

TABLE S1: *Aspergillus* isolates used in this study. *Isolates used for genomic analyses.

| Species/Morphotype | Isolate | Country | Substrate | Aflatoxin | Reference |
|--------------------|-------------|--------------|-------------|-----------|---|
| <i>A. flavus</i> S | AF12* | US | Soil | B | Cotty 1989 |
| | AF70* | US | Soil | B | Cotty 1989 |
| | AZS* | US | Soil | B | P. J. Cotty, personal communication |
| | AF42 | US | Cotton seed | B | Cotty 1989 |
| | TXA35-K | US | Soil | B | Probst et al. 2012 |
| | TXD7-D | US | Soil | B | Probst et al. 2012 |
| | TXEC08BY1-J | US | Maize | B | Probst et al. 2012 |
| | TX08ECBY1-G | US | Maize | B | Probst et al. 2012 |
| | Sanpatong22 | Thailand | Soil | B | Ehrlich et al. 2007; Probst et al. 2012 |
| | Yuin20 | Thailand | Soil | B | Ehrlich et al. 2007; Probst et al. 2012 |
| <i>A. flavus</i> L | 54-P | Rwanda | Maize | B | Probst et al. 2014 |
| | BS01* | US | Cotton seed | B | P. J. Cotty, personal communication |
| | DV901* | US | Cotton seed | B | P. J. Cotty, personal communication |
| | MC04* | US | Cotton seed | B | P. J. Cotty, personal communication |
| | TBA1-A | US | Maize | B | Probst et al. 2014 |
| | AF13 | US | Soil | B | Cotty 1989 |
| | Ak29G-01 | Nigeria | Soil | B | Probst et al. 2014 |
| | MIZAN14 | Phillippines | Soil | B | Probst et al. 2014 |
| | Sukhothai16 | Thailand | Soil | B | Ehrlich et al. 2007; Probst et al. 2014 |
| | BN001-B | Benin | Soil | None | Probst et al. 2014 |
| | BF1-A | Burkina Faso | Maize | B | Probst et al. 2014 |
| | Cam53-D | Cameroon | Maize | None | Probst et al. 2014 |
| | CONGO E1-E | Congo | Maize | None | Probst et al. 2014 |
| | ET48-B | Ethiopia | Maize | None | Probst et al. 2014 |
| | GH2-A | Ghana | Maize | B | Probst et al. 2014 |
| | ML6-B | Mali | Maize | None | Probst et al. 2014 |
| | MZ2-A | Mozambique | Maize | None | Probst et al. 2014 |
| | RW 47-F | Rwanda | Maize | B | Probst et al. 2014 |

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|------------------------------------|------------|--------------|--------|------|--|
| | SN 8-G | Senegal | Maize | None | Probst et al. 2014 |
| | SL5-H | Sierra Leone | Maize | None | Probst et al. 2014 |
| | UG 8-G | Uganda | Maize | None | Probst et al. 2014 |
| | Z15-M | Zambia | Maize | None | Probst et al. 2014 |
| | ZW 4-A | Zimbabwe | Maize | B | Probst et al. 2014 |
| | A5-1 | Australia | Soil | B | Geiser et al. 2000; Probst et al. 2014 |
| | TureganoAQ | Spain | Soil | None | Probst et al. 2014 |
| | TP 4-B | Turkey | Pepper | B | Probst et al. 2014 |
| <i>A. minisclerotigenes</i> | A11611 | Nigeria | Soil | BG | Hesseltine 1970; Probst et al. 2012 |
| | DG4-2 | Australia | Soil | BG | Geiser et al. 2000; Probst et al. 2014 |
| Lineage SBG | A11612 | Nigeria | Soil | BG | Hesseltine 1970; Probst et al. 2012 |
| <i>A. parasiticus</i> | NRRL2999 | Uganda | Soil | BG | Rambo et al 1974; Probst et al. 2012 |

TABLE S2: Protein families (Pfams) expanded in S morphotype genomes and their p-values (< 0.1) from the Pfam enrichment analysis; p-values < 0.05 are in bold.

| Pfam | Name | S morphotype | | | L morphotype | | | p-value |
|---------|---|--------------|------|-----|--------------|-------|------|--------------|
| | | AF12 | AF70 | AZS | BS01 | DV901 | MC04 | |
| PF00391 | PEP-utilising enzyme, mobile domain | 1 | 1 | 1 | 0 | 0 | 0 | |
| PF01326 | Pyruvate phosphate dikinase, PEP/pyruvate binding domain | 1 | 1 | 1 | 0 | 0 | 0 | |
| PF02896 | PEP-utilizing enzyme, TIM barrel domain | 1 | 1 | 1 | 0 | 0 | 0 | |
| PF01126 | Heme oxygenase | 1 | 1 | 1 | 0 | 0 | 0 | |
| PF11402 | Antifungal protein | 1 | 1 | 1 | 0 | 0 | 0 | |
| PF12141 | Protein of unknown function (DUF3589) | 2 | 2 | 2 | 0 | 0 | 0 | 0.015 |
| PF00005 | ABC transporter | 142 | 142 | 142 | 140 | 140 | 134 | |
| PF00006 | ATP synthase alpha/beta family, nucleotide-binding domain | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF00056 | lactate/malate dehydrogenase, NAD binding domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF00067 | Cytochrome P450 | 173 | 171 | 174 | 168 | 163 | 170 | |
| PF00102 | Protein-tyrosine phosphatase | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF00107 | Zinc-binding dehydrogenase | 97 | 95 | 99 | 91 | 93 | 92 | |
| PF00122 | E1-E2 ATPase | 28 | 27 | 28 | 25 | 25 | 25 | |
| PF00132 | Bacterial transferase hexapeptide (six repeats) | 10 | 10 | 10 | 9 | 9 | 9 | |
| PF00205 | Thiamine pyrophosphate enzyme, central domain | 15 | 15 | 15 | 13 | 13 | 13 | |
| PF00306 | ATP synthase alpha/beta chain, C terminal domain | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF00331 | Glycosyl hydrolase family 10 | 8 | 8 | 8 | 6 | 6 | 6 | |
| PF00406 | Adenylate kinase | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF00438 | S-adenosylmethionine synthetase, N-terminal domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF00457 | Glycosyl hydrolases family 11 | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF00581 | Rhodanese-like domain | 11 | 11 | 11 | 10 | 10 | 10 | |
| PF00672 | HAMP domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF00689 | Cation-transporting ATPase, C-terminus | 13 | 12 | 13 | 11 | 11 | 11 | |
| PF00698 | Acyl transferase domain | 39 | 41 | 41 | 38 | 37 | 37 | |
| PF00920 | Dehydratase family | 8 | 8 | 8 | 5 | 5 | 5 | |
| PF00999 | Sodium/hydrogen exchanger family | 10 | 10 | 10 | 8 | 8 | 8 | |

