

**Suppl. Table 1.** 26 down-regulated expression genes in SLE females vs SLE males, which of most genes were linked to Y chromosome

Gene ID	q-valu	Fold	Chrom	Symbol	Full name
	e(%)	Change	osomal		
NM_004653	0	0.0011	chrY	SMCY	Smcy homolog, Y-linked (mouse)
D87072	0	0.0019	chrY	SMCY	Smcy homolog, Y-linked (mouse)
NM_032576	0	0.0021	chrY	CYorf15B	chromosome Y open reading frame 15B
NM_004654	0	0.0027	chrY	USP9Y	ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)
NM_004681	0	0.0028	chrY	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked
BC100905	0	0.0041	chrY	RPS4Y1	ribosomal protein S4, Y-linked 1
NM_004660	0	0.0055	chrY	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
NM_001008	0	0.0072	chrY	RPS4Y1	ribosomal protein S4, Y-linked 1
NM_182659	0	0.0087	chrY	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
AF332239	0	0.0096	chrY	TTTY10	testis-specific transcript, Y-linked 10
<b>NM_001005852</b>	<b>0</b>	<b>0.0102</b>	<b>chrY</b>	<b>CYorf15A</b>	<b>chromosome Y open reading frame 15A</b>
BC035312	0	0.0103	chrY	CYorf15B	chromosome Y open reading frame 15B
BC110817	0	0.0104	chrY	CYorf15A	chromosome Y open reading frame 15A
NM_003411	0	0.0113	chrY	ZFY	zinc finger protein, Y-linked
NM_182660	0	0.0221	chrY	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
NM_007125	0	0.0285	chrY	UTY	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked
BC034942	0	0.0572	chrY	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked
<b>BC093959</b>	<b>4.9773</b>	<b>0.0635</b>	<b>chr8</b>	<b>DEFA4</b>	<b>defensin, alpha 4, corticostatin 348</b>
<b>BC015823</b>	<b>0</b>	<b>0.0849</b>	<b>chr3</b>	<b>LTF</b>	<b>lactotransferrin</b>
<b>BC015822</b>	<b>4.0395</b>	<b>0.0926</b>	<b>chr3</b>	<b>LTF</b>	<b>lactotransferrin 761</b>
NM_001039567	0	0.111	chrY	RPS4Y2	ribosomal protein S4, Y-linked 2
<b>NM_002343</b>	<b>4.9773</b>	<b>0.1161</b>	<b>chr3</b>	<b>LTF</b>	<b>lactotransferrin 348</b>
<b>NM_014893</b>	<b>0</b>	<b>0.1291</b>	<b>chrY</b>	<b>NLGN4Y</b>	<b>neuroligin 4, Y-linked</b>
<b>BC055089</b>	<b>0</b>	<b>0.1412</b>	<b>chr3</b>	<b>CAMP</b>	<b>cathelicidin antimicrobial peptide</b>
BC005248	0	0.2904	chrY	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked
<b>AL133030</b>	<b>4.0395</b>	<b>0.4397</b>	<b>chr22</b>	<b>KIAA1666</b>	<b>KIAA1666 protein 761</b>

\*Bold words showed eight DEGs have non-significant different between healthy females and healthy males.

**Suppl. Table 2.** Enriched signaling pathways with significant association with 26 DEGs (SLE females/ SLE males)

	No. of genes	p-Value
<b>Kegg pathways</b>		
Ribosome	1	0.019865
<b>Genmap pathways</b>		
GO_Samples--Biological process--spermatogenesis	2	2.42E-04
GO_Samples--Cellular component--male gamete generation	2	2.42E-04
GO_Samples--Cellular component--gametogenesis	2	3.68E-04
Tissue-specific--Hs_1-Tissue-Blood_and_Lymph	2	4.30E-04
GO_Samples--Biological process--sexual reproduction	2	5.67E-04
GO_Samples--Biological process--reproduction	2	9.37E-04
Contributed--cellular_process--Hs_Translation_Factors	1	0.009782
Contributed--molecular_function--Hs_Ribosomal_Proteins	1	0.01716
GO_Samples--Molecular function--translation factor activity, nucleic acid binding	1	0.019286
GO_Samples--Biological process--cell ion homeostasis	1	0.019286
GO_Samples--Biological process--di-, tri-valent inorganic cation transport	1	0.019479
GO_Samples--Molecular function--translation regulator activity	1	0.019672
GO_Samples--Molecular function--cysteine-type endopeptidase activity	1	0.020251
GO_Samples--Biological process--ion homeostasis	1	0.021216
GO_Samples--Biological process--cell homeostasis	1	0.021408
GO_Samples--Biological process--ubiquitin-dependent protein catabolism	1	0.021986
GO_Samples--Molecular function--cysteine-type peptidase activity	1	0.024104
GO_Samples--Molecular function--helicase activity	1	0.024872
GO_Samples--Molecular function--serine-type endopeptidase activity	1	0.028517
GO_Samples--Biological process--humoral immune response	1	0.030048
GO_Samples--Molecular Function--catalytic activity	1	0.031386
GO_Samples--Biological process--translation	1	0.03215
GO_Samples--Molecular function--lipid binding	1	0.035961
GO_Samples--Biological process--response to chemical substance	1	0.039189
GO_Samples--Biological process--ubiquitin cycle	1	0.046371
GO_Samples--Cellular component--cytosol	1	0.048818
GO_Samples--Cellular component--extracellular space	1	0.052195

**Suppl. Table 3.** Top ten enriched signaling pathways with significant association with DEGs (SLE females/SLE males)

	No. of genes	p-Value
<b>KEGG pathways</b>		
Ribosome	1	0.019865
<b>Biocarta pathways</b>		
novel		
<b>Genmapp pathways</b>		
spermatogenesis	2	2.42E-04
male gamete generation	2	2.42E-04
gametogenesis	2	3.68E-04
Blood_and_Lymph	2	4.30E-04
sexual reproduction	2	5.67E-04
reproduction	2	9.37E-04
Translation_Factors	1	0.009782
Ribosomal_Proteins	1	0.01716
translation factor activity, nucleic acid binding	1	0.019286
cell ion homeostasis	1	0.019286

**Suppl. Table 4.** Top ten enriched signaling pathways with significant association with estrogen-relevant DEGs (SLE females/SLE males)

	No. of genes	p-Value
<b>KEGG pathways</b>		
Ribosome	1	0.013287258
<b>Biocarta pathways</b>		
novel		
<b>Genmapp pathways</b>		
Blood_and_Lymph	2	1.80E-04
Translation_Factors	1	0.006531869
Ribosomal_Proteins	1	0.011472277
translation factor activity, nucleic acid binding	1	0.012898568
cell ion homeostasis	1	0.012898568
di-, tri-valent inorganic cation transport	1	0.013028145
translation regulator activity	1	0.013157709
ion homeostasis	1	0.014193707
cell homeostasis	1	0.014323143
helicase activity	1	0.016650571

