

Genome-wide association study identifies multiple loci associated with bladder cancer risk

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Candidate gene and genome-wide association studies (GWAS) have identified 11 independent susceptibility loci associated with bladder cancer risk. To discover additional risk variants, we conducted a new GWAS of 2422 bladder cancer cases and 5751 controls, followed by a meta-analysis with two independently published bladder cancer GWAS, resulting in a combined analysis of 6911 cases and 11 814 controls of European descent. TaqMan genotyping of 13 promising single nucleotide polymorphisms with $P < 1 \times 10^{-5}$ was pursued in a follow-up set of 801 cases and 1307 controls. Two new loci achieved genome-wide statistical significance: rs10936599 on 3q26.2 ($P = 4.53 \times 10^{-9}$) and rs907611 on 11p15.5 ($P = 4.11 \times 10^{-8}$). Two notable loci were also identified that approached genome-wide statistical significance: rs6104690 on 20p12.2 ($P = 7.13 \times 10^{-7}$) and rs4510656 on 6p22.3 ($P = 6.98 \times 10^{-7}$); these require further studies for confirmation. In conclusion, our study has identified new susceptibility alleles for bladder cancer risk that require fine-mapping and laboratory investigation, which could further understanding into the biological underpinnings of bladder carcinogenesis.

INTRODUCTION

Each year ~380 000 bladder cancers are diagnosed worldwide, with men being three to four times more likely than women to be diagnosed with the disease (1,2). Family history of bladder cancer is associated with ~2-fold increased risk, suggesting shared genetic and potential environmental contribution to its etiology (3,4). Meta-analyses of established candidate genes and genome-wide association studies (GWAS) have identified 11 loci that harbor bladder cancer susceptibility alleles: 1p13.3 (*GSTM1*), 2q37.1 (*UGT1A* cluster), 3q28 (*TP63*), 4p16.3 (*TMEM129* and *TACC3-FGFR3*), 5p15.33 (*TERT-CLPTMIL*), 8p22 (*NAT2*), 8q24.21, 8q24.3 (*PSCA*), 18q12.3 (*SLC14A1*), 19q12 (*CCNE1*) and 22q13.1 (*CBX6*, *APOBEC3A*) (5–14). Using an approach that estimates the number of susceptibility loci and the distribution of their effect sizes based on previously reported loci (15), many additional common single nucleotide polymorphisms (SNPs) for bladder cancer are yet to be discovered (9). To search for such loci, we performed a new scan of 2422 cases and 5751 controls (National Cancer Institute, NCI-GWAS2). We then conducted a meta-analysis with two previously independently published GWAS [NCI-GWAS1 and Texas Bladder Cancer Study (TXBCS)-GWAS] (9,10). Here, we present our GWAS analysis that included 6911 cases and 11814 cancer-free controls, and follow-up of promising loci with TaqMan genotyping in an independent set of 801 cases and 1307 controls from the TXBCS (TXBCS-TaqMan).

RESULTS

After applying standard quality control metrics, the new bladder cancer GWAS was comprised 2422 cases genotyped with the HumanHap 660w and HumanHap 610 (Illumina, San Diego, CA, USA) and 5751 cancer-free controls selected from previously scanned studies at the NCI (NCI-GWAS2) (Fig. 1, Supplementary Material, Table S1) (9,16–21). Meta-analysis of previously published data for 11 reported bladder cancer susceptibility loci (5–14), including data from NCI-GWAS2, confirmed bladder cancer risk associations close to or below genome-wide significance (Supplementary Material, Table S2). In addition, using a TaqMan-based deletion detection assay, we also confirmed an association with null versus present copy number variation in *GSTM1* (1p13.3) (9) (Supplementary Material, Table S2).

To identify new bladder cancer susceptibility loci, a meta-analysis was performed using the NCI-GWAS2 dataset with two previously published bladder cancer GWAS: NCI-GWAS1 (6,9), and TXBCS-GWAS (10) (Figure 1). The primary analytical approach employed logistic regression models for genotype trend effects (with 1 d.f.) adjusted for study group, age, sex and smoking status. NCI-GWAS1 and NCI-GWAS2 were further adjusted for six eigenvectors (see Materials and Methods, Supplementary Material, Fig. S1). After rigorous quality control metrics were applied across the sets of called genotypes from the three GWAS datasets (see Materials and Methods), 462 190 common genotyped SNPs were available for analysis (Figure 1). A manhattan plot shows the results based on the meta-analysis of the three GWAS (Supplementary Material, Fig. S2).

