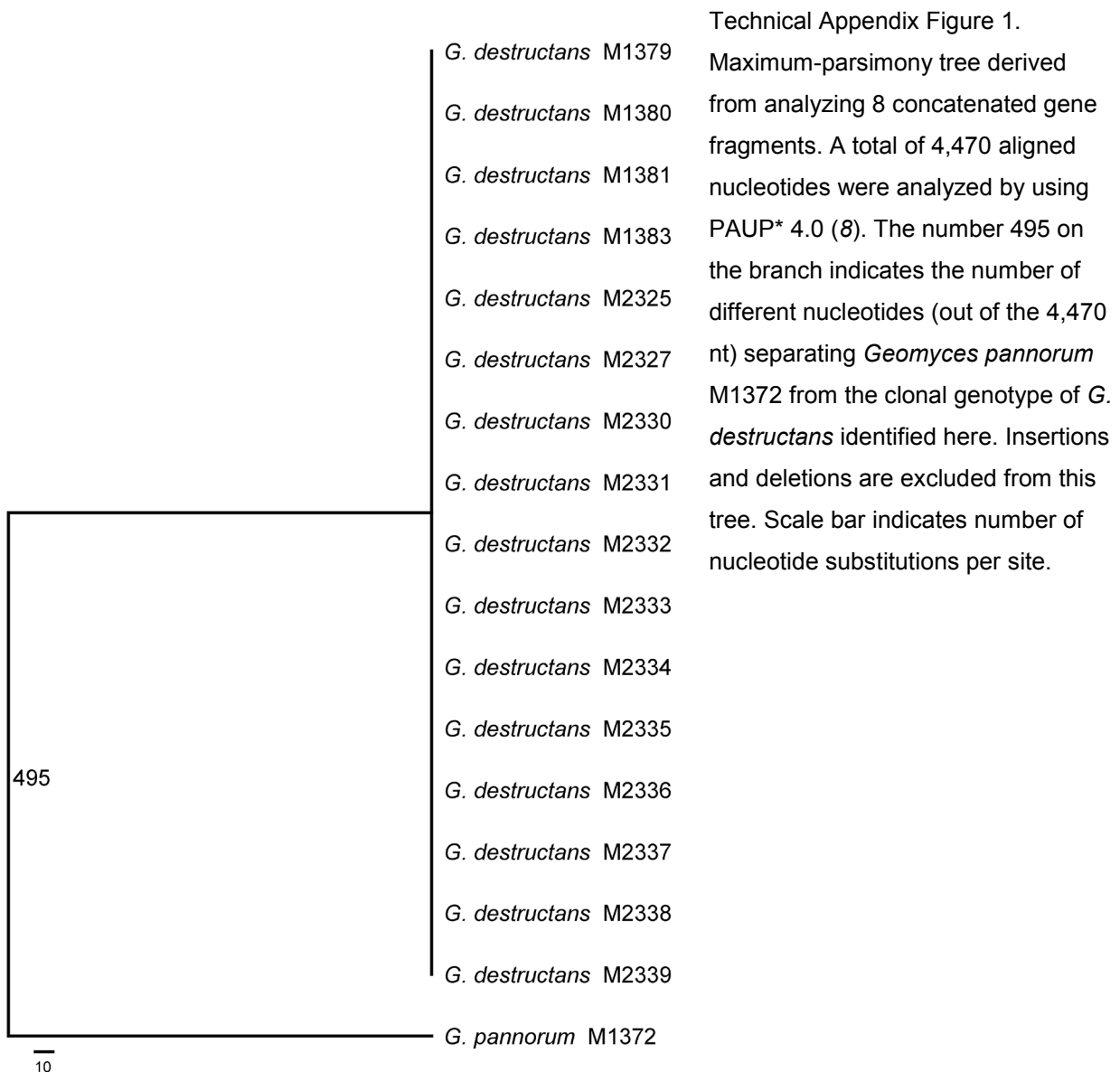
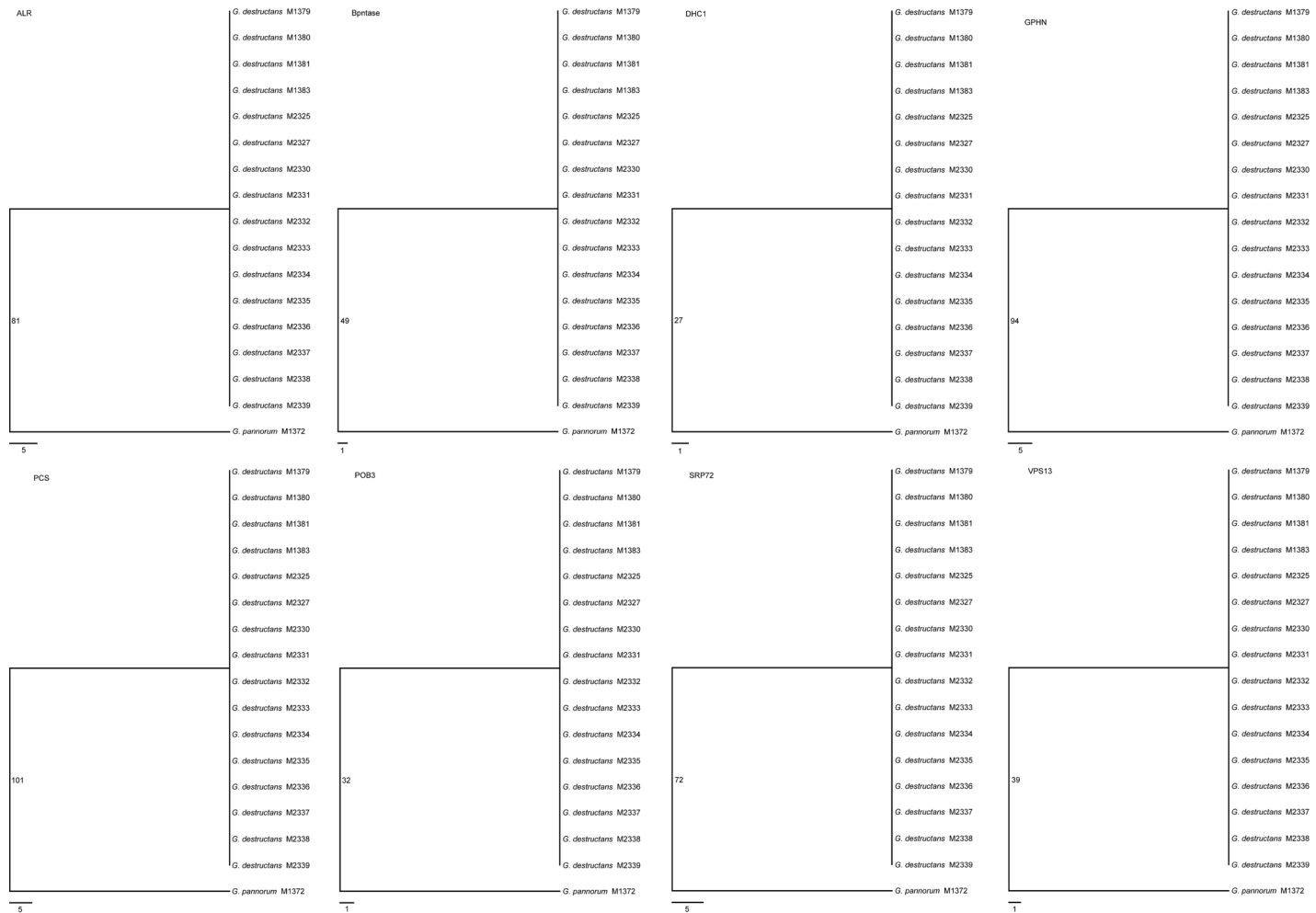


Clonal Genotype of *Geomyces destructans* among Bats with White Nose Syndrome, New York, USA

Technical Appendix





Technical Appendix Figure 2. Maximum parsimony trees derived from individual target sequences. Alpha-L-rhamnosidase (*ALR*), 530 aligned nucleotides with 81 nt difference between *Geomyces destructans* and *G. pannorum*; 3'(2'),5'-bisphosphate nucleotidase (*Bpntase*), 667 nt/49

nucleotide difference; dynein (*DHC1*), 417 nt /27 difference; gephyrin molybdenum cofactor biosynthesis protein (*GPHN*), 522 nt/94 nt difference; peroxisomal-coenzyme A synthetase (*PCS*), 719 nt/101 nt difference; FACT complex subunit (*POB3*), 413 nt/32 nt difference; signal recognition particle protein 72 (*SRP72*), 613 nt/72 nt difference; vacuolar protein sorting-associated protein (*VPS13*), 527 nt/39 nt difference. The tree topologies were identical when neighbor-joining methods were used for analysis. Scale bars indicate number of nucleotide substitutions per site.

Technical Appendix Figure 3 (below). Multiple alignments of 8 target gene fragments. Synonymous substitutions are shaded light gray while nonsynonymous substitution are dark gray and amino acid changes are highlighted in red. A smaller fragment of nucleotides used in phylogenetics construct was used in this comparison. Putative amino acid sequences for *Geomyces destructans* and *G. pannorum* were deduced by using EMBOSS Transeq (EMBL-EBI, Cambridgeshire, UK). Homologous sequences from either *Ajellomyces dermatitidis*, *Arthroderma otae*, *Aspergillus nidulans*, *Aspergillus clavatus*, *Botryotinia fuckeliana*, *Glomerella graminicola*, *Nectria hematococca*, *Sclerotinia sclerotiorum*, and *Verticillium albo-atrum* were included in this comparison.

