

**Supplementary Table 1** Significantly differentially expressed probesets (61 genes) in breast tissue in the DER group identified by SAM analysis with an FDR of 0.38. FC is the average fold change before and after DER for the 10 participants. P val is the unadjusted p value for the pairwise comparison using SAM. <sup>1</sup>Number of probesets expressed (called 'present') out of 6 arrays (3 before and 3 after) in breast epithelium and whole breast tissue in this study. <sup>2</sup>Number of probesets expressed out of 10 arrays in breast ducts and lobules of the study by Turashvili et al (38) and the value in brackets is the median expression level using MAS normalisation (37).

Gene Symbol	Gene title	Affymetrix Probe ID	FC	P val	Expressed whole tissue <sup>1</sup>	Expressed breast LCM <sup>1</sup>	Expressed in ducts <sup>2</sup>	Expressed in lobules <sup>2</sup>
SCD	stearoyl-CoA desaturase	211708_s_at	-16.7	0.0003	6(12635)	5(404)	1(51)	1(32)
SCD	stearoyl-CoA desaturase	211162_x_at	-8.3	0.0000	6(6961)	4(354)	1(32)	0(29)
SCD	stearoyl-CoA desaturase	200831_s_at	-4.2	0.0000	6(6404)	5(437)	1(488)	2(557)
FADS1	fatty acid desaturase 1	208963_x_at	-3.8	0.0001	6(1137)	3(104)	3(215)	4(100)
FADS1	fatty acid desaturase 1	208964_s_at	-3.7	0.0002	5(128)	2(74)	7(547)	3(355)
TF	transferrin	214063_s_at	-2.3	0.0025	6(2990)	6(2507)	9(1637)	9(877)
ALDOC	aldolase C, fructose-bisphosphate	202022_at	-2.3	0.0007	6(797)	4(183)	8(912)	5(624)
LOC389393	NA	222278_at	-2.1	0.0012	6(842)	0(5)	1(20)	2(44)
NID2	nidogen 2 (osteonidogen)	204114_at	-2.0	0.0031	6(1034)	5(186)	9(1188)	6(416)
TMEM135	Transmembrane protein 135	222209_s_at	-2.0	0.0031	6(970)	6(230)	8(796)	7(599)
MCART1	mitochondrial carrier triple repeat 1	238574_at	-1.9	0.0005	6(199)	5(156)	6(470)	4(173)
HK2	hexokinase 2	202934_at	-1.9	0.0015	6(6248)	6(1263)	4(237)	2(278)
THBS4	thrombospondin 4	204776_at	-1.8	0.0002	6(2256)	2(232)	10(992)	8(723)
CD164	CD164 antigen, sialomucin	208653_s_at	-1.8	0.0005	6(2033)	6(1054)	10(919)	9(1025)
C1orf97	chromosome 1 ORF 97	224444_s_at	-1.8	0.0005	4(292)	3(235)	3(146)	0(130)
ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	214033_at	-1.8	0.0004	6(323)	0(34)	2(170)	6(446)
LOXL2	lysyl oxidase-like 2	202998_s_at	-1.8	0.0028	6(748)	6(714)	8(691)	5(392)
ACACA	acetyl-Coenzyme A carboxylase $\alpha$	212186_at	-1.8	0.0003	6(966)	6(1003)	9(1781)	9(1974)
SCD	stearoyl-CoA desaturase	223839_s_at	-1.8	0.0002	6(18384)	6(2475)	6(273)	9(400)
CD164	CD164 antigen, sialomucin	208654_s_at	-1.7	0.0023	6(12491)	6(9708)	10(2547)	10(3016)
SYBL1	synaptobrevin-like 1	202829_s_at	-1.7	0.0010	6(2113)	6(1886)	10(1079)	10(1550)
SCD	stearoyl-CoA desaturase	200832_s_at	-1.7	0.0003	6(14838)	6(1432)	10(2726)	10(3313)
MME	membrane metallo-endopeptidase	203435_s_at	-1.6	0.0023	6(2714)	6(2075)	7(1197)	6(1139)
ACOX1	acyl-Co A oxidase 1, palmitoyl	209600_s_at	-1.6	0.0021	6(7880)	6(3159)	8(752)	10(843)
C14orf50	chromosome 14 ORF 50	237654_at	-1.6	0.0003	3(39)	1(31)	3(113)	2(147)
AGPS	alkylglycerone phosphate synthase	225114_at	-1.6	0.0025	6(1106)	6(739)	8(200)	7(254)
ANKRD38	ankyrin repeat domain 38	229125_at	-1.5	0.0003	6(1266)	3(101)	5(209)	5(438)
IDI1	isopentenyl-diphosphate delta isomerase 1	208881_x_at	-1.5	0.0002	6(2906)	6(3764)	8(840)	10(1214)
2'-PDE	NA	1554915_a_at	-1.5	0.0021	6(1444)	6(1390)	7(61)	5(46)
PRO0149	NA	228373_at	-1.5	0.0002	6(397)	6(259)	9(992)	9(839)
PDHB	pyruvate dehydrogenase (lipoamide) beta	211023_at	-1.5	0.0004	6(4564)	6(4510)	10(3498)	10(4182)
BOLA3	bolA-like 3 ( <i>E. coli</i> )	227291_s_at	-1.4	0.0026	6(2087)	6(2077)	8(649)	8(573)
ALDH3A2	aldehyde dehydrogenase 3 family, member A2	202053_s_at	-1.4	0.0030	6(6907)	6(2559)	7(1352)	5(1413)
MTCH2	mitochondrial carrier homolog 2	217772_s_at	-1.4	0.0011	6(1463)	6(727)	10(1307)	7(905)
GOLGA2	golgi autoantigen	225672_at	-1.4	0.0019	6(462)	6(368)	10(1536)	10(1298)
GCSH	glycine cleavage system protein H	213133_s_at	-1.4	0.0000	6(3921)	6(1974)	9(1023)	10(1401)