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|---------|---|----|----|----|----|----|----|------|
| PF01040 | UbiA prenyltransferase family | 5 | 5 | 5 | 4 | 3 | 3 | |
| PF01061 | ABC-2 type transporter | 44 | 44 | 44 | 41 | 40 | 41 | |
| PF01172 | Shwachman-Bodian-Diamond syndrome (SBDS) protein | 4 | 4 | 4 | 2 | 2 | 2 | |
| PF01222 | Ergosterol biosynthesis ERG4/ERG24 family | 13 | 13 | 12 | 10 | 10 | 11 | |
| PF01287 | Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold | 4 | 4 | 4 | 3 | 3 | 3 | |
| PF01370 | NAD-dependent epimerase/dehydratase family | 35 | 35 | 35 | 33 | 34 | 33 | |
| PF01496 | V-type ATPase 116kDa subunit family | 2 | 2 | 2 | 1 | 1 | 1 | |
| PF01596 | O-methyltransferase | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF01633 | Choline/ethanolamine kinase | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF01738 | Dienelactone hydrolase family | 9 | 9 | 9 | 8 | 7 | 7 | |
| PF01755 | Glycosyltransferase family 25 (LPS biosynthesis protein) | 2 | 2 | 2 | 1 | 1 | 1 | |
| PF02386 | Cation transport protein | 8 | 8 | 8 | 7 | 7 | 7 | |
| PF02417 | Chromate transporter | 6 | 4 | 4 | 2 | 2 | 2 | 0.06 |
| PF02558 | Ketopantoate reductase PanE/ApbA | 10 | 10 | 10 | 8 | 8 | 8 | |
| PF02714 | Calcium-dependent channel, 7TM region, putative phosphate | 7 | 6 | 7 | 5 | 5 | 5 | |
| PF02772 | S-adenosylmethionine synthetase, central domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF02773 | S-adenosylmethionine synthetase, C-terminal domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF02775 | Thiamine pyrophosphate enzyme, C-terminal TPP binding domain | 15 | 15 | 15 | 13 | 13 | 13 | |
| PF02776 | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain | 15 | 15 | 15 | 13 | 13 | 13 | |
| PF02801 | Beta-ketoacyl synthase, C-terminal domain | 41 | 43 | 43 | 39 | 40 | 39 | |
| PF02866 | Lactate/malate dehydrogenase, alpha/beta C-terminal domain | 3 | 3 | 3 | 2 | 2 | 2 | |
| PF02874 | ATP synthase alpha/beta family, beta-barrel domain | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF02900 | Catalytic LigB subunit of aromatic ring-opening dioxygenase | 4 | 4 | 4 | 3 | 3 | 3 | |
| PF03489 | Saposin-like type B, region 2 | 2 | 2 | 2 | 1 | 1 | 1 | |
| PF04371 | Porphyromonas-type peptidyl-arginine deiminase | 2 | 2 | 2 | 1 | 1 | 1 | |
| PF04622 | ERG2 and Sigma1 receptor like protein | 3 | 3 | 3 | 1 | 2 | 2 | |
| PF04969 | CS domain | 5 | 5 | 5 | 4 | 4 | 4 | |
| PF05183 | RNA-dependent RNA polymerase | 5 | 5 | 5 | 3 | 3 | 3 | |
| PF06422 | CDR ABC transporter | 21 | 21 | 21 | 19 | 18 | 18 | |
| PF07716 | Basic region leucine zipper | 6 | 7 | 6 | 5 | 4 | 5 | |
| PF07859 | alpha/beta hydrolase fold | 35 | 35 | 35 | 33 | 32 | 33 | |

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|---------|--|----|----|----|----|----|----|
| PF07969 | Amidohydrolase family | 3 | 3 | 3 | 2 | 2 | 2 |
| PF08659 | KR domain | 26 | 29 | 28 | 25 | 25 | 24 |
| PF11991 | Tryptophan dimethylallyltransferase | 11 | 11 | 11 | 9 | 9 | 9 |
| PF13086 | AAA domain | 12 | 12 | 12 | 10 | 10 | 11 |
| PF13207 | AAA domain | 2 | 2 | 2 | 1 | 1 | 1 |
| PF13246 | Cation transport ATPase (P-type) | 9 | 7 | 8 | 6 | 6 | 6 |
| PF13347 | MFS/sugar transport protein | 2 | 2 | 2 | 1 | 1 | 1 |
| PF13393 | Histidyl-tRNA synthetase | 3 | 3 | 3 | 2 | 2 | 2 |
| PF13602 | Zinc-binding dehydrogenase | 17 | 20 | 18 | 16 | 15 | 16 |
| PF13857 | Ankyrin repeats (many copies) | 16 | 16 | 15 | 12 | 13 | 13 |
| PF13967 | Late exocytosis, associated with Golgi transport | 6 | 6 | 6 | 5 | 5 | 5 |

TABLE S3: Protein families (Pfams) expanded in L morphotype genomes and their p-values (< 0.1) from the Pfam enrichment analysis; p-values < 0.05 are in bold.

| Pfam | Name | S morphotype | | | L morphotype | | | p-value |
|---------|---|--------------|------|-----|--------------|-------|------|--------------|
| | | AF12 | AF70 | AZS | BS01 | DV901 | MC04 | |
| PF00023 | Ankyrin repeat | 11 | 9 | 14 | 17 | 15 | 17 | 0.058 |
| PF00076 | RNA recognition motif. (aka. RRM, RBD, or RNP domain) | 92 | 87 | 92 | 93 | 93 | 93 | |
| PF00089 | Trypsin | 1 | 1 | 1 | 2 | 2 | 2 | |
| PF00171 | Aldehyde dehydrogenase family | 32 | 32 | 33 | 35 | 36 | 34 | |
| PF00175 | Oxidoreductase NAD-binding domain | 21 | 21 | 21 | 22 | 23 | 22 | |
| PF00202 | Aminotransferase class-III | 14 | 15 | 14 | 17 | 16 | 16 | |
| PF00258 | Flavodoxin | 9 | 9 | 9 | 10 | 10 | 10 | |
| PF00270 | DEAD/DEAH box helicase | 45 | 43 | 45 | 47 | 46 | 47 | |
| PF00324 | Amino acid permease | 30 | 27 | 30 | 31 | 31 | 31 | |
| PF00326 | Prolyl oligopeptidase family | 6 | 6 | 6 | 7 | 7 | 7 | |
| PF00364 | Biotin-requiring enzyme | 10 | 10 | 10 | 11 | 11 | 11 | |
| PF00378 | Enoyl-CoA hydratase/isomerase | 19 | 18 | 19 | 20 | 21 | 20 | |
| PF00441 | Acyl-CoA dehydrogenase, C-terminal domain | 12 | 12 | 12 | 13 | 13 | 13 | |
| PF00487 | Fatty acid desaturase | 10 | 10 | 10 | 12 | 12 | 11 | |
| PF00491 | Arginase family | 6 | 6 | 6 | 8 | 8 | 8 | |
| PF00667 | FAD binding domain | 8 | 8 | 8 | 9 | 9 | 9 | |
| PF00732 | GMC oxidoreductase | 36 | 35 | 36 | 38 | 37 | 37 | |
| PF00854 | POT family | 15 | 15 | 15 | 20 | 19 | 21 | 0.08 |
| PF00890 | FAD binding domain | 9 | 10 | 10 | 11 | 11 | 11 | |
| PF01058 | NADH ubiquinone oxidoreductase, 20 Kd subunit | 2 | 2 | 2 | 3 | 3 | 3 | |
| PF01118 | Semialdehyde dehydrogenase, NAD binding domain | 2 | 2 | 2 | 4 | 3 | 3 | |
| PF01419 | Jacalin-like lectin domain | 1 | 1 | 1 | 2 | 2 | 2 | |
| PF01476 | LysM domain | 14 | 11 | 13 | 21 | 19 | 22 | 0.009 |
| PF01485 | IBR domain, a half RING-finger domain | 4 | 3 | 3 | 6 | 6 | 6 | 0.089 |
| PF01565 | FAD binding domain | 59 | 51 | 59 | 60 | 60 | 60 | |
| PF01593 | Flavin-containing amine oxidoreductase | 20 | 21 | 20 | 23 | 24 | 25 | |

