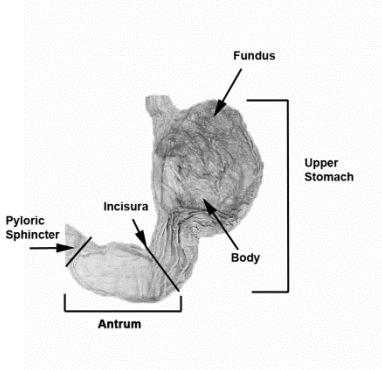
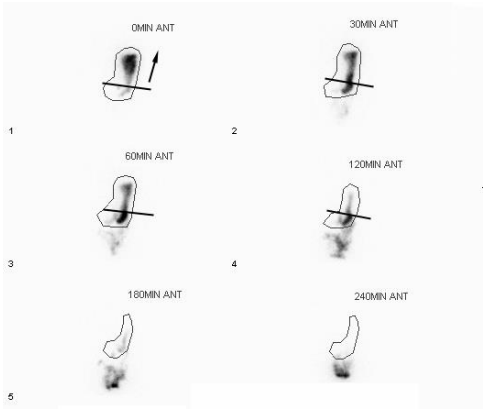
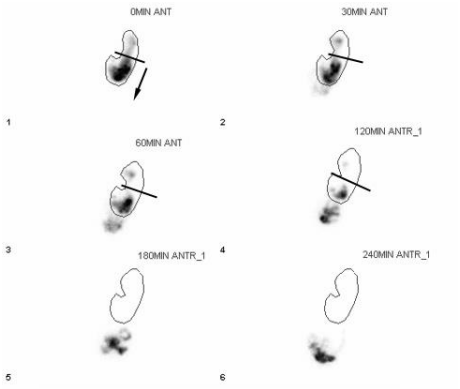
Supplemental Appendix A. Reader Training Interpretive Guide. The following were provided to train the readers how to visually assess fundic accommodation from routine solid-meal gastric emptying scintigraphy.



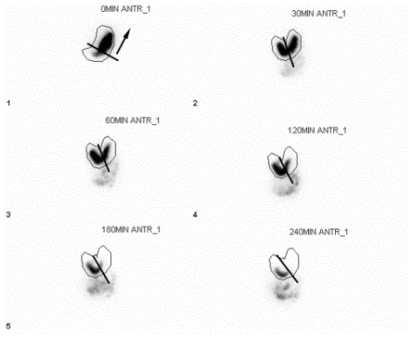
Supplemental Figure 1A: Anatomy. Anatomic and functional correlates used to define gastric regions of interest for fundic accommodation (FA). The proximal stomach includes the fundus to the acute angle of the incisura. After meal ingestion and initial FA of solids the majority of solids (> 50%) should appear in the upper stomach. For confirmation of upper from distal stomach, one should see progression of the solids past the incisura into the antrum in later gastric emptying images.



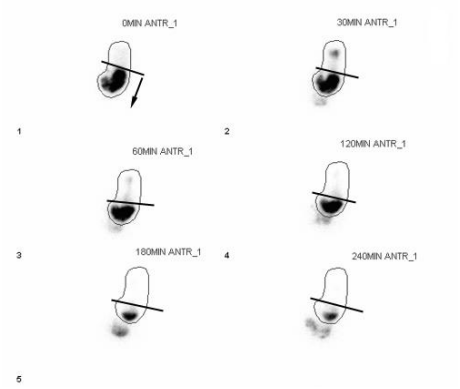
Supplemental Figure 2A: Normal accommodation with normal gastric emptying. Anterior views are shown to demonstrate normal FA with predominant (> 50%) visualization of the radiolabeled solids in the proximal stomach (arrow). The heavy straight line shows where the visualized lower level of the upper stomach is taken using the incisura as a reference. With increasing time (30 min, 60 min, and 120 min), the solids can be seen to progress distally into the antrum which is below the incisura. The thin black line is included to show the large region of interest drawn around the entire stomach used to calculate the total gastric emptying which was normal.



