

1 Cav1.2 and Cav1.3 voltage-gated L-type Ca²⁺ channels in rat white fat
2 adipocytes.

3

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25 **Abstract**

26 L-type channel antagonists are of therapeutic benefit in the treatment of
27 hyperlipidaemia and insulin resistance. Our aim was to identify L-type
28 voltage gated Ca^{2+} channels in white fat adipocytes, and determine if they
29 affect intracellular Ca^{2+} , lipolysis and lipogenesis. We used a
30 multidisciplinary approach of molecular biology, confocal microscopy, Ca^{2+}
31 imaging and metabolic assays, to explore this problem using adipocytes
32 isolated from adult rat epididymal fat pads. $\text{Ca}_v1.2$, $\text{Ca}_v1.3$ and $\text{Ca}_v1.1$
33 α_1 , beta and $\alpha_2\delta$ subunits were detected at the gene expression
34 level. The $\text{Ca}_v1.2$ and $\text{Ca}_v1.3$ α_1 subunits were identified in the plasma
35 membrane at the protein level. Confocal microscopy with fluorescent
36 antibodies labelled $\text{Ca}_v1.2$ in the plasma membrane. Ca^{2+} imaging revealed
37 that the intracellular Ca^{2+} concentration, $[\text{Ca}^{2+}]_i$, was reversibly decreased
38 by removal of extracellular Ca^{2+} , an effect mimicked by verapamil,
39 nifedipine and Co^{2+} , all blockers of L-type channels. Whereas the Ca^{2+}
40 channel agonist BAY-K8644 increased $[\text{Ca}^{2+}]_i$. The finding that the
41 magnitude of these effects correlated with basal $[\text{Ca}^{2+}]_i$ suggests that
42 adipocyte $[\text{Ca}^{2+}]_i$ is controlled by L-type Ca^{2+} channels that are
43 constitutively active at the adipocyte depolarized membrane potential.
44 Pharmacological manipulation of L-type channel activity modulated both
45 basal and catecholamine-stimulated lipolysis but not insulin-induced
46 glucose uptake or lipogenesis. We conclude that white adipocytes have
47 constitutively active L-type Ca^{2+} channels which explains sensitivity of
48 lipolysis to Ca^{2+} channel modulators. Our data suggest $\text{Ca}_v1.2$ as a potential
49 novel therapeutic target in the treatment of obesity.

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51

52

53 **Introduction**

54 White fat adipocytes (WFA) are the major energy depot of the body, storing
55 and releasing energy in response to the calorific demands of the body
56 during periods of excess and need respectively (Arner *et al.* 2011). It is
57 widely accepted that an impairment of WFA triglyceride metabolism in
58 obesity is a major etiological factor of the metabolic syndrome and type 2
59 diabetes. Whereby the inability of WFA to appropriately store energy as fat
60 leads to ectopic disposition of lipids in insulin-responsive tissues such as
61 skeletal muscle, liver and pancreas to promote insulin resistance and
62 associated systemic disorders (Sattar & Gill 2014). To address
63 dysfunctional fat storage, it is first necessary to understand the regulation
64 of lipid storage in healthy WFA.

65

66 Extracellular Ca^{2+} influx is implicated in the processes of fat storage
67 (Arruda & Hotamisligil 2015): lipolysis (Schimmel 1978; Izawa *et al.* 1983;
68 Allen & Beck 2000) and lipogenesis (Avasthy *et al.* 1988). Indeed, studies
69 in *Drosophila* mutants indicate that impaired adipocyte cytosolic Ca^{2+} is
70 associated with increased lipid deposition (Baumbach *et al.* 2014).
71 However, the identity of the Ca^{2+} pathway is unclear (Draznin *et al.* 1988).

72

73 Several routes by which Ca^{2+} enters primary WFA are identified, these
74 include voltage-gated Ca^{2+} channels, VGCC (Clausen & Martin 1977;
75 Pershadsingh *et al.* 1989) store-operated Ca^{2+} channels (El Hachmane &
76 Olofsson 2018), and reverse mode $\text{Na}^+/\text{Ca}^{2+}$ exchange, NCX (Pershadsingh
77 *et al.* 1989; Bentley *et al.* 2014). Although VGCCs play a prominent role in
78 Ca^{2+} entry and function of electrically excitable cells (Lipscombe 2004), this
79 route of influx is ill-defined in non-excitable adipocytes.

80

81 Pharmacological investigations show that verapamil and nifedipine,
82 blockers of L-type VGCCs, can inhibit WFA Ca^{2+} uptake (Martin *et al.* 1975;
83 Pershadsingh *et al.* 1989) and impair glucose transport (Draznin *et al.*
84 1987), lipolysis (Izawa *et al.* 1983) and lipogenesis (Avasthy *et al.* 1988).

85 However, this inference of an association between Ca^{2+} influx and lipid
86 turnover has come from independent studies where animal species, adipose
87 depot as well as experimental conditions differed. To date, no
88 comprehensive synthetic study exists where changes in Ca^{2+} influx and
89 WFA function has been examined in primary adipocytes for the same
90 species under similar experimental conditions of similar age and weight.
91 Furthermore, a detailed molecular and immunohistochemical investigation
92 of L-type VGCC expression in WFA is absent.

93

94 The aim of this study was to use a combination of Ca^{2+} imaging, metabolic,
95 immunocytochemical and molecular biology techniques to identify L-type
96 Ca^{2+} channels in WAT and demonstrate their functional role in lipid
97 turnover.

98

99 **Materials and Methods**

100

101 Unless stated otherwise, adipocyte isolation and experiments were
102 performed in Hank's buffer solution which composed of (in mM): NaCl 138,
103 NaHCO_3 4.2, KCl 5.6, MgCl_2 1.2, CaCl_2 2.6, NaH_2PO_4 1.2, glucose 5 and
104 HEPES 10 (pH 7.4 with NaOH). For, nominally Ca^{2+} free solutions, CaCl_2
105 was equimolarly replaced with MgCl_2 . All % values are weight per volume.
106 Unless stated otherwise drugs and chemicals are from Sigma, Poole, UK

107

108 *Ethical approval*

109 Animal care and experimental procedures were carried out in accordance
110 with either the UK Home Office Animals (Scientific Procedures) Act (1986)
111 or Swedish ethical review board. In both instances the local ethical
112 committees approved the animal procedures. Animals were killed by
113 cervical dislocation or CO_2 .

114

115 *Isolation and preparation of adipocytes*

116 Epididymal fat pads were taken from Wistar rats (*fed ad libitum*, 12 hr
117 dark/light cycle, weight 220–420 g; Charles River Laboratory, Kent, UK).
118 For some experiments tissue from Sprague Dawley rats were used, but
119 since no difference could be detected, data was pooled. Adipocytes were
120 isolated as described previously (Bentley *et al.* 2014).

121

122 *PCR*

123 For reverse transcriptase PCR (RT-PCR) total RNA was isolated by cell lysis
124 in TRI Reagent. Genomic DNA was removed with RQ1 RNase-free DNase
125 (Promega, UK) with RNA quantity and purity determined by the A_{260}/A_{280}
126 ratio (1.98 to 2.02). The RNA integrity numbers (6-8) ascertained samples
127 were suitable for RT-PCR (Schroeder *et al.* 2006). First-strand cDNA
128 synthesis used 1 μg of total RNA with 200 ng random hexamer primers and
129 Avian Myeloblastosis Virus reverse transcriptase (10 units/ μl RNA,
130 Promega).

131 PCR reactions used Dream Taq PCR Master Mix (ThermoFisher, UK) and
132 primers shown in Table 1. PCR was performed at 95°C for 10 min, followed
133 by 40 cycles at 95°C for 45 sec, 58°C for 45 sec, 72°C for 45 sec and
134 terminated by a final extension step at 72°C for 10 min. PCR products were
135 separated on 1% agarose gels, DNA stained with 0.5 $\mu\text{g}/\text{ml}$ ethidium
136 bromide and imaged with GeneSnap software (Syngene, UK). cDNA
137 sequencing (DeepSeq, Nottingham, UK) checked PCR product identity.

138

139 Quantitative PCR (qPCR) reactions were performed in triplicate with SYBR®
140 Green JumpStart™ Taq ReadyMix™. The thermal profile was 10 minutes
141 at 95°C, 40 cycles of denaturation at 95°C for 15 seconds, annealing for
142 20 seconds at the primer specific temperature, and elongation at 72°C for
143 35 seconds. The resultant mean threshold cycle (Ct) values were used for
144 gene normalization and expression analyses. Three, stable, reference
145 genes with the sequences listed in Table 2 were used: glyceraldehyde-3-
146 phosphate dehydrogenase (GAPDH), phosphoglycerate kinase
147 1 (PGK1) and hypoxanthine guanine phosphoribosyl transferase (HPRT1)

148 (Gorzelniaak *et al.* 2001; Fink *et al.* 2008; Silver *et al.* 2008). Relative mRNA
149 levels were quantified by the method of Pfaffl (Pfaffl 2001).

150

151 *Western blot analysis*

152 Cytosolic and solubilized plasma membrane proteins were prepared by
153 differential centrifugation. Cell lysates were prepared at 4°C with a lysis
154 solution that contained 10 µl of protease inhibitor cocktail per 1 ml of lysis
155 buffer (10 mM tris, 250 mM sucrose, 1 mM EDTA, pH 7.4). Protein content
156 was determined by Lowry. 15-20 µg of protein was resolved by SDS-PAGE
157 on 4-20% gradient precast minigels TGX (Biorad, UK) at 170 volts for 40
158 minutes.

159 Protein transfer onto nitrocellulose membranes was performed at 100 volts
160 for 60 minutes in cold transfer buffer; Ponceau S staining confirmed
161 transfer. Membranes were blocked in 5% milk in TBST (25mM Tris, pH 7.6;
162 125 mM NaCl; 0.1% Tween 20) for 3-4 hours, at 20-22°C, followed by
163 overnight incubation at 4°C with primary antibodies: rabbit anti-Cav1.3 at
164 1:200 (ACC-005, Alomone), anti Cav1.2 at 1:500 dilution (ACC-003,
165 Alomone), anti-β-actin at 1:5,000 and anti-Na,K-ATPase at 1:20,000
166 (Abcam, UK). Membranes were washed with TBST and incubated for 1 hour
167 at room temperature with a 1:10,000 dilution of secondary antibodies:
168 IRDye 800 CW goat anti-rabbit IgG (Li-COR™) and IRDye 680 CW goat
169 anti-mouse IgG (Li-COR™). Antibody dilutions were made in 5% milk in
170 TBST. Membranes were then washed with TBST, rinsed in H₂O and imaged
171 with Li-COR Odyssey infrared Imaging System.

