

Table S7 The significantly enriched GO description of BP, CC and MF
for the upregulated mRNA target genes of cattle

Ontology	Term	GO.ID	Significant	Annotated	Qvalue
BP	cellular component	GO:0071840	658	5228	1.14E-11
	organization or biogenesis				
BP	reproductive process	GO:0022414	187	1188	3.10E-08
BP	reproduction	GO:0000003	187	1190	3.40E-08
BP	metabolic process	GO:0008152	1067	9982	0.002728
BP	cellular process	GO:0009987	1505	14842	0.092403
BP	localization	GO:0051179	556	5065	0.094813
BP	multi-organism process	GO:0051704	242	2045	0.095071
BP	establishment of localization	GO:0051234	433	3965	0.357635
CC	organelle	GO:0043226	1476	12576	4.94E-28
CC	organelle part	GO:0044422	988	7853	1.39E-20
CC	membrane-enclosed lumen	GO:0031974	471	3755	6.06E-07
CC	supramolecular fiber	GO:0099512	135	841	8.82E-07
CC	cell part	GO:0044464	1728	16747	0.001307
CC	cell	GO:0005623	1728	16775	0.002938
CC	protein-containing complex	GO:0032991	493	4316	0.008014
CC	synapse	GO:0045202	82	716	0.762281
CC	synapse part	GO:0044456	67	582	0.820478
CC	nucleoid	GO:0009295	7	43	0.856805
MF	catalytic activity	GO:0003824	713	5764	7.85E-17
MF	binding	GO:0005488	1152	10991	2.38E-08
MF	translation regulator activity	GO:0045182	11	39	0.064563