ALR (Alpha-L-rhamnosidase): □450 bases aligned (Gd = *Geomyces destructans*, Gp = *Geomyces pannorum*
An = *Aspergillus nidulans*, Va = *Verticillium albo-atrum*)

Gd-DNA	CTC	TCT	ACA	AAA	CTC	TTG	GCA	CCG	GAT	GCG	CCG	CCC	GTT	ACG	GTC					
Gp-DNA	CTC	TCT	ACA	AAA	CTC	ATC	GCT	CCA	GAT	GCG	CCA	CCC	GTC	ACT	GTG					
An-DNA	CCA	GAG	ACG	CAG	CTG	GTG	GCG	CCA	AAC	GCG	CCA	CCA	GTG	CGA	GTG					
Va-DNA	GAT	ACC	GTC	CAG	CTC	CAT	GCG	GGT	GAC	GCC	GAG	CCT	GTT	CGA	CGC					
Gd-PRO				K	L	L	A	P	D	A	P	P	V	T	V					
Gp-PRO				K	L	I	A	P	D	A	P	P	V	T	V					
An-PRO				Q	L	V	A	P	N	A	P	P	V	R	V					
Va-PRO				Q	L	H	A	G	D	A	E	P	V	R	R					
Gd-DNA	ACA	GAA	GAG	GTC	AAC	CCA	GTC	GAT	ATT	ATC	AAG	ACA	AAG	TCC	GGG	AAA	ACA	GTC	ATT	GAT
Gp-DNA	ACA	GAA	GAG	CTG	AGC	CCA	ACT	GAG	ATT	ATC	AAG	ACA	AAG	TCC	GGC	AAA	ACG	GTC	ATT	GAC
An-DNA	ACC	GAA	GTG	GTC	AAT	CCA	GTT	GAA	ATC	ATT	CGC	ACG	CCG	TCC	GGC	AAA	GTA	ATC	ATT	GAT
Va-DNA	CTC	GAA	ATC	GTC	AAG	CCC	ATC	GAA	AAG	ATC	ACG	ACC	CCC	TCC	GGA	AAG	ACG	GTG	CTT	GAC
Gd-PRO	T	E	E	V	N	P	V	D	I	I	K	T	K	S	G	K	T	V	I	D
Gp-PRO	T	E	E	L	S	P	T	E	I	I	K	T	K	S	G	K	T	V	I	D

An-PRO T E V V N P V E I I R T P S G K V I I D
 Va-PRO L E I V K P L E K I T T P S G K T V L D

Gd-DNA TTT GGG CAG AAC CTG GTA GGC AAG CTT CGT GTC AGC TCC GTC CGA CTC CCC GCG GGT CA
 Gp-DNA TTT GGG CAG AAC CTC GTA GGG AAA CTT CGT GTC AAC TCC GTC CGA CTC CCT GCC GGT GA
 An-DNA TTT GGG CAA AAC CTC GTT GGC CGT GTC CGG ATC CGC TCC GTA AAG AAG ACC GTG GGC CA
 Va-DNA TTT GGG CAG AAC CTC GTA GGC TAC CTT CGG GTC AAC AAA GTC AGG GGT CCC CGC GGC CA
 Gd-PRO F G Q N L V G K L R V S S V R L P A G Q
 Gp-PRO F G Q N L V G K L R V N S V R L P A G E
 An-PRO F G Q N L V G R V R L R S V K K T V G H
 Va-PRO F G Q N L V G Y L R V N K V R G P R G H

Gd-DNA G AAG ATC TCA TTT ACA CAT GTC GAA GTG CTC GAG AAT GGC GAA ATC GGC ACA CGT CCG CT
 Gp-DNA G AAA ATC ACA TTT ACA CAC GTC GAG GTA CTC GAG AAT GGC GAA ATT AGC ACC CGA CCG CT
 An-DNA C TCT ATC ATT CTC AAG CAT GCG GAA GTG CTC GAG AAT AGC GAA CTT GGA ACG CGT CCG CT
 Va-DNA T AAA ATC ACC CTG CTG CAC GCC GAG GTT CTC GAG AAG GGC GAG CTT GGC ATC CGG CCG CT
 Gd-PRO K I S F T H V E V L E N G E I G T R P L
 Gp-PRO K I T F T H V E V L E N G E I S T R P L
 An-PRO S I I L K H A E V L E N S E L G T R P L
 Va-PRO K I T L L H A E V L E K G E L G I R P L

Gd-DNA T CGA GGA GCA GTC TGC GTT GAT ACT ATT GTC TTT TCT GAA AAG GAG CTC CGC GGC ==
 Gp-DNA T CGA GAA GCA GTA CCC GTC GAT ACT GTC ATC TTT TCT GAT AAC GAG CTC CTG AAC ==
 An-DNA G CGA GTG GCC AAG GCC CAG GAC GAG ATC ATC TCA GCA GGA CAG GAG ATT TGT GAC ==
 Va-DNA G CGT GAC TGC AAG GCC CGG GAC ATC TAC ACC CTC TGT GGT GAT GAG GCT GGC GAA TC
 Gd-PRO R G A V C V D T I V F S E K E L R G -
 Gp-PRO R E A V P V D T V I F S D N E L L N -
 An-PRO R V A K A Q D E I I S A G Q E T C D -
 Va-PRO R D C K A R D I Y T L C G D E A G E S

Gd-DNA - TGG TCG CCG AAA TTC ACA TTC CAC GGC TTC CAG TAC GTG CAG GTT GAA GGG TGG CCA GC
 Gp-DNA - TGG TCC CCA AAA TTC ACA TTT CAT GGT TTC CAG TAC GTG CAA GTT GAT GGG TGG CCA GC
 An-DNA - TGG GCT CCT AGC TTT ACT TTC CAT GGC TTC CGG TAT GTT CAG GTT GAT GGA TGG AGC ==
 Va-DNA G TAC GAG CCT CGC TTC ACC TTC CAC GGC TTT CGC TAT GCC CAG GTC GAC GAC TGG CCA ==
 Gd-PRO W S P K F T F H G F Q Y V Q V E G W P A
 Gp-PRO W S P K F T F H G F Q Y V Q V D G W P A
 An-PRO W A P S F T F H G F R Y V Q V D G W S -
 Va-PRO Y E P R F T F H G F R Y A Q V D D W P -

Gd-DNA	A	ACT	GCG	GAT	GCT	GAA	CTC	CCT	---	TAT	AAG	TCT	GAC	TTT	ACT	GCG	CTA	GTC	ATG	CAT	445
Gp-DNA	A	ACT	GCG	GAT	GCT	GAA	CTC	CCA	---	TCT	TTG	TCT	GAC	TTC	ACT	GCA	CTA	GTC	ATG	CAT	452
An-DNA	-	CCT	GAA	GAC	GCC	GAC	ACC	CCT	CTT	ACT	CTA	CAA	AGC	CTG	ACC	GCC	GAA	GTC	ATG	CAT	444
Va-DNA	-	TCC	GCA	GAT	ATT	GAC	---	---	---	ATC	CTG	GAC	TCA	CTC	GAG	GCT	GTG	GTC	TGC	AAT	459
Gd-PRO		T	A	D	A	E	L	P	-	Y	K	S	D	F	T	A	L	V	M	H	
Gp-PRO		T	A	D	A	E	L	P	-	S	L	S	D	F	T	A	L	V	M	H	
An-PRO		P	E	D	A	D	T	P	L	T	L	Q	S	L	T	A	E	V	M	H	
Va-PRO		S	A	D	I	D	-	-	-	I	L	D	S	L	E	A	V	V	C	N	

BPntase (3'(2'),5'-bisphosphate nucleotidase): ~750 bases aligned; Alignment shows 3' region of the protein and the 3' UTR (Ss = *Sclerotinia sclerotiorum*; Af = *Aspergillus fumigatus*)

Gd-DNA										AG	AGC	CAG	CCG	ATC	CGC	ATG	AGC	GAG	AAG	A
Gp-DNA										AG	AGC	CAG	CCA	ATC	CGC	ATG	AGC	GAG	AAG	A
Ss-DNA										AG	GGT	CAA	TCT	ATT	CAA	ATG	AAG	CCA	GTT	A
Af-DNA										AG	AGC	AAG	CCC	ATC	TCG	ATG	CGT	CCC	GTT	C
Gd-PRO										S	Q	P	I	R	M	S	E	K		
Gp-PRO										S	Q	P	I	R	M	S	E	K		
Ss-PRO										G	Q	S	I	Q	M	K	P	V		
Af-PRO										S	K	P	I	S	M	R	P	V		

