Figure S1

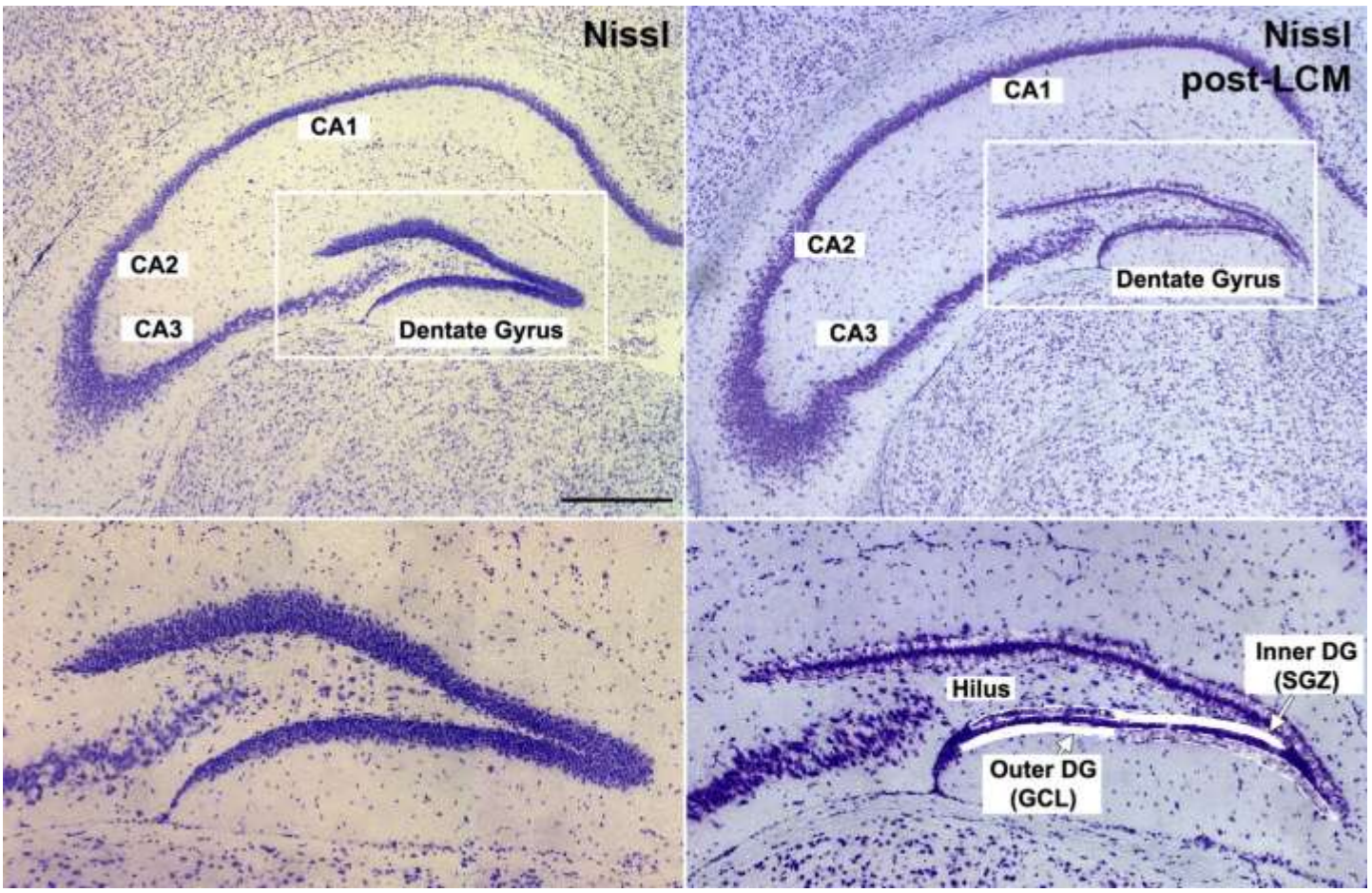

Figure S1, related to Figure 1: Delineation and laser capture microdissection (LCM) of the adult mouse dentate gyrus SGZ and GCL. Left panels shows cresyl violet staining of a 12µm section through the adult mouse hippocampus (top) and dentate gyrus (bottom). Right panels show a nearby cresyl violet-stained section following LCM of the inner portion of the GCL and the outer portion of the GCL independently. In each case a band approximately 2-3 cells thick was isolated. CA1, CA2, CA3: hippocampal subfields; DG: dentate gyrus; SGZ: subgranular zone; GCL: granule cell layer. Scale bar: 500µm.

Figure S2

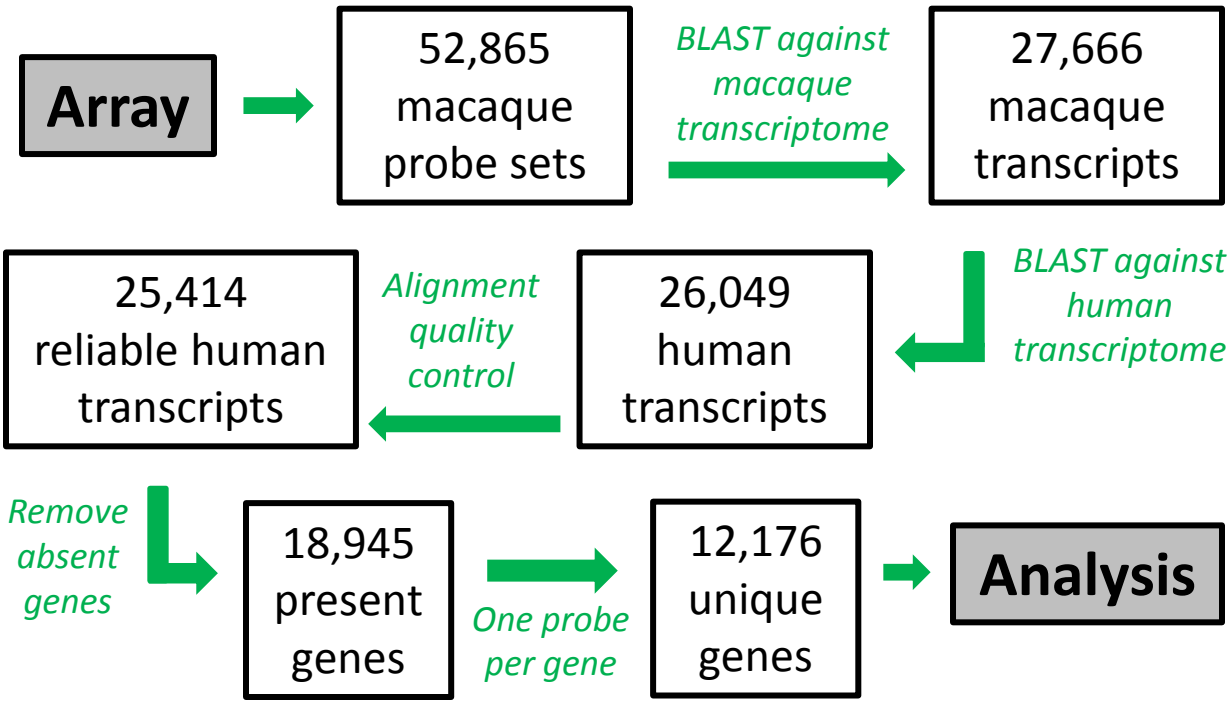

Figure S2, related to Materials and Methods: Schematic of macaque probe to human gene conversions. To allow better comparison with orthologous mouse genes, macaque probe sets were annotated with human gene symbols instead of using the Affymetrix annotation. First, probes were BLASTed against the latest (10/14/2010; Build 1.2) macaque transcriptome and any probe sets with at least 3 probe hits (alignment of >80% sequence length and >90% alignment score) were considered a match to the macaque transcript. Second, macaque transcripts were blasted against the human transcriptome (7/13/2009; RefSeq version 36) to assign human gene symbols to relevant probe sets. Third, results were checked manually and by comparison with several other annotation strategies in order to assess believability of each hit. Finally, gene symbols were renamed for the few probe sets (<10%) where our results disagreed with consistent results from several other annotation strategies (majority rules strategy). These changes typically occurred for genes with several aliases and in situations where the rhesus monkey transcriptome is incomplete. For mouse, the most recent Affymetrix annotation file (6/9/11; Release 32) for MG-U74Av2 was used. Orthologous mouse and macaque genes were found using the Jackson Laboratory orthology table downloaded from http://www.informatics.jax.org/orthology.shtml on 4/23/12. The probe with the highest mean expression was chosen to represent each gene using the function collapseRows in the WGCNA library (Miller et al., 2011), leaving a total of 12,176 macaque genes.

Figure S3

*(**Figure S3** spans the next 62 pages.)*

Figure S3, related to Figure 2: Representative ISH images for the 363 genes identified in adult mouse as showing enrichment in the subgranular zone compared to the overlying granule cell layer. Coronal and sagittal images were selected to illustrate the cellular distribution of each gene in the hippocampus and in some cases the adjacent subventricular zone and rostral migratory stream surrounding the lateral ventricle. Gene labels link to matched ISH images in the Allen Mouse Brain Atlas, which are interactive and are presented at much higher resolution. Scale bar: 500μm.

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Cdca3

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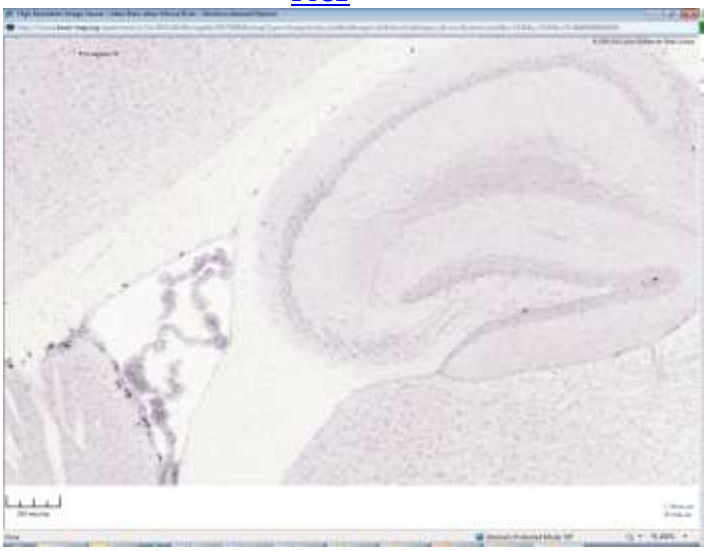
Prc1



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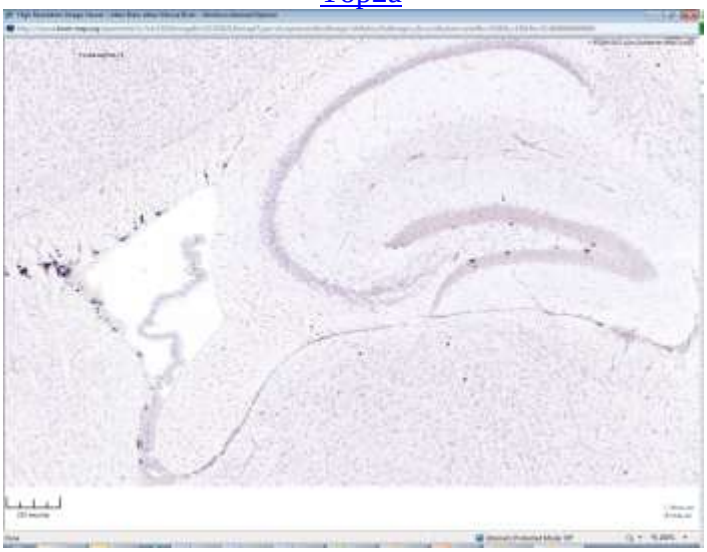

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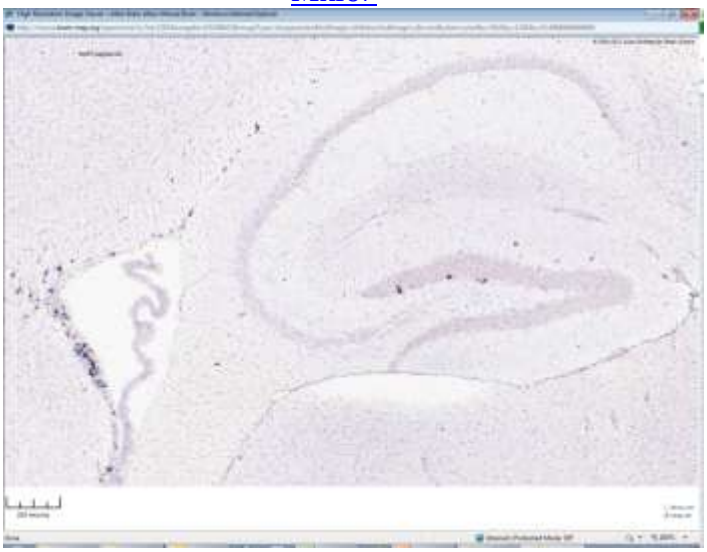

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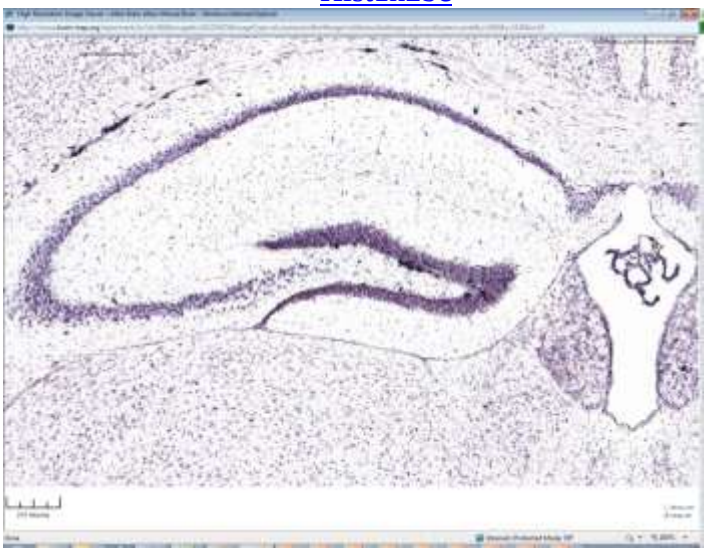

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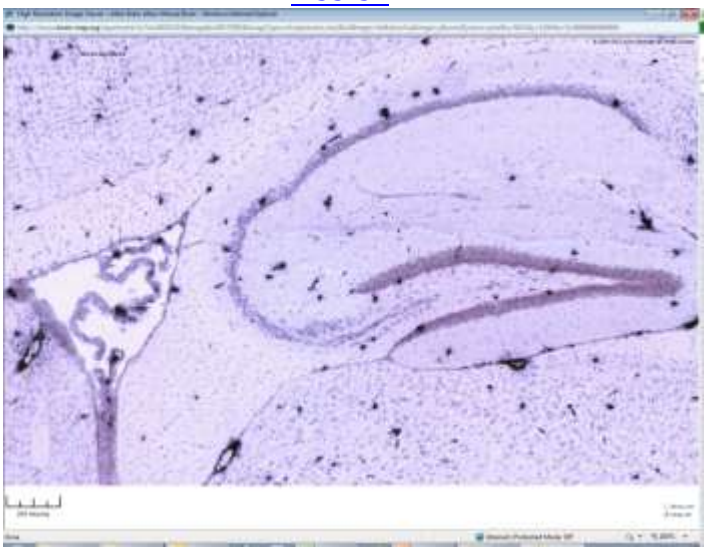
Hbb-b2



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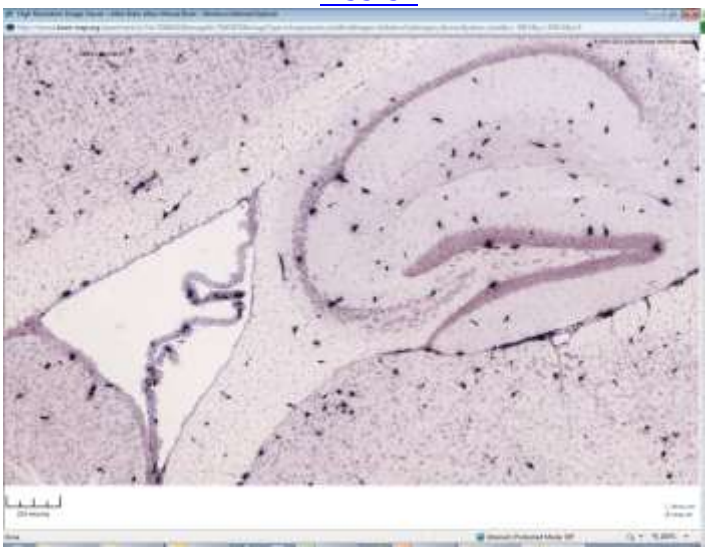

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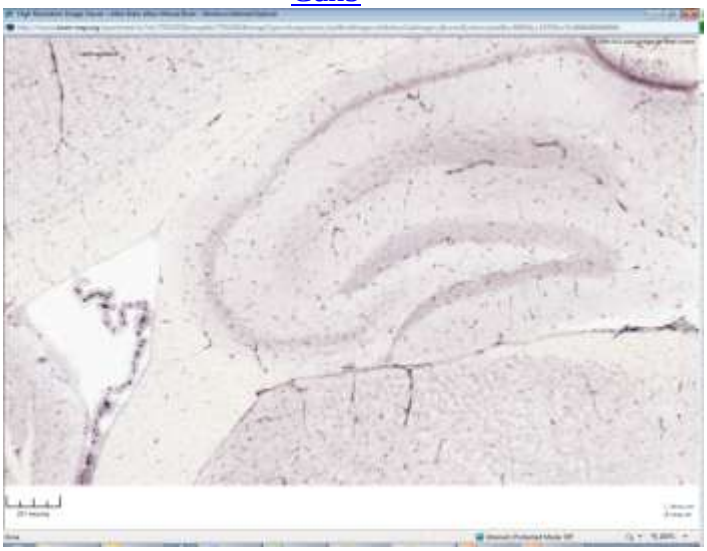

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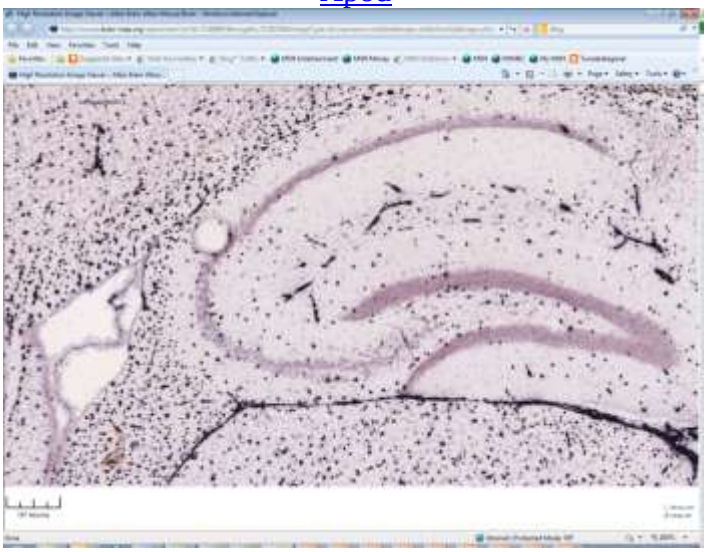

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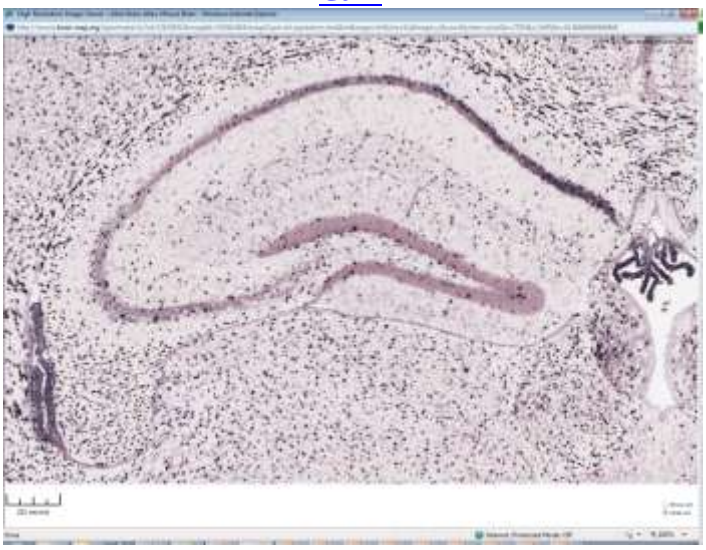

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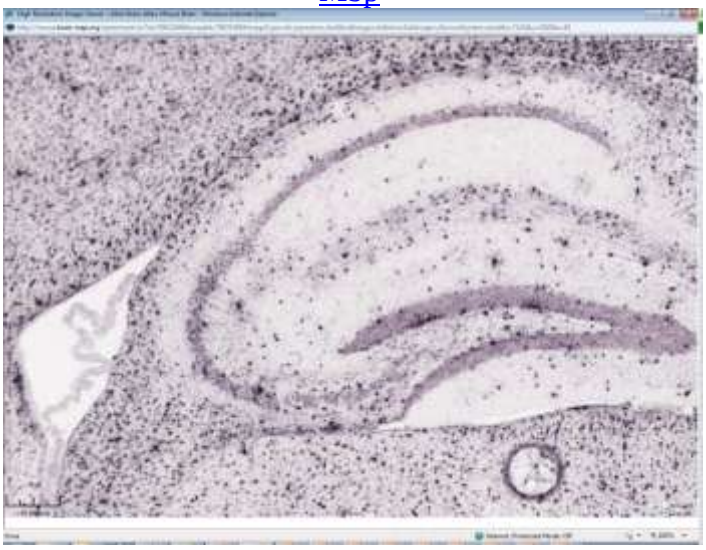

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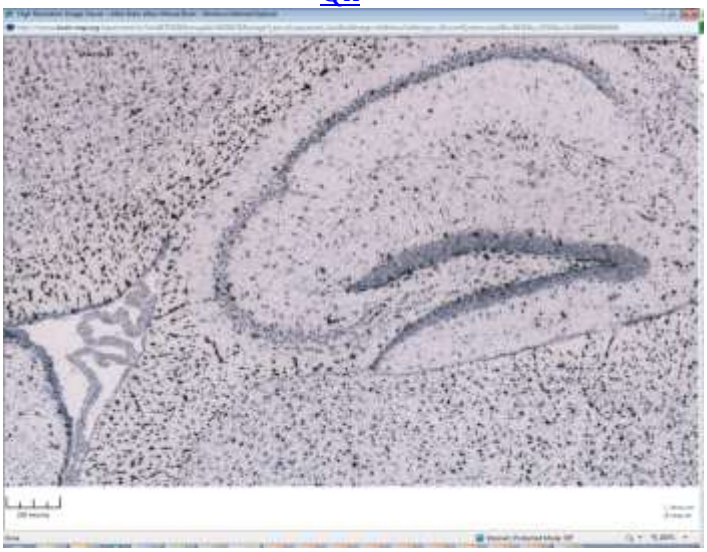

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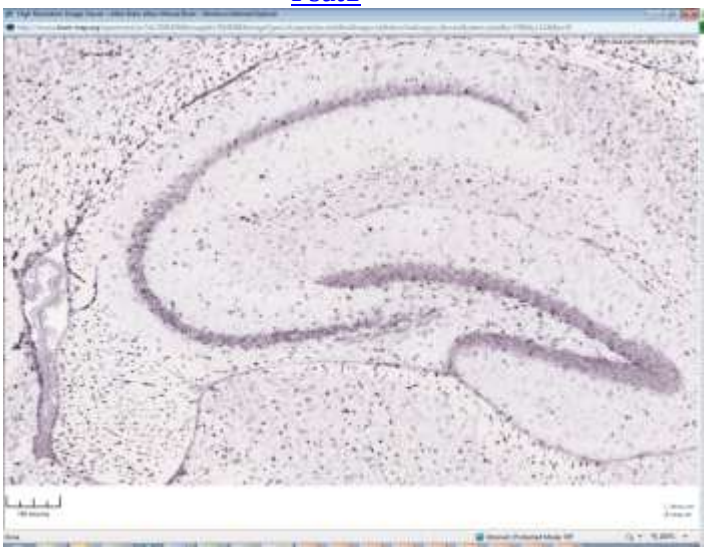

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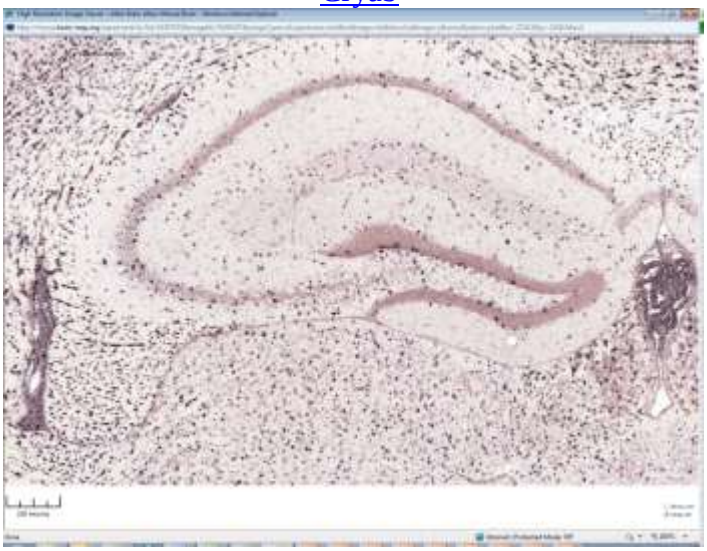

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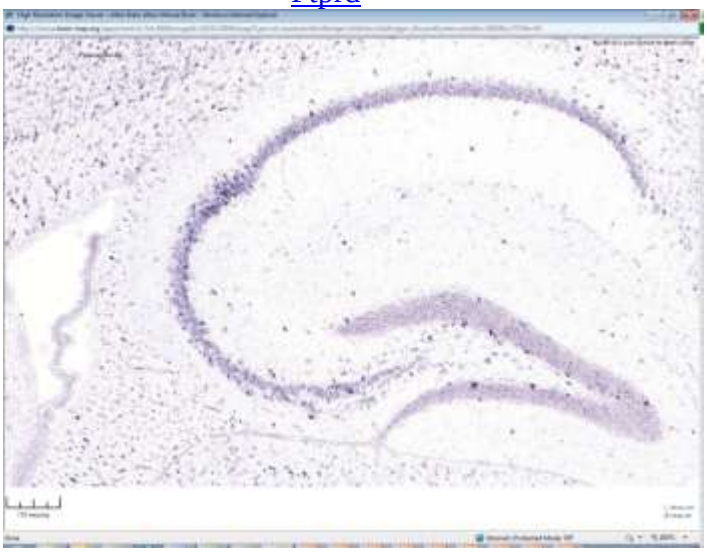

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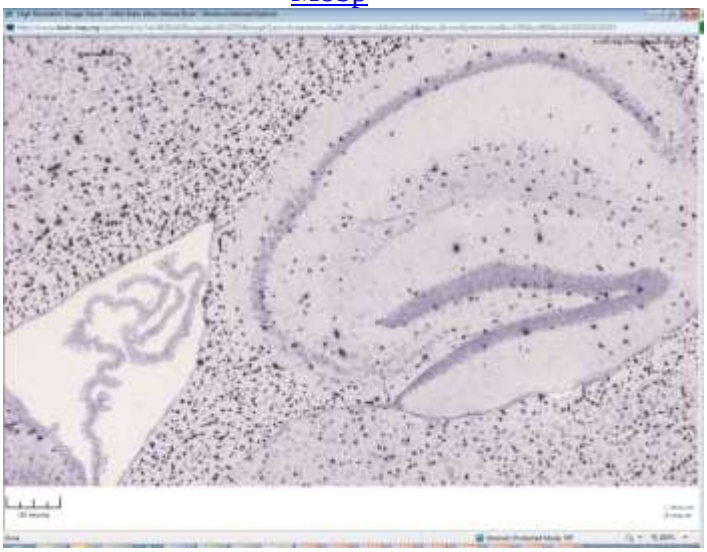

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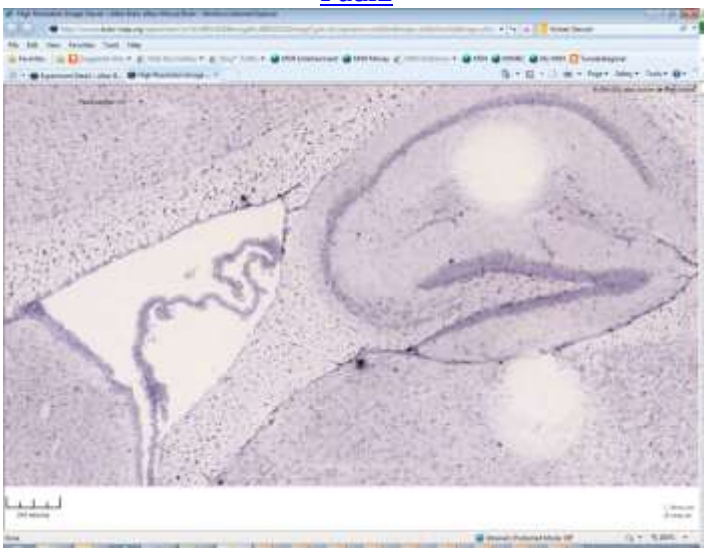

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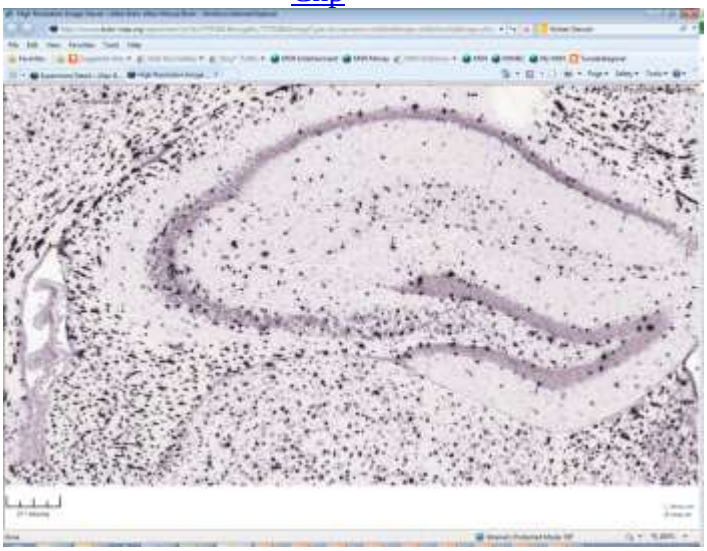

