

1 **Cytoarchitectural changes in hippocampal subregions of the NZB/W F1 mouse model of lupus**

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31

32

33 **Abstract**

34 Over 50% of clinical patients affected by the systemic lupus erythematosus disease display impaired
35 neurological cognitive functions and psychiatric disorders, a form called neuropsychiatric systemic
36 lupus erythematosus. Hippocampus is one of the brain structures most sensitive to the cognitive
37 deficits and psychiatric disorders related to neuropsychiatric lupus. The purpose of this study was to
38 compare, layer by layer, neuron morphology in lupus mice model NZB/W F1 *versus* Wild Type mice.
39 By a morphometric of cells identified on Nissl-stained sections, we evaluated structural alterations
40 between NZB/W F1 and Wild Type mice in seven hippocampal subregions: Molecular dentate gyrus,
41 Granular dentate gyrus, Polymorph dentate gyrus, Oriens layer, Pyramidal layer, Radiatum layer and
42 Lacunosum molecular layer. By principal component analysis we distinguished healthy Wild Type
43 from NZB/W F1 mice. In NZB/W F1 mice hippocampal cytoarchitecture, the neuronal cells resulted
44 larger in size and more regular than those of Wild Type. In NZB/W F1, neurons were usually denser
45 than in WT. The Pyramidal layer neurons were much denser in Wild Type than in NZB/W F1.
46 Application of principal component analysis, allowed to distinguish NZB/W F1 lupus mice from
47 healthy, showing as NZBW subjects presented a scattered distribution and intrasubject variability.
48 Our results show a hypertrophy of the NZB/W F1 hippocampal neurons associated with an increase
49 in perikaryal size within the CA1, CA2, CA3 region and the DG. These results help advance our
50 understanding on hippocampal organization and structure in the NZB/W F1 lupus model, suggesting
51 the hypothesis that the different subregions could be differentially affected in neuropsychiatric
52 systemic lupus erythematosus disease. **Leveraging an in-depth analysis of the morphology of neural**

53 cells in the hippocampal subregions and applying dimensionality reduction using PCA, we propose
54 an efficient methodology to distinguish pathological NZBW mice from WT mice.”

55

56 1. Introduction

57 Systemic Lupus Erythematosus (SLE) is an auto-immune disease that affects a variety of organ
58 systems by altering the regulatory pathways of inflammation (Ghirardello et al. 2004), including the
59 central nervous system (CNS) (Leung et al, 2016). Up to 75% of SLE patients show neurological
60 symptoms involving a range of cognitive deficits, psychiatric disorders (Briani et al., 2009) and
61 memory loss. This form is termed neuropsychiatric SLE (NPSLE). Beyond the existence of these
62 symptoms, the full spectrum of NPSLE manifestation remains poorly understood (Schwartz et al,
63 2019). One of the brain regions most suspected to have marked NPSLE-related changes is the
64 hippocampus. Critically involved in fundamental processes such as learning, emotions, spatial
65 navigation and memory, the hippocampus is among the most studied neural systems in mammals.
66 The *hippocampus proper* comprises the dentate gyrus (DG), CA1, CA2 and CA3 regions, each with
67 their own cellular structure and distinctive functions. The three layers of the DG are the molecular
68 layer (MoDG), granule cell layer (GrDG) and polymorph dentate gyrus (PoDG). Within the CA1,
69 CA2 and CA3 regions, a number of layers are defined. The pyramidal layer (Py), the subregion in
70 which the main cell types are pyramidal neurons, differing in terms of genetics, morphology, and
71 connectivity (Merino-Serra et al., 2020). Deep to the Py is the *stratum oriens* (Or), a relatively cell-
72 free subregion containing mostly fibers and some interneurons. Superficial to the Py is the *stratum*
73 *radiatum* (Rad) and *stratum lacunosum-moleculare* (LMol) containing GABAergic interneurons,
74 which play a critical role in modulating the dynamic activity in hippocampus networks (Jarsky et al.,
75 2005).

76 Anatomical observations and lesioning experiments support the idea that the hippocampus is crucial
77 in memory formation, especially the dentate gyrus (DG) area, while the CA3 area covers the
78 encoding, storage and retrieval of memory (Hainmueller and Bartos, 2020). The hippocampus also

79 plays a major role in the formation of declarative, spatial, and contextual memory, as well as in the
80 processing of emotional information and stress response (Zaletel et al., 2016).

81 The widely used NZB/W F1 (NZBW) murine model offers an opportunity to bridge the gap between
82 neurological deficits and histological lesions underlying NPSLE (Pikman et al., 2017). NZBW mice
83 spontaneously develop generalized auto-immune inflammation providing a powerful translational
84 model to approach human autoimmune disease.

85 The neuronal loss and reduced neuronal density found in NZBW hippocampi were comparable to
86 those described in human NPSLE patients (Ballok et al., 2004). The same year, Kowal and colleagues
87 (Kowal et al., 2004) demonstrated that systemic immune responses could cause cognitive impairment
88 even in the absence of an inflammatory cascade and suggested that the antibodies gained access to
89 the brain to bind preferentially to hippocampal neurons, causing neuronal death with resulting
90 cognitive dysfunction and altered hippocampal metabolism. More recent works focused on cellular
91 and network basis of cognitive processes, allowing further understanding of the hippocampus role in
92 complex memories processes (Lisman et al, 2017).

93 By advance quantitative imaging and statistical methods, over a large number of cells, we would like
94 to contribute to the debate with hard evidence. In order to study quantitatively the fine changes in
95 neuronal changes, and to quantify structural differences in the cytoarchitecture of NZBW and WT
96 mice we set up an automatic pipeline combining image analysis together with a statistical data
97 analysis based on a multivariate, multi-aspect testing approach.

98

99 **2.Materials and methods**

100 *2.1 Mice*

101 A series of 11 NZB/W F1 female mice (22-week-old), purchased from (Harlan Laboratories, Envigo
102 RMS, UD, Italy) and 5 wild type (WT) female mice were housed in the animal facility of the
103 Department of Surgery, Oncology and Gastroenterology of the University of Padova, Padova, Italy.
104 The housing conditions were controlled, with the temperature at 21–23°C and a 12:12 hours light:

105 dark cycle. All animal studies were approved by the Institutional Animal Care and Use Committee
106 of the Albert Einstein College of Medicine. Mice used in this study were littermates. The NZB/W
107 mice used are hybrid of two inbred strains (NZB females X NZW males) that are genetically uniform
108 and heterozygous only for the genes for which the two parental strains differ. The genetic
109 heterozygosity is related to some dominant alleles wherewith the two parental mice strains contribute
110 in the development of the typical lupus-like auto anti-bodies production. Probably due to estrogen
111 action and as it's observed in human, lupus syndrome in the NZB/W F1 strain is strongly biased in
112 favor of female

113 *2.2 Assessment of lupus*

114 Mice were monitored twice a week for the development of proteinuria and autoantibody titers.
115 Urinary protein excretion was measured by dipstick analysis (Uristix; Bayer), where +1 is 30 mg/dl,
116 +2 is 100 mg/dl, +3 is 300 mg/dl, and +4 is ≥ 2000 mg/dl (supplementary material Table 1). Active
117 generalized SLE was present in all mice of the NZBW group, as determined by elevated serum anti-
118 DNA antibodies and by the presence of glomerulonephritis. Mouse IgG anti-double stranded (ds)
119 DNA antibody titers were determined by ELISA, as previously described in detail (Gatto et al., 2016;
120 Gatto et al., 2020). Similar ELISA protocols were also used for anti-chromatin, anti-cardiolipin and
121 anti-N-methyl-D-aspartate receptor antibody ELISAs (Gatto et al., 2016; Gatto et al., 2020). For
122 details of weight, age, values of proteinuria and autoantibody titers analyzed in NZBW mice before
123 death see (supplementary material Table 1).

124

125 *2.3 Brain tissue preparation and Nissl staining*

126 The mouse brains were fixed in a 10% formaldehyde solution. After fixation, the brains were
127 processed for paraffin embedding. The brains were cut into 8- μ m-thick coronal sections. From each
128 sample, continuous brain sections were stained following a routine Nissl protocol (Corain et al.,
129 2020). The topography of the hippocampal region was assessed by comparison with detailed
130 stereotaxic mouse brain atlases (Paxinos and Franklin, 2012). For cytoarchitectural analysis of the

131 hippocampus we selected the range from Bregma was from -2.80 mm to -3.40 mm. In order to
132 evaluate the hippocampal regions extension, we Nissl stained one section every ten per mouse brain
133 in both NZB/WF1 and wild type populations.

134 135 *2.4 Image acquisition and topographical mapping of the hippocampal subregions*

136 Nissl-stained sections were digitalized with a semi-automated microscope (D-Sight v2, Menarini
137 Diagnostics, Italy) with the 20x objective at the best focal plane. The layers of interest were manually
138 segmented on each acquired image using a general-purpose image-editing software (GNU Image
139 Manipulation Program, The GIMP Development Team, 2019). For details see (supplementary
140 material, Figure 1).

141 142 *2.5 Automatic cell identification*

143 Each neuron was identified and segmented through an automatic image analysis method applied on
144 the Nissl-stained section (Grisan et al., 2018). The process identified the position and outline of the
145 visible cells within the manually outlined regions. Briefly, a local space-varying threshold applied to
146 the image separated the stained objects (foreground) from the background. From the local surface
147 density of the foreground objects (mainly cells), a separation of the densest (with clustered and
148 cluttered cells) and sparsest regions is obtained (Poletti et al., 2012; Grisan et al. 2018), and the
149 potential cell cluster were then identified. All identified clusters underwent secondary analyses to
150 separate the cells composing them.

151 152 *2.6 Cells classification by shape type and morphometric descriptors setting*

153 For each cell in each subregion data characterizing its shape and local relationship with surrounding
154 cells were collected (Corain et al., 2020). These data broadly belong to three domains: Size,
155 Regularity and Density (supplementary material, Table 2). Size regarding cell morphology, are
156 composed by shape measurements (area, perimeter, major and minor axis length). Regularity

157 delineate the domain that consider the parameter Extent and the parameters Solidity. Extent is defined
158 as: $\text{Area} / (\text{Area of the bounding box})$; Solidity is defined as the proportion of the pixels in the convex
159 hull that are also in the object; computed as $\text{Area}/\text{Convex Area}$. We defined “more regular” the
160 neurons showing values closer to 1 of Extent and Solidity (cells show a rounded shape) in comparison
161 to the lower values of these parameters (cells tend to be farther from the round shape). Density
162 characterizes the context neighboring each cell by counting the number of cells within a radius of 50
163 μm or within 100 μm from the cell under analysis. Density descriptors are an absolute number of
164 neighbor cells around a given cell. All neural cells were grouped in 4 categories defined by their
165 shape: pyramidal, round, ellipsoid and complex. The total number of cells analyzed for the NZBW
166 mice population and for the Wild Type mice population, in each subregions separately for cell shape
167 is reported in the supplementary material. For details see (supplementary material, Table 2, Table 3
168 and Figure 2).