	(aminomethyl carrier)							
IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	201193_at	-1.4	0.0007	6(3746)	6(1944)	10(4684)	10(3738)
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	217869_at	-1.3	0.0001	6(2526)	6(2565)	10(2393)	10(1613)
DPH5	DPH5 homolog ( <i>S. cerevisiae</i> )	222360_at	-1.3	0.0019	5(114)	4(175)	5(178)	6(277)
FMOD	fibromodulin	202709_at	-1.3	0.0001	6(2473)	6(866)	10(2507)	10(2732)
GNG2	guanine nucleotide binding protein (G protein), gamma 2	224964_s_at	-1.3	0.0012	6(1557)	5(680)	3(42)	4(73)
RSU1	Ras suppressor protein 1	201980_s_at	-1.3	0.0019	6(1417)	6(1962)	10(1621)	9(1148)
NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	203621_at	-1.3	0.0003	6(3348)	6(4335)	10(2150)	10(1989)
GPX1	glutathione peroxidase 1	200736_s_at	-1.3	0.0001	6(1052)	6(379)	10(3639)	10(2818)
HOXA10	homeo box A10	213150_at	-1.3	0.0004	6(404)	6(246)	7(299)	3(108)
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	202004_x_at	-1.3	0.0000	6(1123)	5(295)	8(874)	8(875)
GLUD2	glutamate dehydrogenase 2	215794_x_at	-1.3	0.0011	6(2642)	6(1393)	9(662)	7(366)
C17orf39	chromosome 17 ORF 39	228452_at	-1.2	0.0024	6(616)	6(525)	8(377)	8(504)
DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	209389_x_at	-1.2	0.0000	6(4665)	6(5638)	9(1691)	10(1539)
CNIH4	cornichon homolog 4 ( <i>Drosophila</i> )	223993_s_at	-1.2	0.0019	6(2635)	6(1220)	10(1833)	10(2127)
DBI	diazepam binding inhibitor	211070_x_at	-1.2	0.0003	6(8590)	6(9328)	10(2376)	10(2157)
RPA1	replication protein A1, 70kDa	215088_s_at	-1.2	0.0016	6(14089)	6(13462)	10(1347)	10(1146)
SLC44A1	solute carrier family 44, member 1	228486_at	-1.2	0.0013	6(2646)	6(2718)	8(1132)	6(718)
LTB4DH	leukotriene B4 12-hydroxydehydrogenase	231897_at	-1.2	0.0026	6(4229)	6(2290)	10(1970)	10(1874)
C10orf57	chromosome 10 open reading frame 57	222545_s_at	-1.2	0.0023	2(258)	4(383)	5(484)	3(401)
CD164	CD164 antigen, sialomucin	208405_s_at	-1.2	0.0029	6(11742)	6(11549)	10(11768)	10(13206)
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	220052_s_at	-1.2	0.0020	6(875)	6(1048)	9(1298)	9(1104)
DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	202428_x_at	-1.2	0.0001	6(10278)	6(16661)	10(5451)	10(5976)
PRDX2	peroxiredoxin 2	39729_at	-1.2	0.0014	6(2111)	6(2847)	10(5660)	10(4733)
UBQLN1	ubiquilin 1	222991_s_at	-1.2	0.0027	6(1134)	6(1413)	10(734)	7(486)
SUB1	SUB1 homolog ( <i>S. cerevisiae</i> )	214512_s_at	-1.1	0.0003	6(2755)	6(2370)	9(677)	8(513)
SFT2D1	SFT2 domain containing 1	226836_at	-1.1	0.0031	6(583)	5(438)	4(106)	1(73)
SUB1	SUB1 homolog ( <i>S. cerevisiae</i> )	212857_x_at	-1.1	0.0001	6(15217)	6(12808)	10(7060)	10(8150)
SUB1	SUB1 homolog ( <i>S. cerevisiae</i> )	224586_x_at	-1.1	0.0003	6(7917)	6(6847)	10(5192)	10(6563)
FAM45A	family with sequence similarity 45, member A	225351_at	-1.1	0.0005	6(325)	6(387)	8(454)	9(642)
GTF3A	general transcription factor IIIA	201338_x_at	-1.1	0.0027	6(4819)	6(4931)	10(5511)	10(4812)
NA	NA	230267_at	1.43	0.0001	1(93)	3(105)	3(130)	0(29)
ARIH2	ariadne homolog 2 ( <i>Drosophila</i> )	201230_s_at	1.24	0.0001	6(864)	6(1131)	10(1695)	10(1894)
NIBP	NA	56829_at	1.2	0.0002	3(128)	4(153)	6(642)	8(682)
FOXP1	forkhead box P1	223287_s_at	1.2	0.0001	6(1096)	6(543)	10(2675)	10(2539)
FLJ10099	NA	224688_at	1.17	0.0001	6(3128)	6(1568)	10(3144)	10(3607)