Supplemental Figure 3A: Impaired gastric accommodation with normal gastric emptying. The thin black line is the total gastric region of interest, the thick black line is visual reference to define the proximal stomach and the black arrow now demonstrates that > 50% of the solids are initially (t=0 min) in the distal stomach consistent with lack of normal FA. Measured total gastric emptying was normal.



Supplemental Figure 4A: Normal accommodation with delayed gastric emptying. The thin black line is total gastric region of interest, thick black line is visual reference to define the proximal stomach and the black arrow demonstrates normal FA with > 50% of the solids immediately (t=0 min) in the proximal stomach consistent with normal FA. There is normal progression of solids into the antrum but measured total gastric emptying; however, was delayed (70% retained at 2 hours and 18% at 4 hours).



Supplemental Figure 5A: Abnormal accommodation with delayed gastric emptying. The thin black line is total gastric region of interest, the thick black line is visual reference to define proximal stomach and the black arrow demonstrates abnormal FA with >50% of the solids initially (t=0 min) in the distal stomach consistent with abnormal FA response. There is persistent retention of solids in the antrum and measured total gastric emptying was delayed (80% retained at 2 hours and 22% at 4 hours).

Supplemental Appendix B. Description of computer software

The software developed to compute IMD combines and analyzes the gastric images from all time points and uses MatLab® (MathWorks®, Natick, Massachusetts), a licensed software development tool. There are four fundamental steps that the software takes to process the scintigraphic images. Step one is opening, selecting, and coregistering the images. Step two is finding the gastric region of interest (ROI) boundaries by thresholding and modifying boundaries manually if necessary. Step three is calculating the longitudinal axis and separating the whole-stomach region of interest (ROI) into separate sections. Finally, step four calculates the gastric counts in each region images obtained at the different times including options at: 0, 30, 60, 120, 180, 240 minutes.

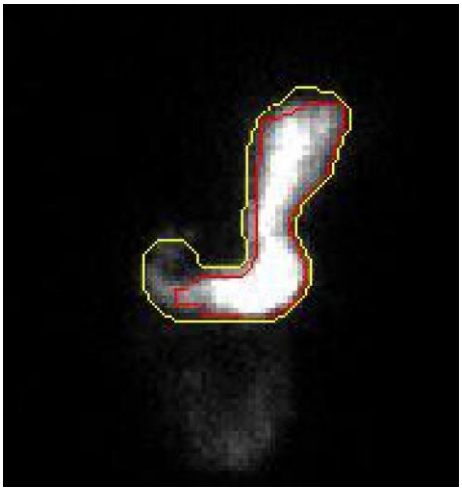
The first step is opening, selecting, and coregistering a composite image set for image alignment. The graphic user interface (GUI) displays all the study images on the screen. The user selects images and can rotate each image if the images are angled askew to optimize alignment. The user drags each image in succession to line up correctly with the 0-minute image. This ensures that the boundaries and regions drawn are positioned appropriately for all images in the set.

The second step defines the boundaries to determine the whole-stomach ROI. First, the software performs a first iteration of the boundaries of the stomach by finding the boundary around the portion of the stomach visible in each image. The software automatically creates a region of interest (ROI) around each individual image using a threshold of 0.25 based on the maximum gastric counts in each image. This can then be reviewed and adjusted for a best fit, if needed, using the graphic user interface (GUI). After creating these ROIs, the software smooths the edges to simplify the boundaries. The software then combines all images and ROIs to reconstruct a final total gastric ROI that contains all the gastric activity seen from time 0 to 4 hours (Figure 1B of Appendix B). The operator can manually modify the calculated boundary if needed by smoothing the edges, expanding it in all directions, or in specified locations, called "bumping" the boundary in the GUI.

