Supplemental Table S1. Assumed variant allele function based on previous literature

Gene	rs#	Allele Substitution	Variant allele function	Reference	LIBCSP Analytic Sample Size			
					Total	Cases	Controls	Variant allele frequency[a]
PTGS-2	rs20417	G > C	↓ Inf	(1)	2106	1030	1076	0.20
PTGS-2	rs5275	T > C	↓ Inf	(1)	2106	1033	1073	0.34
PPAR-α	rs1800206	C > G	↓ Inf	(2)	1815	878	937	0.05
FAS	rs2234767	G > A	↓ Inf	(3)	2106	1030	1076	0.13
FAS	rs1800682	G > A	↑ Inf	(3)	2095	1024	1071	0.47
FASL	rs763110	C > T	↓ Inf	(4)	2110	1035	1075	0.43
TNF-α	rs1800629	G > A	↑ Inf	(5)	2088	1019	1069	0.14
MnSOD	rs4880	C > T	↓ Os	(6)	2063	1006	1057	0.51
MPO	rs2333227	G > A	↓ Os	(7)	2078	1015	1063	0.24
CAT	rs1001179	C > T	↑ Os	(8)	2068	1009	1059	0.20
GPX1	rs1050450	C > T	↑ Os	(9)	2074	1013	1061	0.31
GSTM1	deletion	deletion	↑ Os	(10)	1925	950	975	0.45
GSTP1	rs1695	A > G	↑ Os	(11)	2040	999	1041	0.30
GSTT1	deletion	deletion	↑ Os	(10)	1946	957	989	0.22
GSTA1	rs3957356	G > A	↑ Os	(12)	2075	1013	1062	0.41
COMT	rs4680	G > A	↑ Os	(13)	2084	1020	1064	0.50
COMT	rs737865	C > T	↓ Os	(14)	2064	1002	1062	0.69
CYP17	rs743572	T > C	↑ Es	(15)	2044	1001	1043	0.40

Note: LIBCSP=Long Island Breast Cancer Study, Inf = inflammation, Os = oxidative stress, Es = estrogen

[a]Variant allele frequency among the LIBCSP controls

Supplement Table S2. Multivariable[a]-adjusted odds ratios (ORs) and 95% confidence intervals (95% CIs) for the risk of breast cancer for the interaction between ω-3/ω-6 ratio and putatively functional genetic polymorphisms[b] evaluated on the multiplicative scale in the LIBCSP, 1996-1997

Variant	Genotype	High ω-3/ω-6 (≥ median[c])			Low ω-3/ω-6 (< median)			LRT $\chi 2^{d}$	*p* value
		Ca/Co	OR	95% CI	Ca/Co	OR	95% CI		
PTGS-2	GC/CC	169/198	1.00		208/204	1.00			
rs20417	GG	311/333	1.09	0.84, 1.41	342/341	0.98	0.77, 1.25	0.36	0.55
PTGS-2	TC/CC	264/310	1.00		306/309	1.00			
rs5275	TT	217/222	1.15	0.89, 1.47	246/232	1.05	0.83, 1.34	0.23	0.64
PPAR-α	GC/GG	51/48	1.00		50/44	1.00			
rs1800206	CC	354/416	0.77	0.51, 1.18	423/429	0.86	0.56, 1.32	0.11	0.74
FAS	GA/AA	115/145	1.00		123/106	1.00			
rs2234767	GG	364/387	1.19	0.89, 1.58	428/438	0.82	0.61, 1.11	3.03	0.08
FAS	GG	114/144	1.00		160/157	1.00			
rs1800682	GA/AA	360/386	1.22	0.91, 1.62	390/384	1.00	0.77, 1.30	1.02	0.31
FASL	CT/TT	312/363	1.00		396/361	1.00			
rs763110	CC	170/169	1.18	0.90, 1.53	157/182	0.79	0.61, 1.02	4.63	0.03
TNF-α	GG	346/381	1.00		412/403	1.00			
rs1800629	GA/AA	127/145	0.96	0.73, 1.27	134/140	0.95	0.72, 1.26	0.00	0.97
MnSOD	CC	113/118	1.00		137/141	1.00			
rs4880	CT/TT	353/402	0.92	0.68, 1.23	403/396	1.05	0.80, 1.38	0.42	0.51
MPO	GG	289/304	1.00		340/329	1.00			
rs2333227	GA/AA	183/221	0.87	0.68, 1.13	203/209	0.94	0.74, 1.21	0.17	0.68
CAT	CT/TT	185/180	1.00		210/200	1.00			
rs1001179	CC	283/341	0.80	0.62, 1.04	331/338	0.94	0.73, 1.20	0.77	0.38
GPX1	CT/TT	263/297	1.00		287/255	1.00			
rs1050450	CC	208/226	1.05	0.82, 1.35	255/283	0.80	0.63, 1.02	2.24	0.13
GSTM1	null	221/208	1.00		236/235	1.00			
deletion	present	218/266	0.77	0.59, 1.00	271/261	1.03	0.80, 1.32	2.52	0.11
GSTP1	AG/GG	236/263	1.00		263/269	1.00			
rs1695	AA	229/248	1.03	0.80, 1.33	271/261	1.07	0.84, 1.37	0.05	0.82
GSTT1	null	99/102	1.00		104/112	1.00			

