Supplementary Table 1: detailed search strategy of databases

PubMed: 2015/28/10; NO limitation		updated at April 2107
1	"LSP"[All Fields] OR "LSP1"[All Fields] OR "lymphocyte-specific protein"[All Fields] OR "WP34"[All Fields]	2,902
2	"breast cancer"[All Fields] OR "breast tumor"[All Fields] OR "breast neoplasm"[All Fields]	198,551
	1 & 2	57
ISI: 2015/28/10; NO limitation		
1	(“LSP” OR “LSP1” OR “lymphocyte-specific protein” OR “WP34”)	13,144
2	“breast cancer” OR “breast tumor” OR “breast neoplasm”)	1,271,211
	1 & 2	143
EMBASE: 2015/28/10; NO limitation		
1	(LSP* or lymphocyte-specific protein* or WP34).mp. [mp=title, abstract, heading word, drug trade name, original title, device manufacturer, drug manufacturer, device trade name, keyword]	2897
2	(breast ca* or breast neo* or breast tu*).mp. [mp=title, abstract, heading word, drug trade name, original title, device manufacturer, drug manufacturer, device trade name, keyword]	430,448
3	1 & 2	87

Supplementary table 2. Quality of studies assessing the association between LSP1 gene rs3817198T>C polymorphism and breast cancer

Study (year)	Source of control	Population ethnicity	Sample size	menopausal status
Chen, Y. (2016)	+	-	+	-
Deng, Z. (2016)	+	-	+	-
Tan, Tan. (2016)	+	-	+	-
Mizoo, T. (2013)	+	+	+	+
Butt, S. (2012)	+	-	+	-
Shan, J. (2012)	+	+	+	-
Campa, D. (2011)	+	+	+	-
Sueta, A. (2011)	+	-	+	-
Barnholtz-Sloan, J. S. (2010)	+	+	+	-
Gorodnova, T. V.	+	-	+	-
Latif, A. (2010)	+	+	+	-
Tamimi, R. M. (2010)	+	+	+	-

Year: year of publication;
Source of control means clinic (or hospital) based or population based; population ethnicity means Caucasian, African-American and other ethnicity; sample size means calculable sample size; menopausal status means to provide measure of association for pre/post-menopauses.

Supplementary table 3. Characteristics of literature included in the systematic review evaluating the association between LSP1 rs3817198 Polymorphism and breast cancer.

First author	Date	Country	ethnicity	Study design	Control source	Genotyping methods	Analyzed sample size (case number)	Minor allele frequency (case/control)	Considered confounders*
Tan, T.	2016	China	NS	NS	Population based	TaqMan Genotyping Assay	1203(453)	0.11/0.12	-
Chen, Y.	2016	China	NS	Hospital based	Hospital based	TaqMan SNP Genotyping Assays	487(105)	0.10/0.16	Age
Deng, Z.	2016	China	NS	Hospital based	Population based	Matrix-assisted laser desorption ionization-time of flight	719(136)	0.14/0.11	age + BMI
Mizoo, T.	2013	Japan	Japanese	Hospital based	Hospital based	TaqMan genotyping assay	936(472)	0.15/0.13	Age, BMI, smoking, meat intake, mushroom intake, green and yellow vegetable intake, coffee intake, green tea intake, leisure-time exercise and education.
Butt, S.	2012	Sweden	NS	Population based	Population based	(SEQUENOM MassArray)	1999(669)	0.32/0.29	Socioeconomic status and exposure to HRT
Shan, J.	2012	Tunisia	Tunisian	Hospital based	Population based	TaqMan SNP Genotyping assays	1011(640)	-	-
Campa, D.	2011	International	Mix	Population based	Population based	Taqman assays with reagents by Applied Biosystems	20468(8576)	0.29/0.30	Age and ethnicity
Sueta, A.	2011	Japan	NS	Hospital based	Hospital based	TaqMan SNP Genotyping Assays	2091(697)	-/14.9	Age, age at menarche, menopausal status, age at first live birth, body mass index, regular exercise, family history of breast cancer
Barnholtz-Sloan, J. S.	2010	USA	Mix	Hospital based	Population based	Illumina GoldenGate assay	3745(1970)	-	Age
Gorodnova, T. V.	2010	Russia	NS	Population based	Population based	Real-time PCR	314(140)	0.37/0.29	-
Latif, A.	2010	UK	British	Hospital based	Population based	TaqMan genotyping assay	1398(962)	-	-
Tamimi, R. M.	2010	Sweden	Swedish	Hospital based	Population based	Sequenom iPLEX and Taqman	1417(680)	0.31/0.29	Birth weight