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|---------|--|-----|-----|-----|-----|-----|-----|
| PF01794 | Ferric reductase like transmembrane component | 13 | 12 | 13 | 14 | 15 | 15 |
| PF02136 | Nuclear transport factor 2 (NTF2) domain | 5 | 5 | 5 | 6 | 6 | 6 |
| PF02668 | Taurine catabolism dioxygenase TauD, TfdA family | 24 | 20 | 24 | 25 | 25 | 25 |
| PF02727 | Copper amine oxidase, N2 domain | 6 | 5 | 6 | 7 | 7 | 7 |
| PF02770 | Acyl-CoA dehydrogenase, middle domain | 13 | 14 | 13 | 15 | 15 | 15 |
| PF02771 | Acyl-CoA dehydrogenase, N-terminal domain | 10 | 10 | 10 | 11 | 11 | 12 |
| PF03033 | Glycosyltransferase family 28 N-terminal domain | 6 | 6 | 6 | 7 | 8 | 7 |
| PF03664 | Glycosyl hydrolase family 62 | 2 | 2 | 2 | 3 | 3 | 3 |
| PF04030 | D-arabinono-1,4-lactone oxidase | 2 | 2 | 2 | 3 | 3 | 3 |
| PF04082 | Fungal specific transcription factor domain | 282 | 270 | 281 | 283 | 284 | 285 |
| PF04193 | PQ loop repeat | 17 | 17 | 17 | 18 | 18 | 18 |
| PF04389 | Peptidase family M28 | 13 | 12 | 13 | 14 | 15 | 15 |
| PF05592 | Bacterial alpha-L-rhamnosidase | 11 | 11 | 11 | 12 | 14 | 13 |
| PF05899 | Protein of unknown function (DUF861) | 2 | 2 | 2 | 3 | 3 | 3 |
| PF06202 | Amylo-alpha-1,6-glucosidase | 1 | 1 | 1 | 2 | 2 | 2 |
| PF07264 | Etoposide-induced protein 2.4 (EI24) | 2 | 2 | 2 | 3 | 3 | 3 |
| PF07504 | Fungalysin/Thermolysin Propeptide Motif | 2 | 2 | 2 | 3 | 3 | 3 |
| PF07632 | Protein of unknown function (DUF1593) | 5 | 5 | 5 | 6 | 6 | 6 |
| PF09298 | Fumarylacetoacetate N-terminal | 3 | 2 | 3 | 4 | 4 | 4 |
| PF09365 | Conserved hypothetical protein (DUF2461) | 2 | 2 | 2 | 3 | 3 | 3 |
| PF10165 | Guanine nucleotide exchange factor synembryon | 1 | 1 | 1 | 2 | 2 | 2 |
| PF10294 | Lysine methyltransferase | 7 | 7 | 7 | 8 | 8 | 8 |
| PF11374 | Protein of unknown function (DUF3176) | 6 | 5 | 6 | 7 | 7 | 7 |
| PF11951 | Fungal specific transcription factor domain | 122 | 115 | 122 | 126 | 126 | 126 |
| PF12146 | Serine aminopeptidase, S33 | 1 | 1 | 1 | 2 | 2 | 2 |
| PF12680 | SnoaL-like domain | 2 | 2 | 2 | 3 | 3 | 3 |
| PF12796 | Ankyrin repeats (3 copies) | 194 | 195 | 197 | 206 | 227 | 210 |
| PF13489 | Methyltransferase domain | 26 | 25 | 26 | 28 | 28 | 28 |
| PF13520 | Amino acid permease | 52 | 53 | 52 | 55 | 55 | 57 |
| PF13639 | Ring finger domain | 17 | 16 | 17 | 18 | 18 | 18 |
| PF13738 | Pyridine nucleotide-disulphide oxidoreductase | 21 | 22 | 22 | 25 | 24 | 25 |

0.041

PF14441 OTT_1508-like deaminase

4 4 3 | 6 5 5

TABLE S4: L morphotype proteins encoded by genes present within deleted regions of the S morphotype, using DV901 to represent the L morphotype. Only those with predicted Pfam annotations are listed with their amino acid coordinates for Pfam domains indicated.

| Deleted gene | Pfam ID | Pfam name | Start | End |
|--------------|---------|---|-------|------|
| DV901_09638 | PF01048 | Phosphorylase superfamily | 15 | 291 |
| | PF12796 | Ankyrin repeats (3 copies) | 989 | 1078 |
| | PF12796 | Ankyrin repeats (3 copies) | 1158 | 1251 |
| | PF12796 | Ankyrin repeats (3 copies) | 875 | 977 |
| | PF12796 | Ankyrin repeats (3 copies) | 1082 | 1149 |
| | PF13857 | Ankyrin repeats (many copies) | 1297 | 1351 |
| DV901_10805 | PF01670 | Glycosyl hydrolase family 12 | 45 | 249 |
| DV901_03590* | PF13857 | Ankyrin repeats (many copies) | 1341 | 1385 |
| | PF12796 | Ankyrin repeats (3 copies) | 575 | 645 |
| | PF12796 | Ankyrin repeats (3 copies) | 1491 | 1599 |
| | PF12796 | Ankyrin repeats (3 copies) | 848 | 937 |
| | PF13637 | Ankyrin repeats (many copies) | 977 | 1008 |
| DV901_03591 | PF00120 | Glutamine synthetase, catalytic domain | 118 | 482 |
| DV901_04954* | PF05368 | NmrA-like family | 7 | 225 |
| DV901_04955 | PF00854 | POT family | 327 | 505 |
| | PF00854 | POT family | 172 | 318 |
| DV901_11588 | PF08240 | Alcohol dehydrogenase GroES-like domain | 33 | 97 |
| DV901_11587 | PF08389 | Exportin 1-like protein | 266 | 432 |
| DV901_07543 | PF13637 | Ankyrin repeats (many copies) | 12 | 63 |
| DV901_10657* | PF00067 | Cytochrome P450 | 61 | 492 |
| DV901_02307 | PF04082 | Fungal specific transcription factor domain | 37 | 227 |

*Proteins also identified to be unique to the L morphotype in the morphotype-unique protein analysis (TABLE 10).