**Supplementary Table 2.** Significantly differentially expressed probesets (200, 161 genes) in abdominal adipose tissue in the DER group identified by SAM analysis with an FDR of 0.01. FC is the average fold change before and after DER for the 10 participants. P val is the unadjusted p value for the pairwise comparison using SAM.

Gene Symbol	Gene Title	Affymetrix probe ID	FC	P val
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	211708_s_at	-4.3	2.01E-06
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	211162_x_at	-4.3	1.46E-06
ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	204256_at	-3.6	4.39E-05
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	200831_s_at	-3.2	2.56E-06
SFRP2	secreted frizzled-related protein 2	223121_s_at	-2.8	5.49E-06
CETP	cholesteryl ester transfer protein, plasma	206210_s_at	-2.6	1.10E-06
SFRP2	secreted frizzled-related protein 2	223122_s_at	-2.6	2.74E-06
COL11A1	collagen, type XI, alpha 1	37892_at	-2.6	4.76E-06
CLCA2	chloride channel, calcium activated, family member 2	206165_s_at	-2.6	1.83E-07
GYS2	glycogen synthase 2 (liver)	214621_at	-2.4	4.54E-05
HP	haptoglobin	206697_s_at	-2.3	2.14E-05
ALDOC	aldolase C, fructose-bisphosphate	202022_at	-2.3	3.66E-07
STC1	stanniocalcin 1	230746_s_at	-2.3	6.04E-06
HPR	haptoglobin-related protein	208470_s_at	-2.3	5.61E-05
MXRA5	matrix-remodelling associated 5	209596_at	-2.3	2.19E-06
C20orf50	chromosome 20 open reading frame 50	234018_s_at	-2.2	1.52E-05
NA	CDNA: FLJ22539 fis, clone HRC13227	227491_at	-2.2	4.81E-05
FADS1	fatty acid desaturase 1	208964_s_at	-2.2	3.60E-05
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	204429_s_at	-2.2	2.38E-05
THBS4	thrombospondin 4	204776_at	-2.1	5.49E-07
FADS1	fatty acid desaturase 1	208962_s_at	-2.1	6.09E-05
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	200832_s_at	-2.1	8.96E-06
NA	CDNA FLJ20833 fis, clone ADKA02957	1557832_at	-2.1	4.57E-06
LOC55908	hepatocellular carcinoma-associated gene TD26	220437_at	-2.1	2.16E-05
FASN	fatty acid synthase	212218_s_at	-2.0	7.86E-06
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	206232_s_at	-2.0	6.22E-05
STC1	stanniocalcin 1	204597_x_at	-2.0	3.66E-06
TF	transferrin	203400_s_at	-2.0	3.40E-05
FADS1	fatty acid desaturase 1	208963_x_at	-2.0	5.51E-05
COL11A1	collagen, type XI, alpha 1	204320_at	-2.0	1.32E-05
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	206233_at	-2.0	3.69E-05
DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	226064_s_at	-1.9	6.40E-06
TF	transferrin	214063_s_at	-1.9	2.25E-05
BBOX1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	205363_at	-1.9	5.30E-06
FLJ37543	hypothetical protein FLJ37543	1553426_at	-1.9	1.87E-05
KRT14	keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)	209351_at	-1.9	5.67E-06
ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	207583_at	-1.9	2.56E-05
DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	224327_s_at	-1.9	8.23E-06
FADS2	fatty acid desaturase 2	202218_s_at	-1.8	7.32E-06
CLCA2	chloride channel, calcium activated, family member 2	217528_at	-1.8	7.13E-06
B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	235333_at	-1.8	6.77E-06
AACS	acetoacetyl-CoA synthetase	218434_s_at	-1.8	3.99E-05
FMOD	fibromodulin	202709_at	-1.8	4.39E-06
KRT5	keratin 5 (epidermolysis bullosa simplex, Dowling-	201820_at	-1.8	4.21E-06

