

1 **An insight into intestinal mucosal microbiota disruption after**
2 **stroke**

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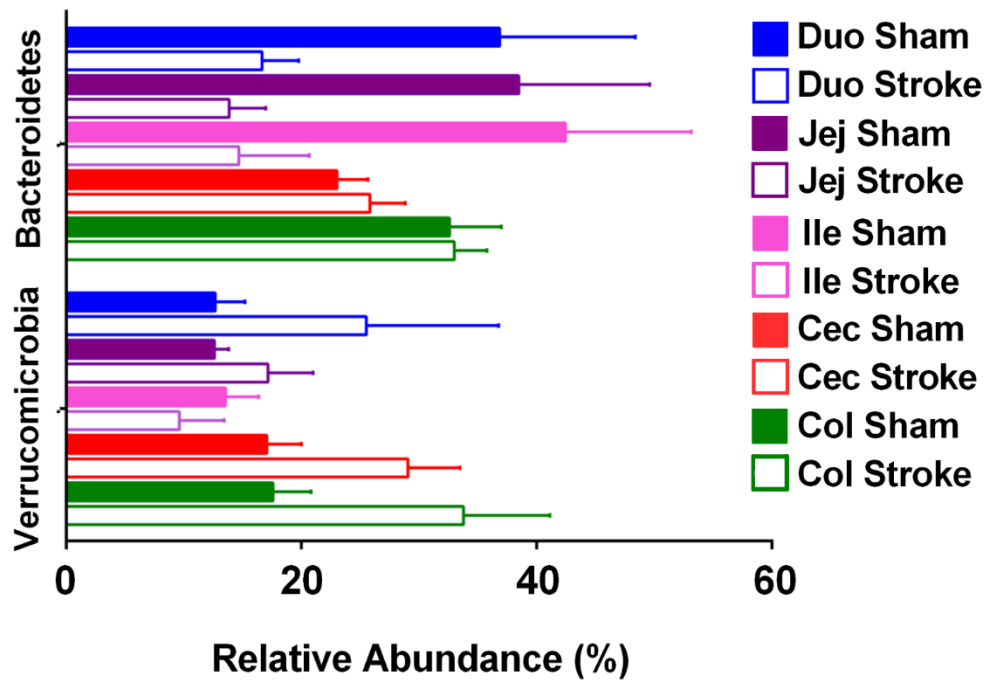
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22 **SUPPLEMENTARY FIGURES: 4**

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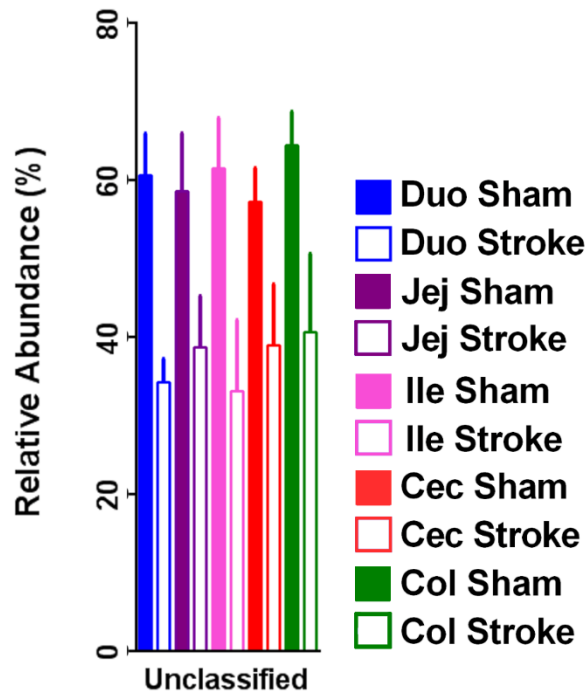
27 **Supplementary Figure 1:** Phylum Bacteroidetes was significantly decreased ($P=5.3E^{-3}$) and

28 Verrucomicrobia ($P=0.045$) were markedly increased in the intestinal mucosal samples

29 isolated from post-stroke mice as compared to sham-operated counterparts, consistently

30 across all 5 GIT sections. $n = 5$ per group.

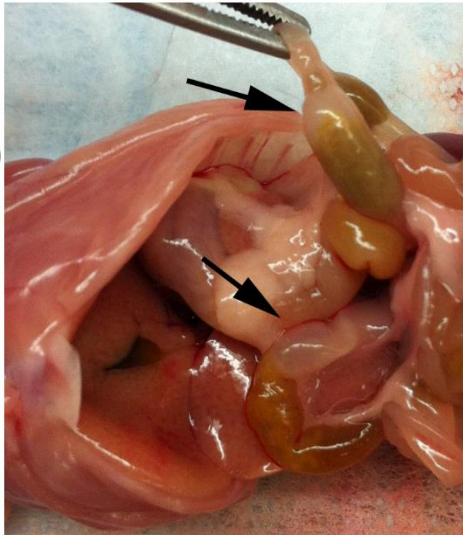
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33 **Supplementary Figure 2:** Genera Unclassified elevated significantly (ANOVA) across the
 34 GIT sections after stroke. GIT sections are abbreviated in labels: duodenum (Duo), jejunum
 35 (Jej), ileum (Ile), cecum (Cec), and colon (Col). $n = 5$ per group.

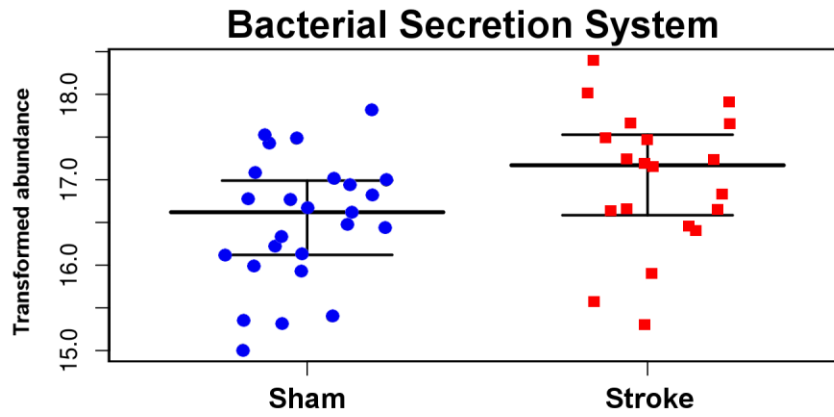
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38 **Supplementary Figure 3:** Representative image of the presence of multiple gas pockets,
39 denoted by black arrows, in the small intestine of post-stroke mice that were completely
40 absent in sham-operated counterparts.

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43 **Supplementary Figure 4:** KEGG level 3 *Bacterial Secretion System* category was
44 significantly ($P=0.042$) higher represented in stroke than in sham mucosa. Y axes represents
45 log₂ transformed functional category abundance.

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