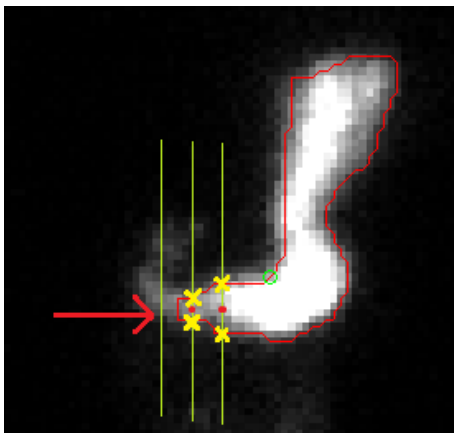
The third step calculates the longitudinal axis, and separates the whole-stomach ROI into equal halves. To produce the long axis, the software finds the two points on the stomach boundary which are most distal, and most proximal. Moving from the most distal point, the computer calculates the midpoints between the boundaries on the combined gastric image (Figure 2B of Appendix B). Using this method, the computer plots approximately fifty midpoints which are located close to the radial center of the stomach, from the most distal point to the most proximal point of the stomach. A best-fit third degree polynomial curve is calculated along these points forming the longitudinal axis. The stomach is divided by taking the midpoint of the longitudinal axis. The line used for separation is perpendicular to the longitudinal axis at its midpoint, dividing the stomach into two regions: a proximal region and a distal region (Figure 3B of Appendix B).

Step four is calculating the gastric counts in each region. The proximal and distal ROIs, are overlaid onto the original, aligned images at each time, and the number of counts in the proximal region and the number of counts in the distal region are obtained, for each image. The ratio of the gastric count in the proximal region to the total gastric count in the whole stomach ROI at the 0-minute image is defined as the intragastric meal distribution (IMD^0).

Supplemental Figure 1B. The software creates a region around each individual image (multiple colored ROIs) using thresholding, combines the images, then expands or contracts the boundaries with user input to create a single (white ROI) for the final composite image.

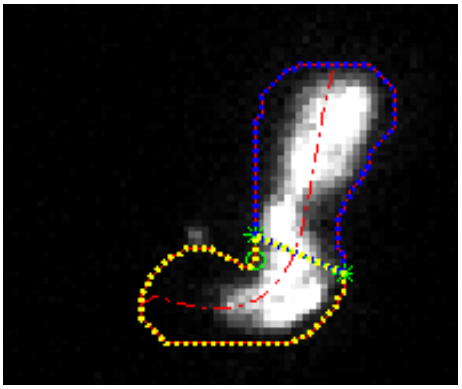


Supplemental Figure 2B. The computer software constructs the long axis by finding midpoints(red dots) between a line drawn between the gastric boundaries (x,x) on the composite image (Figure 1).



Supplemental Figure 3B. The software then computes the length of the long axis and draws a line perpendicular to the long axis (between green x-x) where the stomach is separated into two equal halves.

After the stomach is segmented into proximal and distal halves, the counts in each region are recorded and IMD calculated.



Supplemental Appendix C. Mixture Distribution Analysis Statistical Analysis Methods

Mixture distribution analysis is a numerically intense, probabilistic approach to estimate the "positivity" and its "reliability" or panel consistency of image readings based on a sample of patients' images by a group of expert readers, where independent verification of the imaging diagnosis does not exist. Agreement is considered in the context of one reader agreeing with a panel of readers rather than just another reader. Fundamental to this approach is that the 'true' reading is not known. Within this context, the reading made by a panel of readers is the best reading possible. Therefore, mixture distribution analysis assesses the positivity and its panel consistency (i.e., whether a large group of readers could make a positive or negative diagnosis consistently in a reproducible manner) rather than accuracy (i.e., whether a reader's diagnosis is correct as measured against a known truth or gold standard). For this approach, panel consistency is expressed as the relative percentage "correctly" or consistently diagnosed.

Specifically, images are conceptually categorized by how easy they are to read (i.e., easy or hard) and whether those images are disease-positive or disease-negative. Thus, images can be easy disease-positive, hard disease-positive, hard disease-negative, and easy disease-negative. Based on this categorization, Kundel and Polansky (14) utilize the following parameterization in the MDA analysis that is used to define the mixture distribution on images and readers: p_i is the proportion of images in each group in the target population, where

- p_1 is the proportion of easy disease-positive images,
- p_2 is the proportion of hard disease-positive and hard disease-negative images, and
- p_3 the proportion of easy disease-negative images.