	Meara/Kobner/Weber-Cockayne types)			
SREBF1	sterol regulatory element binding transcription factor 1	202308_at	-1.8	2.41E-05
CLCA2	chloride channel, calcium activated, family member 2	206164_at	-1.8	4.77E-05
SPATA9	spermatogenesis associated 9	223840_s_at	-1.7	8.78E-06
PDGFD	platelet derived growth factor D	222860_s_at	-1.7	6.29E-05
MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	203434_s_at	-1.7	4.94E-06
CLCA2	chloride channel, calcium activated, family member 2	206166_s_at	-1.7	1.61E-05
LOX	lysyl oxidase	204298_s_at	-1.6	9.51E-06
PDGFD	platelet derived growth factor D	219304_s_at	-1.6	3.97E-05
ACACA	acetyl-Coenzyme A carboxylase alpha	212186_at	-1.6	1.74E-05
ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	214033_at	-1.6	2.38E-06
SCD	stearoyl-CoA desaturase (delta-9-desaturase)	223839_s_at	-1.6	2.60E-05
GLYAT	glycine-N-acyltransferase	206930_at	-1.6	1.65E-06
TRD@	T cell receptor delta locus	217143_s_at	-1.6	1.41E-05
LOX	lysyl oxidase	213640_s_at	-1.6	1.37E-05
FAT3	FAT tumor suppressor homolog 3 (Drosophila)	236029_at	-1.6	6.31E-05
TRD@	T cell receptor delta locus	213830_at	-1.6	3.29E-06
TRA@	T cell receptor alpha locus	216191_s_at	-1.6	4.55E-05
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial	225420_at	-1.6	4.37E-05
CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	205999_x_at	-1.6	9.88E-06
GLYAT	glycine-N-acyltransferase	231683_at	-1.6	1.72E-05
FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	236481_at	-1.6	1.26E-05
MGC33657	similar to hypothetical protein	231043_at	-1.6	2.29E-05
LGALS12	lectin, galactoside-binding, soluble, 12 (galectin 12)	223828_s_at	-1.6	2.19E-05
CKMT2	creatine kinase, mitochondrial 2 (sarcomeric)	205295_at	-1.6	7.32E-07
NA	Full length insert cDNA clone ZE12B03	230913_at	-1.6	4.15E-05
KLB	klotho beta	235708_at	-1.6	2.01E-05
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	232081_at	-1.6	1.15E-05
LOX	lysyl oxidase	215446_s_at	-1.6	6.22E-06
ECHDC1	enoyl Coenzyme A hydratase domain containing 1	223088_x_at	-1.6	5.12E-06
STC1	stanniocalcin 1	204595_s_at	-1.6	5.16E-05
THRSP	thyroid hormone responsive (SPOT14 homolog, rat)	1553583_a_at	-1.6	2.67E-05
MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	203435_s_at	-1.6	5.85E-06
ECHDC1	enoyl Coenzyme A hydratase domain containing 1	219974_x_at	-1.5	1.06E-05
GPC6	glypican 6	223730_at	-1.5	1.85E-05
GYS1	glycogen synthase 1 (muscle)	201673_s_at	-1.5	5.67E-05
FLJ30294	hypothetical protein FLJ30294	1555090_x_at	-1.5	5.41E-05
SELENBP1	selenium binding protein 1	214433_s_at	-1.5	3.68E-05
KLB	klotho beta	244276_at	-1.5	1.54E-05
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	209600_s_at	-1.5	3.53E-05
AGTRL1	angiotensin II receptor-like 1	213592_at	-1.5	4.19E-05
ECHDC1	enoyl Coenzyme A hydratase domain containing 1	233124_s_at	-1.5	2.80E-05
ADRA1A	adrenergic, alpha-1A-, receptor	235642_at	-1.5	4.22E-05
GLYAT	glycine-N-acyltransferase	222083_at	-1.5	4.24E-05
RASSF4	Ras association (RalGDS/AF-6) domain family 4	49306_at	-1.5	1.02E-05
FLJ30294	hypothetical protein FLJ30294	238578_at	-1.5	3.07E-05
ANKRD38	ankyrin repeat domain 38	229125_at	-1.5	2.96E-05
GPC6	glypican 6	227059_at	-1.5	4.02E-06
KLHDC8B	kelch domain containing 8B	225755_at	-1.5	3.27E-05
NA	Transcribed locus, strongly similar to XP_527419.1 PREDICTED: similar to bA345L23.2 (novel protein with BTB/POZ (broad complex Tramtrack bric-a-brac/Pox virus and zinc finger) domain) [Pan troglodytes]	239398_at	-1.5	4.85E-05
HSPA12A	heat shock 70kDa protein 12A	214434_at	-1.5	9.33E-06
ECHDC1	enoyl Coenzyme A hydratase domain containing 1	223087_at	-1.4	1.04E-05
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	213501_at	-1.4	1.79E-05
HSD11B1	Hydroxysteroid (11-beta) dehydrogenase 1	237154_at	-1.4	4.70E-05

