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Bovine hepatic differential gene expression in response to perennial ryegrass staggers

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Figure S1. Histogram showing an approximately normal distribution of the normalized log intensities from one chip.

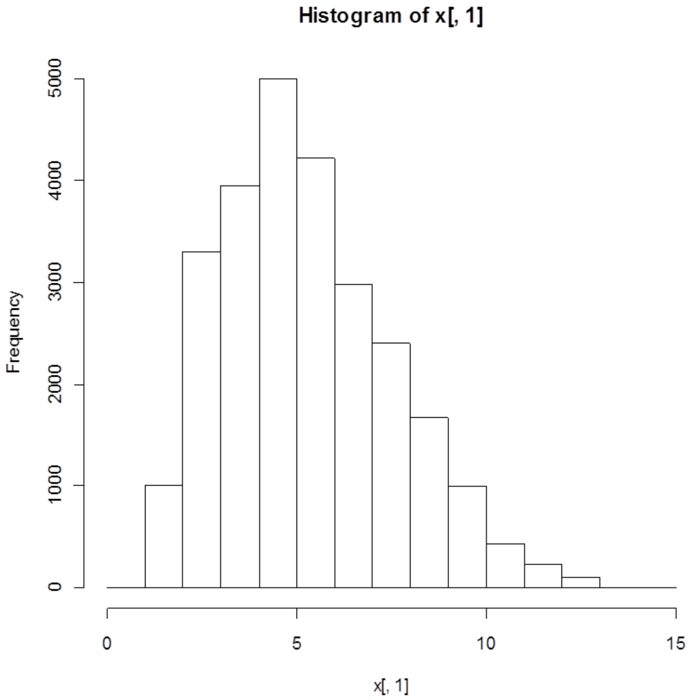

Figure S2. Distribution of *P*-values for comparisons of low (A), mid (B) and high (C) groups for day 64 versus their corresponding control (day 0).

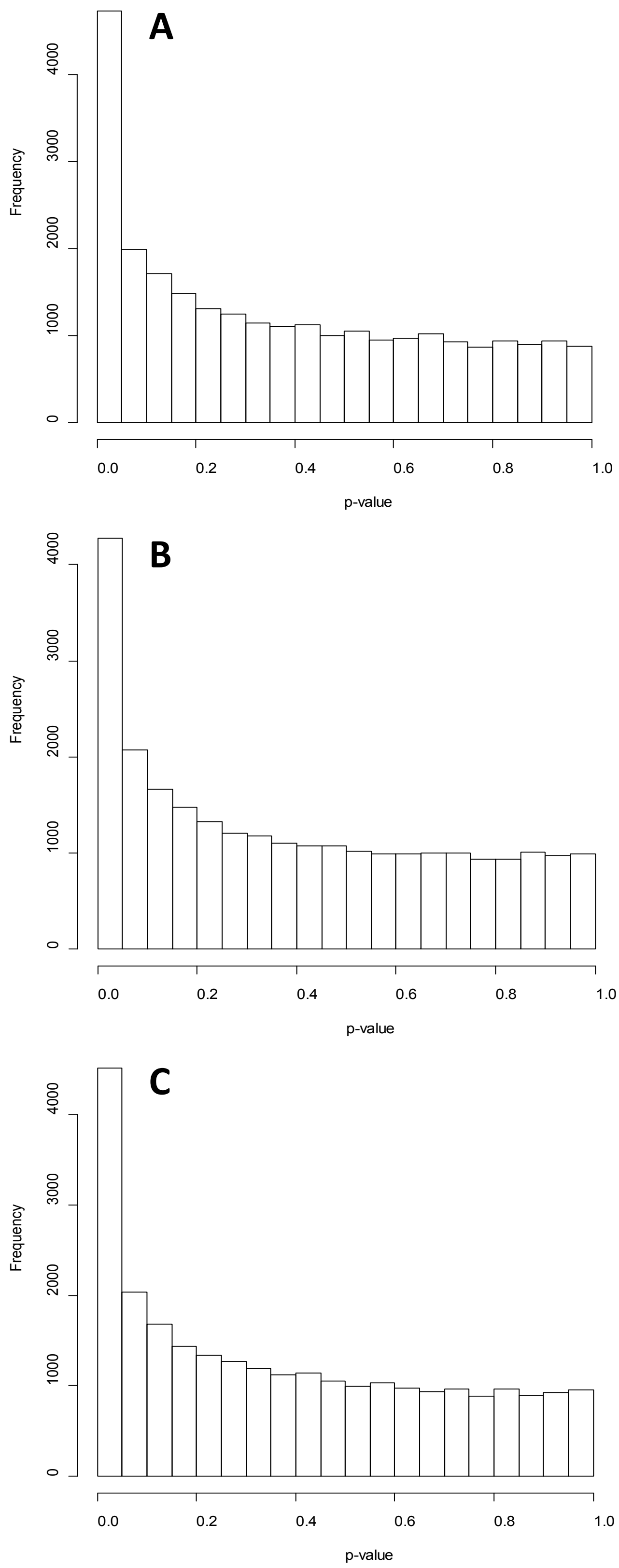

Table S1. Top 50 most significantly differentially expressed genes in hepatic tissue from steers fed 247 (low), 1,554 (mid) or 2,256 (high) µg/kg lolitrem B-containing perennial ryegrass straw over 64 days.

