

No.	miRNA (miRBase ID)	DE or Ref	Thermo Fisher Scientific Assay ID	Thermo Fisher Scientific Catalog Number
1	<i>bta-miR-2415-3p</i>	DE	241869_mat	4440886
2	<i>bta-miR-133a</i>	DE	002246	4427975
3	<i>bta-miR-2419-5p</i>	DE	244440_mat	4440886
4	<i>bta-miR-424-5p</i>	DE	242183_mat	4440886
5	<i>bta-miR-223</i>	DE	002295	4427975
6	<i>bta-miR-155</i>	DE	002623	4427975
7	<i>bta-miR-192</i>	Ref	006776_mat	4427975
8	<i>bta-miR-93</i>	Ref	007615_mat	4440886
9	<i>bta-miR-228x</i>	Ref	464990_mat	4440886
10	<i>bta-let-7b</i>	Ref	002619	4427975

Table S1: All miRNAs used in the qPCR validation with their Thermo Fisher Scientific specifications, DE = differentially expressed miRNA, Ref = to reference miRNA.

Trait	Angus			Charolais			KC		
	L_RFI±SE	H_RFI±SE	P-value	LRFI±SE	HRFI±SE	P-value	LRFI±SE	HRFI±SE	P-value
RFI/kg/day	1.26±0.11	-0.84±0.07	1.13E-08	1.15±0.16	-0.98±0.09	4.19E-07	1.52±0.12	-1.29±0.11	1.18E-08
DMI/kg/day	12.97±0.35	11.46±0.51	0.04	12.23±0.19	10.23±0.12	4.18E-06	12.74±0.36	9.21±0.36	3.95E-05
ADG/kg/day	1.6±0.07	1.88±0.11	0.06	1.68±0.09	1.62±0.05	0.62	1.63±0.07	1.48±0.1	0.26
MWT/kg	115.09±2.56	115.58±5.41	0.94	118.39±2.01	121.17±1.42	0.29	104.67±2.77	99.7±2.7	0.23
FUREA/cm ²	79.72±3.06	84.41±1.56	0.20	88.86±2.41	99±2.7	0.02	8.98±0.45	8.75±0.55	0.75
FUFAT/kg	9.89±0.62	9.23±0.68	0.49	5.67±0.63	6.69±0.91	0.38	74.22±1.52	71.02±2.77	0.34
HCW/kg	754.78±22.47	763.23±44.26	0.87	828.17±10.5	874.17±19.67	0.07	697.33±24.54	656.67±21.52	0.24
AFAT/mm	12.33±1.33	10.67±1.09	0.36	89.83±2.96	97.83±4.95	0.2	76.33±2.23	69.67±2.54	0.08
CREA/cm ²	72±3.79	75.83±2.34	0.41	6.67±0.49	7.67±1.28	0.48	10±0.52	11.67±1.17	0.22
LMY/%	54.59±1.56	56.43±1.18	0.37	61.28±0.77	61.63±1.32	0.82	57.81±0.56	55.79±0.88	0.08
Marbling score	448.33±24.95	393.33±23.47	0.14	393.33±17.44	353.33±16.46	0.13	378.33±20.56	378.33±20.56	1
Slaughter age/day	489.33±5.29	500.33±4.38	0.14	512.5±9.11	519.67±4.14	0.49	445.17±3.44	464±7.08	0.04

Table S2: “*” indicates significant difference (P-value < 0.0042, Bonferroni Correction for 12 multiple testing analyses at P<0.05). DMI = daily dry matter intake, RFI = residual feed intake, ADG = average daily gain, MWT = metabolic body weight, FUREA = final ultrasound ribeye area at

the end of feedlot test; FUFAT = final ultrasound backfat at the end of feedlot test; HCW = hot carcass weight; AFAT = carcass average backfat; REA = carcass ribeye area; LMY = lean meat yield; Marbling score (100–399 = trace marbling or less, 400–499 = slight marbling, 500–799 = small to moderate marbling, and 800–1199 = slightly abundant or more marbling). L_RFI \pm SE= trait mean values for the low RFI group \pm standard error (SE); H_RFI \pm SE= trait mean values for the high RFI steer group \pm standard error (SE).