Furthermore, m_i represents the probability of a large group of readers agreeing that the image is positive given the image is from group *i* corresponding to p_i. Intuitively, if 80% of the readers conclude that disease is present (i.e., $m_1 = 0.8$), then the image is classified as easy disease-positive; if 50% of the readers conclude that disease is present (i.e., $m_2 = 0.5$), then the image is classified as either hard disease-positive or hard disease-negative--in this case, note that there is no definitive "radiologic truth" because it is impossible to distinguish positive from negative; and if only 20% of the readers conclude that disease is present (i.e., $m_3 = 0.2$), then the image is classified as easy disease-negative since 80% of the readers conclude that the disease is absent. Thus, the probability that exactly *r* out of *n* readers will classify an image as positive assuming it is randomly selected from all the possible target images rather than specifically from one of the three groups (or if it is not known which group the image comes from) is:

$$\frac{n!}{r!\,(n-r)!}\sum_{i=1}^{3} p_i m_i r(1-m_i)^{n-r}$$

The likelihood function therefore can be written down based on a set of observed values of r among n readers for a random sample of images taken from the target population. The maximum likelihood estimates of the *m*'s and *p*'s and their 95% confidence intervals can then be found using the expected maximization (EM) algorithm. Furthermore, overall proportion correct (% of "correct" or consistent diagnosis) can be calculated as per Kundel, et. al.:

$$p_1 m_1 + p_2(1 - m_2) + p_3(1 - m_3)$$

Kappa analysis (23,24) was also employed to assess the agreement in assessments of fundic accommodation by any two readers at a time using the scoring 1=definitely abnormal accommodation, 2=probably abnormal accommodation, 3=possibly abnormal accommodation, 4=probably normal accommodation, and 5=definitely normal accommodation. We also simplified this approach by using the condensed scoring of abnormal/impaired/positive accommodation (scores 1, 2, 3) and normal/negative accommodation (scores 4, 5). Both weighted or simple Kappas and their 95% confidence intervals were reported for these two scoring methods. The average of all the pairwise Kappas provided some evidence on the strength of pairwise agreement the four readers evaluated the images.

Note that agreement and consistency refer to slightly different "concepts" here: agreement simply means how agreeable the FA assessments by any two different readers are; whereas consistency refers to the degree a group of readers reach their "correct" consensus under the framework of the Kundel's Mixture Distribution Analysis Approach (i.e., % correct). In essence, Kappa measures the pairwise agreement while Kundel's MDA yields information on panel consistency for the readers' scoring. Kappa is a well-known summary statistic while Kundel's concept is less known. Therefore, Kappa analyses have been used for making the main findings with consistency as a supplement.

Abnormal FA as defined by the expert panel consensus was then compared to computer-derived IMD data via the use of logistic regression and ROC analyses to estimate an optimal cutpoint of IMD for the purposes of diagnosing impaired FA. In these analyses, images that were classified as abnormal/impaired/positive by at least 3 out of the four readers were considered true positives; all others were considered true normal/negatives. Logistic regression model performance can be evaluated based on the area under the ROC curve, also known as the AUC or the c-statistic. The AUC or c-statistic is a measure of classification "accuracy" or "discrimination", that is, the ability of the model to correctly discriminate cases (i.e., positive reads) from non-cases (i.e., negative reads), or the predictive power of the model (25,26,27). Three approaches were used to identify an optimal cutpoint of IMD for classifying impaired/abnormal FA: 1) Maximum Youden's index J (i.e., max{Sensitivity + Specificity – 1}) (Table 2). Under this approach, the optimal cutpoint is at the point of the maximum vertical distance from the diagonal line to the ROC curve (28); 2) The closest-to-(0,1) criterion – The optimal cutpoint is defined as the point of the minimum distance from the ROC curve to the point where the diagnosis is perfect, i.e.,

sensitivity=1 and specificity=1 (the upper-left corner of the ROC plot) (min{sqrt((1-sensitivity)^2+(1-specificity)^2)}) (29); and 3) Sensitivity and Specificity Equality criterion (min{abs(Sensitivity - Specificity)}) – the optimal cutpoint is chosen to be at the point of minimum absolute difference between sensitivity and specificity under this criterion (30). As these approaches are all defined in terms of sensitivity and specificity, corresponding IMD cutpoints (i.e., % retention at time 0) associated with these optimal choices were calculated using the coefficients from the logistic regression model used to derive the ROC curve to facilitate impaired fundic accommodation diagnosis.

