

Table S 2.
Summary of FISH, *in situ*, and methylation data for SYK in tumor epithelium.

Slide name	% DCIS	DCIS Allelic Loss ¹	Benign	DCIS	IDC	Benign	DCIS	IDC	Benign	DCIS	IDC
SYK In situ² SYK Methylation³ Syk Protein⁴											
DCIS ONLY											
38											
8081	100	1.1		2.0			4.0			137.2	
38											
07405	100	1.1	2.0	2.0			7.3		194.0	273.1⁵	
38											
2194	100	0.9	3.0	2.0			N.D.		195.4	196.9	
38											
06830	100	0.8	3.0	3.0			N.D.		93.4	123.7	
38											
06768	100	0.7	3.0			5.8	9.3⁶		206.9		
38											
10095	100	1.0	3.0	2.0			10.3		173.3	208.8	
38											
1855	100	0.9	3.0	2.0			9.8		145.1	80.3	
38											
4205	100	0.9		0.0			9.1		202.5	192.3	
DCIS with IDC											
39											
7038	60	0.9	3.0		0.0		N.D.		N.D.		
36											
2059		0.9	3.0	2.0	2.5		N.D.	3.9	N.D.		
38											
02422	70	0.9		0.0	0.0		9.7	3.4	281.0	224.1	174.7
36											
10462		0.9	1.0	3.0	2.0		10.7	5.0	N.D.		
39											
04168	70	0.8		2.0			4.3		N.D.	246.0	
38											
10443	50	0.8	3.0	0.0			11.2		N.D.		
39											
06013	98	0.5⁷ 	3.0	3.0			7.0		421.5	214.5	
38											
11203	70	0.6	3.0	2.0	0.0		2.2			308.3	350.0
39											
08204	70	0.3	3.0	2.0			5.3	13.5	279.6	253.8	174.8
39											
07489	50	0.6		2.0	0.0		4.5	11.1		121.3	150.6
36											
6362		0.5	3.0	2.5	2.5			7.7		216.5	168.8

<u>Benign ONLY</u>						
35	870	benign	0.8	3.5	6.0	47.6
35						
4850		benign	0.8	3.5	1.7	118.8
36						
11964		benign	0.7	3.0	7.3	
36						
10605		benign	0.8	3.0		
36						
3757		benign	0.7			

¹ Ratio of Syk/ Chromosome 9 Centromere marker, Average of 30 cells, cut off of 0.6

² from Moroni et al., (2004) Progressive loss of Syk and abnormal proliferation in breast cancer cells. Cancer Res 64: 7346-7354.

³ Pyrosequencing, result is average of 4 CpG's, cut off above normal breast control + 1 S.D.

⁴ Immunofluorescence staining for epithelial Syk, average intensity (bold is P < 0.05 for adjacent value).

⁵ Bold indicates protein staining intensity significantly different from tissue to left, P < 0.05.

⁶ Bold indicates methylation value in the positive range (see *Methods*).

⁷ Bold indicates allelic loss (see *Methods*).