Article title: Diets high in corn oil or extra virgin olive oil differentially modify the gene expression profile of the mammary gland and influence experimental breast cancer susceptibility

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Electronic Supplementary Material 4:

Supplementary Table 4

Enriched Gene Ontology (GO) categories in down- and up-modulated genes in mammary gland by effect of the experimental high fat diets.

Modulated genes were sub-classified in “common” (modulated in more than one group) or “specific” (found as modulated in one specific group)

Lists of “common” and “specific” genes found in high fat diet groups at 51 days of age were analyzed using Genecodis program by Babelomics platform setting GO annotations at level 3-6. Only statistically significant enriched categories are indicated.

51 days

Common down-regulated genes (in HCO and HOO)

Gene Ontology category (levels 3-6)	*Items*[a]	*S*[b]	*TS*[c]	*Hyp*[d]	*Genes*[e]
alcohol metabolic process	GO:0006066	18(61)	546(22938)	2, 32E-15	Pdk1, Tkt, Taldo1, Pygl, Aldoa, G6pd, Bche, Sod1, Lss, Insig1, Dhcr7, Dgat2, Cyb5r3, Pdhb, Pc, Mdh1, Ldhb, Gpd1
lipid metabolic process	GO:0006629	19(61)	735(22938)	2, 72E-09	Sod1, Lss, Lpin1, Insig1, Hsd17b12, Dhcr7, Dgat2, Cyb5r3, Akr1c14, Slc27a1, Scd, Pc, Gpd1, Gpam, Fabp4, Elovl6, Acsl1, Acaca, Adora1
cellular lipid metabolic process	GO:0044255	16(61)	622(22938)	4, 62E-07	Sod1, Lss, Insig1, Hsd17b12, Dhcr7, Dgat2, Cyb5r3, Akr1c14, Slc27a1, Scd, Gpd1, Gpam, Fabp4, Elovl6, Acsl1, Acaca
cellular carbohydrate metabolic process	GO:0044262	12(61)	341(22938)	8, 71E-06	Acly, Tkt, Taldo1, Pygl, Aldoa, G6pd, Dgat2, Pdhb, Pc, Mdh1, Ldhb, Gpd1
oxidation reduction	GO:0055114	14(61)	564(22938)	1, 96E-05	Sod3, Akr7a2, G6pd, Sod1, Hsd17b12, Dhcr7, Cyb5r3, Akr1c14, Scd, Pdhb, Me1, Mdh1, Ldhb, Gpd1
organic acid metabolic process	GO:0006082	13(61)	567(22938)	2, 49E-05	Slc27a1, Scd, Pdhb, Pc, Me1, Mdh1, Ldhb, Gpd1, Gpam, Fabp4, Elovl6, Acsl1, Acaca
lipid biosynthetic process	GO:0008610	11(61)	299(22938)	3, 60E-05	Sod1, Lss, Hsd17b12, Dhcr7, Dgat2, Cyb5r3, Scd, Pc, Gpam, Elovl6, Acaca
cofactor metabolic process	GO:0051186	10(61)	230(22938)	4, 87E-05	Tkt, Taldo1, Mgst1, G6pd, Sod1, Pdhb, Mdh1, Ldhb, Gpd1, Acaca
carbohydrate metabolic process	GO:0005975	13(61)	674(22938)	1, 95E-04	Pdk1, Acly, Tkt, Taldo1, Pygl, Aldoa, G6pd, Dgat2, Pdhb, Pc, Mdh1, Ldhb, Gpd1
carboxylic acid metabolic process	GO:0019752	13(61)	566(22938)	2, 44E-04	Slc27a1, Scd, Pdhb, Pc, Me1, Mdh1, Ldhb, Gpd1, Gpam, Fabp4, Elovl6, Acsl1, Acaca
generation of precursor metabolites and energy	GO:0006091	6(61)	335(22938)	2, 62E-04	Pygl, Atp5o, Aldoa, Pdhb, Mdh1, Ldhb
chemical homeostasis	GO:0048878	7(61)	483(22938)	2, 87E-04	Pygl, Slc2a4, Sod1, Scd, Fabp4, Acaca, Adora1
hexose metabolic process	GO:0019318	10(61)	291(22938)	4, 72E-04	Pdk1, Tkt, Taldo1, Aldoa, G6pd, Pdhb, Pc, Mdh1, Ldhb, Gpd1
fat cell differentiation	GO:0045444	3(61)	60(22938)	5, 50E-04	Slc2a4, Lpin1, Fabp4
regulation of multicellular organism growth	GO:0040014	3(61)	61(22938)	5, 77E-04	G6pd, Sod1, Gpam
mitochondrial transport	GO:0006839	3(61)	63(22938)	6, 34E-04	Slc25a10, Slc25a1, Atp5o
response to hormone stimulus	GO:0009725	6(61)	399(22938)	6, 61E-04	Aldoa, Bche, Lpin1, Insig1, Me1, Fabp4
regulation of blood vessel size	GO:0050880	3(61)	77(22938)	1, 14E-03	G6pd, Sod1, Adora1
response to organic cyclic substance	GO:0014070	4(61)	178(22938)	1, 30E-03	Aldoa, G6pd, Acsl1, Acaca