	Reads > 28bp	Reads < 15bp	rRNA	tRNA	snRNA	snoRNA	Retained Reads
Angus	43.22%	8.15%	0.25%	0.14%	0.03%	0.03%	48.18%
Charolais	33.65%	8.75%	0.25%	0.15%	0.03%	0.03%	57.15%
KC	33.87%	7.96%	0.25%	0.14%	0.03%	0.03%	57.73%
Average	36.91%	8.29%	0.25%	0.14%	0.03%	0.03%	54.35%

Table S3: Quality control processing and filtration summaries.

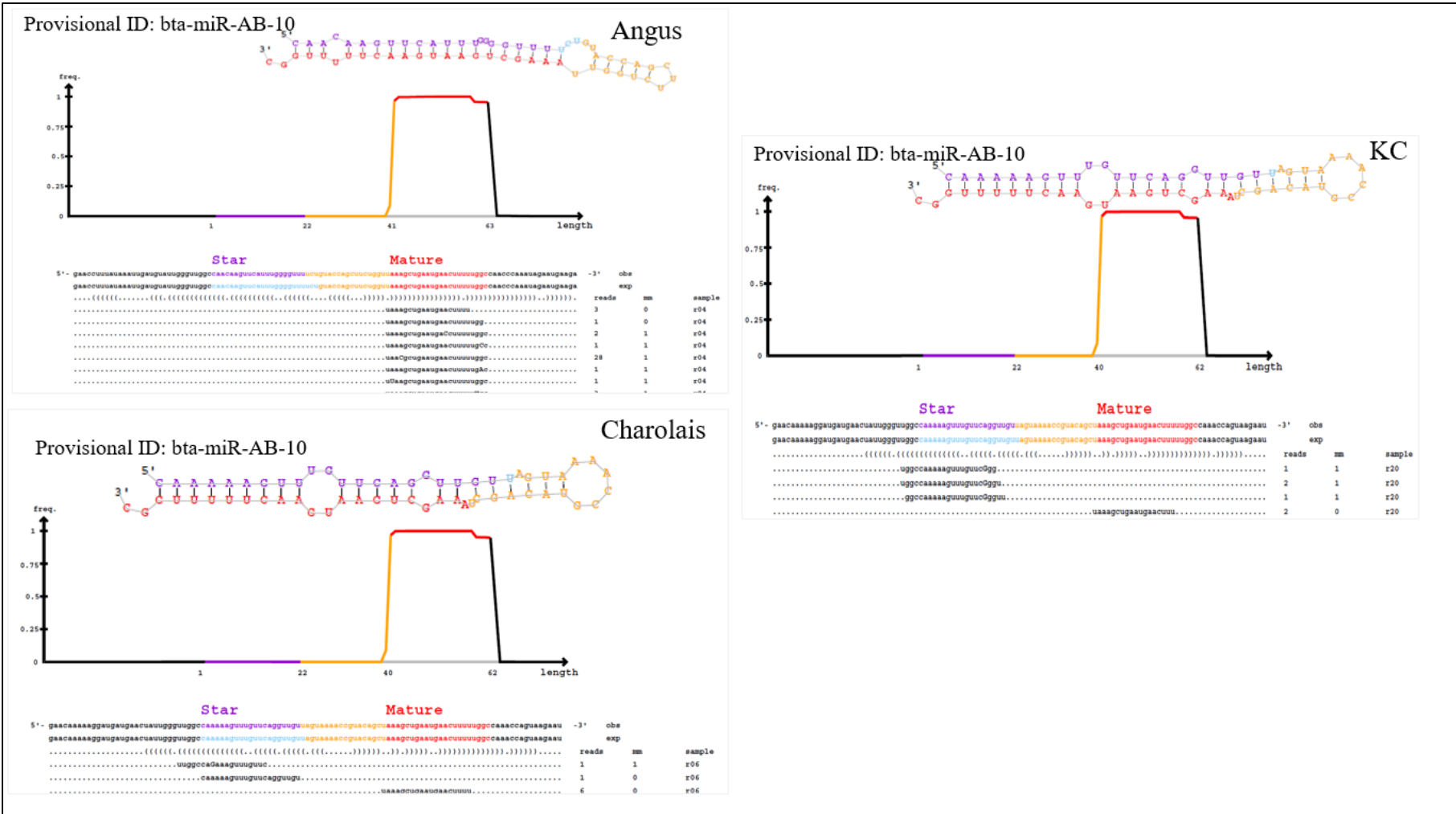


Figure S1: Precursor hairpin structure and alignment summary of the most expressed novel miRNA (bta-miR-AB-10) across liver tissue of the three studied populations (Angus, Charolais and KC steers).



