SUPPLEMENTARY MATERIAL

SUPPLEMENTARY METHODS

QrtPCR of Brain Gene Transcripts In the Endocannabinoid System: The following TaqMan® specific gene expression probe primers from Life Technologies™ (Carlsbad, CA) were used to determine brain mRNA levels of: cannabinoid receptor-1 (*Cnr1*, Mm01212171_s1); cannabinoid receptor-2 (*Cnr2*, Mm02620087_s1); diacylglycerol lipase α (*Dagla*, Mm00813830_m1); diacylglycerol lipase β (*Daglb*, Mm00523381_m1); fatty acid amide hydrolase (*Faah*, Mm00515684_m1); fatty acid binding protein-3 (*Fabp3*, Mm02342494_m1); fatty acid binding protein-5 (*Fabp5*, Mm00783731_s1); fatty acid binding protein-7 (*Fabp7*, Mm01246302_m1); 2-monoacylglycerol lipase (*Mgll*, Mm00449274_m1); N-acylethanolamine hydrolyzing acid amidase (*Naah*, Mm01341699_m1); N-acylphosphatidylethanolamine phospholipase D (*Napepld*, Mm00724596_m1); sterol carrier protein-2 (*Scp2*, Mm01257982_m1). Two replicates of each sample reaction (20 μL total volume each) were performed on 96-well optical reaction plates (Applied Biosystems®, Foster City, CA). ABI Prism 7000 SDS software (Applied Biosystems®, Foster City, CA) established the threshold cycle from each well. The housekeeping gene 18S RNA was used to normalize QrtPCR data for mRNA expression of *Cnr1*, *Cnr2*, *Dagla*, *Daglb*, *Faah*, *Fabp3*, *Fabp5*, *Fabp7*, *Mgll*, *Naah*, *Napepld*, and *Scp-2* as described earlier (Klipsic *et al.* 2015;Martin *et al.* 2016a;Martin *et al.* 2016b).

SUPPLEMENTARY FIGURE LEGENDS

SUPPLEMENTARY FIGURE 1. Impact of *Fabp1* gene ablation (LKO) on ability of high fat diet (HFD) to alter brain mRNA levels of cytosolic binding/chaperone proteins of ARA and endocannabinoids. All conditions were as in Figure 1 except that QrtPCR was performed to determine mRNA levels of (A) *Fabp3*, (B) *Fabp5*, (C) *Fabp7*, and (D) *Scp-2* as described in Supplementary Methods. Levels of mRNA were normalized to an internal control (18S RNA), values compared to male WT set to 1, results expressed as the relative ratio of each protein in High-Fat/Control diet, and data presented as mean ± SEM (n = 8); *, $P < 0.05$ for LKO *vs* WT; #, $P < 0.05$ for female (F) *vs* male (M).

SUPPLEMENTARY FIGURE 2. Effect of *Fabp1* gene ablation (LKO) on ability of high fat diet (HFD) to impact mRNA levels of brain proteins involved in endocannabinoid synthesis and degradation. All conditions were as described in Figure 1 except that QrtPCR was used as described in Supplementary Methods to determine mRNA levels of: (A) *Napepld*, (B) *Dagla*, (C) *Daglb*, (D) *Faah*, (E) *Naaa*, (F) *Mgll*, (G) *Cnr1*, and (H) *Cnr2*. Levels of mRNA were normalized to an internal control (18S RNA), values compared to male WT set to 1, results expressed as the relative ratio of each protein in High-Fat/Control diet, and data presented as mean ± SEM (n = 8); *, $P < 0.05$ for LKO *vs* WT; #, $P < 0.05$ for female (F) *vs* male (M).

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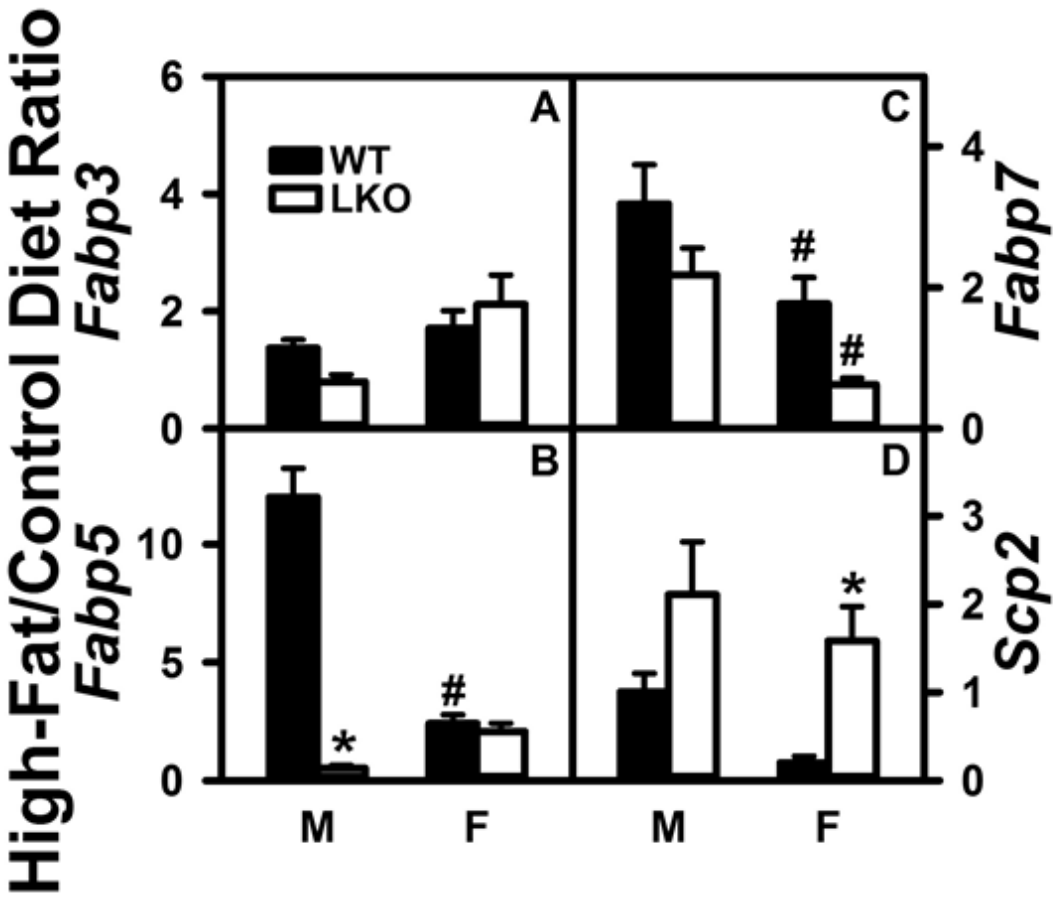
Supplementary Figure 1



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Supplementary Figure 2