Supplemental Table 1. Summary odd ratios (OR) estimates and 95% confidence intervals (CI) derived from study-specific results on single nucleotide polymorphism in *HSD17B1* and breast cancer risk overall

SNP	No. of Studies	Random-effects summaries		Fixed-effects summaries		p-value for between-study heterogeneity
		OR (95% CI)	p-value	OR (95% CI)	p-value	
rs676387 (IVS4-150 C>A)						
CC	7	1.00		1.00		
CA		1.04 (0.97, 1.12)	1.05	1.06 (1.00, 1.12)	0.07	0.20
AA		1.12 (0.99, 1.27)	0.08	1.14 (1.02, 1.27)	0.02	0.30
rs605059[5] (Ex6+220 G>A)						
AA	10	1.00		1.00		
AG		0.93 (0.87, 0.99)	0.03	0.93 (0.87, 0.99)	0.02	0.39
GG		0.95 (0.85, 1.07)	0.41	0.93 (0.86, 1.01)	0.07	0.06

Supplemental Table 2. Summary odd ratios (OR) estimates and 95% confidence intervals (CI) derived from study-specific results on single nucleotide polymorphism in *HSD17B1* and risk of breast tumors expressing the estrogen receptor (ER-positive) and those not expressing the estrogen receptor (ER-negative)

SNP	No. of Studies	ER-positive tumors vs. controls					No. of Studies	ER-negative tumors vs. controls				
		Random-effects summaries		Fixed-effects summaries		p-value for between-study heterogeneity		Random-effects summaries		Fixed-effects summaries		p-value for between-study heterogeneity
		OR (95% CI)	p-value	OR (95% CI)	p-value			OR (95% CI)	p-value	OR (95% CI)	p-value	
rs676387 (IVS4-150 C>A)												
CC	6	1.00		1.00			6	1.00		1.00		
CA		1.07 (0.97, 1.18)	0.16	1.09 (1.01, 1.18)	0.03	0.23		0.87 (0.65, 1.17)	0.35	0.93 (0.82, 1.06)	0.28	0.001
AA		1.05 (0.91, 1.22)	0.51	1.05 (0.91, 1.22)	0.51	0.95		1.02 (0.70, 1.50)	0.91	1.19 (0.94, 1.51)	0.16	0.11
rs605059[5] (Ex6+220 G>A)												
AA	6	1.00		1.00			6	1.00		1.00		
AG		0.94 (0.87, 1.03)	0.17	0.94 (0.87, 1.03)	0.17	0.48		1.02 (0.86, 1.21)	0.83	1.00 (0.86, 1.15)	0.96	0.30
GG		0.97 (0.84, 1.11)	0.65	0.95 (0.87, 1.05)	0.31	0.16		1.18 (0.78, 1.80)	0.44	1.07 (0.90, 1.27)	0.45	0.001

Supplemental Table 3. Age- and center-adjusted odds ratios (OR) and 95% confidence intervals (CI) for the association between HSD17β1 haplotype-tagging SNPs and breast cancer stratified by age