172 Band intensity was measured using the Li-COR Odyssey software version
173 2.1 (Li-COR Bioscience, USA) and analyzed using Image Studio Lite Version
174 5.2. For each protein band the signal intensity was normalized to that of β-
175 actin expression, which was then expressed relative to that in brain. In
176 initial experiments GAPDH was used as a control, but since comparison of
177 the ratios obtained with that of β-actin expression showed no difference,
178 the two set of data were pooled. For Cav1.2 in brain, bands spanning 130-
179 250 kD were combined before normalization to β-actin. Samples probed

180 with the primary antibodies in the absence of primary antiserum indicated
181 absence of non-specific binding

182

183 *Immunocytochemistry*

184 Adipocytes were attached to poly-L-lysine (25-100 $\mu\text{g ml}^{-1}$) coated
185 coverslips and fixed with 4% PFA for 10 min. Cells were permeabilised in
186 blocking buffer (PBS with 3% BSA and 0.5% Triton-100x) for 10 min then
187 stained with primary anti-Calcium Channel L-type alpha 1C subunit
188 (cacna1C) antibody conjugated with Atto 594 (ACC-003-AG, Alomone,) at
189 1:200 dilution for 16 hours (Raifman *et al.* 2017). To visualize nuclei cells
190 were stained with Hoechst 33342 (8 μM for 30 min). Positive controls were
191 initially performed with pancreatic beta-cell that express Cav1.2 (Schulla *et*
192 *al.* 2003). Images were captured on a Zeiss LSM880C confocal microscope
193 with excitation wavelengths of 405nm for Hoechst33342 and 633nm for the
194 anti-CaV1.2-ATTO antibody.

195

196 *Measurement of $[Ca^{2+}]_i$*

197 Adipocytes attached to coverslips were incubated with the Ca^{2+} fluorophore
198 Fluo-4 AM (1 μM ; Molecular Probes) in Hank's solution with 0.01% BSA for
199 30 minutes at 21-23°C in the dark. Coverslips were mounted in a perfusion
200 chamber on an Axiovert 135 Inverted microscope equipped for
201 epifluorescence (Carl Zeiss Ltd, UK). Cells were focused to maximize
202 equatorial circumference and fluorescence. Adipocytes were identified
203 under Kohler illumination as 50-100 μm diameter spheroids with a nuclear
204 protuberance (Fig. 3). Experiments were performed 1-4 hour post isolation.

205

206 Fluo-4 was excited at 450-490 nm, the emitted light band-pass filtered at
207 515-565 nm and the signal detected using a Photonics Science ISIS-3
208 camera with image intensification (luminous gain 8,000:1). Fluorescence
209 emission was integrated for 900 ms and captured at 1Hz with an 8-bit frame
210 grabber (DT3155, Data Translation, Basingstoke, UK) and Imaging
211 Workbench Ver. 6.0 software (Indec Biosystems, Santa Clara, CA, USA).

212 Cells were perfused at 1 ml min⁻¹. Since dye extrusion occurred at
213 temperatures >30°C, experiments were performed at 27-28°C.

214

215 For data analysis, a region of interest (ROI) was drawn around each cell,
216 background corrected and the time course of its mean fluorescent intensity
217 calculated. Fluorescence was calibrated by a two-point method (Ni *et al.*
218 1994): the maximum fluorescence value, F_{max}; determined by
219 permeabilization of the cells with Triton X-100 (0.0125-0.1%) followed by
220 10mM EGTA to determine the minimum, F_{min}. [Ca²⁺]_i was calculated with
221 the equation (Equation 1):

$$222 \quad [Ca^{2+}]_i = Kd \times \frac{(F - F_{min})}{(F_{max} - F)}$$

223 Where F is the background corrected fluorescence, and Kd the dissociation
224 constant of Fluo-4: 345 nM (Bentley *et al.* 2014). Over 75% of basal [Ca²⁺]_i
225 values measured were below the Kd of the dye and thus within its linear
226 region of sensitivity. Data was only used from cells in which [Ca²⁺]_i was
227 stable and had a basal value within the 5-95% percentile range (60-380
228 nM).

229

230 To visualize spatial variation of [Ca²⁺]_i it is necessary to mitigate
231 fluorescent signal heterogeneity due to uneven dye loading or/and
232 differences in cytoplasmic volume. In the absence of extracellular Ca²⁺,
233 Ca²⁺ influx is abolished and heterogeneity in fluorescence was assumed to
234 reflect variation in only cell volume and dye loading. Since these
235 parameters proportionally affect Fluo-4 fluorescence, a ratio of the
236 fluorescence signal in the presence of extracellular Ca²⁺ with that in its
237 absence was undertaken Using ImageJ2 with floating point arithmetic
238 (Rueden *et al.* 2017) to normalize these confounders to reveal true
239 differences in spatial [Ca²⁺]_i.

240

241 *Biochemical assays*

242 To control for differences in adipocyte cell-density, biochemical data were
243 normalized to paired values measured under basal or control conditions.
244 Experiments were performed at 37°C.

245

246 *Free fatty acid assay*

247 Free fatty acid (FFA) release was used to measure lipolysis. Adipocytes
248 were incubated for 60 minutes under different experimental conditions in 1
249 ml of Hank's. After which, 100 μ l of supernatant was removed and stored
250 at -20°C prior to assay. FFA was assayed with a non-esterified FFA assay
251 kit (WAKO chemicals). After subtraction of blank, data was normalized to
252 the absorbance of the FFA standard (17 μ M oleic acid) and corrected for
253 dilution.

254

255 *Glucose uptake*

256 Glucose-utilization was measured via 14 C glucose uptake. After a 30 minute
257 pre-incubation under different experimental conditions, 14 C glucose was
258 added and the cells incubated for a further 30 minutes, final volume 0.5
259 ml. For the assay, cells were separated from the medium by centrifugation
260 and their 14 C content measured via scintillation counting. The GLUT-
261 dependent glucose uptake was determined by subtraction of non-specific
262 measured in the presence of 10 μ M Cytochalasin B. For analysis, 14 C uptake
263 was normalized to that measured in the absence of insulin and drug
264 additions under control conditions.

265

266 *Lipogenesis*

267 Lipogenesis was measured via 3- 3 H-glucose incorporation. Adipocytes were
268 incubated for 30 minutes under different experimental conditions with a
269 fixed activity of 3- 3 H-glucose. For the assay, cells were separated from the
270 medium by centrifugation and the 3 H content determined via scintillation
271 counting. Lipogenesis was determined as the difference of cellular counts
272 to that measured in the absence of 3- 3 H-glucose. For analysis, lipogenesis

273 was normalized to that measured in the absence of insulin and drug
274 additions under control conditions.

275

276 *Justification of drug concentrations employed*

277 Verapamil and nifedipine were used at concentrations employed by others
278 to block L-type VGCCs in this cell type (Martin *et al.* 1975; Begum *et al.*
279 1992; Ni *et al.* 1994). Moreover, concentrations were employed to mitigate
280 their adsorption by serum (>90%) (Rumiantsev *et al.* 1989) and
281 absorption by the adipocytes (Louis *et al.* 2014).

282

283 *Statistical analysis*

284 Data were checked with the D'Agostino & Pearson omnibus normality test
285 with the appropriate inferential test given in the text. Graphical data are
286 shown as box and whisker plots as median, interquartile range, 10, and
287 90% confidence intervals. Unless otherwise stated, experiments were
288 performed as repeated measures. Numerical data are quoted as means \pm
289 S.E.M. or median with 5 to 95% confidence intervals (95% C.I.), where n
290 is the number of determinations. Experimental data was collated from at
291 least four animals. Fitting of equations to data used a least squares
292 algorithm with the parameters given in text. Statistical analysis was
293 performed using Graphpad PRISM version 8.2 (San Diego, California USA).
294 Data were considered statistically significant difference when $p < 0.05$ and
295 in graphics is flagged as *, ** when $P < 0.01$, *** when $P < 0.001$ and ****
296 when $P < 0.0001$.

297

298

299 **Results**

300 *Molecular Evidence and identification of VGCC in WAT*

301 RT-PCR indicated the presence of mRNA for Cav1.1, Cav1.2 and Cav1.3 but
302 not Cav1.4 L-type α_1 subunits in epididymal WFA (Fig. 1A); mRNA for
303 L-type VGCCs β_2 subunits: *cacnb2*, *cacnb3* and *cacnb4*, and $\alpha_2\delta$
304 subunits, *cacna2d1*, *cacna2d2* and *cacna2d3* were also detected. cDNA
305 sequence analysis of the PCR products for Cav1.1, Cav1.2 and Cav1.3 gave
306 98.7 ± 0.3 (n=3), $98.5\pm 0.2\%$ (n=6) and $97.8\pm 0.7\%$ (n=6) identity to the
307 rat VGCC subunits α_1S (*Cacna1s*), α_1C (*Cacna1c*) and α_1D
308 (*Cacna1d*) respectively. Quantification of mRNA levels by qPCR gave a rank
309 expression order of Cav1.2 > Cav1.3 > Cav1.1 (Fig. 1B).

310

311 Western blots of the plasma membrane fraction revealed a 260 kD Cav1.3
312 α -subunit (Fig. 2B) (N’Gouemo *et al.* 2015) and an extended form of
313 Cav1.2 of >250 kD (Fig. 2A); the latter bigger than the canonical neuronal
314 isoform of 210 kD (Raifman *et al.* 2017). Cav1.2 protein expression was 10
315 fold greater than that of Cav1.3 (Fig. 2C; $p < 0.001$, Mann Whitney); a ratio
316 comparable the qPCR results (Fig. 1B)

317

318 *Immunohistochemical evidence of VGCC in WAT*

319 Confocal microscopy revealed that fixed adipocytes preserved their
320 morphology (Fig. 3A) as demonstrated by retention of their nucleus and
321 spherical form. Atto 594 labeled antibodies identified Cav1.2 in the plasma
322 membrane; this was granular in appearance and densest near the nucleus
323 (Fig. 3B). Given this finding, the spatial distribution of $[Ca^{2+}]_i$ was examined
324 (Fig. 3C). Figure 3C shows six adipocytes with identifiable nuclei, all of
325 which responded with a reversible decrease in $[Ca^{2+}]_i$ on removal of bath
326 Ca^{2+} (Fig. 5A). Although the change in $[Ca^{2+}]_i$ was uniformly distributed in
327 the extra-nuclear cell membrane for all six cells, three had a higher $[Ca^{2+}]_i$
328 in the perinuclear region (Fig. 3D); data which supports a higher density of
329 VGCCs in this region.