169

170 *2.7 Statistical Analysis*

171 The statistical analysis was performed comparing WT and NZBW populations for each domain within
172 the 7 layers and the 4 shape types. As multiple cells recorded in each image are not independent,
173 resampling-based the method proposed by (Finos and Basso, 2012) was used to account for repeated
174 measures. The method is as follows: each image the mean of each feature is computed and used as
175 pseudo-observation. The pseudo-observations are now independent, but not homoscedastic. They are
176 randomly permuted among groups, while an adequate test statistics accounts for the
177 heteroscedasticity. The p-value is the proportion of test statistics computed on randomly permuted
178 pseudo-observations that exceeds the one computed on observed data.

179 This approach takes into account the joint distribution of the tests and allows for the multivariate
180 inference via nonparametric Fisher combination of the univariate test. The tests are combined by
181 morphometric descriptors, subregion and cell type. Significance level was set to $\alpha=0.05$. The
182 analysis was performed with R software (R Core Team, 2021) and flip package (Finos, 2018). For

183 descriptive purposes, a Principal Component Analysis was performed for each layer after
184 standardization of the morphometric descriptors. A bi-plot of the first two principal components was
185 drawn also reporting the explained variance of each component.

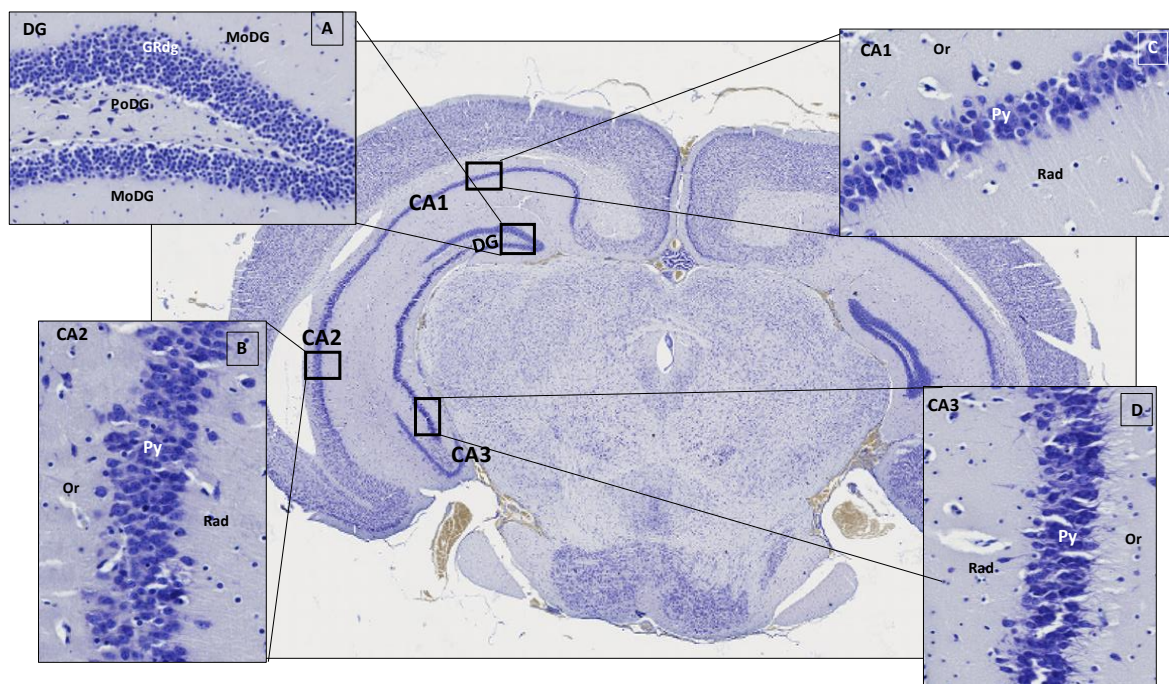
186

187 3. Results

188 3.1 Lamination of the hippocampal region and subregion

189 The DG, CA1, CA2 and CA3 regions were identified as well as the 7 subregions PoDG, Or, Py, Rad,
190 LMol, MoDG and GrDG and their cytoarchitecture, in all mice (Figure 1). Within each subregion,
191 the 4 categories of cells type (pyramidal, round, ellipsoid and complex) were found in both NZBW
192 and WT population. The general anatomy of the hippocampus followed its well-known description
193 (Figure 1).

194



195

196 **Figure 1:** A. Image of a Nissl stained coronal section of WT mouse brain showing the Dg, CA1, CA2 and
197 CA3 hippocampal regions (X20). A. Enlargement of DG showing details of neuronal cells in the PoDG, GrDG
198 and MoDG subregions. B. Enlargement of CA2 region showing details of neuronal cells in the Py, Or and Rad
199 subregions. C. Enlargement of CA1 region showing details of neuronal cells in the Or, Py, Rad, subregions.
200 D. Enlargement of CA3 region showing details of neuronal cells in the Py, Or and Rad subregion.

201

202 *3.2 Neurons in the NZBW hippocampus showed larger body size than WT neurons.*

203 The cells in the hippocampal neurons of NZBW mice were larger than neurons of WT mice in all
204 subregions (Figure 2). The Py subregion, where neurons had a larger perimeter in WT than NZBW
205 mice, was an exception. Representation of the results, separately for each morphometric descriptor
206 are shown in Figure 2. Inferential analysis demonstrated a strongly statistically significant difference
207 ($p \leq 0.01$) in NZBW mice in the PoDG, Or, Py, Rad subregions, and a statistically significant
208 difference ($p \leq 0.05$) in the GrDG and LMol subregions (Table 1). No difference in the size of neurons
209 was found in the MoDg or the GrDG subregion. The analysis performed by categories and by
210 subregion revealed which cell shape type contributed to the statistical significance (Table 1).

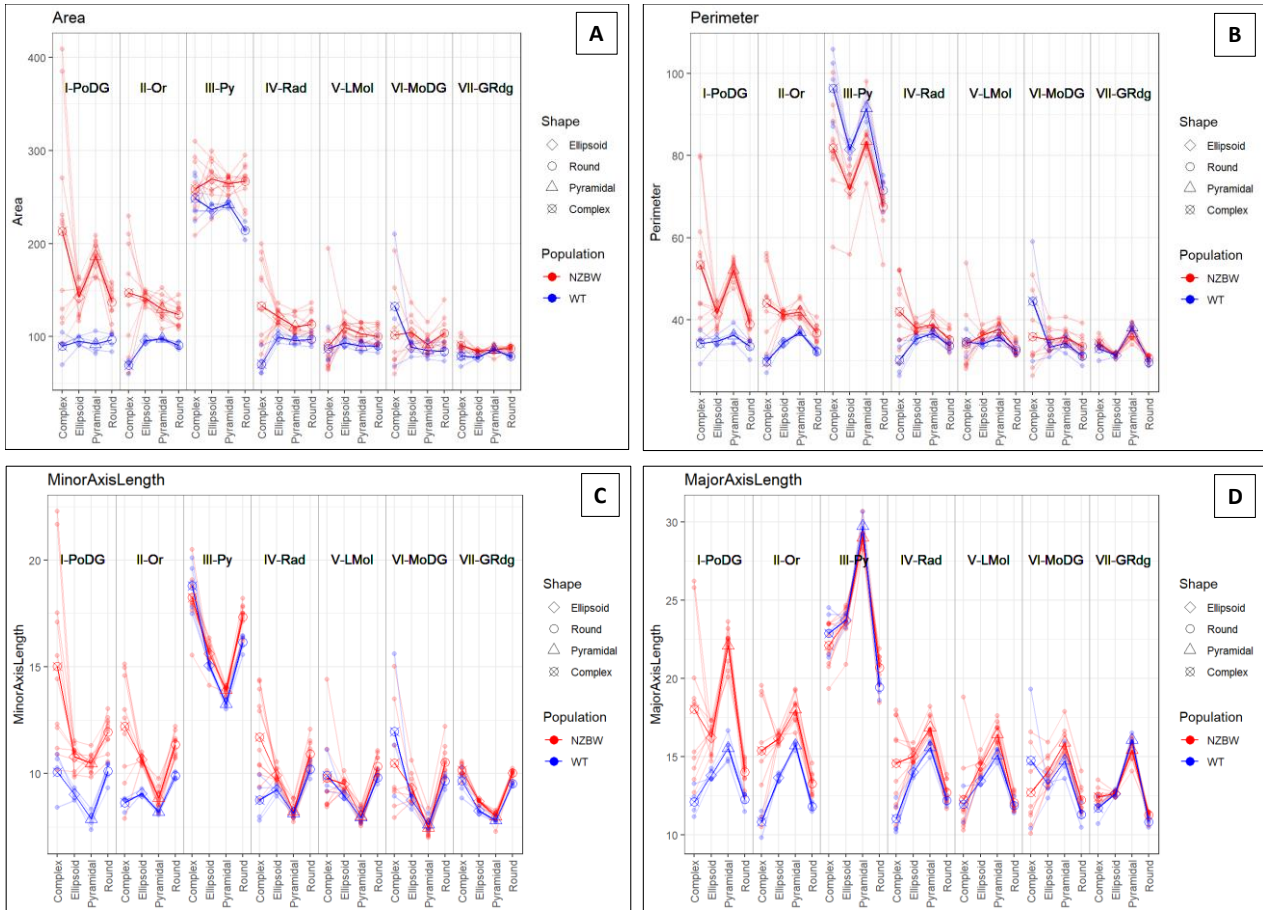
211 Details of the mean difference and standard error are reported separately for each morphometric
212 descriptor in the section “Additional statistical results, (supplementary material). Moreover, detailed
213 results of the p-values combined for domains subregions, cell shape and morphometric descriptor are
214 reported in the in the section “Additional statistical results”, (supplementary material).