Table 1C of Supplemental Appendix C. Estimated proportion of images in each group (Mixing Proportions) and the probability that a large group of readers concludes "Positive" impaired fundic accommodation (Point Distributions) and CIs using Kundel's Mixture Distribution analysis (n=99 Test Subjects)†

	Mixing Proportions			Point Distributions			Proportion Correct
	p_1	p_2	p_3	m_1	m_2	m_3	
Mean	0.109	0.267	0.624	0.872	0.410	0.053	0.844
95% CI	(0.030, 0.223)	(0.067, 0.578)	(0.363, 0.753)	(0.602, 1.000)	(0.119, 0.734)	(0.000, 0.113)	(0.779, 0.894)

†Table entries are the means and 95% bootstrap confidence intervals calculated with the EM algorithm. CI = confidence interval.

Table 2C of Supplemental Appendix C. Optimal cutpoint for the IMD^0 at baseline by approach based on data from 99 test subjects$

Approach	*Optimal Cutpoint*	*Sensitivity*	*Specificity*	*No. of Correctly Predicted Events*	*No. of Correctly Predicted Nonevents*	*No. of Nonevents Predicted as Events*	*No. of Events Predicted as Nonevents*
Youden's Index J	0.568	0.867	0.917	13	77	7	2
The closest-to-(0,1)	0.568	0.867	0.917	13	77	7	2
Sensitivity and Specificity Equality	0.590	0.867	0.869	13	73	11	2

$Based on these analyses, the optimal cutpoint for the IMD^0 or % retention at time 0 is 0.568 since there is no obvious advantage with regard to sensitivity or specificity by selecting 0.590 as the cutpoint.

Appendix D. Results of IMD analysis in 177 patients in the NIH Gastroparesis Registry

Figure 1D of Supplemental Appendix D. Distribution of the IMD^0 for 177 patients of the NIH Gastroparesis Registry

