

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 μ M, 1 h) in vitro.

Gene Clade	Auxin Related ¹		CK Related ¹	
	ARE	DEG ²	CRE ³	DEG ²
<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 ⁴		0.93		0.87

¹All data in the table are presented per gene averaged.

²Each 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.

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

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