High group (2,256 µg/kg lolitrem B)					
No.	**Gene ID[a]**	**Symbol**	**Definition**	**logFC[b]**	**FDR[c]**
1	12821369	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	3.663	4.85E-06
2	12714225	ACSS2	acyl-CoA synthetase short-chain family member 2	2.533	6.74E-06
3	12818863	LOC100337286	acyl-CoA desaturase-like	3.157	8.27E-06
4	12730451	LOC789567	similar to steroid dehydrogenase homolog	1.105	9.40E-06
5	12762782	TMEM97	transmembrane protein 97	1.008	2.33E-05
6	12834425	FADS1	fatty acid desaturase 1	2.068	2.33E-05
7	12730813	CRYAB	crystallin, alpha B	1.413	0.00012103
8	12703239	MBOAT2	membrane bound O-acyltransferase domain containing 2	3.488	0.000270381
9	12843282	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	1.042	0.000413212
10	12735174	LOC506707	similar to complement component 4 binding protein, alpha chain	1.343	0.000481905
11	12793713	C21H14orf147	chromosome 14 open reading frame 147 ortholog	0.605	0.000626767
12	12744650	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	0.905	0.000682734
13	12836065	S100A10	S100 calcium-binding protein A10	1.152	0.000728771
14	NA	NA	NA	0.823	0.000728771
15	12702548	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.932	0.000728771
16	12821712	OAT	ornithine aminotransferase	1.637	0.000766711
17	12907179	S100G	S100 calcium binding protein G	1.333	0.000855025
18	12829453	TM7SF2	transmembrane 7 superfamily member 2	1.133	0.000855025
19	12784256	MGC152346	Uncharacterized protein LOC285141 homolog	1.520	0.000855025
20	12794313	LTF	lactotransferrin	0.925	0.000855025
21	12873166	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	1.927	0.000862103
22	12868313	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.730	0.000862103
23	12695051	SGPP1	sphingosine-1-phosphate phosphatase 1	0.800	0.000876451
24	12801442	SLC17A1	solute carrier family 17 (sodium phosphate), member 1	1.087	0.000876451
25	12877228	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	0.937	0.000876451

26	12885334	TMEM205	transmembrane protein 205	0.752	0.000876451
27	12785671	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	1.000	0.000928368
28	12693994	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	1.242	0.000953313
29	12859755	LOC516241	similar to cysteine sulfinate decarboxylase	1.725	0.001085131
30	12757637	NQO1	NAD(P)H dehydrogenase, quinone 1	0.850	0.001085131
31	12892052	LOC781732	similar to interferon alpha G	-0.588	0.001099869
32	12791768	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.812	0.001127836
33	NA	NA	NA	-0.780	0.001127836
34	12794535	TKT	transketolase	1.085	0.001275782
35	12755996	RTN2	reticulon 2	0.765	0.001275782
36	12755702	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.640	0.001305293
37	12703045	ACYP2	acylphosphatase 2, muscle type	0.610	0.001336513
38	12760706	FASN	fatty acid synthase	0.900	0.001521313
39	12865696	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	-0.722	0.001846189
40	12853903	CDK6	cyclin-dependent kinase 6	0.585	0.00186431
41	12872011	CASP6	caspase 6, apoptosis-related cysteine peptidase	0.663	0.0022221
42	12882137	C7H5orf32	chromosome 5 open reading frame 32 ortholog	0.477	0.002693534
43	12836074	UGT1A6	UDP glucuronosyltransferase 1 family, polypeptide A6	2.617	0.002693534
44	12837370	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	0.503	0.003136354
45	12863892	CD9	CD9 molecule	0.763	0.003136354
46	12844465	MFSD2A	major facilitator superfamily domain containing 2A	1.187	0.003545649
47	12767240	ACACA	acetyl-coenzyme A carboxylase alpha	0.808	0.003645926
48	12897412	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	0.630	0.003645926
49	12863971	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	0.630	0.003645926
50	12696623	C10H14ORF1	chromosome 14 open reading frame 1 ortholog	0.868	0.003996274