330

331 *Evidence for constitutive Ca²⁺ influx*

332 Epifluorescent imaging of adherent adipocytes revealed a skewed basal
333 [Ca²⁺]_i and Gaussian cell diameter distributions with median values of 135
334 nM (129 to 145 nM, 95% C.I., n = 555) and 80 μm (79 to 81 μm, 95%
335 C.I., n = 580) respectively (Fig. 4A, B). [Ca²⁺]_i values are similar to those
336 previously reported (Schwartz *et al.* 1991; Hardy *et al.* 1992; Ni *et al.* 1994;
337 Gaur *et al.* 1998).

338

339 Both basal [Ca²⁺]_i (Spearman r = 0.17, 0.084 to 0.25 95% C.I., p <
340 0.0001, Fig. 4C) and body weight (Spearman r = 0.13, 0.01 to 0.26 95%
341 C.I., p < 0.05, Fig. 4D) were positively correlated with adipocyte diameter,
342 although [Ca²⁺]_i did not correlate with individual animal weight (Spearman,
343 Fig. 4E).

344

345 To explore Ca²⁺ influx, the effect of equimolar substitution of extracellular
346 Ca²⁺ with Mg²⁺ was investigated. Removal of bath Ca²⁺ reversibly
347 decreased [Ca²⁺]_i, Δ[Ca²⁺]_i, by 30% (25 to 34%, 95% C.I ; p<0.0001,
348 Friedman; Figs. 5A, B). Δ[Ca²⁺]_i was negatively correlated with basal
349 [Ca²⁺]_i: that is cells with the highest basal values underwent the largest
350 percentage decrease on Ca²⁺ removal (Spearman r = -0.32, P<0.001; Fig.
351 5C). Δ[Ca²⁺]_i was unrelated to cell diameter or body weight (Spearman).
352 Prolonged exposure to Ca²⁺ removal for over three hours did not affect cell
353 integrity which suggest that this intervention is not cytotoxic.

354

355 Doubling the extracellular Ca²⁺ concentration produced a 9% increase in
356 [Ca²⁺]_i (4 to 16%, 95% C.I; p<0.0001 Wilcoxon Signed Rank; Figs. 5D, E).
357 Conversely, addition of 2.5 mM Co²⁺, an inorganic inhibitor of VGCCs,
358 irreversibly decreased [Ca²⁺]_i by 13% (8 to 17%, 95% C.I; p<0.0001
359 Wilcoxon Signed Rank; Fig. 5D); a magnitude comparable to that seen
360 with removal of extracellular Ca²⁺ (Fig. 5E).

361

362 *Pharmacological manipulation of Ca²⁺ influx*

363 We next tested a variety of pharmacological agents that affect VGCC
364 activity. Although both verapamil and nifedipine significantly decreased
365 $[Ca^{2+}]_i$ relative to DMSO control (Fig. 6) ($p < 0.001$ and $p < 0.0001$
366 respectively, Wilcoxon Signed Rank), the effect of nifedipine was small
367 (Figs. 6B, F). Verapamil decreased $\Delta[Ca^{2+}]_i$ to a similar extent to Ca^{2+}
368 removal (Kruskal Wallis, Fig. 6F). In the presence of nifedipine Ca^{2+}
369 removal further decreased $[Ca^{2+}]_i$ (Figs. 6B, G). In any given cell, the
370 amount by which verapamil decreased $[Ca^{2+}]_i$ positively correlated with
371 that seen with extracellular Ca^{2+} removal (Pearson $r = 0.77$, slope $0.66 \pm$
372 0.13 , $p < 0.001$; Fig. 6H).

373

374 We next explored the pharmacology of $[Ca^{2+}]_i$ recovery following re-
375 addition of Ca^{2+} to the bath after its removal. Both verapamil (Figs. 7B, F,
376 J) and nifedipine (Figs. 7C, G, J) significantly affected $[Ca^{2+}]_i$ recovery
377 (Figs. 7A, E, J); did. The NCX inhibitor SN-6 neither affected basal $[Ca^{2+}]_i$
378 or its recovery (Figs. 7H, J). BAY-K8644, an agonist of L-type VGCCs,
379 significantly enhanced recovery (Figs. 7D, I, J).

380

381 *L-type Ca^{2+} influx stimulates basal lipolysis*

382 Since Ca^{2+} modulates the lipolytic cascade in WFA (Schimmel 1978; Izawa
383 *et al.* 1983; Allen & Beck 2000), we investigated if L-type VGCCs affected
384 lipolysis (Fig. 9). Isoprenaline stimulated lipolysis with a pEC_{50} of 7 (6.7 to
385 7.3, 95% C.I) and Hill coefficient of 0.8 (0.43 to 1.2, 95% C.I; Fig. 9A). At
386 10 μM , isoprenaline stimulated lipolysis 9.8 ± 0.63 fold ($p < 0.001$, One
387 Sample t test; $n = 39$). Consistent with previous reports (Izawa *et al.* 1983;
388 Allen & Beck 2000), removal of extracellular Ca^{2+} neither affected the EC_{50}
389 or Hill coefficient for isoprenaline, but decreased lipolysis by $\sim 30\%$
390 ($p < 0.0004$; Figs. 8A, C). Insulin inhibited the beta-adrenoceptor stimulated
391 lipolysis with a pEC_{50} of 9.4 (9.6 to 9.3, 95% C.I; Fig. 9B).

392

393 Interventions that promoted Ca^{2+} influx: BAY-K8644 or elevation of $[K^+]_o$
394 (Bentley *et al.* 2014), stimulated basal, but not isoprenaline-stimulated,

395 lipolysis (Figs. 8C, D). Interventions that decreased Ca^{2+} influx: removal of
396 extracellular Ca^{2+} or verapamil inhibited both isoprenaline-stimulated and
397 basal lipolysis (Fig. 8C, D). Insulin stimulated basal lipolysis (Fig. 8D), an
398 effect consistent with its ability to elevate $[\text{Ca}^{2+}]_i$ (Clausen & Martin 1977).
399 The capacity of 20 nM insulin to block beta-adrenoceptor stimulated
400 lipolysis was unaffected by interventions that affected $[\text{Ca}^{2+}]_i$ (Fig. 8E).

401

402 We checked if intracellular Ca^{2+} handling affected lipolysis. 1 μM oxytocin,
403 which mobilizes intracellular Ca^{2+} (Kelly *et al.* 1989), did not affect basal
404 lipolysis (Fig. 8G), but consistent with others (Fain *et al.* 1997) inhibited
405 isoprenaline-stimulated lipolysis (Fig. 8F). Neither store depletion with 1
406 μM thapsigargin (El Hachmane *et al.* 2018), or increased cytosolic Ca^{2+}
407 buffering with 10 μM BAPTA-AM (Komai *et al.* 2014) affected
408 isoprenaline-stimulated lipolysis (Fig. 8F); however, both treatments
409 impaired basal lipolysis (Fig. 8G); actions consistent with the greater
410 sensitivity of basal lipolysis to $[\text{Ca}^{2+}]_i$ compared to that stimulated by
411 isoprenaline (Figs. 8C, D).

412

413 Although alpha-adrenoceptor activation mobilizes intracellular Ca^{2+} stores
414 in WFA (Hardy *et al.* 1992), like others (Blackmore, PF; Augert 1989;
415 Seydoux *et al.* 1996), we did not see an increase in $[\text{Ca}^{2+}]_i$ with beta-
416 adrenoceptor activation ($n = 7$).

417

418 *L-type Ca^{2+} influx does not affect glucose uptake or lipogenesis*

419 Insulin at 2 nM maximally stimulated glucose uptake 5 fold ($p < 0.001$, One
420 Sample t test) (Fig. 9A). Insulin-stimulated glucose uptake was unaffected
421 by either 5 μM nifedipine or 1 μM BAY-K8644 (Figs. 9A, B); outcomes that
422 were independent of insulin concentration. Lipogenesis was also maximally
423 stimulated by 2 nM insulin (~ 9 fold, $p < 0.001$, One Sample t test) (Figs.
424 10C, D). However, neither 5 μM nifedipine or 1 μM BAY-K8644 significantly
425 affected lipogenesis (Figs. 10C, D).

426

428 **Discussion**

429

430 *Molecular evidence for L-type Ca²⁺ channels*

431 Our Western blot, PCR and in-situ immunolabelling data demonstrates
432 expression of Cav1.2 and Cav1.3 L-type VGCCs in primary white fat
433 adipocytes. The presence of Cav1.2/Cav1.3 in WFA is consistent with
434 transcriptomic data published for human (Fagerberg *et al.* 2014) and
435 mouse fat tissue (Yue *et al.* 2014); however, in contrast to these, we failed
436 to detect Cav1.4. Although the 250 kD Cav1.2 protein band went undetected
437 in our brain tissue control we did detect its 210 KD proteolytic cleavage
438 product (Hell *et al.* 2017; Shi *et al.* 2017). Using the same antibody, others
439 have also detected just a 210 kD Cav1.2 band (N’Gouemo *et al.* 2015). The
440 140 kD band may relate to the 130 kD or 150 kD non-Cav1.2 epitope that
441 this antibody recognized in Cav1.2 knock out mice (Bavley *et al.* 2017; Hell
442 *et al.* 2017). Though adipocytes possessed a Cav1.2 immuno-positive band,
443 they did not show any further proteolytic cleavage products, data that
444 suggests that this protein has post-translational modification with a
445 polymorphic proteolytic cleavage site. For Cav1.3, we only obtained positive
446 immunoblots with early batches of antibody, a recognized problem with
447 commercial antibodies to Cav1.3 (Hell *et al.* 2017). In WFA, Cav1.3 was
448 comparable in molecular weight to that observed in our brain controls and
449 heart (268kD) (Le Scouarnec *et al.* 2008). The presence of mRNA for L-
450 type VGCC alpha₁, beta₂ and alpha₂delta subunits suggests that adipocytes
451 have the capacity to traffic and assemble functional VGCCs (Dolphin 2016).

