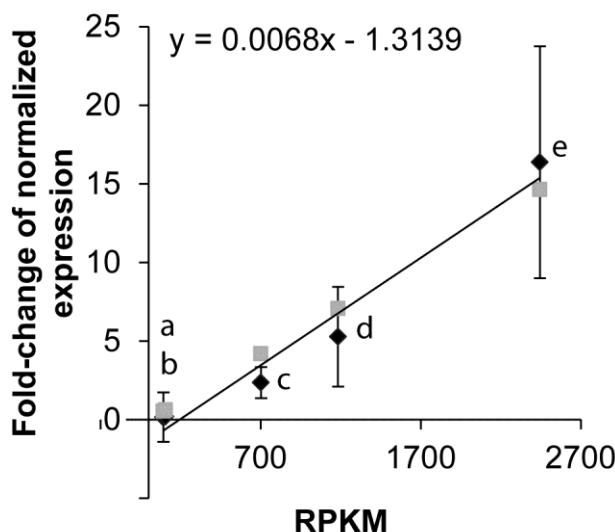


a)**b)**

Representative isoform	Corresponding dot in figure	Name	Sequence
Isotig01227		Tubulin Fwd	TGCAGAGGGCTGTTGCATGA
Isotig01227		Tubulin Rev	ACCCACGTACCAAGTGAACAAAAG
Isotig02972	a	Art v 2 Fwd	GGCTGATCAAAGGAAGGACTGCAA
Isotig02972	a	Art v 2 Rev	TGCACCGCGTATGAACCATTGA
Isotig03100	b	Amb a 10 Fwd	GACGAGCTATTGCCATCCTGAAA
Isotig03100	b	Amb a 10 Rev	GCTAATGAAACCATGCCATCTGC
Contig32361	c	Amber 8 2 Fwd	GAATTCGATGCCAGCTGGTACCCCTT
Contig32361	c	Amb a 8.2 Rev	GGGCTTCGTAATGCCAACAC
Isotig03734	d	Clathrin Fwd	AGGCCTTCATTGCGCTTACTA
Isotig03734	d	Clathrin Rev	ATCCTGGAGATCCTGCAACCAAAC
Isotig02293	e	02293 Fwd	AGCTCACTGGATGCTCACCTTCT
Isotig02293	e	02293 Rev	CCATGGCAAGGTGGAAGTTGTA

Figure S6. Comparison of high and low expressed transcripts, qRT-PCR vs. RPKM. **a)** Fold-change of tubulin normalized expression data are plotted against high and low RPKM-values of transcripts from control plants (black) ($n=3$). RPKM-values normalized to tubulin are shown in grey. Pearson-correlation $r = 0.984$. **b)** Corresponding isoforms with primer sequences are indicated.