

Figure S4. Alignment of pathway regulator DsAfIR from 19 *D. septosporum* strains

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0_NZE10      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
1_ALP3       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
2_AUS4       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
3_BHU1       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
4_CAN3       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
5_CHI17      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
6_COLN       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
7_COLS       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
8_DEN1       1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
9_ECU13      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
10_GUA1      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
11_GRE1      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
12_GUA2      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
13_NZE2      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
14_NZE8      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
15_RUS1      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
16_SAF4      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
17_SLV1      1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
18_USA12     1 MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRTSHATAQK0000R00000SQQEAADRRVSQS 100
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0_NZE10      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
1_ALP3       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
2_AUS4       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
3_BHU1       101 AVPVANMLPDVDEFISPMSLQESSILSPALMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
4_CAN3       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
5_CHI17      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
6_COLN       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
7_COLS       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
8_DEN1       101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
9_ECU13      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
10_GUA1      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
11_GRE1      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
12_GUA2      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
13_NZE2      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
14_NZE8      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
15_RUS1      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
16_SAF4      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
17_SLV1      101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
18_USA12     101 AVPVANMLPDVDEFISPMSLQESSILSPTLMPDLSTSGSQAGLDQWNSDLWSTMFAPNEPSSNNTPANTMQTHGGNGNDIDHLFNDLTSYSMLGEPTDTA 200
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0_NZE10 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMTNCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
1_ALP3 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
2_AUS4 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
3_BHU1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
4_CAN3 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
5_CHI17 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
6_COLN 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
7_COLS 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
8_DEN1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
9_ECU13 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
10_GUA1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
11_GRE1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
12_GUA2 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
13_NZE2 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMTNCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
14_NZE8 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMTNCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
15_RUS1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
16_SAF4 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
17_SLV1 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
18_USA12 201 MSNQHTHTFSDTSSSISPFDQLTSVSDMGSQDFSNIDL SMANCTPAIQQSVEPANCLTVALGFMTQLCATASSSCTMPGSHNGNTTLPTIDSVITENRQ 300
*****v*****

0_NZE10 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
1_ALP3 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
2_AUS4 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
3_BHU1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
4_CAN3 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
5_CHI17 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
6_COLN 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSDRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
7_COLS 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSDRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
8_DEN1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
9_ECU13 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
10_GUA1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSDRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
11_GRE1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
12_GUA2 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSDRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
13_NZE2 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
14_NZE8 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
15_RUS1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
16_SAF4 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
17_SLV1 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
18_USA12 301 IVDQIVKILECPCSHDEYLLTIVHLVVFVMAWYAAAAREKPSLAEEINWTDQQSGRPRSRTHSEEVLRFPPSIDGYSSDGDNGRMAAQLVLSSELHRVQ 400
*****c*****v*****

0_NZE10	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
1_ALP3	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
2_AUS4	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
3_BHU1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
4_CAN3	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
5_CHI17	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
6_COLN	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
7_COLS	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
8_DEN1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
9_ECU13	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
10_GUA1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
11_GRE1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
12_GUA2	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
13_NZE2	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
14_NZE8	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
15_RUS1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
16_SAF4	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
17_SLV1	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479
18_USA12	401	RLVNLLSQRLEGVRLRNHVASSGSSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS	479

Figure S4. Alignment of pathway regulator DsAflR from 19 *D. septosporum* strains.

Amino acid changes compared to strain NZE10 are highlighted in blue (these sites also variant between AflR sequences of *D. septosporum*, *C. fulvum*, *Aspergillus parasiticus* and *A. nidulans*; (Chettri et al., 2013)) or in green (at sites conserved between those four species). The Zn₂Cys₆ zinc binuclear domain is highlighted in pink; the linker sequence thought to determine DNA-binding specificity in grey; the acidic glutamine-rich motif in yellow and C-terminal arginine residues implicated in AflJ binding in red.