Table 4. Genes that best discriminate systemic lupus erythematosus from control peripheral blood mononuclear cells are enriched for IFN-regulated genes

Criteria Used to Define Genes as "IFN-Regulated"	Criteria Used to Define Genes as "Dysregulated in SLE"	# of IFN-Regulated Transcripts Observed	# Expected by Chance Alone	Ratio: Observed/Expected	P value (Chi-Test)
Fold Change > 2, AD Difference > 500, 4/4 Experiments (193)	p<0.001, Fold Change > 1.5, Difference > 100 (161)	23 (14.3%)	6.8 (4.2%)	3.4	1.0×10^{-10}
	p<0.001, Fold Change > 1.5, Difference > 200 (141)	22 (15.6%)	6.0	3.7	9.9×10^{-12}
	p<0.001, Fold Change > 1.6, Difference > 100 (130)	22 (16.9%)	5.5	4.0	2.9×10^{-13}
	p<0.001 (465)	33 (7.1%)	19.7	1.7	1.2×10^{-3}
Fold Change > 2, Difference > 500, 3/4 Experiments (551)	p<0.001, Fold Change > 1.5, Difference > 100 (161)	40 (24.8%)	19.4 (12.1%)	2.1	4.0×10^{-7}
	p<0.001, Fold Change > 1.5, Difference > 200 (141)	38 (27.0%)	17.0	2.2	3.6×10^{-8}
	p<0.001, Fold Change > 1.6, Difference > 100 (130)	36 (27.7%)	15.7	2.3	2.9×10^{-8}
	p<0.001 (465)	67 (14.4%)	56.1	1.2	0.10
p<0.001 (63)	p<0.001, Fold Change > 1.5, Difference > 100 (161)	9 (5.6%)	2.2 (1.4%)	4.1	3.1×10^{-6}
	p<0.001, Fold Change > 1.5, Difference > 200 (141)	9 (6.4%)	1.9	4.6	2.3×10^{-7}
	p<0.001, Fold Change > 1.6, Difference > 100 (130)	7 (5.4%)	1.8	3.9	7.1×10^{-5}
	p<0.001 (465)	16 (3.4%)	6.4	2.5	5.8×10^{-5}
p<0.005 (225)	p<0.001, Fold Change > 1.5, Difference > 100 (161)	16 (9.9%)	7.9 (4.9%)	2.0	2.8×10^{-3}
	p<0.001, Fold Change > 1.5, Difference > 200 (141)	16 (11.3%)	6.9	2.3	3.5×10^{-4}
	p<0.001, Fold Change > 1.6, Difference > 100 (130)	14 (10.8%)	6.4	2.2	1.8×10^{-3}
	p<0.001 (465)	40 (8.6%)	22.9	1.7	1.1×10^{-4}
p<0.01 (365)	p<0.001, Fold Change > 1.5, Difference > 100 (161)	24 (14.9%)	12.9 (8.0%)	1.9	9.9×10^{-4}
	p<0.001, Fold Change > 1.5, Difference > 200 (141)	24 (17.0%)	11.3	2.1	5.9×10^{-5}
	p<0.001, Fold Change > 1.6, Difference > 100 (130)	22 (16.9%)	10.4	2.1	1.4×10^{-4}
	p<0.001 (465)	62 (13.3%)	37.2	1.7	7.5×10^{-6}