Gd-DNA	AG	GAC	ATC	ACC	GAT	GCC	ACT	TTC	TGC	GAG	AGT	GTT	GAG	GCT	GGC	CAC	TCA	TCT	CAC	GAC	G
Gp-DNA	AG	GAT	ATC	ACC	GAT	GCC	ACT	TTC	TGC	GAG	AGT	GTT	GAG	GCT	GGC	CAC	TCG	TCG	CAT	GAC	G
Ss-DNA	CG	GAT	TTA	AGT	CAA	GCT	ACA	TTC	TGT	GAG	AGT	GTT	GAG	GCA	GGT	CAC	TCT	TCC	CAT	GGC	G
Af-DNA	CG	GAT	ATA	AAA	CAG	GCT	GTC	TTC	TGT	GAA	GGA	GTT	GAG	GCT	GCC	CAC	TCT	GCT	CAA	GGC	G
Gd-PRO	K	D	I	T	D	A	T	F	C	E	S	V	E	A	G	H	S	S	H	D	
Gp-PRO	K	D	I	T	D	A	T	F	C	E	S	V	E	A	G	H	S	S	H	D	
Ss-PRO	T	D	L	S	Q	A	T	F	C	E	S	V	E	A	G	H	S	S	H	G	
Af-PRO	P	D	I	K	Q	A	V	F	C	E	G	V	E	A	A	H	S	A	Q	G	

Gd-DNA	AC	CAA	TCT	CAG	ATC	GCC	CAG	AAG	CTG	CAG	ATC	AGC	AAG	CCG	AGC	GTG	CGG	ATG	GAT	TCG	C
Gp-DNA	AC	CAG	TCT	CAG	ATC	GCA	CAG	AAG	CTG	CAG	ATT	AGC	AAG	CCA	AGC	GTG	CGA	ATG	GAT	TCG	C
Ss-DNA	AT	CAA	CAT	GCC	ATT	GCT	ACC	AAA	TTG	GGT	GTT	ACC	AAG	GCT	AGT	GTC	CGA	ATG	GAT	TCG	C
Af-DNA	AC	AAC	GCT	GCC	GTC	GCT	CAG	CTC	CTG	GGT	ATC	ACC	TCC	CCC	AGC	GTG	CGA	CTC	GAC	TCG	C
Gd-PRO	D	Q	S	Q	I	A	Q	K	L	Q	I	S	K	P	S	V	R	M	D	S	
Gp-PRO	D	Q	S	Q	I	A	Q	K	L	Q	I	S	K	P	S	V	R	M	D	S	

Ss-PRO	D	Q	H	A	I	A	T	K	L	G	V	T	K	A	S	V	R	M	D	S	
Af-PRO	D	N	A	A	V	A	Q	L	L	G	I	T	S	P	S	V	R	L	D	S	
Gd-DNA	AG	GCC	AAG	TAT	GCC	TCG	ATC	GCC	CGT	GGC	GCT	GGG	GAT	ATT	TAC	CTG	AGA	CTT	CCA	ACC	A
Gp-DNA	AG	GCA	AAG	TAT	GCC	TCG	ATC	GCT	CGT	GGT	GCG	GGG	GAT	ATT	TAC	CTC	AGA	CTT	CCA	ACC	A
Ss-DNA	AA	GCT	AAA	TAT	GGA	TCG	ATC	GCG	AGA	GGT	GCT	GGA	GAC	ATT	TAC	CTT	AGA	CTT	CCC	GTT	A
Af-DNA	AG	GCC	AAG	TAC	TGC	TCA	ATT	GCT	AGA	GGC	GCA	GGC	GAT	ATC	TAC	CTA	CGG	CTA	CCT	GTC	A
Gd-PRO	Q	A	K	Y	A	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	T	
Gp-PRO	Q	A	K	Y	A	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	T	
Ss-PRO	Q	A	K	Y	G	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	V	
Af-PRO	Q	A	K	Y	C	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	V	
Gd-DNA	GC	GCA	ACG	TAC	CAA	GAG	AAG	ATC	TGG	GAT	CAC	GCT	GCT	GGA	GAC	CTG	ATT	GTT	CGA	GAG	G
Gp-DNA	GC	GCA	ACG	TAC	CAG	GAG	AAG	ATC	TGG	GAT	CAC	GCT	GCT	GGA	GAC	CTG	ATT	GTT	AGG	GAG	G
Ss-DNA	GC	GCG	ACT	TAC	CAA	GAG	AAG	ATT	TGG	GAT	CAT	GCT	GCT	GGA	GAT	CTT	ATT	GTA	AGA	GAG	G
Af-DNA	GA	AAG	GAC	TAC	CAG	GAG	AAG	ATC	TGG	GAT	CAT	GCG	GCT	GGC	GAT	CTC	ATT	GTC	CGC	GAG	G
Gd-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Gp-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Ss-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Af-PRO	R	K	D	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Gd-DNA	CG	GGA	GGA	CAG	GTT	ACG	GAT	TCA	CTA	GGC	AGA	CGT	CTG	GAT	TTC	AGC	AAG	GGT	AGA	ACT	T
Gp-DNA	CA	GGA	GGA	CAG	GTT	ACG	GAT	TCA	CTG	GGC	AGA	CGT	CTG	GAT	TTC	AGC	AAG	GGT	AGA	ACC	T
Ss-DNA	CA	GGT	GGA	CAG	GTT	ACT	GAT	TCT	CTC	GGA	CGA	AGA	TTG	GAT	TTC	AGC	AAG	GGA	AGA	ACT	T
Af-DNA	CT	GGT	GGA	CAA	GTG	ACC	GAT	ATC	TAT	GGC	CAG	CGC	TTG	GAT	TTC	AGC	AAG	GGA	CGC	ACT	T
Gd-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Gp-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Ss-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Af-PRO	A	G	G	Q	V	T	D	I	Y	G	Q	R	L	D	F	S	K	G	R	T	
Gd-DNA	TG	GCT	GAG	AAT	AAG	GGT	GTC	GTT	GCC	GCA	CCA	CAG	GCT	CTA	CAC	GCA	CGA	GTC	CTT	GAG	G
Gp-DNA	TG	GCT	GAG	AAT	AAG	GGT	GTC	GTT	GCC	GCA	CCA	CAG	GCT	CTA	CAT	GCA	CGA	GTC	CTT	GAG	G
Ss-DNA	TG	GCT	GAA	AAC	AAG	GGT	GTC	GTT	GCA	GCT	CCC	GCA	GCC	ATT	CAC	GAC	CAC	GTT	TTG	GAG	G
Af-DNA	TG	GCT	GCC	AAC	AAG	GGA	GTC	GTC	GCC	GCT	CCA	GAG	GCC	ATC	CAG	GAC	CAG	GTT	ATT	AGT	G
Gd-PRO	L	A	E	N	K	G	V	V	A	A	P	Q	A	L	H	A	R	V	L	E	
Gp-PRO	L	A	E	N	K	G	V	V	A	A	P	Q	A	L	H	A	R	V	L	E	
Ss-PRO	L	A	E	N	K	G	V	V	A	A	P	A	A	I	H	D	H	V	L	E	
Af-PRO	L	A	A	N	K	G	V	V	A	A	P	E	A	I	Q	D	Q	V	I	S	

Gd-DNA	TT	GTC	AAG	GAG	GTC	CTT	GGC	AAG	AAG	GGA	AAC	CTA	TAG	-----CAGATATGA
Gp-DNA	TT	GTC	AAA	GAA	GTC	CTG	GGC	AAG	AAA	GGA	AAC	CTA	TAG	-----TAGATATGA
Ss-DNA	TG	GTT	AAG	GAG	GTT	TTG	GGG	CCC	AAG	AAA	TAA	---	ATTGTTTCATATATTCGTCACAA	
Af-DNA	CC	GTC	AAG	ACG	GTC	CTG	AAG	CTA	TGA	AGGATGACGCGAACCGGACCAACTGTTGTATCGA				
Gd-PRO	V	V	K	E	V	L	G	K	K	G	N	L	*	
Gp-PRO	V	V	K	E	V	L	G	K	K	G	N	L	*	
Ss-PRO	V	V	K	E	V	L	G	P	K	K	*			
Af-PRO	A	V	K	I	V	L	K	L	*					

Gd-DNA	ACAATTGAAATAGATTCTA---CATATCGTATAACT-ATCCGCTTGG-GACCCTCCAATT
Gp-DNA	ACAGCTG---TAGATTCTA---CATATCGTATAACT-ATCCGCTTGA-GACTCCACAATT
Ss-DNA	ATAAAAGCCATGATACCTTGATCCACTTGTACATCG-ACACCATAGATATATCTACAATA
Af-DNA	ATCACTAAACCCGTTCTAA--ACCTTTGTTAGATCCTGCACGCTTGATGCGCCTAAAAGT

Gd-DNA	CTATGACA-----ATATAAG---AGCAATATAATAC-ATGGACG--AATCGTCTATTT
Gp-DNA	CTATGACA-----ATATAAG---AACAATATAATAC-ATGGACG--AATCGTCTATTT
Ss-DNA	CCTACAAATG-----ACATTAT---CTCTAGAGATTAT-TTGGATATTCATCCACTACTT
Af-DNA	ACATGAGATAGATACCAATTGGGAAAACAGGAGACTCTGCTGGAAT--ATACATGTACAG