homeostatic process	GO:0042592	8(61)	840(22938)	1, 65E-03	Pygl, Slc2a4, G6pd, Sod1, Scd, Fabp4, Acaca, Adora1
regulation of lipid metabolic process	GO:0019216	3(61)	88(22938)	1, 67E-03	Sod1, Dhcr7, Adora1
peptide metabolic process	GO:0006518	3(61)	88(22938)	1, 67E-03	Mgst1, G6pd, Sod1
regulation of blood pressure	GO:0008217	3(61)	95(22938)	2, 08E-03	G6pd, Sod1, Adora1
sulfur metabolic process	GO:0006790	3(61)	98(22938)	2, 27E-03	Mgst1, G6pd, Sod1
response to nutrient levels	GO:0031667	4(61)	227(22938)	3, 14E-03	G6pd, Bche, Sod1, Acsl1
response to steroid hormone stimulus	GO:0048545	4(61)	236(22938)	3, 60E-03	Aldoa, Bche, Insig1, Fabp4
response to extracellular stimulus	GO:0009991	4(61)	245(22938)	4, 12E-03	G6pd, Bche, Sod1, Acsl1
regulation of growth	GO:0040008	4(61)	250(22938)	4, 42E-03	Tkt, G6pd, Sod1, Gpam
cellular macromolecule catabolic process	GO:0044265	11(61)	485(22938)	5, 44E-03	Ubc, Tkt, Taldo1, Pygl, Aldoa, G6pd, Sod1, Pdhb, Mdh1, Ldhb, Gpd1
glycerolipid metabolic process	GO:0046486	3(61)	136(22938)	5, 71E-03	Dgat2, Gpd1, Gpam
response to oxidative stress	GO:0006979	3(61)	165(22938)	9, 70E-03	Sod3, G6pd, Sod1
cytokine production	GO:0001816	3(61)	166(22938)	9, 86E-03	G6pd, Sod1, Fabp4
blood circulation	GO:0008015	3(61)	184(22938)	1, 30E-02	G6pd, Sod1, Adora1
transmission of nerve impulse	GO:0019226	4(61)	355(22938)	1, 47E-02	Bche, Sod1, Scd, Adora1
cellular amino acid and derivative metabolic process	GO:0006519	4(61)	357(22938)	1, 50E-02	Mgst1, G6pd, Bche, Sod1
vitamin metabolic process	GO:0006766	6(61)	99(22938)	2, 54E-02	Tkt, Taldo1, G6pd, Mdh1, Ldhb, Gpd1
heterocycle metabolic process	GO:0046483	4(61)	424(22938)	2, 63E-02	Tkt, Pygl, Atp5o, Adora1
response to external stimulus	GO:0009605	6(61)	913(22938)	3, 40E-02	G6pd, Bche, Sod1, Fabp4, Acsl1, Adora1
response to organic substance	GO:0010033	11(61)	746(22938)	3, 80E-02	Mgst1, Aldoa, G6pd, Bche, Sod1, Lpin1, Insig1, Me1, Fabp4, Acsl1, Acaca
response to biotic stimulus	GO:0009607	3(61)	289(22938)	4, 17E-02	Ifitm2, Mgst1, Aldoa
steroid metabolic process	GO:0008202	7(61)	177(22938)	4, 44E-02	Sod1, Lss, Insig1, Hsd17b12, Dhcr7, Cyb5r3, Akr1c14

Specific down-regulated genes (only in HCO)