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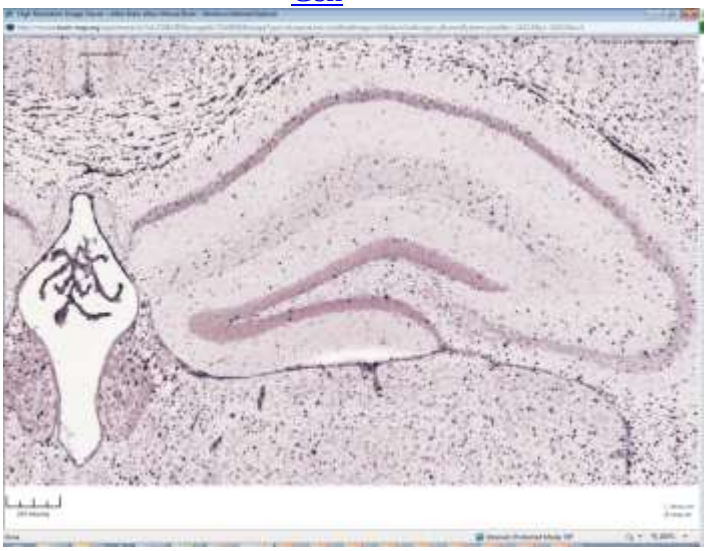

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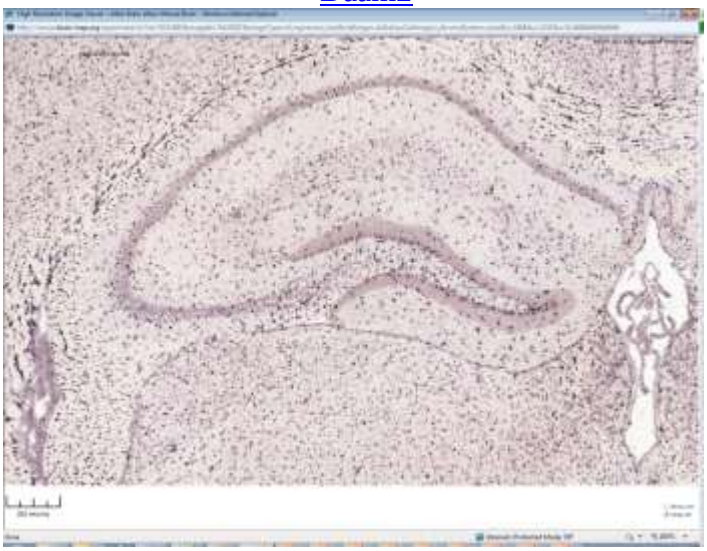

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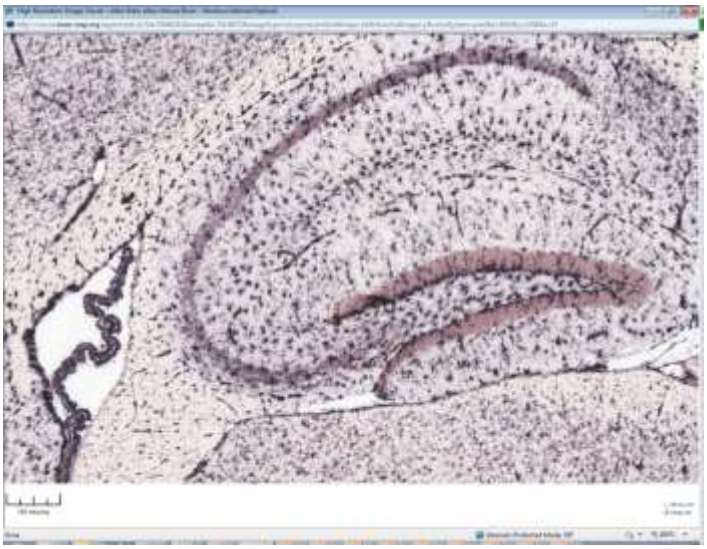

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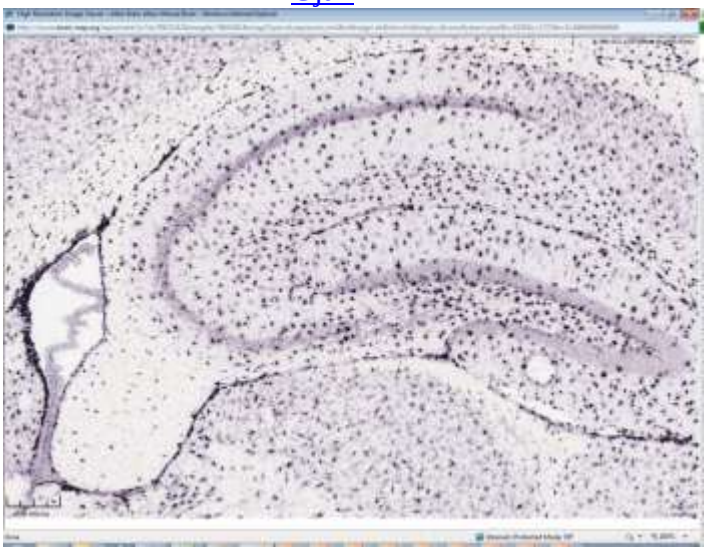

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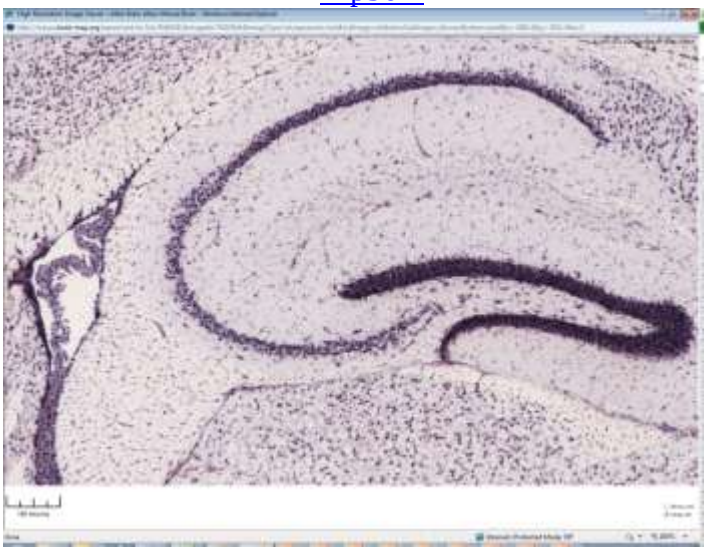

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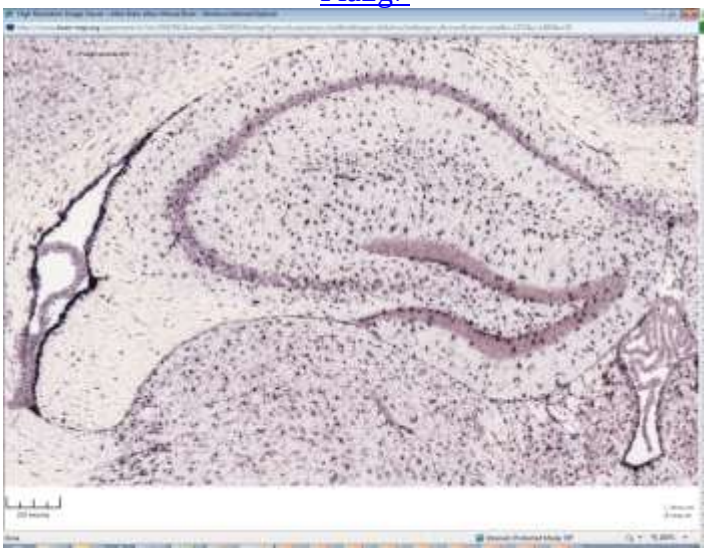

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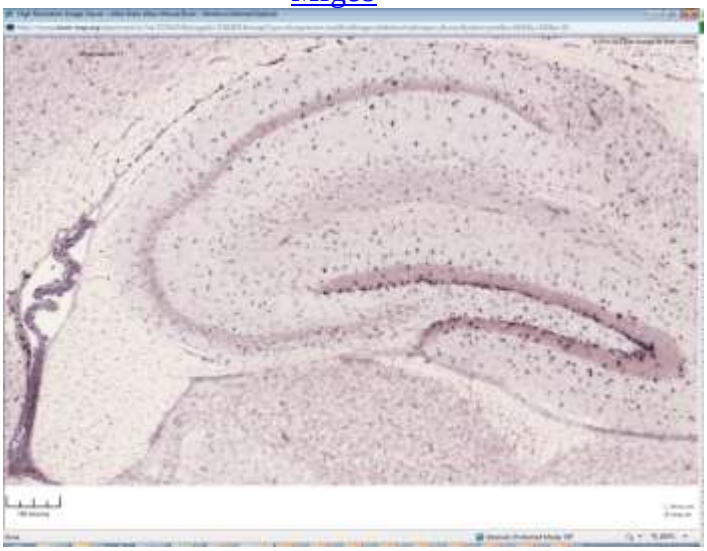

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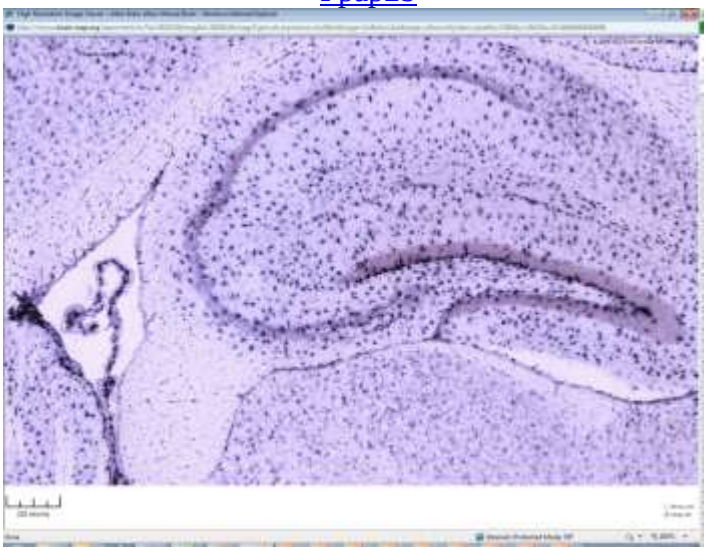

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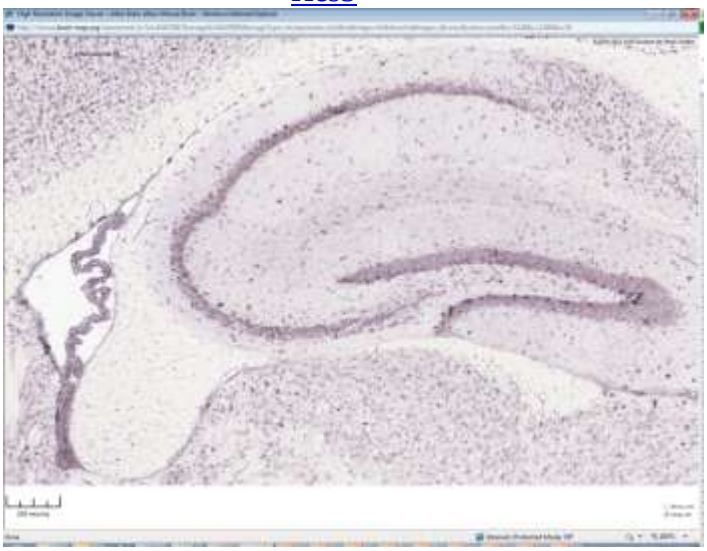

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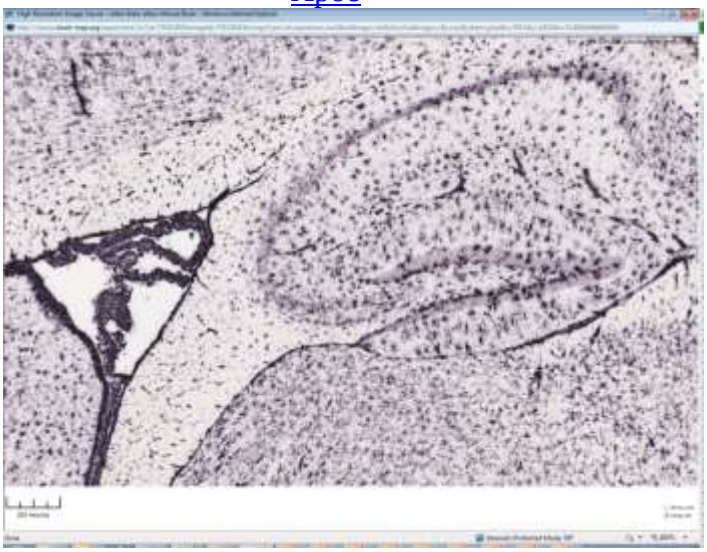

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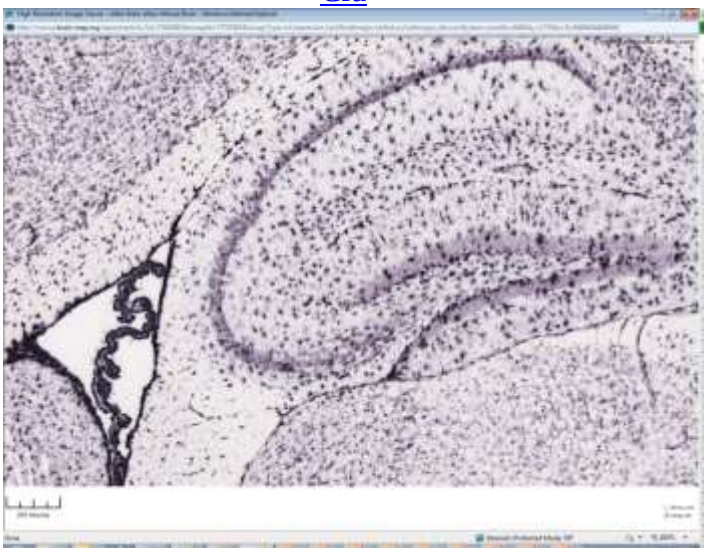

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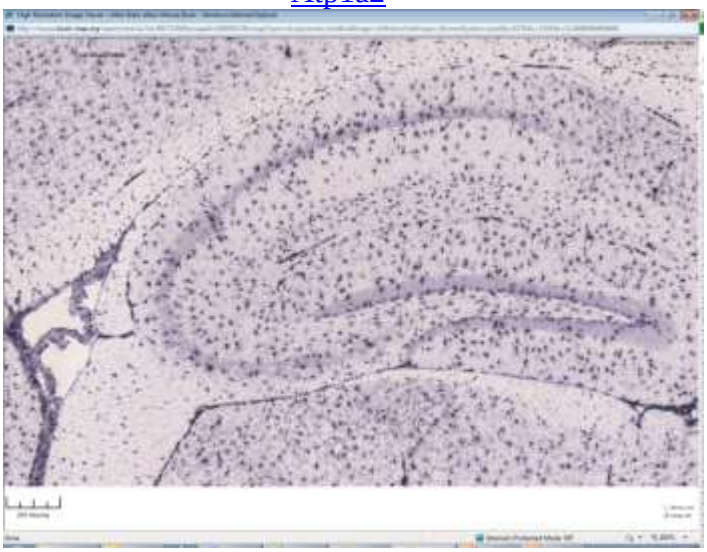

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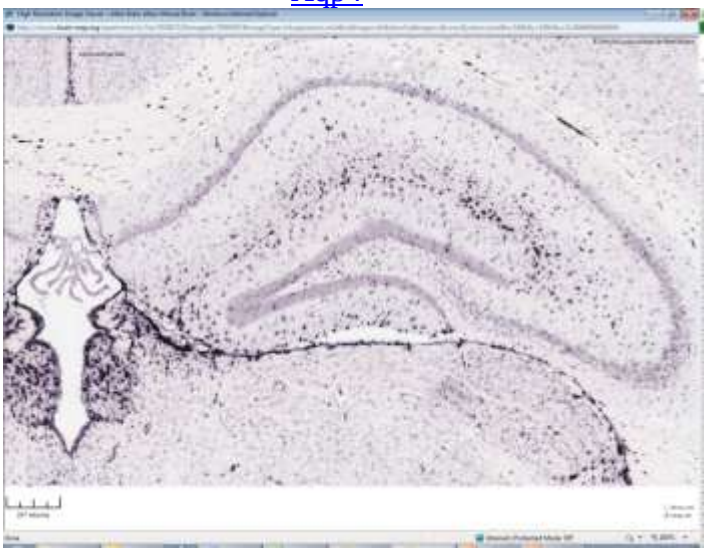

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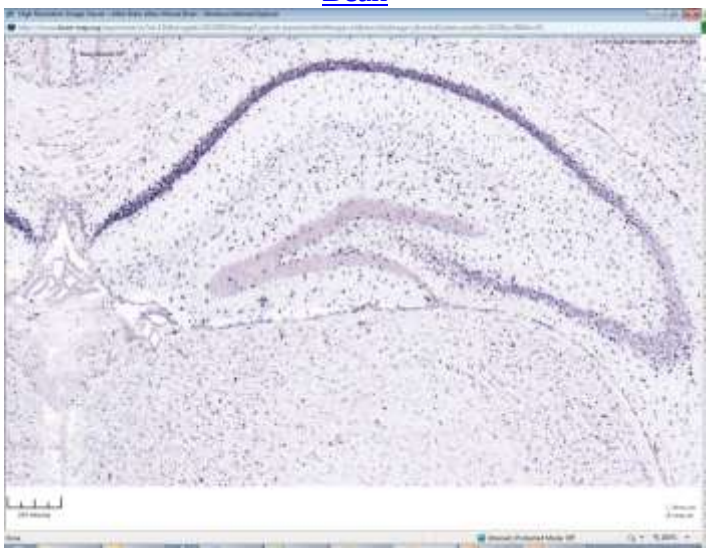

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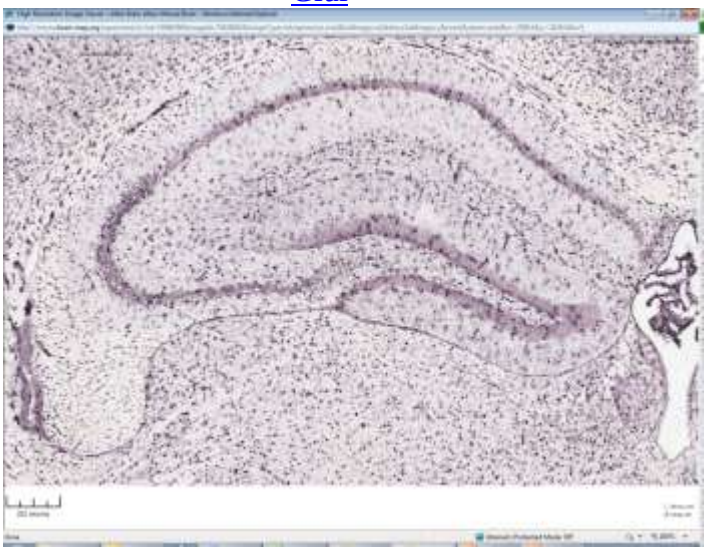

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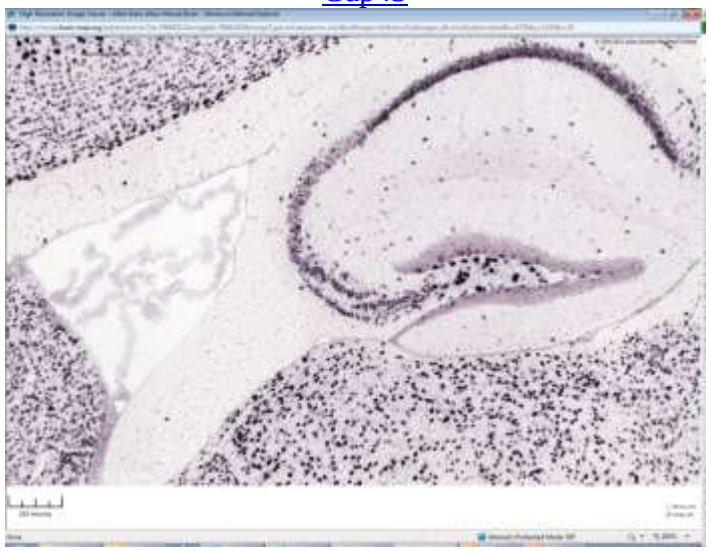

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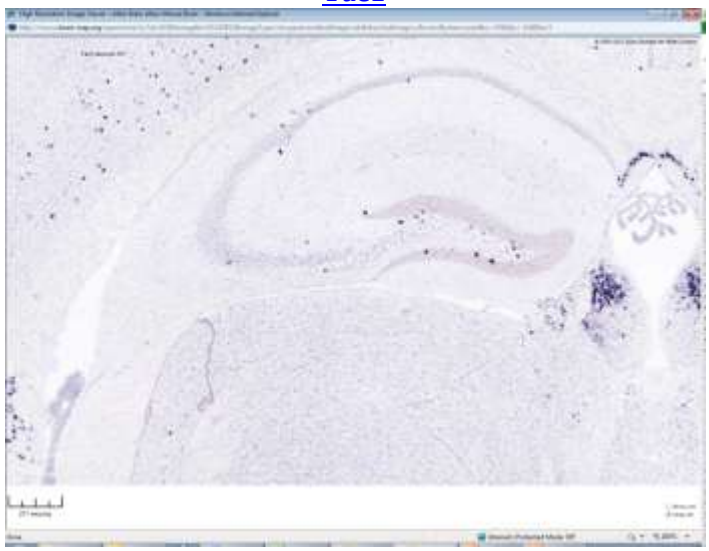

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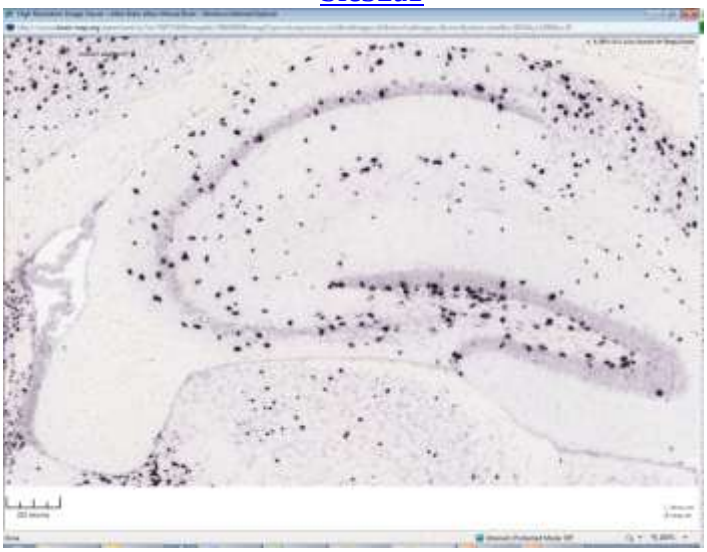

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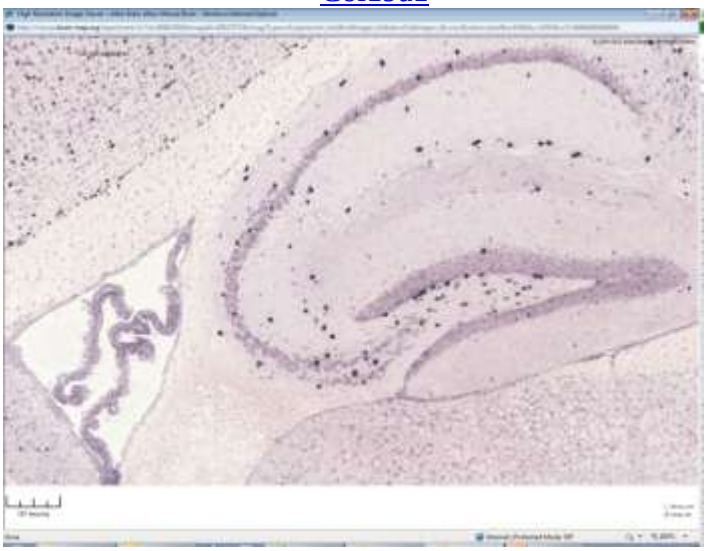

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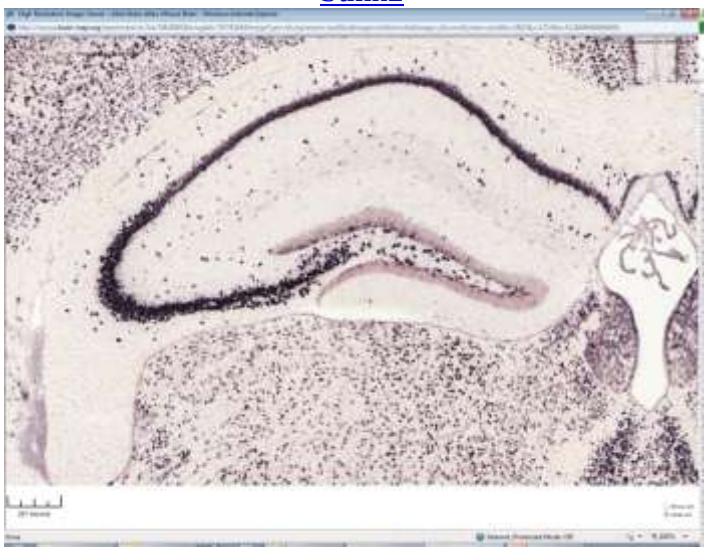

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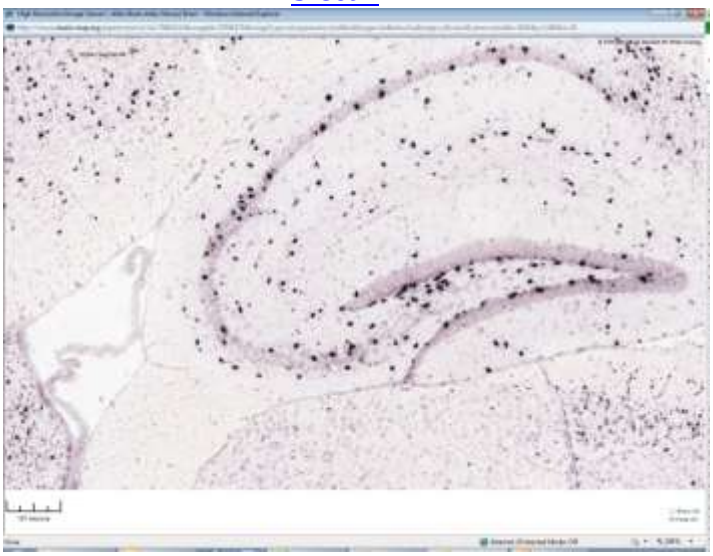

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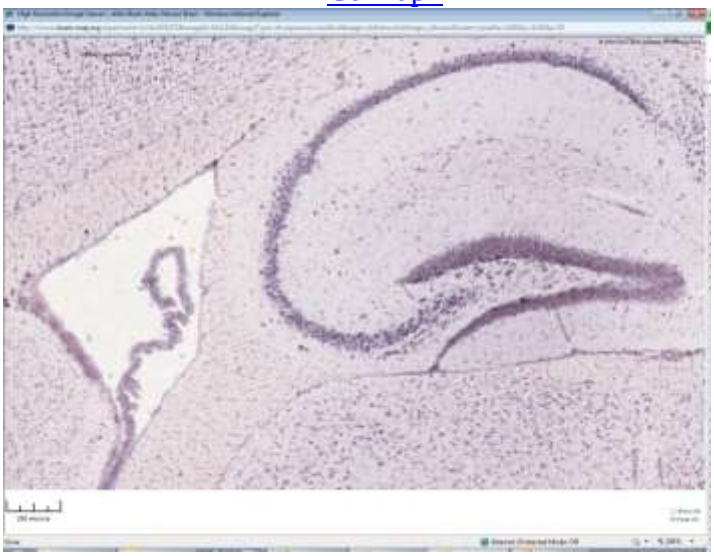

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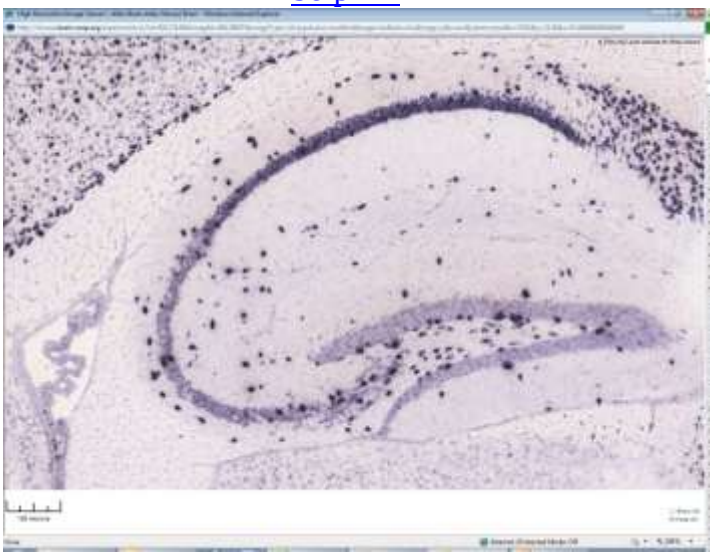