Mid group (1,554 µg/kg lolitrem B)					
No.	**Gene ID[a]**	**Symbol**	**Definition**	**logFC[b]**	**FDR[c]**
1	12821369	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	3.472	1.17E-05
2	12730451	LOC789567	similar to steroid dehydrogenase homolog	1.103	1.37E-05
3	12762782	TMEM97	transmembrane protein 97	1.078	1.37E-05
4	12714225	ACSS2	acyl-CoA synthetase short-chain family member 2	2.275	1.90E-05
5	12818863	LOC100337286	acyl-CoA desaturase-like	2.830	2.83E-05
6	12834425	FADS1	fatty acid desaturase 1	2.000	3.93E-05
7	12829453	TM7SF2	transmembrane 7 superfamily member 2	1.298	0.000305744
8	12693994	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	1.468	0.000305744
9	12859656	LPCAT3	lysophosphatidylcholine acyltransferase 3	0.910	0.000423338
10	12755702	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.760	0.000423338
11	12702548	RETSAT	retinol saturase (all-trans-retinol 13,14-reductase)	0.982	0.000423338
12	12696623	C10H14ORF1	chromosome 14 open reading frame 1 ortholog	1.137	0.000423338
13	12680528	CBR1	carbonyl reductase 1	0.978	0.000423338
14	NA	NA	NA	-1.447	0.00050781
15	12843282	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	0.973	0.000658234
16	12794535	TKT	transketolase	1.175	0.000864731
17	12744650	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	0.868	0.000864731
18	12875732	UGT2B4	UDP glucuronosyltransferase 2 family, polypeptide B4	1.143	0.001029698
19	12885334	TMEM205	transmembrane protein 205	0.760	0.001029698
20	12785671	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)	0.992	0.001341588
21	12859755	LOC516241	similar to cysteine sulfinate decarboxylase	1.735	0.001341588
22	NA	NA	NA	-1.492	0.001341588
23	12839924	DHCR24	24-dehydrocholesterol reductase	1.198	0.00153772
24	12897137	ACAT2	acetyl-Coenzyme A acetyltransferase 2	0.752	0.00153772
25	NA	NA	NA	-0.753	0.001664157
26	12868313	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.687	0.001684821
27	12757637	NQO1	NAD(P)H dehydrogenase, quinone 1	0.828	0.001709955

28	12703239	MBOAT2	membrane bound O-acyltransferase domain containing 2	2.778	0.001917005
29	NA	NA	NA	-1.027	0.002239133
30	12783426	KLF7	Kruppel-like factor 7 (ubiquitous)	0.585	0.002239133
31	12824957	GSR	glutathione reductase	0.553	0.002742367
32	NA	NA	NA	-0.837	0.002742367
33	12834190	TMEM135	transmembrane protein 135	0.735	0.002742367
34	NA	NA	NA	-1.083	0.002742367
35	12849070	ASB15	ankyrin repeat and SOCS box-containing 15	-1.837	0.002742367
36	12905830	NSDHL	NAD(P) dependent steroid dehydrogenase-like	1.148	0.002742367
37	12747786	BRI3BP	BRI3 binding protein	0.612	0.002742367
38	12695051	SGPP1	sphingosine-1-phosphate phosphatase 1	0.707	0.002908523
39	12805318	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	0.762	0.003099463
40	12843470	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	0.575	0.003099463
41	12680419	MCM2	cyclin L1	-1.060	0.003181465
42	12839691	MRPL24	mitochondrial ribosomal protein L24	0.488	0.003270932
43	12747823	HSPB8	heat shock 22kDa protein 8	0.522	0.003405986
44	NA	NA	NA	-1.687	0.003405986
45	12784543	OPRD1	opioid receptor, delta 1	-0.612	0.003427444
46	12744453	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	0.550	0.003454508
47	NA	NA	NA	-0.955	0.003454508
48	12826638	C28H10orf58	chromosome 10 open reading frame 58 ortholog	0.698	0.004213662
49	12700001	10-Sep	septin 10	0.458	0.004213662
50	12892785	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	1.118	0.004213662

