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*Supplement of*

## **The microRNA gene *bta-mir-2313* in cattle: an atlas of regulatory elements and an association analysis with growth and carcass traits in the Slovenian Simmental cattle breed**

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**Supplement Table S1:** Genomic location of 17 QTL, overlapping the *bta-miR-2313* gene.

QTL symbol	QTL ID	QTL trait	QTL peak (cM)	QTL span (cM)	QTL span (bp), chromosome 15
AD	5122	Abomasum displacement	67.8	58.3-74.1	28737753-36469420
BFCI	1594	Body form composite index	65	54.286-75.71	31549304-37655364
FA-C13:0	19626	Tridecylic acid content	41.81	0.00-83.62	20-59060134
FERIND	62361	Fertility index	48.31	47.61-49.00	34177504-35177124
FTPL	1595	Teat placement - front	65	54.286-75.71	31549304-37655364
KPHCWT	1335	Kidney, pelvic, and heart fat percentage	45	21-69	9532674-36158521
LIVP	12195	Liver percentage	56	39.07-73.63	19145683-36123213
MARBL	10999	Marbling score	77.94	59.27-84.89	29452266-40819540
MHT	11001	Height (mature)	84.89	59.27-104.9	29452266-50231208
MWT	10997	Body weight (mature)	59.27	59.27-77.94	29452266-36441038
PTAT	1597	PTA type	65	54.286-75.71	31549304-37655364
SF	20794	Shear force	44.90	44.02-45.78	31599942-63827753
THUWDT	1599	Thurl width	65	54.286-75.71	31549304-37655364
UC	1600	Udder cleft	65	54.286-75.71	31549304-37655364
UCI	1602	Udder composite index	65	54.286-75.71	31549304-37655364
WWT	10996	Body weight (weaning)	59.27	54.29-77.94	31552250-36441038
WWT	10998	Body weight (weaning)	59.27	54.29-77.94	31552250-36441038

**Supplement Figure S1:** Polymorphism rs41761413C>T within mature miRNA *bta-miR-2313* seed region causing formation of a novel seed region, annotated to a miRNA gene *bta-miR-3600*. Polymorphism within the seed region also causes a change in the number of predicted targets (3393/3789).