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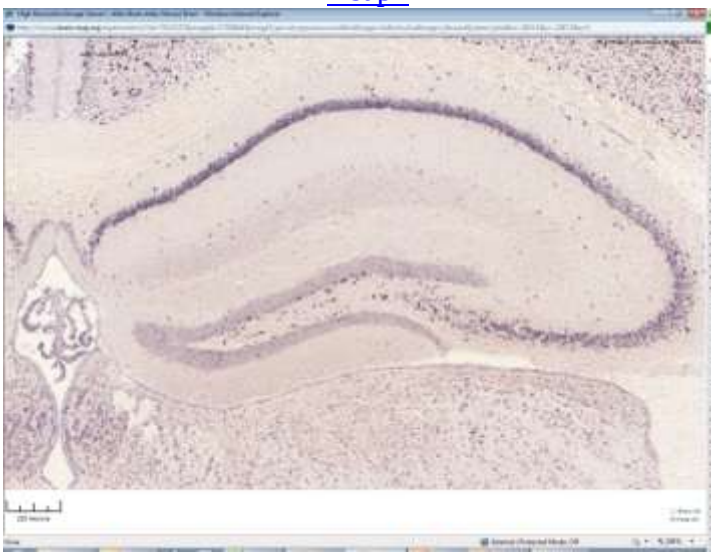

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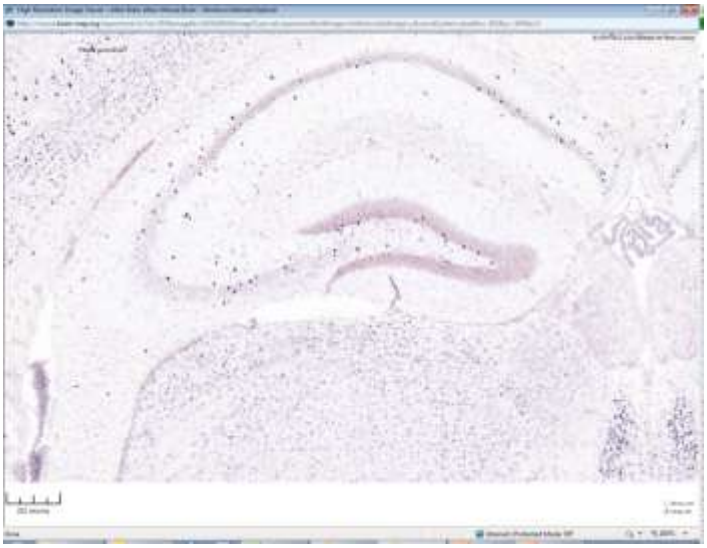

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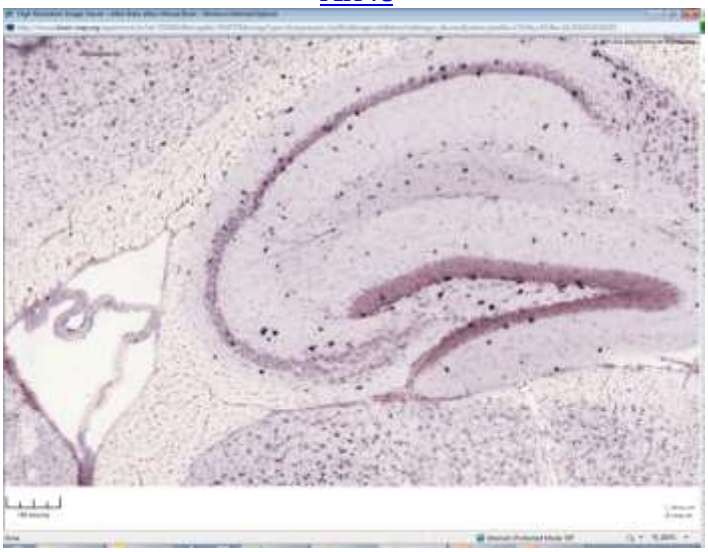

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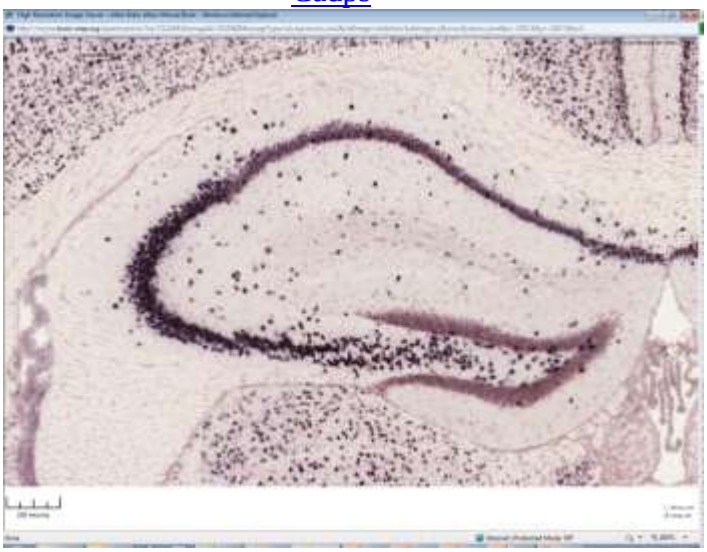

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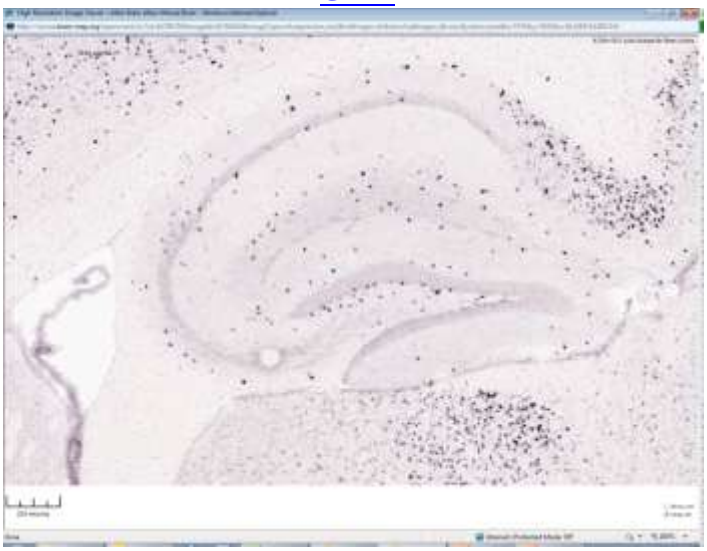

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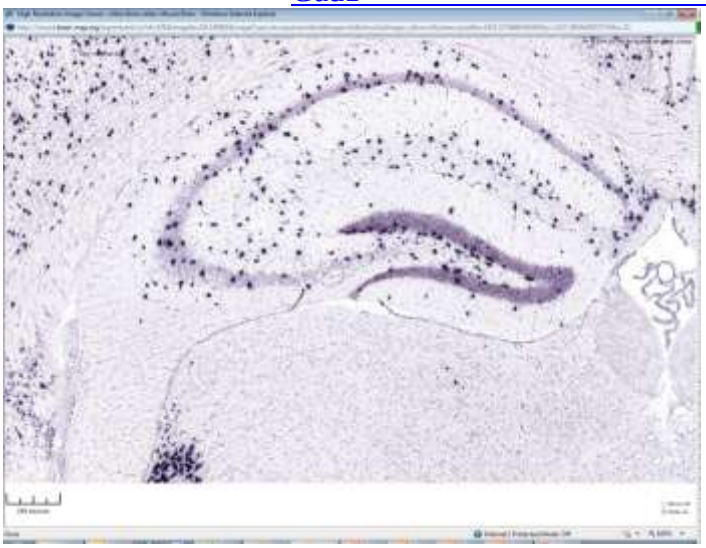

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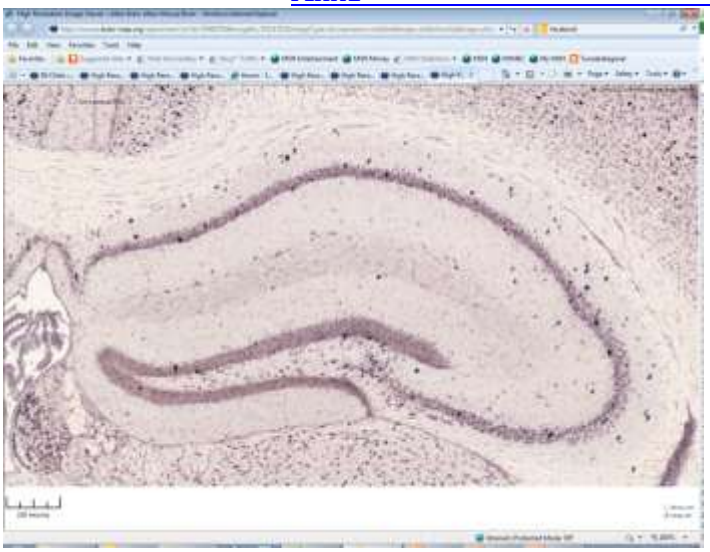

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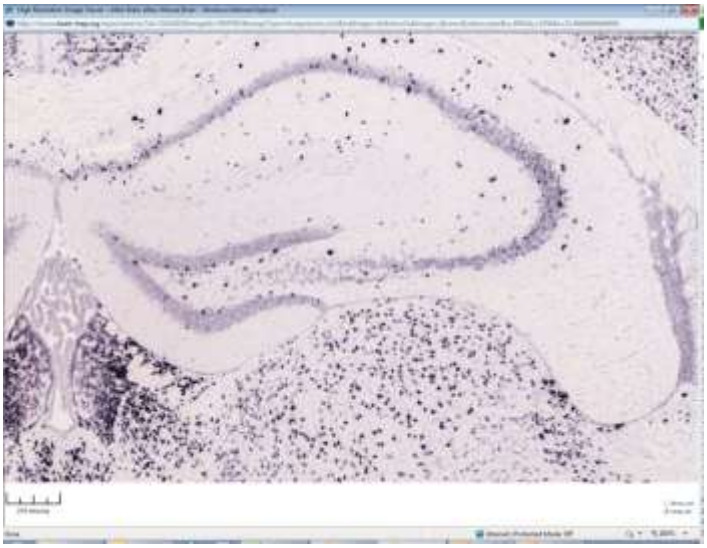

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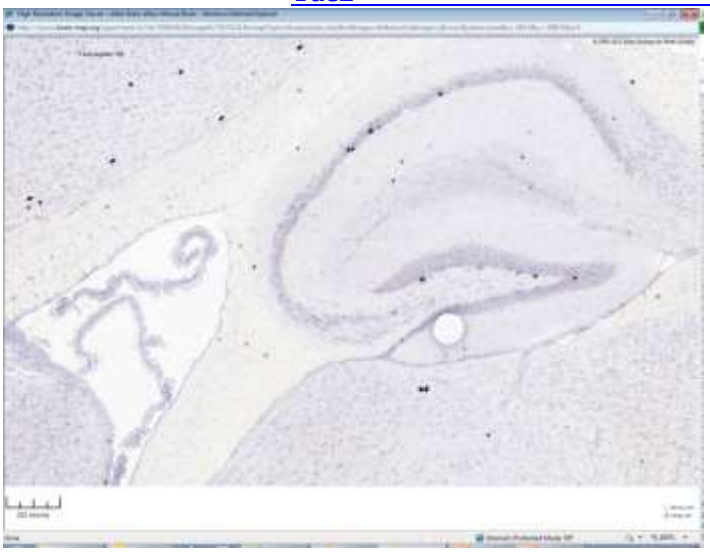

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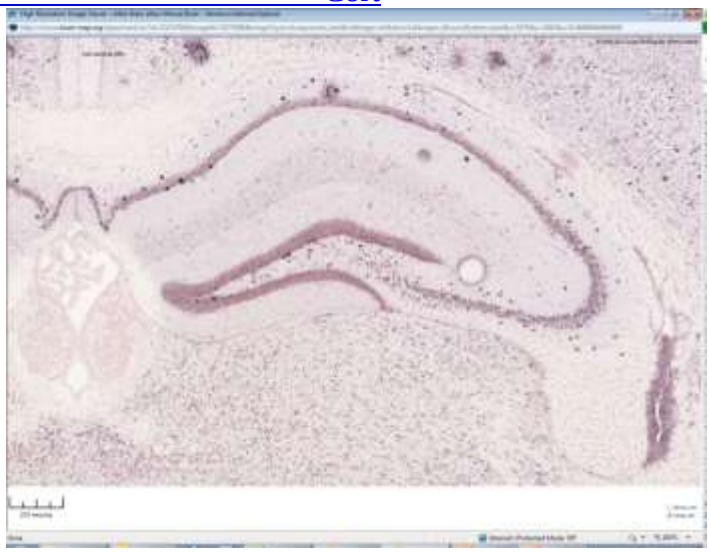

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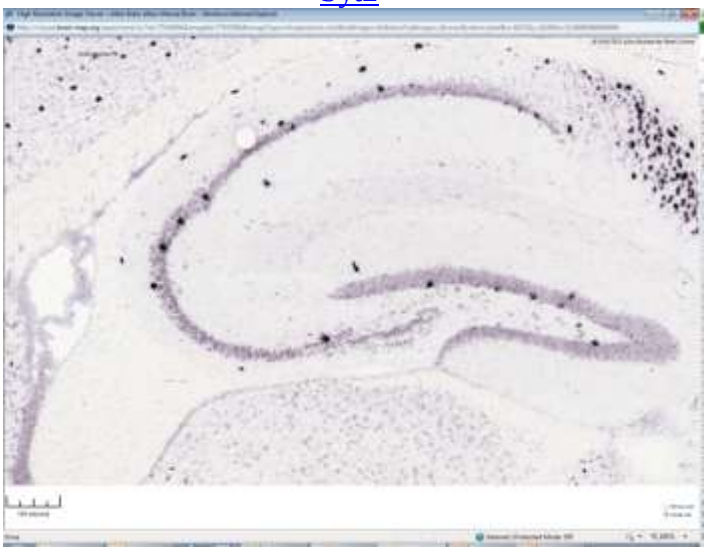

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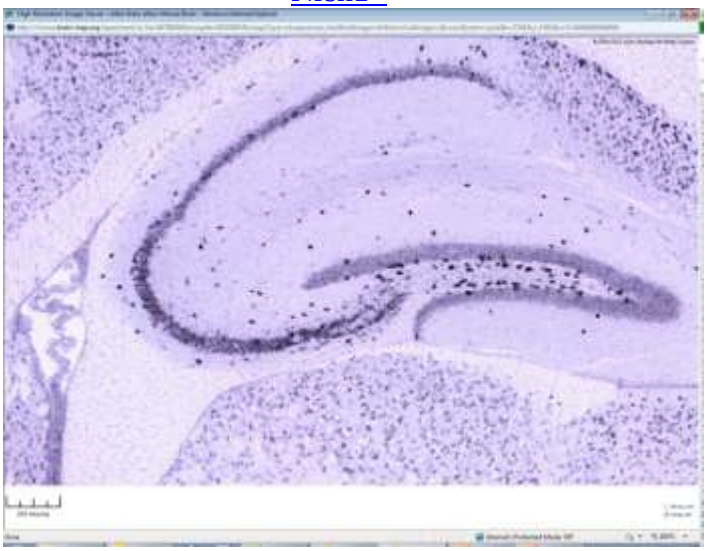

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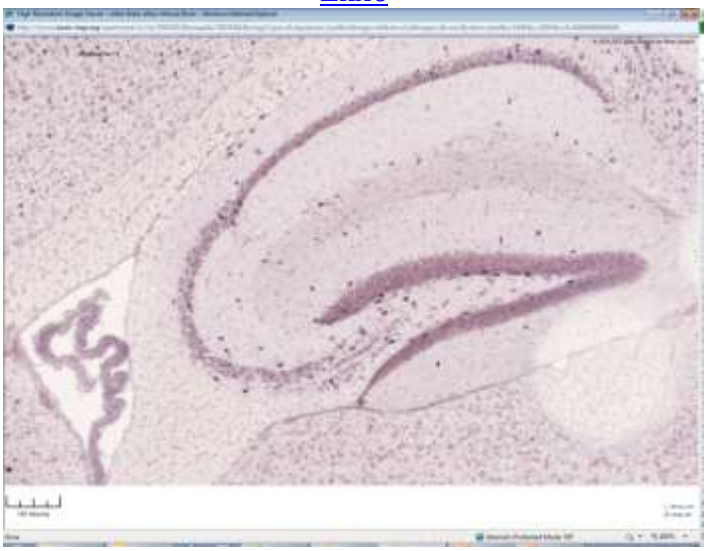

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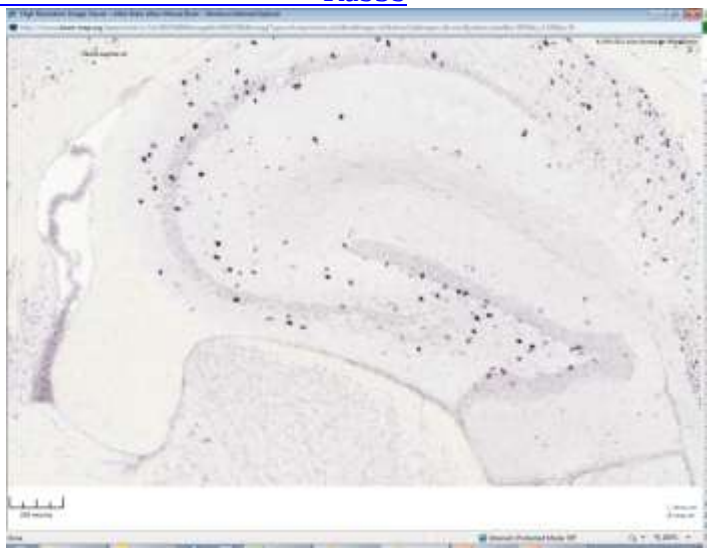

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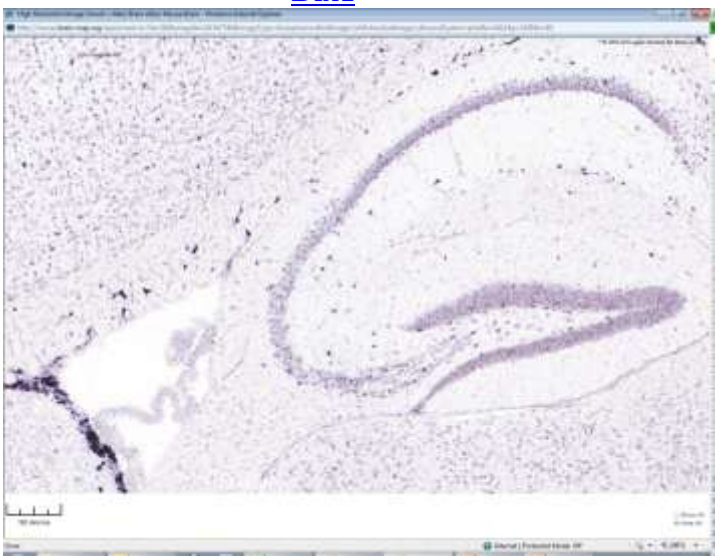

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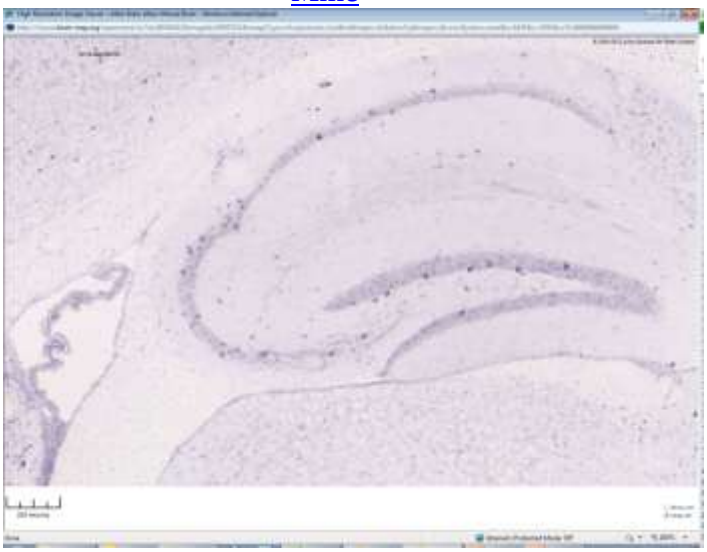

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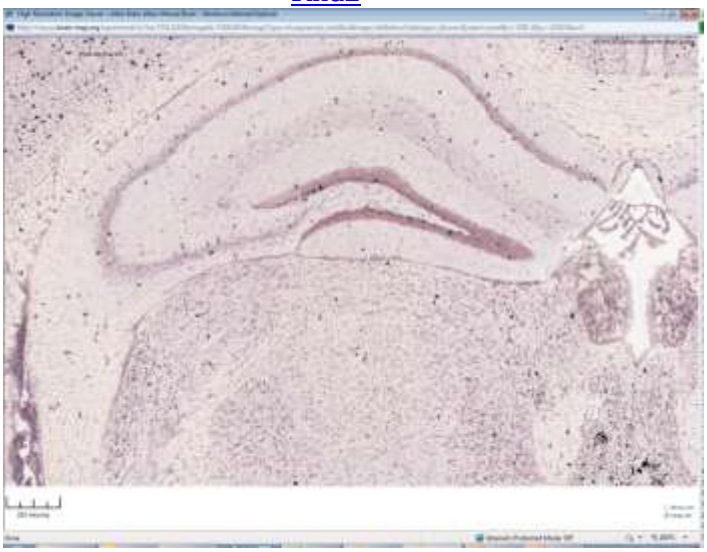

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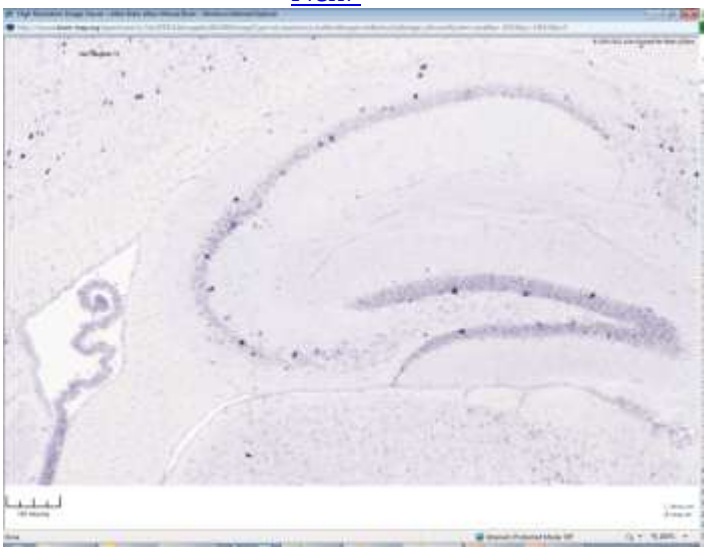

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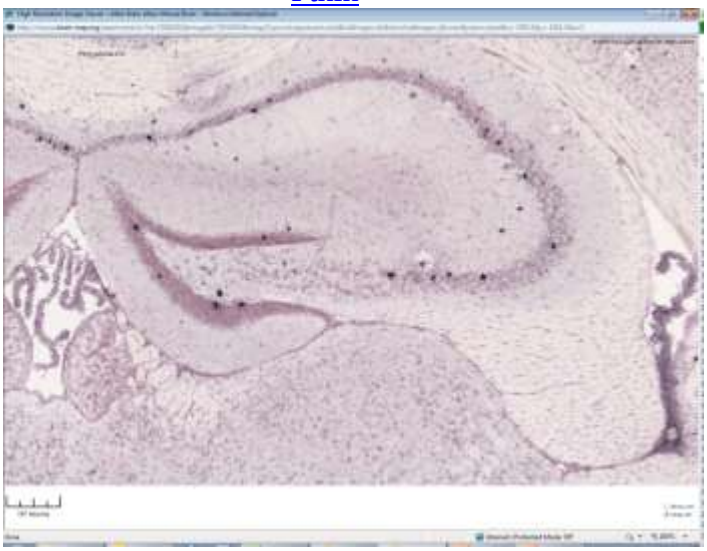

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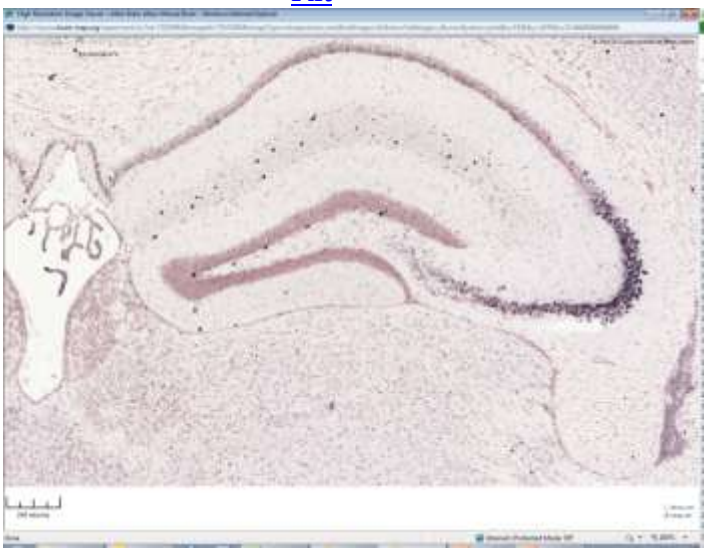

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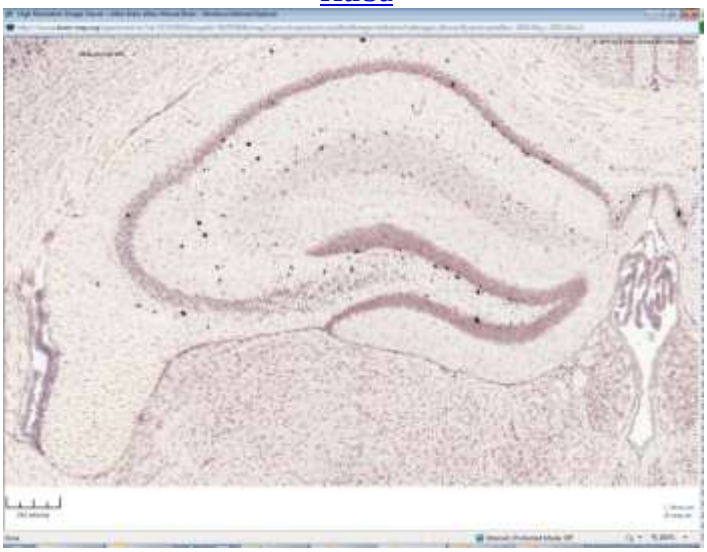

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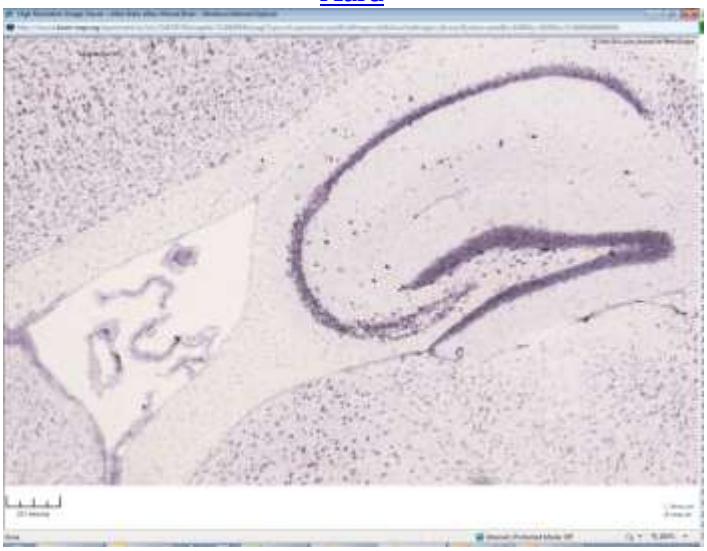

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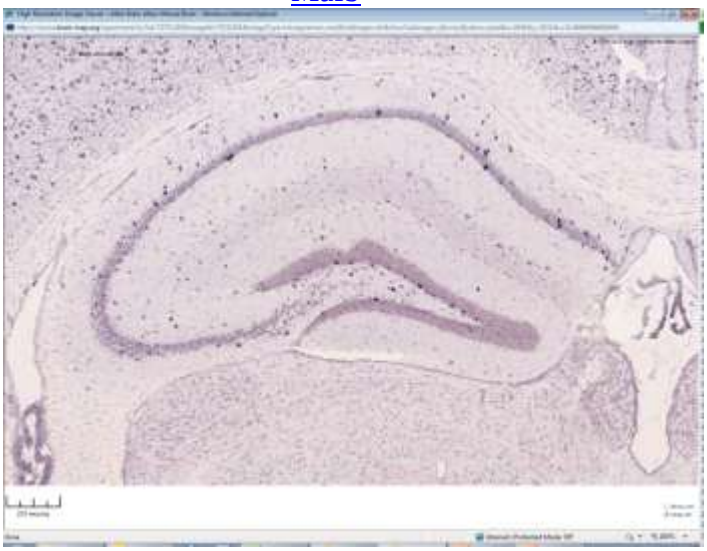

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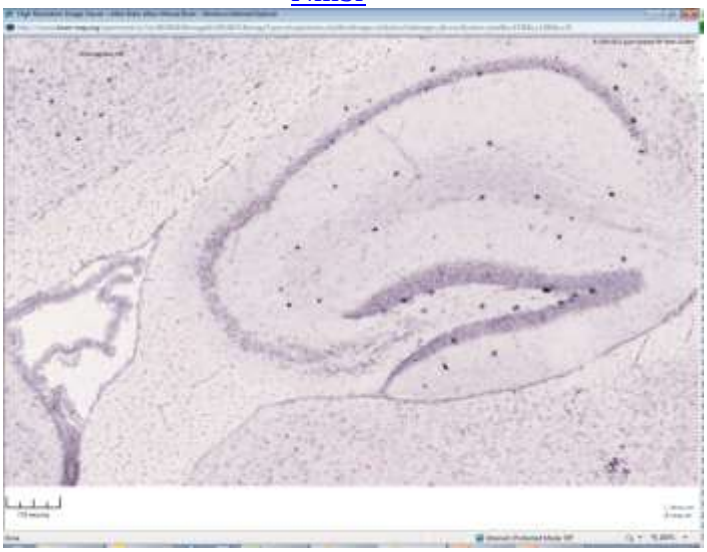