452

453 *Constitutive Ca²⁺ influx through L-type Ca²⁺ channels.*

454 Our finding that both Co²⁺ and verapamil decreased [Ca²⁺]_i by similar
455 amounts to Ca²⁺ removal is indicative of a Ca²⁺-influx pathway mediated
456 by L-type VGCCs. This notion is reinforced by enhancement of Ca²⁺ influx
457 by the L-type VGCCs dihydropyridine agonist BAY-K8644. Our data
458 contrasts to studies where neither nitrendipine or verapamil affected [Ca²⁺]_i
459 under basal conditions (Gaur *et al.* 1996a, b). One possible reason for this

460 discrepancy is that we corrected for the effect of DMSO on fluorescence to
461 reveal a block whereas previous studies had not.

462 The fact that removal of bath Ca^{2+} had a larger effect in adipocytes with
463 higher basal $[\text{Ca}^{2+}]_i$ suggests that basal $[\text{Ca}^{2+}]_i$ is set by the prevalent VGCC
464 activity. These findings, combined with the ability of verapamil and
465 nifedipine to prevent, and BAY-K8644 to enhance Ca^{2+} recovery, suggest
466 that basal $[\text{Ca}^{2+}]_i$ in WFA is maintained by a constitutive Ca^{2+} influx via L-
467 type VGCCs; an idea supported by impairment of $^{45}\text{Ca}^{2+}$ uptake in WFA by
468 L-type VGCCs antagonists (Martin *et al.* 1975).

469

470 The resting membrane potential of primary white adipocytes, measured by
471 ourselves (Bentley *et al.* 2014) and others (Ramírez-Ponce *et al.* 1990; Lee
472 & Pappone 1997), is around -30 mV. As this voltage is within the activation
473 range of L-type VGCCs (Xu & Lipscombe 2001) a “window Ca^{2+} current”
474 (Fleischmann *et al.* 1994) is expected. Constitutive L-type VGCC activity in
475 electrically non-excitable cells is not unique; for example it has been
476 recorded at a similar V_m (-30 mV) in osteoclasts (Miyachi *et al.* 1990). To
477 be constitutively active, inactivation of these VGCCs must be incomplete.

478

479 Although whole-cell voltage-clamp would have been ideal for
480 electrophysiological characterization of the VGCCs we did not attempt this
481 for technical reasons. First, the adipocyte cytoplasm is a relatively thin ~ 0.3
482 μm layer wrapped around a lipid droplet of $\sim 80 \mu\text{m}$ diameter (Bentley *et al.*
483 *et al.* 2014); this creates a membrane time constant of 100's of ms (Bentley
484 *et al.* 2014), compared to ~ 2 ms for a neuron (Coombs *et al.* 1956) of
485 similar diameter (Henneman & Mendell 2010). This difference precludes
486 voltage-clamping of VGCCs under physiological conditions due to space
487 clamp considerations and “voltage escape” (Armstrong & Gilly 1992).
488 Secondly, although Ca^{2+} influx can affect $[\text{Ca}^{2+}]_i$, we have previously shown
489 that it is too small to affect V_m (Bentley *et al.* 2014), a result indicative of
490 low channel density. Indeed, $^{45}\text{Ca}^{2+}$ tracer studies (Martin *et al.* 1975) have
491 measured the DHP-sensitive Ca^{2+} influx in WFA at $\sim 0.024 \text{ pmoles s}^{-1} \text{ cm}^{-2}$:

492 ~ 1.5 amoles s^{-1} cell $^{-1}$ or ~ 0.3 pA of whole-cell inward Ca^{2+} current, a value
493 too low to measure with whole-cell voltage-clamp.

494

495 *Constitutive Ca^{2+} influx modulates lipid metabolism*

496 Our data confirms that both basal and stimulated lipolysis require
497 extracellular Ca^{2+} (Bleicher *et al.* 1966; Ziegler *et al.* 1980; Allen & Beck
498 2000). However, we now show that lipolysis is sensitive to agents that
499 modulate L-type VGCC activity. Although, isoprenaline-stimulated lipolysis
500 could not be enhanced by interventions that increase $[Ca^{2+}]_i$, presumably
501 because it was already maximal, like basal lipolysis, it was impaired by
502 verapamil and Ca^{2+} removal. The idea that Ca^{2+} -influx promotes lipolysis
503 is also supported by the action of high K^+ , where substitution of bath Na^+
504 with K^+ elevates $[Ca^{2+}]_i$ by reverse Na^+-Ca^{2+} exchange (Bentley *et al.*
505 2014).

506

507 Multiple targets exist for extracellular Ca^{2+} during beta-adrenoceptor
508 stimulated lipolysis. Extracellular Ca^{2+} enhances beta-adrenoceptor
509 stimulated cAMP production (Ziegler *et al.* 1980) and is also required for
510 undefined lipolytic processes downstream of cytosolic cAMP (Allen & Beck
511 2000). Indeed, lipolysis can be potentiated by increasing $[Ca^{2+}]_i$ with Ca^{2+}
512 ionophores in the absence of cAMP elevation (Gaion & Krishna 1982) or
513 conversely, as shown here, depressed with Ca^{2+} chelators (Efendić *et al.*
514 1970). However, the exact mechanisms by which Ca^{2+} , and indeed Ca^{2+}
515 influx modulates basal lipolysis remains unknown; it is unlikely to involve
516 the Ca^{2+} -sensitive, isoform III, of adenylyl cyclase found in WFA (Wang *et al.*
517 2009) since changes in Ca^{2+} influx do not affect adipocyte cAMP levels
518 under basal conditions (Ziegler *et al.* 1980). However, adipocyte lipoprotein
519 lipase is positively modulated by Ca^{2+} (Efendić *et al.* 1970; Soma *et al.*
520 1989; Carmen & Víctor 2006).

521

522 *Translational context*

523 The idea that Ca^{2+} influx via $\text{Cav}1.2/\text{Cav}1.3$ regulates basal lipolysis agrees
524 with translational data. Rats with chronic renal failure are hyperlipidaemic
525 and possess WFA with elevated intracellular Ca^{2+} levels (Ni *et al.* 1995).
526 The observation that verapamil reversed these phenomena suggests that
527 exacerbated Ca^{2+} -influx via L-type VGCCs may be responsible for the
528 elevated basal lipolysis. This notion is also supported by the ability of
529 nicardipine to decrease plasma levels of FFA in spontaneously hypertensive
530 rats (Cignarella 1994). Moreover, in humans, verapamil can also decrease
531 basal plasma FFA levels, again data suggestive of VGCC mediated Ca^{2+} -
532 influx dependent lipolysis (Hvarfner *et al.* 1988). Such effects do not arise
533 through impairment of beta-adrenoceptor activation since
534 antihypertensives such as nicardipine and verapamil actually promote
535 catecholamine levels through activation of baroreflex mediated
536 sympathetic output. The failure of the DHP L-type channel antagonists to
537 affect plasma FFA in man can be reconciled by the binding of these drugs
538 to $\text{Cav}1.2/1.3$ being compromised by FFA (Pepe *et al.* 2006).

539

540 **Conclusion**

541 Our study provides direct, corroborative, evidence for the existence of
542 $\text{Cav}1.2/\text{Cav}1.3$ L-type voltage-gated Ca^{2+} channels in white adipocytes. The
543 basal concentration of intracellular Ca^{2+} appears to reflect the ambient level
544 of VGCC activity on an individual cell basis, apparently unrelated to
545 adipocyte size or animal weight. Importantly, $\text{Cav}1.x$ channels contribute
546 to a persistent state of Ca^{2+} influx in WFA, without the need for cell
547 excitability, and appear to have a key role in lipolysis. Consequently,
548 dysregulation of $\text{Cav}1.x$ in WFA may contribute to lipid storage disorders
549 that may contribute to, or indeed precipitate, the metabolic syndrome. As
550 such, these cation channels may be a potential therapeutic target for the
551 treatment of hyperlipidaemia, peripheral insulin resistance and obesity.

552

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562

563

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810
811

812 **Table 1.** Primer sequences

Name	Accession number	Sequence	Product Size (bp)
Beta-actin	V01217	FWD: 5'-AGGCCAGAGCAAGAGAG-3' REV: 5'-CCTCATAGATGGGCACAGT-3'	333
18s rRNA	V01270	FWD: 5'-TCTGCCCTATCAACTTTCGATG-3' REV: 5'-AATTTGCGCGCCTGCTGCCTTCCTT-3'	137
Cacna1s (CaV1.1)	U31816.1	FWD: 5'-CAAGTCCTTCCAGGCCCTG-3' REV: 5'-CGTAGTCAGACTCCGGGTCG-3'	271
Cacna1c (CaV1.2)	M67515.1	FWD: 5'-CGCATTGTCAATGACACGATC-3' REV: 5'-CGGCAGAAAGAGCCCTTGT-3'	217
Cacna1d (CaV1.3)	M57682.1	FWD: 5'-TTGGTACGGACGGCTCTCA-3' REV: 5'-CCCCACGGTTACCTCATCAT-3'	156
Cacna1f (CaV1.4)	U31816.1	FWD: 5'-AGCACAAGACCGTAGTGGTG-3' REV: 5'-ATACCCCAATGCCACACAG-3'	168
Cacnb1	NM_017346.1	FWD: 5'-AGTGCCAACAGAAGCAGAAGT-3' REV: 5'-GTGTTTGCTGGGGTTGTTGAG-3'	237
Cacnb2	NM_053851.1	FWD: 5'-CTCTTCTCCCTGCACCAA-3' REV: 5'-GCCTCGGCTAAGAGCAGTTT-3'	237
Cacnb3	NM_012828	FWD: 5'-CCTACGCCCGGGTTTGA-3' REV: 5'-CAAATGCCACAGTTTGTGCT-3'	174
Cacnb4	NM_001105733.1	FWD: 5'-ATGCCAGGTCTGCATGTCTC-3' REV: 5'-ACATGGGGGTCTGGTGATCC-3'	231
Cacna2d1	NM_012919.3	FWD: 5'-CCAAATCTCAGGAGCCGGT-3' REV: 5'-GCAATACCAAGGCCAAACTGT-3'	219
Cacna2d2	NM_175592.2	FWD: 5'-CTGCAGGTCAAGTTGCCAAT-3' REV: 5'-AGACGCGTTCCACTAACTGC-3'	262
Cacna2d3	NM_175595	FWD: 5'-TGGACGAGAGGCTGCTTTTG-3' REV: 5'-ATGTACGCTTCGGTCCACAC-3'	180
Cacna2d4	NM_001191751.1	FWD: 5'-ATCGCCTTCGACTGCAGAAA-3' REV: 5'-CTCTCGGTTGTCTCGATCCG-3'	255