215

Subregion	cell population Size difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.0020	0.0030	0.0020	0.0010	0.0410
Or	0.0020	0.0020	0.0010	0.0030	0.0450
Py	0.0080	0.0040	0.0040	0.0020	0.1550
Rad	0.0050	0.0670	0.0020	0.0150	0.0090
LMol	0.0410	0.1530	0.0040	0.0290	0.9530
MoDG	0.0570	0.1530	0.0040	0.0290	0.9530
GrDG	0.0150	0.0010	0.0130	0.1120	0.0200

216 **Table 1:** significant p-value combined by subregion and cells shape type for the domain Size with adjustment
 217 by multiplicity. The 1% statistically significant p-values are highlighted in bold.

218



219

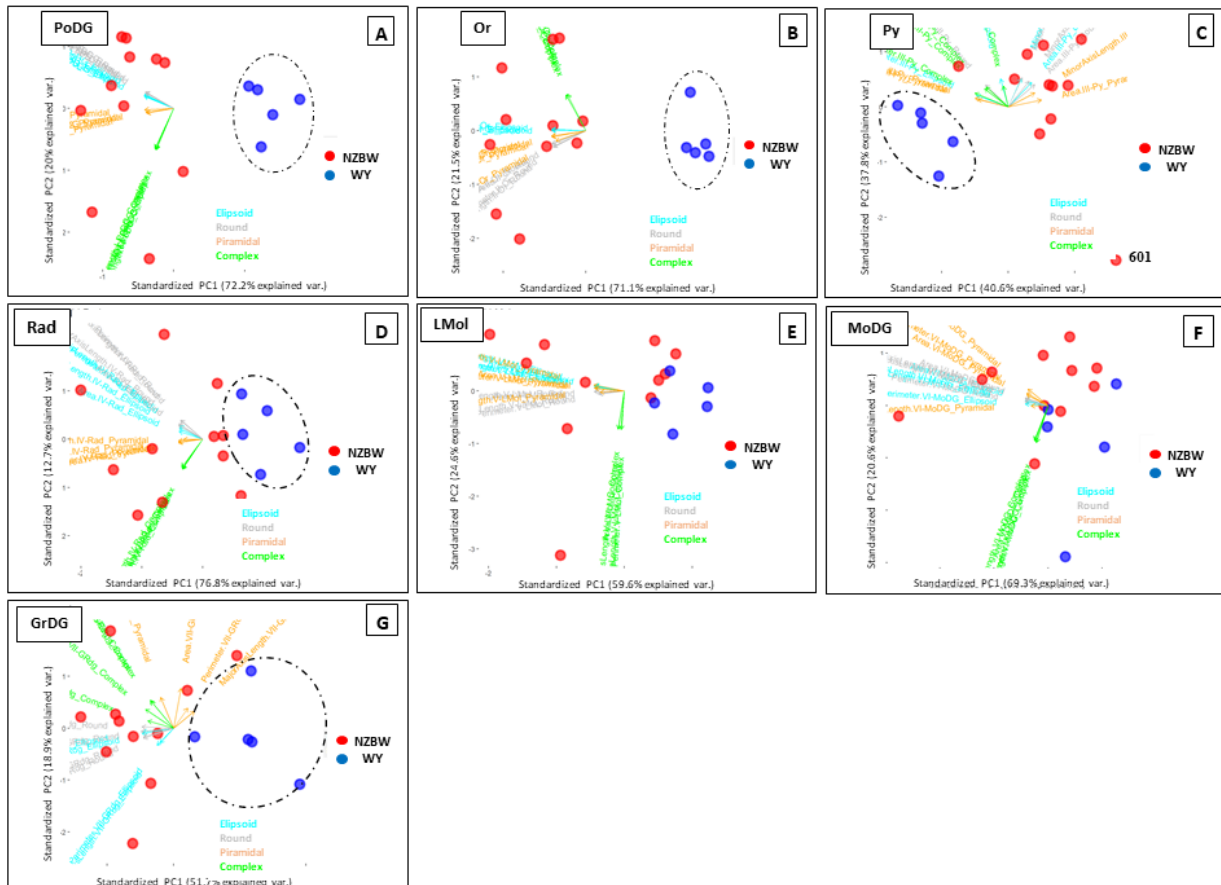
220 **Figure 2:** Graphical representation of the Size morphometric descriptors. Results are presented by subject and
 221 by subregion, separately per cell shape types, in the two populations NZBW (red lines) and WT (blue lines).
 222 In **A**, plot of the area (in microns²). In **B**, plot of the perimeter (microns). In **C**, plot of minor axis length. **The**
 223 **parameter “minor axis length” corresponds to the length of the minor axis of the cell body expressed in μm.**
 224 In **D**, plot of major axis length. **The parameter major axis length corresponds to the length of the major axis of**
 225 **the cell body expressed in μm.** The mean values for each morphometric descriptor are reported for the NZBW
 226 mice (red bold line) and for the WT mice (blue bold line).

227

228 3.3 WT mice showed a distinct clustering compared to NZBW for the domain Size

229 The principal components analysis score plot was applied to visualize the sample distribution patterns
 230 (Figure 3). The two-dimensional scatter plot was defined by the first and second principal components

231 (PC1 and PC2, respectively). In all subregions except the MoDG, the NZBW mice were clearly
 232 separated from WT. In the PoDG, OR Py Rad and LMol subregions, the PC1 and 2 accounted for >
 233 80% of the total variance, indicating that WT subjects were well distinguished from NZBW,
 234 accounting for a large part of the statistically significant differences between them (Figure 3).



235
 236 **Figure 3:** plot of the first (x-axis) against second (y-axis) PCA, for the Size domain, separated for each
 237 subregion, showing similarities (closer points) and differences (distant points) between each of the subjects bi-
 238 dimensionally separately for hippocampal subregion: **in the plot A the PoDG; in B the Or, in C the Py, in D**
 239 **the Rad, in E the LMol, in F the MoDG, in G the GrDG.** Each data point corresponds to one subject in function
 240 of the first two principal components of the morphometric descriptors. The single subjects resulted grouped
 241 by multiple inter-correlated variables and for the four types of cells shape considered (light blue, green, gray
 242 and yellow color). NZBW mice (red dots) and WT mice (blue dots).

243

244 *3.4 Neurons in the hippocampus of NZBW mice showed more regular cell shape than WT neurons.*

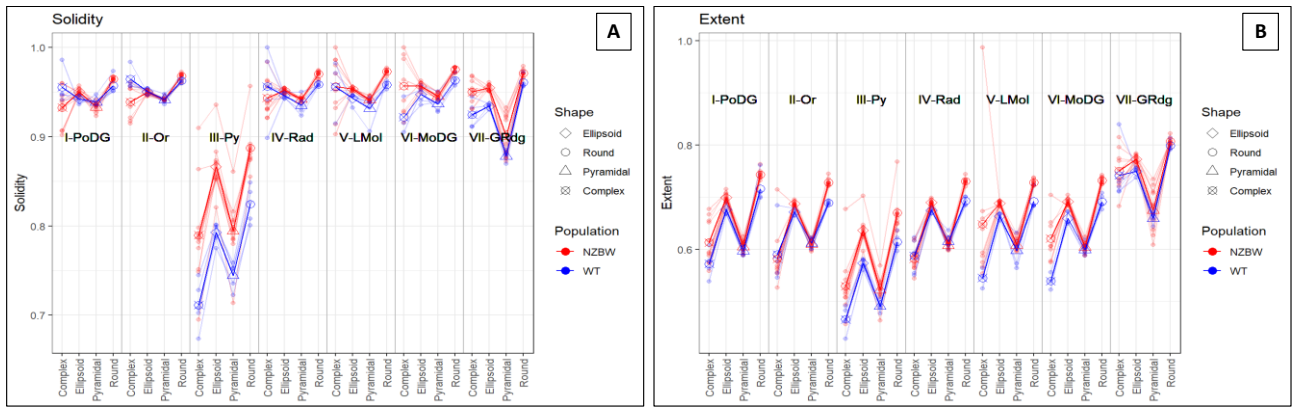
245 The results for the Regularity morphometric descriptors revealed that NZBW neurons were more
 246 regular ($p \leq 0.01$) than WT neurons in all subregions (Figure 4).
 247 Inferential results obtained separately for each shape type revealed that round, ellipsoid and pyramidal
 248 cell contributed strongly ($p \leq 0.01$) to the statistical difference, while the complex shape type did not
 249 show differences (Table 2). Again, graphically, the Py neurons seemed to differ more between them
 250 and across cell shape.

251

Subregion	cell population Regularity difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.0010	0.0010	0.0010	0.0040	0.3570
Or	0.0010	0.0010	0.0030	0.0010	0.5070
Py	0.0010	0.0140	0.0010	0.0010	0.0840
Rad	0.0010	0.0010	0.0040	0.0010	0.8310
LMol	0.0010	0.0010	0.0010	0.0010	0.2690
MoDG	0.0010	0.0030	0.0030	0.0010	0.0900
GrDG	0.0010	0.0250	0.0510	0.0510	0.2490

252 **Table 2:** statistically significant p-value combined by subregion and cells shape type for the Regularity domain
 253 with adjustment by multiplicity. The 1% statistically significant p-values are highlighted in bold.