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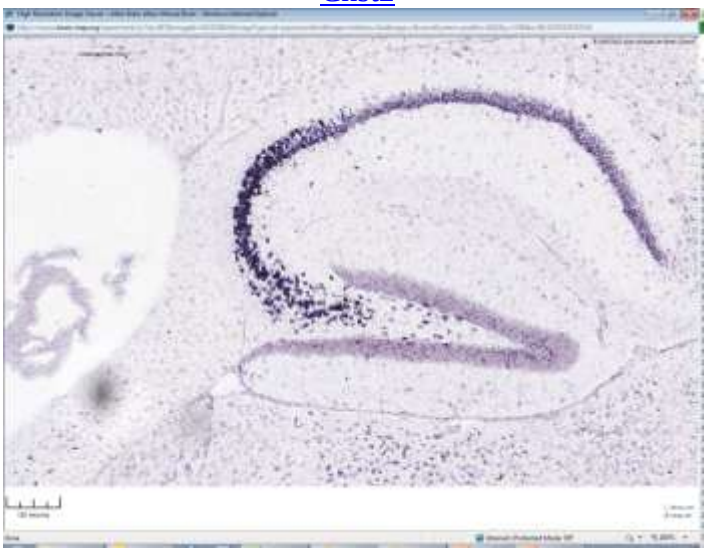

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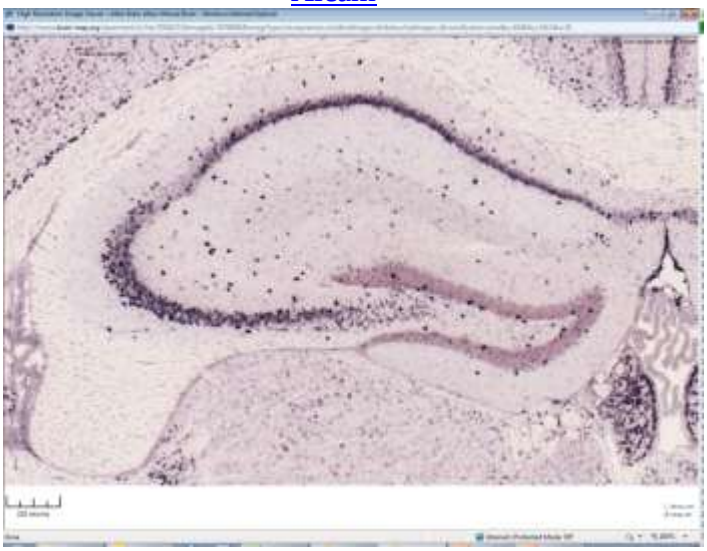

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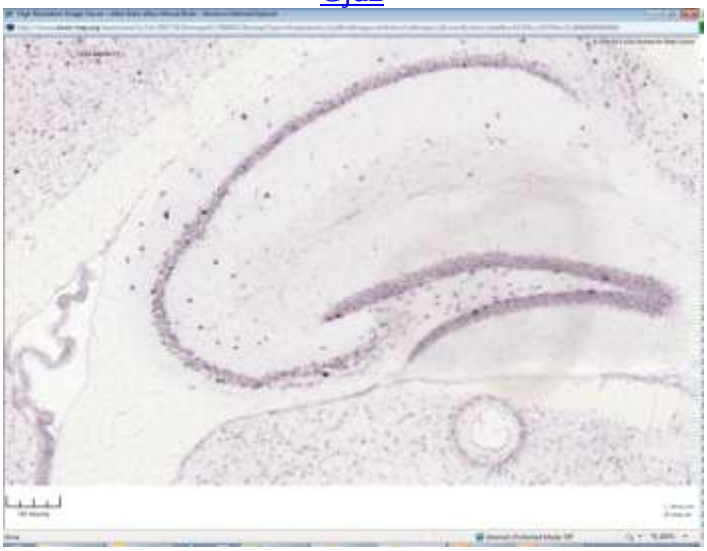

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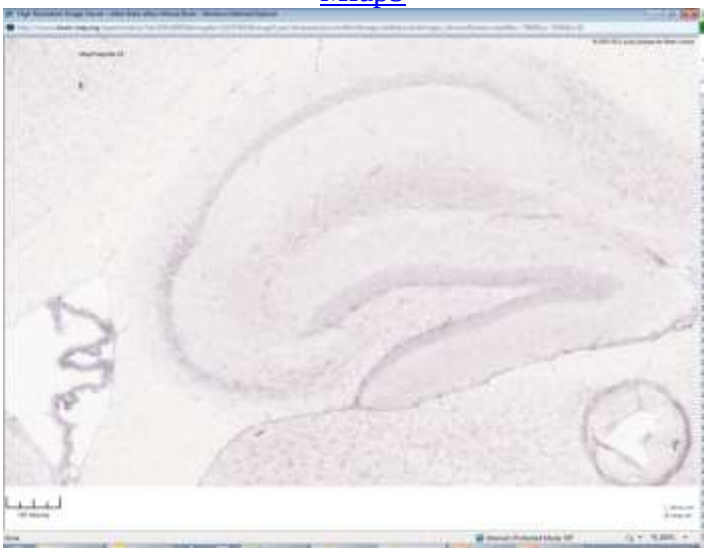

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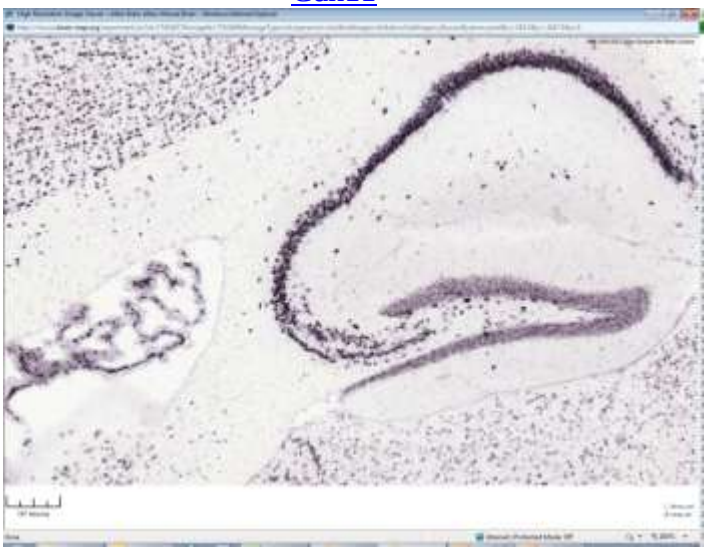

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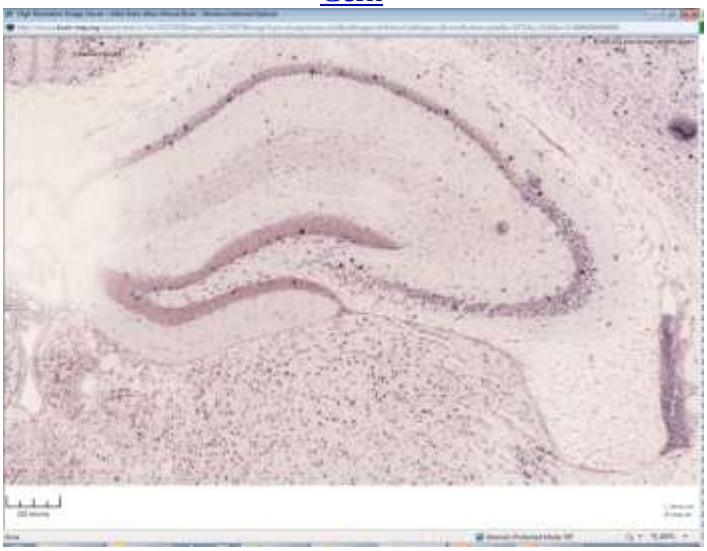

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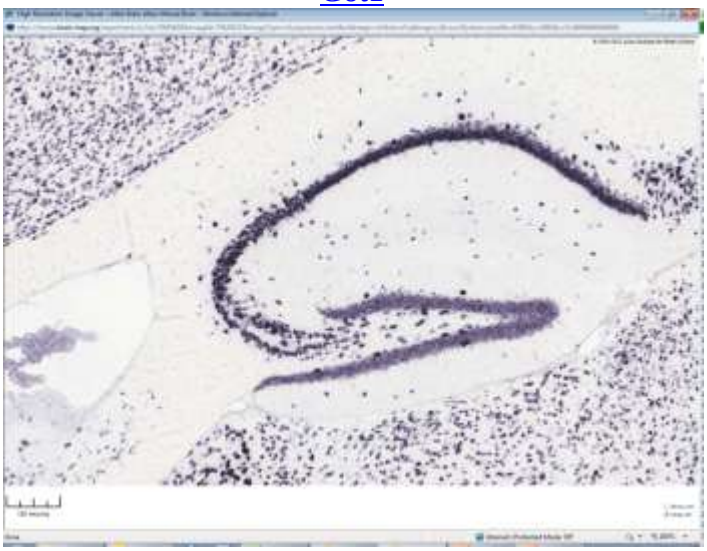

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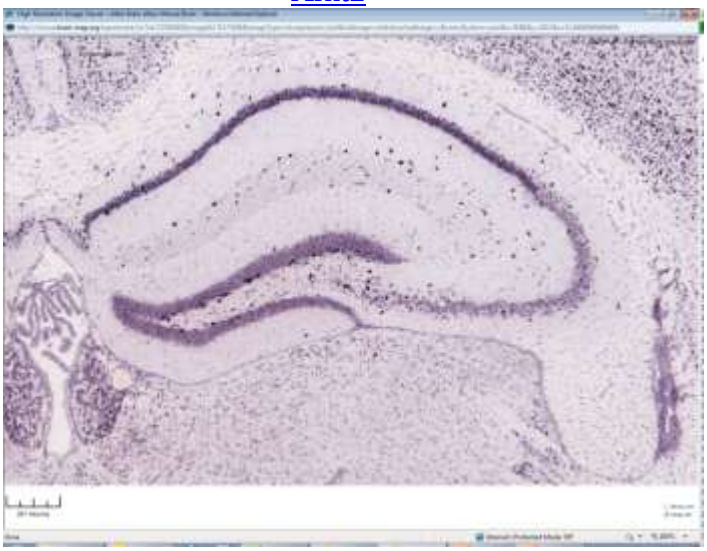

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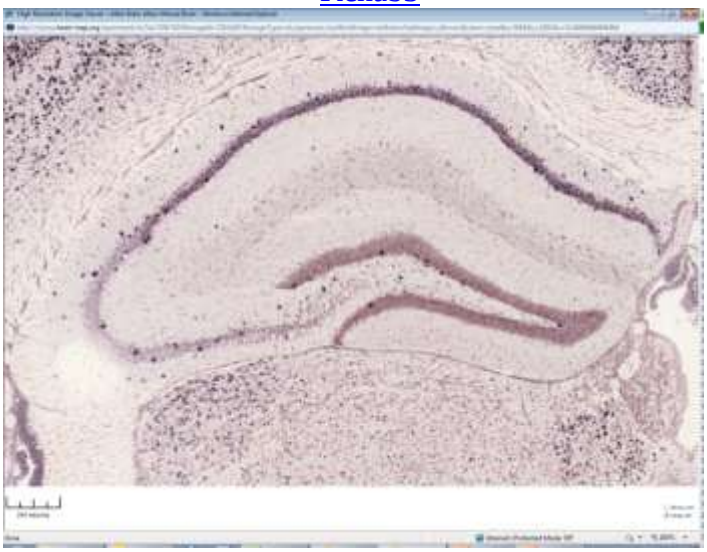

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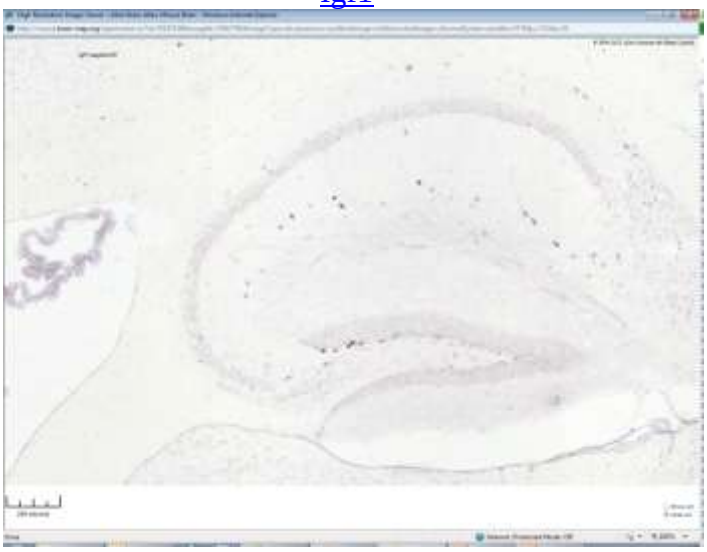

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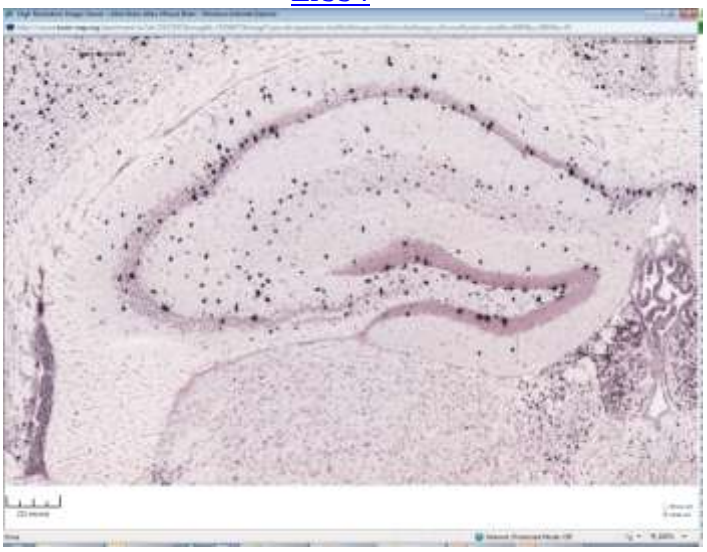

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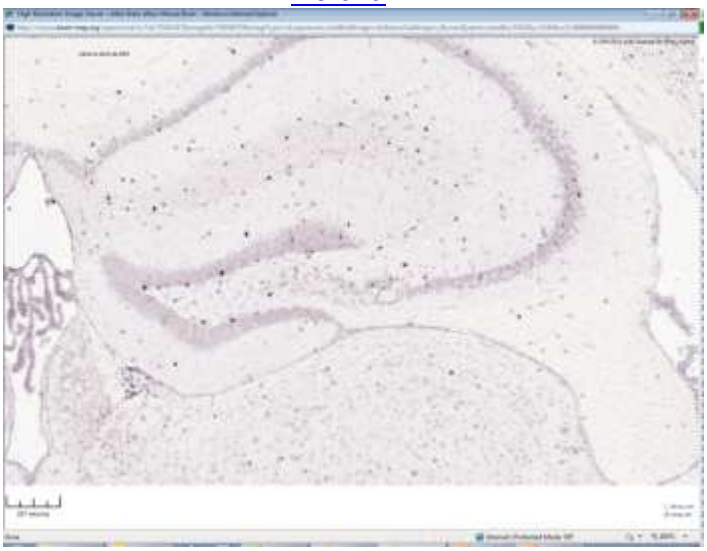

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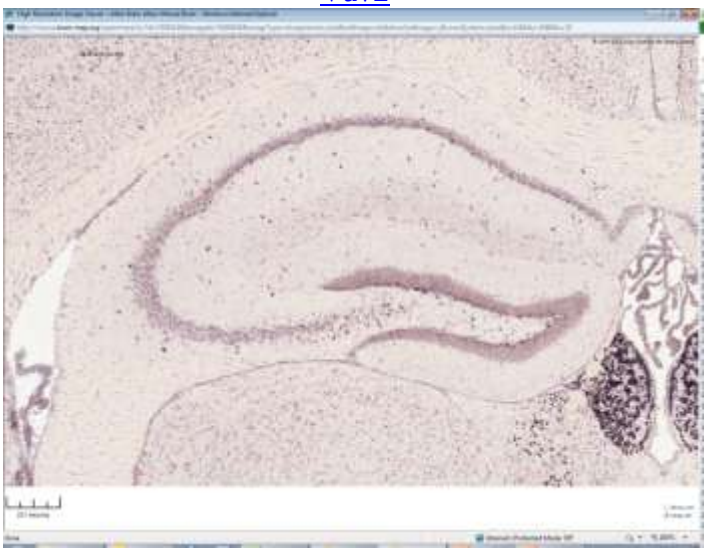

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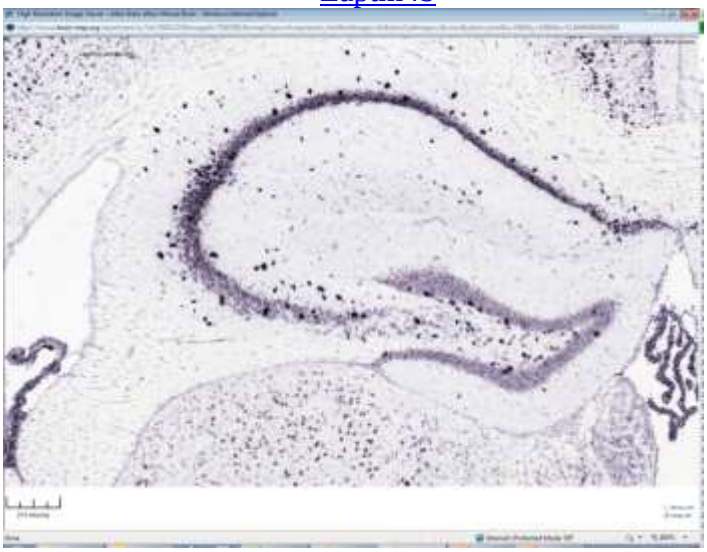

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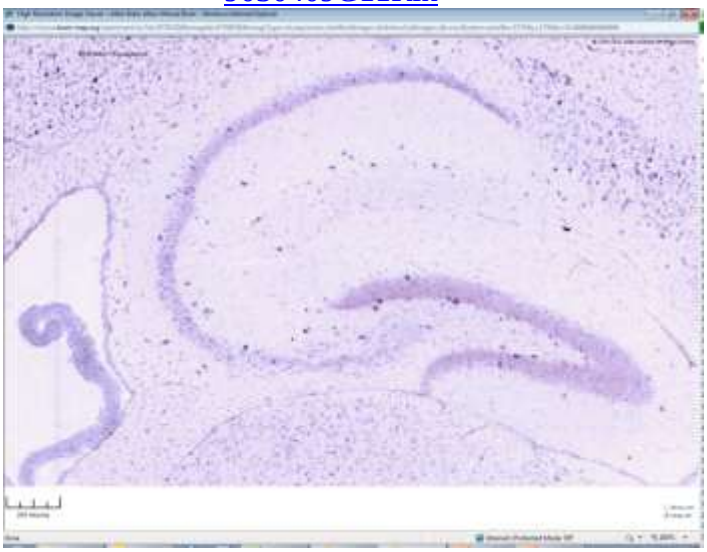

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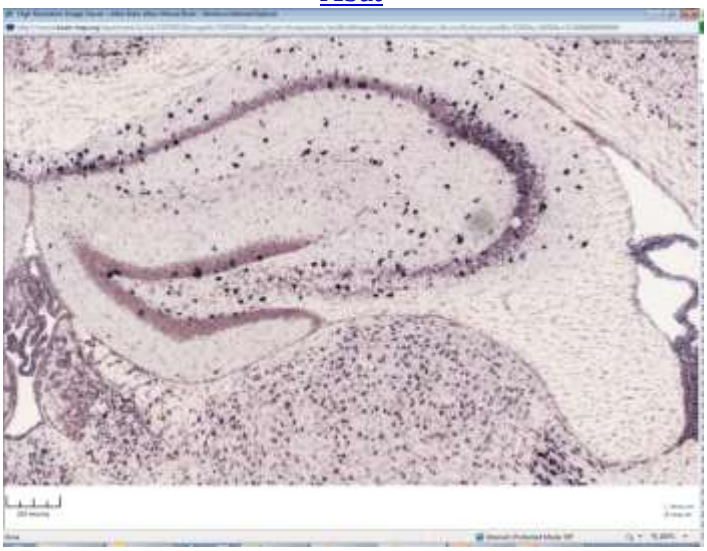

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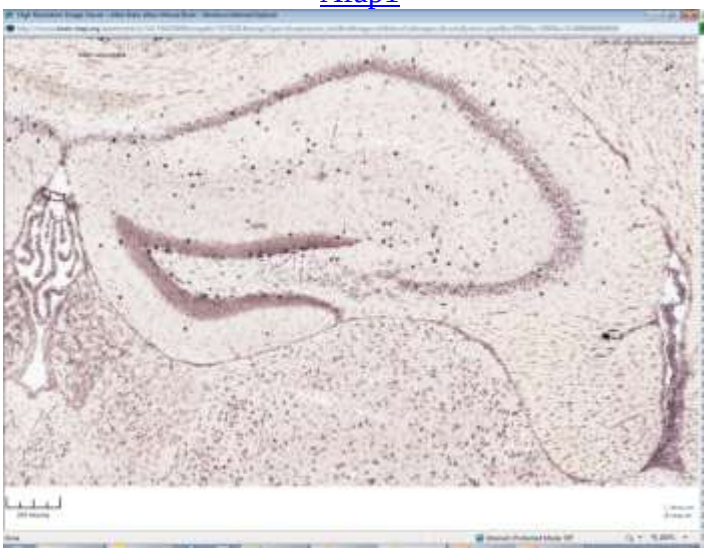

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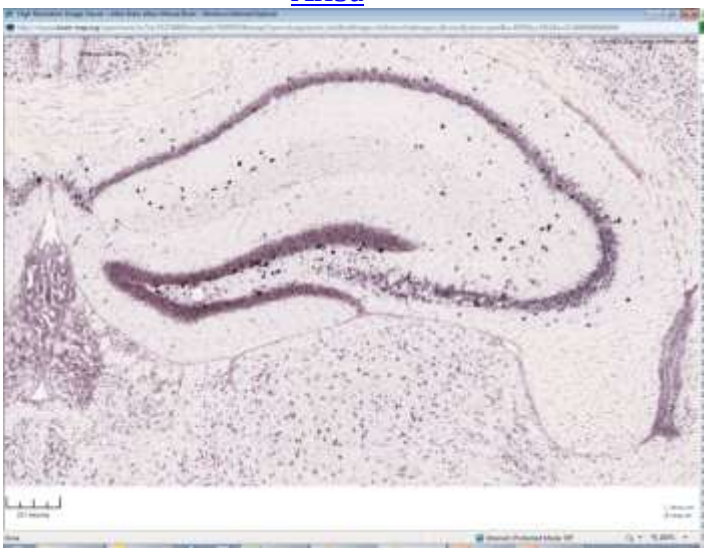

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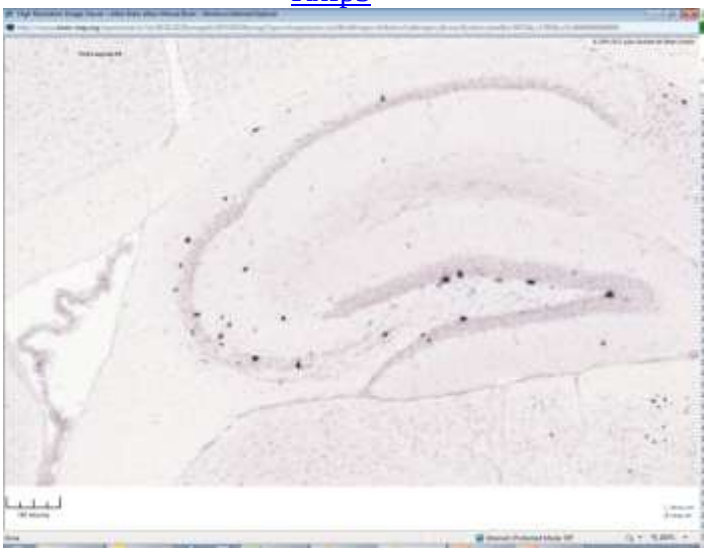

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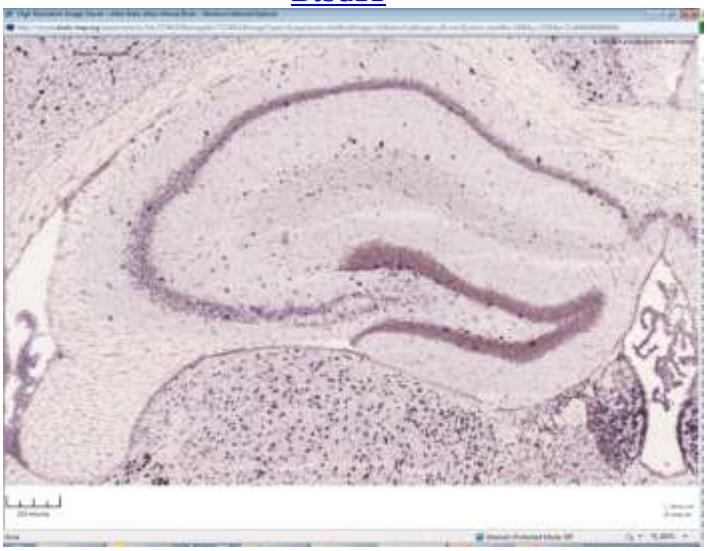

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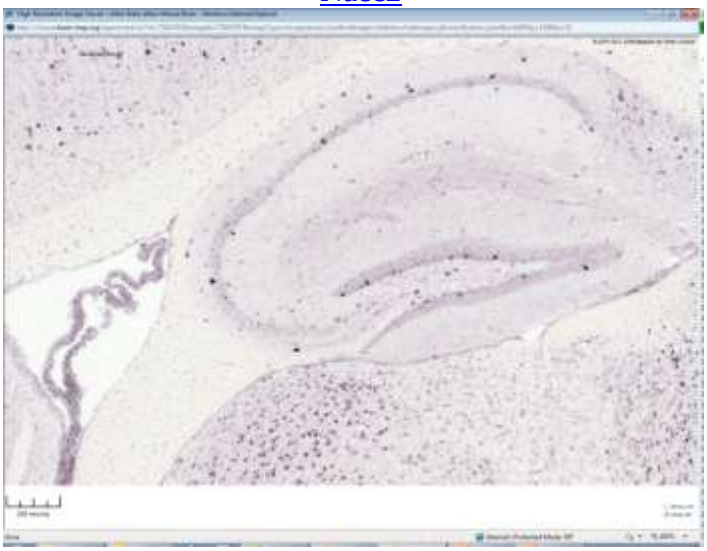

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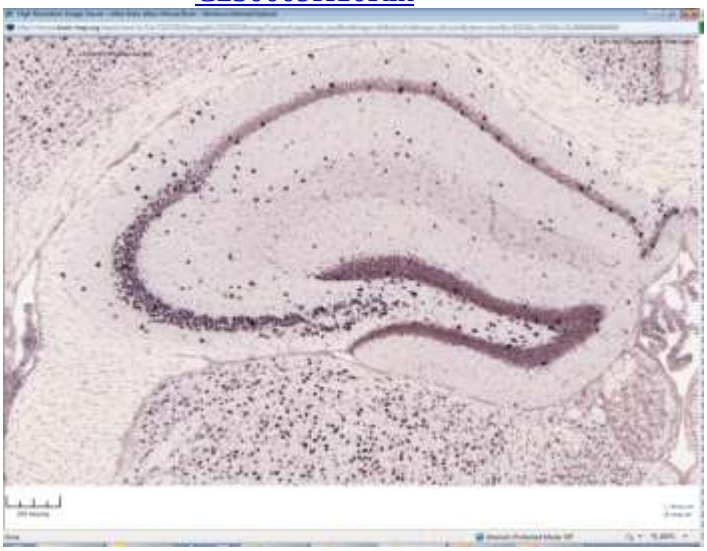

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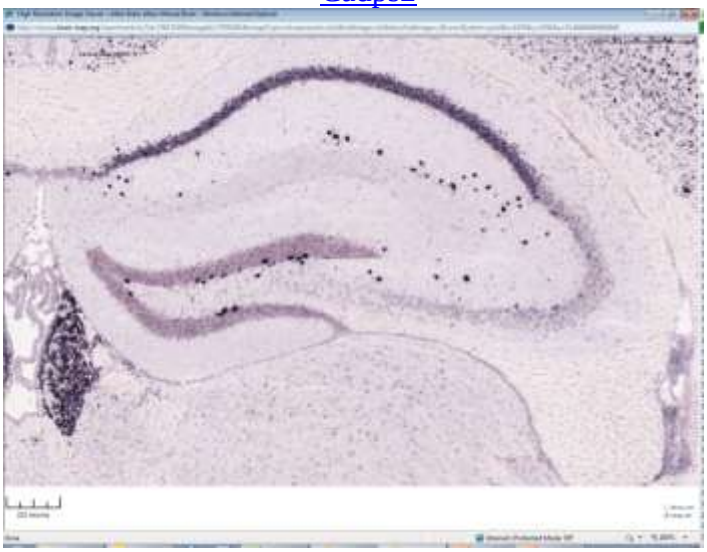

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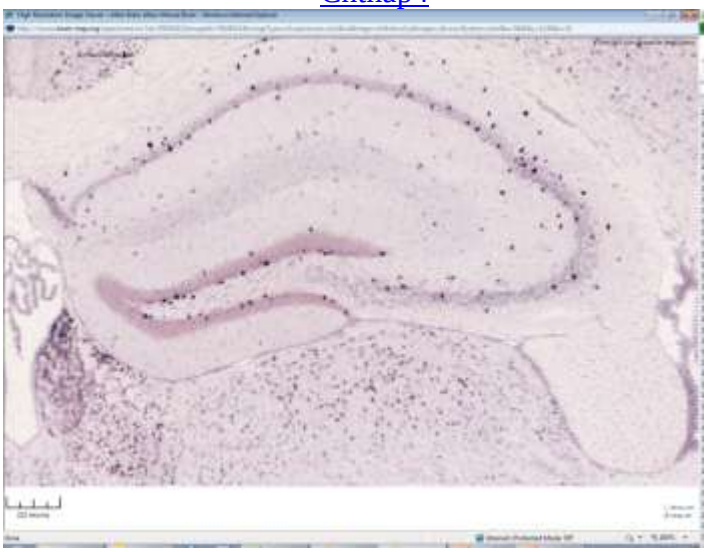

