**Supplementary Dataset S4.** Differentially expressed *Epichloë festucae* genes related to transport at false discovery rate adjusted *p* < 0.01

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| **Gene** | **Log2 FCa** |
| EfM3.017590\_2 Major facilitator superfamily, possible iron siderophore transporter | 12.9 |
| EfM3.019610\_1 *Efe*-MfsB; membrane transporter protein | 4.5 |
| EfM3.028310\_1 Major facilitator superfamily, sugar transporter | 4.1 |
| EfM3.054480\_1 ABC type transporter | 2.5 |
| EfM3.054490\_2 Major facilitator superfamily, sugar transporter | 4.6 |
| EfM3.059060\_1 Golgi transport complex subunit COG4 | 13.5 |
| EfM3.073030\_1 Mitochondrial amino acid transporter arg-13 | 2.5 |
| EfM3.076540\_1 Oligopeptide transporter OPT superfamily | 3.6 |
| EfM3.056950\_1 Amino acid permease | 13.6 |
| EfM3.014910\_1 Major facilitator superfamily, multidrug resistance transporter | 4.4 |
| EfM3.001040\_2 Vacuolar protein sorting vps16 | 14.6 |
| EfM3.025350\_1 Aquaglyceroporin | 3.7 |
| EfM3.038260\_1 Magnesium-translocating P-type ATPase | 3.3 |
| EfM3.070700\_1 Vacuolar protein sorting protein DigA | 12.7 |
| EfM3.073880\_1 Aminophospholipid translocase | 3.9 |
| EfM3.014790\_1 ABC multidrug transporter | -6.8 |
| EfM3.017940\_1 Major facilitator superfamily transporter | -5.5 |
| EfM3.027570\_1 Major facilitator superfamily, possible peptide transporter | -3.8 |
| EfM3.029870\_1 Major facilitator superfamily transporter | -2.6 |
| EfM3.047170\_1 Permease, cytosine/purine, uracil, thiamine, allantoin | -2.5 |
| EfM3.056220\_1 ABC-type multidrug transport system | -5.7 |
| EfM3.069880\_1 Major facilitator superfamily transporter | -4.0 |
| EfM3.082040\_1 Major facilitator superfamily transporter | -2.4 |

a Positive Log2 fold change (FC) value indicates the gene was more highly expressed in the choke stroma tissue and negative fold change value indicates the gene was more highly expressed in the asymptomatic inflorescence tissue.