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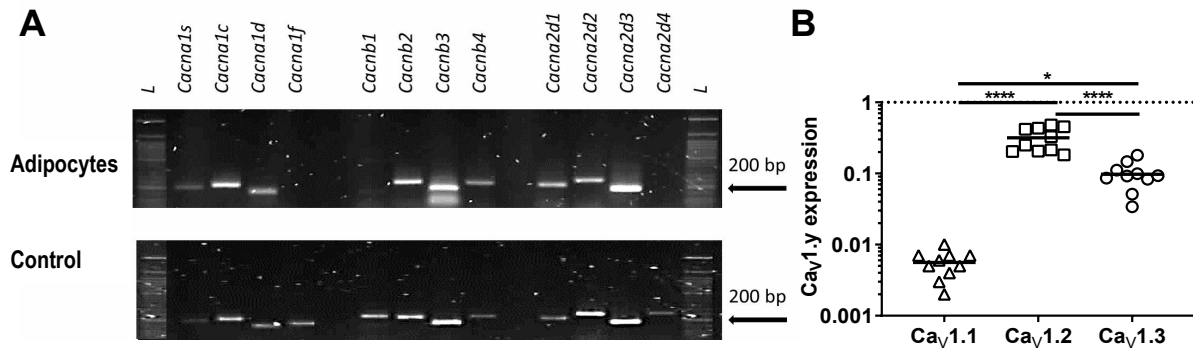
814 **Table 2.** Primer sequences used for qPCR analysis

Name	Sequence	Product Size (bp)
Hprt1	FWD:5'- CGAGGAGTCCTGTTGATGTTGC -3' REV:5'- CTGGCCTATAGGCTCATAGTGC -3'	172
Pgk1	FWD:5'- TAGTGGCTGAGATGTGGCACAG -3' REV:5'- GCTCACTTCCTTTCTCAGGCAG -3'	166
GAPDH	FWD:5'- GGCAAGTTCAATGGCACAGT -3' REV:5'- TGGTGAAGACGCCAGTAGACTC -3'	183

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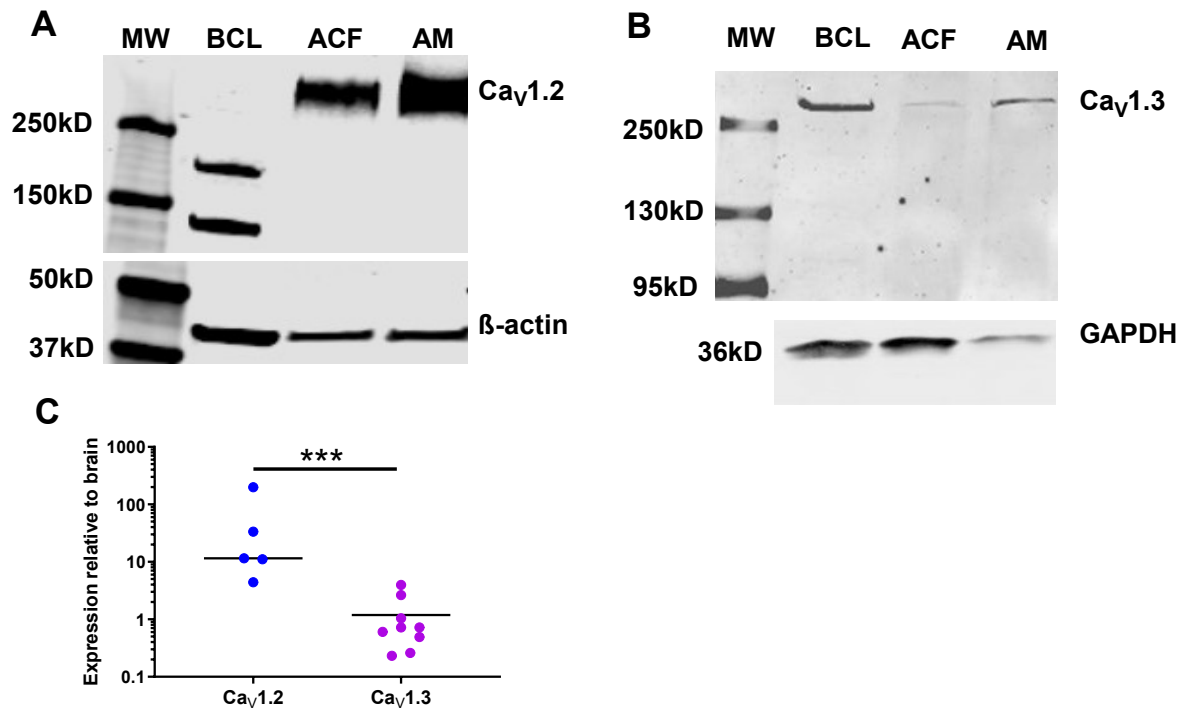
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819 **Figure 1. Cav1.1, 1.2 and 1.3 mRNA are expressed in rat**820 **adipocytes.** A) RT-CPR products (*Rattus norvegicus*) of voltage-dependent821 L-type calcium channels Cav1.1, Cav1.2, Cav1.3 and Cav1.4 alpha₁822 (*cacna1s*, *cacna1c*, *cacna1d* and *cacna1f*), beta₂ (*cacnb1*, *cacnb2*, *cacnb3*823 and *cacnb4*) and alpha₂delta (*cacna2d1*, *cacna2d2*, *cacna2d3* and824 *cacna2d4*) subunits for white fat adipocytes and for control: skeletal muscle825 for *cacna1s* (Ca_v1.1) and whole brain for all other genes; L , DNA 50 bp826 ladder. PCR product sizes are in Table 1. B) Relative expression of Ca_v1.1,827 Ca_v1.2 and Ca_v1.3 alpha-1 subunits as determined by qPCR. Data is828 normalized to mRNA expression of Ca_v1.2 in rat brain. Each point

829 represents a different animal (n=10), horizontal line is mean. Statistical

830 significance is by one-way ANOVA, with Tukey's multiple comparison test.

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833 **Figure 2. White fat adipocytes express Cav1.2 and Cav1.3 protein**834 **in membrane fractions.** Representative Western blots of Ca_v1.2 (A) and835 Ca_v1.3 (B) in adipocyte cell lysate fraction (ACF) and membrane fraction

836 (AM) of white fat adipocytes. Note the larger molecular weight (MW) of the

837 Ca_v1.2 protein in adipocytes: >250 kD compared to the proteolytic

838 cleavage product of 210 kD in the whole brain cell lysate (BCL) positive

839 control. C) Relative protein expression of Ca_v1.2 (n=5) to Ca_v1.3 (n=9) in

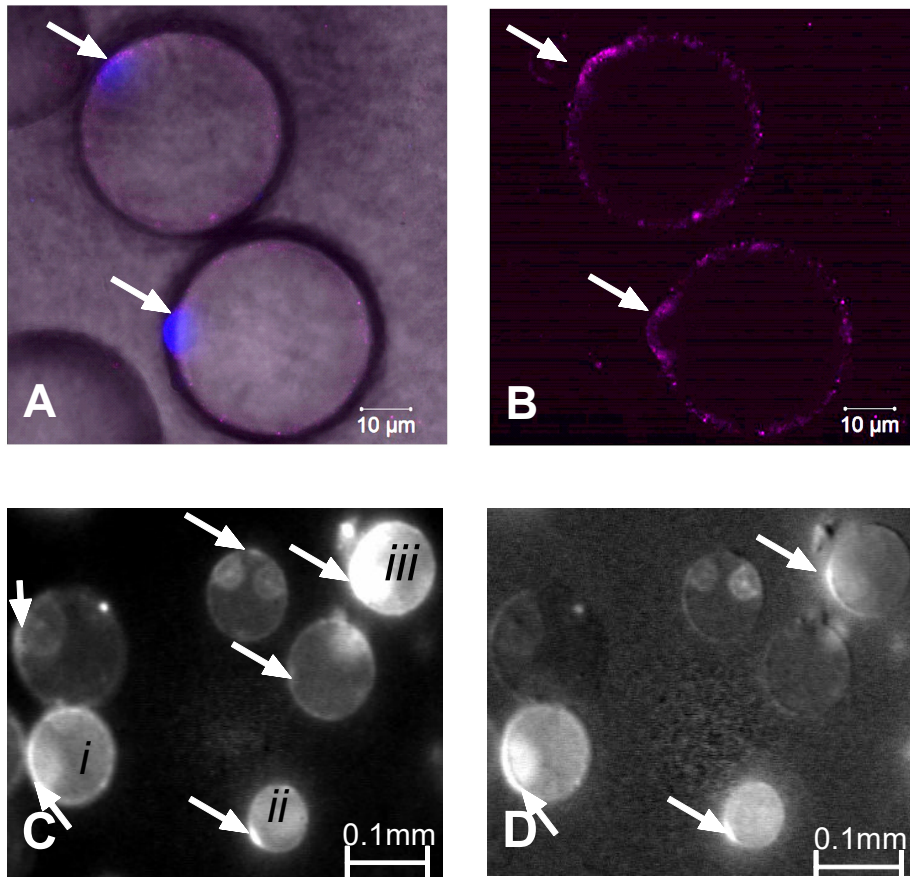
840 membrane fractions from white fat adipocytes. Data normalized to beta-

841 actin. Horizontal lines are the medians. Statistical significance is by Mann

842 Whitney.

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846 **Figure 3. Cav1.2 in the plasma-membrane.** A and B Confocal images of

847 fixed rat epididymal white fat adipocytes. A) Blue, nucleus stained with

848 Hoechst 33342; Magenta, Atto 594 labelled antibody to Cav1.2. Image

849 captured over 62s. B) Magenta only channel to highlight Cav1.2 labelling

850 which is densest in the nuclear region. Arrows indicate associated nuclei.

