

Additional file 5. PARE and RNA-seq data for rice *MIR156* and *MIR529* precursors.

miRNA precursors	PARE libraries				Total	RNA-seq library	sRNA-seq library
	Three-week-old wild-type seedlings (SC938) <sup>a</sup>	Wild-type young panicle (INF939)	Wild-type young inflorescences (4-6cm; INF9311a)	Three-week-old wild-type seedlings (NPBs)		Wild-type leaf tissue <sup>b</sup>	Wild-type leaf tissue <sup>b</sup>
<i>MIR156a</i>	23	49	1	97	170	n.d.	<15,000
<i>MIR156b</i>	23	49	1	97	170	<10	<15,000
<i>MIR156c</i>	23	49	1	103	176	<10	<15,000
<i>MIR156d</i>	34	109	3	257	403	>10	>80,000
<i>MIR156e</i>	23	49	1	73	146	n.d.	<15,000
<i>MIR156f</i>	31	126	24	197	378	>10	>80,000
<i>MIR156g</i>	23	49	7	113	192	>10	<15,000
<i>MIR156h</i>	37	120	4	199	360	>10	>80,000
<i>MIR156i</i>	23	49	1	78	151	n.d.	<15,000
<i>MIR156k</i>	0	3	1	4	8	n.d.	<100
<i>MIR156l</i>	0	0	3	14	17	n.d.	<100
<i>MIR529a</i>	0	0	69	40	109	n.d.	<15,000
<i>MIR529b</i>	0	0	0	10	10	n.d.	<100

<sup>a</sup>Sequence abundance for all PARE samples was normalized to TP10M (transcript per 10 million reads). Data were retrieved from publicly available database ([https://mpss.udel.edu/dbs/index.php?SITE=rice\\_pare](https://mpss.udel.edu/dbs/index.php?SITE=rice_pare)).

<sup>b</sup>Sequence abundance from RNA-seq and sRNA-seq libraries was normalized to TP10M. Data were retrieved from Stroud et al. (2013). N.d, not detected.

Reference:

Stroud H, Ding B, Simon SA, Feng S, Bellizzi M, Pellegrini M, Wang GL, Meyers BC, Jacobsen SE. 2013. Plants regenerated from tissue culture contain stable epigenome changes in rice. *Elife*. 2:e00354.