Low group (247 μg/kg lolitrem B)					
No.	Gene ID[a]	Symbol	Definition	logFC[b]	FDR[c]
1	12821369	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	3.455	8.74E-06
2	12730813	CRYAB	crystallin, alpha B	1.798	8.74E-06
3	12730451	LOC789567	similar to steroid dehydrogenase homolog	1.130	8.74E-06
4	12873166	SULT1E1	sulfotransferase family 1E, estrogen-preferring, member 1	2.660	3.84E-05
5	12818863	LOC100337286	acyl-CoA desaturase-like	2.702	5.09E-05
6	12714225	ACSS2	acyl-CoA synthetase short-chain family member 2	2.082	5.09E-05
7	12762782	TMEM97	transmembrane protein 97	0.907	8.87E-05
8	NA	NA	NA	0.942	0.000193024
9	12688156	ANXA2	annexin A2	1.147	0.000237205
10	12877228	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	1.087	0.000237205
11	12793713	C21H14orf147	chromosome 14 open reading frame 147 ortholog	0.640	0.000237205
12	12791768	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.968	0.000237205
13	12695051	SGPP1	sphingosine-1-phosphate phosphatase 1	0.915	0.000237205
14	12713983	CTSZ	cathepsin Z	0.635	0.000277108
15	12868313	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	0.812	0.000279869
16	NA	NA	NA	-0.838	0.000783421
17	12906231	LOC786942	similar to rCG61730	-2.337	0.001023945
18	12865696	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	-0.793	0.001023945
19	12859656	LPCAT3	lysophosphatidylcholine acyltransferase 3	0.815	0.001023945
20	12802388	RPL7L1	ribosomal protein L7-like 1	0.590	0.001023945
21	12834425	FADS1	fatty acid desaturase 1	1.458	0.001157992
22	12709549	ATP11A	ATPase, class VI, type 11A	0.735	0.001157992
23	12829596	CTSC	cathepsin C	1.158	0.001173826
24	12734464	ENO1	enolase 1, (alpha)	0.613	0.001173826
25	NA	NA	NA	-0.793	0.001173826
26	12827916	ZMYND17	zinc finger, MYND-type containing 17	-0.687	0.001379487
27	12794535	TKT	transketolase	1.095	0.001433347

28	12794313	LTF	lactotransferrin	0.867	0.00149234
29	12755702	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	0.638	0.001633751
30	12694950	LOC515823	similar to Keratin 8	0.943	0.001633751
31	12879784	PRELID1	PRELI domain containing 1	0.408	0.001915063
32	12875828	LOC616908	hypothetical protein LOC616908	-0.688	0.001961484
33	12687580	LOC100137993	similar to Uncharacterized protein C14orf45	-0.977	0.001970826
34	12849070	ASB15	ankyrin repeat and SOCS box-containing 15	-1.872	0.002173594
35	NA	NA	NA	-1.147	0.002173594
36	12824957	GSR	glutathione reductase	0.557	0.002173594
37	12885741	NHP2	NHP2 ribonucleoprotein homolog (yeast)	0.808	0.002173594
38	NA	NA	NA	0.773	0.002173594
39	12775947	FKBP7	FK506 binding protein 7	0.955	0.002222936
40	NA	NA	NA	-0.708	0.002356474
41	12882137	C7H5orf32	chromosome 5 open reading frame 32 ortholog	0.482	0.002419138
42	12791600	LGMN	legumain	0.660	0.002543454
43	12823094	PDLIM1	PDZ and LIM domain 1	0.585	0.00257193
44	12714816	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-0.913	0.002672697
45	12874454	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	-1.165	0.002817074
46	12795077	ASB14	ankyrin repeat and SOCS box-containing 14	-0.653	0.002817074
47	12853718	SNX10	sorting nexin 10	0.525	0.002817074
48	12757637	NQO1	NAD(P)H dehydrogenase, quinone 1	0.763	0.002817074
49	12761977	CCDC45	coiled-coil domain containing 45	-0.518	0.002828081
50	12786883	GHR	growth hormone receptor	-0.697	0.002842434

[a]Affymetrix Bovine Gene v1 Array probe ID
[b]log FC = log fold-change
[c]FDR = adjusted P-value (Benjamini *et al.*, 1995)

Table S2. Primers used for qPCR validation.

Symbol	Name	Forward primer	Reverse primer	Product length	Access #
SCD	stearoyl-CoA desaturase	CGACGTGGCTTTTTCTTCTC	GATACCATGGCACGAGTGTG	190 bp	NM_173959
ACSS2	acyl-CoA synthetase short-chain family member 2	TCAGCCGCCTATGGAATATC	AGGCCTCAGGGTTGATAGGT	168 bp	NM_001105339
LASS6	LAG1 homolog, ceramide synthase 6	GGCTTGAACTGCTTCTGGTC	GGGTTCTTTCCTGGAGGTTC	140 bp	NM_001193132
ARG1	arginase, liver	GGCTGGTCTGCTTGAGAAAC	GGAGTGTTGATGTCCGTGTG	297 bp	NM_001046154
GPX4	glutathione peroxide 4	ACCCTCTGTGGAAATGGATG	GAAGGCTTCTCGGAACACAG	228 bp	NM_174770
GAPDH	glyceraldehyde 3-phosphate dehydrogenase	GGGTCATCATCTCTGCACCT	GGTCATAAGTCCCTCCACGA	176 bp	NM_001034034