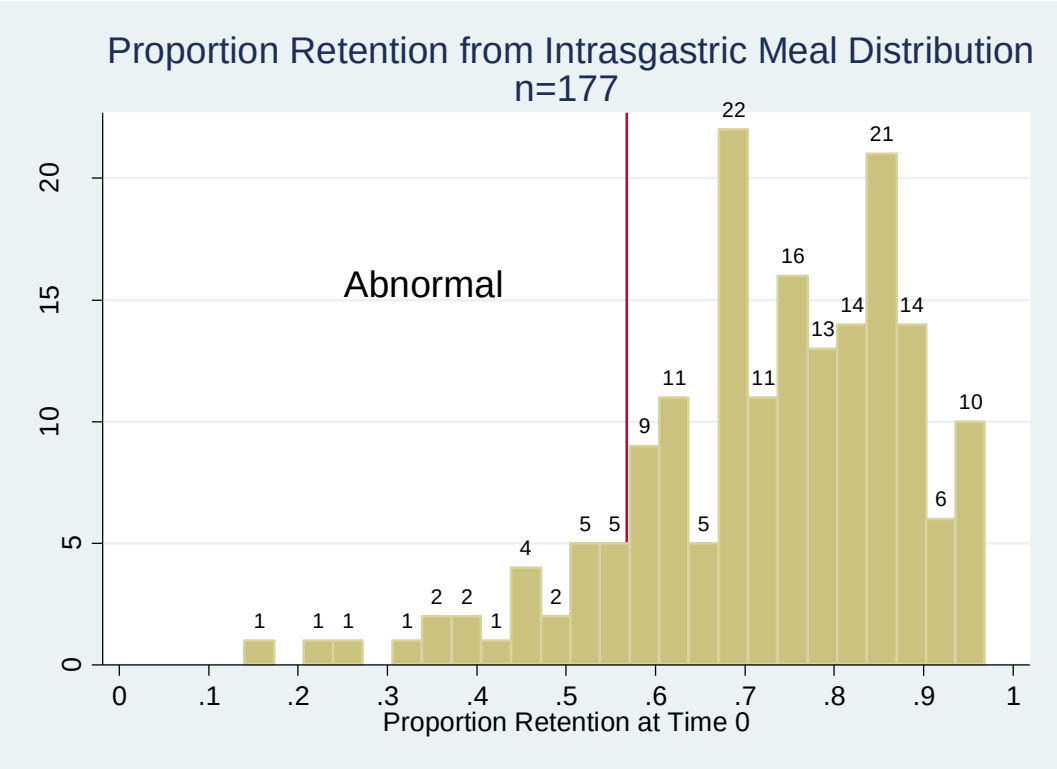


Table 1D of Supplemental Appendix D. Association of intragastric meal distribution status (normal vs. borderline vs. impaired) with characteristics of patients with gastroparesis at screening visit

	Intragastric Meal Distribution‡				
	Normal (n=132)	**Borderline* (n=20)**	**Impaired* (n=25)**	**Total (n=177)**	**p-value**
Demographics					
Age – yrs	42 (14)	45 (18)	47 (17)	43 (15)	0.10
Male gender	14%	0%	16%	13%	0.73
Anthropometric					
BMI – kg/m2	27 (7)	26 (8)	23 (6)	27 (7)	0.006
Weight change since Gp dx					0.06
Decrease	47%	50%	72%	51%	
Same	3%	10%	4%	4%	

Increase	50%	40%	24%	45%	
Weight change in past 6 mo					0.24
Decrease	42%	35%	56%	43%	
Same	26%	45%	16%	27%	
Increase	33%	20%	28%	31%	
Metabolic					
HbA1c - %	6.5 (1.9)	6.0 (1.7)	6.0 (1.6)	6.4 (1.8)	0.15
Gp characteristics					
Etiology					0.37
Diabetes	33%	25%	16%	30%	
Idiopathic	64%	75%	80%	67%	
Fundoplication	3%	0%	4%	3%	
Acute onset of symptoms	35%	40%	36%	36%	0.81
Initial infectious prodrome	23%	25%	12%	22%	0.27
Duration – yrs	6.6 (6.9)	4.3 (4.0)	8.7 (9.7)	6.7 (7.2)	0.42
Gp symptom severity - (0-5)	3.0 (0.6)	2.8 (0.5)	2.9 (0.5)	3.0 (0.5)	0.46
Gp severity - % severe	15%	10%	8%	14%	0.29
Predominant symptom					0.13
Nausea / vomiting	31%	50%	56%	37%	
Abdominal pain	23%	15%	12%	21%	
Other	45%	35%	32%	42%	
Co-morbidities					
Diabetes	39%	25%	16%	34%	0.01
Type I	58% (30/52)	40% (2/5)	50% (2/4)	56% (34/61)	0.56
Post Nissan Fundoplication	5%	0%	8%	5%	0.83
Gastric emptying					
Delayed Gastric Emptying†	77%	65%	64%	73%	0.13
1 hr solid gastric retention - %	78 (16)	75 (12)	67 (18)	76 (16)	0.001
2 hr solid gastric retention - %	58 (22)	57 (19)	43 (20)	56 (22)	0.002
4 hr solid gastric retention - %	26 (20)	21 (24)	18 (14)	24 (20)	0.05
1 hr liquid gastric retention - %	48 (17)	46 (14)	44 (21)	47 (17)	0.29
PAGI-SYM at screening visit					
GCSI					
Nausea (0-5)	3.2 (1.5)	3.1 (1.7)	3.5 (1.0)	3.2 (1.4)	0.39
Retching (0-5)	1.5 (1.7)	1.0 (1.2)	1.5 (1.5)	1.4 (1.6)	0.64
Vomiting (0-5)	1.5 (1.8)	0.6 (1.3)	1.5 (1.7)	1.4 (1.7)	0.49
Nausea subscore (0-15)	6.1 (4.1)	4.7 (3.5)	6.4 (3.1)	6.0 (3.9)	0.86
Stomach fullness (0-5)	3.6 (1.3)	4.0 (1.4)	3.9 (0.9)	3.7 (1.3)	0.19
Not able to finish meal (0-5)	3.4 (1.5)	3.8 (1.7)	4.1 (1.0)	3.5 (1.5)	0.02
Feeling excessively full (0-5)	3.8 (1.3)	3.8 (1.6)	4.1 (1.0)	3.8 (1.3)	0.34
Loss of appetite (0-5)	2.8 (1.5)	2.7 (1.8)	3.0 (1.2)	2.8 (1.5)	0.53
Fullness subscore (0-20)	13.6 (4.6)	14.3 (5.6)	15.1 (3.1)	13.9 (4.6)	0.12
Bloating (0-5)	3.2 (1.6)	3.7 (1.5)	3.7 (1.2)	3.3 (1.5)	0.10

