

Table 1 Suppl. Quantitative analysis of anthocyanins and carotenoids [$\mu\text{g g}^{-1}(\text{f.m.})$] in *Strelitzia reginae* during different stages. Means \pm SDs, $n = 3$. n.d. - not detected.

Pigment group	Compound	Bud period blue petals	Blooming period blue petals	Bud period orange sepals	Blooming period orange sepals
Anthocyanins	6-hydroxycyanidin 3-glucoside	0.57 \pm 0.12	5.31 \pm 0.54	n.d.	n.d.
	delphinidin 3-glucoside	5.23 \pm 0.34	54.82 \pm 0.41	n.d.	n.d.
Carotenoids	lutein	n.d.	n.d.	1.43 \pm 0.12	3.87 \pm 0.38
	β -cryptoxanthin	n.d.	n.d.	4.86 \pm 0.3	322.28 \pm 31.53
	β -carotene	n.d.	n.d.	23.99 \pm 2.13	825.80 \pm 95.43

Table 2 Suppl. Candidate genes related to flower pigmentation of *Strelitzia reginae*.

Function	Gene	Enzyme	Number of all genes	Number of upregulated genes in blue petals	Number of upregulated genes in orange sepals
Anthocyanin biosynthesis	<i>CHS</i>	chalcone synthase	13	2	1
	<i>CHI</i>	chalcone isomerase	2	1	1
	<i>F3H</i>	flavanone 3-hydroxylase	3	1	0
	<i>F3'H</i>	flavonoid 3'-hydroxylase	1	1	0
	<i>F3'5'H</i>	flavonoid 3',5'-hydroxylase	8	1	1
	<i>DFR</i>	dihydroflavonol 4-reductase	3	1	0
Anthocyanin modification	<i>ANS</i>	anthocyanidin synthase	1	1	0
	<i>UA3GT</i>	anthocyanidin 3-O-glucosyltransferase	11	1	0
	<i>3'GT</i>	anthocyanidin 3'-O-glucosyltransferase	5	1	1
	<i>AA5GT</i>	cyanidin 3-O-glucoside 7-O-glucosyltransferase	4	0	0
	<i>5AT</i>	anthocyanidin 5-O-aromatic acyltransferase	2	0	0
	<i>GT1</i>	anthocyanidin 5,3-O-glucosyltransferase	3	2	0
Flavone and flavonol biosynthesis	<i>5Mat1</i>	anthocyanin 3-O-glucoside-6"-O-malonyltransferase	5	0	0
	<i>FLS</i>	flavonol synthase	6	2	0
	<i>F4ST</i>	flavonol 4'-sulphotransferase	3	1	1
Flavanone biosynthesis	<i>ANR</i>	anthocyanidin reductase	3	1	0
Carotenoid biosynthesis	<i>PSY</i>	phytoene synthase	5	0	3
	<i>PDS</i>	phytoene synthase	2	0	2
	<i>ZDS</i>	ζ -carotene desaturase	2	0	1
	<i>LCYB</i>	lycopene β -cyclase	3	0	3
	<i>LCYE</i>	lycopene-cyclase	1	0	0
	<i>CRTISO</i>	carotenoid isomerase	1	0	0
	<i>CHYB</i>	β -carotene hydroxylase	3	0	2
	<i>ZEP</i>	zeaxanthin epoxidase	6	0	0
	<i>VDE</i>	violaxanthin de-epoxidase	2	0	0
	<i>NCED</i>	9- <i>cis</i> -epoxycarotenoid dioxygenase	4	0	0

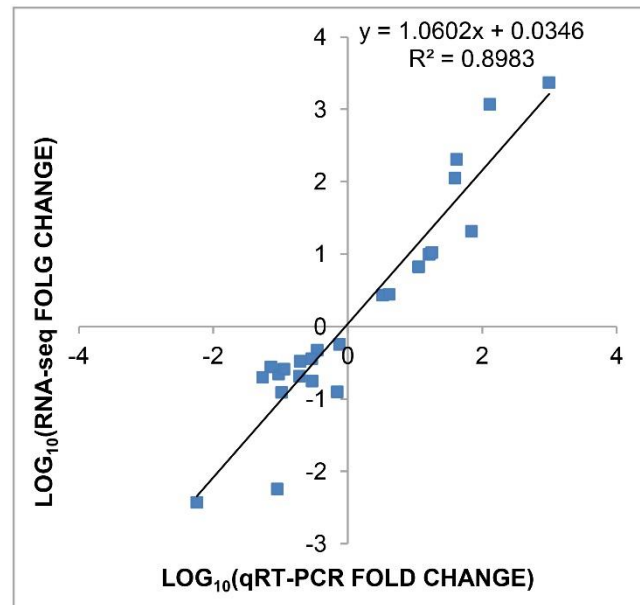


Fig. 1 Suppl. Correlation analysis of the fold change between the RNA sequencing and the quantitative real-time PCR. The RNA sequencing fold change refers to the ratios of fragments per kilobase of transcript per million mapped reads values of petals to sepals for selected transcripts, whereas the quantitative real-time PCR fold change is the relative quantity of petals normalized to the expression in sepals.