Date: year of publication; NS: not state; USA: United State of America; UK: United kingdom
* Confounders in multivariate analysis

Supplementary table 4. List of excluded studies after detailed assessment of literature

NO.	Article Information	Cause of Exclusion
1	Chen, Hai, et al. "Correlation between LSP1 polymorphisms and the susceptibility to breast cancer." *International journal of clinical and experimental pathology* 8.5 (2015): 5798.	Different Gene polymorphism (LSP1 rs569550)
2	Long, Jirong, et al. "Evaluation of breast cancer susceptibility loci in Chinese women." *Cancer Epidemiology Biomarkers & Prevention* 19.9 (2010): 2357-2365.	Lack of Calculable (OR) For Genetic Models
3	Andersen, Shaneda Warren, et al. "The associations between a polygenic score, reproductive and menstrual risk factors and breast cancer risk."*Breast cancer research and treatment* 140.2 (2013): 427-434.	Lack of Calculable (OR) For Genetic Models
4	Tapper, William, et al. "The influence of genetic variation in 30 selected genes on the clinical characteristics of early onset breast cancer." *Breast Cancer Research* 10.6 (2008): 1-10.	Different Gene polymorphsm (LSP1 rs661348)
5	Gaudet, Mia M., et al. "Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk." *PLoS Genet* 9.3 (2013): e1003173.	Lack of Calcuable (OR) For Genetic Models
6	Nickels, Stefan, et al. "Evidence of gene–environment interactions between common breast cancer susceptibility loci and established environmental risk factors." *PLoS Genet* 9.3 (2013): e1003284.	Lack of Calcuable (OR) For Genetic Models
7	Barnes, D. R., et al. "Estimating single nucleotide polymorphism associations using pedigree data: applications to breast cancer." *British journal of cancer* 108.12 (2013): 2610-2622.	Lack of Calcuable (OR) For Genetic Models
8	Couch, Fergus J., et al. "Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk."*PLoS Genet* 9.3 (2013): e1003212.	Lack of Calcuable (OR) For Genetic Models
9	Hemminki, Kari, et al. "Low-risk variants FGFR2, TNRC9 and LSP1 in German familial breast cancer patients." *International Journal of Cancer*126.12 (2010): 2858-2862.	Different Gene polymorhoism (LSP1 rs2271439)
10	Milne, Roger L., et al. "Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study." *Breast Cancer Res* 12.6 (2010): R110.	Lack of Calcuable (OR) For Genetic Models
11	Travis, Ruth C., et al. "Gene–environment interactions in 7610 women with breast cancer: prospective evidence from the Million Women Study." *The Lancet* 375.9732 (2010): 2143-2151.	Lack of Calcuable (OR) For Genetic Models
12	Turnbull, Clare, et al. "Genome-wide association study identifies five new breast cancer susceptibility loci." Nature genetics 42.6 (2010): 504-507.	Lack of Calcuable (OR) For Genetic Models
13	Antoniou, Antonis C., et al. "Common breast cancer susceptibility alleles and the risk of breast cancer for BRCA1 and BRCA2 mutation carriers: implications for risk prediction." Cancer research 70.23 (2010): 9742-9754.	NO measure of association was provided for four genetic model
14	Chen, Min-Bin, et al. "Association of a LSP1 gene rs3817198T> C polymorphism with breast cancer risk: evidence from 33,920 cases and 35,671 controls." Molecular biology reports 38.7 (2011): 4687-4695.	A meta-analysis study
15	Easton, Douglas F., et al. "Genome-wide association study identifies novel breast cancer susceptibility loci." Nature 447.7148 (2007): 1087-1093.	Lack of Calcuable (OR) For dominant and recessive Genetic Models
16	Garcia-Closas, Montserrat, and Stephen Chanock. "Genetic susceptibility loci for breast cancer by estrogen receptor status." Clinical Cancer Research 14.24 (2008): 8000-8009.	Lack of Calcuable (OR) For dominant and recessive Genetic Models
17	Risk of genome-wide association study newly identified genetic variants for breast cancer in Chinese women of Heilongjiang Province	Lack of Calcuable (OR) For dominant and recessive Genetic Models