

Table S1 Composition and nutrient levels of basal diets (air-dry basis) %

Item	Content
	1 to 3 weeks
Ingredients	
Corn	61.38
Soybean meal	31.00
Fish meal	2.00
Soybean oil	2.00
Limestone	1.50
CaHPO ₄	1.30
<i>DL</i> -Met	0.22
NaCl	0.30
Premix ¹⁾	0.20
Choline chloride	0.10
Total	100.00
Nutrient levels ²⁾	
ME/(MJ/kg)	12.47
CP	20.55
CF	4.59
Ca	0.95
AP	0.46
Lys	1.10
Met	0.55

¹⁾The premix provided the following per kg of diets: VA 8000 IU, VB₁ 4.2 mg, VB₂ 4 mg, VB₆ 4.5 mg, VB₁₂ 0.02 mg, VD₃ 3000 IU, VE 20 IU, VK₃ 2 mg, biotin 0.15 mg, folic acid 1.0 mg, *D*-pantothenic acid 11 mg, nicotinic acid 10 mg, Cu (as copper sulfate) 10 mg, Fe (as ferrous sulfate) 80 mg, Mn (as manganese sulfate) 80 mg, Zn (as zinc sulfate) 75 mg, I (as potassium iodide) 0.40 mg, Se (as sodium selenite) 0.30 mg.

²⁾The nutrient levels were calculated values.

Table S2 Protein data statistics table

Items	Number
Total protein number	784
Total peptide number	5099
Unique peptides	4087

Table S3 Comparison of the proteomics analysis between DEX and CON groups by KEGG

ID	Description	GeneRati			p.adjust	qvalue	geneID	Count
		o	BgRatio	pvalue				
gga0451					0.0106680	0.0083419		
2	ECM-receptor interaction	5/32	70/3644	0.0003048	5	3	COL6A3/ITGA6/CD36/ITGAV/CD47	5
gga0451			169/364	0.0030155	0.0228770		COL6A3/ITGA6/ITGAV/ILK/RAP1A/ZY	
0	Focal adhesion	6/32	4	8	2	0.0178888	X	6
gga0481	Regulation of actin		169/364	0.0030155	0.0228770		GSN/ITGA6/KRAS/ITGAV/WASF2/BAIA	
0	cytoskeleton	6/32	4	8	2	0.0178888	P2	6
gga0414			170/364	0.0031064	0.0228770		CLTC/RAB7A/HSPA2/CHMP5/BF2/CHM	
4	Endocytosis	6/32	4	7	2	0.0178888	P1A	6
gga0414			118/364	0.0032681	0.0228770			
5	Phagosome	5/32	4	5	2	0.0178888	CD36/ITGAV/RAB7A/TUBB/BF2	5
gga0332				0.0112647	0.0657111	0.0513831		
0	PPAR signaling pathway	3/32	54/3644	6	1	2	FABP6/CD36/ILK	3
gga0452				0.0170984	0.0854924	0.0668512		
0	Adherens junction	3/32	63/3644	9	7	6	WASF2/BAIAP2/PTPRJ	3
gga0305				0.0333063	0.1457152	0.1139427		
0	Proteasome	2/32	33/3644	4	2	3	PSMA3/PSMA5	2
gga0451	Cell adhesion molecules				0.1869657	0.1461987		
4	(CAMs)	3/32	94/3644	0.0480769	2	6	ITGA6/ITGAV/BF2	3
gga0077	Pantothenate and CoA			0.1005797	0.3296032			
0	biosynthesis	1/32	12/3644	8	9	0.2577349	VNN1	1
gga0461	Renin-angiotensin system	1/32	13/3644	0.1085041	0.3296032	0.2577349	AGT	1

