine_synthase	100	unclear	Magnapo	C44	1	>1
61	58	<i>M. incrustans.scf40_91.g81</i>	tripeptidyl-peptidase_sed4	100	Clade_ABC	Magnapo	S53	1	>1
62	59	<i>M. incrustans.scf43_84.g22</i>	leucoanthocyanidin_reductase	99	Clade_BC	Magnapo	CE12	1	>1
63	60	<i>M. incrustans.scf50_60.g58</i>	glucose_transporter_hxt1	100	Clade_BC	Colleto		1	>1
64	61	<i>M. incrustans.scf54_86.g81</i>	arylsulfatase_protein	100	Clade_B	unknown	CBM20 GH15	0	1
65	62	<i>M. incrustans.scf55_68.g61</i>	fatty-acid_amide_hydrolase	100	Clade_B	unknown		1	>1
66	63	<i>M. incrustans.scf55_68.g64</i>	major_facilitator_superfamily_transporter	99	Clade_BC	unknown	TC-DB	1	>1
67	64	<i>M. incrustans.scf61_80.g17</i>	mfs_multidrug_transporter	100	Clade_BC	Magnapo		1	>1
68	65	<i>M. incrustans.scf61_80.g18</i>	c6_finger_domain-containing_protein	100	Clade_BC	Magnapo		1	>1
69	66	<i>M. incrustans.scf61_80.g74</i>	glycoside_hydrolase_family_43_protein	96	Clade_C	Magnapo		1	>1
70	67	<i>M. incrustans.scf63_70.g23</i>	endoplasmic_reticulum_protein	99	Clade_ABC	Magnapo		1	>1
71	68	<i>M. incrustans.scf65_53.g1</i>	ankyrin_repeat-containing	100	Clade_C	unknown		0	1
72	69	<i>M. incrustans.scf65_53.g44</i>	mas3_protein	89	Clade_BC	Magnapo		1	>1
73	70	<i>M. incrustans.scf66_71.g16</i>	general_amino_acid_permease_agp2	100	Clade_BC	Colleto	TC-DB	1	>1
74	71	<i>M. incrustans.scf68_59.g21</i>	nitroreductase_family_protein	100	Clade_A	Magnapo		1	1
75	72	<i>M. incrustans.scf7_130.g116</i>	glycosyl_hydrolase	100	Clade_BC	Magnapo	GH92	1	>1
76	73	<i>M. incrustans.scf7_130.g118</i>	sulphydryl_oxidase	100	Clade_B	Magnapo		1	>1

77	74	<i>M. incrustans.scf75_46.g36</i>	glycosyltransferase_family_90_protein	100	Clade_BC	Magnapo	GT90		1	1
78		<i>M. incrustans.scf83_65.g53</i>		100	Clade_ABC	Magnapo	GT90		1	1
79	75	<i>M. incrustans.scf8_147.g137</i>	polyketide_synthase	100	Clade_ABC	unknown	GT2		1	>1
80	76	<i>M. incrustans.scf8_147.g65</i>	abc_transporter	100	Clade_ABC	Magnapo			1	>1
81	77	<i>M. incrustans.scf8_147.g9</i>	secreted_glucosidase	100	Clade_BC	Magnapo	GH16		1	>1
82	78	<i>M. incrustans.scf81_37.g22</i>	rhamnogalacturonan_acetylerase	100	Clade_A	unknown	CE12		1	>1
83	79	<i>M. incrustans.scf83_65.g47</i>	choline_dehydrogenase	100	Clade_ABC	Colleto	AA3		1	>1
84	80	<i>M. incrustans.scf86_70.g25</i>	aminotransferase_class_i_and_ii	100	Clade_B	unknown			1	1
85	81	<i>M. incrustans.scf86_70.g26</i>	epoxide_hydrolase_2	100	Clade_B	Magnapo		S33	1	1
86	82	<i>M. incrustans.scf86_70.g27</i>	cytochrome_p450	100	Clade_B	Magnapo			1	1
87	83	<i>M. incrustans.scf9_129.g18</i>	nacht_and_tpr_domain-containing_protein	99	Clade_ABC	Colleto			1	>1
88	84	<i>M. incrustans.scf9_129.g28</i>	glycoside_hydrolase_family_18_protein	98	Clade_C	unknown	CBM18		0	1
89	85	<i>M. incrustans.scf9_129.g61</i>	calcium-transporting_atpase	97	Clade_ABC	Colleto		TC-DB	1	>1
90	86	<i>M. incrustans.scf91_52.g17</i>	hypothetical_protein_GGTG_06400	94	Clade_BC	unknown			1	>1
91	87	<i>M. incrustans.scf94_48.g2</i>	high-affinity_nicotinic_acid_transporter	99	Clade_ABC	unknown		TC-DB	1	>1
92	88	<i>M. incrustans.scf94_48.g8</i>	major_facilitator_superfamily_transporter	99	Clade_BC	Magnapo			1	>1
93	89	<i>M. incrustans.scf97_44.g2</i>	phospholipase_carboxylesterase	94	Clade_B	Magnapo			1	>1

* Genes in transferred genomic segments are shown in bold face.

¹ Magnaporthales comprise three major clades (i.e., clades A, B and C). This column indicates tentatively which Magnaporthales clades were involved in the gene transfer with *Colletotrichum*.

² The putative donor of the gene transfers between Magnaporthales and *Colletotrichum*.

³ If one or more transferred *Colletotrichum* genes are located in long contigs (encoding ≥ 5 genes), value (1) is assigned. Value (0) is assigned otherwise.

⁴ Number of *Colletotrichum* species involved in the individual HGT instance.