RHOF	Ras homolog gene family, member F (in filopodia)	219154_at	-1.4	3.09E-05
HIST1H4H	histone 1, H4h	208180_s_at	-1.4	3.79E-05
DHCR24	24-dehydrocholesterol reductase	200862_at	-1.4	3.55E-05
LRRN3	leucine rich repeat neuronal 3	209840_s_at	-1.4	1.70E-05
MECR	mitochondrial trans-2-enoyl-CoA reductase	218664_at	-1.4	1.13E-05
ACOX1	acyl-Coenzyme A oxidase 1, palmitoyl	227962_at	-1.4	2.10E-05
ACSL1	acyl-CoA synthetase long-chain family member 1	207275_s_at	-1.4	1.94E-05
ACAD11	acyl-Coenzyme A dehydrogenase family, member 11	225573_at	-1.4	8.60E-06
PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	202884_s_at	-1.4	3.64E-05
ATP2B4	ATPase, Ca <sup>++</sup> transporting, plasma membrane 4	212135_s_at	-1.4	4.17E-05
MTCH2	mitochondrial carrier homolog 2 ( <i>C. elegans</i> )	222403_at	-1.4	1.19E-05
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	32837_at	-1.4	1.30E-05
AQP11	aquaporin 11	229526_at	-1.4	2.47E-05
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	204059_s_at	-1.4	3.29E-05
C20orf7	chromosome 20 open reading frame 7	227160_s_at	-1.4	2.52E-05
DUSP14	dual specificity phosphatase 14	203367_at	-1.4	4.48E-05
CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	209616_s_at	-1.4	2.62E-05
SLC25A10	solute carrier family 25 (mitochondrial carrier)	218275_at	-1.4	5.69E-05
LOC399959	Hypothetical gene supported by BX647608	236640_at	-1.3	1.44E-05
NA	NA	226192_at	-1.3	2.18E-05
ALAD	aminolevulinatase, delta-, dehydratase	218489_s_at	-1.3	6.20E-05
SHMT1	serine hydroxymethyltransferase 1 (soluble)	209980_s_at	-1.3	3.35E-05
SGCG	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	207302_at	-1.3	3.26E-05
COL4A1	collagen, type IV, alpha 1	211981_at	-1.3	6.36E-05
ENSA	endosulfine alpha	228852_at	-1.3	5.07E-05
MCART1	mitochondrial carrier triple repeat 1	238574_at	-1.3	2.65E-05
LOXL2	lysyl oxidase-like 2	202998_s_at	-1.3	3.71E-05
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	211113_s_at	-1.3	2.27E-05
NA	MRNA; cDNA DKFZp779M2422 (from clone DKFZp779M2422)	229498_at	-1.3	3.57E-05
ALDH9A1	aldehyde dehydrogenase 9 family, member A1	201612_at	-1.3	5.83E-05
GPBAR1	G protein-coupled bile acid receptor 1	1552501_a_at	-1.3	4.92E-05
PRDX2	peroxiredoxin 2	211658_at	-1.3	2.23E-05
HSPG2	heparan sulfate proteoglycan 2 (perlecan)	201654_s_at	-1.3	4.65E-05
FAT	FAT tumor suppressor homolog 1 ( <i>Drosophila</i> )	201579_at	-1.3	5.80E-05
SEMA5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	205405_at	-1.3	2.74E-05
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	200980_s_at	-1.3	1.35E-05
LOC338799	hypothetical locus LOC338799	1556042_s_at	-1.3	4.76E-05
NA	Hypothetical protein LOC644005	1555753_x_at	-1.3	5.49E-05
MSTO1	misato homolog 1 ( <i>Drosophila</i> )	218296_x_at	-1.3	1.01E-05
OXCT1	3-oxoacid CoA transferase 1	202780_at	-1.3	2.83E-05
MACF1	microtubule-actin crosslinking factor 1	208633_s_at	-1.3	4.46E-05
ATP2C1	ATPase, Ca <sup>++</sup> transporting, type 2C, member 1	209934_s_at	-1.3	5.78E-05
BMSC-MCP	PNC1 protein	223296_at	-1.3	1.28E-05
EGFL6	EGF-like-domain, multiple 6	219454_at	-1.3	5.76E-05
MGC45438	hypothetical protein MGC45438	229177_at	-1.3	4.06E-05
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	1555864_s_at	-1.3	5.89E-05
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	203039_s_at	-1.2	4.30E-05
SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	202283_at	-1.2	3.22E-05
LRRN6A	leucine rich repeat neuronal 6A	227933_at	-1.2	6.18E-05
MDH1	malate dehydrogenase 1, NAD (soluble)	200978_at	-1.2	2.87E-05
RARRES1	retinoic acid receptor responder (tazarotene induced) 1	221872_at	2.13	3.33E-05
ATF3	activating transcription factor 3	202672_s_at	1.89	2.03E-05
TSRC1	thrombospondin repeat containing 1	226071_at	1.76	1.28E-06