Stomach visibly larger (0-5)	2.9 (1.8)	3.4 (2.0)	3.3 (1.4)	3.0 (1.7)	0.16
Bloating subscore (0-10)	6.1 (3.2)	7.1 (3.4)	7.0 (2.4)	6.3 (3.1)	0.11
Total score (0-45)	25.8 (9.1)	26.1 (10.9)	28.5 (6.2)	26.2 (9.0)	0.20
Upper abdominal pain (0-10)	6.0 (2.9)	5.4 (3.5)	5.9 (2.6)	5.9 (2.9)	0.68
Lower abdominal pain (0-10)	3.9 (3.2)	4.2 (3.5)	4.7 (2.6)	4.1 (3.1)	0.28
GERD (0-35)	11.9 (9.6)	10.8 (9.3)	14.6 (7.6)	12.2 (9.3)	0.31
Constipation (0-5)	2.8 (1.7)	2.6 (2.0)	2.9 (1.5)	2.8 (1.7)	0.86
Diarrhea (0-5)	1.6 (1.6)	1.4 (1.7)	1.5 (1.8)	1.6 (1.6)	0.63
Satiety testing					
Water (mL)	368 (199)	313 (112)	413 (248)	368 (200)	0.53
Nutrient bar - % consumed	88 (22)	91 (16)	87 (23)	88 (22)	0.90
Medication use					
Prokinetics	30%	45%	20%	30%	0.66
Narcotics	33%	25%	28%	32%	0.48
Source of nutrition					0.34
Enteral	2%	0%	0%	2%	
Parenteral	0%	0%	0%	0%	
Oral	98%	100%	100%	98%	
Treatments					
Botox	25%	35%	44%	29%	0.04
G tube	2%	0%	0%	2%	0.34
J Tube	2%	0%	0%	2%	0.34
Central line	2%	0%	0%	2%	0.34
Gastric stimulator	8%	15%	0%	8%	0.33

‡Table entry = mean (SD) or %.

*Normal, borderline, and impaired intragastric meal distribution defined as (proximal counts / total time-0 ROI counts) at baseline at Gastric Emptying 0 min from >0.642, 0.568 to 0.642, and <0.568, respectively.

†Delayed Gastric Emptying defined as gastric retention >60% at 2 hours or >10% at 4 hours.

Appendix E. Relationships of gastric emptying and water load testing to symptoms.

Table 1E of Supplemental Appendix E. Association of Gastric Retention at 4 hours with PAGI-SYM items (n=172)†