254



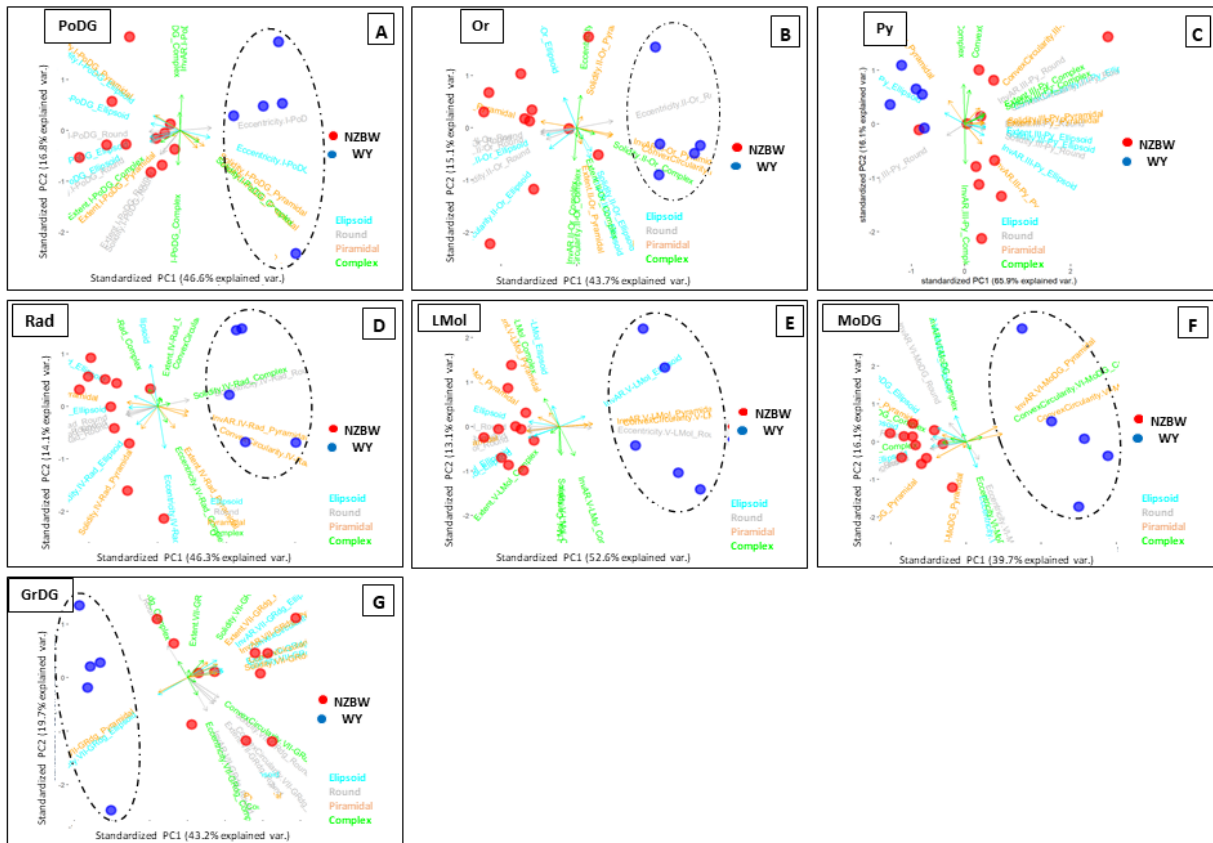
255

256 **Figure 4:** Graphical representation of the Regularity morphometric descriptors solidity (plot A) and extent
 257 (plot B). Results are described by subject and by subregion, separately per cell shape types; NZBW (red lines)
 258 and WT (blue lines). The mean value for each morphometric descriptor is reported for the NZBW mice (red
 259 bold line) and for the WT mice (blue bold line).

260

261 *3.5 Principal component analysis of NZBW populations and WT populations for the Regularity*
 262 *domain*

263 In all subregions, the PCA demonstrated a clear segregation of the WT and NZBW populations
 264 (Figure 5). In Rad, PoDG but most prominently in Lmol and MoDG, the NZBW were closely
 265 clustered while WT were more widely distributed. In the Or and Py subregions, WT subjects formed
 266 a homogeneous group, while the subjects of the NZBW population exhibited a much wider
 267 distribution.



268

269 **Figure 5:** plot of the first (x-axis) against second (y-axis) PCA, for the Regularity domain, separated for each
 270 subregion, showing similarities (closer points) and differences (distant points) between each of the subjects bi-
 271 dimensionally: **in the plot A the PoDG; in B the Or, in C the Py, in D the Rad, in E the LMol, in F the MoDG,**
 272 **in G the GrDG.** Each data point corresponds to one subject in function of the first two principal components
 273 of the morphometric descriptors. The single subjects resulted grouped by multiple inter-correlated variables
 274 and for the four types of cells shape considered (light blue, green, gray and yellow color). NZBW mice (red
 275 dots) and WT mice (blue dots).

276

277 3.6 Neurons in the hippocampus of NZBW mice were denser than neurons in WT

278 NZBW neurons were denser than WT in most cases, except in Py and GrDG subregion (Figure 6).
 279 The NZBW mice presented higher cell density in the Or, Rad, LMol and MoDG than the WT mice
 280 (Figure 6). Multivariate analysis indicated a strong statistically significant difference ($p \leq 0.01$) in the
 281 Py, Rad LMol and MoDG, and statistically significant in Or ($p \leq 0.05$), (Table 3).

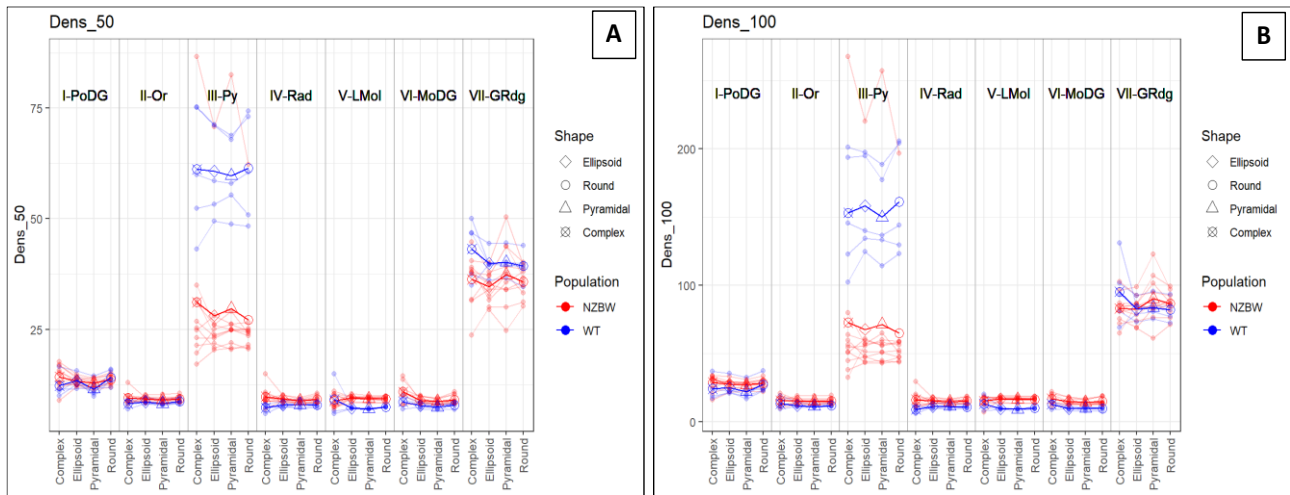
282 Interestingly, the density in the Py subregion was lower in NZBW than in WT, and that was true for
 283 all the cell shape types (Figure 6). The PoDG and GrDG subregions did not significant variation in
 284 cells density between the two mice populations (Table 3). In MoDg, Or and Lmol, the complex shapes
 285 were not significantly different from WT; neither were the pyramidal cells in MoDG.
 286

Subregion	cell population Density difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.2330	0.5490	0.4430	0.0550	0.2350
Or	0.0240	0.0200	0.0110	0.0070	0.2210
Py	0.0090	0.0030	0.0040	0.0080	0.0190
Rad	0.0080	0.0030	0.0040	0.0080	0.0080
LMol	0.0090	0.0020	0.0020	0.0020	0.6990
MoDG	0.0090	0.0060	0.0020	0.0020	0.1410
GrDG	0.2330	0.1530	0.0960	0.4110	0.0960

287 **Table 3:** statistically significant p-value combined by subregion and cells shape type for the Density domain
 288 with adjustment by multiplicity. The 1% statistically significant p-values are highlighted in bold.

289

290



291

292 **Figure 6:** Graphical representation of the morphometric descriptors Ngb_50 (plot A) and Ngb_100 (plot B),
 293 belonging to the Density domain. Results are described by subject and by subregion, separately per the cell
 294 shape types; NZBW (red lines) and WT (blue lines). The mean value for each morphometric descriptor is
 295 reported for the NZBW mice (red bold line) and for the WT mice (blue bold line).

296

297

298 3.7 Principal component analysis of NZBW populations and WT populations for the Density domain

299 The PCA showed that, in Py and Lmol, NZBW mice formed a very homogeneous group while WT
 300 subjects revealed a more spread-out distribution (Figure 7).

301 The subjects of the NZBW population in the Py subregion formed a well-defined group (Figure 7).

302 Control mice were homogeneous and close to each other in the Py, Lmol and MoDG. The two groups

303 were clearly demarcated in the context of the Py, the Lmol and relatively so in the MoDG where the

304 PC1 explained 97.5%, 74.6% and 78.2% of the variance, respectively. This was not the case in PoDG,

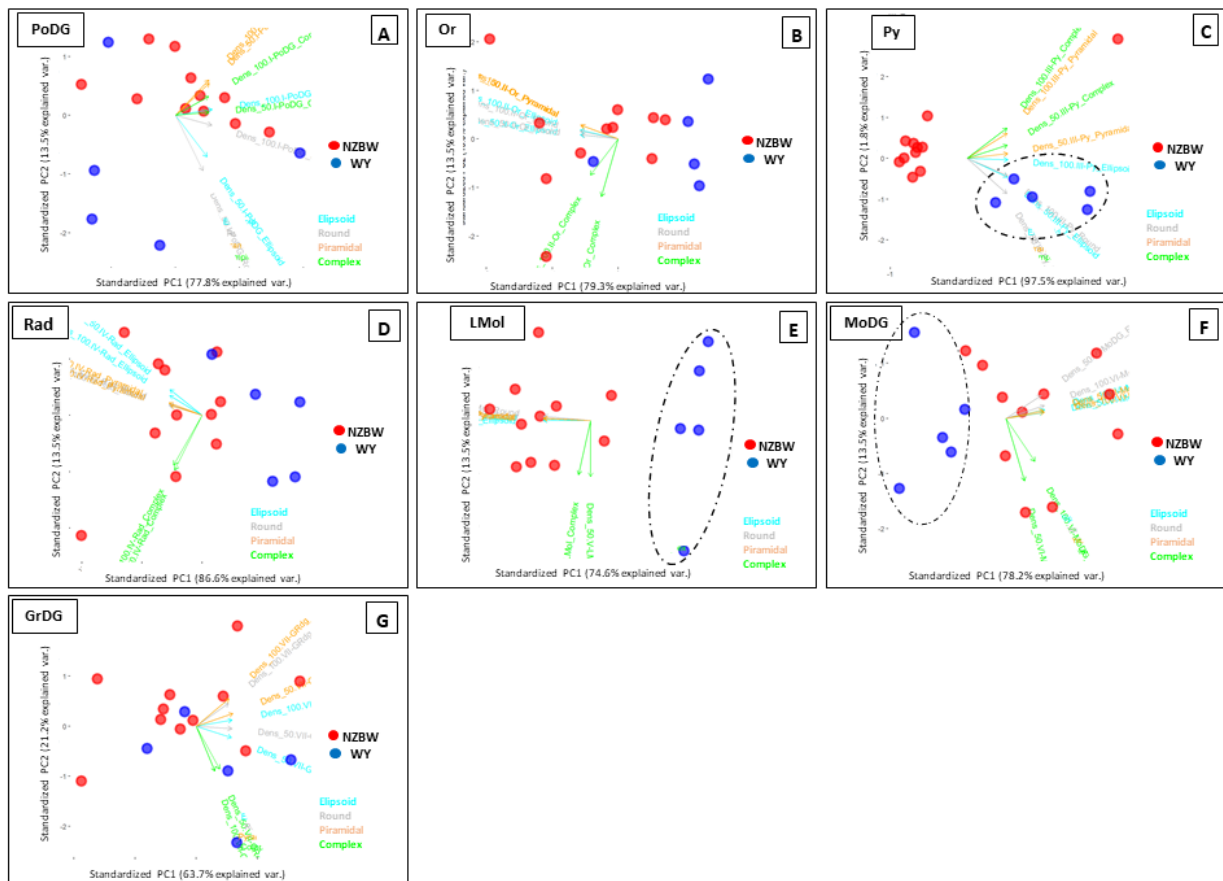
305 Or, Rad and GrDG, (Figure 7). In Py and Lmol specifically, the two populations seemed most

306 segregated.