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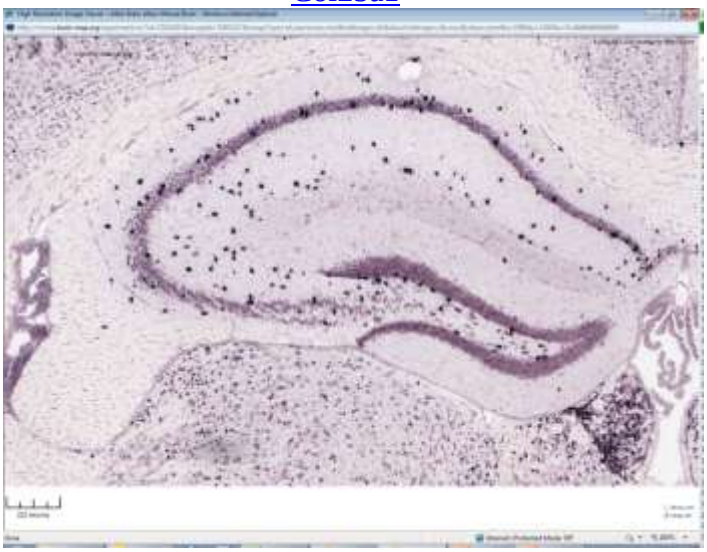

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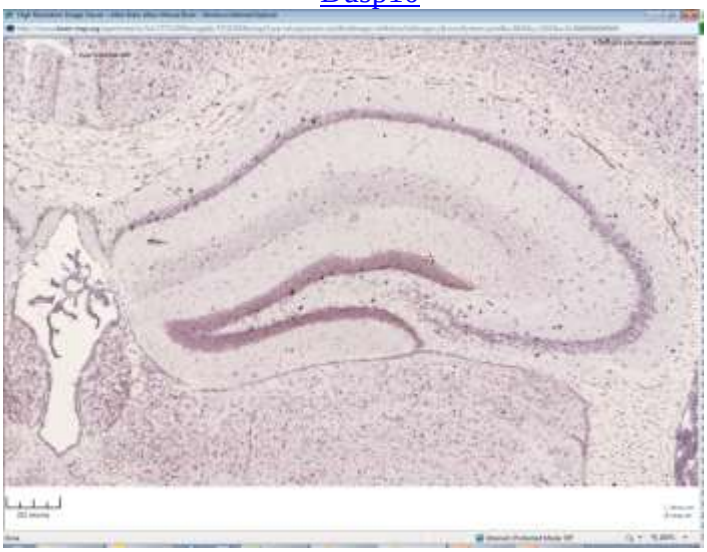

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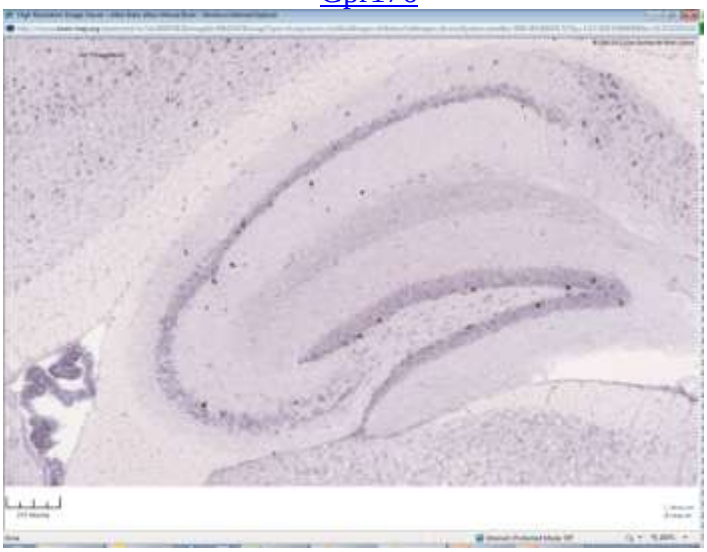

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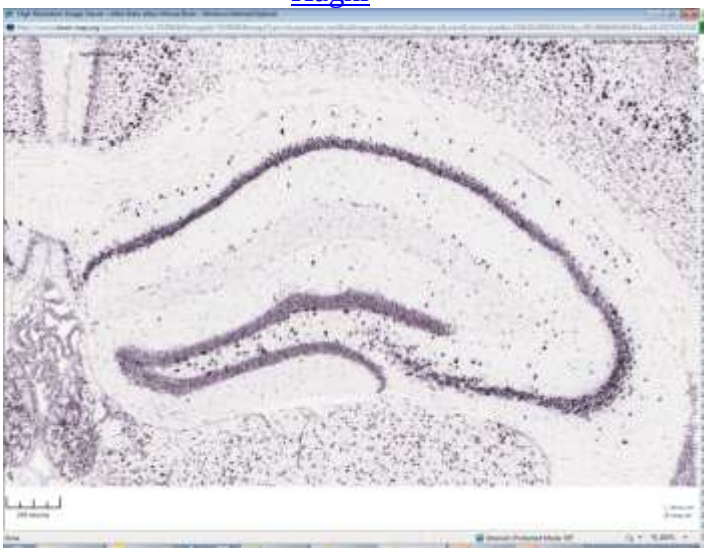

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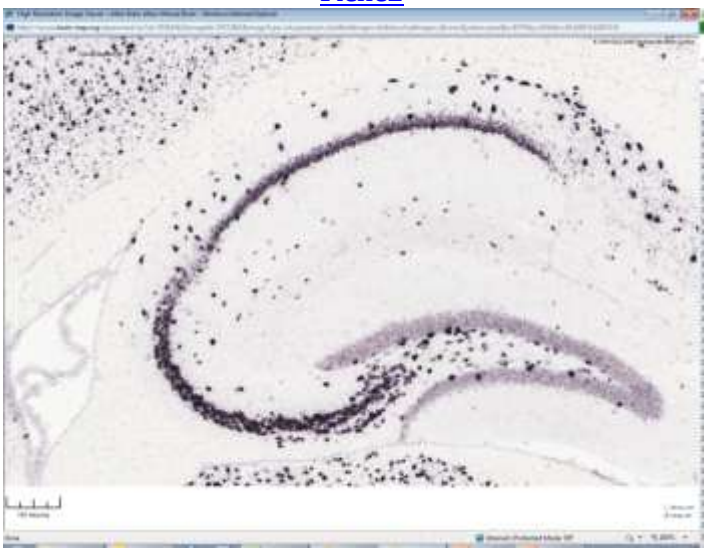

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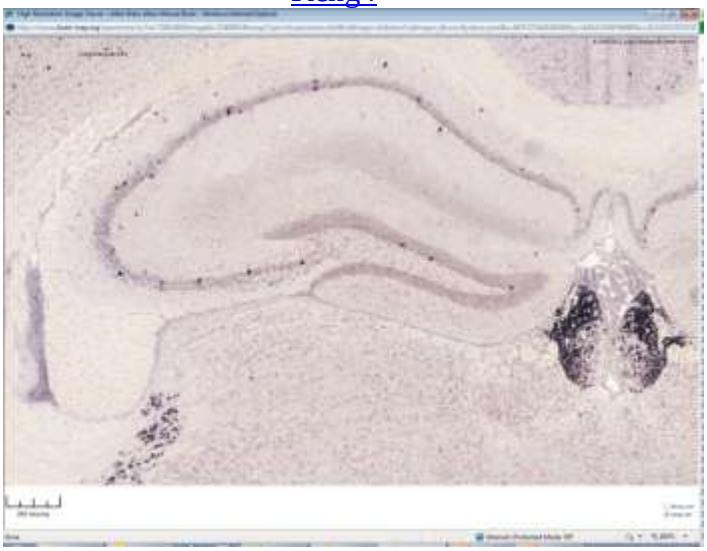

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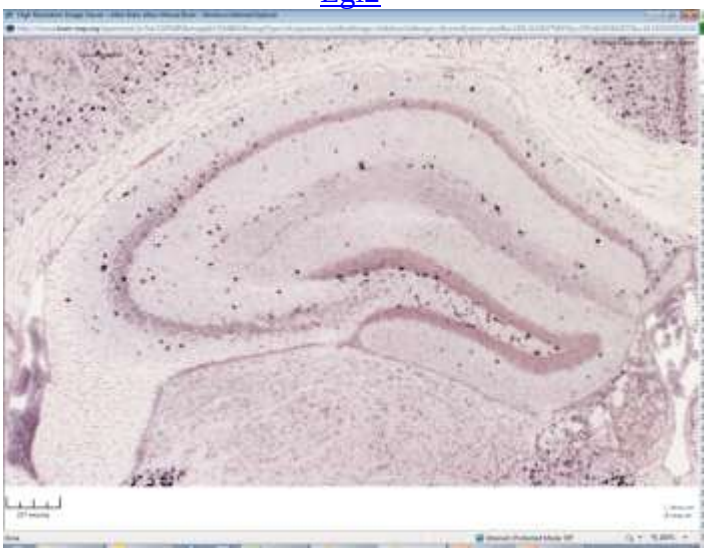

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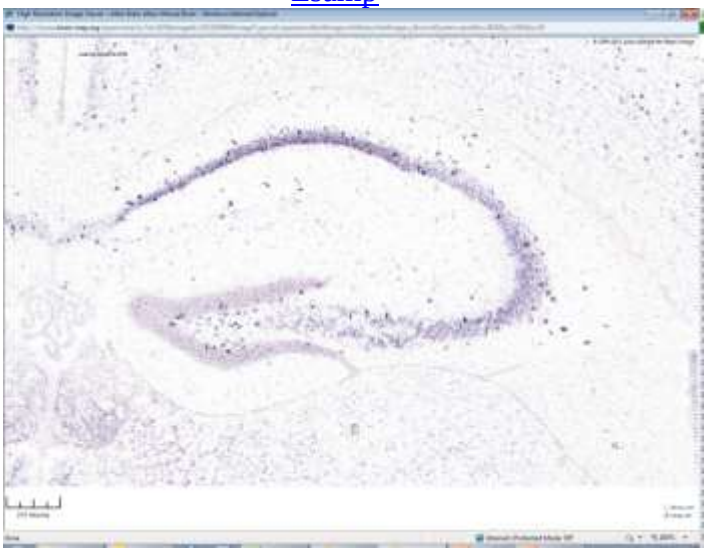

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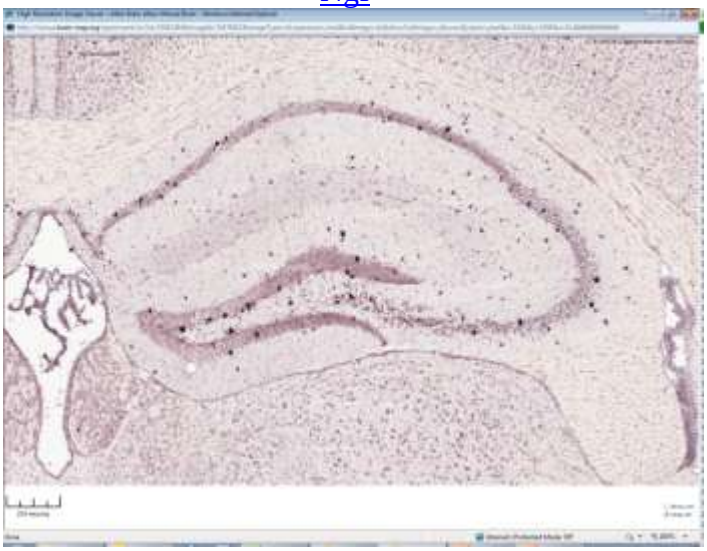

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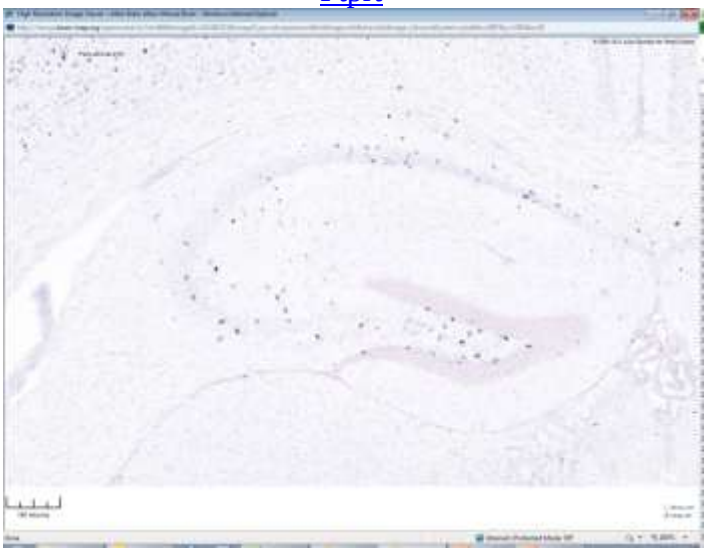

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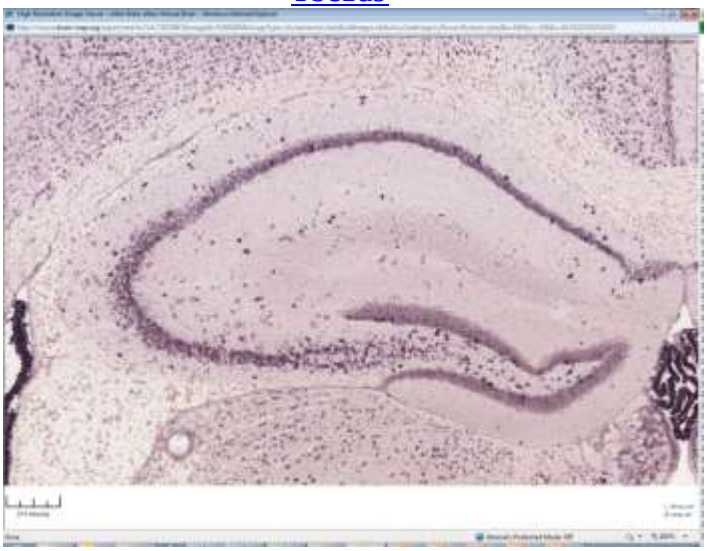

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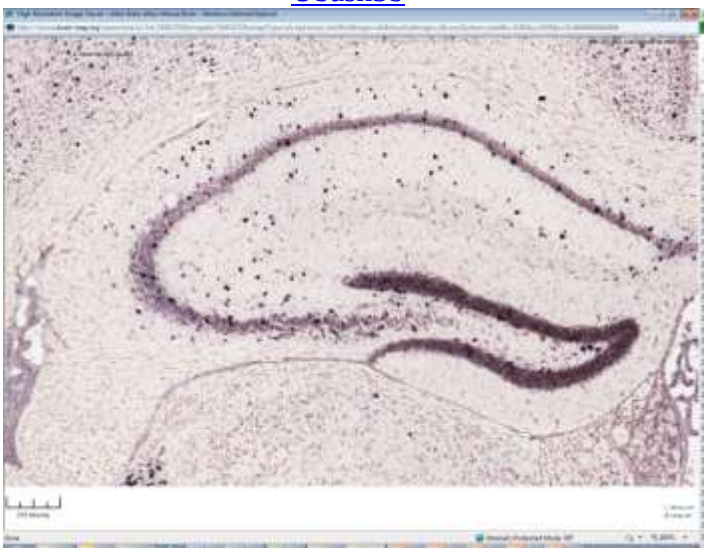

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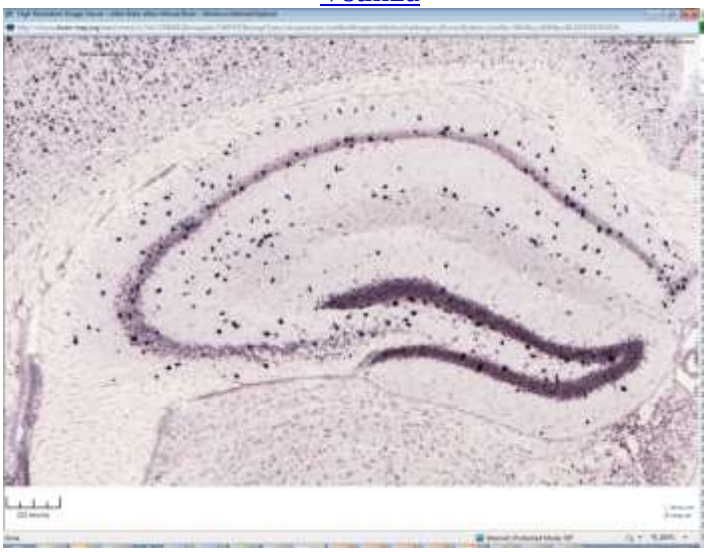

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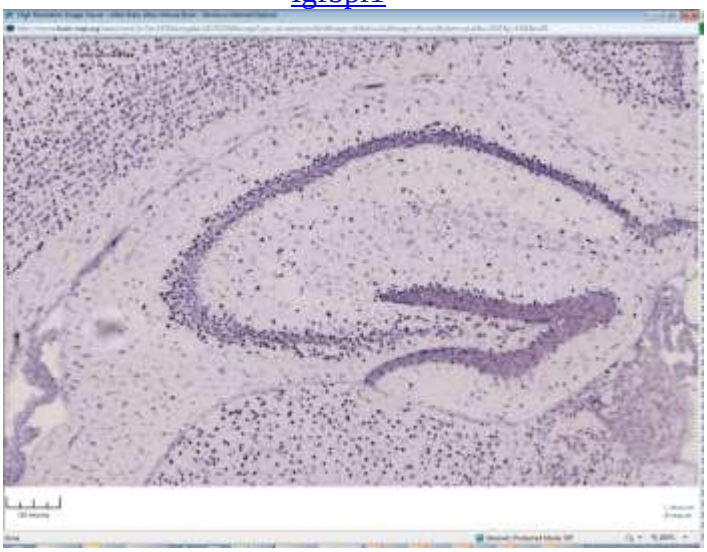

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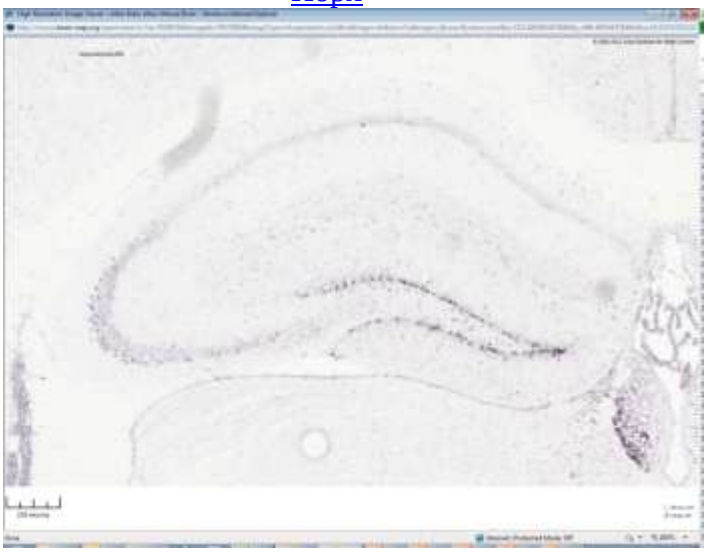

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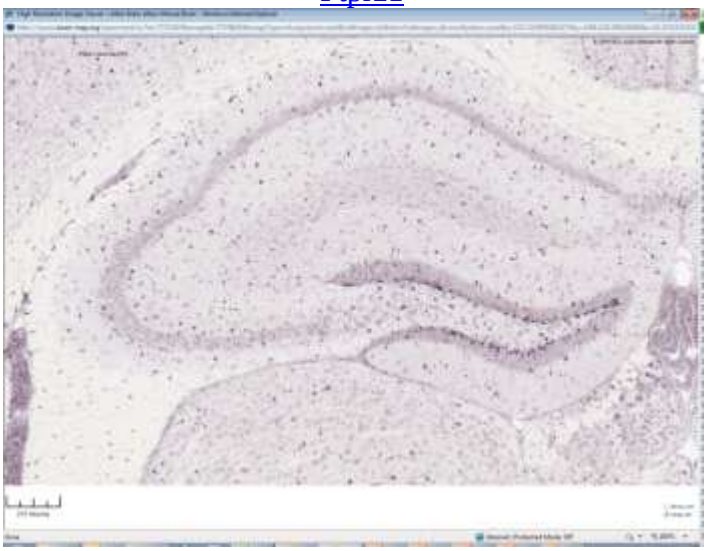

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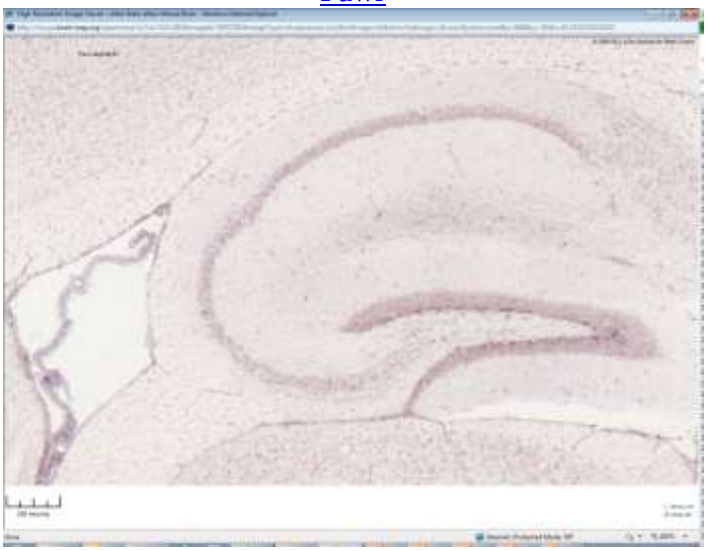

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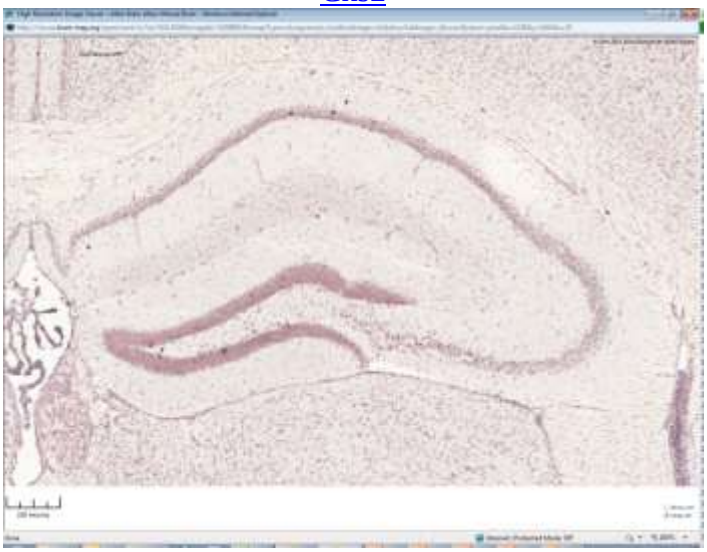

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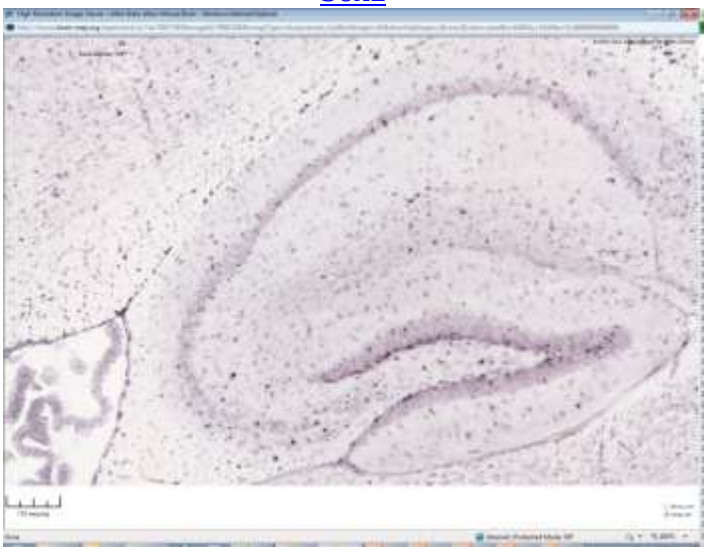

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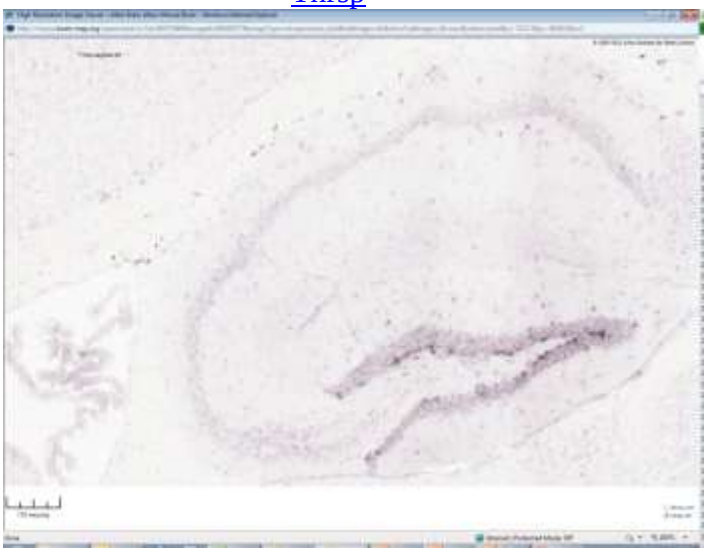

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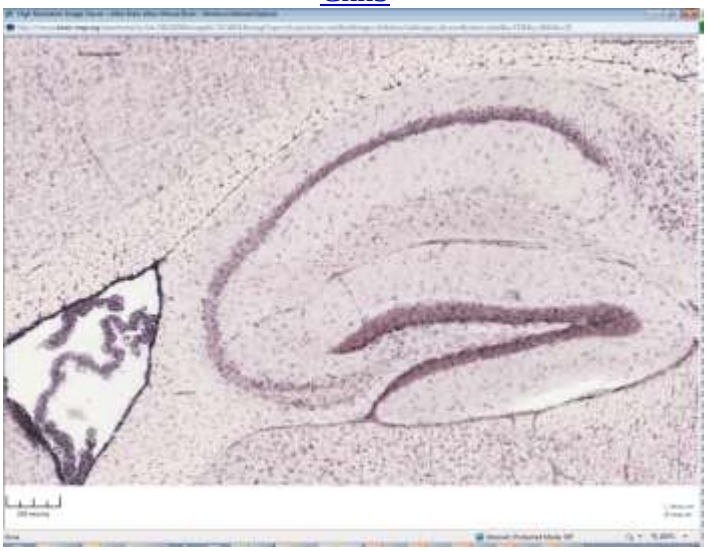

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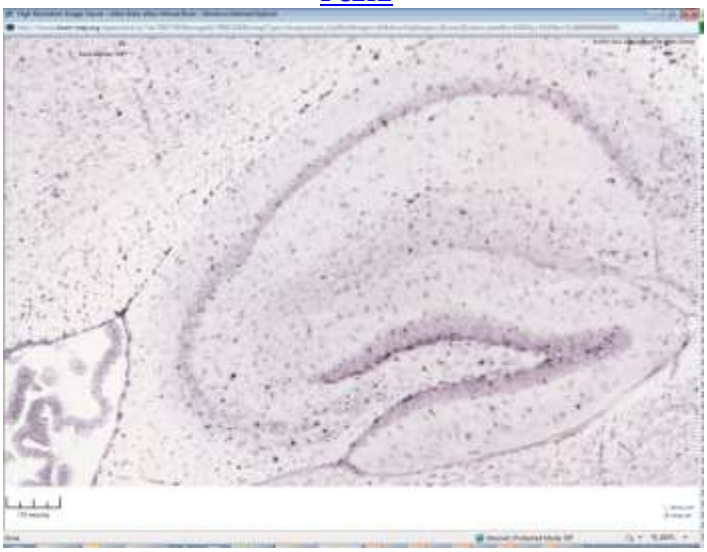

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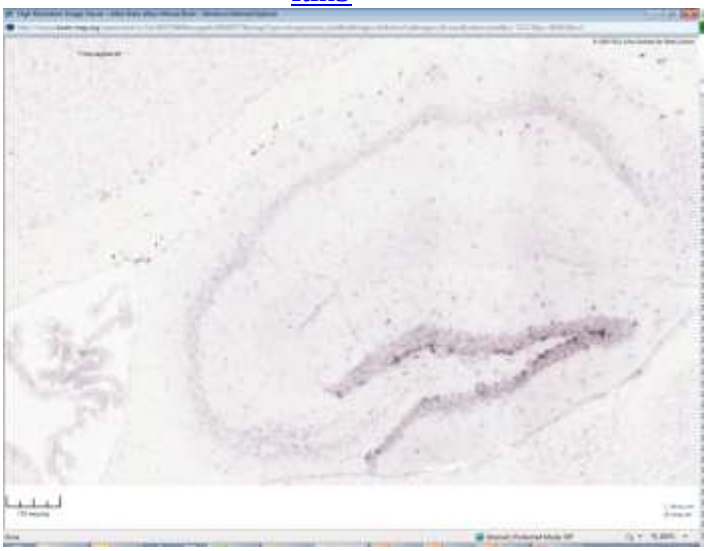

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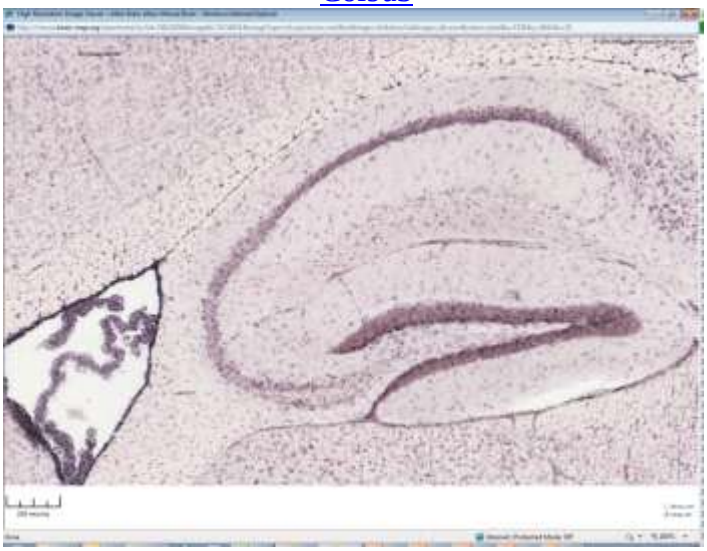