Gd-DNA	GATCTTCTTGGCCTTCAACCTGATCGTCTCACCGTTGACGAAAATTCCCTTCCCCT--TG
Gp-DNA	GATCTTCTTGCCTTTCAGCTTGATCGTCTCGCCATTGACGAAGATTCCCTTCCCCT--TA
Ss-DNA	AATCTTCTTATTCTTCAACTTAATCTCCTCTCCATTGACAAAAGATTCCCTTCCCCT--TA
Af-DNA	AAACAGCCCCAGACCCTGTTCCAAGAAAATGCCAAAGTAAAATAGAAACCACCCAGATC

Gd-DNA	TATGGCTCAGGCTTCCCTCCACTGGCGGATTTCCGCAGCAAAGTGCAGAACCCTT---CC
Gp-DNA	TATGGCTCAGGCTTCCCTCCATTACGAATTTCCGCAGCGAACTGGAGAACAACCT---CC
Ss-DNA	TACGGTTCTGGAAGTCTCCACTTTCTAATTTGCGCAGCGAAAAGTAATACAACCT---CC
Af-DNA	ACCGAATCTT-CTTGGCCTTCAGTCTGATTGTCTCTCCGTTACAAAAATACCCTTGCCC

Gd-DNA	TTCTCCGGGCCCT-CCAGCAATATTCTCGTTGGCTGCGGTGTGCTGGCCGTCATGCCCTT
Gp-DNA	TTCTCTGGGCCCT-CCAGCAATATTCTCGTTGGCTGCGGTGTGCTAGCCGTCATGCCCTT
Ss-DNA	TTCTCTGGTCCTT-CTAACAATATACGTGTAGGTTGTGGTGTGCTCGCTTTCACAAATCT
Af-DNA	TTGTAAGGCTCTGGCTTCCGCCATTCTC-TGATTTCCGCCGCGAATTGTGTACAAACGTT

Gd-DNA	CGGCACTGGCAACTCGA-TAGGATGTGAGTAG 744
Gp-DNA	CGGCACTGGCAACTCGA-TTGGATGTGAGTAC 741

Ss-DNA TGGAACGGGTAATTTCGA-TAGGATGAGAGTAC 759
 Af-DNA TTTGTCTGACTCCCTCAAGCAGAATACGAGTAG 775

DHC1 (Cytoplasmic dynein heavy chain): 418 bases aligned (Ss = *Sclerotinia sclerotiorum*, Bf = *Botryotinia fuckeliana*)

Ss-DNA	GAT	GCT	GAA	TAC	CTA	GAT	CCA	ATC	CTT	AAC	CAC	GTT	CTT	AAC	AAA	GAG	TAT	CAA	AAG	ACT	60
Bf-DNA	GAT	GCC	GAA	TAC	CTG	GAC	CCA	ATT	CTT	AAC	CAC	GTT	CTC	AAC	AAA	GAG	TAC	CAA	AAG	ACT	60
Gd-DNA	GAT	GCC	GAG	CAT	TTG	GAT	CCA	ATC	CTT	AAC	CAC	GTC	CTC	AAC	AAG	GAA	TAC	CAA	AAG	ACT	60
Gp-DNA	GAT	GCC	GAG	CAT	TTG	GAT	CCG	ATC	CTT	AAT	CAT	GTC	CTC	AAC	AAG	GAG	TAC	CAA	AAG	ACT	60
Ss-PRO	D	A	E	Y	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Bf-PRO	D	A	E	Y	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Gd-PRO	D	A	E	H	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Gp-PRO	D	A	E	H	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	

Ss-DNA	GGT	GGA	CGT	GTT	CTT	ATT	CAG	CTT	GGT	AAG	CAA	GAA	ATT	GAC	TTT	TCG	CCC	GCA	TTT	AAG	120
Bf-DNA	GGT	GGG	CGT	GTT	CTC	ATC	CAG	CTT	GGG	AAG	CAA	GAA	ATC	GAT	TTC	TCG	CCC	GCA	TTC	AAG	120
Gd-DNA	GGT	GGA	CGT	GTC	CTC	ATC	CAG	CTC	GGT	AAA	CAA	GAG	ATC	GAT	TTC	TCC	CCA	GCC	TTC	AAG	120
Gp-DNA	GGC	GGG	CGT	GTT	CTC	ATC	CAG	CTT	GGC	AAA	CAA	GAA	ATC	GAT	TTC	TCC	CCA	GCC	TTC	AAG	120
Ss-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Bf-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Gd-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Gp-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	

Ss-DNA	ATC	TAC	CTT	TCC	ACT	AGA	GAT	CCA	TCT	GCA	ACA	TTC	GCA	CCG	GAT	ATT	TGC	AGT	CGG	ACA	180
Bf-DNA	ATT	TAC	CTT	TCC	ACC	AGA	GAT	CCA	TCT	GCA	ACA	TTC	GCA	CCG	GAC	ATT	TGC	AGT	CGC	ACA	180
Gd-DNA	ATC	TAC	CTC	TCG	ACC	AGA	GAT	CCA	TCT	GCT	ACG	TTT	GCA	CCA	GAC	ATA	TGC	AGT	CGC	ACA	180
Gp-DNA	ATC	TAT	CTC	TCA	ACC	AGA	GAT	CCA	TCT	GCT	ACA	TTT	GCA	CCA	GAT	GTA	TGC	AGT	CGC	ACA	180
Ss-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Bf-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Gd-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Gp-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	V	C	S	R	T	

Ss-DNA	ACG	TTT	GTC	AAT	TTC	ACT	GTC	ACA	CAA	AGC	AGT	TTA	CAA	ACA	CAG	TCA	CTT	AAT	GAC	GTC	240
Bf-DNA	ACA	TTT	GTT	AAT	TTC	ACA	GTC	ACA	CAG	AGT	AGT	TTG	CAA	ACA	CAG	TCA	CTC	AAT	GAC	GTT	240

Gd-DNA	ACT	TTC	GTC	AAT	TTC	ACC	GTC	ACC	CAG	AGC	AGT	CTC	CAA	ACG	CAA	TCA	TTG	AAC	GAA	GTC	240
Gp-DNA	ACC	TTC	GTG	AAT	TTC	ACT	GTC	ACC	CAG	AGC	AGT	CTC	CAA	ACA	CAA	TCA	TTG	AAC	GAA	GTC	240
Ss-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	D	V	
Bf-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	D	V	
Gd-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	E	V	
Gp-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	E	V	
Ss-DNA	CTC	AAA	TCT	GAG	CGA	CCT	GAT	GTG	GAT	GAG	AGG	CGC	TCA	AAT	CTC	ATC	AAA	TTA	CAG	GGT	300
Bf-DNA	CTC	AAA	TCC	GAA	CGA	CCT	GAT	GTG	GAC	GAG	AGA	CGC	TCT	AAT	CTC	ATC	AAG	TTA	CAA	GGC	300
Gd-DNA	CTG	AAA	TCT	GAG	CGA	CCT	GAC	GTG	GAT	GAG	CGA	AGA	TCC	AAC	CTG	ATC	AAA	TTA	CAG	GGA	300
Gp-DNA	CTG	AAA	TCT	GAG	CGA	CCT	GAC	GTG	GAT	GAA	CGA	AGA	TCC	AAC	CTG	ATC	AAA	TTG	CAG	GGA	300
Ss-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Bf-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Gd-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Gp-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Ss-DNA	GAA	TTC	AAA	GTT	CAT	CTT	AGA	CAG	CTC	GAG	AAA	CGC	TTG	TTG	CAA	GCA	TTG	AAC	GAA	TCA	360
Bf-DNA	GAA	TTC	AAA	GTT	CAC	CTC	AGG	CAG	CTC	GAG	AAG	CGC	TTG	CTG	CAA	GCC	CTG	AAC	GAA	TCA	360
Gd-DNA	GAA	TTC	AAG	GTC	CAT	CTT	CGC	CAA	TTG	GAG	AAG	CGT	CTT	TTG	CAA	GCT	TTG	AAC	GAG	TCC	360
Gp-DNA	GAA	TTC	AAG	GTC	CAC	CTT	CGC	CAA	TTG	GAG	AAG	CGT	CTT	TTG	CAG	GCT	TTG	AAC	GAG	TCC	360
Ss-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Bf-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Gd-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Gp-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Ss-DNA	CGT	GGC	AAT	ATT	CTC	GAT	GAT	GAT	AAC	GTC	ATT	GAA	ACT	CTC	GAA	ACT	TTG	AAG	AAG	G	418
Bf-DNA	CGT	GGC	AAT	ATT	CTT	GAT	GAT	GAC	AAC	GTC	ATT	GAA	ACT	CTT	GAG	ACT	TTG	AAG	AAG	G	418
Gd-DNA	CGT	GGC	AAT	ATC	TTG	GAT	GAT	GAC	AAC	GTC	ATT	GAG	ACT	CTC	GAG	ACG	TTG	AAG	AAG	G	418
Gp-DNA	CGT	GGT	AAT	ATC	TTG	GAT	GAT	GAC	AAC	GTT	ATT	GAA	ACT	CTC	GAA	ACG	TTG	AAG	AAG	G	418
Ss-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Bf-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Gd-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Gp-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		

GPHN (Gephyrin): ~300 bases aligned; the alignment starts with non-coding miscellaneous feature

