Supplementary Table S1. Demographic characteristics of study populations.

| | US Radiologic Technologist | | | | Poland | | | |
|---|---|---|---|---|---|---|---|---|
| | Cases | | Controls | | Cases | | Controls | |
| Age[a] | N | % | N | % | N | % | N | % |
| 20-29 | 15 | 2 | 0 | 0 | 4 | 0.2 | 4 | 0.2 |
| 30-39 | 139 | 16 | 0 | 0 | 62 | 3 | 89 | 4 |
| 40-49 | 354 | 41 | 146 | 14 | 506 | 25 | 565 | 25 |
| 50-59 | 214 | 25 | 353 | 34 | 674 | 34 | 787 | 34 |
| 60-69 | 97 | 11 | 323 | 31 | 510 | 26 | 603 | 26 |
| 70-79 | 37 | 4 | 165 | 16 | 239 | 12 | 248 | 11 |
| 80+ | 4 | 0.5 | 61 | 6 | 0 | 0 | 0 | 0 |
| Time from Dx To Blood Draw | | | | | | | | |
| < 5 years | 43 | 5 | | | 1995 | 100 | | |
| 5-9 years | 311 | 37 | | | | | | |
| 10-14 yers | 243 | 28 | | | | | | |
| 15+ years | 259 | 30 | | | | | | |
| Age at Menarche | | | | | | | | |
| <12 | 431 | 53 | 497 | 50 | 566 | 29 | 514 | 23 |
| 13 | 233 | 29 | 306 | 31 | 433 | 22 | 530 | 23 |
| 14 | 98 | 12 | 128 | 13 | 528 | 27 | 637 | 28 |
| 15 | 42 | 5 | 55 | 6 | 215 | 11 | 258 | 11 |
| 16+ | 10 | 1 | 13 | 1 | 240 | 12 | 330 | 15 |
| Number of full-term births | | | | | | | | |
| 0 | 168 | 20 | 188 | 18 | 290 | 15 | 253 | 11 |
| 1 | 119 | 14 | 140 | 14 | 689 | 35 | 682 | 30 |
| 2 | 275 | 33 | 304 | 29 | 803 | 40 | 1016 | 44 |
| 3+ | 270 | 32 | 401 | 39 | 213 | 11 | 345 | 15 |
| Age at first full-term birth (parous) | | | | | | | | |
| <20 | 21 | 3 | 43 | 5 | 189 | 11 | 286 | 14 |
| 20-24 | 267 | 40 | 420 | 50 | 841 | 49 | 1050 | 51 |
| 25-29 | 254 | 38 | 258 | 31 | 455 | 27 | 511 | 25 |
| 30+ | 122 | 18 | 124 | 15 | 220 | 13 | 196 | 10 |
| Oral Contraceptive | | | | | | | | |
| Never | 396 | 46 | 510 | 49 | 1731 | 88 | 2019 | 89 |
| Ever | 463 | 54 | 536 | 51 | 231 | 12 | 238 | 11 |

The number of subjects for each variable do not add to the total number of subjects in each study due to missing values.

[a] In the USRT study, age is age at diagnosis for cases and age as of 1999 for controls.

Supplementary Table S2. Details of Assays for *ATM* Variants.