4				9	9				
gga0301				0.1278450	0.3296032				
0	Ribosome	2/32	71/3644	3	9	0.2577349	RPL6/RPL24		2
gga0401				0.1367650	0.3296032				
2	ErbB signaling pathway	2/32	74/3644	2	9	0.2577349	CAMK2D/KRAS		2
gga0454				0.1397699	0.3296032				
0	Gap junction	2/32	75/3644	7	9	0.2577349	KRAS/TUBB		2
gga0491				0.1458244	0.3296032				
2	GnRH signaling pathway	2/32	77/3644	2	9	0.2577349	CAMK2D/KRAS		2
gga0432				0.1546492	0.3296032				
0	Dorso-ventral axis formation	1/32	19/3644	8	9	0.2577349	KRAS		1
gga0491				0.1643110	0.3296032				
6	Melanogenesis	2/32	83/3644	3	9	0.2577349	CAMK2D/KRAS		2
gga0306				0.1695102	0.3296032				
0	Protein export	1/32	21/3644	6	9	0.2577349	HSPA5		1
gga0401			203/364	0.2626356	0.4838024	0.3783116			
0	MAPK signaling pathway	3/32	4	1	5	9	KRAS/HSPA2/RAP1A		3
gga0033	Arginine and proline			0.2796246		0.3826442			
0	metabolism	1/32	37/3644	3	0.4893431	3	CKM		1
gga0414	Protein processing in		132/364	0.3238078	0.5396797	0.4220052			
1	endoplasmic reticulum	2/32	4	5	5	2	HSPA5/HSPA2		2
gga0411					0.5883303	0.4600477			
5	p53 signaling pathway	1/32	53/3644	0.3755357	1	6	CD82		1
gga0492	Adipocytokine signaling			0.3866170	0.5883303	0.4600477			
0	pathway	1/32	55/3644	6	1	6	CD36		1

gga0437					0.6030113	0.4715276		
0	VEGF signaling pathway	1/32	60/3644	0.4134935	5	7	KRAS	1
gga0465	Natural killer cell mediated			0.4442414	0.6219379	0.4863274		
0	cytotoxicity	1/32	66/3644	2	9	5	KRAS	1
gga0491	Progesterone-mediated			0.4686665	0.6308972	0.4933331		
4	oocyte maturation	1/32	71/3644	1	3	7	KRAS	1
gga0411				0.5482782	0.6997186	0.5471484		
4	Oocyte meiosis	1/32	89/3644	9	8	4	CAMK2D	1
gga0414				0.5603705	0.6997186	0.5471484		
2	Lysosome	1/32	92/3644	8	8	4	CLTC	1
gga0304					0.6997186	0.5471484		
0	Spliceosome	1/32	98/3644	0.5836215	8	4	HSPA2	1
gga0491			107/364	0.6162792	0.6997186	0.5471484		
0	Insulin signaling pathway	1/32	4	2	8	4	KRAS	1
gga0453			108/364	0.6197508	0.6997186	0.5471484		
0	Tight junction	1/32	4	3	8	4	KRAS	1
gga0431			122/364	0.6652722	0.7276415	0.5689828		
0	Wnt signaling pathway	1/32	4	5	2	4	CAMK2D	1
gga0402			142/364	0.7212610	0.7649738	0.5981750		
0	Calcium signaling pathway	1/32	4	8	8	6	CAMK2D	1
gga0408	Neuroactive ligand-receptor		235/364	0.8826571	0.9086176	0.7104979		
0	interaction	1/32	4	1	1	8	C5AR1	1

Table S4 Comparison of the proteomics analysis between P8+DEX and DEX groups by KEGG

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
					0.3334840	0.3233224		
gga04012	ErbB signaling pathway	3/23	74/3644	0.0106349	4	8	PAK3/KRAS/CAMK2D	3
				0.0178696	0.3334840	0.3233224		
gga03050	Proteasome	2/23	33/3644	4	4	8	PSMA5/PSMA3	2
				0.0447113	0.3334840	0.3233224		
gga03320	PPAR signaling pathway	2/23	54/3644	1	4	8	ILK/FABP6	2
				0.0732730	0.3334840	0.3233224		
gga00770	Pantothenate and CoA biosynthesis	1/23	12/3644	1	4	8	VNN1	1
				0.0791416	0.3334840	0.3233224		
gga04614	Renin-angiotensin system	1/23	13/3644	1	4	8	AGT	1
				0.0838129	0.3334840	0.3233224		
gga04912	GnRH signaling pathway	2/23	77/3644	4	4	8	KRAS/CAMK2D	2
				0.0879375	0.3334840	0.3233224		
gga04510	Focal adhesion	3/23	169/3644	9	4	8	PAK3/SPP1/ILK	3
				0.0879375	0.3334840	0.3233224		
gga04810	Regulation of actin cytoskeleton	3/23	169/3644	9	4	8	PAK3/KRAS/RDX	3
				0.0891544	0.3334840	0.3233224	RABEP1/RAB7A/VPS37	
gga04144	Endocytosis	3/23	170/3644	7	4	8	C	3
				0.0953018	0.3334840	0.3233224		
gga04916	Melanogenesis	2/23	83/3644	2	4	8	KRAS/CAMK2D	2
				0.0965348	0.3334840	0.3233224		
gga00910	Nitrogen metabolism	1/23	16/3644	5	4	8	CA2	1
					0.3388172	0.3284931		
gga04320	Dorso-ventral axis formation	1/23	19/3644	0.1136136	3	6	KRAS	1

