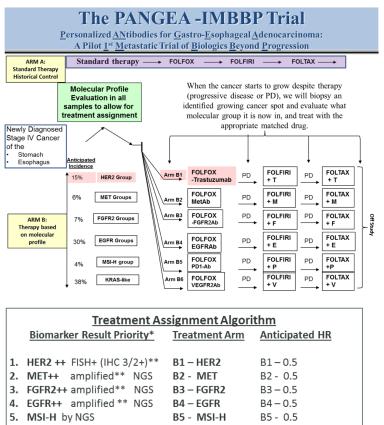
Supplementary Figures

- Fig S1. PANGEA trial design (S2A) and treatment algorithm (S2B).
- **Fig. S2.** Serial ctDNA *EGFR* copy number versus serum tumor marker while on therapy for patients 1-4
- **Fig. S3.** "Genogram" figures by each treated patient indicating features of each case at baseline with low values at the center and high values towards the periphery. These factors serve as a framework to assisting in predicting favorable response to therapy, in addition to classical prognostic features including age, histopathology, tumor burden, comorbidities, etc. See also Figure 4G. Duration of therapy (Also see table S3): Pt 1, 43 weeks; Pt 2, 42 weeks; Pt 4, 14 weeks; Pt 5, 17 weeks; Pt 6, 6 weeks (censored); Pt 7, 43 weeks.

Figure S1. PANGEA trial design (Figure S1A) and treatment algorithm (Figure S1B).



<u>Treatment Assignment Algorithm</u>			
	Biomarker Result Priority*	Treatment Arm	Anticipated HR
1.	HER2 ++ FISH+ (IHC 3/2+)**	B1 – HER2	B1 - 0.5
2.	MET++ amplified** NGS	B2 - MET	B2 - 0.5
3.	FGFR2++ amplified** NGS	B3 – FGFR2	B3 - 0.5
4.	EGFR++ amplified ** NGS	B4 – EGFR	B4 - 0.5
5.	MSI-H by NGS	B5 - MSI-H	B5 - 0.5
6.	VEGFR2++ by NGS	B6 – VEGFR2	B6 - 0.75
	 KDR/VEGFA amplified 		
	- KRAS amplified		
	- KRAS mutant		
	- RAF mutant		
	- MEK/ERK mutant		
	- PIK3CA mutant		
	- PTEN/mTOR/AKT mutant		
	- RAS/PIK3CA/AKT alteration		
7.	All negative, EGFR+ by MS	B4 - EGFR	B4 - 0.75
8.	All negative, VEGFR2+	B6 – VEGR2	<u>B6 – 0.75</u>
			Aggregate HR = 0.67
*Proceed to subsequent line if previous is negative.			
** Prioritize by highest Gene/Control ratio.			

Catenacci et al. Towards personalized treatment for gastroesophageal adenocarcinoma: Strategies to address inter- and intra- patient tumor heterogeneity – PANGEA. J Clin Oncol 32, 2014 (suppl 3; abstr 66)

Figure S2. Serial ctDNA *EGFR* copy number versus serum tumor marker while on therapy for patients 1-4

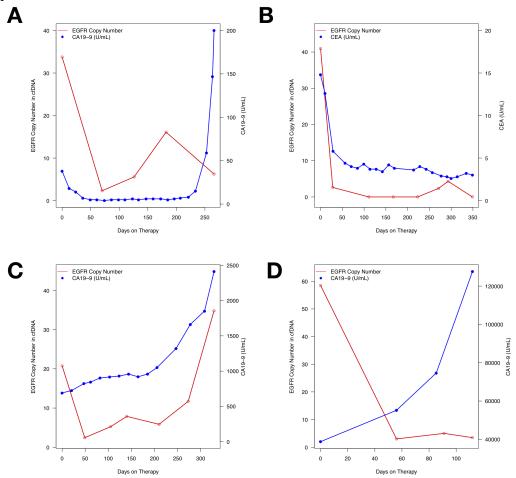


Figure S3. "Genogram" by patient.