Gd-DNA	TA	AGC	TCT	AGC	GGA	TCT	CAC	GCT	GGC	CAT	CAC	GGC	TAT	GGT	CAC	GGT	CAC	GAC	CA	303
Gp-DNA	TA	GGC	TCT	GGT	GGA	GCT	CAT	GCT	GGA	CAT	CAT	GGC	CAC	AGC	CAT	GGT	CAC	GGC	CA	318
Nh-DNA	TA	TCA	GGT	GGA	AAG	CCC	CAA	CCT	GCT	GCC	AGC	CAC	AGT	CAC	GGA	TGC	CAC	AGA	CA	324
Ac-DNA	TA	GCC	CCC	AAT	GAT	CCG	CGC	TCG	GAA	AGT	CAA	GGA	CAG	CAG	CAT	GAT	CAC	CAT	CA	354
Gd-PRO	I	S	S	S	G	S	H	A	G	H	H	G	Y	G	H	G	H	D		
Gp-PRO	I	G	S	G	G	A	H	A	G	H	H	G	H	S	H	G	H	G		
Nh-PRO	L	S	G	G	K	P	Q	P	A	A	S	H	S	H	G	C	H	H		
Ac-PRO	V	A	P	N	D	P	R	S	E	S	Q	G	Q	Q	H	D	H	H		

PCS (Peroxisomal-coenzyme A synthetase): ~480 bases aligned; Alignment shows the exonic region and a predicted intronic region (Ac = *Aspergillus clavatus*; Ao = *Arthroderma otae*)

Gd-DNA										GTA	CCC	TTG	ACA	CAC	A
Gp-DNA										GTG	CCC	TTG	ACA	CAC	A
Ac-DNA										GTT	CCC	CTG	ACG	CAC	A
Ao-DNA										GTA	CCG	CTC	TCA	CAT	A
Gd-PRO										V	P	L	T	H	
Gp-PRO										V	P	L	T	H	
Ac-PRO										V	P	L	T	H	
Ao-PRO										V	P	L	S	H	

Gd-DNA	GG	AAT	TTG	ACG	AGG	ACA	ATG	AGTATGCA--AGCCCCGCTAGTGGCTAGTGGGAGATTCTCA
Gp-DNA	GG	AAT	TTG	ACA	AGG	ACT	ATG	AGTATGTA--AATCCGCCCGTGG-----GAGATTTCCA
Ac-DNA	AG	AAC	CTG	ACC	ACT	AGC	ATG	AGTGAGTAC--AACATCCCTGTGT-----GATGTAACTG
Ao-DNA	AA	AAC	CTG	ACC	AGG	ACA	ATG	AGTGGGTGTTGGCTAGTTTTGTTG-----GAGATTTTTTA
Gd-PRO	R	N	L	T	R	T	M	
Gp-PRO	R	N	L	T	R	T	M	
Ac-PRO	K	N	L	T	T	S	M	
Ao-PRO	K	N	L	T	R	T	M	

Gd-DNA	----	ATTGCTAA-CA--ATT-GACA-GAG	AAC	ATC	CAG	GCA	ACA	TAT	GAG	TTG	AGC	CCT	G
Gp-DNA	----	ATTGCTAA-CA--ATTTGGCA-GAG	AAC	ATA	CAG	GCA	ACA	TAT	GAG	CTG	AGC	CCT	G
Ac-DNA		GAAGACCACTGA-CGCGGTATCACAAGAC	AAC	ATC	CGG	GCT	ACA	TAT	AAG	TTG	ACC	CCC	G
Ao-DNA		TTGTCATGCTAAATACATTCTCGTTAGGA	AAC	ATC	CAA	GCT	ACA	TAC	TCT	CTG	ACG	GGT	A
Gd-PRO			N	I	Q	A	T	Y	E	L	S	P	
Gp-PRO			N	I	Q	A	T	Y	E	L	S	P	

Ac-PRO
Ao-PRO

N I R A T Y K L T P
N I Q A T Y S L T C

Gd-DNA CT GAC CGA ACC ATG CTT GTC ATG CCT CTT TTC CAC GTC CAC GGC CTT CTC GCC GGG CTC
Gp-DNA CT GAC CGA ACC ATG CTC GTC ATG CCT CTT TTC CAC GTC CAC GGC CTT CTT GCC GGG TTC
Ac-DNA AG GAT CGC ACC TAC TTG GTG ATG CCT CTA TTC CAC GTC CAC GGC CTG TTG GCC GGA TTC
Ao-DNA AT GAC CGA ACT TAT CTT GTT ATG CCG CTC TTC CAC GTC CAC GGC CTT CTC GCC GCT TTC
Gd-PRO A D R T M L V M P L F H V H G L L A G L
Gp-PRO A D R T M L V M P L F H V H G L L A G F
Ac-PRO E D R T Y L V M P L F H V H G L L A G F
Ao-PRO N D R T Y L V M P L F H V H G L L A A F

Gd-DNA CTC GCC CCT CTT CTT TCC GGA GGC TCT GTC GTT GTC CCT GCC AAG TTC AGC GCC ACT ACC
Gp-DNA CTT GCC CCT CTA CTT TCC GGA GGG TCC GTC GTT GTC CCT GCC AAG TTC AGC GCC ACT ACT
Ac-DNA CTC GCC CCC CTT TTG TCT GGA GGC TCC GTA ATT GTG CCT CCC AGA TTC TCC GCA TCG GAG
Ao-DNA CTC GCC CCG TTA CAG TCT GGA GGG TCC GTC GTT GTG CCT CCC AAG TTC TCT GCT ACC GAT
Gd-PRO L A P L L S G G S V V V P A K F S A T T
Gp-PRO L A P L L S G G S V V V P A K F S A T T
Ac-PRO L A P L L S G G S V T V P P R F S A S E
Ao-PRO L A P L Q S G G S V V V P P K F S A T D

Gd-DNA TTC TGG GAG GAT TTC ATC ACG CAT AAA GCC AAC TGG TAC ACT GCT GTG CCC ACC ATC CAC
Gp-DNA TTC TGG GAA GAC TTT ATC AAT TAT AAA GCT AAC TGG TAC ACT GCT GTG CCC ACC ATC CAC
Ac-DNA TTC TGG GCG GAT TTC GTT GGA TTC CAC GCG AAC TGG TAC ACA GCT GTG CCT ACG ATC CAT
Ao-DNA TTC TGG TCG GAT TTC ATC ACG TAC AAG GCC AAC TGG TAT ACG GCG GTG CCG ACC ATA CAC
Gd-PRO F W E D F I T H K A N W Y T A V P T I H
Gp-PRO F W E D F I N Y K A N W Y T A V P T I H
Ac-PRO F W A D F V G F H A N W Y T A V P T I H
Ao-PRO F W S D F I T Y K A N W Y T A V P T I H

Gd-DNA CAG ATT CTC CTC AGA AAC CCT CCT CCG TCC ACC AAG CCC AAC ATT CGA TTC ATT CGC TCT
Gp-DNA CAG ATC CTT CTC AGA AAC CCA CCC CCG TCA GCC AAA CCT AAC ATT CGA TTT ATC CGG TCC
Ac-DNA CAG ATC CTC CTT AAG ACA CCG CTG CCG AAC CCC ATT CCC AAG ATC CGG TTC ATT CGC TCA
Ao-DNA CAG ATC CTA CTC AAG CAT CCA TTC CCA TCT CCC ATG CCA AAG ATC CGT TTC GTC CGC TCT
Gd-PRO Q I L L R N P P P S T K P N I R F I R S
Gp-PRO Q I L L R N P P P S A K P N I R F I R S
Ac-PRO Q I L L K T P L P N P T P K I R F I R S
Ao-PRO Q I L L K H P F P S P M P K I R F V R S

Gd-DNA	TGC	TCG	TCG	CCT	CTT	TCG	CCA	ACA	ACC	TTC	CAC	CAG	CTT	GAG	GAG	CAG	TAC	AAT	GCC	CCT
Gp-DNA	TGC	TCG	TCT	CCT	TTA	TCG	CCA	ACA	ACC	TTT	TAC	CAA	CTC	CAG	GAG	CAG	TAC	AAT	GCT	CCT
Ac-DNA	TGC	TCA	TCG	CCG	CTG	TCG	CCA	AAG	ACT	TTC	GAG	GAT	CTG	GAA	AAG	ACG	TTC	AAG	GCC	CCC
Ao-DNA	TGC	TCG	TCA	CCG	CTG	TCT	CCC	AAG	ACA	TTC	CAC	GAA	ATA	GAA	CGT	GCA	TTC	AAT	GCT	CCG
Gd-PRO	C	S	S	P	L	S	P	T	T	F	H	Q	L	E	E	Q	Y	N	A	P
Gp-PRO	C	S	S	P	L	S	P	T	T	F	Y	Q	L	Q	E	Q	Y	N	A	P
Ac-PRO	C	S	S	P	L	S	P	K	T	F	E	D	L	E	K	T	F	K	A	P
Ao-PRO	C	S	S	P	L	S	P	K	T	F	H	E	I	E	R	A	F	N	A	P