TABLE S5: S morphotype proteins encoded by genes present within deleted regions of the S morphotype, using AZS to represent the S morphotype. Only those with predicted Pfam annotations are listed with their amino acid coordinates for Pfam domains indicated.

| Deleted gene | Pfam ID | Pfam name | Start | End |
|--------------|---------|---|-------|------|
| AZS_10233 | PF08244 | Glycosyl hydrolases family 32 C terminal | 419 | 537 |
| AZS_07769 | PF01557 | Fumarylacetoacetate (FAA) hydrolase family | 1 | 187 |
| | PF00501 | AMP-binding enzyme | 222 | 448 |
| AZS_03413 | PF00438 | S-adenosylmethionine synthetase, N-terminal domain | 12 | 106 |
| | PF02773 | S-adenosylmethionine synthetase, C-terminal domain | 211 | 341 |
| | PF02772 | S-adenosylmethionine synthetase, central domain | 126 | 196 |
| AZS_03559 | PF00026 | Eukaryotic aspartyl protease | 727 | 774 |
| | PF00026 | Eukaryotic aspartyl protease | 444 | 697 |
| | PF00248 | Aldo/keto reductase family | 30 | 334 |
| AZS_03412* | PF00107 | Zinc-binding dehydrogenase | 79 | 155 |
| AZS_03557* | PF01565 | FAD binding domain | 22 | 133 |
| AZS_03411* | PF00067 | Cytochrome P450 | 57 | 482 |
| AZS_03556* | PF00248 | Aldo/keto reductase family | 43 | 122 |
| | PF00248 | Aldo/keto reductase family | 122 | 245 |
| AZS_03410 | PF07690 | Major Facilitator Superfamily | 28 | 307 |
| | PF07690 | Major Facilitator Superfamily | 320 | 464 |
| AZS_03558* | PF11905 | Domain of unknown function (DUF3425) | 227 | 321 |
| AZS_00217* | PF00135 | Carboxylesterase family | 2 | 239 |
| AZS_00226* | PF02900 | Catalytic LigB subunit of aromatic ring-opening dioxygenase | 160 | 315 |
| AZS_00227* | PF01494 | FAD binding domain | 11 | 169 |
| | PF01494 | FAD binding domain | 249 | 328 |
| AZS_00218* | PF00135 | Carboxylesterase family | 80 | 243 |
| | PF00135 | Carboxylesterase family | 250 | 552 |
| AZS_04020 | PF00848 | Ring hydroxylating alpha subunit (catalytic domain) | 98 | 154 |
| AZS_06878* | PF14765 | Polyketide synthase dehydratase | 844 | 1148 |
| | PF13602 | Zinc-binding dehydrogenase | 1898 | 2035 |

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|------------|---------|---|------|------|
| | PF00109 | Beta-ketoacyl synthase, N-terminal domain | 1 | 165 |
| | PF08242 | Methyltransferase domain | 1323 | 1430 |
| | PF00550 | Phosphopantetheine attachment site | 2355 | 2420 |
| | PF16197 | Ketoacyl-synthetase C-terminal extension | 294 | 362 |
| | PF02801 | Beta-ketoacyl synthase, C-terminal domain | 174 | 291 |
| | PF08659 | KR domain | 2060 | 2237 |
| | PF00698 | Acyl transferase domain | 451 | 792 |
| AZS_04277* | PF00067 | Cytochrome P450 | 23 | 194 |
| AZS_04445* | PF00732 | GMC oxidoreductase | 2 | 136 |
| | PF05199 | GMC oxidoreductase | 268 | 409 |
| AZS_04446* | PF00732 | GMC oxidoreductase | 3 | 60 |
| AZS_10720 | PF13602 | Zinc-binding dehydrogenase | 2099 | 2236 |
| | PF08240 | Alcohol dehydrogenase GroES-like domain | 1943 | 2011 |
| | PF00550 | Phosphopantetheine attachment site | 2556 | 2617 |
| | PF00698 | Acyl transferase domain | 613 | 940 |
| | PF08242 | Methyltransferase domain | 1518 | 1630 |
| | PF02801 | Beta-ketoacyl synthase, C-terminal domain | 336 | 452 |
| | PF08659 | KR domain | 2260 | 2436 |
| | PF00109 | Beta-ketoacyl synthase, N-terminal domain | 78 | 327 |
| | PF14765 | Polyketide synthase dehydratase | 1010 | 1329 |
| AZS_10718* | PF00067 | Cytochrome P450 | 49 | 474 |
| AZS_10717* | PF07859 | alpha/beta hydrolase fold | 127 | 366 |
| AZS_10719* | PF07690 | Major Facilitator Superfamily | 22 | 403 |
| AZS_10722 | PF01636 | Phosphotransferase enzyme family | 7 | 182 |
| | PF04082 | Fungal specific transcription factor domain | 283 | 487 |
| AZS_05421* | PF01040 | UbiA prenyltransferase family | 62 | 312 |
| AZS_05420 | PF00067 | Cytochrome P450 | 67 | 493 |
| AZS_12891* | PF13857 | Ankyrin repeats (many copies) | 340 | 392 |
| | PF00023 | Ankyrin repeat | 503 | 571 |

*Proteins also identified to be unique to the S morphotype in the morphotype-unique protein analysis (TABLE 9).