| Unequivocal reference[a] | Common SNP Name | CGF Name[b] | F Primer | R primer | VIC Probe | FAM probe | Conditions |
|---|---|---|---|---|---|---|---|
| rs189037 | -4518A>G | ATM-06 | | | | | |
| rs228589 | IVS1+19A>T | NPAT-01 | | | | | |
| rs4585 | IVS10-12792C>A | MGC33948-02 | | | | | |
| rs664677 | IVS21-77C>T | ATM-27 | | | | | |
| rs600329 | IVS31+213T>C | ATM-23 | | | | | |
| rs664143 | IVS62+60G>A | ATM-01 | | | | | |
| rs1800054 | S49C | ATM-09 | gcctgattcgagatcctgaaacaat | gaatacctaaaaacagcatcccaattcaa | ccttgtttggaatctg | cttgtttgcaatctg | Taqman 5' nuclease[c] |
| rs4986761 | S707P | ATM-10 | gatcgctgtcttctgggattatcag | ccttcctaacagtttaccaaagttgaatcata | atctcacctcagatgagtaa | tcacctcaggtgagtaa | Taqman 5' nuclease |
| rs1800056 | F858L | ATM-28 | atggaggtggaggatcagtca | tgcatcactaacactactatcagggtaa | tccatgaatctatttaacg | ccatgaatctacttaacg | Taqman 5' nuclease |
| rs1800889 | P1526P | ATM-02 | cttactgtaaggatgctctagaaaacca | ctgaacctccacctgctcatac | ttggtacacttatacccccttgt | ttggtacacttatacctcttgt | Taqman 5' nuclease |
| rs1800057 | P1054R | | accacagttcttttcccgtagg | acttcatttacaggaaagtcttttcccatt | ccattttgaataggatcag | ccattttgaataacgatcag | Taqman 5' nuclease |
| rs1800058 | L1420F | | tttttactaaatctgtttatttttctaggattcctatcagaa | aacattatttgtttcagctgcttgct | atatggcaagaagaatt | atatggcaaaaagaatt | Taqman 5' nuclease |
| c.1563-1564delAG | 1563delAG | | tggagccataattcagggtagttta | gcaggctgacccagtaaataactt | aggttgacagagagaa | tgacagagaattct | Taqman 5' nuclease |
| c.3576G>A | K1192K_spl | | gagaatggattagaacctcaccttgt | ttcacagtgacctaaggaagcttct | atccatatatacctttttc | catccatatatacttttttc | Taqman 5' nuclease |
| c.3802delG | 3802delG | | aggttttgattccacatctggtgat | tttccagtcctcttgaatctgattagc | aatggacttcacctcatc | aatggacttcactcatc | Taqman 5' nuclease |
| rs800059 | S1691R | | ttgggagaagtgggtcctatagatt | cttaagggccttggtataagatgca | catagctatacaacatagtaaag | atagctatacaacatcgtaaag | Taqman 5' nuclease |
| rs17174393 | IVS62+1G>A | | gggcattacgggtgttgaag | gacatcaaaaattatttccctccttt | tgtcttcagaaggtaagt | tgtcttcagaagataagt | Taqman 5' nuclease |
| g.82970T>G | IVS10-6T>G | | acagcgaaactctggctcaaa | 6FAM-tgatcttttattacttcccagcctagt | | | PCR-RFLP[d] |
| c.7271T>G | V2424G | | acaagcaagctctcctgaaaaga | gtcacttgtagaaacctagttacctgtt | ctaaggagacctacttcct | aggagacctccttcct | Taqman 5' nuclease |
| c.7775C>G | S2592C | | ggtagccagaagaagcagaataact | acacttctaaaaggtacgtatgtttaatcca | caagctgagagcttt | caagctgacagcttt | Taqman 5' nuclease |
| c.7636-7644del9 | 7636del9 | | atgcaggcatacacgctcta | ttgcatttgctaaggccagt | | | DHPLC[e] |
| c.9139C>T | R3047X | | gGcaggccatagaccccaaa | cacacccaagctttccatcct | tcagccgactttt | ctcagctgactttt | Taqman 5' nuclease |

[a] "rs" reference SNP number for variants in dbSNP(http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Snp); "c." represents the nucleotide position, starting from "1" of the ATG start codon, of Genbank record NM_000051.3; "g." represents nucleotide position within Genbank record AP001925.5.

[b] SNP name used at the NCI's Core Genotyping Facility (CGF) (http://snp500cancer.nci.nih.gov/assay_list.cfm). Sequences and other assay information available at their web site. SNPs with entries in both the CGF Name and primer columns were designed and performed independently in both the Laboratory of Population Genetics and the CGF. Primer sequences are those used in the Laboratory of Population Genetics..

[c]Taqman assays were performed according to manufacturer's instructions (Applied Biosystems, Foster City, CA, U.S.A., https://www2.appliedbiosystems.com/).

[d] Performed according to Chenevix-Trench (Chenevix-Trench et al. 2002), with slight modifications. The reverse primer was labeled with a fluorescent dye (6-FAM), the PCR product was digested with RsaI and analyzed as a fragment length polymorphism on an ABI 3730 analyzer and GeneMapper software(Applied Biosystems, Foster City, CA, U.S.A.). Samples were prepared in 384-well format.
[e] dHPLC conditions 52$^0$C; 50% Buffer B (25% ACN), minutes 0-0.5; Buffer B gradient 53% Buffer B- 59% Buffer B, minutes 0.5-3.5.