307

308

309



310

311 **Figure 7:** plot of the first PCA versus the second, for the Density domain, showing the be-dimensional
 312 visualization of similarities and differences between each of the subjects. Each point corresponds to one subject
 313 with a 2-D (the first two principal components) projection of the morphometric descriptors. The single subjects
 314 resulted grouped by multiple inter-correlated variables and for the four types of cells shape considered (light
 315 blue, green, gray and yellow color). NZBW mice (red dots) and WT mice (blue dots).

316

317 3.8 Summary of results

318 ▪ **Size:** NZBW hippocampal neurons were larger in size than those of WT. No differences were found
 319 in the MoDg and GrDG subregion.

320 ▪ **Regularity:** NZBW hippocampal neurons were significantly more regular than those of WT mice
 321 in all the subregions. However, the complex cell shape did not contribute to the statistical significance
 322 in any subregion.

323 ▪ **Density:** In NZBW, neurons were usually denser than in WT. Interestingly, Py neurons were much
 324 denser in WT than in NZBW. The PoDG and GrDG did not show difference in cell density.

325 **4.Discussion**

326 This study is aimed at investigating alterations in the internal hippocampal cytoarchitecture of the
327 NZBW mice lupus model. Our results revealed that neurons in the hippocampus of NZBW mice were
328 denser, larger and showed a more a regular cell body than WT mice, apart in the Py subregion, where
329 density of NZBW neurons was lower than in WT. Finally, PCA allow to distinguish healthy WT
330 subjects from NZBW subjects.

331 332 *4.1 How does NPSLE induce hippocampal damage? Two alternative hypotheses*

333 The studies performed on possible hippocampal damages in both human SLE patients and in lupus
334 mice models highlighted two alternative hypotheses: one suggests that NPSLE induces hippocampal
335 damage and atrophy by either reducing the number of neurons (Ballok et al 2004) or reducing the
336 volume of the hippocampal structures (Appenzeller et al., 2006, Bódi et al., 2017; Liu et al., 2020).
337 Conversely, the other hypothesis also proposes that NPSLE causes hippocampal damages, but
338 increasing the local volumes, cells hypertrophy, and cells number (Zimmerman et al., 2017). Other
339 works have argued that, regarding the whole brain, volumetric variations do not scale well with
340 alterations in cognitive abilities, and that the total number of neurons appears to be a much more
341 accurate predictor of cognitive ability (Herculano-Houzel, 2011).

342 Recently, efforts have been focused on the involvement of microglia in NPSLE cognitive dysfunction,
343 revealing an aberrant overexpression of these cells in lupus mice hippocampi (Qiao et al., 2021).
344 Additionally, Grovola and colleagues assessed neuropathological and neuroinflammatory changes in
345 subregions of the dentate gyrus of the pig (Grovola et al., 2020). They found mossy cell hypertrophy
346 with a statistically significant increase in neuron density, specifically in the MoDG, at 7, 30 days and
347 1-year post brain injury, suggesting that microglial activation after brain injury may play a role in
348 hippocampal circuit and/or synaptic remodeling (Grovola et al., 2020).

349 Despite contrasting results resulting in two hypotheses, most of these studies provide evidence on the
350 presence of structural abnormalities in the brain linked to NPSLE manifestations. Whether neuron

351 morphology might be affected and, eventually, which types or groups of neurons may be responsible
352 for the differential effects on cognitive ability remains a subject of debate. The reason behind different
353 and sometime contrasting results (Ota et al 2022) could be related to the fact that no unifying
354 pathophysiological processes has been found in the etiology of NPSLE.

355 Using advance quantitative imaging and statistical methods, over a large number of cells, we
356 contributed to the discussion with hard evidence, showing as NZBW hippocampus possess cells
357 hypertrophy (denser and larger neurons) than WT mice

358 This finding support the hypothesis that NPSLE causes hippocampal cells hypertrophy. Conversely,
359 the Py subregion in NZBW mice present lower density than in WT mice supporting the hypothesis
360 that NPSLE induce hippocampal damage by reducing the number of neurons.

361

362 *4.2 Analysis combined by subregion and by cell shape allowed to highlight hidden differences*

363 We carried out the present analysis separately for the 7 hippocampal subregions, considering 4 types
364 of neuronal shape. Using this focal approach, we were able to identify the hippocampal subregions in
365 which the cytoarchitecture was altered and the type of neurons involved. An accurate account of the
366 internal hippocampal cytoarchitecture is a key step towards the elucidation of the pathogenic
367 mechanisms underlying NPSLE and virtually in all neurological disorders. In this sense the
368 characterization of neuronal morphometry *via* descriptors at the cytoarchitecture meso-scale of an
369 organ or a layer appears to be a powerful indicator of neural cells functions in health *vs.* pathology
370 (Herculano-Houzel, 2011).

371

372 *4.3 The NZBW mice had larger body size and were denser than WT mice in PoDG, Or, Py, Rad, LMol*

373 The Or, Rad and LMol subregions are relatively cell-free areas containing subpopulations of
374 interneurons. An interesting aspect in the LMol subregions is the presence of specific interneurons
375 type, the so-called neuroglia-form cells that mediate powerful inhibition of CA1 pyramidal cells
376 (Capogna 2011). These interneurons play an important role in the regulation of local circuits in the

377 hippocampus proper, selectively regulating specific groups of neurons to enhance their function or
378 protect vulnerable neurons from damage (Houser, 2007). Our results show that interneurons density
379 and soma size tended to increase in the Or, Rad and LMol subregions of NZBW mice. Despite the
380 lack of data regarding interneuron morphology of patients with SLE or in lupus mice models,
381 evidence of hypertrophy of interneurons in the hippocampus were described in several
382 neuropathological conditions, including mice after epileptogenetic hippocampal lesion (Sieu et al.,
383 2017) and in the mouse model for the neurodegenerative disorder's neuronal ceroid lipofuscinoses
384 (Cooper et al., 1999).

385 Pyramidal neurons are responsible to provide organized responses to spatial stimuli, non-spatial
386 stimuli, and time in the Py subregions (Lisman et al., 2017). An increase in the soma size of the
387 pyramidal neurons associated to cytoplasmic accumulations of phosphorylated neurofilament was
388 demonstrated in neuropathological condition as hippocampal sclerosis in human (Thom et al., 1999).
389 Hypertrophy of the hippocampus associated with an increase in perikarya size of pyramidal neurons
390 was found also in transgenic synRas mice (Gärtner et al., 2004), suggesting an involvement of the
391 Ras-signaling (Rat sarcoma virus) in morpho-regulatory and structural maintenance of hippocampal
392 pyramidal neurons.

393 In prior works, variation in cell regularity have been considered to evaluate damages in brain areas
394 due to ischemia or to highlight differences in cerebellum of bovine affected from Freemartin
395 syndrome.

396 Leyh and colleagues, in the murine hippocampus and neocortex analyzed shape and regularity of cells
397 (convex areas, circularities and other parameters) between control hemisphere and ischemic-affected
398 hemisphere. They showed as microglia cells had larger convex hull area and soma circularities, within
399 the control hemisphere compared to the ischemic-affected hemisphere (Leyh et al., 2021).

400 In a recently work Corain and colleagues set up a method to analyzed the cell shape, regularity and
401 density in bovine cerebellar neurons, to quantify dimorphism in the cytoarchitecture among male,

402 female and bovine affected from the freemartin syndrome, showing as the Freemartin granule neurons
403 were the largest, most regular and dense (Corain et al., 2020).

404

405 *4.4 No difference was found in neural density among NZBW and WT mice in the PoDG and GrDG*
406 *subregion*

407 Differences in neural density between NZBW and WT mice were not significant in the GrDG
408 subregion. A possible explanation of the steady state of granule cells number in NZBW could be the
409 result of the turnover process due to neurogenesis well described in the dentate gyrus of adult
410 mammals (Amaral et al., 2017; Abbott and Nigussie, 2020). Although evidence indicate that
411 neurogenesis in the dentate gyrus persists in the adult mammalian brain and appears to be under
412 environmental control, (Abbott and Nigussie, 2020), studies have shown that the total number of
413 granule cells does not vary in adult animals (Abbott and Gallagher, 1996), demonstrating that there
414 is a steady state turnover of granule cells rather than a continuous accretion. These could explain way
415 no difference was found in GrDG neural density between NZBW and WT mice.

416 The axons of the excitatory granule neurons in the GrDG reach direct to mossy cells in the PoDG
417 (Scharfman, 2016). The loss of mossy cells, which are excitatory neurons making synaptic contact
418 with granule cells, basket cells, and CA3 pyramidal neurons, has been demonstrated to contribute to
419 DG dysfunction (Scharfman, 2016), resulting in the dysregulation of granule cell excitability, which
420 in turn leads to abnormal behaviors such as anxiety and impaired pattern separation (Jinde et al.,
421 2012).

422

423 *4.5 WT subjects formed a defined cluster from the scattered NZBW subjects*

424 The PCA analysis grouped the subjects, distinguishing WT subjects from NZBW subjects.
425 Furthermore, it is worth noting that the variability among subjects within NZBW population was
426 much larger than in WT mice.

427 The variability within NZBW subjects could be mainly due to multisystem involvement and
428 confounding aspects (proteinuria levels) that occur in lupus disease. These multisystem aspects could
429 also be the reason why experimental studies have not yet been able to explain the main causes and
430 mechanisms involved in the pathogenesis of NPSLE (Bruyn, 1995).