Gene Ontology category (levels 3-6)	*Items*	*S*	*TS*	*Hyp*	*Genes*
lipid catabolic process	GO:0016042	4(38)	152(22938)	1, 15E-04	Smpdl3a, Prdx6, Echs1, Cebpa
transmembrane transport	GO:0055085	4(38)	165(22938)	1, 57E-04	Atp5i, Atp5e, Atp5g3, Atp5g2

response to organic substance	GO:0010033	7(38)	746(22938)	1, 96E-04	Hsp90ab1, Atp5g3, Atp5g2, Uqcrfs1, Aldh2, Mif, Cebpa
generation of precursor metabolites and energy	GO:0006091	9(38)	334(22938)	2, 97E-04	Atp5i, Atp5e, Atp5g3, Atp5g2, Uqcrfs1, Cat, Pfkfb3, Mif, Cebpa
ion transport	GO:0006811	7(38)	873(22938)	5, 08E-04	Slc36a2, Atp5i, Atp5e, Atp5g3, Atp5g2, Vdac1, Mif
response to biotic stimulus	GO:0009607	4(38)	289(22938)	1, 30E-03	Mx1, Hsp90ab1, Mif, Cebpa
response to nutrient	GO:0007584	3(38)	158(22938)	2, 27E-03	Cox4i1, Mif, Cebpa
cellular response to stimulus	GO:0051716	5(38)	616(22938)	3, 31E-03	Aldh2, Prdx6, Cat, Mif, Cebpa
response to hormone stimulus	GO:0009725	4(38)	398(22938)	4, 14E-03	Uqcrfs1, Aldh2, Mif, Cebpa
heterocycle metabolic process	GO:0046483	4(38)	424(22938)	5, 17E-03	Atp5i, Atp5e, Atp5g3, Atp5g2
response to other organism	GO:0051707	3(38)	225(22938)	6, 10E-03	Mx1, Mif, Cebpa
response to nutrient levels	GO:0031667	3(38)	227(22938)	6, 25E-03	Cox4i1, Mif, Cebpa
response to steroid hormone stimulus	GO:0048545	3(38)	235(22938)	6, 88E-03	Aldh2, Mif, Cebpa
response to extracellular stimulus	GO:0009991	3(38)	245(22938)	7, 71E-03	Cox4i1, Mif, Cebpa
cellular macromolecule catabolic process	GO:0044265	4(38)	485(22938)	8, 25E-03	Pfkfb3, Mif, Dnase2a, Cebpa
apoptosis	GO:0006915	5(38)	790(22938)	9, 37E-03	Vdac1, Cstb, Cat, Dnase2a, Cebpa
programmed cell death	GO:0012501	5(38)	798(22938)	9, 76E-03	Vdac1, Cstb, Cat, Dnase2a, Cebpa
cell death	GO:0008219	5(38)	826(22938)	1, 12E-02	Vdac1, Cstb, Cat, Dnase2a, Cebpa
inflammatory response	GO:0006954	3(38)	294(22938)	1, 26E-02	Ddt, Mif, Cebpa
immune system development	GO:0002520	3(38)	304(22938)	1, 38E-02	LOC364236, Dnase2a, Cebpa
cellular carbohydrate metabolic process	GO:0044262	3(38)	338(22938)	1, 83E-02	Pfkfb3, Mif, Cebpa
central nervous system development	GO:0007417	3(38)	374(22938)	2, 38E-02	Pfkfb3, Mif, Cebpa
cellular response to stress	GO:0033554	3(38)	430(22938)	3, 40E-02	Prdx6, Cat, Mif
behavior	GO:0007610	3(38)	443(22938)	3, 67E-02	Cstb, Mif, Cebpa
homeostatic process	GO:0042592	4(38)	839(22938)	4, 91E-02	Prdx6, LOC364236, Dnase2a, Cebpa

Specific down-regulated genes (only in HOO)

Gene Ontology category (levels 3-6)	*Items*	*S*	*TS*	*Hyp*	*Genes*
response to external stimulus	GO:0009605	6(23)	915(22938)	2, 23E-04	Scnn1b, Gas6, Tgfb3, C6, Timp3, Pparg

