

Supplemental Table 2

This table shows the 39 miRNAs whose estimated expression level changed by more than 10% due to cross-mapping, their estimated sequence counts before and after the cross-mapping correction, and the origin of cross-mapping short RNAs for each locus.

miRNA	Sequence counts before cross-mapping correction	Sequence counts after cross-mapping correction	Origin of cross-mapping short RNAs
let-7c	178.2746	25.84297	let-7b
miR-18b	286.9698	42.7678	miR-18a
miR-20b	151.9674	86.15918	miR-17
miR-23b	760.0213	615.459	miR-23a
miR-27b	7854.829	2157.724	miR-27a
miR-28-3p	237.0677	329.2775	L2 repeat region
miR-28-5p	538.7714	615.5236	unannotated region
miR-30a-5p	739.3997	623.7123	miR-30d
miR-106a	1528.125	207.4155	miR-17
miR-107	2788.881	2151.148	miR-103
miR-144	13.83333	15.83039	unannotated region
miR-151-3p	41.49637	65.89941	L2 repeat region
miR-151-5p	36.58438	54.76452	unannotated region
miR-186	27.77205	37.35529	unannotated region
miR-188-5p	2140.717	2383.239	unannotated region
miR-194	131.4829	146.881	unannotated region
miR-199b-3p	77.55168	69.42541	miR-199a
miR-320b	57.19626	29.57442	miR-320c
miR-320c	17.03359	6.573378	miR-320b
miR-324-3p	200.9468	262.5874	unannotated region
miR-326	224.2341	297.7247	unannotated region
miR-339-5p	1010.039	2125.895	unannotated region
miR-545	34.48889	51.51938	unannotated region

miR-548d-3p	11.06082	13.59609	unannotated region
miR-550	25.63333	28.94677	unannotated region
miR-574-3p	84.6052	96.63905	unannotated region; MER1_type repeat region
miR-576-5p	8.592857	10.6245	unannotated region
miR-584	9.5	11.89443	unannotated region
miR-625	52.04329	68.06676	L1 repeat region
miR-720	89.96229	191.4881	tRNA-Thr; unannotated region
miR-886-3p	598.3825	789.1534	unannotated region
miR-886-5p	16.65	19.16806	L1 repeat region
miR-940	86.96863	133.6656	unannotated region
miR-1260	107.354	159.7671	L2 repeat region; unannotated region;
miR-1274a	55.26929	8.38666	tRNA-Lys; miR-1274b
miR-1274b	2241.256	5352.133	unannotated region; tRNA-Lys; Simple_repeat repeat region
miR-1280	10.18861	3.809237	tRNA_Leu
miR-1285	4.46882	21.28288	Alu repeat region; unannotated region
miR-1286	9.176923	10.98179	tRNA-Gln; L1 repeat region; unannotated region; MaLR repeat region
miR-1296	37.07143	45.00981	unannotated region
miR-1308	23.9942	6.194658	tRNA repeat region