C5R1	complement component 5 receptor 1 (C5a ligand)	220088_at	1.75	3.11E-05
RGS17	regulator of G-protein signalling 17	220334_at	1.74	9.14E-07
DFNA5	deafness, autosomal dominant 5	203695_s_at	1.69	3.15E-05
ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	209614_at	1.6	3.37E-05
CIDEA	cell death-inducing DFFA-like effector a	221295_at	1.6	3.84E-05
MCOLN3	mucolipin 3	229797_at	1.59	2.07E-05
NA	CDNA: FLJ23573 fis, clone LNG12520	232538_at	1.55	6.95E-06
NAP1L1	nucleosome assembly protein 1-like 1	1556121_at	1.55	7.68E-06
CPT1B	carnitine palmitoyltransferase 1B (muscle)	210069_at	1.55	7.50E-06
THBS1	thrombospondin 1	201108_s_at	1.55	1.43E-05
ANGPTL4	angiopoietin-like 4	221009_s_at	1.53	2.71E-05
MAP3K5	mitogen-activated protein kinase kinase kinase 5	203837_at	1.53	1.50E-05
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	223427_s_at	1.52	9.14E-06
AQP3	aquaporin 3	39248_at	1.51	3.20E-05
FN5	chromosome 11 open reading frame 75	219806_s_at	1.49	3.82E-05
NAP1L1	nucleosome assembly protein 1-like 1	208754_s_at	1.48	2.36E-05
AP1S2	adaptor-related protein complex 1, sigma 2 subunit	228415_at	1.48	1.23E-05
ATOH8	atonal homolog 8 (Drosophila)	1558706_a_at	1.47	2.05E-05
CAMTA1	calmodulin binding transcription activator 1	1555370_a_at	1.46	1.10E-05
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	220161_s_at	1.45	1.39E-05
CRIP1	cysteine-rich protein 1 (intestinal)	205081_at	1.45	3.84E-06
GPRASP1	G protein-coupled receptor associated sorting protein 1	204793_at	1.45	1.63E-05
FPRL2	formyl peptide receptor-like 2	230422_at	1.44	3.77E-05
ACY1L2	aminoacylase 1-like 2	225421_at	1.43	3.18E-05
PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	202847_at	1.42	2.78E-05
NAP1L1	nucleosome assembly protein 1-like 1	204528_s_at	1.42	9.69E-06
LPAAT	lysophosphatidic acid acyltransferase theta	224480_s_at	1.41	1.12E-05
IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	203126_at	1.39	2.45E-05
PES1	pescadillo homolog 1, containing BRCT domain (zebrafish)	236434_at	1.39	1.88E-05
NA	Full-length cDNA clone CS0DF032YA11 of Fetal brain	230968_at	1.38	8.05E-06
MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	205429_s_at	1.37	1.83E-06
NA	NA	239775_at	1.36	3.88E-05
NAP1L1	nucleosome assembly protein 1-like 1	208753_s_at	1.36	3.86E-05
NA	CDNA clone IMAGE:5263177	228108_at	1.36	6.58E-06
ANAPC5	anaphase promoting complex subunit 5	235926_at	1.36	1.68E-05
OPN3	opsin 3 (encephalopsin, panopsin)	226350_at	1.36	3.62E-05
CBX7	chromobox homolog 7	212914_at	1.35	3.13E-05
DENND2D	DENN/MADD domain containing 2D	221081_s_at	1.35	2.12E-05
RTN1	reticulon 1	203485_at	1.33	1.17E-05
SLC43A3	solute carrier family 43, member 3	213113_s_at	1.33	2.54E-05
CPT1B	carnitine palmitoyltransferase 1B (muscle)	210070_s_at	1.32	3.24E-05
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	226974_at	1.31	3.80E-05
TCEA3	transcription elongation factor A (SII), 3	226388_at	1.3	3.75E-05
SNF1LK2	SNF1-like kinase 2	213221_s_at	1.3	3.66E-05
NIPSNAP3B	nipsnap homolog 3B (C. elegans)	229015_at	1.3	3.73E-05
SART2	squamous cell carcinoma antigen recognized by T cells 2	218854_at	1.28	1.55E-05
MATN2	matrilin 2	202350_s_at	1.27	3.51E-05
TBC1D2	TBC1 domain family, member 2	222173_s_at	1.27	2.34E-05
ALMS1	Alstrom syndrome 1	214221_at	1.27	3.04E-05
KIAA1815	KIAA1815	218342_s_at	1.19	2.32E-05

**Supplementary Table 3** Gene ontology categories significantly (P-value  $\leq 0.01$ ) represented by genes down-regulated by DER in the breast tissue. Bold = those categories also represented by genes down-regulated by DER in the adipose tissue.

