

Supplementary Table VI. Selected KEGG pathway enrichments among differentially expressed mRNAs in SLE patients [*n* (%)]

Pathway ID	Pathway name	DEGs with pathway annotation (2,200)	<i>P</i> -value
ko00630	Glyoxylate and dicarboxylate metabolism	13 (0.59)	0.002
ko04710	Circadian rhythm	11 (0.50)	0.002
ko04666	Fcγ R-mediated phagocytosis	59 (2.68)	0.002
ko00900	Terpenoid backbone biosynthesis	10 (0.45)	0.004
ko04915	Estrogen signaling pathway	33 (1.50)	0.005
ko04022	cGMP-PKG signaling pathway	47 (2.14)	0.015
ko00640	Propanoate metabolism	11 (0.50)	0.016
ko05223	Non-small cell lung cancer	17 (0.77)	0.020
ko04922	Glucagon signaling pathway	27 (1.23)	0.022
ko03018	RNA degradation	91 (4.14)	0.025
ko04918	Thyroid hormone synthesis	19 (0.86)	0.030
ko00532	Glycosaminoglycan biosynthesis-chondroitin sulfate/dermatan sulfate	8 (0.36)	0.033
ko04971	Gastric acid secretion	25 (1.14)	0.040
ko04910	Insulin signaling pathway	42 (1.91)	0.047
ko00010	Glycolysis/Gluconeogenesis	16(0.73)	0.047
ko04020	Calcium signaling pathway	46 (2.09)	0.049