TABLE S6: S morphotype-unique proteins with predicted Pfam, CAZy, MEROPS, and SMURF annotations.

| S morphotype-unique genes | | | Annotation | | CAZy ^a | MEROPS ^b | SMURF ^c |
|---------------------------|------------|-----------|------------|---|-------------------|---------------------|--------------------|
| AF12 | AF70 | AZS | Pfam ID | Pfam name | | | |
| AF12_04868 | AF70_01446 | AZS_11530 | PF03171 | 2OG-Fe(II) oxygenase superfamily | | | |
| | | | PF14226 | non-haem dioxygenase in morphine synthesis N-terminal | | | |
| AF12_08060 | AF70_09348 | AZS_08273 | PF13086 | AAA domain 11 | | | |
| | | | PF13087 | AAA domain 12 | | | |
| | | | PF05183 | RNA-dependent RNA polymerase | | | |
| AF12_05761 | AF70_02921 | AZS_06878 | PF00698 | Acyl transferase domain | | | lovF |
| | | | PF02801 | β-ketoacyl synthase, C-terminal domain | | | |
| | | | PF00109 | β-ketoacyl synthase, N-terminal domain | | | |
| | | | PF16197 | Ketoacyl-synthetase C-terminal extension | | | |
| | | | PF08659 | KR domain | | | |
| | | | PF08242 | Methyltransferase domain | | | |
| | | | PF14765 | Polyketide synthase dehydratase | | | |
| | | | PF00550 | Phosphopantetheine attachment site | | | |
| | | | PF13602 | Zinc-binding dehydrogenase | | | |
| AF12_13225 | AF70_12828 | AZS_13022 | PF00406 | Adenylate kinase | | | |
| AF12_08338 | AF70_08552 | AZS_08570 | PF08240 | Alcohol dehydrogenase GroES-like domain | | | |
| | | | PF00107 | Zinc-binding dehydrogenase | | | |
| AF12_05552 | AF70_08618 | AZS_03556 | PF00248 | Aldo/keto reductase family | | | |
| AF12_02647 | AF70_03415 | AZS_10717 | PF07859 | α/β hydrolase fold | CE10 | S09X | bah |
| AF12_04354 | AF70_04122 | AZS_04444 | PF00023 | Ankyrin repeat | | | |
| | | | PF12796 | Ankyrin repeats (3 copies) | | | |
| AF12_12472 | AF70_12718 | AZS_12891 | PF00023 | Ankyrin repeat | | | |
| | | | PF13857 | Ankyrin repeats (many copies) | | | |
| AF12_10042 | AF70_10036 | AZS_11587 | PF12796 | Ankyrin repeats (3 copies) | | | |
| AF12_13125 | AF70_13108 | AZS_01307 | PF12796 | Ankyrin repeats (3 copies) | | | |
| AF12_09918 | AF70_09912 | AZS_06018 | PF11402 | Antifungal protein | | | |
| AF12_06194 | AF70_03533 | AZS_00770 | PF01400 | Astacin (Peptidase family M12A) | | M10B, M12A | |

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|------------|------------|-----------|---------|---|------|------|
| AF12_10480 | AF70_10044 | AZS_12084 | PF00795 | Carbon-nitrogen hydrolase | | |
| AF12_00961 | AF70_01808 | AZS_00217 | PF00135 | Carboxylesterase family | CE10 | S09X |
| AF12_00962 | AF70_01809 | AZS_00218 | PF00135 | Carboxylesterase family | CE10 | S09X |
| AF12_06861 | AF70_11549 | AZS_06389 | PF00135 | Carboxylesterase family | CE10 | S09X |
| AF12_00970 | AF70_01817 | AZS_00226 | PF02900 | Catalytic LigB subunit of aromatic ring-opening dioxygenase | | |
| AF12_08131 | AF70_09419 | AZS_08344 | PF04969 | CS domain | | |
| AF12_02648 | AF70_03416 | AZS_10718 | PF00067 | Cytochrome P450 | | TRI4 |
| AF12_03157 | AF70_07238 | AZS_04277 | PF00067 | Cytochrome P450 | | |
| AF12_05406 | AF70_12346 | AZS_03411 | PF00067 | Cytochrome P450 | | |
| AF12_08673 | AF70_08977 | AZS_09568 | PF00067 | Cytochrome P450 | | |
| AF12_12788 | AF70_13194 | AZS_13126 | PF00067 | Cytochrome P450 | | |
| AF12_12805 | AF70_13211 | AZS_13143 | PF00067 | Cytochrome P450 | | |
| AF12_12793 | AF70_13199 | AZS_13131 | PF00920 | Dehydratase family | | |
| AF12_12794 | AF70_13200 | AZS_13132 | PF00920 | Dehydratase family | | |
| AF12_12795 | AF70_13201 | AZS_13133 | PF00920 | Dehydratase family | | |
| AF12_13145 | AF70_11766 | AZS_11940 | PF01965 | DJ-1/Pfpl family | C56 | |
| AF12_06641 | AF70_13072 | AZS_06171 | PF11807 | Domain of unknown function (DUF3328) | | |
| AF12_05554 | AF70_08620 | AZS_03558 | PF11905 | Domain of unknown function (DUF3425) | | |
| AF12_06190 | AF70_03529 | AZS_00766 | PF06441 | Epoxide hydrolase N terminus | S33 | |
| AF12_13017 | AF70_12836 | AZS_13030 | PF04622 | ERG2 and Sigma1 receptor like protein | | |
| AF12_08335 | AF70_08555 | AZS_08573 | PF01287 | Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold | | |
| AF12_00971 | AF70_01818 | AZS_00227 | PF01494 | FAD binding domain | | |
| AF12_05553 | AF70_08619 | AZS_03557 | PF01565 | FAD binding domain | AA7 | |
| AF12_12785 | AF70_13191 | AZS_13123 | PF01557 | Fumarylacetoacetate (FAA) hydrolase family | | |
| AF12_12803 | AF70_13209 | AZS_13141 | PF01557 | Fumarylacetoacetate (FAA) hydrolase family | | |
| AF12_07169 | AF70_06898 | AZS_07768 | PF04082 | Fungal specific transcription factor domain | | |
| | | | PF00172 | Fungal Zn(2)-Cys(6) binuclear cluster domain | | |
| AF12_12786 | AF70_13192 | AZS_13124 | PF04082 | Fungal specific transcription factor domain | | |
| | | | PF00172 | Fungal Zn(2)-Cys(6) binuclear cluster domain | | |
| AF12_12792 | AF70_13198 | AZS_13130 | PF04082 | Fungal specific transcription factor domain | | |
| AF12_13223 | AF70_12826 | AZS_13020 | PF04082 | Fungal specific transcription factor domain | | |