851 C and D greyscale epifluorescent Ca²⁺ images of a field of 6 rat epididymal

852 white fat adipocytes. C) Adipocytes under basal conditions, arrows indicate

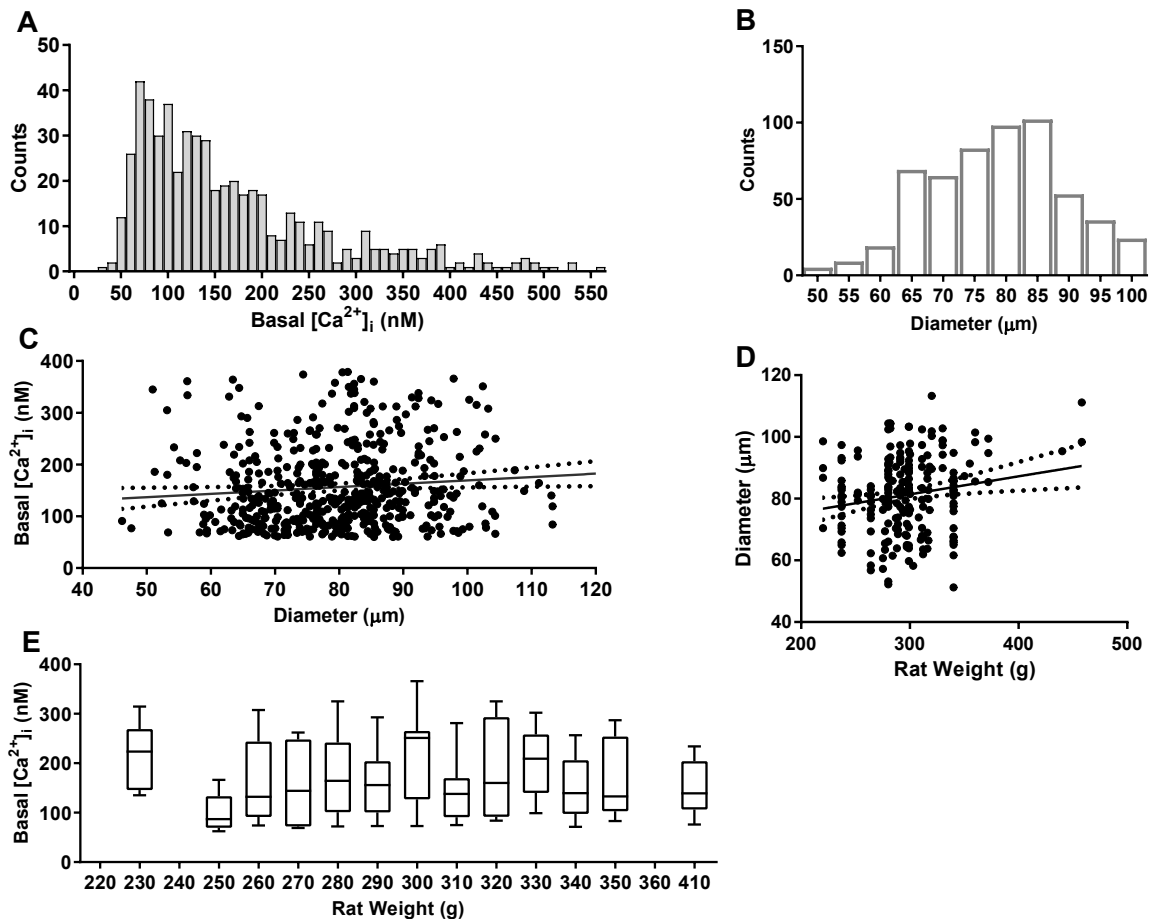
853 nuclei. Note nuclear protuberances and brighter circumferential

854 fluorescence where the cytoplasm has the deepest volume parallel to the

855 plane of illumination. D) Image shown in C is ratioed to that observed in

856 the absence of extracellular Ca²⁺ to normalize dye loading and cytoplasmic857 volume. The brighter fluorescence in the perinuclear region of cells *i*, *ii*, and858 *iii* indicates a higher Ca²⁺ level. C and D are averages of 100 frames.

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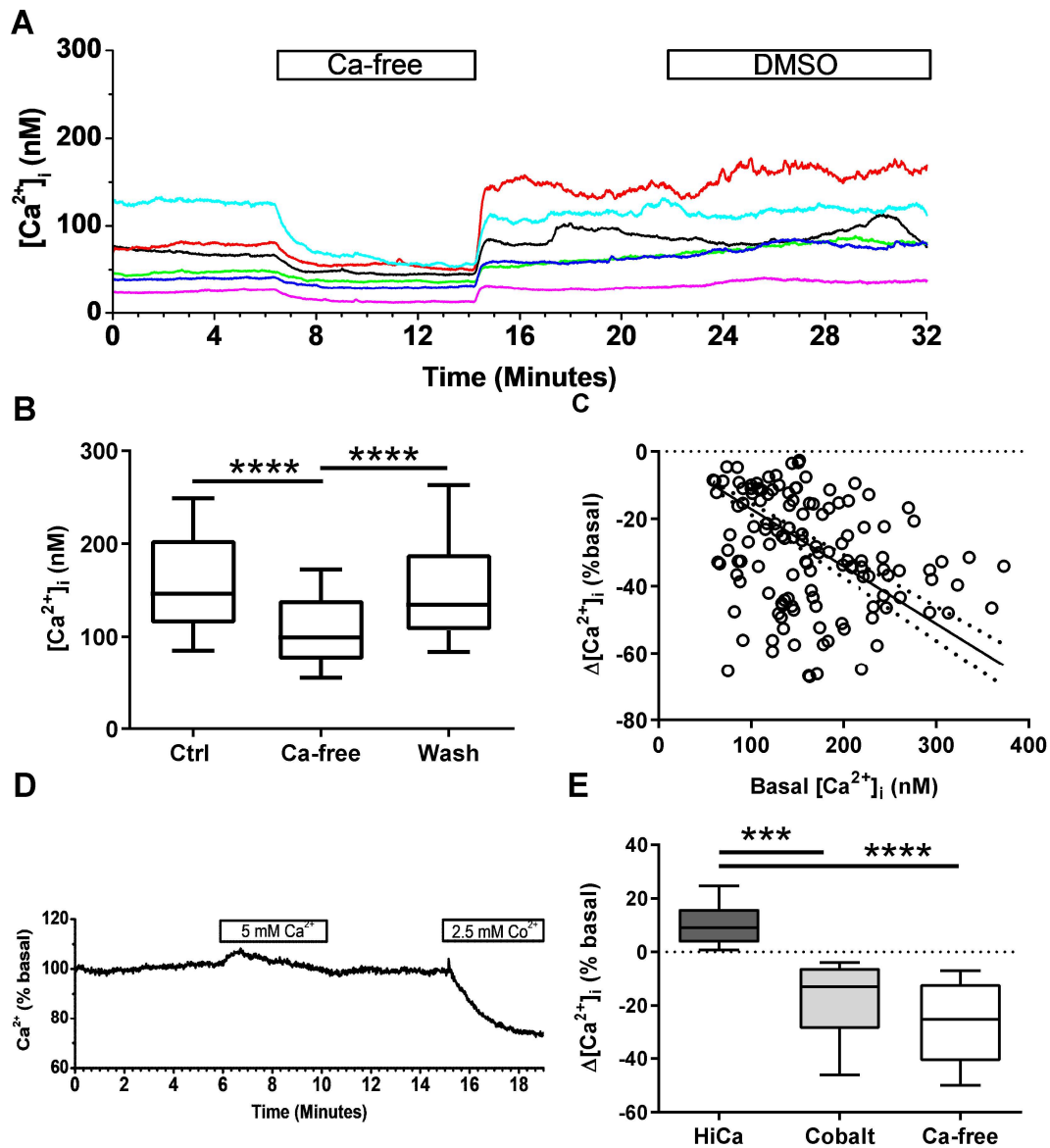
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864 **Figure 4. Measurement of intracellular $[Ca^{2+}]_i$ in isolated adipocytes**

865 A) Distribution of basal $[Ca^{2+}]_i$ ($n = 588$). B) Distribution of adipocyte
866 diameters ($n = 547$). C) Scatter plot of $[Ca^{2+}]_i$ versus cell diameter ($n =$
867 495). D) Scatter plot of cell diameter for 233 adipocytes with each vertical
868 data set taken from a given weighed animal (45 in total). Solid lines in C)
869 & D) are drawn by linear regression with slopes of $0.65 \pm 0.29 \text{ nM } \mu\text{M}^{-1}$ ($p <$
870 0.03) and $0.058 \pm 0.02 \text{ } \mu\text{m g}^{-1}$ ($p < 0.01$) respectively. Dotted lines are
871 95% C.I. for the fits shown. E) Individual distributions of basal $[Ca^{2+}]_i$ for
872 epididymal adipocytes from 13 different rats ($n = 7-40$). Note the variation
873 in $[Ca^{2+}]_i$ within any given animal was greater than between animals
874 (ANOVA).

