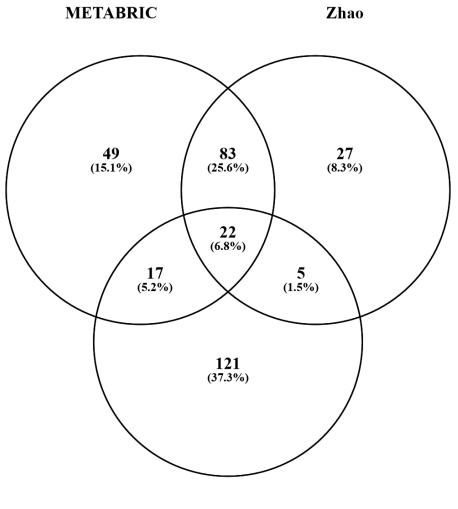
## Replicated RNA/cell lineage associated with nodal metastasis: Total Population

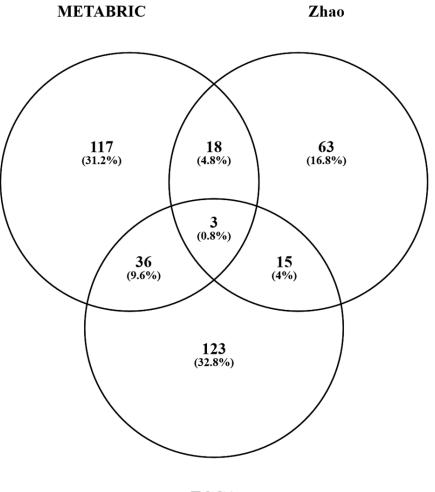


**TCGA** 

Table 1: Effect of data set upon nodal metastasis status

Data Set	<b>METABRIC</b>	(N=772)	χ2	ZHAO	(N=927)	χ2	TCGA	(N=650)	χ2
Nodal Metastases	None	Any		None	Any		None	Any	
	389 (50.4%)	383 (49.6%)		620 (66.9%)	307 (33.1%)		293 (45.1%)	357 (54.9%)	
Broad breast subtype*		(	0.05			0.013			0.06
- Her2	41 (10.5%)	61 (16.0%)		68 (13.9%)	53 (20.3%)		9 ( 3.4%)	21 (6.3%)	
- Luminal	258 (66.3%)	247 (64.8%)		299 (61.0%)	162 (62.1%)		212 (80.3%)	276 (82.6%)	
- TNBC	90 (23.1%)	73 (19.2%)		123 (25.1%)	46 (17.6%)		43 (16.3%)	37 (11.1%)	
* Category includes missing observations									

Replicated RNA/cell lineage associated with nodal metastasis: Luminal tumors only



**TCGA** 

Replicated RNA/cell lineage associated with nodal metastasis: TNBC tumors only