tissue development	GO:0009888	5(23)	607(22938)	2, 89E-04	Gas6, Tgfb3, Timp3, Nsdhl, Pparg
cellular carbohydrate metabolic process	GO:0044262	4(23)	340(22938)	3, 36E-04	Lalba, Hk2, Nsdhl, Hsd11b1
GO:0016052	GO:0016052	3(23)	143(22938)	3, 83E-04	Chi3l1, Hk2, Hsd11b1
carbohydrate metabolic process	GO:0005975	5(23)	673(22938)	4, 65E-04	Lalba, Chi3l1, Hk2, Nsdhl, Hsd11b1
reproductive process in a multicellular organism	GO:0048609	4(23)	405(22938)	6, 50E-04	Rgs2, Tgfb3, Hk2, Kit
response to steroid hormone stimulus	GO:0048545	3(23)	237(22938)	1, 66E-03	Tgfb3, Timp3, Pparg
nuclear transport	GO:0051169	3(23)	242(22938)	1, 76E-03	Rnd3, Rab34, Tgfb3
regulation of catalytic activity	GO:0050790	4(23)	567(22938)	2, 25E-03	Tgfb3, C6, Kit, Pparg
positive regulation of cell death	GO:0010942	3(23)	294(22938)	3, 05E-03	Tgfb3, C6, Timp3
cellular lipid metabolic process	GO:0044255	4(23)	622(22938)	3, 15E-03	Nsdhl, Kit, Hsd11b1, Pparg
regulation of programmed cell death	GO:0043067	4(23)	642(22938)	3, 52E-03	Tgfb3, C6, Timp3, Kit
positive regulation of catalytic activity	GO:0043085	3(23)	343(22938)	4, 70E-03	Tgfb3, C6, Kit
lipid metabolic process	GO:0006629	4(23)	736(22938)	5, 72E-03	Nsdhl, Kit, Hsd11b1, Pparg
protein transport	GO:0015031	4(23)	752(22938)	6, 17E-03	Rnd3, Rab34, Tgfb3, Pparg
establishment of protein localization	GO:0045184	4(23)	762(22938)	6, 47E-03	Rnd3, Rab34, Tgfb3, Pparg
response to hormone stimulus	GO:0009725	3(23)	400(22938)	7, 19E-03	Tgfb3, Timp3, Pparg
programmed cell death	GO:0012501	4(23)	799(22938)	7, 63E-03	Tgfb3, C6, Timp3, Kit
cell death	GO:0008219	4(23)	827(22938)	8, 60E-03	Tgfb3, C6, Timp3, Kit
regulation of cell differentiation	GO:0045595	3(23)	433(22938)	8, 94E-03	Tgfb3, Kit, Pparg
protein localization	GO:0008104	4(23)	869(22938)	1, 02E-02	Rnd3, Rab34, Tgfb3, Pparg
cellular macromolecule catabolic process	GO:0044265	3(23)	484(22938)	1, 21E-02	Timp3, Hk2, Hsd11b1
response to abiotic stimulus	GO:0009628	3(23)	491(22938)	1, 26E-02	Timp3, Kit, Pparg
cellular protein localization	GO:0034613	3(23)	509(22938)	1, 38E-02	Rnd3, Rab34, Tgfb3
alcohol metabolic process	GO:0006066	3(23)	545(22938)	1, 66E-02	Hk2, Nsdhl, Hsd11b1
negative regulation of metabolic process	GO:0009892	3(23)	547(22938)	1, 68E-02	Tgfb3, Timp3, Pparg
oxidation reduction	GO:0055114	3(23)	562(22938)	1, 80E-02	Aox3, Nsdhl, Hsd11b1

regulation of cell proliferation	GO:0042127	3(23)	584(22938)	1, 99E-02	Tgfb3, Kit, Pparg
intracellular transport	GO:0046907	3(23)	657(22938)	2, 71E-02	Rnd3, Rab34, Tgfb3
organ morphogenesis	GO:0009887	3(23)	675(22938)	2, 90E-02	Gas6, Tgfb3, Pparg
regulation of signal transduction	GO:0009966	3(23)	734(22938)	3, 59E-02	Rgs2, Tgfb3, Kit
cell proliferation	GO:0008283	3(23)	747(22938)	3, 75E-02	Tgfb3, Kit, Pparg
response to organic substance	GO:0010033	3(23)	748(22938)	3, 77E-02	Tgfb3, Timp3, Pparg
positive regulation of metabolic process	GO:0009893	3(23)	749(22938)	3, 78E-02	Tgfb3, Kit, Pparg
apoptosis	GO:0006915	3(23)	791(22938)	4, 33E-02	Tgfb3, C6, Timp3
regulation of developmental process	GO:0050793	3(23)	819(22938)	4, 72E-02	Tgfb3, Kit, Pparg

[a]*: enriched Gene Ontology caterogies*
[b]*: number of genes in the input list that have been matched in the enriched set and the total number of genes in the list*
[c]*: number of genes in the reference list that match with the enriched set and total number of genes in the reference list*
[d]*: pvalue calculated by the hypergeometric function*
[e]*: the genes of the input list that match with the enriched items*