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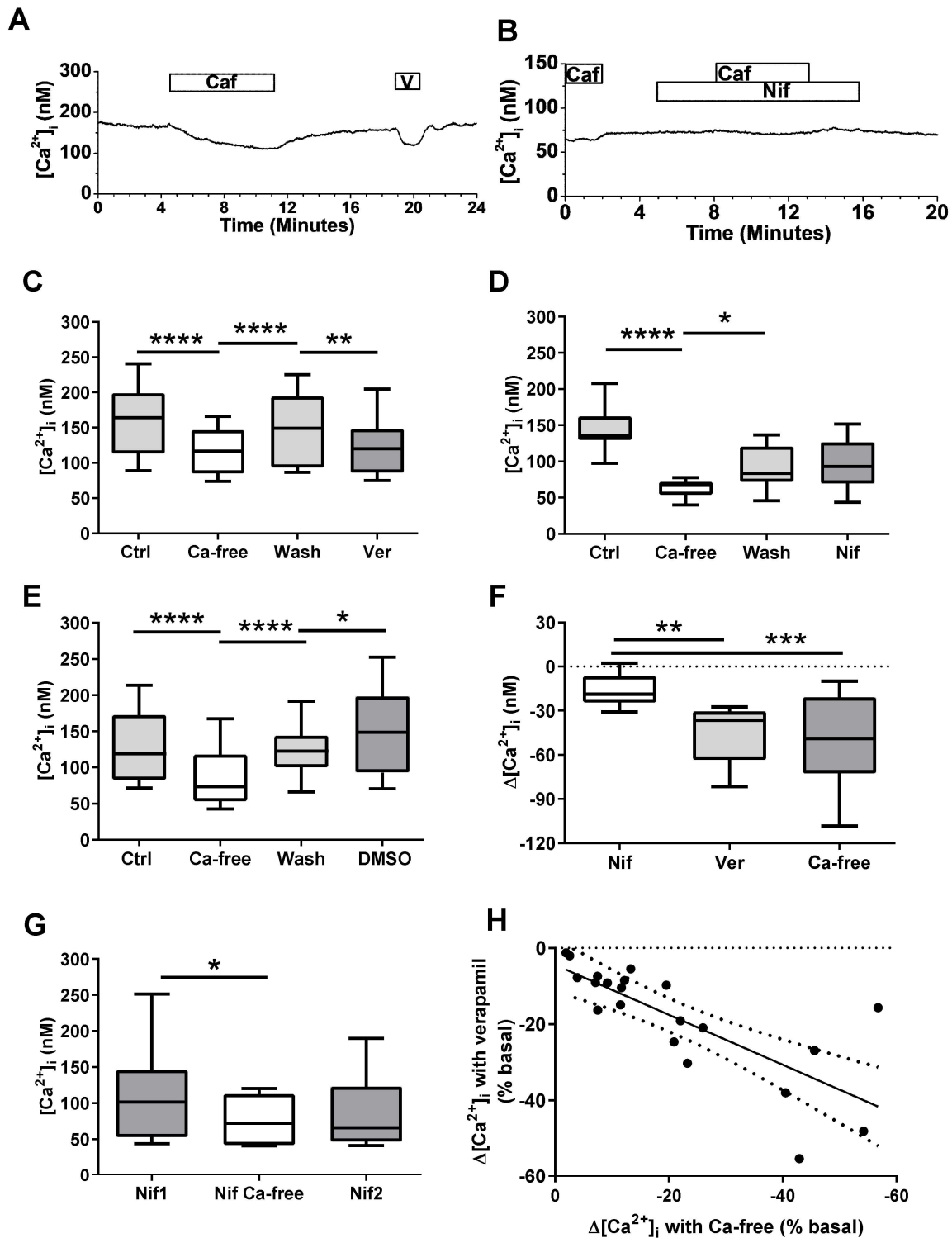
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878 **Figure 5. Extracellular Ca^{2+} removal decreases intracellular**
 879 **$[\text{Ca}^{2+}]_i$** A) $[\text{Ca}^{2+}]_i$ time courses measured for 6 adipocytes within a single
 880 field in response to removal of bath Ca^{2+} (Ca-free), followed by 0.1%
 881 DMSO. B) $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of extracellular Ca^{2+} (Ca-
 882 free) and recovery (Wash) ($n = 138$). Statistical inference by Friedman with
 883 Dunn's multiple comparison tests. C) Relationship between the decrease
 884 in $[\text{Ca}^{2+}]_i$, $\Delta[\text{Ca}^{2+}]_i$, on removal of bath Ca^{2+} and basal $[\text{Ca}^{2+}]_i$. Solid line
 885 drawn by linear regression with a slope of $-0.17 \pm 0.01 \text{ \% nM}^{-1}$ ($p <$
 886 0.0001). Dotted lines are the 95% C.I. for the fit shown. D) Mean time

887 course of $[Ca^{2+}]_i$ for 5 adipocytes in response to 5 mM $CaCl_2$ (HiCa) followed
888 by 2.5 mM $CoCl_2$ (Cobalt) added to the bath. E) $\Delta[Ca^{2+}]_i$ responses to HiCa
889 ($n = 17$), Cobalt ($n = 19$) and removal of extracellular Ca^{2+} (Ca-free; $n =$
890 140). Dashed line indicates no effect. Data is from 7 animals. Statistical
891 inference was by Kruskal-Wallis with Dunn's multiple comparison tests.
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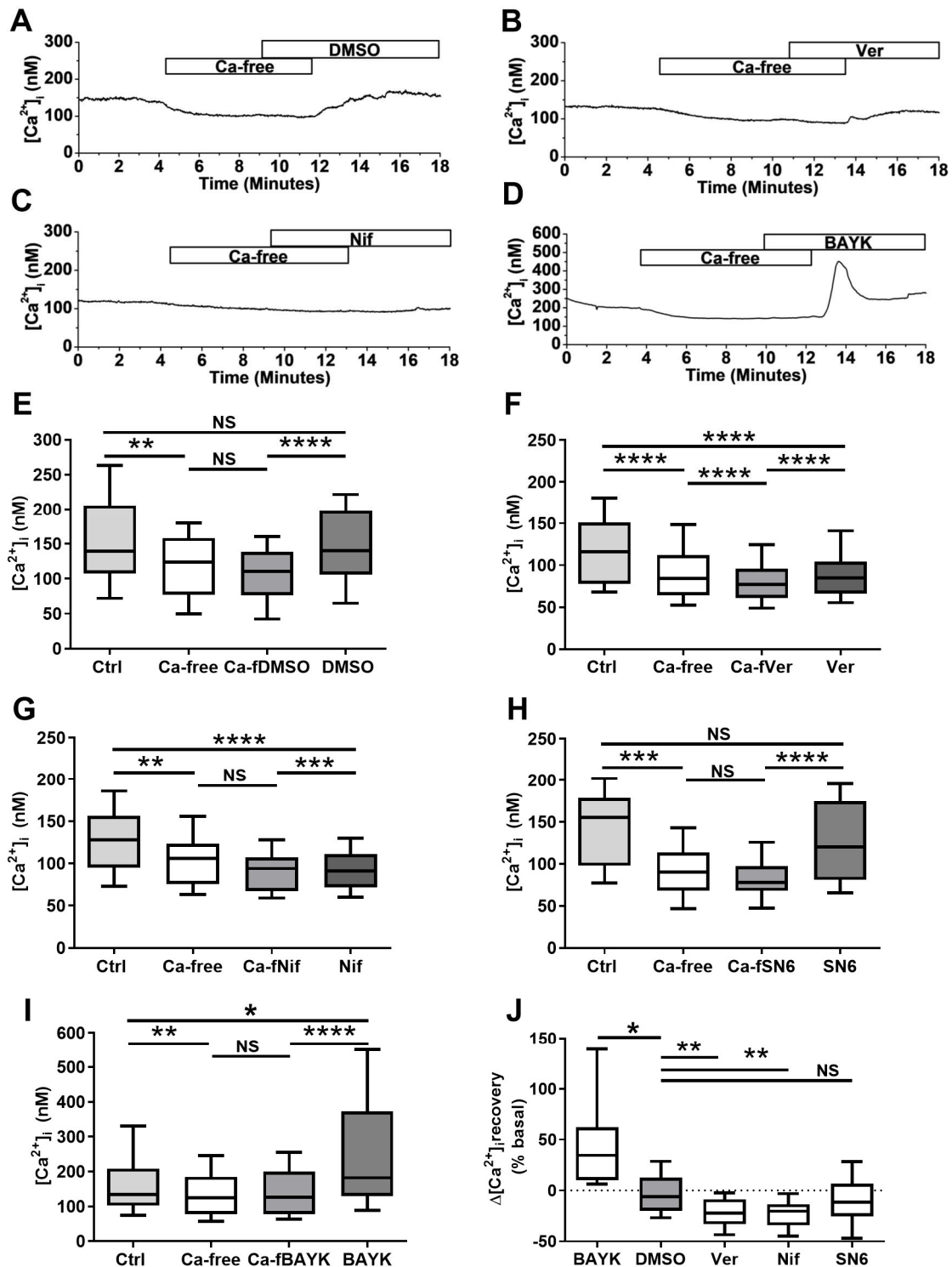
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Figure 6. Verapamil and nifedipine decrease the intracellular Ca^{2+} concentration, $[\text{Ca}^{2+}]_i$ A) Mean time course of $[\text{Ca}^{2+}]_i$ measured for 11 adipocytes within a single field in response to removal of bath Ca^{2+} (Caf), followed by 20 μM verapamil (V). B) Mean time course of $[\text{Ca}^{2+}]_i$ measured for a field of 5 adipocytes in response to removal of bath Ca^{2+} (Caf) in the

899 absence and then presence of 20 μM nifedipine (Nif). Note block by
900 nifedipine is countered by a positive DMSO effect on fluorescence. C) $[\text{Ca}^{2+}]_i$
901 in control (Ctrl), after removal of extracellular Ca^{2+} (Ca-free) and recovery
902 (Wash) followed by 20 μM verapamil (Ver) (n= 19 from 6 animals). D)
903 $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of extracellular Ca^{2+} (Ca-free) and
904 recovery (Wash) followed by the addition of 20 μM nifedipine (Nif) (n = 15
905 from 4 animals). E) $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of extracellular
906 Ca^{2+} (Ca-free) and recovery (Wash) followed by 0.1% DMSO (n = 36 from
907 6 animals). F) Comparison of $\Delta[\text{Ca}^{2+}]_i$ produced by removal of bath Ca^{2+}
908 (Ca-free), 20 μM nifedipine (Nif; n = 15) and 20 μM verapamil (Ver; n =
909 19). Data are from C and D and are corrected for DMSO effects shown in E
910 (n = 137). G) $[\text{Ca}^{2+}]_i$ in the continuous presence of 20 μM nifedipine (Nif1)
911 where Ca^{2+} is removed from the bath (Nif Ca-free) and added back again
912 (Nif2) (n= 9 from 2 animals). For C-G, statistical comparison between
913 groups was by Kruskal-Wallis with Dunn's multiple comparison tests. H)
914 Relationship between $\Delta[\text{Ca}^{2+}]_i$ produced by 20 μM verapamil and removal
915 of bath Ca^{2+} (n = 21) for the same cell. Solid line is linear regression of
916 data with a slope of 0.66 ± 0.13 . The dotted lines are the 95% C.I. of the
917 fit.
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920 **Figure 7. Pharmacological exploration of Ca^{2+} recovery.** A-D)921 Representative mean time courses of $[Ca^{2+}]_i$ in response to removal of bath922 Ca^{2+} (Ca-free) followed by the addition of drugs as indicated.: A) 0.1%923 vovl/vol DMSO; B) 20 μ M verapamil (V); C) 20 μ M nifedipine (Nif); D) 10924 μ M BAY-K8644 (BAYK) all in Ca^{2+} free. E) $[Ca^{2+}]_i$ in control (Ctrl), after

925 removal of extracellular Ca^{2+} (Ca-free), after addition of 0.1% DMSO (Ca-
926 fDMSO), then re-addition of bath Ca^{2+} in the presence of DMSO (DMSO) (n
927 = 19 from 12 animals). F) $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of
928 extracellular Ca^{2+} (Ca-free), followed by 20 μM verapamil in Ca^{2+} free (Ca-
929 fVer), then re-addition of bath Ca^{2+} in verapamil (Ver) (n = 67 from 12
930 animals). G) $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of extracellular Ca^{2+}
931 (Ca-free), followed by 20 μM nifedipine in Ca^{2+} free (Ca-fNif), then re-
932 addition of bath Ca^{2+} in nifedipine (Nif) (n = 33 from 6 animals). H) $[\text{Ca}^{2+}]_i$
933 in control (Ctrl), after removal of extracellular Ca^{2+} (Ca-free), followed by
934 10 μM SN6 in Ca^{2+} free (Ca-fSN6), then re-addition of bath Ca^{2+} in SN6
935 (SN6) (n = 18 from 5 animals). I) $[\text{Ca}^{2+}]_i$ in control (Ctrl), after removal of
936 extracellular Ca^{2+} (Ca-free), followed by 10 μM BAY-K8644 in Ca^{2+} free
937 (Ca-fBAYK), then re-addition of bath Ca^{2+} in BAY-K8644 (BAYK) (n = 18
938 from 8 animals). All data uncorrected for DMSO effect. J) Percentage
939 change in basal $[\text{Ca}^{2+}]_i$ after recovery on re-addition of bath Ca^{2+} with the
940 various treatments as shown. Statistical comparison was by Friedman with
941 Dunn's multiple comparison multiple comparison.

