Supplemental Data

Supplemental Table 1. NF-κB consensus sequence in genes overexpressed in NOS2 high ER- breast tumors.

Gene symbol	Fold change[A]	Location[B]	Strand[C]	Gene name	Basal-like signature gene[D]
KRT6A	42.1	548	-	Keratin 6A	yes
KRT6C	42.1	548	-	Keratin 6C	yes
FLJ21511	12.2	172	+	Hypothetical protein FLJ21511	no
		687	+		
IL8	6.8	477	+	Interleukin 8	no
		477	-		
S100A8	5.0	1091	-	S100 calcium binding protein A8	yes
		1107	-		
		1108	+		
		1228	+		
		1228	-		
CDH3	4.3	652	+	P-cadherin	yes
		1639	-		
SLC7A5	4.2	11	-	Solute carrier family 7, member 5	no
		11	+		
		71	+		
		123	+		
		360	-		
		360	+		
C16ORF60	4.1	425	-	Chromosome 16 open reading frame 60	no
		614	+		
ANXA8	3.9	378	+	Annexin A8	yes
		453	-		
		639	+		
SLC6A8	3.9	10	-	Solute carrier family 6, member 8	no
		59	+		
		213	-		
		214	+		
		735	+		
		961	-		

		1107	+		
		1107	-		
TRIM29	3.8	233	-	Tripartite motif-containing 29	yes
		405	-		
KLF5	3.4	39	-	Kruppel-like factor 5	yes
GGH	3.2	487	+	Gamma-glutamyl hydrolase	
		612	+		
KLK8	3.2	562	+	Kallikrein 8	yes
		562	-		
		858	-		
		1042	-		
		1043	+		
		1074	+		
CYP39A1	3.1	73	+	Cytochrome P450, family 39, subfamily A, polypeptide 1	yes
		722	+		
		722	-		
		954	-		
		954	+		
SRD5A1	2.9	214	+	Steroid-5-alpha-reductase, alpha polypeptide 1	yes
		277	+		
		609	-		
HMGB3	2.8	126	+	High-mobility group box 3	no
		344	+		
SFN	2.8	33	+	Stratifin	yes
		33	-		
PTPLB	2.6	92	-	Protein tyrosine phosphatase-like, member b	yes
		437	-		
		437	+		
CD59	2.4	270	+	CD59 molecule	yes
		431	+		
WNT5A	2.4	395	-	Wingless-type MMTV integration site family, member 5A	no

		782	-		
RPE	2.3	454	+	Ribulose-5-phosphate-3-epimerase	no
ASS	2.3	169	+	Arginosuccinate synthetase	no
		169	-		
SLC35A2	2.1	656	-	Solute carrier family 35, member A2	no
TPI1	2.0	263	+	Triosephosphate isomerase 1	no
		359	+		
HCCS	2.0	28	-	Holocytochrome c synthase	yes
		195	-		
		470	-		
ENO1	2.0	590	-	Enolase 1	no
CD44	2.0	891	+	CD44 molecule	yes
		969	+		
CALU	1.9	379	-	Calumenin	no
		655	+		
MRPL3	1.8	637	-	Mitochondrial ribosomal protein L3	no
		638	+		
PPP1CB	1.7	411	+	Protein phosphatase 1, catalytic subunit, beta isoform	no
		438	+		
		438	-		

[A] Fold change in High vs. Low Expressing NOS2 Tumors (Glynn et al, JCI 2010).

[B] Base pairs from TSS.

[C] Sense (+) or anti-sense (-) DNA strand.

[D] Previously published basal-like signature genes (from Glynn et al, JCI 2010).