431 The PCA method is useful when data sets from different modalities are combined or if the analysis is
432 complex that there is a need for dimension reduction. Despite is very difficult to clarify how
433 neuroanatomical changes are relating to clinical symptoms of **neurodegenerative diseases**, the PCA
434 showed the possibility to differentiate healthy patients from schizophrenic patients (Caprihan et al.,
435 2008; Rotarska-Jagiela et al., 2008). The application of PCA was proposed also to improve the
436 performance of Alzheimer's disease detection (Halebeedu et al., 2021).

437 Recently, in the field of SLE, the PCA performed well in in lupus nephritis patients, identifying
438 important risk factors and thus enabling clinicians to identify subjects at-risk and either implement
439 preventative strategies or manage current treatments (Huang et al., 2020). The PCA was also used to
440 determine which groups of cytokines have the greatest influence across disease activity states helping
441 to describe the influence of complex cytokine interactions in SLE (Raymond et al., 2019). The PCA
442 was also applied as a tool to identify lesioned skin patterns in cutaneous lupus erythematosus, helping
443 to characterize where on the body lesions of cutaneous lupus erythematosus tend to occur in patients
444 (Prasad et al., 2020).

445 The methodology we propose based on in-depth analysis of the morphology of neural cells, provides
446 a collection of valuable data on the morphology of multiple cells, acquired and analyzed individually.
447 In the context of the investigation of pathological changes in structures of the brain areas, due to SLE
448 disease, the application of PCA as technique for reducing the dimensionality of such datasets, allows
449 the increasing interpretability but at the same time minimizing information loss. The collection of
450 large datasets are increasingly common in pathological investigation and the method we proposed
451 could be a powerful tool to distinguish healthy from pathological neurons in postmortem sample
452 analysis.

453 **5.Conclusion**

454 The methodology we set-up consists of multivariate and multi-aspect testing for cytoarchitecture-
455 ranking, based on neuronal cell shape analysis, among populations defined by factors, such as sex,
456 age or pathology. This tool could be a powerful instrument to carry out morphometric analysis
457 providing a robust basis for objective tissue screening, especially in the field of neurodegenerative
458 pathologies.

459 The analysis carried out separately for each hippocampal subregion provided a baseline to highlight
460 hidden effects on the neuronal cytoarchitecture with respect to analyses conducted without this
461 subdivision.

462 **The application of PCA methodology represents a possible approach to understanding the effects of**
463 **lupus disease in the brain, optimizing the interpretation of complex data in diagnostics of neurolupus**
464 **consequences.**

465 Despite the statistically significant morphologic alterations that we found in the NZBW lupus mice
466 hippocampal cytoarchitecture, it remains to be determined whether these structural modifications are
467 associated with the progress of the autoimmune disease and whether these modifications are
468 functionally important.

469 We are aware that the pathogenetic aspects of lupus in NZBW mice are not entirely representative of
470 the of human pathology. However, this murine model can significantly contribute towards the
471 understanding of lupus.

472

473

474 **Abbreviation**

475 NZB/W F1 (NZBW)

476 Systemic Lupus Erythematosus (SLE)

477 Central nervous system (CNS)

478 Neuropsychiatric SLE (NPSLE)

479 Dentate gyrus (DG),
480 Molecular layer (MoDG),
481 Granule cell layer (GrDG)
482 Polymorph dentate gyrus (PoDG)
483 Pyramidal layer (Py)
484 Stratum oriens (Or)
485 *Stratum radiatum* (Rad)
486 *Stratum lacunosum-moleculare* (LMol)

487

488 **Declarations:**

489 **Ethics approval and Consent to Participate:** All experimental procedures were previously
490 approved by the “Padova University Animal Ethic Committee and Italian Ministry of Health with the
491 authorization number 720/2017-PR under the Italian Law Dlgs 26/2014”.

492

493 **Consent to publication:** The authors declare that they consent to publication.

494

495 **Availability of data and material:** The authors declare that data and material can be freely given
496 upon request.

497

498 **Authors' contributions:** Antonella Peruffo: Conceptualization, Supervision, Writing, Original draft,
499 Writing - review & editing. Jean-Marie Graïc: Conceptualization, Methodology, Writing - review &
500 editing. Tommaso Gerussi: Methodology, Writing - review & editing. Bruno Cozzi:
501 Conceptualization, Writing - review & editing. Andrea Doria: Conceptualization, Writing - review &
502 editing. Mariella Gatto: Writing - review & editing. Livio Finos: Methodology, Writing - review &
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509 **References**

