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SNPs	Minor Allele (%)	Interacting SNPs*	Alteration	Function	Breast Cancer Association§	Selected Biological Processes¶
Higher Rank (Direct Functional Evidence)						
XPD-[Lys751Gln]	C: 32.3	Yes	Missense	Gln (C) allele has decreased DNA repair capacity [15-18]	Yes [83]	transcription-coupled nucleotide-excision repair, ATP-dependent DNA helicase activity
COMT-[Met108/158Val]	G: 47.3	Yes	Missense	Met (A) allele has lower enzymatic activity [20,21]	Yes [84]	neurotransmitter catabolism, catecholamine metabolism
GSTP1-[Ile105Val]	G: 31.2	Yes	Missense	Val (G) allele is associated with reduced enzymatic activity [22,23]	Yes [85]	Metabolism, glutathione transferase activity
MTHFR-[Ala222Val]	T: 35.6	No	Missense	Val (T) allele is associated with reduced enzyme activity [19]	Yes† [86]	Folate metabolism, methylene-tetrahydrofolate reductase (NADPH) activity
CCND1-[Pro241Pro]	A: 46.1	Yes	Splice Variant	(A) allele affects protein stability [24-27]	Yes [87]	G1/S transition of mitotic cell cycle
MMPI1-[IG(-1607)2G]	Ins: 49.7	No	Regulatory	(Ins) allele shows increased transcription [28,29]	No	collagen catabolism, interstitial collagenase activity
IL10-[G(-1082)A]	G: 47.6	Yes	Regulatory	G allele is associated with increased expression [30-32]	No	cell-cell signaling, B-cell differentiation and proliferation, anti-apoptosis.
Medium Rank (Indirect Functional Evidence)						
BARD1-[Pro24Ser]	T: 37.5	Yes	Missense	Proline to serine change is a significant alteration	No	response to DNA damage, protein ubiquitination, regulation of apoptosis
IL13-[Arg130Gln]	A : 18.3	No	Missense	Gln allele associated with increased IgE levels [41]	No	immune response, inflammatory response, signal transduction,
p27-[Val109Gly]	G: 19.4	No	Missense	Possible function [33]	No	regulation of cyclin dependent protein kinase activity
GSTM3-[4595 (3bp ins/del)]	Del: 16.8	No	UTR	creates recognition site for transcription factor YY1 [34]	No	Metabolism, glutathione transferase activity
TNFA-[G(-308)A]	A: 17.6	No	UTR	increased transcriptional activity; also no functional change [35-38]	No	inflammatory response, signal transduction, regulation of transcription, apoptosis
CYP17-[C(518)T]	C: 34.3	No	Regulatory	Associated with increased serum estradiol [39,40]	Yes [4]	C21-Steroid hormone metabolism,

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