Figure S2: Correlation plot between expression levels (expressed as $\log_2(\text{Fold-change})$) of the six validation miRNAs in low-RFI animals relative to high-RFI animals as estimated using RNAseq and qPCR methods

qPCR validation results

miRNA	Fold-Change	logFC	P-value	Breed
bta-miR-2415-3p	2.135	1.095	0.144	Charolais
bta-miR-133a	1.555	0.637	0.003	Charolais
bta-miR-2419-5p	1.521	0.605	0.273	Charolais
bta-miR-424-5p	1.358	0.441	0.086	KC
bta-miR-223	1.350	0.433	0.054	KC
bta-miR-155	1.852	0.889	0.314	KC

Table S4: qPCR validation results showing the $\log_2(\text{Fold-Change})$ or logFC, and the P-values for the t-tests between relative expression differences between high and low-RFI steers. **Fold changes and $\log_2(\text{Fold-Change})$ show expression in low-RFI steers liver tissue relative to high-RFI**

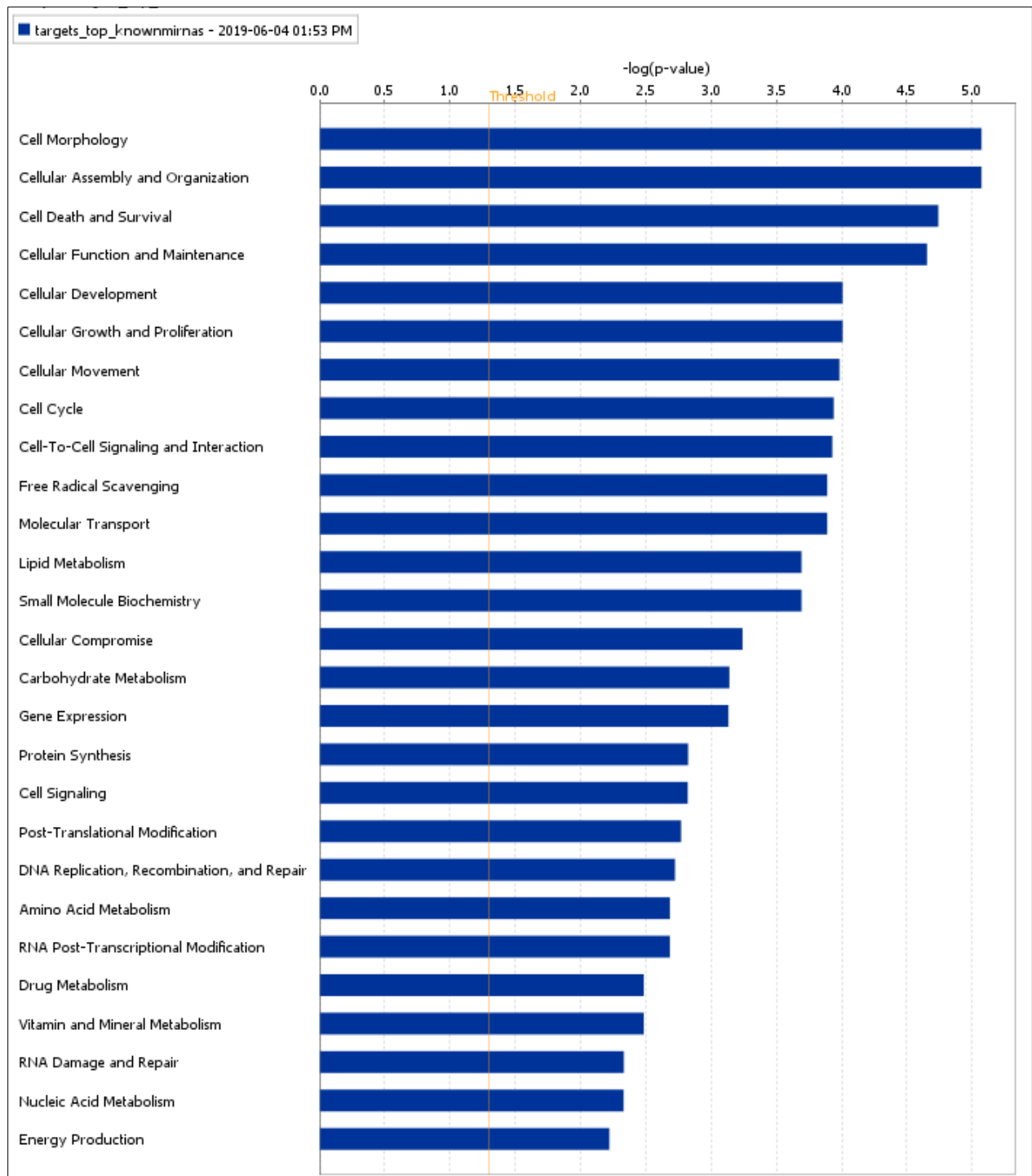


Figure S3: All enriched cellular and molecular functions enriched by target genes for the 16 top expressed known miRNAs across the liver tissues of steers from the three populations.

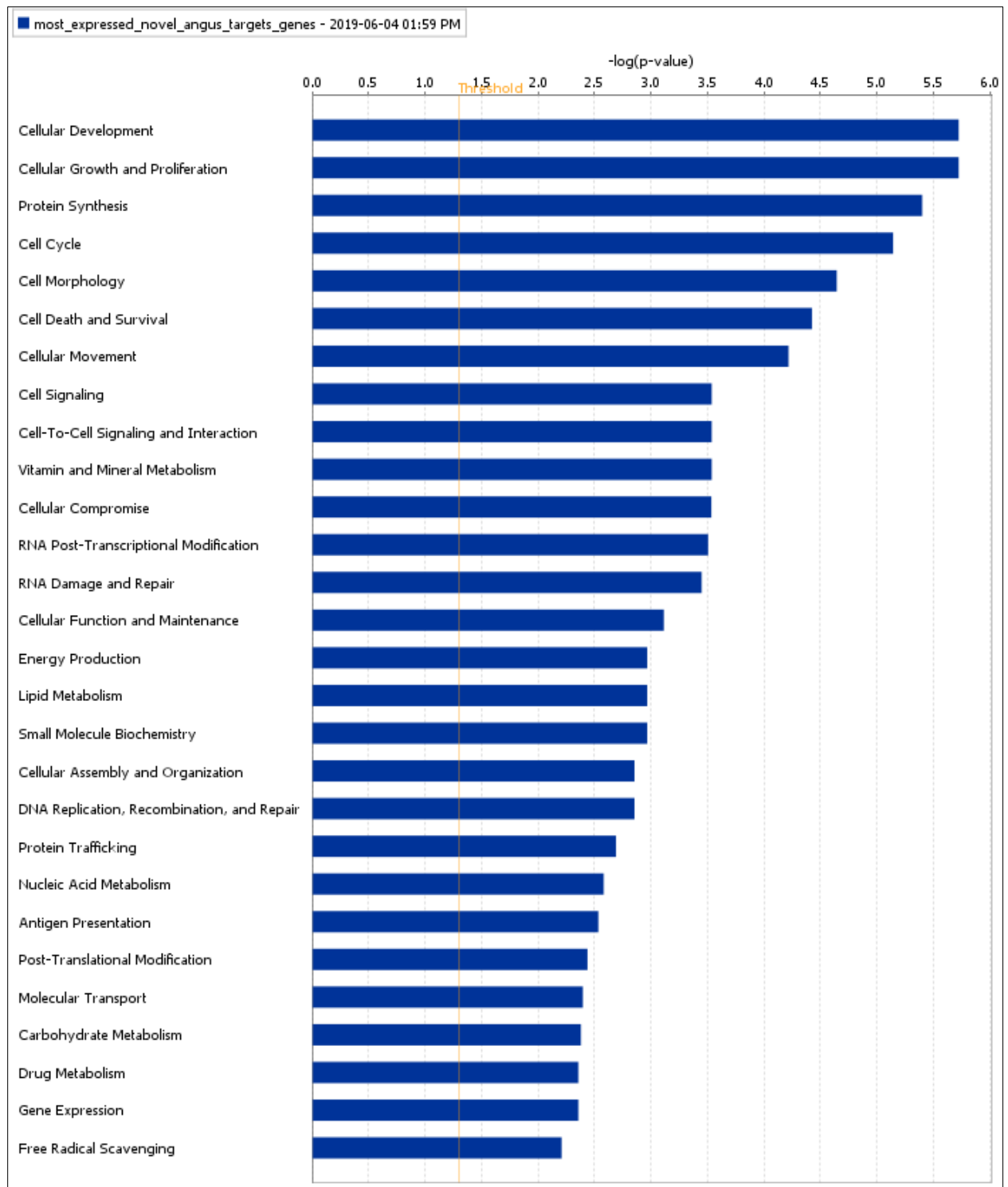


Figure S4: All enriched cellular and molecular functions enriched by target genes for the 20 highly expressed novel miRNAs in the liver tissue of Angus steers.