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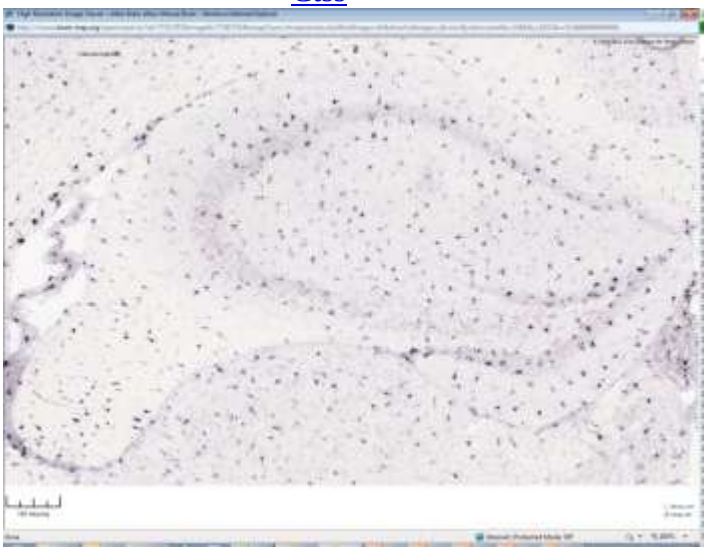

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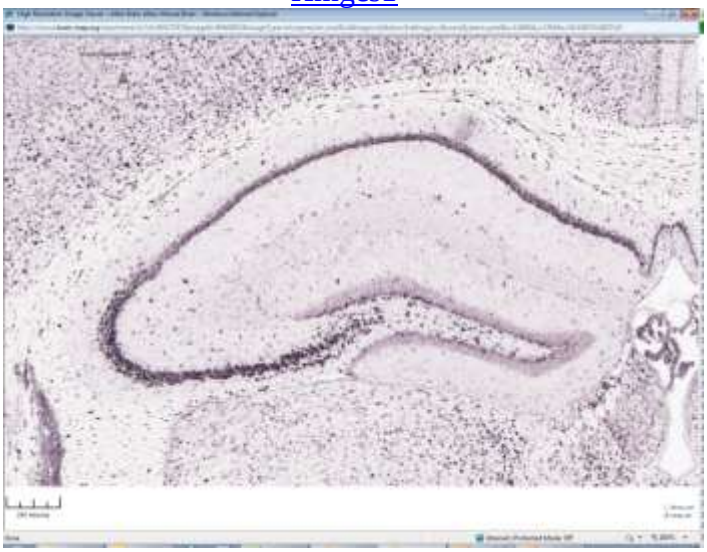

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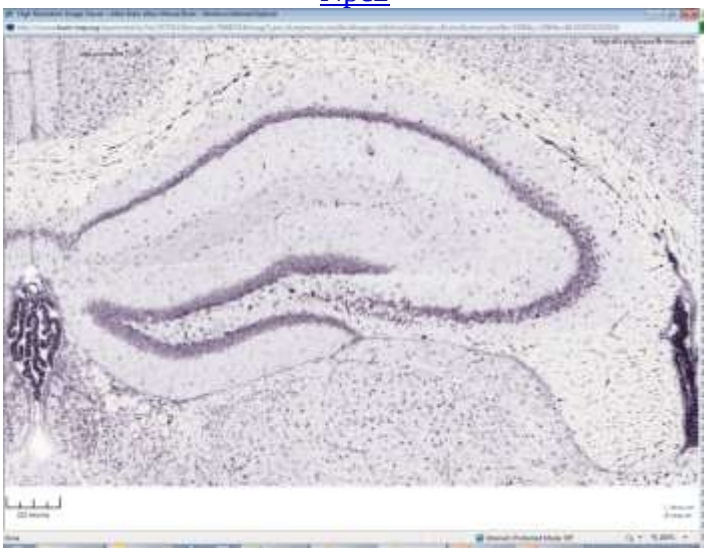

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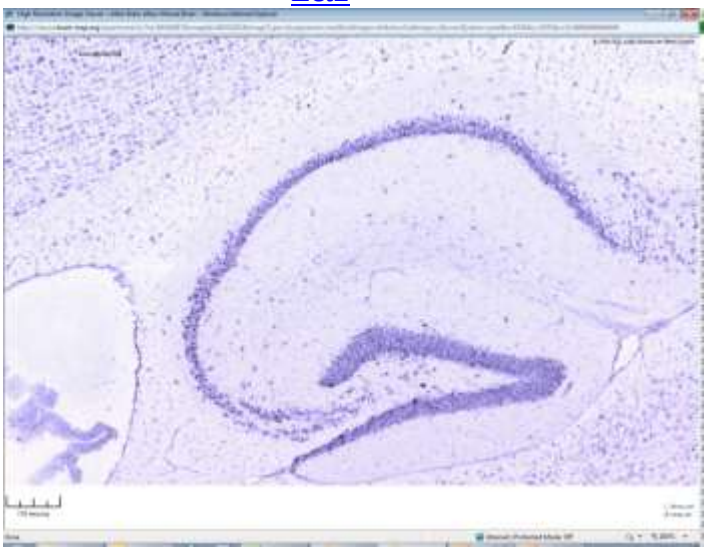

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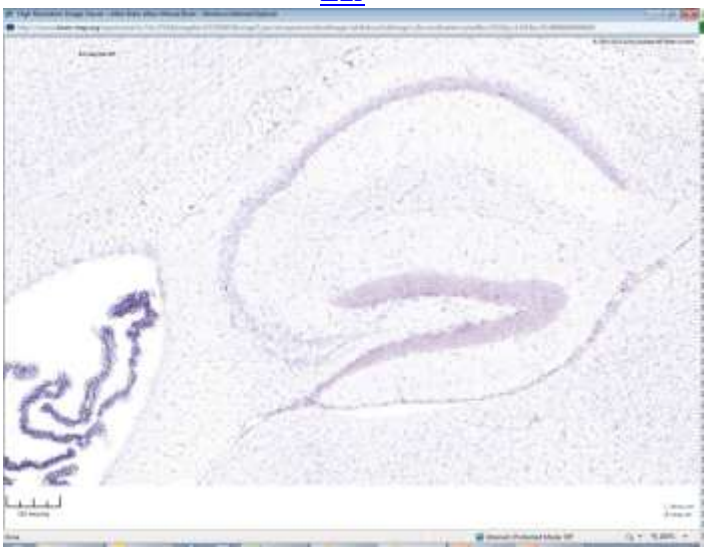

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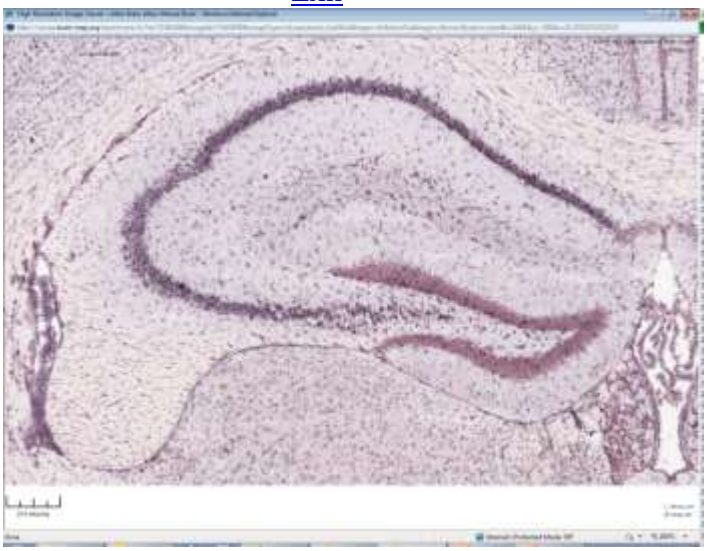

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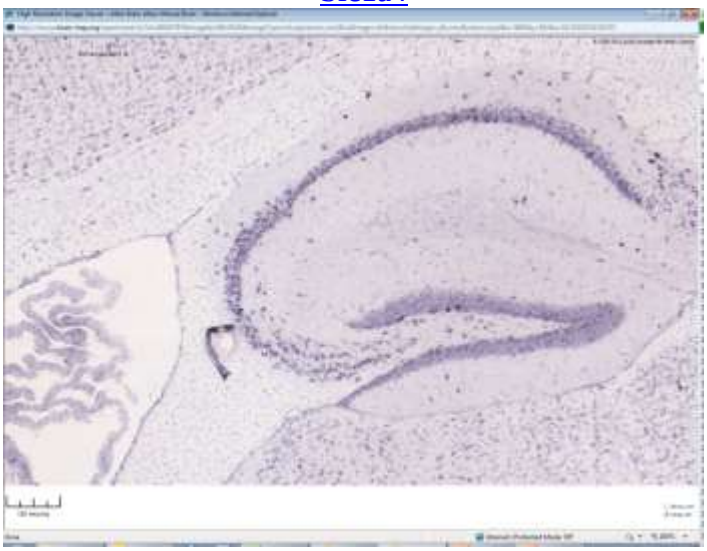

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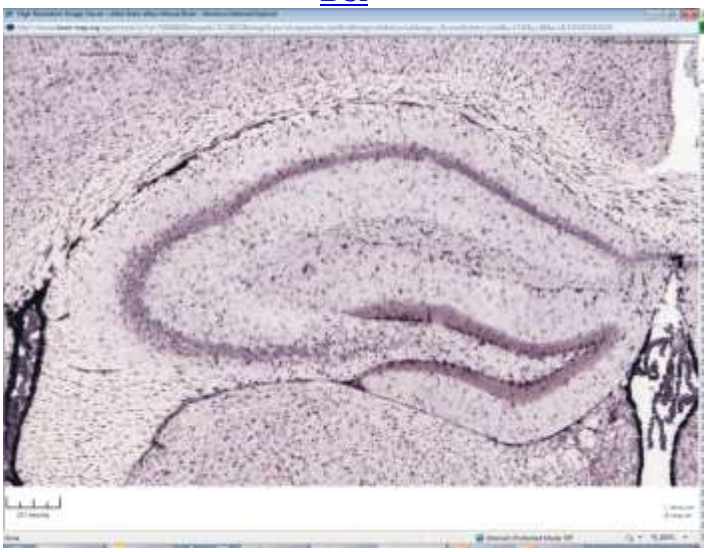

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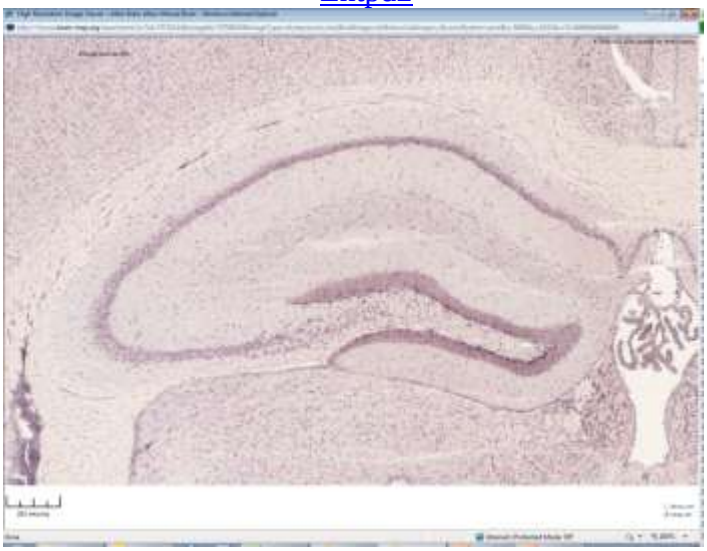

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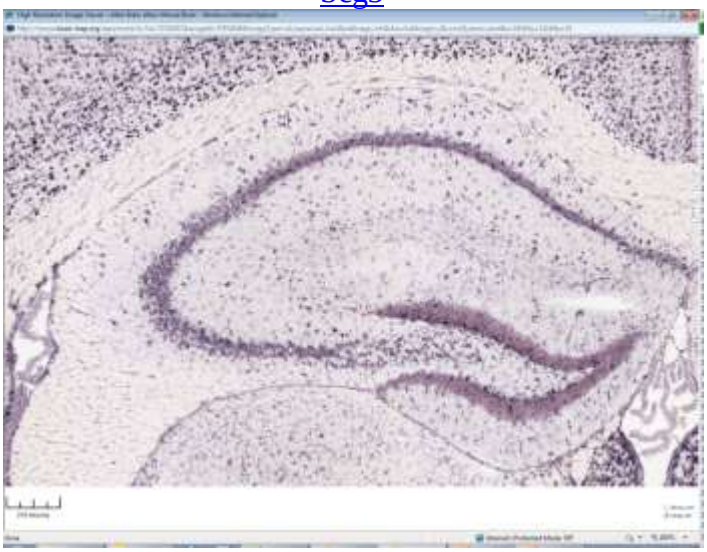

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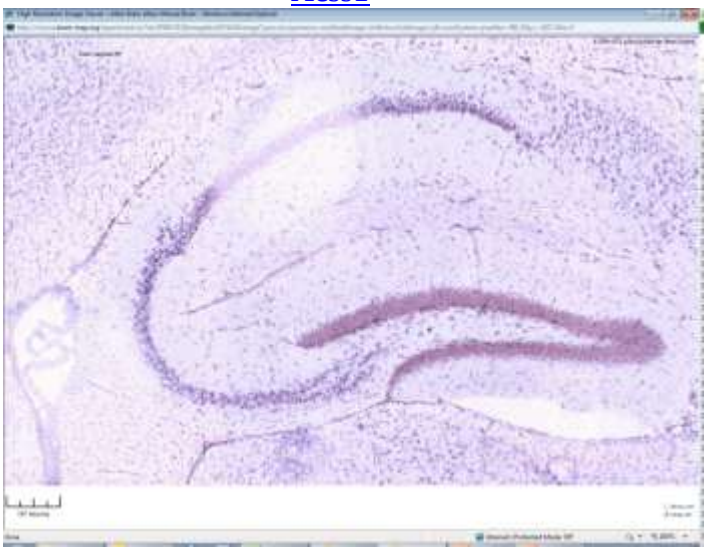

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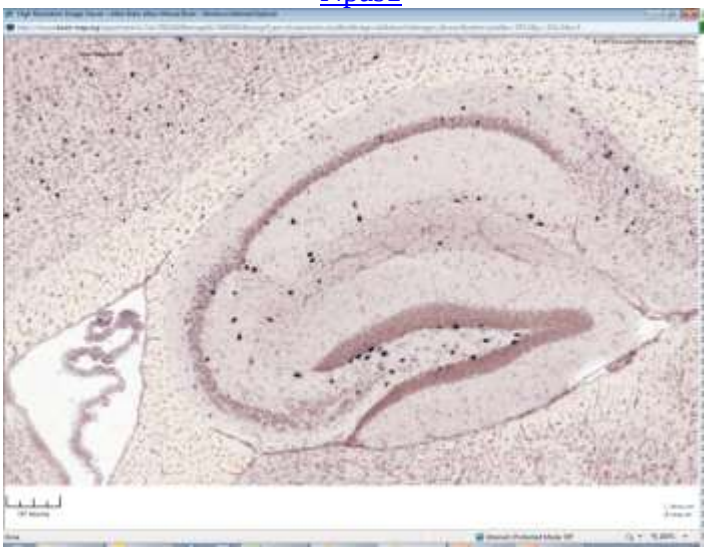

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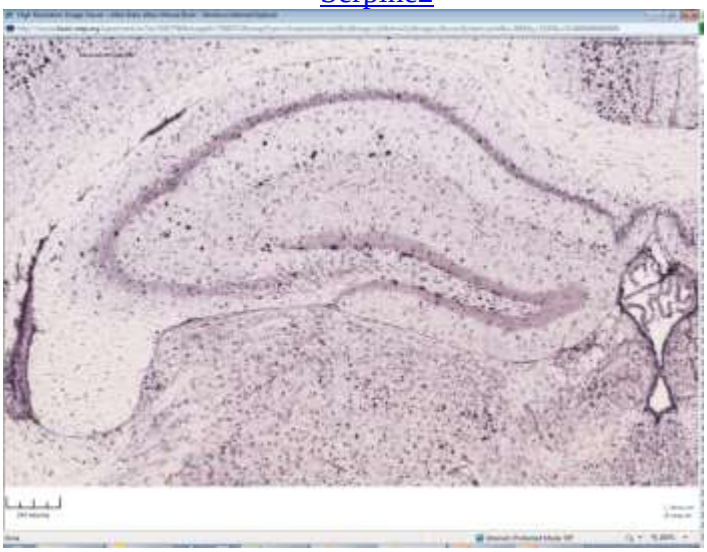

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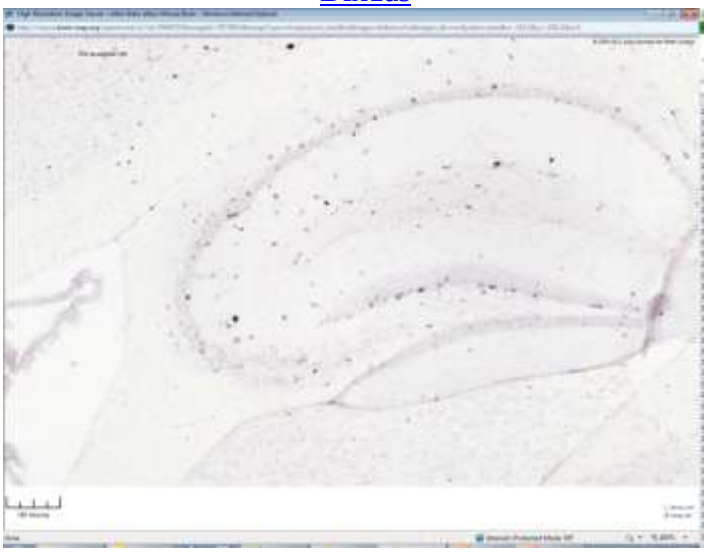

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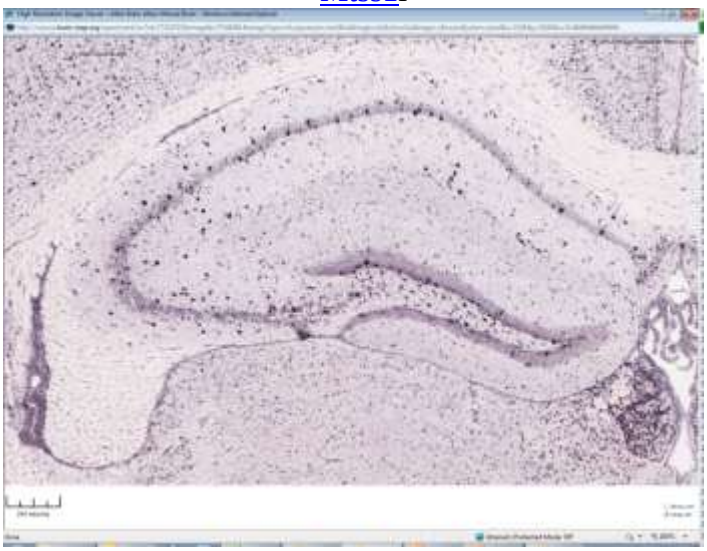

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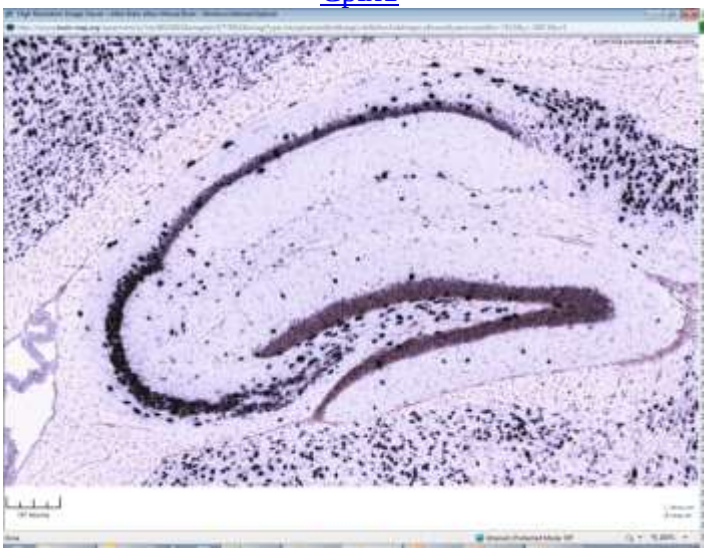

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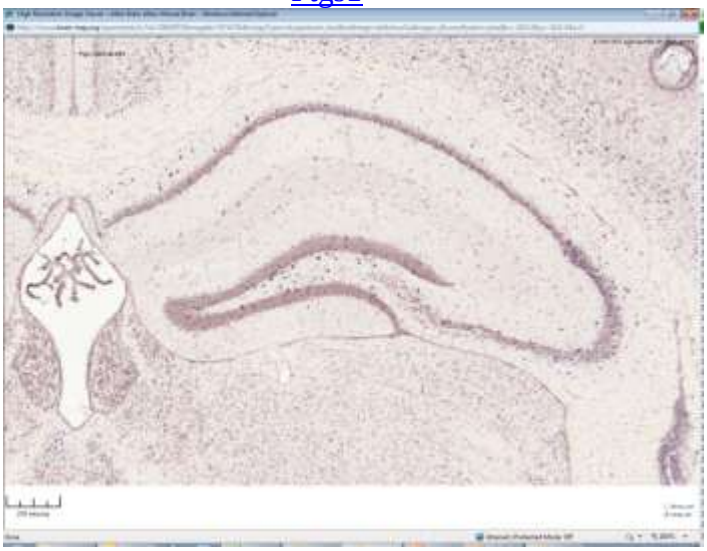

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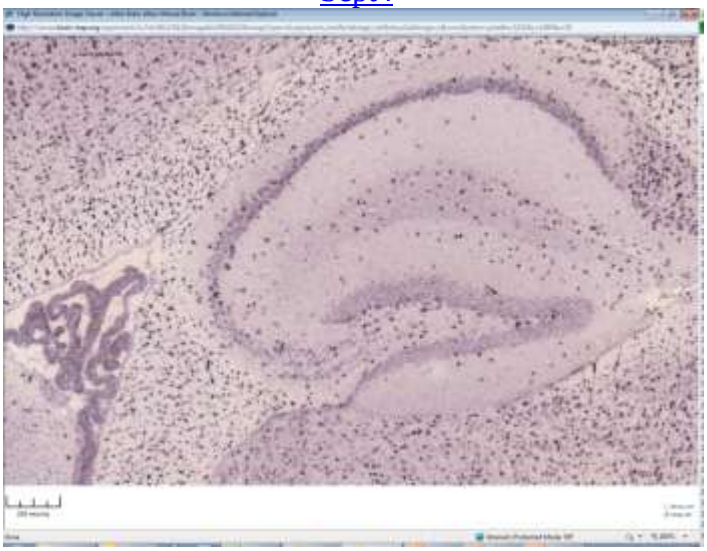

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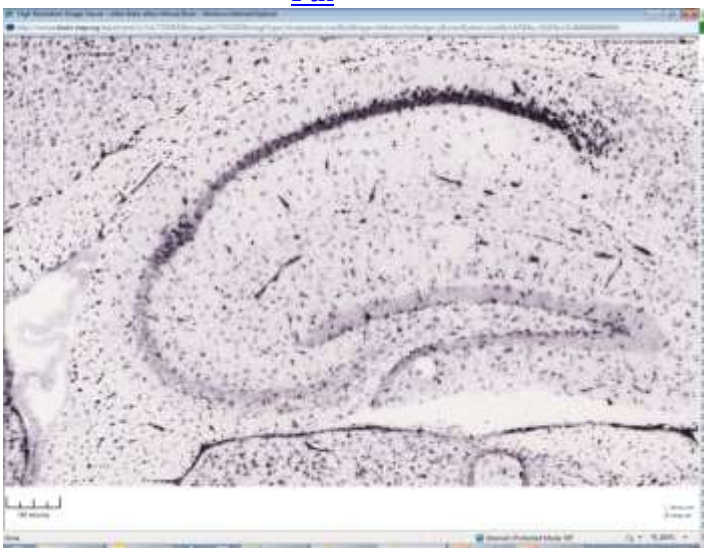

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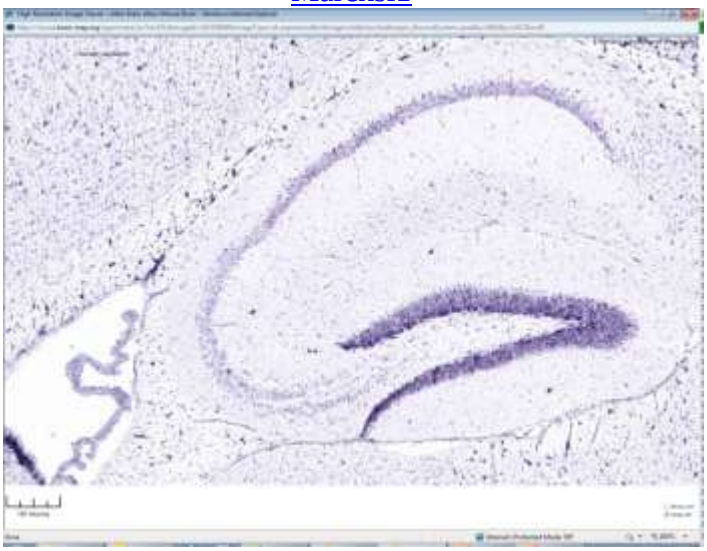

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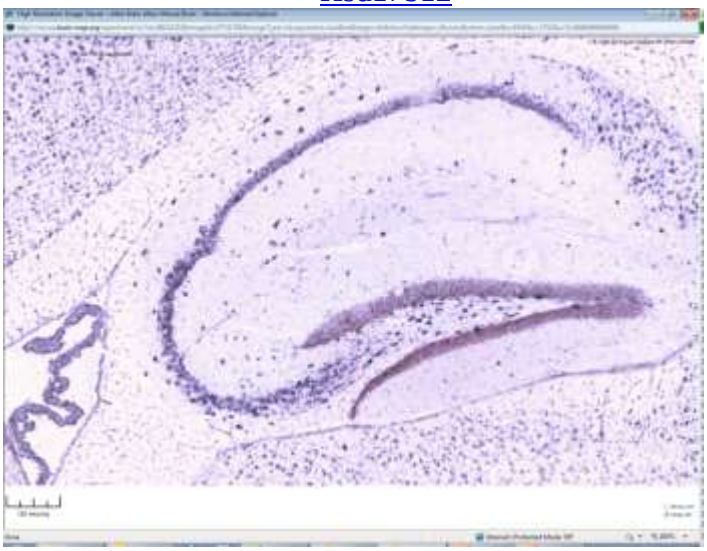

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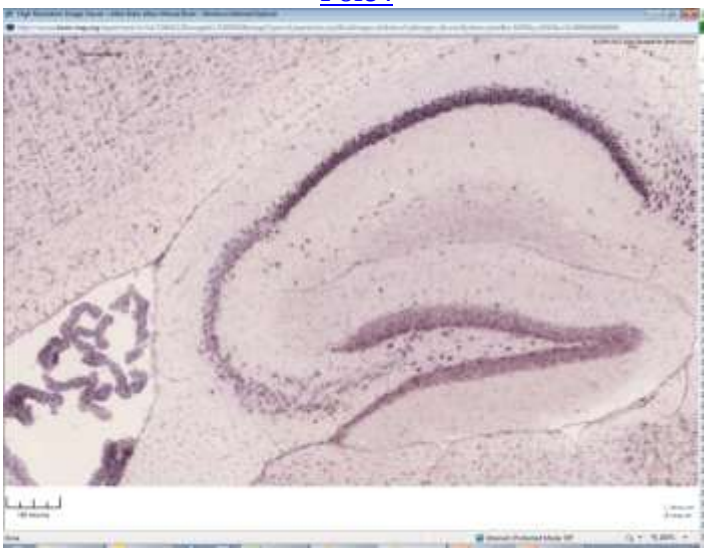

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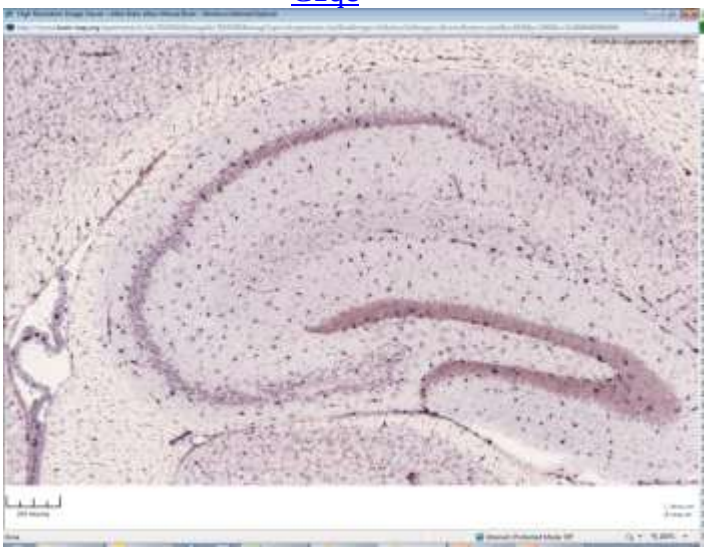

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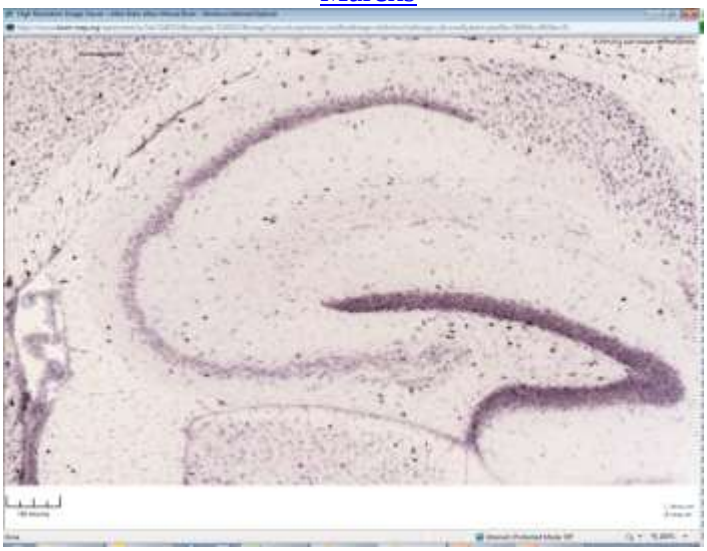