GO ID	Term	Total no. genes in category	No. genes down-reg.	P-Val
6631	<b>fatty acid metabolism</b>	180	6	0.000
6629	<b>lipid metabolism</b>	718	10	0.000
6536	glutamate metabolism	19	3	0.000
6099	tricarboxylic acid cycle	24	3	0.000
6092	<b>main pathways of carbohydrate metabolism</b>	118	5	0.000
6082	<b>organic acid metabolism</b>	597	10	0.000
19752	<b>carboxylic acid metabolism</b>	595	10	0.000
8610	<b>lipid biosynthesis</b>	282	7	0.000
6091	<b>generation of precursor metabolites and energy</b>	660	9	0.000
44255	<b>cellular lipid metabolism</b>	612	9	0.000
51186	<b>cofactor metabolism</b>	232	6	0.000
9109	coenzyme catabolism	30	3	0.000
46356	acetyl-CoA catabolism	25	3	0.000
6636	<b>fatty acid desaturation</b>	7	2	0.000
6084	acetyl-CoA metabolism	36	3	0.000
51187	cofactor catabolism	36	3	0.000
6732	<b>coenzyme metabolism</b>	193	5	0.000
6979	response to oxidative stress	113	4	0.000
15980	<b>energy derivation by oxidation of organic compounds</b>	206	5	0.000
9060	aerobic respiration	50	3	0.001
6096	<b>glycolysis</b>	54	3	0.001
9064	glutamine family amino acid metabolism	57	3	0.001
45333	cellular respiration	59	3	0.001
6800	oxygen and reactive oxygen species metabolism	142	4	0.001
6007	glucose catabolism	68	3	0.001
6633	<b>fatty acid biosynthesis</b>	71	3	0.001
19320	hexose catabolism	78	3	0.002
46365	monosaccharide catabolism	78	3	0.002
6081	aldehyde metabolism	21	2	0.002
6694	steroid biosynthesis	81	3	0.002
46164	alcohol catabolism	83	3	0.002
16053	<b>organic acid biosynthesis</b>	84	3	0.002
46394	<b>carboxylic acid biosynthesis</b>	84	3	0.002
6749	glutathione metabolism	23	2	0.002
42049	cell acyl-CoA homeostasis	1	1	0.003
316	sulfite transport	1	1	0.003
9058	<b>biosynthesis</b>	1459	11	0.003
44248	cellular catabolism	683	7	0.004
6414	translational elongation	32	2	0.004
302	response to reactive oxygen species	33	2	0.004

GO ID	Term	Total no. genes in category	No. genes down-reg.	P-Val
50875	<b>cellular physiological process</b>	9595	36	0.005
6790	sulfur metabolism	114	3	0.005
44275	cellular carbohydrate catabolism	114	3	0.005
42775	ATP synthesis coupled electron transport (sensu Eukaryota)	35	2	0.005
16052	carbohydrate catabolism	116	3	0.005
6690	icosanoid metabolism	36	2	0.005
42773	ATP synthesis coupled electron transport	36	2	0.005
43449	alkene metabolism	36	2	0.005
6006	<b>glucose metabolism</b>	122	3	0.006
46292	formaldehyde metabolism	2	1	0.006
42026	protein refolding	2	1	0.006
6118	<b>electron transport</b>	390	5	0.006
8152	<b>metabolism</b>	7250	30	0.006
44237	cellular metabolism	6899	29	0.006
9408	response to heat	40	2	0.007
44262	<b>cellular carbohydrate metabolism</b>	402	5	0.007
9056	catabolism	775	7	0.008
6102	isocitrate metabolism	3	1	0.009
7181	transforming growth factor beta receptor complex assembly	3	1	0.009
2040	sprouting angiogenesis	3	1	0.009



**Supplementary Table 4** Gene ontology categories significantly (P-value  $\leq 0.01$ ) represented by genes down-regulated by DER in the subcutaneous adipose tissue. Bold = those categories also represented by genes down-regulated by DER in the breast tissue.