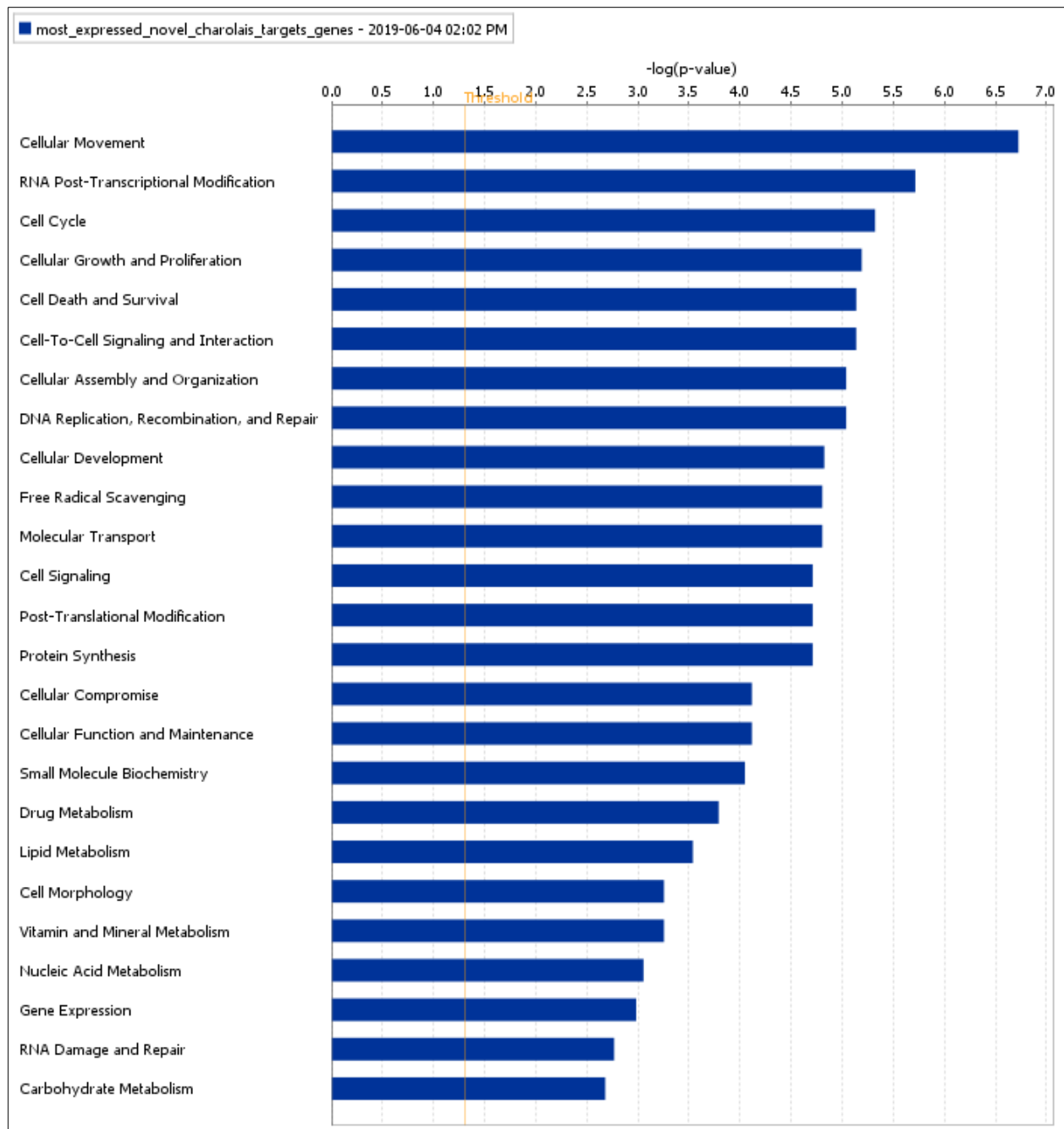


Figure S5: All enriched cellular and molecular functions enriched by target genes for the 20 highly expressed novel miRNAs in the liver tissue of Charolais steers.

