

Table S2 Quality of sequencing data ($n=3$)

Sample	Genes Num-R NA	Ratio-R NA	total	rRNA	snRNA	snoRNA	tRNA	known mirna num	novel mirna num	miRNA _numbe r	target_g ene_nu mber
Con	67300± 988	0.92±0. 01	841909								
			±25275	6725±1			2378±9			1145±3	23850±
			3	338	615±46	158±7	8	424±43	721±65	2	13
MT25- M	67823± 1166	0.92±0. 02	725271								
			±22838	6590±5			2265±1			1082±4	23819±
			2	91	703±77	159±18	25	408±71	674±34	5	79
MT50- M	67709± 551	0.92±0. 01	773402								
			±29053	8817±1			2753±7	504±10		1238±5	23961±
			1	612	754±59	198±31	2	9	734±78	3	70
MT100 -M	68633± 873	0.93±0. 01	720409								
			±26674	8650±2			2681±1		691±10	1105±8	23822±
			1	77	756±32	150±13	51	414±37	0	4	69