	Classification Based on Gastric retention at 4 hours‡			
PAGI-SYM items	**Very Abnormal >35% (n=43)**	**Moderately Abnormal >10-35% (n=80)**	**Normal ≤10% (n=49)**	**p-value***
GCSI				
Nausea (0-5)	3.4 (1.6)	3.1 (1.5)	3.2 (1.3)	0.57
Retching (0-5)	1.5 (1.8)	1.5 (1.6)	1.2 (1.6)	0.43
Vomiting (0-5)	1.9 (2.0)	1.3 (1.7)	1.1 (1.5)	0.03
Nausea subscore (0-15)	6.8 (4.3)	5.9 (3.9)	5.5 (3.5)	0.13
Stomach fullness (0-5)	3.8 (1.4)	3.6 (1.2)	3.7 (1.2)	0.80
Not able to finish meal (0-5)	3.5 (1.6)	3.5 (1.5)	3.5 (1.4)	1.00
Feeling excessively full (0-5)	4.0 (1.4)	3.8 (1.3)	3.8 (1.3)	0.58
Loss of appetite (0-5)	3.0 (1.4)	2.7 (1.5)	2.8 (1.5)	0.63
Fullness subscore (0-20)	14.2 (5.0)	13.5 (4.5)	13.8 (4.5)	0.71
Bloating (0-5)	3.5 (1.7)	3.1 (1.6)	3.4 (1.4)	0.85
Stomach visibly larger (0-5)	3.1 (1.8)	2.9 (1.6)	3.1 (1.8)	0.95
Bloating subscore (0-10)	6.6 (3.3)	6.1 (3.0)	6.5 (3.1)	0.90
Total score (0-45)	27.6 (9.8)	25.5 (9.2)	25.9 (8.2)	0.37
Upper abdominal pain (0-10)	6.3 (3.1)	5.5 (2.8)	5.9 (3.0)	0.53
Lower abdominal pain (0-10)	4.2 (3.4)	4.0 (3.0)	4.0 (3.2)	0.86
GERD (0-35)	13.1 (9.2)	11.7 (9.6)	11.5 (9.0)	0.43
Constipation (0-5)	3.3(1.7)	2.5 (1.7)	2.8 (1.7)	0.19
Diarrhea (0-5)	1.4 (1.7)	1.6 (1.7)	1.4 (1.5)	0.99

*Based on linear regression of each PAGI-SYM item on ordered classification categories of gastric retention at 4 hours.

†5 patients missing gastric retention at 4 hours data.

‡Table entry = mean (SD) severity of the PAGI-SYM item.

Table 2E of Supplemental Appendix E. Association of Satiety Water Load with PAGI-SYM items (n=173)†

	Classification Based on Satiety Water Load‡			
PAGI-SYM items	**Very Abnormal ≤ 240 mL (n=51)**	**Moderately Abnormal 241-500 mL (n=94)**	**Normal 501+ mL (n=28)**	**p-value***
GCSI				
Nausea (0-5)	3.5 (1.4)	3.1 (1.5)	2.9 (1.4)	0.05
Retching (0-5)	1.4 (1.6)	1.3 (1.7)	1.6 (1.6)	0.71
Vomiting (0-5)	1.6 (1.7)	1.3 (1.7)	1.4 (1.7)	0.43
Nausea subscore (0-15)	6.6 (3.8)	5.7 (4.0)	5.9 (3.9)	0.37
Stomach fullness (0-5)	3.7 (1.2)	3.7 (1.3)	3.5 (1.1)	0.75
Not able to finish meal (0-5)	3.7 (1.4)	3.6 (1.5)	3.2 (1.7)	0.23
Feeling excessively full (0-5)	3.9 (1.3)	3.9 (1.3)	3.6 (1.4)	0.31
Loss of appetite (0-5)	3.2 (1.4)	2.6 (1.5)	2.7 (1.5)	0.06
Fullness subscore (0-20)	14.5 (4.7)	13.8 (4.5)	13.0 (5.0)	0.17
Bloating (0-5)	3.4 (1.6)	3.3 (1.5)	3.1 (1.4)	0.42
Stomach visibly larger (0-5)	3.1 (1.7)	3.0 (1.8)	2.8 (1.7)	0.35
Bloating subscore (0-10)	6.5 (3.2)	6.3 (3.2)	5.8 (2.9)	0.36
Total score (0-45)	27.6 (8.7)	25.8 (9.1)	24.8 (9.5)	0.16
Upper abdominal pain (0-10)	6.5 (2.8)	5.6 (3.0)	5.5 (2.8)	0.09
Lower abdominal pain (0-10)	5.4 (2.9)	3.9 (3.1)	2.4 (2.9)	<0.0001
GERD (0-35)	12.9 (9.8)	11.4 (.1)	13.2 (9.2)	0.89
Constipation (0-5)	3.0 (1.6)	2.7 (1.8)	2.5 (1.8)	0.17
Diarrhea (0-5)	2.1 (1.6)	1.3 (1.6)	1.2 (1.7)	0.01

*Based on linear regression of each PAGI-SYM item on ordered classification categories of satiety water load.
†4 patients missing satiety water load data.
‡Table entry = mean (SD) severity of the PAGI-SYM item.