GO ID	Term	Total no. genes in category	No. genes down-reg.	P-Val
6636	<b>fatty acid desaturation</b>	7	3	0
6633	<b>fatty acid biosynthesis</b>	71	6	0
6631	<b>fatty acid metabolism</b>	180	11	0
6629	<b>lipid metabolism</b>	718	24	0
6091	<b>generation of precursor metabolites and energy</b>	660	17	0
6082	<b>organic acid metabolism</b>	597	21	0
44255	<b>cellular lipid metabolism</b>	612	22	0
9058	<b>biosynthesis</b>	1461	23	0
16053	<b>organic acid biosynthesis</b>	84	7	0
19752	<b>carboxylic acid metabolism</b>	595	21	0
8610	<b>lipid biosynthesis</b>	282	13	0
46394	<b>carboxylic acid biosynthesis</b>	84	7	0
6092	<b>main pathways of carbohydrate metabolism</b>	118	6	0.0001
9437	carnitine metabolism	3	2	0.0001
45329	carnitine biosynthesis	3	2	0.0001
15980	<b>energy derivation by oxidation of organic compounds</b>	206	8	0.0001
10033	response to organic substance	46	4	0.0002
6767	water-soluble vitamin metabolism	54	4	0.0004
43526	neuroprotection	5	2	0.0004
6108	malate metabolism	6	2	0.0006
5975	carbohydrate metabolism	523	11	0.0006
6100	tricarboxylic acid cycle intermediate metabolism	28	3	0.0008
51186	<b>cofactor metabolism</b>	232	7	0.0008
43648	dicarboxylic acid metabolism	7	2	0.0009
15909	long-chain fatty acid transport	7	2	0.0009
42221	response to chemical stimulus	653	12	0.0011
30005	di-, tri-valent inorganic cation homeostasis	178	6	0.0011
9626	hypersensitive response	8	2	0.0012
44262	<b>cellular carbohydrate metabolism</b>	403	9	0.0013
6066	alcohol metabolism	328	8	0.0014
9628	response to abiotic stimulus	861	14	0.0014
50875	<b>cellular physiological process</b>	9607	75	0.0014
6875	metal ion homeostasis	189	6	0.0015
8203	cholesterol metabolism	75	4	0.0015
9987	cellular process	10895	81	0.0018
44249	cellular biosynthesis	1329	18	0.0023
30003	cation homeostasis	204	6	0.0023
8152	<b>metabolism</b>	7258	61	0.0023
16125	sterol metabolism	86	4	0.0025

GO ID	Term	Total no. genes in category	No. genes down-reg.	P-Val
6873	cell ion homeostasis	216	6	0.003
6766	vitamin metabolism	92	4	0.0032
15908	fatty acid transport	13	2	0.0032
6869	lipid transport	94	4	0.0034
5978	glycogen biosynthesis	14	2	0.0037
7568	aging	48	3	0.0039
6118	<b>electron transport</b>	390	8	0.0041
9743	response to carbohydrate stimulus	15	2	0.0043
42398	amino acid derivative biosynthesis	50	3	0.0043
50801	ion homeostasis	232	6	0.0043
7582	physiological process	10429	78	0.0045
6096	<b>glycolysis</b>	54	3	0.0054
6641	triacylglycerol metabolism	17	2	0.0055
8202	steroid metabolism	179	5	0.0065
1985	negative regulation of heart contraction rate in baroreceptor response to increased blood pressure	1	1	0.0066
6741	NADP biosynthesis	1	1	0.0066
6565	L-serine catabolism	1	1	0.0066
19464	glycine decarboxylation via glycine cleavage system	1	1	0.0066
44238	primary metabolism	6723	56	0.007
9814	defense response to pathogen, incompatible interaction	20	2	0.0076
7584	response to nutrient	21	2	0.0083
6006	<b>glucose metabolism</b>	122	4	0.0086
19725	cell homeostasis	270	6	0.0088
6732	<b>coenzyme metabolism</b>	193	5	0.0089
188	inactivation of MAPK activity	22	2	0.0091
165	MAPKKK cascade	197	5	0.0097
42592	homeostasis	363	7	0.01

**Supplementary Table 5** Two way ANOVA demonstrating that variability in gene expression of breast tissue from different individuals is greater than variability in expression between samples taken from different regions of the breasts in a single individual.

	<b>P-value for variance between quadrants</b>	<b>P-value for variance between individuals</b>
AREG	0.1831	0.0031
CD24	0.6128	0.1811
KRT14	0.5801	0.0341*
KRT18	0.5006	0.0003
MUC1	0.1193	0.0220*
MYBPC1	0.5878	0.3737
PGR	0.0899	0.0789
SCGB2A2	0.0708	0.159
TFF1	0.4502	0.3819
B2M	0.6375	0.0001*
BACT	0.0783	<0.0001*
L14	0.056	<0.0001*
YWHAZ	0.0714	0.0002*