Supplementary Table S3. Association between all *ATM* variants and breast cancer status in the U.S. Radiologic Technologist (USRT) Study.

| Unequivocal reference[a] | Common SNP Name | Genotype[b] | Cases N | Cases % | Controls N | Controls % | Adjusted OR (95% CI)[c] | *P* |
|---|---|---|---|---|---|---|---|---|
| AT-assoc or function relev[d] | | | | | | | | |
| c.1563-1564 delAG | 1563delAG | Hz WT | 852 | 99.9 | 1037 | 100 | | |
| | | Het | 1 | 0.1 | 0 | | | |
| c.3576G>A | K1192K_spl | Hz WT | 854 | 100 | 1043 | 100 | | |
| c.3802delG | 3802delG | Hz WT | 848 | 100 | 1039 | 100 | | |
| rs1800059 | S1691R | Hz WT | 853 | 99.5 | 1038 | 99.7 | | |
| | | Het | 4 | 0.5 | 3 | 0.3 | | |
| rs17174393 | IVS62+1G>A | Hz WT | 850 | 100 | 1044 | 100 | | |
| c.9139C>T | R3047X | Hz WT | 854 | 100 | 980 | 100 | | |
| g.82970T>G | IVS10-6T>G | Hz WT | 837 | 99.6 | 1021 | 99.6 | | |
| | | Het | 3 | 0.4 | 4 | 0.4 | | |
| c.7271T>G | V2424G | Hz WT | 854 | 100 | 1037 | 100 | | |
| c.7775C>G | S2592C | Hz WT | 851 | 100 | 1043 | 100 | | |
| c.7636-7644 del9 | 7636del9 | Hz WT | 837 | 99.9 | 1036 | 100 | | |
| | | Het | 1 | 0.1 | 0 | | | |
| | Any mutation[e] | All WT | 852 | 99.0 | 1041 | 99.3 | | |
| | | Het | 9 | 1.0 | 7 | 0.7 | 1.87 (0.58 – 5.96) | 0.3 |
| Missense changes | | | | | | | | |
| rs1800054 | S49C | Hz WT | 821 | 96.1 | 1013 | 97.4 | 1.0 | |
| | | Het | 33 | 3.9 | 27 | 2.6 | 1.60 (0.88 – 2.90) | 0.1 |
| rs4986761 | S707P | Hz WT | 837 | 98.4 | 999 | 96.7 | 1.0 | |
| | | Het | 14 | 1.6 | 34 | 3.3 | 0.47 (0.23 – 0.93) | 0.03 |
| rs1800056 | F858L | Hz WT | 826 | 96.5 | 1023 | 98.2 | 1.0 | |
| | | Het | 30 | 3.5 | 19 | 1.8 | 2.03 (1.05 – 3.90) | 0.03 |
| rs1800057 | P1054R | Hz WT | 808 | 94.4 | 985 | 94.9 | 1.0 | |
| | | Het | 48 | 5.6 | 53 | 5.1 | 1.08 (0.68 – 1.70) | 0.7 |
| rs1800058 | L1420F | Hz WT | 819 | 96.0 | 1001 | 95.9 | 1.0 | |
| | | Het | 34 | 4.0 | 43 | 4.1 | 0.87 (0.52 – 1.45) | 0.6 |
| Silent Change | | | | | | | | |
| rs1800889 | P1526P | Hz WT | 791 | 94.2 | 951 | 91.6 | 1.0 | |
| | | Het | 47 | 5.6 | 87 | 8.4 | 0.75 (0.48 – 1.11) | |
| | | Hz Var | 2 | 0.2 | 0 | | Inf. | |
| | | | | | | | | 0.4 (df=2)[f] |

[a] "rs" reference SNP number for variants in dbSNP(http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Snp); "c." represents the nucleotide position within genbank record NM_000051.3; "g." represents nucleotide position within genbank record AP001925.5.
[b] Hz WT subjects are homozygous for the reference/wild-type allele; Het subjects are heterozygous for the variation; Hz Var subjects are homozygous for the non-reference/variant allele.
[c] Odds ratio, adjusted for age (below 50, 50-59, 60-69, 70+).
[d] *ATM* mutations identified in 5 or more AT patients more than one population group or from British AT patients (http://www.vmresearch.org/investigators/concannon_patrick/atmut-t.htm as of June 2000), and those showing functional significance in a biochemical assay (S2592C (Scott et al. 2002), 7636del9(Chenevix-Trench et al. 2002), V2424G(Chenevix-Trench et al. 2002), IVS10-6G>T(Bonnen et al. 2002; Tamimi et al. 2004; Lee et al. 2005)).
[e] Subjects carrying any of the above 10 mutations.
[f] *P* value for unadjusted likelihood ratio chi square test with 2 degrees of freedom for overall difference in genotype frequencies between cases and controls.