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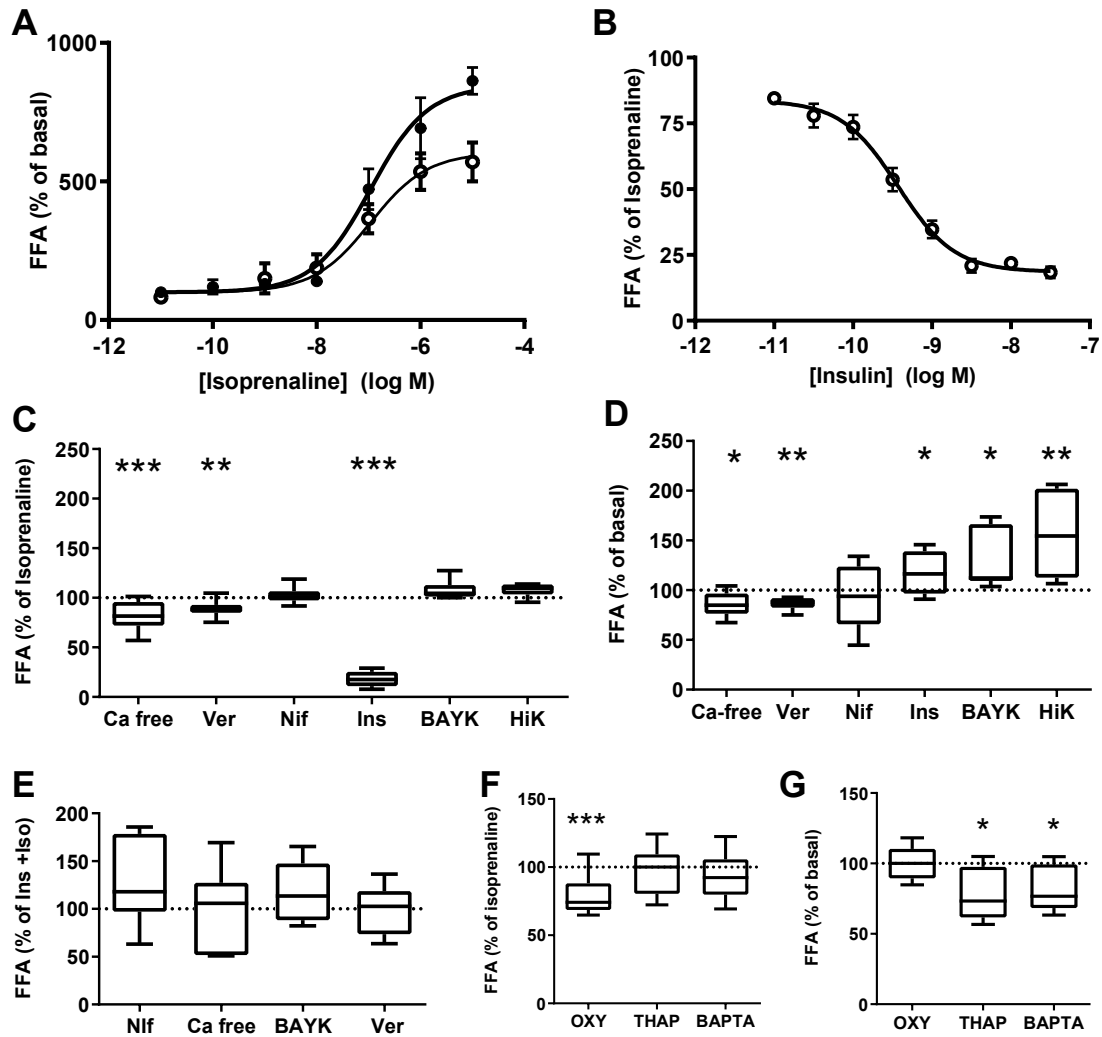
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950 **Figure 8. Extracellular Ca²⁺-influx potentiates lipolysis.** A) Lipolysis

951 as a function of isoprenaline in the presence (●) and absence (○) of bath

952 Ca²⁺. Solid lines are fits of the data with sigmoidal dose response curves

953 with parameters given in the text. Data means ± S.E.M (n = 4-5). B)

954 Inhibition of lipolysis by insulin. Solid line is a fit of the data to dose-

955 response curve with parameters given in the text. Data are means ± S.E.M

956 (n = 5-9). C) Effects of interventions on lipolysis stimulated by 10 μM

957 isoprenaline: Ca free, removal of bath Ca²⁺; Ver, 5 μM verapamil; Nif, 20

958 μM nifedipine; Ins, 20 nM insulin; BAYK, 1 μM BAY-K8644; HiK, 50 mM

959 bath [K⁺]_o (n = 6-16). D) Effects of interventions on basal lipolysis. Key as

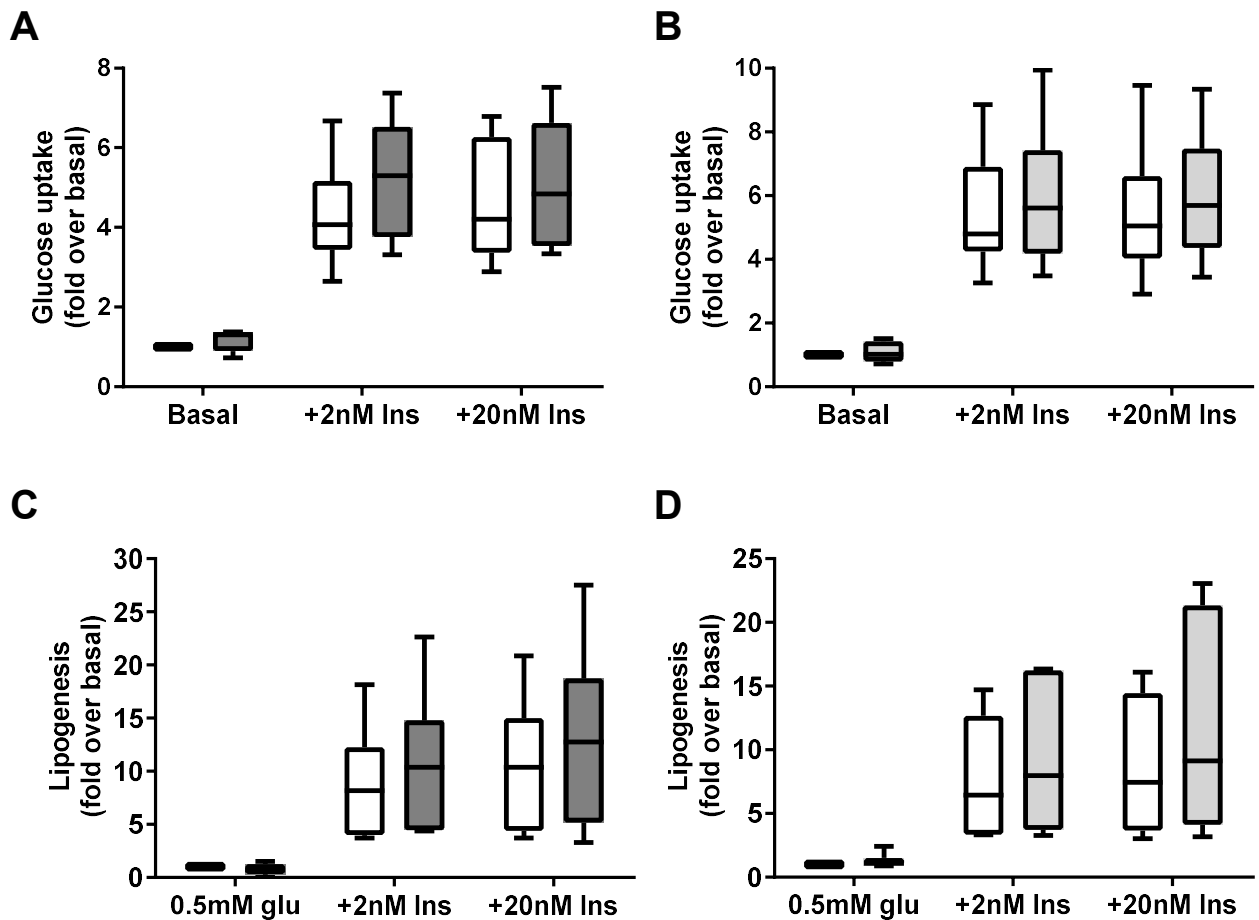
960 for C (n = 6-16). E) Effects of interventions on beta-adrenoceptor mediated

961 lipolysis inhibited by 20 nM insulin: Key as for C (n = 6-10). F) Effects of

962 interventions on 10 μM isoprenaline stimulated lipolysis: OXY, 1 μM

963 oxytocin; THAP, 10 μ M thapsigargin; BAPTA, 10 μ M BAPTA-AM (n = 9–21).
964 G) Effects of interventions as shown in F on basal lipolysis. (n = 6–10).
965 DMSO the solvent for verapamil, nifedipine, and BAY-K8644 was without
966 effect on lipolysis. Statistics are Wilcoxon Sign test relative to 100%.
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971 **Figure 9. Ca^{2+} -influx via L-Type VGCC does not affect glucose**972 **uptake and lipogenesis.** A) Effect of 5 μM nifedipine on glucose uptake.973 B) Effect of 1 μM BAY-K 8644 on glucose uptake. C) Effect of 5 μM nifedipine974 on lipogenesis. D) Effect of 1 μM BAY-K 8644 on lipogenesis. Drug additions

975 are indicated by filled bars, controls by open bars, conditions are as

976 indicated. Ins, insulin, glu, glucose. Data are all paired with $n=5$ for each

977 condition. Statistical inference by Friedman's test.

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