				0.1174657	0.3388172	0.3284931		
gga04514	Cell adhesion molecules (CAMs)	2/23	94/3644	2	3	6	VCAM1/L1CAM	2
					0.3388172	0.3284931		
gga03060	Protein export	1/23	21/3644	0.1248274	3	6	HSPA5	1
				0.1468492	0.3720180	0.3606823		
gga00640	Propanoate metabolism	1/23	25/3644	4	8	5	LDHB	1
				0.1788909	0.4115579	0.3990173		
gga00270	Cysteine and methionine metabolism	1/23	31/3644	2	2	7	LDHB	1
				0.1841180	0.4115579	0.3990173		
gga00620	Pyruvate metabolism	1/23	32/3644	2	2	7	LDHB	1
				0.2097796	0.4428681	0.4293735		
gga00330	Arginine and proline metabolism	1/23	37/3644	4	3	3	CKM	1
				0.2444121	0.4888242	0.4739293		
gga00010	Glycolysis / Gluconeogenesis	1/23	44/3644	3	5	3	LDHB	1
				0.3182036	0.5419536	0.5254398		
gga04370	VEGF signaling pathway	1/23	60/3644	7	6	4	KRAS	1
	Natural killer cell mediated			0.3440560	0.5419536	0.5254398		
gga04650	cytotoxicity	1/23	66/3644	3	6	4	KRAS	1
				0.3566279	0.5419536	0.5254398		
gga04350	TGF-beta signaling pathway	1/23	69/3644	5	6	4	AMH	1
				0.3607671	0.5419536	0.5254398		
gga04512	ECM-receptor interaction	1/23	70/3644	2	6	4	SPP1	1
				0.3648808	0.5419536	0.5254398		
gga03010	Ribosome	1/23	71/3644	2	6	4	RPL6	1
gga04914	Progesterone-mediated oocyte	1/23	71/3644	0.3648808	0.5419536	0.5254398	KRAS	1

	maturation			2	6	4		
				0.3810838	0.5419536	0.5254398		
gga04540	Gap junction	1/23	75/3644	1	6	4	KRAS	1
				0.3850723	0.5419536	0.5254398		
gga04620	Toll-like receptor signaling pathway	1/23	76/3644	4	6	4	SPP1	1
					0.5900004	0.5720226		
gga04114	Oocyte meiosis	1/23	89/3644	0.4347372	8	3	CAMK2D	1
				0.4972085	0.6339388	0.6146221		
gga04910	Insulin signaling pathway	1/23	107/3644	2	2	3	KRAS	1
				0.5004780	0.6339388	0.6146221		
gga04530	Tight junction	1/23	108/3644	2	2	3	KRAS	1
				0.5320738	0.6462008	0.6265104		
gga04145	Phagosome	1/23	118/3644	8	2	9	RAB7A	1
				0.5441691	0.6462008	0.6265104		
gga04310	Wnt signaling pathway	1/23	122/3644	1	2	9	CAMK2D	1
	Protein processing in endoplasmic			0.5731128	0.6574298	0.6373973		
gga04141	reticulum	1/23	132/3644	2	5	6	HSPA5	1
					0.6574298	0.6373973		
gga04020	Calcium signaling pathway	1/23	142/3644	0.6002937	5	6	CAMK2D	1
				0.6055274	0.6574298	0.6373973		
gga04060	Cytokine-cytokine receptor interaction	1/23	144/3644	9	5	6	AMH	1
				0.7335237	0.7742750	0.7506821		
gga04010	MAPK signaling pathway	1/23	203/3644	1	2	5	KRAS	1
	Neuroactive ligand-receptor			0.7852015	0.8064232	0.7818507		
gga04080	interaction	1/23	235/3644	8	5	9	C5AR1	1

Table S5 Multiple reaction monitoring (MRM) analysis of plasmal exosomal proteins

