

Table 5. Summary of transcription data analysis for genes with known regulation by XlnR (*A. niger* and *A. oryzae*) or known regulation on xylose (*A. nidulans*).

Sign. regul.	Trid. hit	Gene ID	Gene name	log2-ratio	Adjusted P
Ng	N	JGI52071	xylanase-B (<i>xlnB/xydB</i>)	-5.13	8.23E-06
NgO	Y	JGI55136	1,4- β -D-arabinoxylan arabinofuranohydrolase (<i>axhA</i>)	-1.18	2.16E-03
Ng	Y	JGI211551	acetyl xylan esterase (<i>axeA</i>)	-0.67	7.72E-03
Ng	N	JGI51662	ferulic acid esterase A (<i>faeA</i>)	-6.90	1.44E-06
Ng	N	JGI211053	endoglucanase A (<i>eglA</i>)	-4.54	1.43E-04
NgO	Y	JGI51764	β -galactosidase (<i>lacA</i>)	-3.17	1.08E-03
Ng	Y	JGI207264	α -galactosidase (<i>aglB</i>)	-1.47	2.22E-02
Ng	Y	JGI53159	1,4- β -D-glucan cellobiohydrolase A (<i>cbhA</i>)	-0.62	4.09E-03
NdNgO	Y	JGI51997	D-xylose reductase (<i>xyrA</i>)	-8.45	3.52E-06
NdNgO	Y	JGI205670	β -xylosidase (<i>xlnD</i>)	-7.80	1.44E-06
NdNgO	Y	JGI56619	α -glucuronidase (<i>aguA</i>)	-5.12	1.58E-06
NdNgO	Y	JGI209771	D-xylylulokinase (<i>xkiA</i>)	-5.31	1.44E-06
	N	JGI209376	Endoglucanase B (<i>eglB</i>)	-0.29	1.41E-01
	N	JGI206333	Endoglucanase C (<i>eglC</i>)	-0.14	4.19E-01
	N	JGI51773	1,4- β -D-glucan cellobiohydrolase B (<i>cbhB</i>)	0.37	9.73E-02
NdNgO	Y	AO90005000986	β -xylosidase (<i>xyIA</i>)	-6.03356	8.11E-06
O	N	AO90103000423	Endoxylanase F1 (<i>xymF1</i>)	-1.24	2.84E-03
O	N	AO90001000111	Endoxylanase G1 (<i>xymG1</i>)	-0.82	3.68E-03
O	N	AO90120000026	Endoxylanase G2 (<i>xymG2</i>)	-4.14	1.85E-05
	N	AO90026000102	Endoglucanase A (<i>celA</i>)	0.03	8.94E-01
	N	AO90010000314	Endoglucanase B (<i>celB</i>)	-0.56	1.78E-01
	N	AO90001000348	Cellobiohydrolase C (<i>celC</i>)	-0.34	2.38E-01
	N	AO90012000941	Cellobiohydrolase C (<i>celD</i>)	0.08	6.87E-01
	N	AN3613	Xylanase X22 (<i>xlnA</i>)	-2.00	1.75E-01
	N	AN9365	Xylanase X24 (<i>xlnB</i>)	-4.86	5.27E-02

The first columns show which of the species have significant regulation of the gene and tri-directional best hit (if such exist). Nd, Ng and O are *A. nidulans*, *A. niger* and *A. oryzae* respectively. The column "Trid. hit" shows if the given gene has tri-directional best hits. A negative log2-ratio represents an up-regulation on xylose relative to glucose. A positive value represents up-regulation on glucose.