

Table S3. Proteomic analysis of wild-type and *sff* adult heads

Protein	Peptides	Genotype	Charge	XCorr
Endoribonuclease Dcr-1 (Control)	LEFLGDAVL DYLI TRHLYEDPR*	wild-type	2	2.0
		<i>sff</i> ^{B22}	2	1.5
Guanine nucleotide releasing factor 2 (Control)	NISHSQTMNIMPMSK*	wild-type	2	1.0
		<i>sff</i> ^{B22}	2	1.6
Sff peptides with Xcorr ≥ 1.2 in wild type or <i>sff</i>	RQVIENDMENDSIFSYK*	wild-type	2	2.2
		<i>sff</i> ^{B22}	nd	
	IERRDSLRL	wild-type	2	1.6
		<i>sff</i> ^{B22}	nd	
	LGVHVIGK [†]	wild-type	2	1.2
		<i>sff</i> ^{B22}	2	0.5
	VEREIAIMK [‡]	wild-type	2	0.8
		<i>sff</i> ^{B22}	2	1.6
	LEKTLGKGQTGLVK	wild-type	2	0.7
		<i>sff</i> ^{B22}	2	1.3
Sff peptides with Xcorr<1.2	17 additional peptides	wild-type	1-5	<1.2
	6 additional peptides [§]	<i>sff</i> ^{B22}	1-2	<1.2

nd denotes that the peptide was not detected in *sff* mutant.

*See Fig. S6 in the supplementary material for LC-MS/MS base peak chromatograms.

[†]Detected as its carbamidomethylated form in wild type and as a missed cleavage (LGVHVIGKKVAIK) in *sff* mutant.

[‡]Oxidized in wild type.

[§]Two of the six additional peptides detected in *sff* mutant heads were also detected in wild type.