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|------------|------------|-----------|---------|--|----------|
| | | | PF00172 | Fungal Zn(2)-Cys(6) binuclear cluster domain | |
| AF12_06859 | AF70_11547 | AZS_06387 | PF01755 | Glycosyltransferase family 25 (LPS biosynthesis protein) | GT25 |
| AF12_12802 | AF70_13208 | AZS_13140 | PF00903 | Glyoxalase/Bleomycin resistance protein/Dioxygenase | |
| AF12_04355 | AF70_04123 | AZS_04445 | PF05199 | GMC oxidoreductase C-terminal | AA3 |
| | | | PF00732 | GMC oxidoreductase N-terminal | |
| AF12_04356 | AF70_04124 | AZS_04446 | PF00732 | GMC oxidoreductase N-terminal | |
| AF12_13130 | AF70_13086 | AZS_01312 | PF01126 | Heme oxygenase | |
| AF12_13331 | AF70_10037 | AZS_12077 | PF06985 | Heterokaryon incompatibility protein (HET) | |
| AF12_03478 | AF70_04821 | AZS_05413 | PF14602 | Hexapeptide repeat of succinyl-transferase | |
| AF12_06169 | AF70_02518 | AZS_07288 | PF00857 | Isochorismatase family | |
| AF12_10529 | AF70_03957 | AZS_01207 | PF08659 | KR domain | |
| | | | PF00550 | Phosphopantetheine attachment site | |
| | | | PF13602 | Zinc-binding dehydrogenase | |
| AF12_13118 | AF70_13239 | AZS_13298 | PF02866 | lactate/malate dehydrogenase, α/β C-terminal domain | |
| | | | PF00056 | lactate/malate dehydrogenase, NAD binding domain | |
| AF12_04742 | AF70_04509 | AZS_05944 | PF06293 | Lipopolysaccharide kinase (Kdo/WaaP) family | PUF |
| AF12_08333 | AF70_08557 | AZS_08575 | PF01823 | MAC/Perforin domain | |
| AF12_02650 | AF70_03418 | AZS_10719 | PF07690 | Major Facilitator Superfamily | C3H1.06c |
| AF12_12796 | AF70_13202 | AZS_13134 | PF07690 | Major Facilitator Superfamily | |
| AF12_12797 | AF70_13203 | AZS_13135 | PF07690 | Major Facilitator Superfamily | |
| AF12_04602 | AF70_04369 | AZS_05803 | PF13847 | Methyltransferase domain | |
| AF12_04864 | AF70_01451 | AZS_11534 | PF13649 | Methyltransferase domain | |
| AF12_02370 | AF70_03145 | AZS_06651 | PF05729 | NACHT domain | |
| AF12_12450 | AF70_07768 | AZS_05004 | PF01370 | NAD-dependent epimerase/dehydratase family | |
| AF12_08371 | AF70_08519 | AZS_10384 | PF13450 | NAD(P)-binding Rossmann-like domain | |
| AF12_07914 | AF70_00904 | AZS_03162 | PF00024 | PAN domain | |
| AF12_13117 | AF70_13240 | AZS_13299 | PF00391 | PEP-utilizing enzyme, mobile domain | |
| | | | PF02896 | PEP-utilizing enzyme, TIM barrel domain | |
| | | | PF01326 | Pyruvate phosphate dikinase, PEP/pyruvate binding domain | |
| AF12_07167 | AF70_06895 | AZS_07766 | PF01048 | Phosphorylase superfamily | |
| AF12_12013 | AF70_12620 | AZS_13244 | PF01048 | Phosphorylase superfamily | |

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|------------|------------|-----------|---------|--|------|
| AF12_06189 | AF70_03528 | AZS_13362 | PF00069 | Protein kinase domain | |
| AF12_13312 | AF70_13336 | AZS_01325 | PF00069 | Protein kinase domain | |
| AF12_06576 | AF70_13021 | AZS_06107 | PF11374 | Protein of unknown function (DUF3176) | |
| AF12_13128 | AF70_13105 | AZS_01310 | PF12141 | Protein of unknown function (DUF3589) | GT91 |
| AF12_09917 | AF70_09911 | AZS_06019 | PF12311 | Protein of unknown function (DUF3632) | |
| AF12_13044 | AF70_13190 | AZS_13273 | PF00856 | SET domain | |
| AF12_08672 | AF70_08978 | AZS_09569 | PF00106 | short chain dehydrogenase | |
| AF12_12448 | AF70_07766 | AZS_05002 | PF00106 | short chain dehydrogenase | |
| AF12_08334 | AF70_08556 | AZS_08574 | PF01172 | Shwachman-Bodian-Diamond syndrome (SBDS) protein | |
| AF12_08340 | AF70_08550 | AZS_08568 | PF01172 | Shwachman-Bodian-Diamond syndrome (SBDS) protein | |
| AF12_08342 | AF70_08548 | AZS_08566 | PF00999 | Sodium/hydrogen exchanger family | |
| AF12_12755 | AF70_12001 | AZS_01349 | PF06687 | SUR7/Pall family | |
| AF12_06860 | AF70_11548 | AZS_06388 | PF03151 | Triose-phosphate Transporter family | |
| AF12_03470 | AF70_04813 | AZS_05421 | PF01040 | UbiA prenyltransferase family | |
| AF12_05407 | AF70_12345 | AZS_03412 | PF00107 | Zinc-binding dehydrogenase | |
| AF12_08168 | AF70_09455 | AZS_08379 | PF00107 | Zinc-binding dehydrogenase | |
| AF12_00870 | AF70_01718 | AZS_00126 | | | CE5 |
| AF12_12226 | AF70_01587 | AZS_12586 | | | PUF |
| AF12_02646 | AF70_03414 | AZS_10716 | | | PUF |
| AF12_02652 | AF70_03420 | AZS_10721 | | | PUF |
| AF12_05073 | AF70_01242 | AZS_02819 | | | PUF |
| AF12_05074 | AF70_01241 | AZS_02820 | | | PUF |

^aCAZy - auxiliary activities (AA), carbohydrate esterases (CE), glycosyltransferases (GT).

^bMEROPS - prolyl aminopeptidase family/serine peptidase (S33), PfPI endopeptidase family/cysteine peptidase (C56), metallopeptidase (M10), astacin/adamalysin family/metallopeptidase (M12), prolyl oligopeptidase family/serine peptidase (S09).

^cAnnotated by SMURF to be similar to the following proteins: Lovastatin diketide synthase LovF (*Aspergillus terreus*) (lovF), acetyl-hydrolase (*Streptomyces hygroscopicus*) (bah), Trichodiene oxygenase (*Fusarium sporotrichioides*) (TRI4), Uncharacterized_transporter C3H1.06c (*Schizosaccharomyces pombe*) (C3H1.06c), protein of unknown function (PUF).