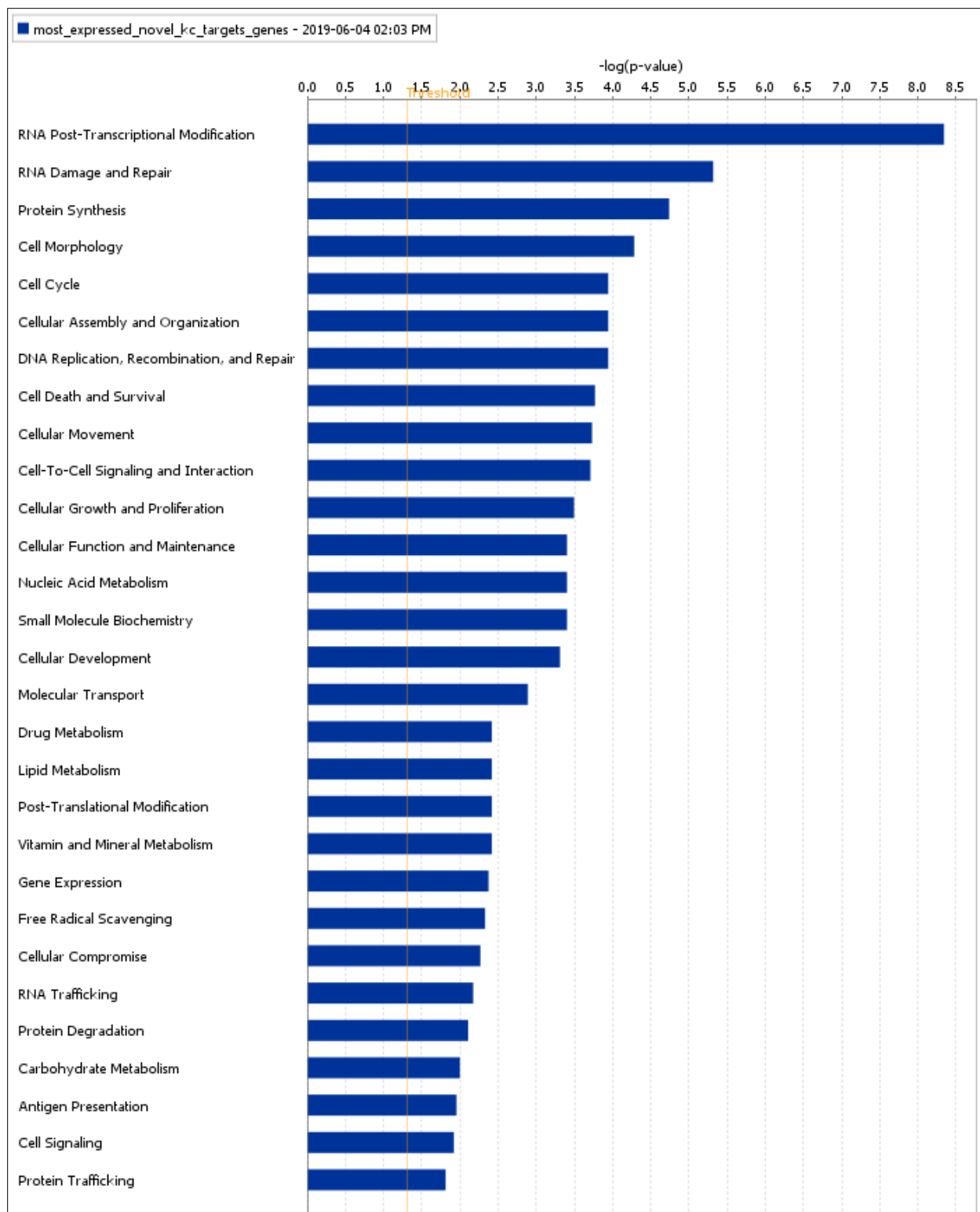


Figure S6: All enriched cellular and molecular functions enriched by target genes for the 20 highly expressed novel miRNAs in the liver tissue of KC steers.