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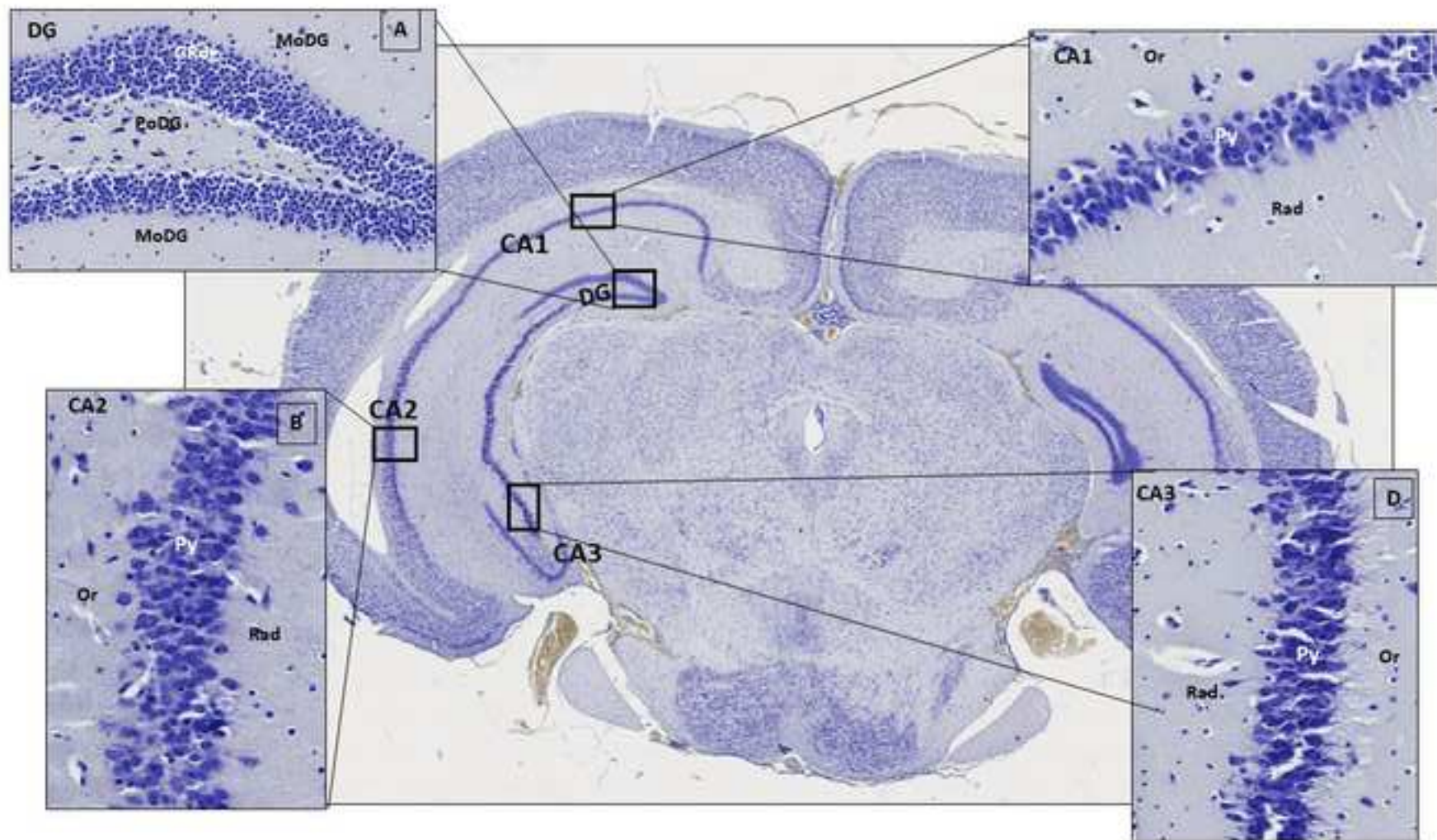
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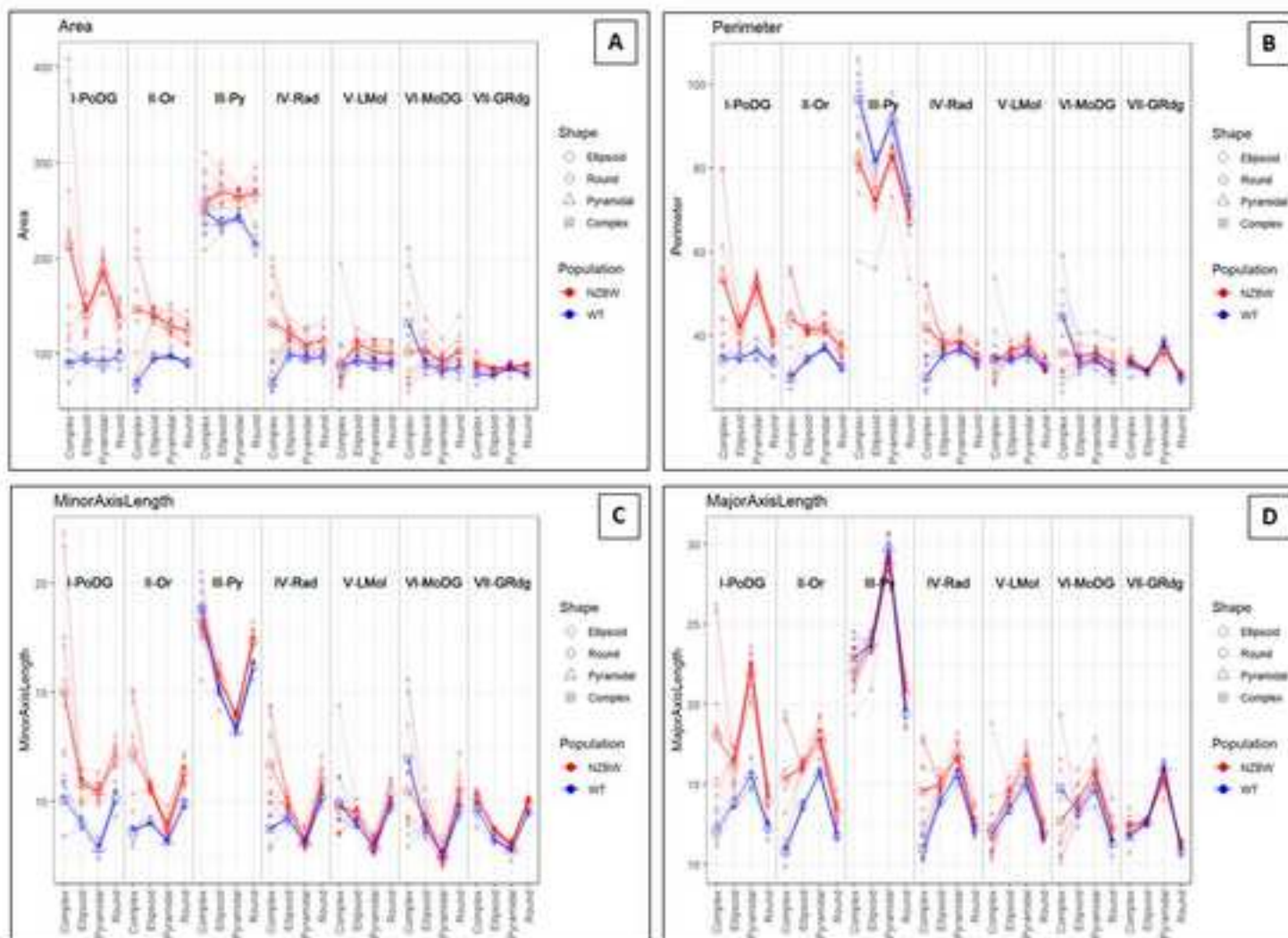
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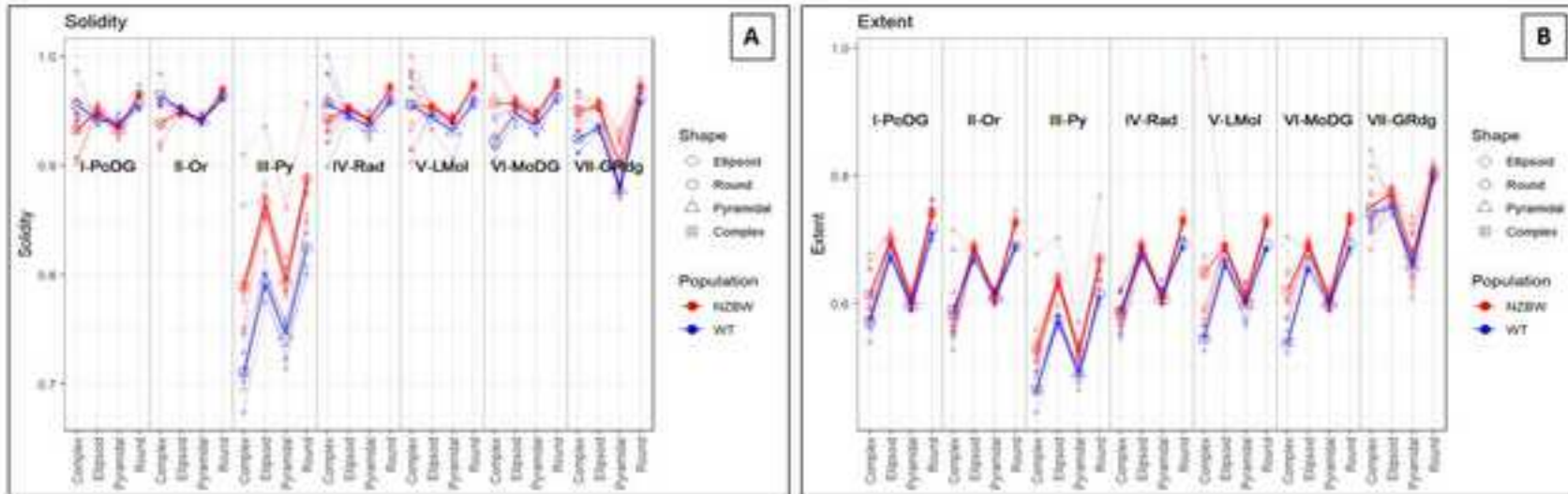
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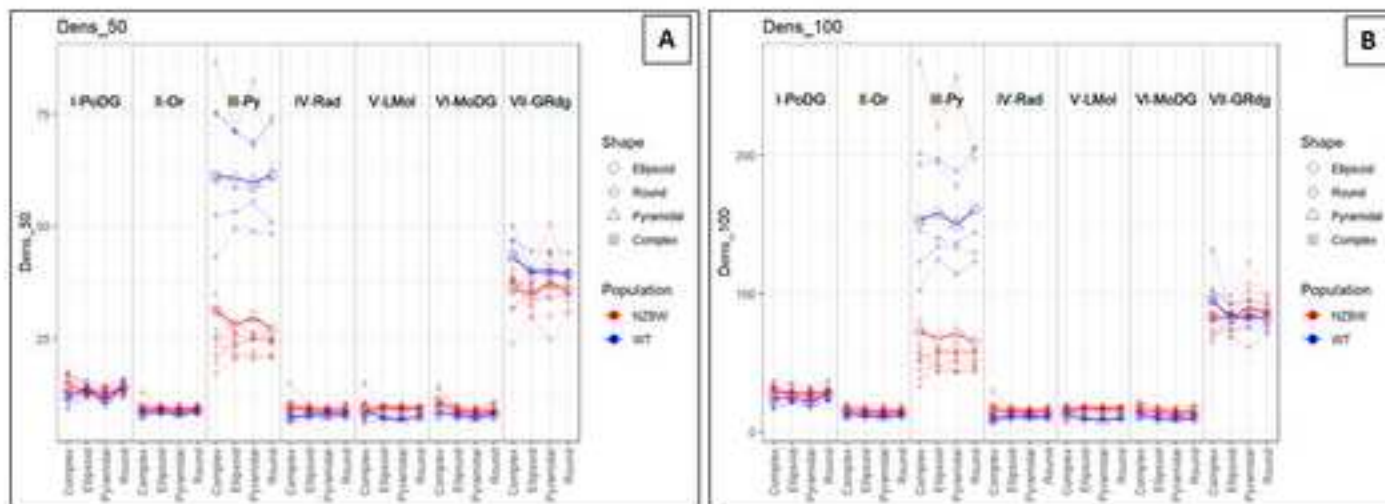
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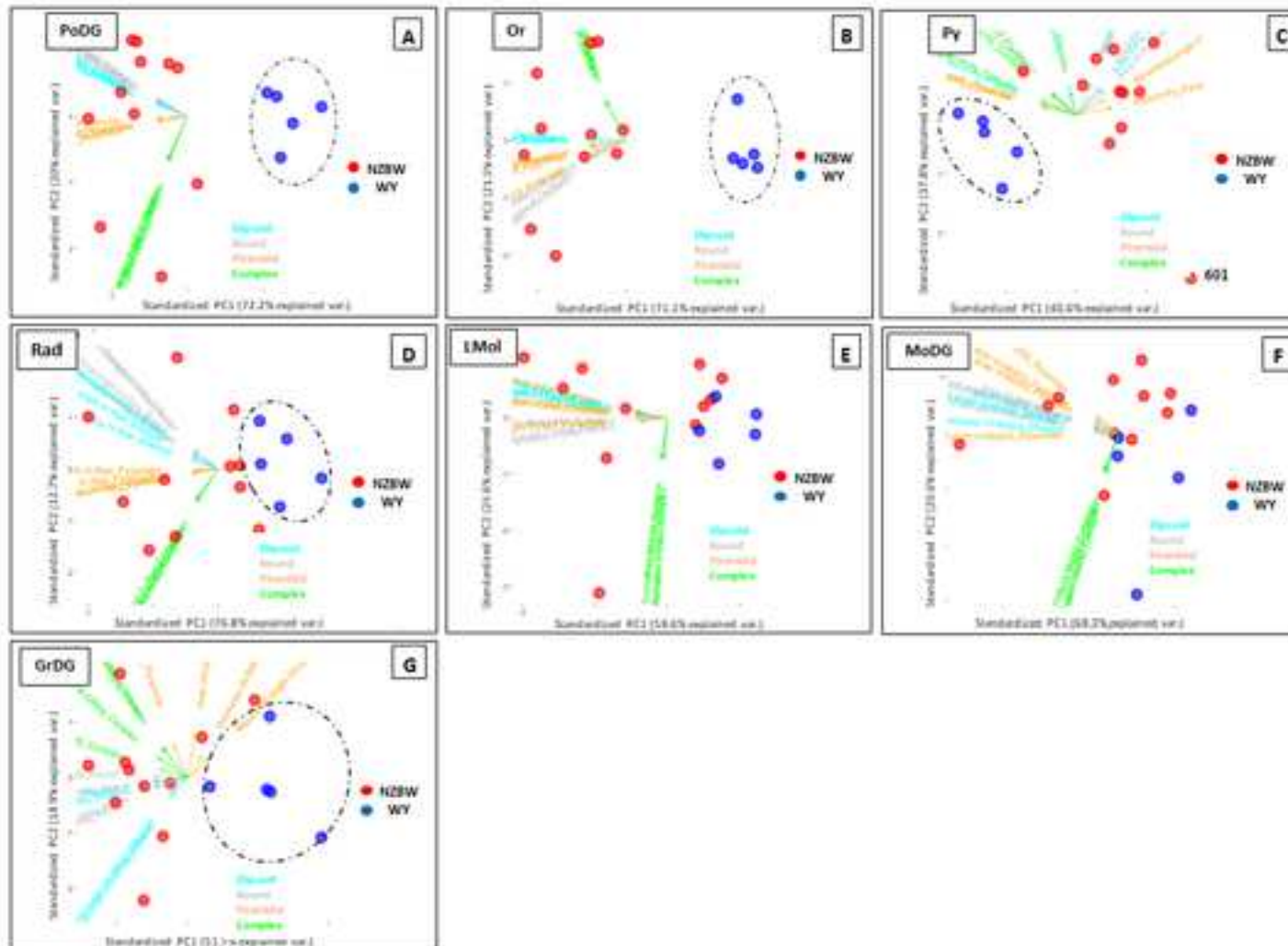
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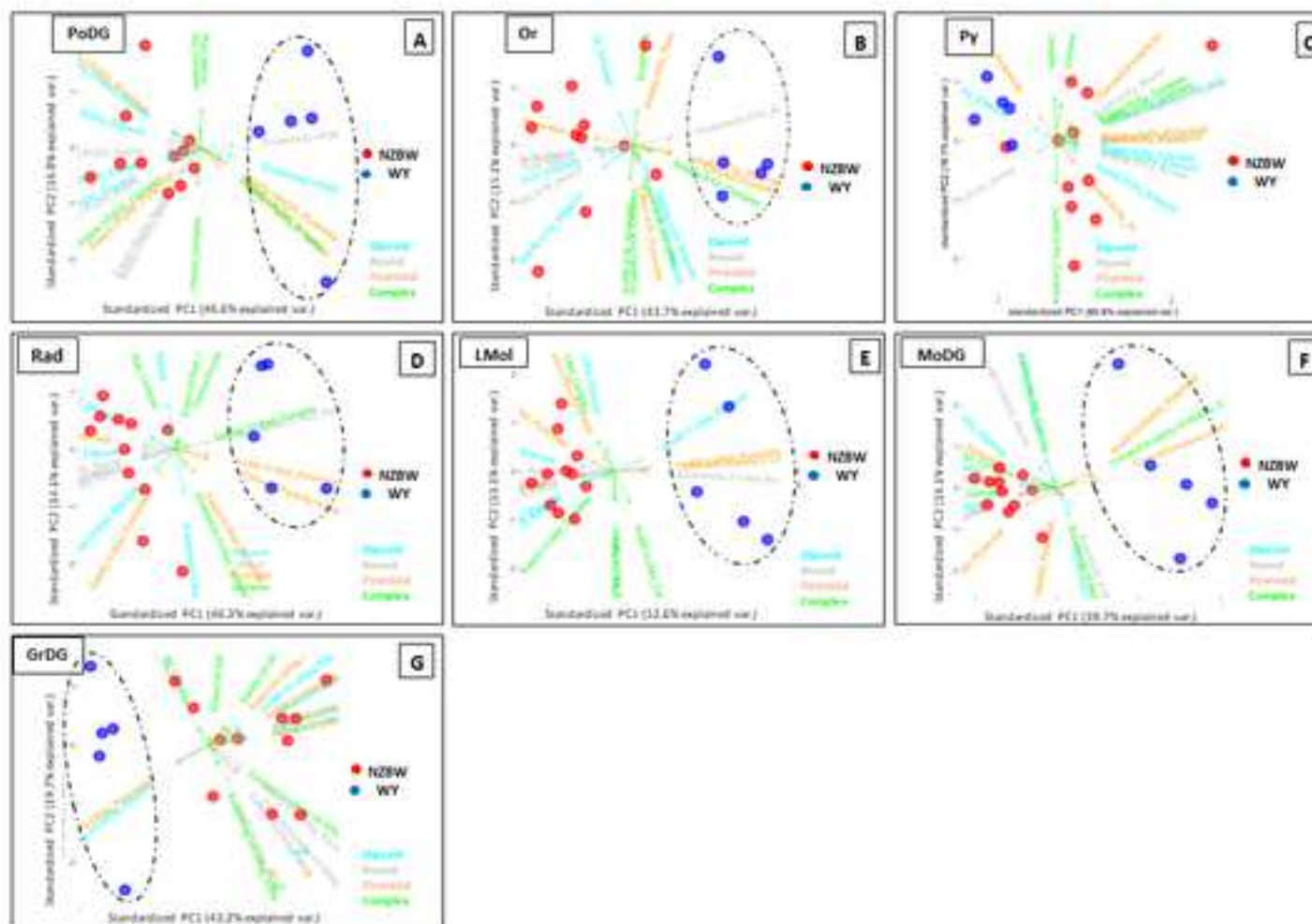


