Table S2. Relative expression of potential interacting genes in 5-week-old mammary glands

Gene	TEBs versus stroma			Ducts versus stroma		
	Overall signal (mean±s.d.)	Ratio (mean±s.d.)	P	Overall signal (mean±s.d.)	Ratio (mean±s.d.)	P
Adam9	1053±428	0.49±0.08	<0.0005	3102±2099	0.93±0.08	NS
Adam10	1968±812	1.42±0.36	0.052	2793±642	2.27±0.29	<0.0005
Adam10	544±129	1.62±0.42	0.016	788±255	1.47±0.24	0.010
Adam12	806±267	0.91±0.26	NS	656±175	0.73±0.16	0.041
Adam15	1140±311	1.09±0.19	NS	1194±470	1.06±0.11	NS
Adam17	1465±419	0.92±0.16	NS	1992±405	1.04±0.14	NS
Adam19	1104±276	1.35±1.07	<0.0005	1257±360	1.07±0.11	NS
Adam33	397±95	0.70±1.23	0.020	511±64	1.01±0.06	NS
Areg	873±300	12.96±3.92	<0.0001	836±380	10.23±4.28	0.003
Btc	336±78	1.28±0.33	NS	360±62	1.35±0.28	0.045
Hbegf	214±28	1.09±0.06	0.028	226±31	1.03±0.06	NS
Egf	237±39	0.98±0.08	NS	268 ±30	0.96±0.11	NS
Epgn	232±42	1.15±0.20	NS	291±103	0.99±0.04	NS
Ereg	226±44	1.09±0.17	NS	330±47	1.05±0.12	NS
Tgfa	325±43	1.80±0.38	0.004	306±47	1.24±0.26	NS
Nrg3	227±47	1.08±0.04	0.015	240±50	1.01±0.03	NS
Nrg4	1761±568	0.29±0.05	0.0001	3458±995	0.58±0.06	<0.0005
Tnf	275±65	1.18±0.16	0.055	269±37	1.00±0.12	NS
Egfr	1553±623	1.09±0.31	NS	2337±662	1.29±0.37	NS
Erbb4	260±34	1.02±0.09	NS	276±41	1.29±0.33	NS
Timp1	1313±321	7.09±2.13	0.0001	815±198	1.52±0.54	NS
Timp2	1506±974	0.99±0.18	NS	3711±2266	1.10±0.23	NS
Timp3	2316±448	0.34±0.06	0.0001	4645±983	1.09±0.15	NS
Timp4	418±86	0.55±0.09	0.001	516±158	0.65±0.09	0.003
Krt1-14	681±137	2.88±0.56	<0.0005	1558±379	7.27±2.47	<0.0005
Krt1-18	2805±1038	37.51±9.07	<0.0001	3903±1985	33.67±12.36	<0.0005
Ucp1	14454±2890	0.09±0.02	<0.0001	35010±16238	0.33±0.18	0.02
Hprt1	1561±723	1.00±0.13	NS	3237±2038	1.04±0.06	NS

Values represent normalized arithmetic means and standard deviations obtained after converting the mean overall signal intensities $A = 0.5[\log_2(Cy5) + \log_2(Cy3)]$ and expression ratios $M = \log_2(Cy5/Cy3)$ for each of six independent arrays to linear values. Ratios greater than 1 represent relative enrichment in the epithelial compartment, whereas ratios less than 1 indicate stromal enrichment. P values for rejecting the hypothesis that the mean expression ratio = 1 were corrected to control for the false discovery rate over the entire array (Benjamini and Hochberg, 1995). Mean overall signals of less than 256 (A=8) were difficult to distinguish from background. *Krt1-14* (keratin 14, a myoepithelial cell marker), *Krt1-18* (keratin 18, a luminal epithelial cell marker), *Ucp1* (uncoupling protein 1, an adipocyte marker) and *Hprt1* (hypoxanthine guanine phosphoribosyl transferase 1, a housekeeping gene) are included as controls. NS, not significant.