

Table 2 Gene expression stability ranks of eight candidate reference genes in different sets of *C. speciosa* samples evaluated by *geNorm* (GN) and *NormFinder* (NF) statistical algorithms

Gene	All samples		All treatments		Developmental stages		Tissues		MeJA treatment		CPPU treatment		GA ₃ treatment		PP ₃₃₃ treatment	
	GN	NF	GN	NF	GN	NF	GN	NF	GN	NF	GN	NF	GN	NF	GN	NF
<i>GAPDH</i>	1	1	6	2	4	2	1	1	1	2	3	2	3	3	3	5
<i>60S</i>	3	4	3	4	7	7	4	7	3	4	1	7	4	4	6	6
<i>ACTIN</i>	5	7	7	7	3	4	1	3	2	1	4	8	1	1	1	3
<i>TUA2</i>	8	8	8	8	8	8	5	5	8	8	7	3	5	6	2	7
<i>TUB1</i>	4	2	4	1	5	5	3	2	6	5	2	4	2	5	4	1
<i>TIF5</i>	2	3	1	5	1	3	7	6	4	6	5	6	6	2	5	2
<i>UBQ</i>	7	6	2	3	6	6	6	4	5	3	6	1	8	8	7	4
<i>EF2</i>	6	5	5	6	2	1	8	8	7	7	8	5	7	7	8	8