Activating HER2 mutations in HER2 gene amplification negative breast cancer

Supplementary Table 1. Previously published studies reporting HER2 somatic mutations in breast cancer. L755S was observed in two patients in the Lee et al. 2006 (1) study, as indicated by the parentheses. Similarly, S310F was observed in two patients in the Banerji et al. 2012 study (2). The sequencing methods employed in each used are as follows: Lee et al.2006 (1) – Sanger sequencing of ERBB2, Shah et al.2009 (3) – whole genome/exome sequencing on 1 patient followed by focused sequencing on 192 additional patients, Kan et al.2010 (4) – mismatch repair detection sequencing of 1,507 candidate genes in 156 breast cancer patients, Shah et al. 2012 (5), Stephens et al 2012 (6) and Banerji et al 2012 (2) – exome/whole genome sequencing of the indicated number of patients.

Publication	Number of HER2 mutations	Number of patients screened	Mutations identified	Notes
Lee et al. 2006 (1)	4	94	L755S (2), R896C, del.755-759+S760A	Korean patient population
Shah et al. 2009 (3)	4 (3 in lobular breast cancer)	193 (113 are lobular breast cancer)	I767M, L755S, D769Y, del.755-759	
Kan et al. 2010 (4)	2	156	G309E – found in a HER2+ patient V777L – found in a hormone receptor+ patient	
Shah et al. 2012 (5)	2 (both cases were Triple Negative)	104	S310F+L755S - two mutar patient Y835F	tions present in 1
Stephens et al. 2012 (6)	1 (this case was ER-, HER2-)	100	P780-Y781insertionGSP	
Banerji et al., 2012 (2)	3	108	S310F (2) – both patients a ER+, lobular breast cance triple negative breast can G1201V – found in a HER2	er. The other is a cer.

Additional sequencing studies utilized here include: 1) Ellis et al., 2012 (7), which performed whole genome/exome sequencing on 77 patients and focused sequencing on 160 additional patients and 2) TCGA Breast Cancer project (8), which performed exome sequencing on 507 patients, 39 of whom had lobular breast cancer. Thus a total of 1,499 patients under genome or focused gene sequencing among these 8 studies.

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