Gd-DNA	GTT	CTC	GAG	GCA	TAT	GCC	ATG	ACT	GAA	GCC	GCC	CAT	CAA	ATG	ACA	TCC	AGC	CCT	CTC	CCA	484
Gp-DNA	GTC	CTC	GAG	GCA	TAT	GCC	ATG	ACG	GAA	GCT	GCC	CAC	CAA	ATG	ACC	TCC	AAC	CCA	CTT	CCA	478
Ac-DNA	GTC	CTG	GAA	GCG	TAC	GCG	ATG	ACC	GAG	GCT	TCG	CAC	CAG	ATG	ACC	AGC	AAC	CCT	CTC	CCG	486
Ao-DNA	GTT	CTC	GAA	GCA	TAT	GCC	ATG	ACC	GAA	GCC	TCA	CAT	CAA	ATG	ACA	AGC	AAC	CCT	CTA	CCG	488
Gd-PRO	V	L	E	A	Y	A	M	T	E	A	A	H	Q	M	T	S	S	P	L	P	
Gp-PRO	V	L	E	A	Y	A	M	T	E	A	A	H	Q	M	T	S	N	P	L	P	
Ac-PRO	V	L	E	A	Y	A	M	T	E	A	S	H	Q	M	T	S	N	P	L	P	
Ao-PRO	V	L	E	A	Y	A	M	T	E	A	S	H	Q	M	T	S	N	P	L	P	

POB3 (FACT complex subunit): ~400 bases aligned; The alignment starts with non-coding miscellaneous feature (Va = *Verticillium albo-atrum*, Gg = *Glomerella graminicola*)

Gd-DNA	--CAATTGGCGCA-----CCCTCTAACCT-ATG-----TA	CAG	GAC	---	TTC	GAC	CG
Gp-DNA	--CGATTGGCGCA-----CCTTCTAACGT-ATG-----TA	CAG	GAC	---	TTC	GAC	CG
Va-DNA	CGCGACACCCGCA-----TCATCCAGCTCGACGGCTTCC-CG	CAG	GAC	GAG	TTC	GAG	CG
Gg-DNA	CCCAGTAAGTGGGGGAAGCCGAGCTAATTGAACACCCGGCGTG	CAG	GAC	---	TAC	GAG	CG
Gd-PRO		Q	D	-	F	D	R
Gp-PRO		Q	D	-	F	D	R
Va-PRO		Q	D	E	F	E	R
Gg-PRO		Q	D	-	Y	E	R

Gd-DNA	C	CTG	ACG	AAA	GTA	TTC	AAG	AAC	TGG	TAC	AGC	ACG	AAC	CTC	GAG	ACG	AAG	GAG	CAC	GCA	TT
Gp-DNA	C	CTG	ACG	AAA	GTG	TTC	AAG	AAC	TGG	TAC	AGC	ACG	AAC	CTC	GAG	ACG	AAG	GAA	CAC	GCA	TT
Va-DNA	C	CTG	TCG	AAG	CTC	TTC	AAA	AAC	TGG	TAC	AGC	ACG	ACC	CTC	GAG	AAC	AAG	GAG	CAC	GCC	CT
Gg-DNA	C	CTC	GCA	AAG	ATT	TTC	AAG	AAT	TGG	TAC	AGC	ACC	GCC	CTC	GAG	AAT	AAG	GAG	CAC	GCC	CT
Gd-PRO		L	T	K	V	F	K	N	W	Y	S	T	N	L	E	T	K	E	H	A	L

Gp-PRO	L	T	K	V	F	K	N	W	Y	S	T	N	L	E	T	K	E	H	A	L
Va-PRO	L	S	K	L	F	K	N	W	Y	S	T	T	L	E	N	K	E	H	A	L
Gg-PRO	L	A	K	I	F	K	N	W	Y	S	T	A	L	E	N	K	E	H	A	L

Gd-DNA	A	CGA	GGA	TGG	AAC	TGG	GGC	AAG	GCG	GAA	TTC	GGA	AAG	GCG	GAA	TTG	GCA	TTC	AAC	GTG	CA
Gp-DNA	A	CGA	GGA	TGG	AAC	TGG	GGG	AAA	GCG	GAG	TTC	GGA	AAG	GCG	GAG	CTG	GCA	TTC	AAT	GTG	CA
Va-DNA	G	CGC	GGC	TGG	AAC	TGG	GGC	AAG	GCG	GAG	TTC	GGC	AAG	GCT	GAG	CTG	TCC	TTC	AAC	GTG	CA
Gg-DNA	G	AGA	GGA	TGG	AAC	TGG	GGC	AAG	GCC	GAA	TTC	GGA	AAG	GCC	GAG	CTT	TCC	TTC	AAC	GTC	CA
Gd-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	A	F	N	V	Q	
Gp-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	A	F	N	V	Q	
Va-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	S	F	N	V	Q	
Gg-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	S	F	N	V	Q	

Gd-DNA	G	AAC	AGA	CCT	GCG	TTT	GAG	ATC	CCC	TAC	TCG	GAG	ATC	TCG	AAT	ACG	AAT	TTG	GCT	GGG	AA
Gp-DNA	G	AAC	AGA	CCT	GCG	TTT	GAA	ATT	CCT	TAC	TCG	GAG	ATC	TCG	AAT	ACG	AAT	TTG	GCT	GGA	AA
Va-DNA	G	AAT	CGT	CCG	GCC	TTT	GAG	GTG	CCC	TAC	TCG	GAA	ATC	TCC	AAC	ACC	AAC	CTC	GCT	GGC	CG
Gg-DNA	G	AAC	CGA	CCT	GCT	TTT	GAA	ATC	CCT	TAC	TCC	GAG	ATC	TCA	AAT	ACC	AAC	CTG	GCA	GGT	CG
Gd-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	K	
Gp-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	K	
Va-PRO	N	R	P	A	F	E	V	P	Y	S	E	I	S	N	T	N	L	A	G	R	
Gg-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	R	

Gd-DNA	G	AAC	GAG	GTG	GCG	GTT	GAG	TTC	TCG	TTG	CCG	GCT	GGT	---	GGC	GAT	GAG	GGC	GCA	AAC	G
Gp-DNA	G	AAC	GAG	GTG	GCA	GTC	GAG	TTT	TCG	TTG	CCG	GCG	GGT	---	GGC	GAC	GAG	GGC	GCA	AAC	G
Va-DNA	C	AAC	GAG	GTC	GCC	GTC	GAG	TTT	GCC	GCC	CCC	ACC	GAC	GAG	AAC	GAC	ACA	GGC	ACC	AAC	G
Gg-DNA	C	AAC	GAA	GTC	GCC	GTC	GAA	TTC	TCT	GCC	CCG	ACG	GAC	CAG	AAC	GAT	ACC	GGC	ACG	AAT	G
Gd-PRO	N	E	V	A	V	E	F	S	L	P	A	G	-	G	D	E	G	A	N		
Gp-PRO	N	E	V	A	V	E	F	S	L	P	A	G	-	G	D	E	G	A	N		
Va-PRO	N	E	V	A	V	E	F	A	A	P	T	D	E	N	D	T	G	T	N		
Gg-PRO	N	E	V	A	V	E	F	S	A	P	T	D	Q	N	D	T	G	T	N		

Gd-DNA	GA	AGC	TTG	GGT	GGT	GCG	AAG	GGG	AAG	GGG	AAG	AAG	GCT	GGC	GCG	GGG	AAG	GAT	CAG	TTG	G	359
Gp-DNA	GA	AGC	TTG	GGC	GGT	GCG	AAG	GGG	AAG	GGC	AAG	AAG	GCC	GGC	GCA	GGG	AAG	GAT	CAA	TTA	G	393
Va-DNA	GG	ACT	CTC	GAC	GGT	GCG	CGT	GGC	AAG	GGC	AAG	AAG	GCG	GGT	GCT	GGC	AAG	GAC	CAG	CTC	G	459
Gg-DNA	GC	CAC	TTG	GGC	GGC	GCG	CGA	GGA	AAG	GGC	AAG	AAG	GCC	GGA	GCC	GGC	AAA	GAT	CAG	CTC	G	465
Gd-PRO	G	S	L	G	G	A	K	G	K	G	K	K	A	G	A	G	K	D	Q	L		
Gp-PRO	G	S	L	G	G	A	K	G	K	G	K	K	A	G	A	G	K	D	Q	L		
Va-PRO	G	T	L	D	G	A	R	G	K	G	K	K	A	G	A	G	K	D	Q	L		

Gg-PRO G **H** L G G A R G K G K K A G A G K D Q L

SRP72 (Signal recognition particle protein 72): ~400 bases aligned; Region shown include 5' UTR and 5' region of the protein (Ss = *Sclerotinia sclerotiorum*, Ad = *Ajellomyces dermatiditis*)

Gd-DNA CTAAATATACATATACATGGAATGAAACATATGCCGCGCATATAATACATATGATATCAGCTTACTCAAGTGCGCCCAAT
 Ss-DNA GCCGCGCTAGCTCAGCAGTTGATCGCTTTTTGACACCATCTCCATATCGCATGGCTACAGTAAATAGGAACCCATCGCCCTA
 Gp-DNA GGAGATATACATACACATGGACTGAAATATATATGGCCTCGCATATAATCAACATATCAGTTTACTCAAGTGCGCCTAATA
 Ad-DNA TTATTCCGCAACCTTCTTTCTTTTTTATTTCTTTAAACAATCCTTTTTCGGGAGCCAGTGCGGCGCCTGAACAGCCCTTGAA