SNP Name	Geno-type	Among women younger than age 45			Among women age 45 - 55			Among women older than age 55			p for inter action
		Cases	Controls		Cases	Controls		Cases	Controls		
		N (%)	N (%)	OR (95% CI)	N (%)	N (%)	OR (95% CI)	N (%)	N (%)	OR (95% CI)	
Polish Breast Cancer Study											
	CC	170 (58.8)	171 (59.4)	1.00	533 (60.3)	571 (60.9)	1.00	602 (57.4)	700 (61.2)	1.00	
rs676387	CA	96 (33.2)	98 (34.0)	0.99 (0.69, 1.41)	296 (33.5)	323 (34.4)	0.99 (0.81, 1.20)	388 (37.0)	384 (33.6)	1.18 (0.99, 1.41)	
(IVS4-150 C>A)	AA	23 (8.0)	19 (6.6)	1.26 (0.66, 2.42)	55 (6.2)	44 (4.7)	1.34 (0.89, 2.03)	58 (5.5)	60 (5.2)	1.12 (0.77, 1.64)	
	per allele			1.06 (0.82, 1.38)			1.06 (0.91, 1.24)			1.12 (0.97, 1.29)	0.58
	AA	85 (30.0)	83 (29.0)	1.00	239 (27.4)	259 (28.2)	1.00	298 (29.2)	299 (26.8)	1.00	
rs605059	AG	141 (49.8)	138 (48.3)	1.04 (0.70, 1.52)	423 (48.5)	451 (49.0)	1.02 (0.81, 1.27)	482 (47.2)	566 (50.7)	0.85 (0.70, 1.05)	
(Ex6+220 G>A)	GG	57 (20.1)	65 (22.7)	0.88 (0.55, 1.41)	211 (24.2)	210 (22.8)	1.09 (0.84, 1.41)	242 (23.7)	252 (22.6)	0.96 (0.76, 1.22)	
	per allele			0.95 (0.75, 1.19)			1.04 (0.91, 1.19)			0.97 (0.86, 1.10)	0.91
SEARCH											
	CC	440 (52.0)	28 (50.9)	1.00	1080 (51.2)	585 (54.0)	1.00	705 (50.2)	1784 (52.7)	1.00	
rs676387	CA	334 (39.5)	19 (34.6)	1.10 (0.58, 2.07)	854 (40.5)	423 (39.0)	1.07 (0.92, 1.26)	577 (41.1)	1335 (39.5)	1.14 (0.99, 1.32)	
(IVS4-150 C>A)	AA	72 (8.5)	8 (14.6)	0.50 (0.20, 1.25)	177 (8.4)	77 (7.1)	1.21 (0.90, 1.62)	123 (8.8)	264 (7.8)	1.17 (0.91, 1.49)	
	per allele			0.81 (0.53, 1.26)			1.09 (0.96, 1.23)			1.11 (1.00, 1.23)	0.39
	AA	281(33.7)	21 (38.2)	1.00	675 (32.3)	313 (29.0)	1.00	488 (35.1)	1072 (32.4)	1.00	
rs605059	AG	407 (48.8)	25 (45.5)	1.51 (0.80, 2.89)	1003 (47.9)	563 (52.2)	0.79 (0.67, 0.95)	664 (47.7)	1573 (47.5)	0.95 (0.82, 1.10)	
(Ex6+220 G>A)	GG	146 (17.5)	9 (16.4)	1.63 (0.69, 3.86)	414 (19.8)	202 (18.7)	0.95 (0.76, 1.18)	240 (17.2)	665 (20.1)	0.76 (0.63, 0.92)	
	per allele			1.32 (0.86, 2.03)			0.95 (0.85, 1.06)			0.88 (0.80, 0.97)	0.15
Pooled Analysis											
	CC	610 (53.7)	199 (58.0)	1.00	1613 (53.9)	1156 (57.1)	1.00	1307 (53.3)	2484 (54.9)	1.00	
rs676387	CA	430 (37.9)	117 (34.1)	1.02 (0.75, 1.38)	1150 (38.4)	746 (36.9)	1.03 (0.91, 1.17)	965 (39.3)	1719 (38.0)	1.13 (1.01, 1.26)	
(IVS4-150 C>A)	AA	95 (8.4)	27 (7.9)	0.91 (0.54, 1.56)	232 (7.8)	121 (6.0)	1.25 (0.99, 1.59)	181 (7.4)	324 (7.2)	1.15 (0.94, 1.41)	
	per allele			0.98 (0.79, 1.23)			1.08 (0.98, 1.18)			1.10 (1.01, 1.19)	0.27
	AA	366 (32.8)	104 (30.5)	1.00	914 (30.8)	572 (28.6)	1.00	786 (32.6)	1371 (31.0)	1.00	
rs605059	AG	548 (49.1)	163 (47.8)	1.04 (0.75, 1.44)	1426 (48.1)	1014 (50.8)	0.89 (0.77, 1.01)	1146 (47.5)	2139 (48.3)	0.91 (0.81, 1.02)	
(Ex6+220 G>A)	GG	203 (18.2)	74 (21.7)	0.93 (0.62, 1.39)	625 (21.1)	412 (20.6)	1.01 (0.85, 1.19)	482 (20.0)	917 (20.2)	0.87 (0.75, 1.01)	
	per allele			0.97 (0.80, 1.19)			0.99 (0.91, 1.08)			0.93 (0.87, 1.00)	0.59