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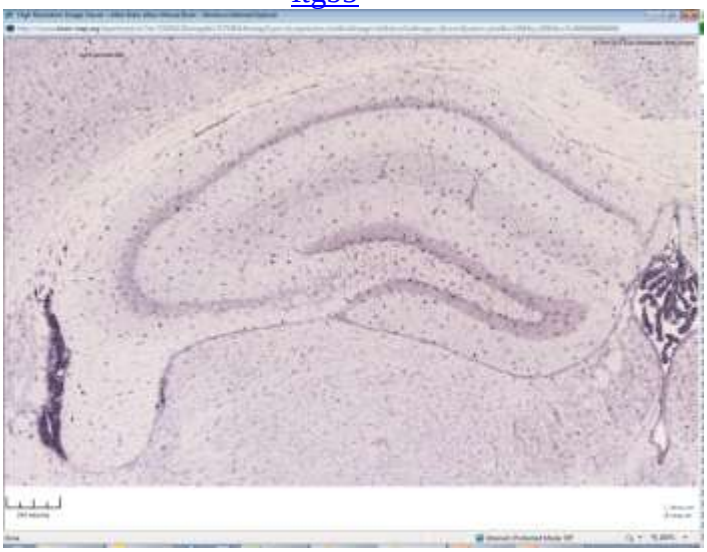

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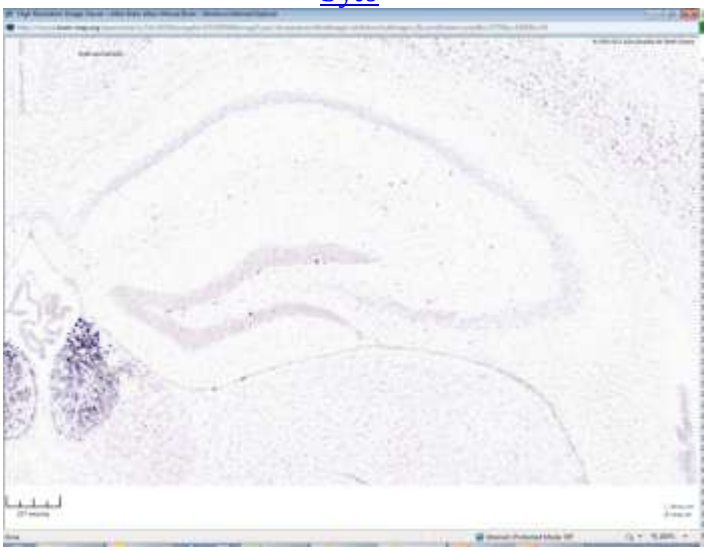

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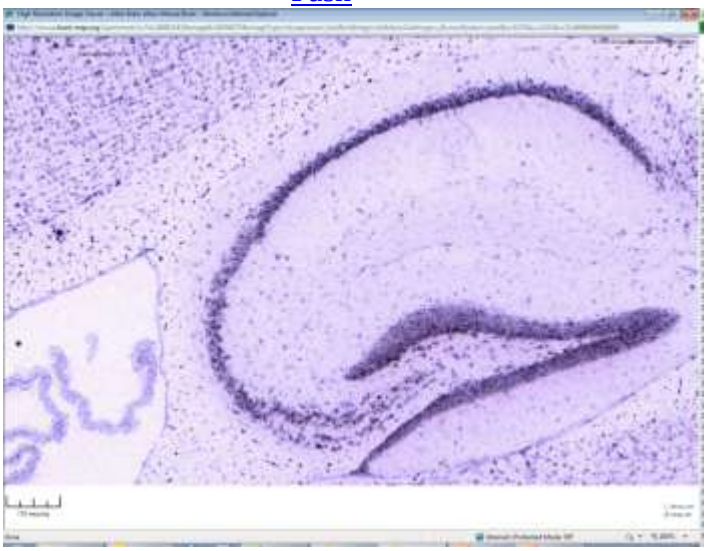

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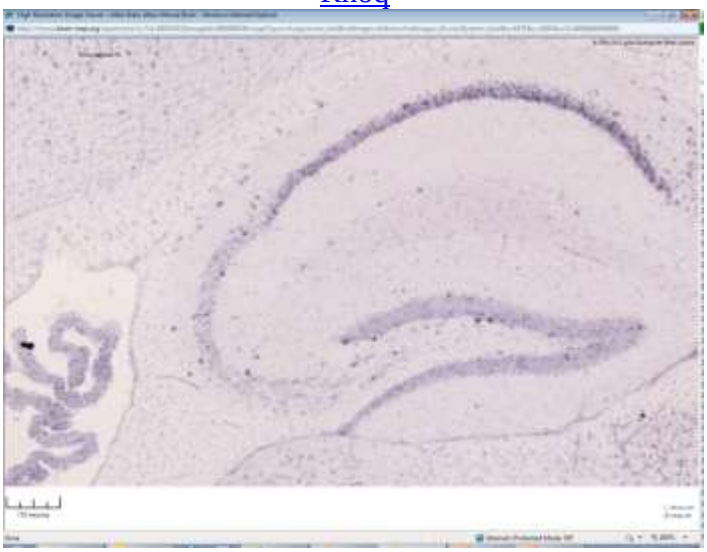

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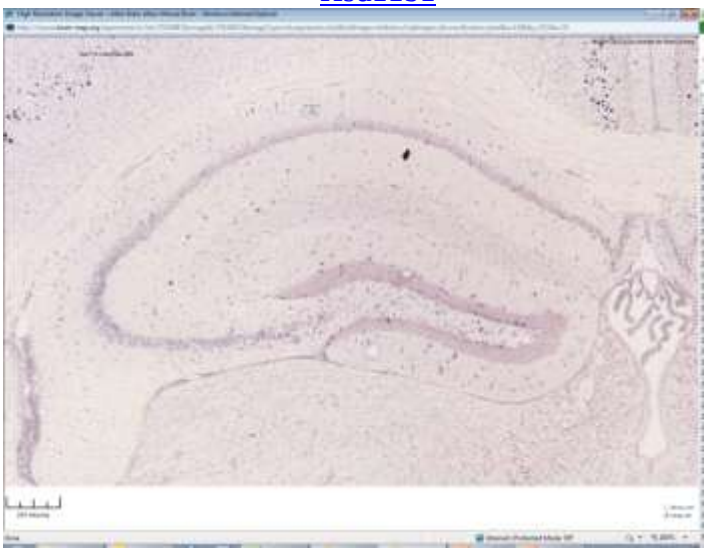

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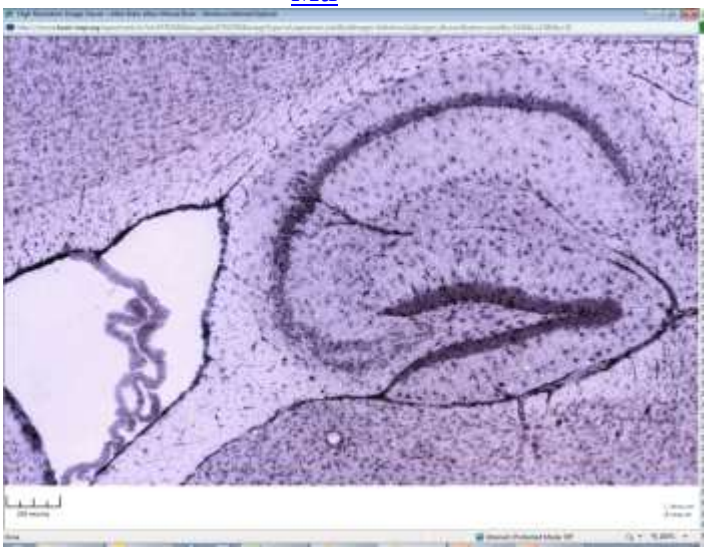

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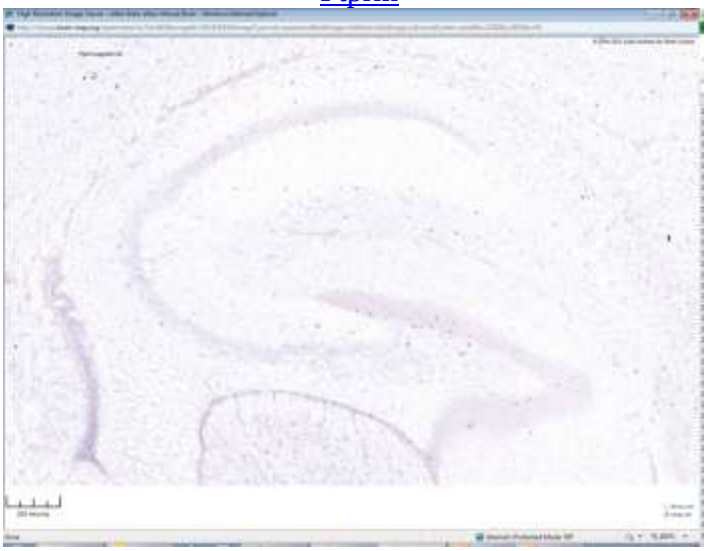

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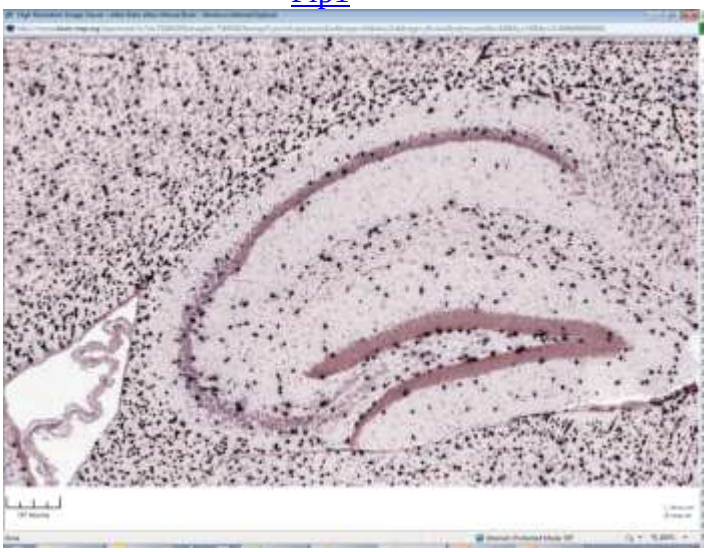

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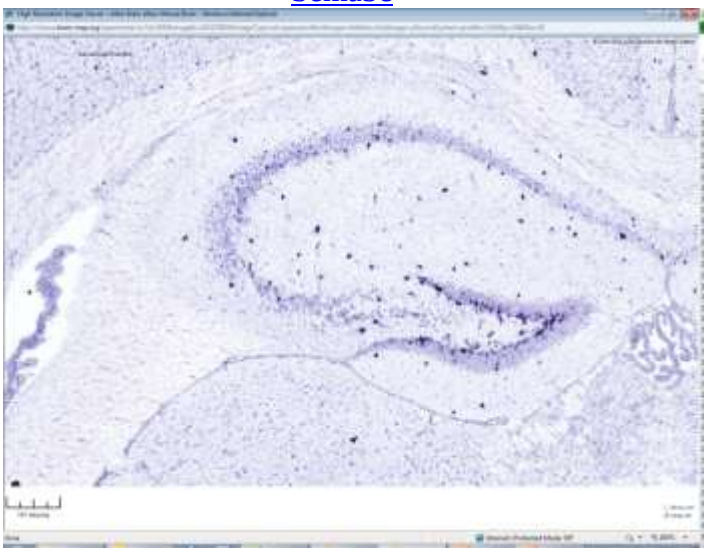

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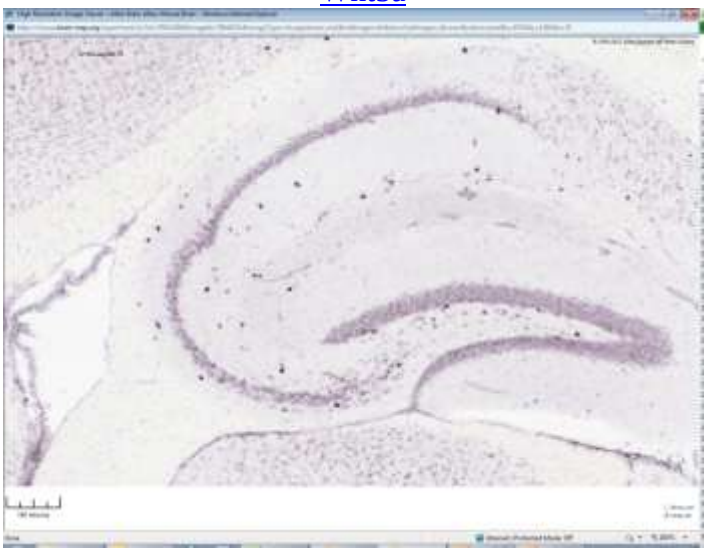

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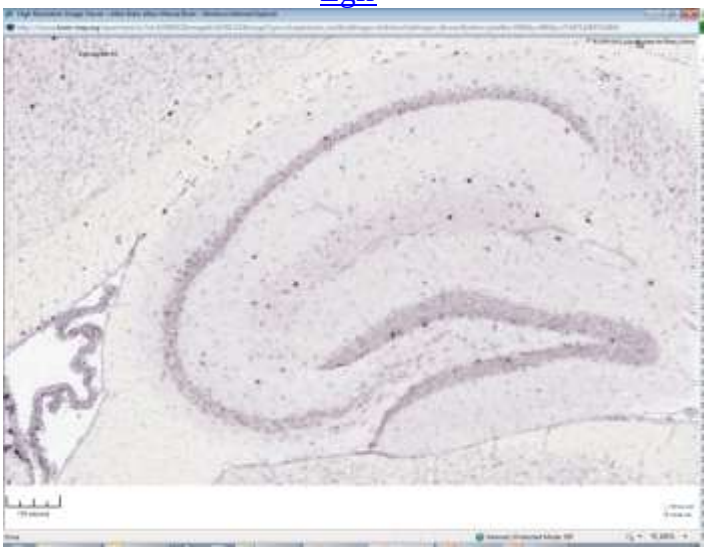

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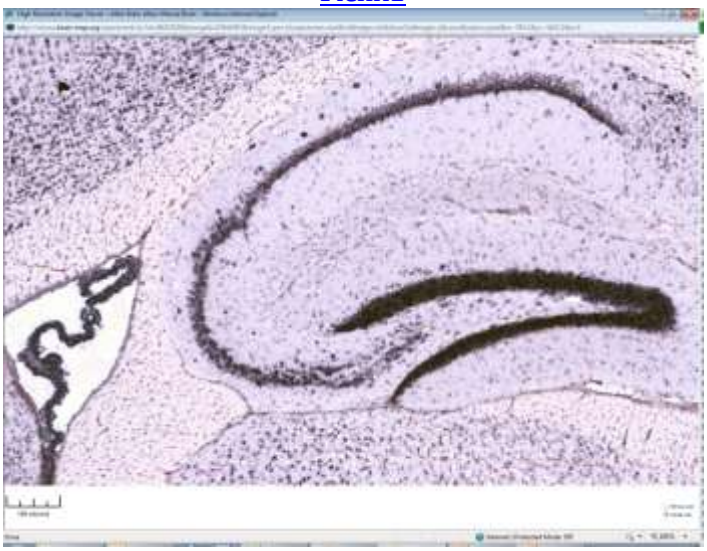

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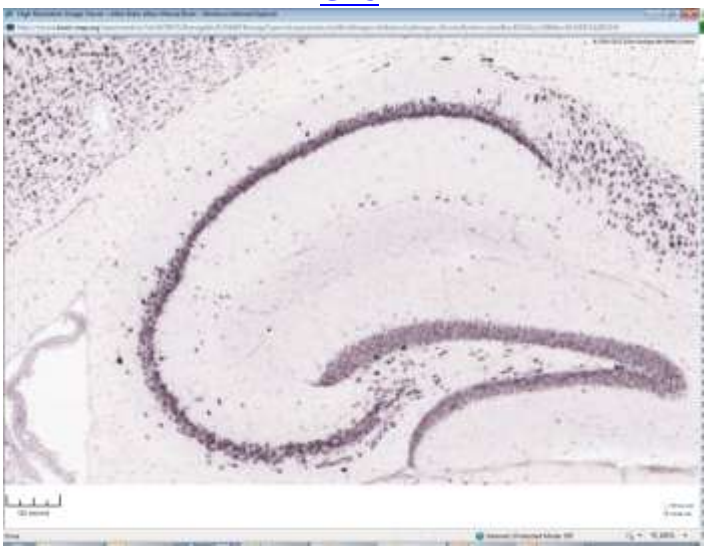

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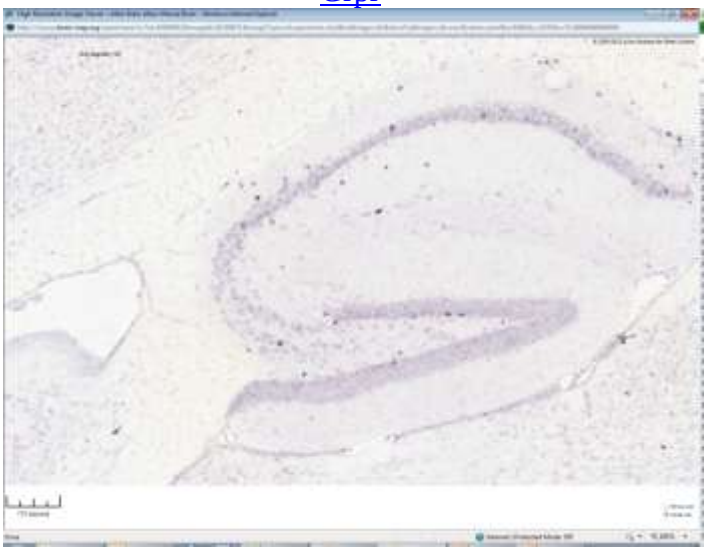

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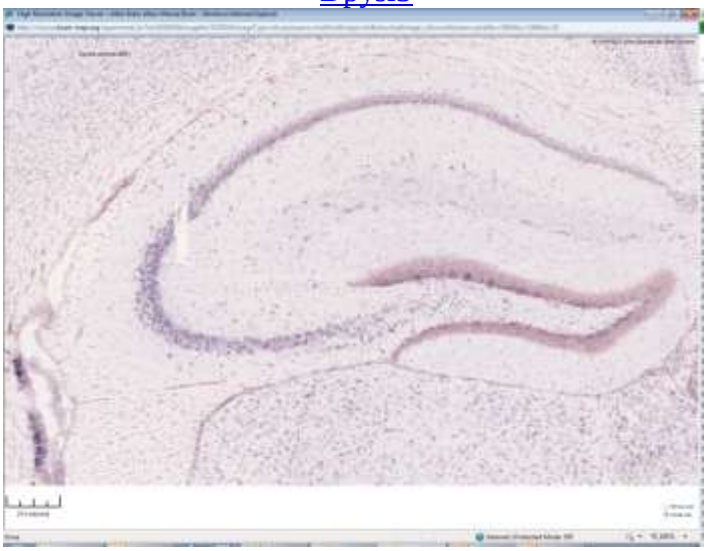

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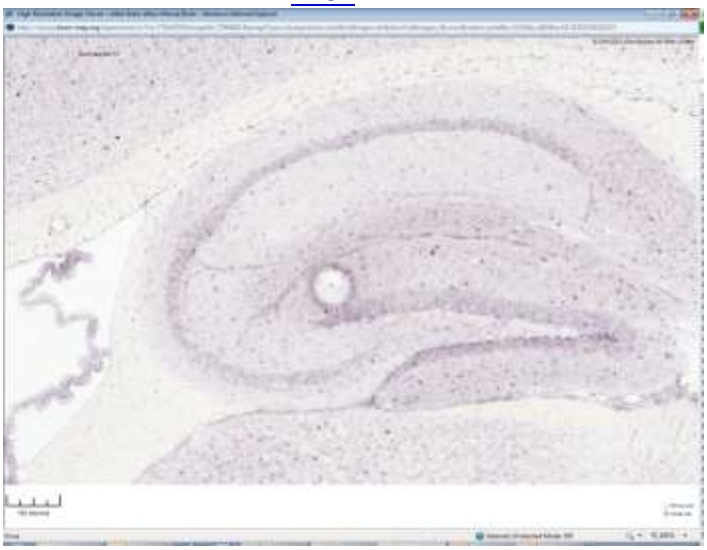

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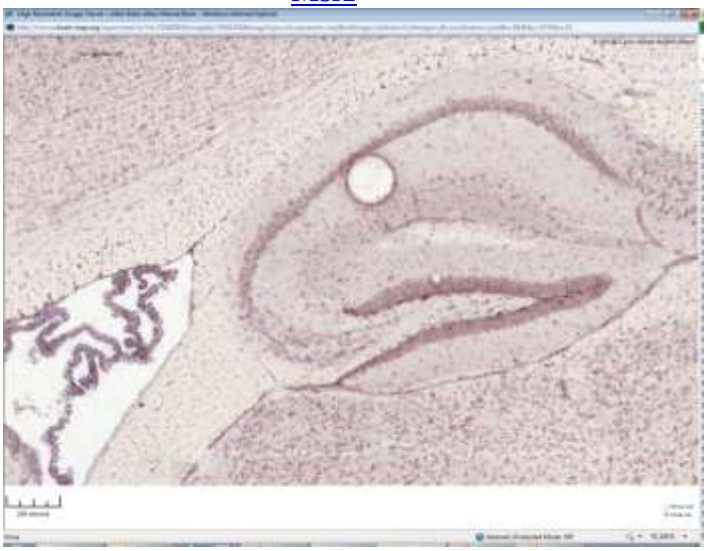

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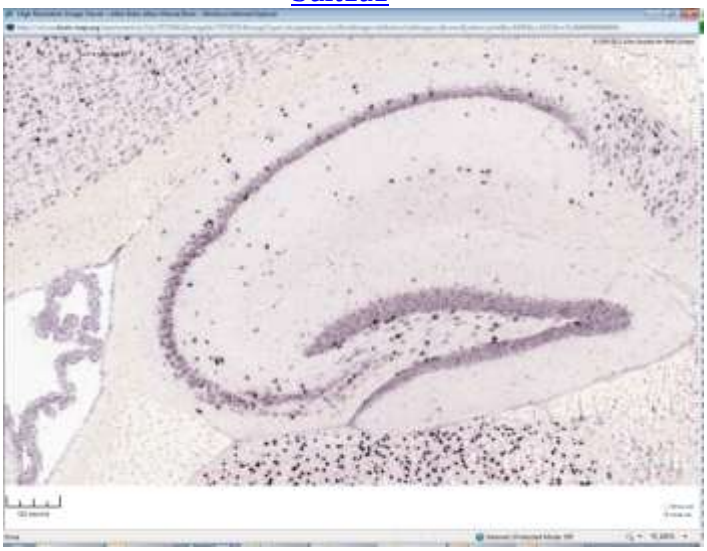

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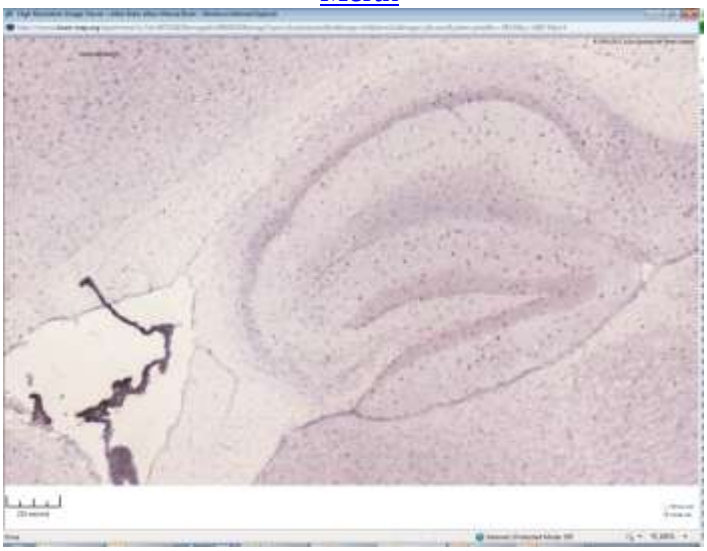

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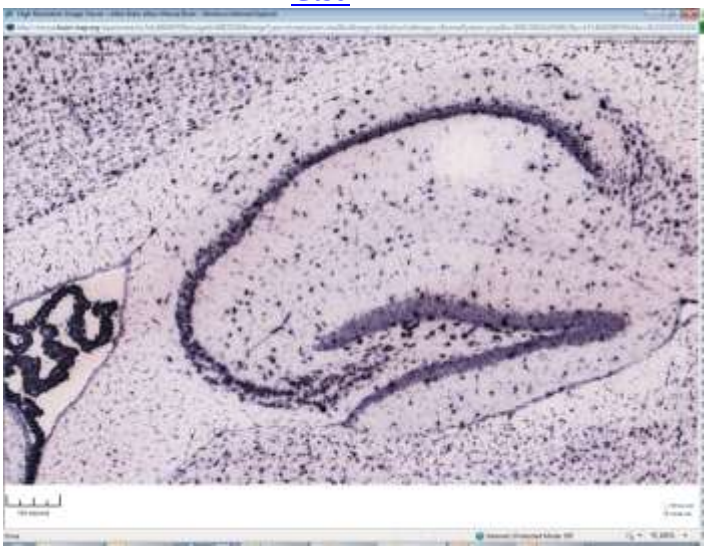

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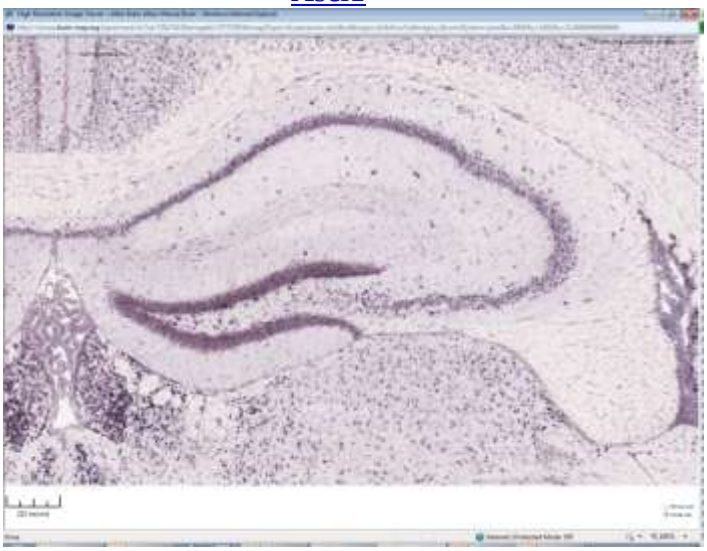

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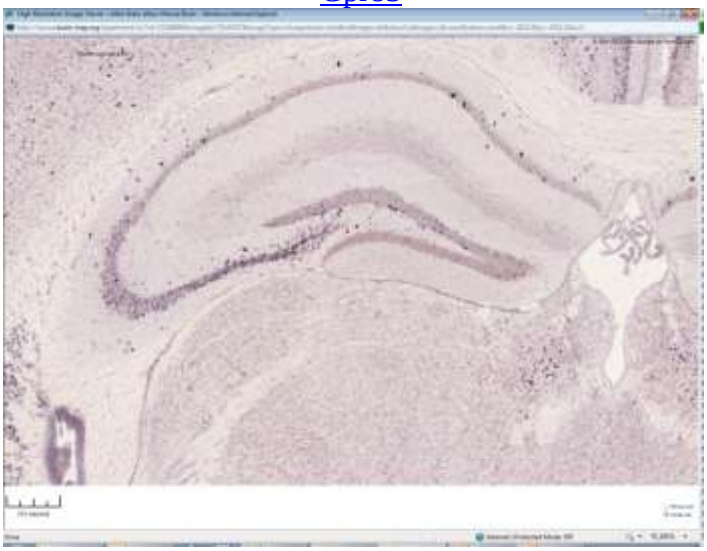

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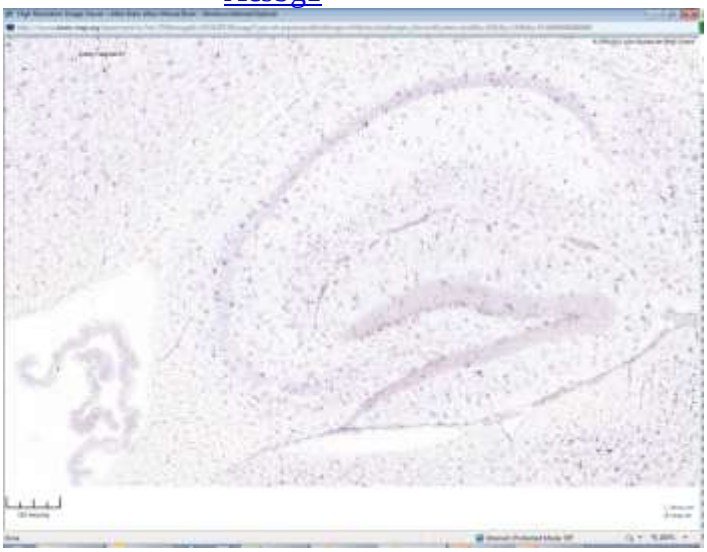