TABLE S7: L morphotype-unique proteins with predicted Pfam, CAZymes, MEROPS, and SMURF annotations.

| L morphotype-unique genes | | | Annotation | | | CAZy ^a | MEROPS ^b | SMURF ^c |
|---------------------------|-------------|------------|------------|--|--|-------------------|---------------------|--------------------|
| BS01 | DV901 | MC04 | Pfam ID | Pfam name | | | | |
| BS01_12639 | DV901_12528 | MC04_02044 | PF00441 | Acyl-CoA dehydrogenase, C-terminal domain | | | | |
| | | | PF02770 | Acyl-CoA dehydrogenase, middle domain | | | | |
| | | | PF02771 | Acyl-CoA dehydrogenase, N-terminal domain | | | | |
| BS01_13233 | DV901_00148 | MC04_09345 | PF08240 | Alcohol dehydrogenase GroES-like domain | | | | |
| | | | PF13602 | Zinc-binding dehydrogenase | | | | |
| BS01_13086 | DV901_03501 | MC04_11055 | PF00248 | Aldo/keto reductase family | | | norB | |
| BS01_03302 | DV901_03140 | MC04_00889 | PF12697 | Alpha/beta hydrolase family | | | | |
| BS01_12688 | DV901_04439 | MC04_02090 | PF12695 | Alpha/beta hydrolase family | | | | |
| BS01_12110 | DV901_04433 | MC04_02096 | PF13520 | Amino acid permease | | | S33 | |
| BS01_03033 | DV901_03590 | MC04_10968 | PF12796 | Ankyrin repeats (3 copies) | | | | |
| | | | PF13637 | Ankyrin repeats (many copies) 4 | | | | |
| | | | PF13857 | Ankyrin repeats (many copies) 5 | | | | |
| BS01_12416 | DV901_04939 | MC04_11989 | PF12796 | Ankyrin repeats (3 copies) | | | | |
| BS01_00005 | DV901_09207 | MC04_06115 | PF13637 | Ankyrin repeats (many copies) | | | | |
| | | | PF01048 | Phosphorylase superfamily | | | | |
| BS01_09349 | DV901_12786 | MC04_12384 | PF00491 | Arginase family | | | | |
| BS01_00297 | DV901_01296 | MC04_06405 | PF09365 | Conserved hypothetical protein (DUF2461) | | | | |
| BS01_10978 | DV901_09227 | MC04_08572 | PF07883 | Cupin domain | | | | |
| BS01_07386 | DV901_10657 | MC04_06594 | PF00067 | Cytochrome P450 | | | | |
| BS01_00081 | DV901_09130 | MC04_06190 | PF00270 | DEAD/DEAH box helicase | | | | |
| | | | PF00076 | RNA recognition motif (aka. RRM, RBD, or RNP domain) | | | | |
| BS01_09346 | DV901_12784 | MC04_12386 | PF00378 | Enoyl-CoA hydratase/isomerase | | | | |
| BS01_13239 | DV901_13248 | MC04_13132 | PF05705 | Eukaryotic protein of unknown function (DUF829) | | | | |
| BS01_03630 | DV901_03468 | MC04_01221 | PF01565 | FAD binding domain | | | | |
| BS01_12111 | DV901_04432 | MC04_02097 | PF01593 | Flavin-containing amine oxidoreductase | | | | |
| BS01_10980 | DV901_09229 | MC04_08570 | PF09298 | Fumarylacetoacetate N-terminal | | | | |
| | | | PF01557 | Fumarylacetoacetate (FAA) hydrolase family | | | | |

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|------------|-------------|------------|--------------------|---|----------|
| BS01_09329 | DV901_12368 | MC04_11211 | PF04082 PF00172 | Fungal specific transcription factor domain Fungal Zn(2)-Cys(6) binuclear cluster domain | C1F7.11c |
| BS01_09344 | DV901_12782 | MC04_12388 | PF11951 PF00172 | Fungal specific transcription factor domain Fungal Zn(2)-Cys(6) binuclear cluster domain | |
| BS01_11831 | DV901_01850 | MC04_11826 | PF11951 | Fungal specific transcription factor domain | |
| BS01_12108 | DV901_04435 | MC04_02094 | PF11951 PF00172 | Fungal specific transcription factor domain Fungal Zn(2)-Cys(6) binuclear cluster domain | |
| BS01_12115 | DV901_04428 | MC04_02101 | PF04082 | Fungal specific transcription factor domain | |
| BS01_12220 | DV901_01516 | MC04_05924 | PF04082 | Fungal specific transcription factor domain | |
| BS01_13072 | DV901_03487 | MC04_11068 | PF04082 PF00172 | Fungal specific transcription factor domain Fungal Zn(2)-Cys(6) binuclear cluster domain | |
| BS01_09385 | DV901_12825 | MC04_12344 | PF07504 | Fungalysin/Thermolysin Propeptide Motif | |
| BS01_02533 | DV901_05174 | MC04_03151 | PF10294 | Lysine methyltransferase | |
| BS01_01386 | DV901_04831 | MC04_02983 | PF01476 | LysM domain | CBM50 |
| BS01_05997 | DV901_02224 | MC04_05543 | PF01476 | LysM domain | CBM50 |
| BS01_12401 | DV901_04954 | MC04_12003 | PF05368 | NmrA-like family | |
| BS01_07818 | DV901_11317 | MC04_01734 | PF14441 | OTT_1508-like deaminase | |
| BS01_07819 | DV901_11318 | MC04_01735 | PF14441 | OTT_1508-like deaminase | |
| BS01_09384 | DV901_12824 | MC04_12345 | PF04389 | Peptidase family M28 | M28E |
| BS01_00331 | DV901_01263 | MC04_06440 | PF11374 | Protein of unknown function (DUF3176) | |
| BS01_11832 | DV901_01851 | MC04_11827 | PF04479 | RTA1-like protein | |
| BS01_13234 | DV901_00147 | MC04_09346 | PF00106 | Short-chain dehydrogenase | |
| BS01_12219 | DV901_01517 | MC04_05923 | PF12680 | SnoaL-like domain | |
| BS01_12909 | DV901_12554 | MC04_02020 | PF00083 | Sugar (and other) transporter | |
| BS01_10177 | DV901_12102 | MC04_07220 | PF00089 | Trypsin | S01A |
| BS01_06107 | DV901_02339 | MC04_05427 | | | PUF |

^aCAZy - carbohydrate-binding modules (CBM).

^bMEROPS - prolyl aminopeptidase family/serine peptidase (S33), aminopeptidase Y family/metallopeptidase (M28), chymotrypsin family/serine peptidase (S01).

^cAnnotated by SMURF to be similar to the following proteins: Norsolorinic acid reductase B (*Aspergillus parasiticus*) (norB), Uncharacterized transcriptional regulatory_protein C1F7.11c (*Schizosaccharomyces pombe*) (C1F7.11c), protein of unknown function (PUF).

