Table S7 Gene expression analysis for putative functional SNPs using 1,006 breast tumor samples in TCGA

SNP ID	Gene	Effect Allele	Ref Allele	Beta [a]	P-value
Signal 1					
rs812020	PTHLH	A	C	0.03	0.65
rs812020	CCDC91	A	C	0.06	0.27
Signal 2					
rs788463	PTHLH	A	T	0.04	0.69
rs10843066	PTHLH	T	C	0.07	0.41
rs788463	CCDC91	A	T	0.01	0.88
rs10843066	CCDC91	T	C	0.03	0.70
Signal 3					
rs10843110	PTHLH	T	G	0.13	0.02
rs56318627	PTHLH	C	T	0.15	0.01
rs11049453	PTHLH	G	A	0.15	0.01
rs10843110	CCDC91	T	G	-0.11	0.08
rs56318627	CCDC91	C	T	-0.11	0.07
rs11049453	CCDC91	G	A	-0.13	0.03

[a] The regression coefficient for each SNP estimated in the residual linear regression.