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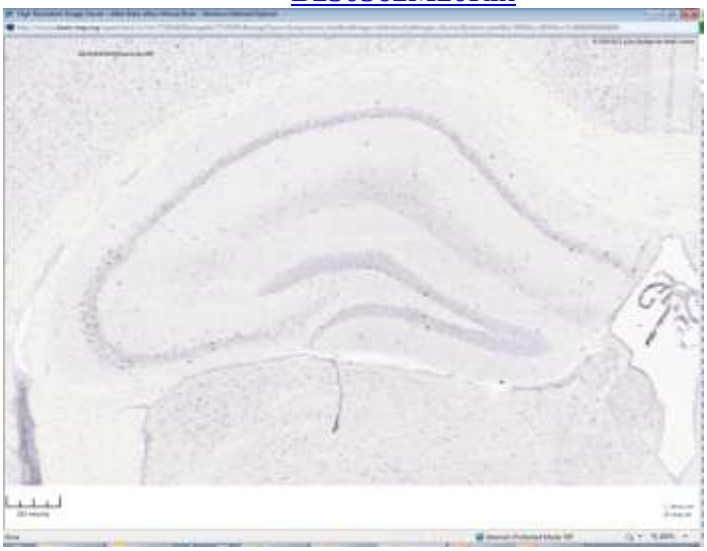

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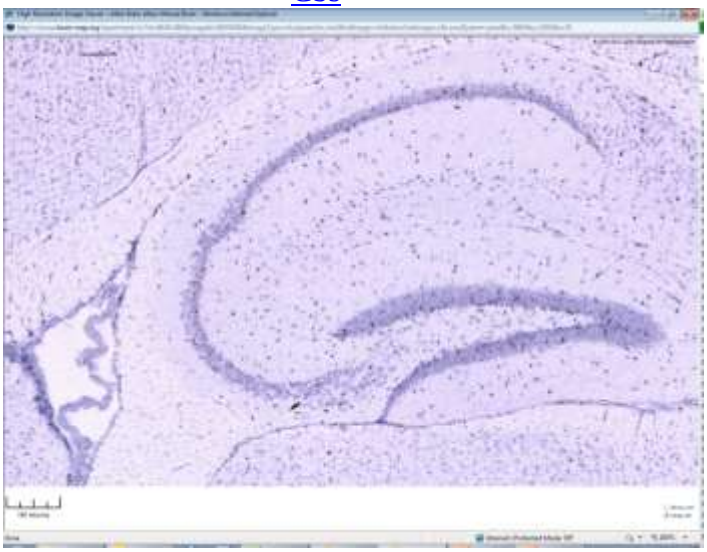

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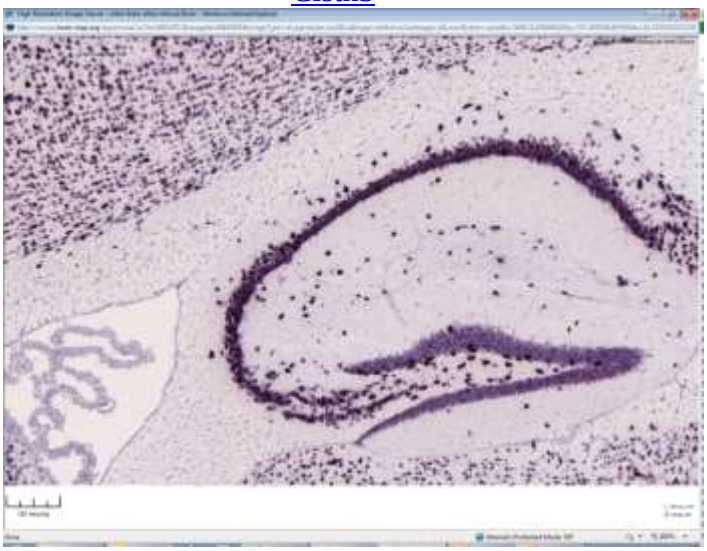

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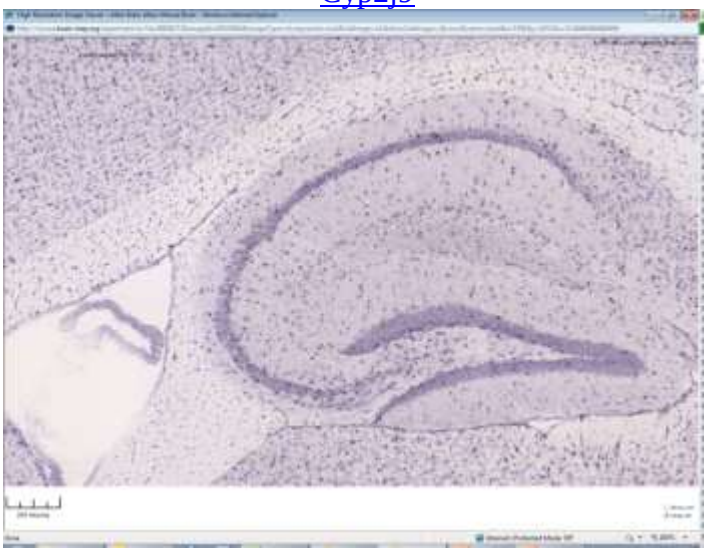

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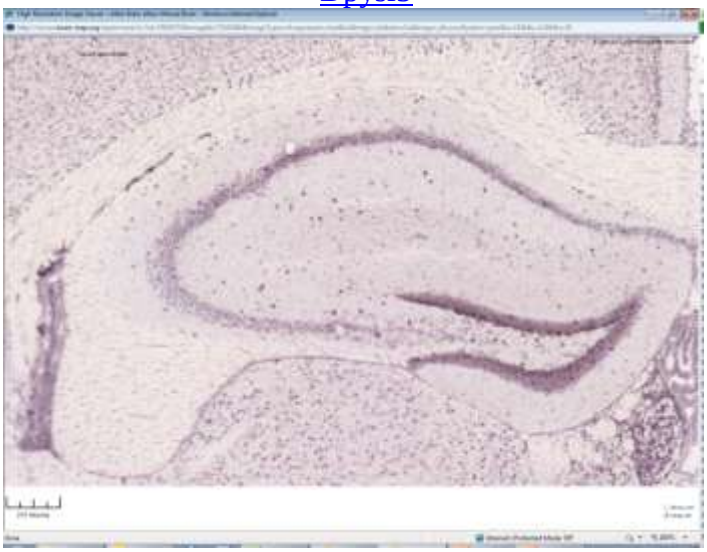

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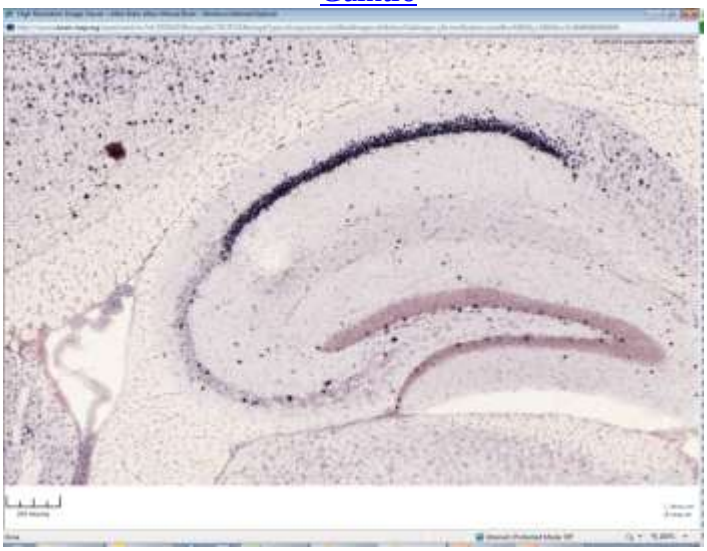

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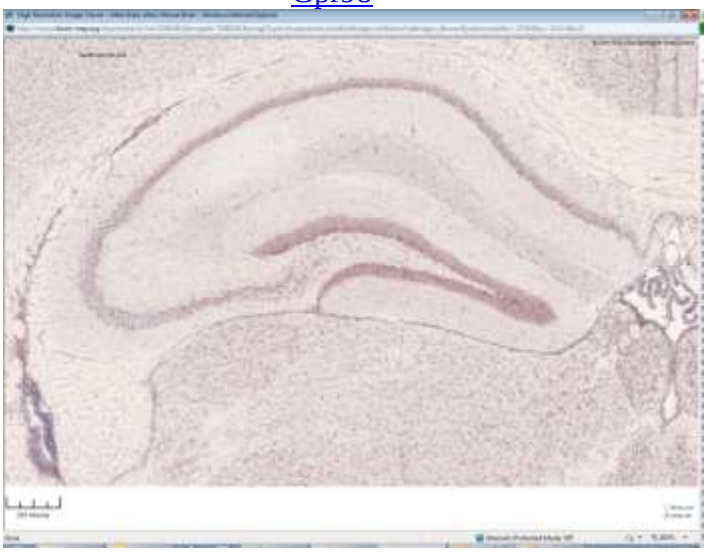

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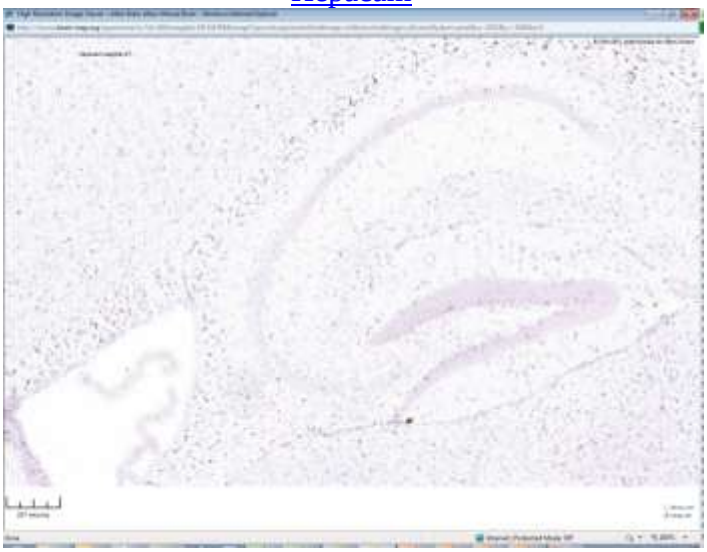

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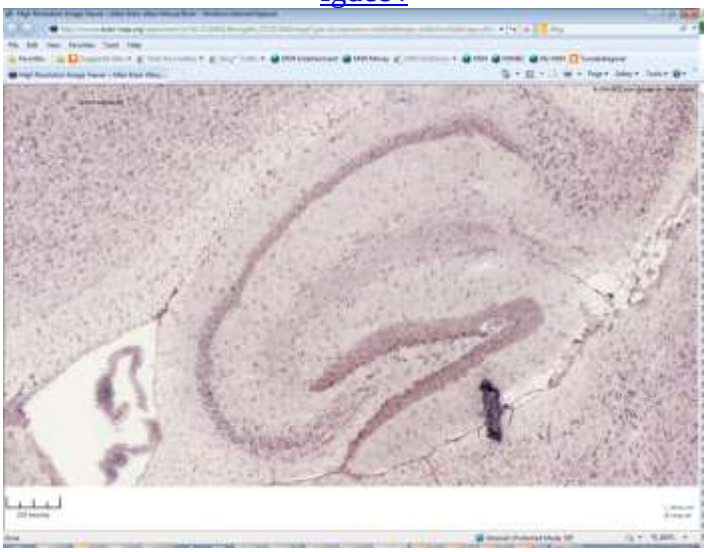

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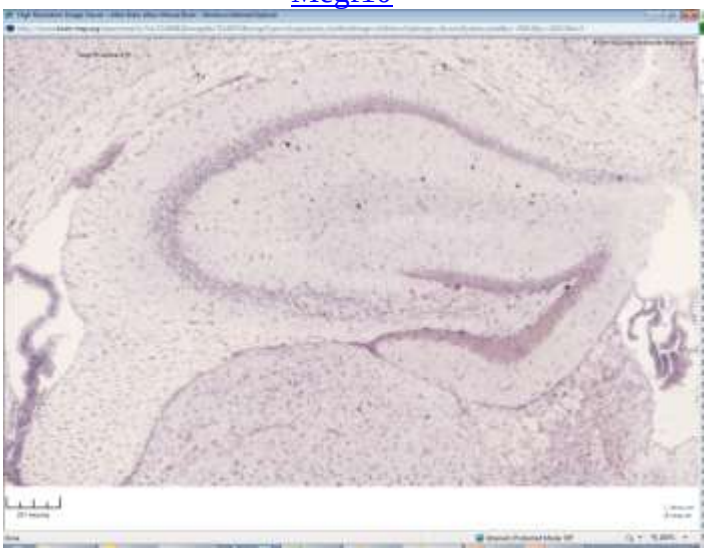

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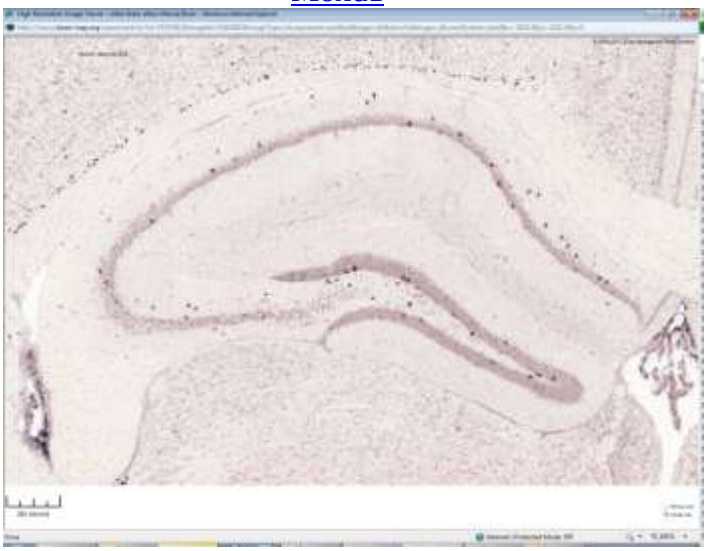

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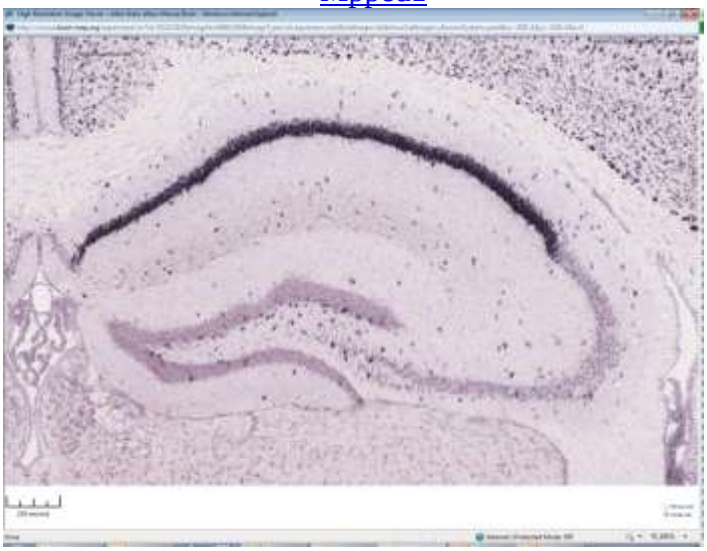

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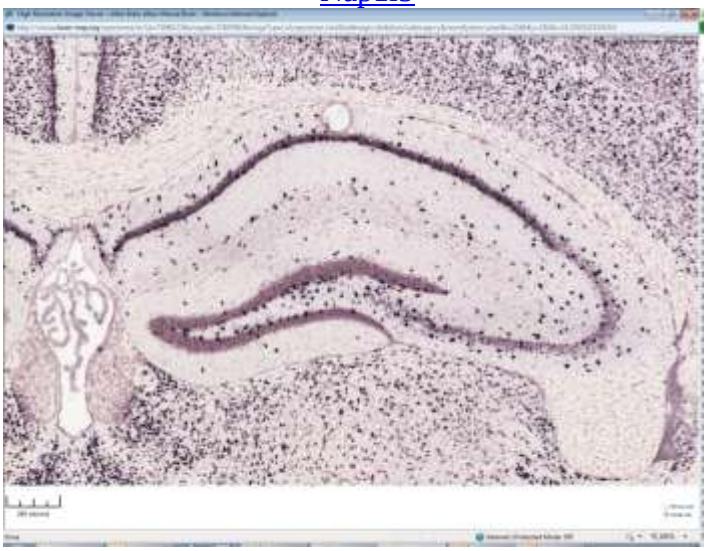

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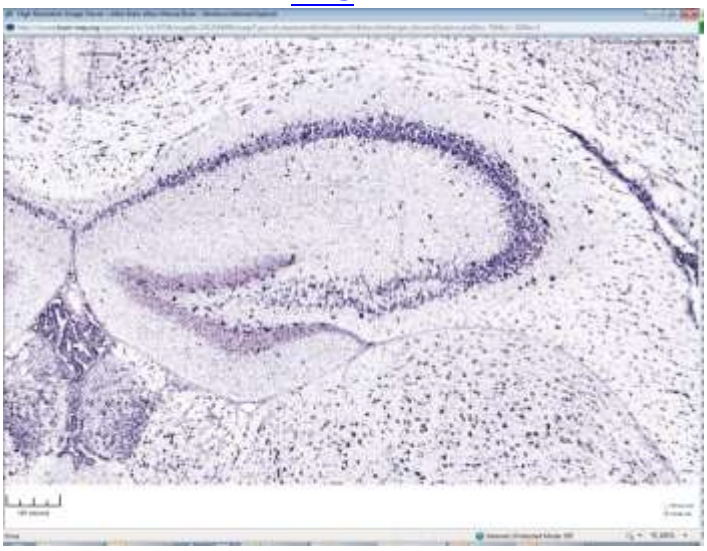

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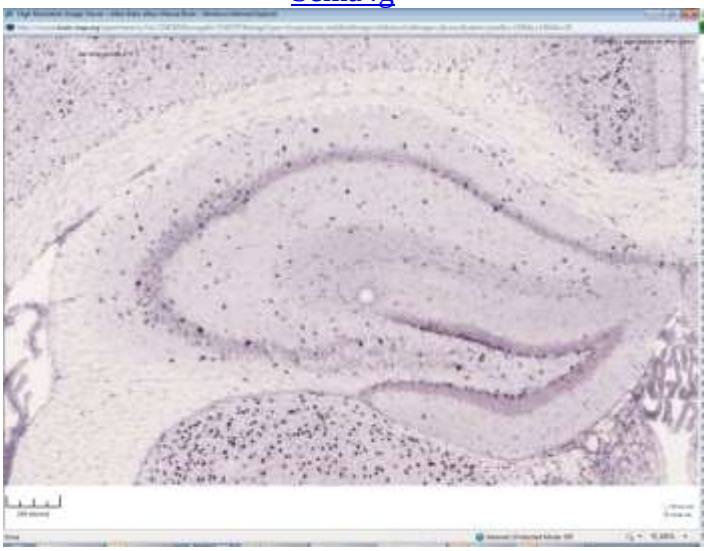

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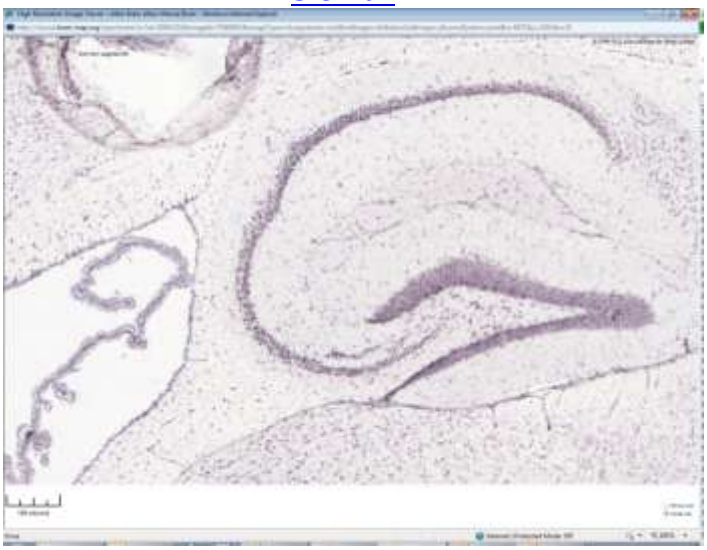

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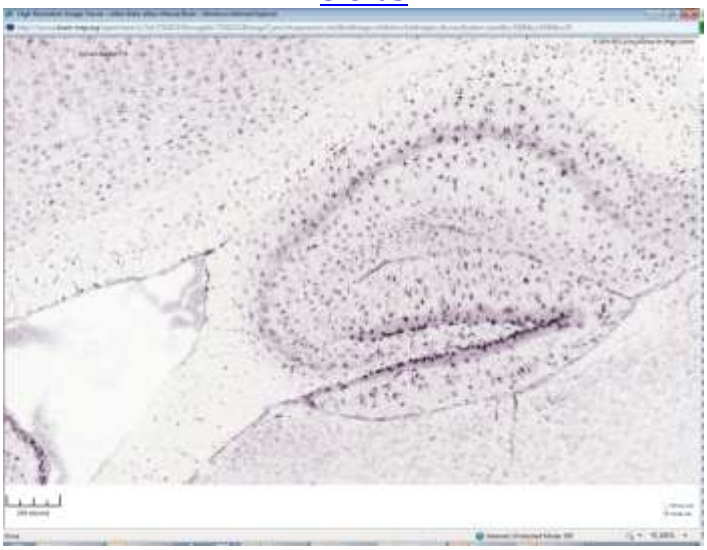

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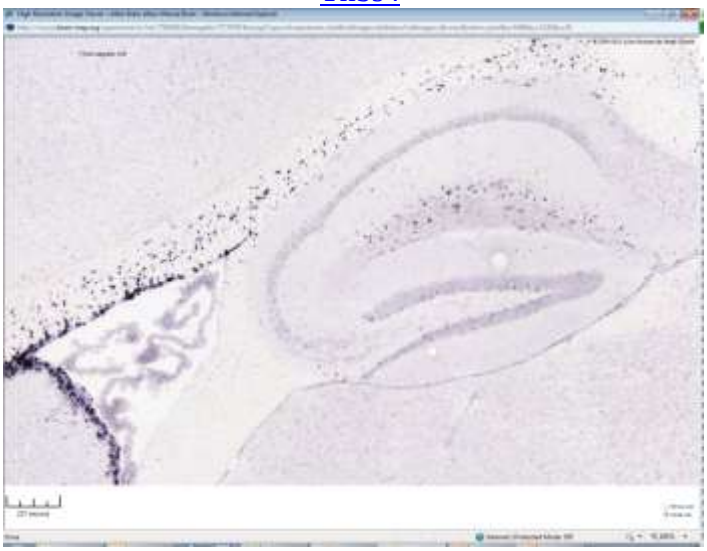

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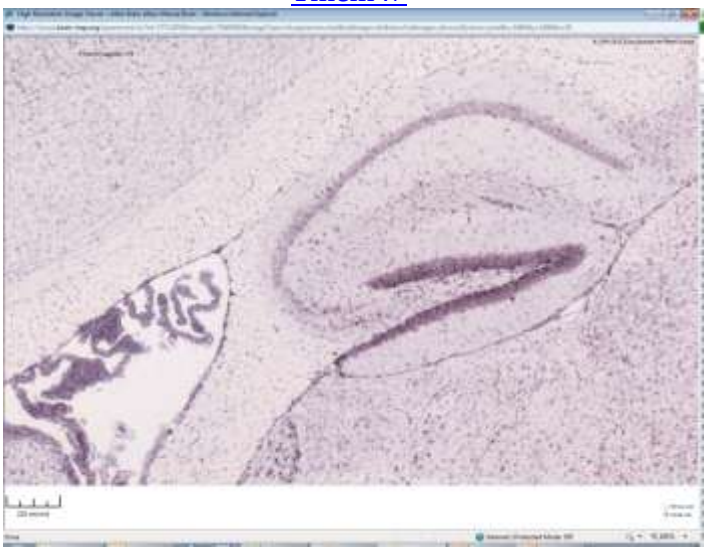

Zfp804a

Figure S4

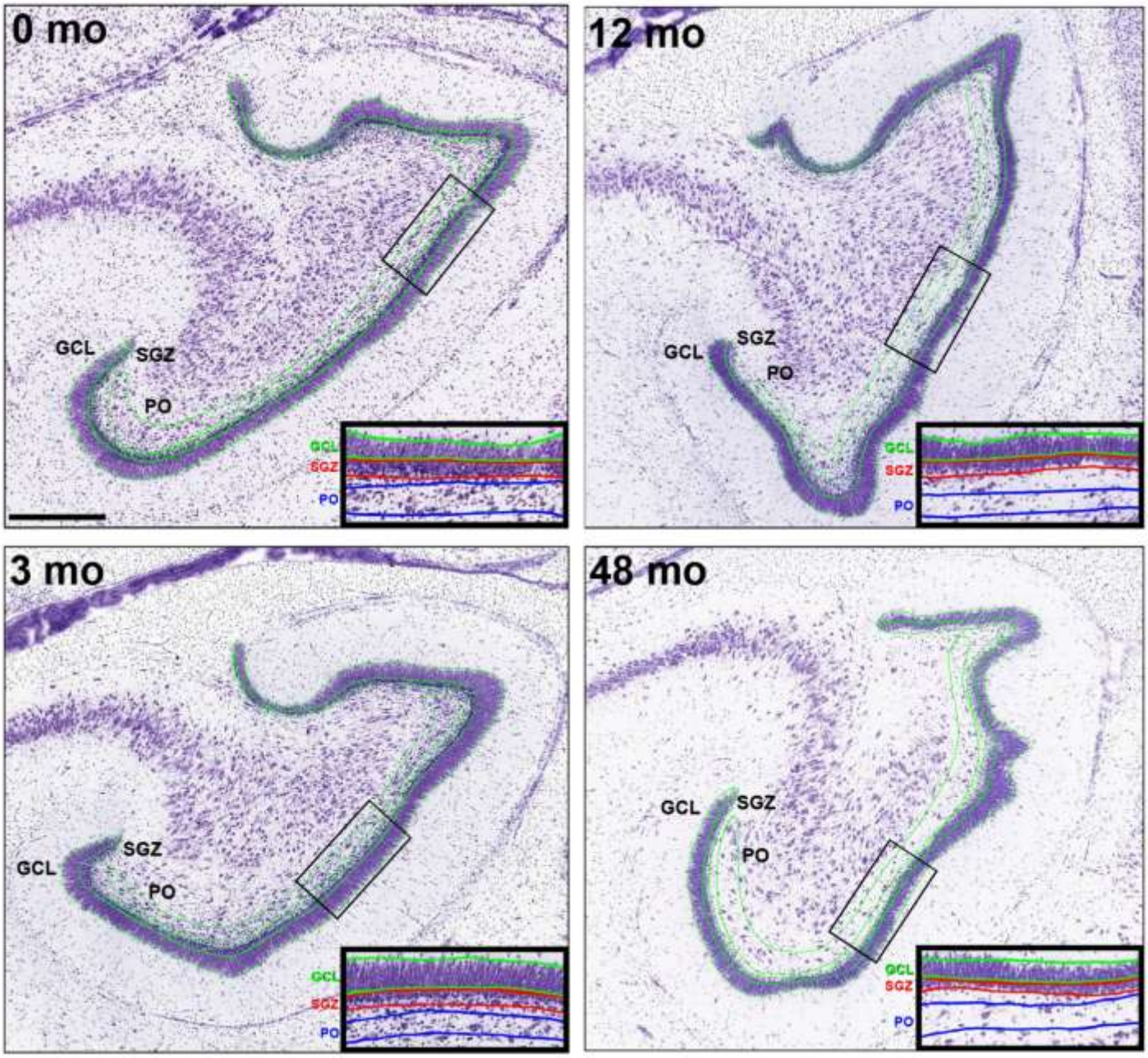

Figure S4, related to Figure 4: Delineation of the developing rhesus monkey dentate gyrus subgranular zone (SGZ), granule cell layer (GCL) and polymorphic layer (PO) for laser microdissection (LMD). Each panel shows a cresyl violet-stained 14µm section at the age indicated. Insets show high magnification views of the boxed regions in low magnification images. Colored lines indicate approximate boundaries of the GCL, SGZ and PO isolated at each age, although the actual regions isolated were somewhat more conservative with respect to boundaries to prevent overlap between samples. PO: polymorphic layer of the dentate gyrus. Scale bar: 500µm.

Table S1.

Download Table S1

Table S2.

Download Table S2

Table S3.

Download Table S3

Table S4.

Download Table S4

Table S5: Enriched categories in 18 macaque co-expression modules.

Module	Gene Category	Source	# Genes	P-value
cyan	response to external stimulus	GO_BP	29	7.44E-03
cyan	nerve maturation	GO_BP	4	7.57E-02
cyan	Astrocyte (10+ fold enrichment)	Cahoy	19	1.93E-11
cyan	Oligodendrocyte marker	ABA	14	8.38E-11
cyan	Astrocyte marker	ABA	7	3.49E-04
cyan	Oligodendrocyte (10+ fold enrichment)	Cahoy	10	9.10E-04
greenyellow	Astrocyte (10+ fold enrichment)	Cahoy	22	5.51E-11
greenyellow	Astrocyte marker	ABA	10	9.12E-07
midnightblue	morphogenesis	GO_BP	24	2.60E-01
midnightblue	Astrocyte (10+ fold enrichment)	Cahoy	11	3.42E-03
tan	neurogenesis	GO_BP	18	3.87E-02
tan	development	GO_BP	39	5.29E-02
---	---	---	--	---
blue	immune response	GO_BP	68	2.18E-06
blue	response to external stimulus	GO_BP	114	2.79E-06
brown	ubiquitin cycle	GO_BP	13	4.98E-02
lightcyan	Neuron (10+ fold enrichment)	Cahoy	13	2.10E-02
lightgreen	metal ion transport	GO_BP	9	6.09E-02
orange	transport	GO_BP	29	8.24E-03
orange	Neuron (10+ fold enrichment)	Cahoy	12	8.43E-03
turquoise	Neuron (10+ fold enrichment)	Cahoy	49	1.10E-03

Table S5: Enriched categories in 18 macaque co-expression modules. Categories for the four SGZ-enriched modules are shown first (above dashed lines). Labeling as in Table 1. Several redundant categories were omitted for clarity. Enrichments shaded in grey may be of interest, despite failing to reach the $p<0.05$ threshold after Bonferroni correcting for multiple comparisons.