Supplementary Table S4. Association between all *ATM* variants and breast cancer status in the Polish Breast Cancer Case-control Study.

| rs num[a] | SNP Name | Genotype[b] | Cases N | Cases % | Controls N | Controls % | Unadjusted OR (95% CI)[c] | *P* |
|---|---|---|---|---|---|---|---|---|
| Intron/non-coding SNPs[d] | | | | | | | | |
| 189037 | -4518A>G | AA | 582 | 29.5 | 633 | 27.9 | 1.0 | |
| | | AG | 988 | 50.0 | 1168 | 51.4 | 0.92 (0.80 – 1.06) | |
| | | GG | 405 | 20.5 | 470 | 20.7 | 0.94 (0.79 – 1.17) | 0.5 (df=2)[f] |
| 228589 | IVS1+19A>T | AA | 571 | 28.9 | 628 | 27.6 | 1.0 | |
| | | AT | 992 | 50.3 | 1172 | 51.5 | 0.93 (0.81 – 1.07) | |
| | | TT | 411 | 20.8 | 474 | 20.8 | 0.95 (0.80 – 1.14) | 0.6 (df=2)[f] |
| 4585 | IVS10-12792C>A | CC | 581 | 29.7 | 637 | 28.2 | 1.0 | |
| | | CA | 952 | 48.6 | 1135 | 50.2 | 0.92 (0.80 – 1.06) | |
| | | AA | 424 | 21.7 | 488 | 21.6 | 0.95 (0.80 – 1.13) | 0.5 (df=2)[f] |
| 664677 | IVS21-77C>T | CC | 594 | 29.9 | 649 | 28.4 | 1.0 | |
| | | CT | 990 | 49.8 | 1173 | 51.3 | 0.92 (0.80 – 1.06) | |
| | | TT | 402 | 20.2 | 466 | 20.4 | 0.94 (0.79 – 1.12) | 0.5 (df=2)[f] |
| 600329 | IVS31+213T>C | CC | 568 | 29.4 | 644 | 28.8 | 1.0 | |
| | | CT | 953 | 49.3 | 1123 | 50.2 | 0.99 (0.83 – 1.11) | |
| | | TT | 411 | 21.3 | 470 | 21.0 | 1.01 (0.95 – 1.07) | 0.9 (df=2)[f] |
| 664143 | IVS62+60G>A | GG | 579 | 29.5 | 637 | 28.2 | 1.0 | |
| | | GA | 983 | 50.0 | 1165 | 51.5 | 0.93 (0.81 – 1.07) | |
| | | AA | 404 | 20.5 | 461 | 20.4 | 0.97 (0.81 – 1.15) | 0.6 (df=2)[f] |
| Missense changes[e] | | | | | | | | |
| 1800054 | S49C | Hz WT | 1933 | 97.7 | 2258 | 98.8 | 1.0 | |
| | | Het | 45 | 2.3 | 28 | 1.2 | 1.88 (1.17 – 3.02) | 0.009 |
| 4986761 | S707P | Hz WT | 1923 | 97.9 | 2231 | 98.3 | 1.0 | |
| | | Het | 42 | 2.1 | 39 | 1.7 | 1.25 (0.08 – 1.94) | 0.3 |
| 1800056 | F858L | Hz WT | 1924 | 98.5 | 2230 | 98.6 | 1.0 | |
| | | Het | 30 | 1.5 | 31 | 1.4 | 1.12 (0.67 – 1.86) | 0.7 |
| Silent Change[e] | | | | | | | | |
| 1800889 | P1526P | Hz WT | 1702 | 85.9 | 1962 | 85.9 | 1.0 | |
| | | Het | 273 | 13.8 | 308 | 13.5 | 1.02 (0.9 – 1.2) | |
| | | Hz Var | 7 | 0.4 | 14 | 0.6 | 0.58 (0.23 – 1.43) | 0.5 (df=2)[f] |

[a] Reference SNP number (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Snp).
[b] Hz WT subjects are homozygous for the reference/wild-type allele; Het subjects are heterozygous for the variation; Hz Var subjects are homozygous for the non-reference/variant allele.
[c] Odds ratio, adjusted for age (below 50, 50-59, 60-69, 70+).
[d] SNPs chosen for study based on preliminary analyses in the USRT Study.
[e] SNPs from prior studies of *ATM* with assay available at the NCI's Core Genotyping Facility (http://snp500cancer.nci.nih.gov/assay_list.cfm as of Jan 2004).
[f] *P* value for unadjusted likelihood ratio chi square test with 2 degrees of freedom for overall difference in genotype frequencies between cases and controls.