Gd-DNA CTC GCT AGC ATG GCG TCC AAC CCC ACC GCT ACG TTG AGC AAA CTA CTC GGC TCA GCA ACT A
 Ss-DNA GAG TTT AAA ATG GCC --- GAT CAA ACA GCA ACG CTC AGC GCC CTC CTT CGT AAT TCT TCA A
 Gp-DNA CTC GCT AGC ATG GCG TCC AAC CCC ACC GCT ACC TTG AGC AAA CTC CTC GGC TCA GCA ACT A
 Ad-DNA CTT CTC CGT ATG GCG --- --- --- ACC CAG AGC ATC AGT GCG TTG GTT CAG CGA AGC ACA A
 Gd-PRO M A S N P T A T L S K L L G S A T
 Ss-PRO M A - D Q T A T L S **A** L L **R** **N** **S** **S**
 Gp-PRO M A S N P T A T L S K L L G S A T
 Ad-PRO M A - - - T **Q** **S** I S **A** L **V** **Q** **R** **S** T

Gd-DNA TG GAG GAC CAT GAG GAG ATT CTG AGA GCC GCC AAT GCC GTT CTC AAG AAG TCG AAA ACA A
 Ss-DNA TT ACA GAC CAT GAA GAG ATC CTC AAA GCT ACA AAT GAC GTA TTA AAG ACT TCT AAA CTC G
 Gp-DNA TC GAT GAC CAC GAG GAG GTT CTG AGA GCC GCC AAT GCT ATT CTC AAG AAG TCG AAA ACA G
 Ad-DNA TC GAC GAC CAT GAA GAA GTC ATC AAA GCT TGC AAT GCG GTA CTG AAA ACG TCC AAA AAC G
 Gd-PRO **M** **E** D H E E I L R A A N A V L K K S K T
 Ss-PRO I **T** D H E E I L **K** A **T** N **D** V L K **T** S K **L**
 Gp-PRO I D D H E E **V** L R A A N A **I** L K K S K T
 Ad-PRO I D D H E E **V** **I** K A **C** N A V L K **T** S K **N**

Gd-DNA AC CAG GAT GCG CTG CGT ACT CGC GTT ATT GCA CTC CTC AAG CTA GAC CGC TAC GCA GAT G
 Ss-DNA AC CCC GAT GCC TTG CAT ACC CGC GCT ATT GCT CTC CTC AAA CTT GAT CGA TTC GAC GAT G
 Gp-DNA AC CAG GAT GCG CTA CGT ACT CGT GTC ATT GCG CTG CTT AAG CTA GAC CGC TAC GCA GAT G
 Ad-DNA AT CTC AAT GCC CTC CAT GTA AAA ACT GTT GCC CTG GTC AAA TTG GAC CGT TTC GAA GAT G
 Gd-PRO **N** Q D A L R T R V I A L L K L D R Y A D
 Ss-PRO D **P** D A L **H** T R **A** I A L L K L D R **F** **D** D
 Gp-PRO D Q D A L R T R V I A L L K L D R Y A D
 Ad-PRO D **L** **N** A L **H** **V** **K** **T** **V** A L **V** K L D R **F** **E** D

Gd-DNA	CC	CTC	CGC	GCC	CTC	GAC	GAC	GGG	GGC	GAA	GCT	CTC	AGC	GAA	AGC	TGC	CAC	GTT
Ss-DNA	CA	CTA	AAA	GCC	CTC	GAC	GAA	GGT	GGA	GAT	AAA	TTG	GCT	TCT	CAA	TGT	ATT	CTC
Gp-DNA	CT	CTC	CGC	GCC	CTC	GAC	GAC	GGG	GGA	GAT	GCT	CTC	AGC	GAA	ATC	TGC	CAC	GTT
Ad-DNA	CG	ATT	CGA	GTG	ATC	GAG	GAT	GGC	GGG	GAT	GCG	CTG	AAA	AAG	AAA	GTC	CCT	CTG
Gd-PRO	A	L	R	A	L	D	D	G	G	E	A	L	S	E	S	C	H	V
Ss-PRO	A	L	K	A	L	D	E	G	G	D	K	L	A	S	Q	C	I	L
Gp-PRO	A	L	R	A	L	D	D	G	G	D	A	L	S	E	I	C	H	V
Ad-PRO	A	I	R	V	I	E	D	G	G	D	A	L	K	K	K	V	P	L

Gd-DNA	GAG	AAG	TCG	TAC	GCC	CTT	TAC	AAA	ACA	GGC	CAG	CTC	GAG	GCC	GCA	CAG	AAG	ATT	TTC	G
Ss-DNA	GAA	CGC	GCT	TAT	GCT	CTC	TAC	AAG	ACA	GGG	AAA	CTG	GCA	GAT	GCG	GCG	AAA	GTA	TGT	G
Gp-DNA	GAG	AAA	TCG	TAC	GCG	CTT	TAC	AAA	ACA	GGC	CAA	CTC	GAG	GCC	GCA	CAG	AAA	ATT	TTC	G
Ad-DNA	GAA	TGG	TCT	TAC	GCT	TTA	TAT	AAG	GTC	GGG	CAA	TTA	GAA	GAT	GCG	ATA	AAA	CTG	GCC	G
Gd-PRO	E	K	S	Y	A	L	Y	K	T	G	Q	L	E	A	A	Q	K	I	F	
Ss-PRO	E	R	A	Y	A	L	Y	K	T	G	K	L	A	D	A	A	K	V	C	
Gp-PRO	E	K	S	Y	A	L	Y	K	T	G	Q	L	E	A	A	Q	K	I	F	
Ad-PRO	E	W	S	Y	A	L	Y	K	V	G	Q	L	E	D	A	I	K	L	A	

VPS13 (Vacuolar protein sorting-associated protein): ~545 bases aligned (Ss = *Sclerotinia sclerotiorum*, Bf = *Botryotinia fuckeliana*)

Gd-DNA	GG	ATC	CCA	GAT	AGT	GGT	GGA	GCG	TTT	AGA	CTC	ACG	ATT	TAC	AGT	CCT	TAC	ATC	ATT	TTG	A
Gp-DNA	GA	ATC	CCA	GAC	GGC	GGT	GGA	GCG	TTT	AGA	CTC	ACA	ATT	TAC	AGT	CCT	TAT	GTC	ATT	TTG	A
Ss-DNA	AG	ATT	CCA	GAT	AGT	GGA	GGA	GCA	TTT	AGA	GTA	ACT	GTC	TAC	AGT	CCT	TAC	GTT	ATC	CTA	A
Bf-DNA	AG	ATT	CCA	GAT	AGT	GGT	GGA	GCT	TTT	AGA	GTC	ACC	GTA	TAC	AGT	CCT	TAT	GTA	ATC	CTA	A
Gd-PRO		I	P	D	S	G	G	A	F	R	L	T	I	Y	S	P	Y	I	I	L	
Gp-PRO		I	P	D	G	G	A	F	R	L	T	I	Y	S	P	Y	V	V	I	L	
Ss-PRO		I	P	D	S	G	G	A	F	R	V	T	V	Y	S	P	Y	V	I	L	
Bf-PRO		I	P	D	S	G	G	A	F	R	V	T	V	Y	S	P	Y	V	I	L	

Gd-DNA	AT	AAA	ACT	GGC	CTG	GAT	ATC	AAT	ATC	AAG	GCC	AAG	TCG	TTA	CTG	CAG	CAA	GCA	CGG	ACG	G
Gp-DNA	AT	AAA	ACA	GGC	CTG	GAT	ATC	AAC	ATC	AAG	GCG	AAG	TCG	TTA	CTG	CAG	CAA	GCG	CGG	ACT	G
Ss-DNA	AT	AAA	ACC	GGA	CTG	GAG	ATC	AAC	ATC	AAA	CAG	AAG	TCA	TTG	TTG	CAG	CAA	GCA	AAG	ACG	G
Bf-DNA	AT	AAG	ACT	GGC	CTA	GAG	ATC	AAC	ATC	AAA	CAA	AAA	TCG	CTA	TTG	CAG	CAA	GCA	AAG	ACG	G
Gd-PRO	N	K	T	G	L	D	I	N	I	K	A	K	S	L	L	Q	Q	A	R	T	
Gp-PRO	N	K	T	G	L	D	I	N	I	K	A	K	S	L	L	Q	Q	A	R	T	

