

**Table S4.** A comparison of *cis* response elements (ARE, CRE) content in promoters of functional gene clades associated with auxin/cytokinin signaling with their transcriptomic responses to auxin (IAA) or cytokinin (BA) treatments of the whole 'Désirée' potato plants (1  $\mu$ M, 1 h) in vitro.

Gene Clade	Auxin Related <sup>1</sup>		CK Related <sup>1</sup>	
	ARE	DEG <sup>2</sup>	CRE <sup>3</sup>	DEG <sup>2</sup>
<i>StTIR1/AFB</i>	0.667	1.043	0.667	1.104
<i>StAux/IAA</i>	1.750	2.835	1.000	1.259
<i>StARF</i>	0.167	0.986	1.167	1.148
<i>StHK</i>	0.333	0.863	1.000	1.105
<i>StHPt</i>	0.667	1.265	0.333	1.076
<i>StRR-A</i>	0.750	1.133	3.750	1.757
<i>StRR-B</i>	0.250	1105	1.500	1.609
Correlation coefficient <sup>4</sup>		0.93		0.87

<sup>1</sup>All data in the table are presented per gene averaged.

<sup>2</sup>Each number in DEG column is a normalized integral indicator which characterizes the averaged hormonal effect on the expression of a distinct gene clade. Here each gene expression value is a mean of seven DEG index determinations of the given gene expressed in the main potato organs regardless of the sucrose content in the growth medium.

<sup>3</sup>Each value represents normalized number of CREs in 300 bp-proximal promoter area.

<sup>4</sup>Extent of correlation (CC) between two columns of each pair was calculated by means of the Excel program.