Accession	Gene Symbol	DEX/CON FC	DEX/CON p_value	DEX+P8/C ON FC	DEX+P8/C ON p_value	DEX+P8/D EX FC	DEX+P8/D EX p_value	CON_aver age	DEX_aver age	DEX+P8_aver age
A0A1D5PG		1.1009068	0.7550594			0.37741019	0.06120464	664305.666	731338.666	
T3	BAIAP2	62	17	0.41549347	0.02010349	2	4	7	7	276014.6667
A0A1D5PM		3.1821924	0.0467276	2.79059796	0.10194933	0.87694193	0.72993714			
A3	NELL2	12	74	2	4	2	1	859218	2734197	2397732
A0A3Q2U50		1.2077623	0.4897297	0.66234558	0.19084499	0.54840722	0.07173971	2042723.66	2467124.66	
4	PROS1	16	15	4	1	8	1	7	7	1352989
A0A3Q2UFJ		1.2356395			0.01802243	0.46955910	0.02050655	3157682.33	3901757.33	
3	CAMK2D	99	0.2951612	0.58020582	8	1	6	3	3	1832105.667
B5BSS3		0.8753621	0.7643922		0.51747720	0.78911613	0.47765300			
	BF2	15	71	0.69076237	5	6	9	412162	360791	284706
E1C007		0.9737639	0.9708582	0.37654628	0.24567549	0.38669153	0.38345951	15448873.6	15043556.6	
	PACSIN2	77	35	6	4	4	5	7	7	5817216
E1C3Y3		0.9822350	0.9343658	1.28260131	0.58047973	1.30579881	0.55223361	9718178.33		
	TSPAN8	11	48	7	8	9	3	3	9545535	12464548.33
F1NEB3		1.0211664	0.9057686	0.97021449	0.90571794			13736156.6	14026901.6	
	HABP2	01	84	7	1	0.95010421	0.815898	7	7	13327018.33

F1NIW7	CUBN	0.5549430	0.2239295		0.04297254	0.20725570	0.00348189	10884433.6	6040240.66	
		36	54	0.11501511	4	4	6	7	7	1251874.333
F1NLE7	AIMP1	0.6154844	0.3844414		0.02188659	0.08683463	0.13315780	1824211.66		
		97	2	0.05344537	6	2	7	7	1122774	97495.66667
F1NM67	ITGB2	1.3396357	0.2488904	0.42111004	0.00294768	0.31434668	0.02037987	805742.666	1079401.66	
		32	17	8	9	3	6	7	7	339306.3333
F1NQD9	RDX	1.2111119	0.2878094	0.24363058	0.01076754	0.20116273				
		24	22	6	8	4	0.00055016	4101450	4967315	999238.6667
F1NSA8	RAP1A	0.7674534	0.0485213	0.96989043	0.84360517	1.26377752	0.17464370	10959386.3		
		64	86	7	7	3	8	3	8410819	10629404
F1NUJ7	FABP6	1.6448510	0.0003558	1.09491971	0.33573770	0.66566497	0.00461756	915250.666		
		28	6	6	7	3	9	7	1505451	1002126
F1NV09	EPCAM	1.9687530	0.0168985	0.88081274	0.41765304	0.44739626	0.01093201			
		38	81	8	4	1	4	401223	789909	353402.3333
H9L0D7	WASF2	1.6230619	0.1338390	1.01606437		0.62601699	0.06855245	124976.333	202844.333	
		66	27	5	0.97006436	5	6	3	3	126984
P35062	HIST1H2A3	1.0372102	0.8256832	0.96103005	0.86994725	0.92655283		6292422.33	6526564.66	
		06	73	8	9	6	0.71354855	3	7	6047207
Q5W9C5	BF1	0.8703154	0.7348435	0.75525584	0.58083759	0.86779547	0.59091803		2575862.33	
		97	06	7	8	1	4	2959688	3	2235321.667
Q7SX63	HSPA2	1.3135884	0.4048487	0.61676543	0.22664755	0.46952713	0.02900557	732618.333		
		76	2	7	8	8	6	3	962359	451853.6667
Q90824	TNC	0.8548722	0.7306834	0.57186291	0.37808480	0.66894542	0.21771032		19217838.6	
		96	24	5	5	9	8	22480362	7	12855685.33
Q9DER4	ZP1	2.0477955	0.1428157	0.99724674	0.99409856	0.48698550	0.17808125	964190.666	1974465.33	961536

		26	87	1	4	6	9	7	3	
R4GKL8		0.6178575	0.0439357	0.15140146	0.00321063	0.24504266	8.11659E-	559023.666		
	C1QTNF3	62	34	1	8	1	05	7	345397	84637
