Table S2. Percent identity matrix between the GH1 β-glucosidases amino acid sequences. The multiple sequence alignment was performed using the Clustal Omega server (http://www.ebi.ac.uk/Tools/msa/clustalo/).

	KU201604	KKP02477.1	KKP05610.	KKO98105.1	KKP06709.1
KU201604	**100.00**	99.57	53.78	31.04	29.02
KKP02477.1	99.57	**100.00**	53.78	31.28	29.02
KKP05610.1	53.78	53.78	**100.00**	30.86	27.46
KKO98105.1	31.04	31.28	30.86	**100.00**	50.16
KKP06709.1	29.02	29.02	27.46	50.16	**100.00**