

Supplementary table S4. Top 10 genes with highest centrality/MM per module. MM: Module Membership, WGCNA: Weighted Gene Co-expression Network Analysis, CTL: control, ELS: early-life stress, HRD: high ω_6/ω_3 ratio diet, LRD: low ω_6/ω_3 ratio diet, SAL: saline, LPS: lipopolysaccharide.

WGCNA module	geneSymbol	MM	p-value
Blue module: Condition (CTL/ELS)	Gaa	0.95106593	2.52E-33
	Syn1	0.94969747	5.81E-33
	Ubqln2	0.94935591	7.13E-33
	Sez6l	0.94424387	1.30E-31
	Sez6	0.94082588	7.82E-31
	Igsf8	0.93379499	2.29E-29
	Atp2b3	0.92858186	2.22E-28
	Pianp	0.92448286	1.18E-27
	Fasn	0.92059425	5.26E-27
	Pom121	0.92044793	5.55E-27
Brown module: Diet (HRD/LRD)	H13	0.93275507	3.65E-29
	Efna3	0.92213248	2.93E-27
	Ypel3	0.91348068	6.75E-26
	2900097C17Rik	0.91109813	1.51E-25
	Camk1d	0.89835297	7.92E-24
	Gm7292	0.87084334	8.70E-21
	Abhd17a	0.86305111	4.74E-20
	Tnfrsf21	0.85834721	1.26E-19
	Gpr135	0.85113784	5.23E-19
Tmem127	0.84966363	6.93E-19	
Turquoise module: challenge (SAL/LPS)	Cdkn1a	0.98914054	2.38E-53
	Gbp4	0.98667079	1.32E-50
	Gbp10	0.98651192	1.90E-50
	Mt2	0.98628127	3.20E-50
	Ctla2a	0.984339	1.89E-48
	Bcl2a1a	0.98375082	5.87E-48
	Gbp2	0.98367457	6.78E-48
	Cd274	0.98355697	8.46E-48
	P2ry12	-0.9827977	3.39E-47
Igtp	0.9826898	4.11E-47	