Ss-PRO	N	K	T	G	L	E	I	N	I	K	Q	K	S	L	L	Q	Q	A	K	T	
Bf-PRO	N	K	T	G	L	E	I	N	I	K	Q	K	S	L	L	Q	Q	A	K	T	
Gd-DNA	CG	GCT	GGC	CAG	AAG	GTA	GTG	CGC	GAT	CTC	CTT	GGG	GAT	GAC	GAA	CAG	AAG	GCG	CTG	CCT	C
Gp-DNA	CA	GCT	GGA	CAG	AAG	GTC	GTG	CGC	GAT	CTC	CTC	AGC	GAT	GAC	GAG	CAG	AAG	GCG	CTG	CCT	T
Ss-DNA	CG	GCC	GGT	CAA	GGG	TTT	CGT	ACA	GAT	TCG	GCT	GAT	TCA	GAA	CGG	CGT	AAG	GCA	CTA	CCT	T
Bf-DNA	CA	GCA	GGT	CAA	GGG	TTC	CAT	ACT	GAC	TCA	GTC	GAT	TCT	GAA	CGG	CGC	AAA	GCA	CTA	CCA	T
Gd-PRO	A	A	G	Q	K	V	V	R	D	L	L	G	D	D	E	Q	K	A	L	P	
Gp-PRO	A	A	G	Q	K	V	V	R	D	L	L	S	D	D	E	Q	K	A	L	P	
Ss-PRO	A	A	G	Q	G	F	R	T	D	S	A	D	S	E	R	R	K	A	L	P	
Bf-PRO	A	A	G	Q	G	F	H	T	D	S	V	D	S	E	R	R	K	A	L	P	
Gd-DNA	TG	ATG	TTT	GCG	TTC	AGT	GGC	GAC	GAC	CAG	CGC	AAC	CGC	GTC	ATC	CTC	AAA	GTC	GGC	GAG	T
Gp-DNA	TG	ATG	TTT	GCG	TTC	AGT	GGC	GAC	GAC	CAG	CGT	AAC	CGC	GTC	ATC	CTC	AAA	GTT	GGC	GAG	T
Ss-DNA	AT	ATG	TTC	GCA	TAT	GGC	GGA	GAT	GAT	CAA	AGG	AAT	CGT	GCT	ATA	TTG	AAG	GTT	GGC	GAC	T
Bf-DNA	AC	ATG	TTC	GCG	TAT	GGC	GGA	GAT	GAT	CAA	CGA	AAT	CGT	GCT	TTA	ATG	AAG	GTC	GGT	GAC	T
Gd-PRO	L	M	F	A	F	S	G	D	D	Q	R	N	R	V	I	L	K	V	G	E	
Gp-PRO	L	M	F	A	F	S	G	D	D	Q	R	N	R	V	I	L	K	V	G	E	
Ss-PRO	Y	M	F	A	Y	G	G	D	D	Q	R	N	R	A	I	L	K	V	G	D	
Bf-PRO	Y	M	F	A	Y	G	G	D	D	Q	R	N	R	A	L	M	K	V	G	D	
Gd-DNA	CG	AAC	TGG	AGT	AAA	CCG	CAG	AGT	TTC	GAC	GCC	ATT	GGC	AGC	ACA	ATC	GAT	GTG	GTT	CTA	C
Gp-DNA	CG	AAC	TGG	AGT	AAA	CCG	CAG	AGT	TTC	GAC	GCC	ATT	GGC	AGC	ACG	ATT	GAT	GTT	GTT	CTA	C
Ss-DNA	CG	AAT	TGG	AGT	AAA	CCA	CAA	AGT	CTG	GAT	GCC	ATC	GGT	AGT	AAT	GTC	GAT	GTT	GTT	TTA	T
Bf-DNA	CC	AAC	TGG	AGT	AAA	CCG	CAA	AGT	TTG	GAT	GCT	ATC	GGC	AGC	AAT	GTA	GAT	GTC	ATA	TTG	C
Gd-PRO	S	N	W	S	K	P	Q	S	F	D	A	I	G	S	T	I	D	V	V	L	
Gp-PRO	S	N	W	S	K	P	Q	S	F	D	A	I	G	S	T	I	D	V	V	L	
Ss-PRO	S	N	W	S	K	P	Q	S	L	D	A	I	G	S	N	V	D	V	V	L	
Bf-PRO	S	N	W	S	K	P	Q	S	L	D	A	I	G	S	N	V	D	V	I	L	
Gd-DNA	CG	TCA	GCA	ACT	CAG	AAT	ACT	GAG	ATC	CAT	GTT	GGA	ATC	AGC	ATC	GAG	AAT	GGA	GAC	GGG	A
Gp-DNA	CC	TCG	GCA	ACT	CAG	AAT	ACC	GAG	ATA	CAC	GTT	GGA	ATC	AGT	ATC	GAG	AAC	GGG	GAC	GGG	A
Ss-DNA	CT	TCT	TCT	AAA	AAC	AAC	ACC	GAG	ATA	CAC	GTG	GGC	ATC	AAT	GTT	GAA	TCA	GGA	GAG	GGC	A
Bf-DNA	CT	TCC	TCA	AAG	AAC	AAT	ACC	GAA	ATT	CAT	GTA	GGT	ATC	AGT	GTC	GAA	GCA	GGA	GAG	GGT	A
Gd-PRO	P	S	A	T	Q	N	T	E	I	H	V	G	I	S	I	E	N	G	D	G	
Gp-PRO	P	S	A	T	Q	N	T	E	I	H	V	G	I	S	I	E	N	G	D	G	
Ss-PRO	S	S	S	K	N	N	T	E	I	H	V	G	I	N	V	E	S	G	E	G	

Bf-PRO	P	S	S	K	N	N	T	E	I	H	V	G	I	S	V	E	A	G	E	G	
Gd-DNA	AA	TAC	AAG	ATG	ACC	AAG	GTC	GTT	ACG	CTT	GCG	CCG	AGA	TTT	GTG	CTG	AAG	AAT	CGC	ATG	A
Gp-DNA	AA	TAC	AAG	ATG	ACC	AAG	GTC	GTT	ACG	CTT	GCA	CCG	AGA	TTT	GTG	CTG	AAG	AAT	CGC	ATG	A
Ss-DNA	AA	TAC	AAA	ATG	ACG	AAG	GTA	GTC	ACT	CTT	GCT	CCC	CGC	TTT	GTT	CTG	AAG	AAT	CAG	ATG	A
Bf-DNA	AA	TAT	AAG	ATG	ACG	AAG	GTT	GTC	ACA	CTT	GCT	CCT	CGC	TTT	GTT	TTA	AAG	AAT	CAA	ATG	A
Gd-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	R	M	
Gp-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	R	M	
Ss-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	Q	M	
Bf-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	Q	M	
Gd-DNA	GC	GAG	GAA	ATC	AGC	GCC	AGG	GAA	CCT	GGA	TCG	TCG	GAG	CTT	ATG	ACT	TTG	AAG	CGG	GGA	G
Gp-DNA	GT	GAG	GAA	ATC	AGC	GCC	AGG	GAA	CCT	GGA	TCG	TCG	GAG	CTC	ATG	ACT	TTG	AAG	CCG	GGA	G
Ss-DNA	AC	GAG	GAA	ATA	AAT	GTC	AGG	GAA	CCC	GGG	TCG	TCT	GAA	CTC	TGG	ACT	TTG	AAG	CCA	CAG	G
Bf-DNA	GC	GAA	GAA	CTA	AAC	GTT	AGA	GAG	CCT	GGG	TCA	TCT	GAA	CTT	TGG	ACT	TTG	AAG	CCA	CAA	G
Gd-PRO	S	E	E	I	S	A	R	E	P	G	S	S	E	L	M	T	L	K	R	G	
Gp-PRO	S	E	E	I	S	A	R	E	P	G	S	S	E	L	M	T	L	K	P	G	
Ss-PRO	N	E	E	I	N	V	R	E	P	G	S	S	E	L	W	T	L	K	P	Q	
Bf-PRO	S	E	E	L	N	V	R	E	P	G	S	S	E	L	W	T	L	K	P	Q	
Gd-DNA	AA	CTG	AAG	GCT	CTT	CAC	TTC	CTT	CAA	AAG	TCG	GCG	GTT	AAG	CAA	CTG	TGC	CTT	TGC	TTC	C
Gp-DNA	AA	CTG	AAA	GCT	CTT	CAC	TTC	CTT	CAA	AAG	TCG	GCG	GTG	AAG	CAA	CTG	TGC	CTT	TGC	TTC	C
Ss-DNA	CC	CTA	GAA	CCT	CTT	CAT	TTC	CTC	CAG	AAG	AGT	CCC	GTC	AAG	CAA	CTT	ACG	CTA	TGC	TTC	C
Bf-DNA	CT	TTA	GAG	CCT	CTT	CAT	TTC	CTT	CAG	AAG	AGT	CAT	GTA	AAA	CAA	CTC	ACG	ATG	TGC	TTC	C
Gd-PRO	E	L	K	A	L	H	F	L	Q	K	S	A	V	K	Q	L	C	L	C	F	
Gp-PRO	E	L	K	A	L	H	F	L	Q	K	S	A	V	K	Q	L	C	L	C	F	
Ss-PRO	A	L	E	P	L	H	F	L	Q	K	S	P	V	K	Q	L	T	L	C	F	
Bf-PRO	A	L	E	P	L	H	F	L	Q	K	S	H	V	K	Q	L	T	M	C	F	
Gd-DNA	CC	GGC																			
Gp-DNA	CG	GGC																			
Ss-DNA	CT	GGA																			
Bf-DNA	CA	GGA																			
Gd-PRO	P	G																			
Gp-PRO	P	G																			
Ss-PRO	P	G																			
Bf-PRO	P	G																			