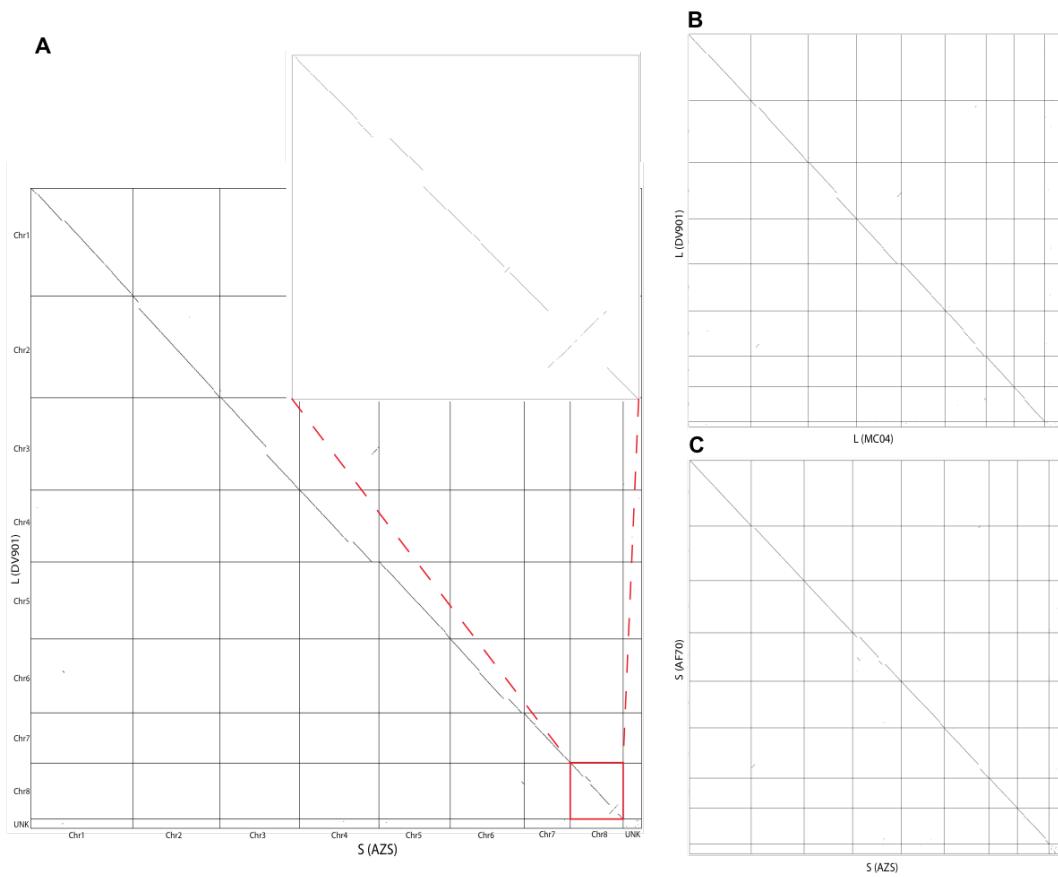


FIGURE S1: Synteny analysis showing a >530 kb inversion on chromosome 8 between S and L morphotype genomes. (A) Synteny analysis of S vs L morphotype genomes (AZS vs DV901) using Symap (Soderlund et al., 2011) reveals an inversion on chromosome 8. The inversion was present in all other S vs L morphotype comparisons as well. (B and C) Synteny analyses of L vs L morphotype genomes (MC04 vs DV901) and S vs S morphotype genomes (AZS vs AF70) show the absence of the inversion on chromosome 8 in comparisons within a morphotype. The inversion was absent in all other L vs L morphotype and S vs S morphotype comparisons as well. Chromosome numbers in B and C are the same as in A.

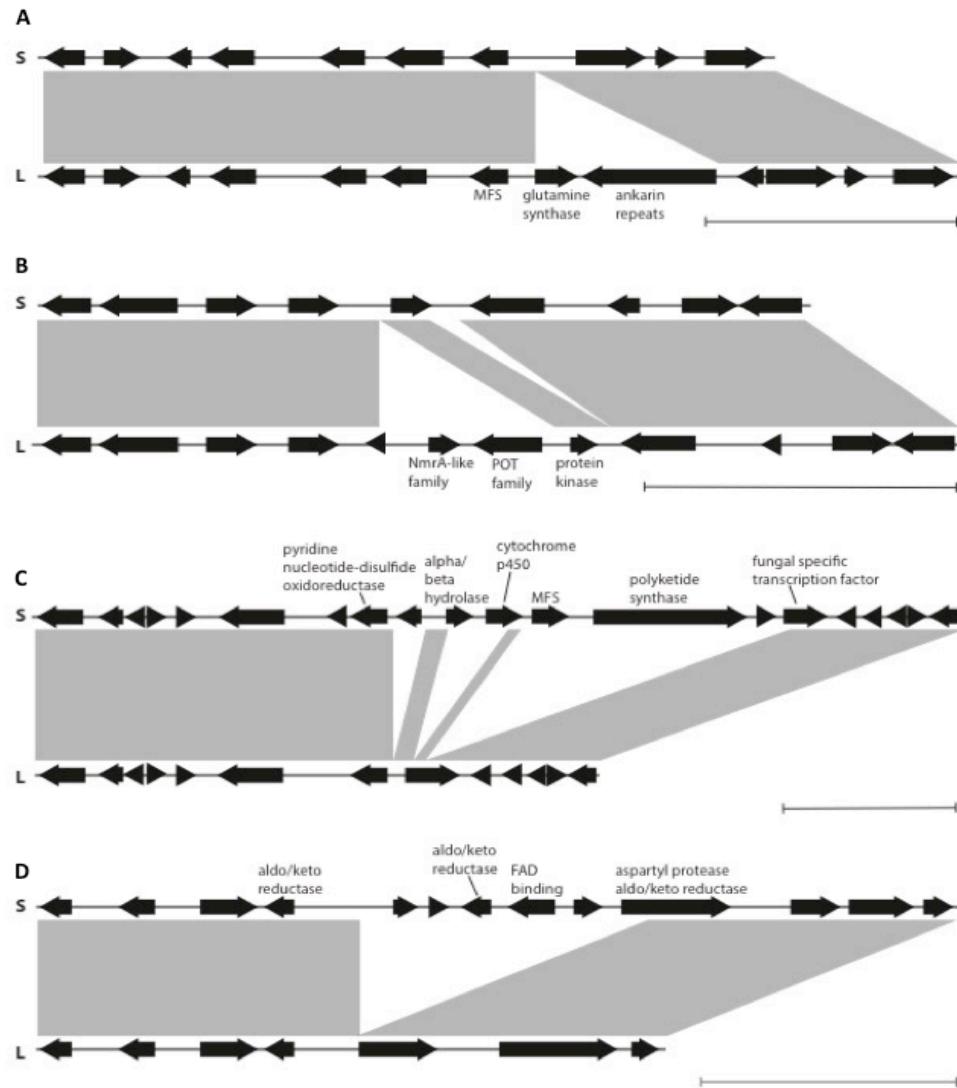


FIGURE S2: Schematic diagrams of deleted regions in S and L morphotype genomes. The bar on the bottom right of each diagram represents a length of 10 kb. Pfam annotations are indicated for genes encoding a protein with a predicted protein family. (A and B) The two largest deletions in S morphotype genomes. (C and D) The two largest deletions in L morphotype genomes.