

Table S1 Statistical analysis of phenotypes

	Ant	Md	Mx	leg	Ug	abdomen	DC
Tc-ff1 (n=205)	34%	69%	3%	40%	16%	16%	19%
Tc-ff2 (n=113)	77%	73%	16%	67%	17%	19%	20%
Tc-ff1/ff2 (n=113)	57%	70%	9%	43%	27%	19%	35%

Statistical analysis of affected appendages in single- and double *flipflop* RNAi experiments. Ant antenna; DC dorsal closure defect; Md mandible; Mx maxilla.

Table S2 Number of inverted appendages per analysable cuticle.

	1	2	3	4	5	6	7	8	9	10
	% n	% n	% n	% n	% n	% n	% n	% n	% n	% n
Tc-ff1	27 43	25 40	21 33	11 18	4 7	6 9	3 4	1 1	1 1	2 3
Tc-ff2	28 14	16 12	14 11	14 11	10 8	10 8	6 5	4 3	4 3	3 2
Tc-ff1/ff2	17 16	17 16	19 18	22 21	10 9	7 7	3 3	3 3	0 0	1 1

Only clearly identified appendages include legs, mandibles, antennae and urogomphi have been taken into this analysis.

Table S3 Statistical quantification of the wildtype and "empty egg" phenotype

	WT	empty egg
Tc-ff1 (n=443)	15%	25%
Tc-ff2 (n=322)	4%	55%
Tc-ff1/ff2 (n=287)	3%	43%