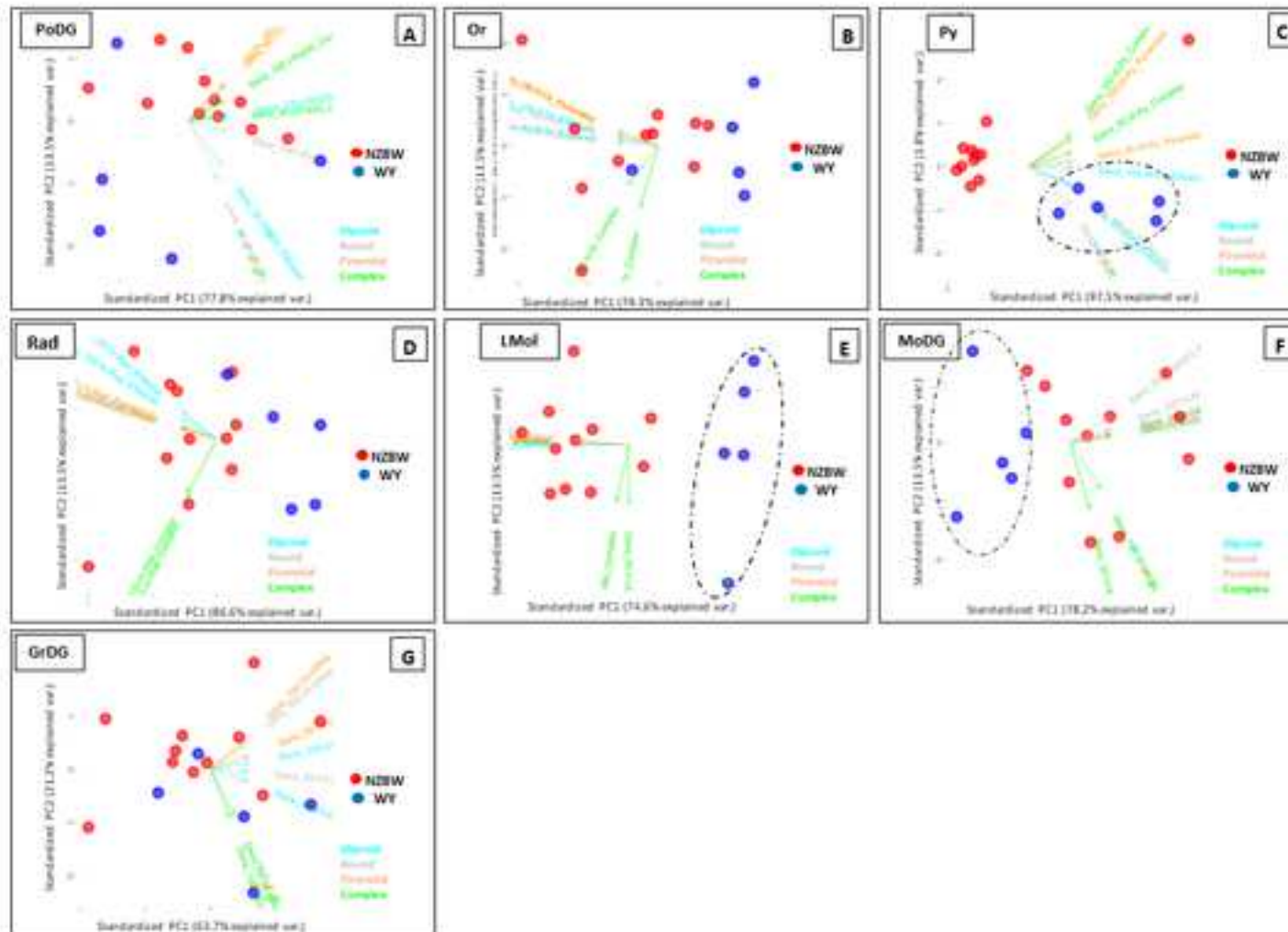












Tables

Table 1

Subregion	cell population Size difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.0020	0.0030	0.0020	0.0010	0.0410
Or	0.0020	0.0020	0.0010	0.0030	0.0450
Py	0.0080	0.0040	0.0040	0.0020	0.1550
Rad	0.0050	0.0670	0.0020	0.0150	0.0090
LMol	0.0410	0.1530	0.0040	0.0290	0.9530
MoDG	0.0570	0.1530	0.0040	0.0290	0.9530
GrDG	0.0150	0.0010	0.0130	0.1120	0.0200

Table 1: significant p-value combined by subregion and cells shape type for the domain Size with adjustment by multiplicity. The 1% statistically significant p-values are highlighted in bold.

Table 2

Subregion	cell population Regularity difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.0010	0.0010	0.0010	0.0040	0.3570
Or	0.0010	0.0010	0.0030	0.0010	0.5070
Py	0.0010	0.0140	0.0010	0.0010	0.0840
Rad	0.0010	0.0010	0.0040	0.0010	0.8310
LMol	0.0010	0.0010	0.0010	0.0010	0.2690
MoDG	0.0010	0.0030	0.0030	0.0010	0.0900
GrDG	0.0010	0.0250	0.0510	0.0510	0.2490

Table 2: statistically significant p-value combined by subregion and cells shape type for the Regularity domain with adjustment by multiplicity. The 1% statistically significant p-values are highlighted in bold.

Table 3

Subregion	cell population Density difference p-value				
	Whole subregion	Round cells	Ellipsoid cells	Pyramidal cells	Complex cells
PoDG	0.2330	0.5490	0.4430	0.0550	0.2350
Or	0.0240	0.0200	0.0110	0.0070	0.2210
Py	0.0090	0.0030	0.0040	0.0080	0.0190
Rad	0.0080	0.0030	0.0040	0.0080	0.0080
LMol	0.0090	0.0020	0.0020	0.0020	0.6990
MoDG	0.0090	0.0060	0.0020	0.0020	0.1410
GrDG	0.2330	0.1530	0.0960	0.4110	0.0960

Table 3: statistically significant p-value combined by subregion and cells shape type for the Density domain with adjustment by multiplicity. The 1% statistically significant p-values are highlighted in bold.

1 **Highlights**

2 Hippocampus is one of the brain structures most sensitive to psychiatric disorders related to
3 neuropsychiatric lupus.

4 The NZBW murine model offers an opportunity to bridge the gap between neurological deficits and
5 histological lesions underlying NPSLE.

6 Our results show a hypertrophy of the NZB/W F1 hippocampal neurons associated with an increase
7 in perikaryal size.

8

9 By principal component analysis we distinguished healthy Wild Type from NZB/W F1 mice.

10

11 Hippocampal structure in the NZB/W F1 lupus model, suggests the hypothesis that the different
12 subregions could be differentially affected in neuropsychiatric systemic lupus erythematosus disease.

13

14

15



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Supplementary Material

Supplementary material 08 05 2023.docx