deletion	present	345/379	0.94	0.68, 1.28	409/396	1.09	0.81, 1.48	0.49	0.49
GSTA1	GA/AA	329/343	1.00		350/347	1.00			
rs3957356	GG	143/181	0.83	0.63, 1.08	191/191	1.00	0.78, 1.29	1.03	0.31
COMT	AG/AA	347/414	1.00		393/383	1.00			
rs4680	GG	130/112	1.37	1.02, 1.83	150/155	0.93	0.71, 1.22	3.60	0.06
COMT	CC	38/50	1.00		61/60	1.00			
rs737865	CT/TT	427/474	1.16	0.74, 1.81	476/478	1.01	0.69, 1.48	0.21	0.64
CYP17	TT	168/204	1.00		177/171	1.00			
rs743572	TC/CC	295/310	1.16	0.89, 1.50	361/358	0.95	0.74, 1.23	1.05	0.31

Note: LIBCSP = Long Island Breast Cancer Study Project, Ca = cases, Co = controls, LRT = likelihood ratio test

[a]All models adjusted for matching factor, 5-year age group, and total energy intake (kcal/day).

[b]Genotypes dichotomized using dominant genetic model.

[c]Median ω-3/ω-6 ratio in the LIBCSP = 0.14.

[d]LRT $\chi 2$ calculated using nested models for the multiplicative interaction.

Online Supplemental References

1. Lee YS, Kim H, Wu TX, Wang XM, Dionne RA (2006) Genetically mediated interindividual variation in analgesic responses to cyclooxygenase inhibitory drugs. Clin Pharmacol Ther. 79: 407-418.
2. Flavell DM, Torra IP, Jamshidi Y, Evans D, Diamond JR, et al. (2000) Variation in the PPARalpha gene is associated with altered function in vitro and plasma lipid concentrations in Type II diabetic subjects. Diabetologia. 43: 673-680.
3. Huang QR, Morris D, Manolios N (1997) Identification and characterization of polymorphisms in the promoter region of the human Apo-1/Fas (CD95) gene. Mol Immunol. 34: 577-582.
4. Wu J, Metz C, Xu X, Abe R, Gibson AW, et al. (2003) A novel polymorphic CAAT/enhancer-binding protein beta element in the FasL gene promoter alters Fas ligand expression: a candidate background gene in African American systemic lupus erythematosus patients. J Immunol Baltim Md 1950. 170: 132-138.
5. Elahi MM, Asotra K, Matata BM, Mastana SS (2009) Tumor necrosis factor alpha -308 gene locus promoter polymorphism: an analysis of association with health and disease. Biochim Biophys Acta. 1792: 163-172.
6. Bastaki M, Huen K, Manzanillo P, Chande N, Chen C, et al. (2006) Genotype-activity relationship for Mn-superoxide dismutase, glutathione peroxidase 1 and catalase in humans. Pharmacogenet Genomics. 16: 279-286.
7. Hansson M, Olsson I, Nauseef WM (2006) Biosynthesis, processing, and sorting of human myeloperoxidase. Arch Biochem Biophys. 445: 214-224.
8. Forsberg L, Lyrenas L, Faire U de, Morgenstern R (2001) A common functional C-T substitution polymorphism in

the promoter region of the human catalase gene influences transcription factor binding, reporter gene transcription and is correlated to blood catalase levels. Free Radic Biol Med.30: 500-505.

9. Hu YJ, Diamond AM (2003) Role of glutathione peroxidase 1 in breast cancer: loss of heterozygosity and allelic differences in the response to selenium. Cancer Res. 63: 3347-3351.
10. Garte S, Gaspari L, Alexandrie AK, Ambrosone C, Autrup H, et al. (2001) Metabolic gene polymorphism frequencies in control populations. Cancer Epidemiol Biomark Prev Publ Am Assoc Cancer Res Cosponsored Am Soc Prev Oncol. 10: 1239-1248.
11. Lin HJ, Johansson AS, Stenberg G, Materi AM, Park JM, et al. (2003) Naturally occurring Phe151Leu substitution near a conserved folding module lowers stability of glutathione transferase P1-1. Biochim Biophys Acta. 1649: 16-23.
12. Morel F, Rauch C, Coles B, Ferrec EL, Guillouzo A (2002) The human glutathione transferase alpha locus: genomic organization of the gene cluster and functional characterization of the genetic polymorphism in the hGSTA1 promoter. Pharmacogenetics. 12: 277-286.
13. Lachman HM, Papolos DF, Saito T, Yu YM, Szumlanski CL, et al (1996) Human catechol-O-methyltransferase pharmacogenetics: description of a functional polymorphism and its potential application to neuropsychiatric disorders. Pharmacogenetics. 6: 243-250.
14. Dempster EL, Mill J, Craig IW, Collier DA (2006) The quantification of COMT mRNA in post mortem cerebellum tissue: diagnosis, genotype, methylation, and expression. BMC Med Genet. 7: 10.
15. Feigelson HS, Shames LS, Pike MC, Coetzee GA, Stanczyk FZ, et al. (1998) Cytochrome P450c17alpha gene (CYP17) polymorphism is associated with serum estrogen and progesterone concentrations. Cancer Res. 58: 585-587.