After excluding previously identified regions associated with bladder cancer in our primary analysis, we identified 13 SNPs with $P < 1 \times 10^{-5}$, for which we developed TaqMan assays for follow-up analysis in an independent set of 801 cases and 1307 controls not included in the GWAS analysis from the TXBCS (Figure 1). Combined meta-analysis for the 13 SNPs adjusted for smoking, gender, age, study group and six eigenvectors for NCI-GWAS2 and NCI-GWAS1, identified two new loci below genome-wide statistical significance (Table 1, Supplementary Material, Table S3): rs10936599 on 3q26.2 ($P = 4.53 \times 10^{-9}$) and rs907611 on 11p15.5 ($P = 4.11 \times 10^{-8}$). Study-specific estimates are shown in Supplementary Material, Figure S3.

The most significant finding was for rs10936599 at 3q26.2 (OR_{adj} per T allele = 0.85, 95% CI 0.81–0.90, $P = 4.53 \times 10^{-9}$; Table 1), which maps to a multigenic region that includes *TERC*, *ACTRT3* (also known as *ARPM1*), *MYNN* and *LRRC34* (Fig. 2a). Using ENCODE resources (22), including HaploReg (23) and RegulomeDB (24), there were 35 highly correlated SNPs with rs10936599 with $r^2 > 0.8$ (based on 1000 Genomes CEU). We evaluated these 35 SNPs and found many of them to be located within the areas predicted to act as enhancers or promoter based on specific chromatin modification marks (Supplementary Material, Table S4). The 40 kb linkage disequilibrium (LD) block surrounding rs10936599, includes a coding synonymous variant rs10936599 (His6His) within *MYNN*, missense variants rs6793295 (Ser249Gly) and rs10936600 (Leu254Ile) within *LRRC34* (Supplementary Material, Table S4). Imputation analysis did not yield any signals with a stronger association (Fig. 2a). RNA-sequencing analysis in tumor ($n = 7$) and adjacent normal ($n = 5$) bladder tissue showed expression of *ACTRT3*, *MYNN* and *LRRC34* while expression of *TERC* was below the level of confident detection by RNA sequencing (Supplementary Material, Fig. S4a). Expression analysis of individual transcripts using more sensitive TaqMan assays in a larger set of bladder tissues (41 muscle-invasive tumors and 40 adjacent normal samples) showed higher expression of these transcripts in tumors compared with normal tissues: *TERC* ($P = 3.2 \times 10^{-21}$), *MYNN* ($P = 2.4 \times 10^{-4}$) and *ACTRT3* ($P = 4.8 \times 10^{-4}$), but did not show significant differences in relation to rs10936599 genotypes (Supplementary Material, Fig. S5).

The next most significant finding was rs907611 on 11p15.5, which maps upstream of the *LSP1* gene (OR_{adj} per A allele = 1.15, 95% CI 1.09–1.21, $P = 4.11 \times 10^{-8}$). Data for the rs907611 SNP were missing for one study. The American Cancer Society's Cancer Prevention Study II due to <90% completion rates, but there was no evidence of significant heterogeneity by study group among those studies with SNP data that passed quality control metrics ($I^2 = 9.1\%$, $P = 0.36$) (Supplementary Material, Fig. S3); TaqMan genotyping of 376 unique samples (145 cases and 231 controls) from seven studies showed 100% concordance with GWAS data for this SNP. The rs907611 SNP lies 130 bp upstream of the transcription start site for the longer transcript of the *LSP1* gene (Fig. 2b). The 10 kb LD block includes 11 SNPs highly correlated ($r^2 > 0.8$) with rs907611 (based on 1000 Genomes CEU), all located within the first exon and part of the intron of *LSP1* gene, which also includes *miRNA-4298* (Fig. 2b, Supplementary Material, Fig. S4b). Imputation analysis did not yield any signals with a stronger association (Fig. 2b). TaqMan expression analysis in

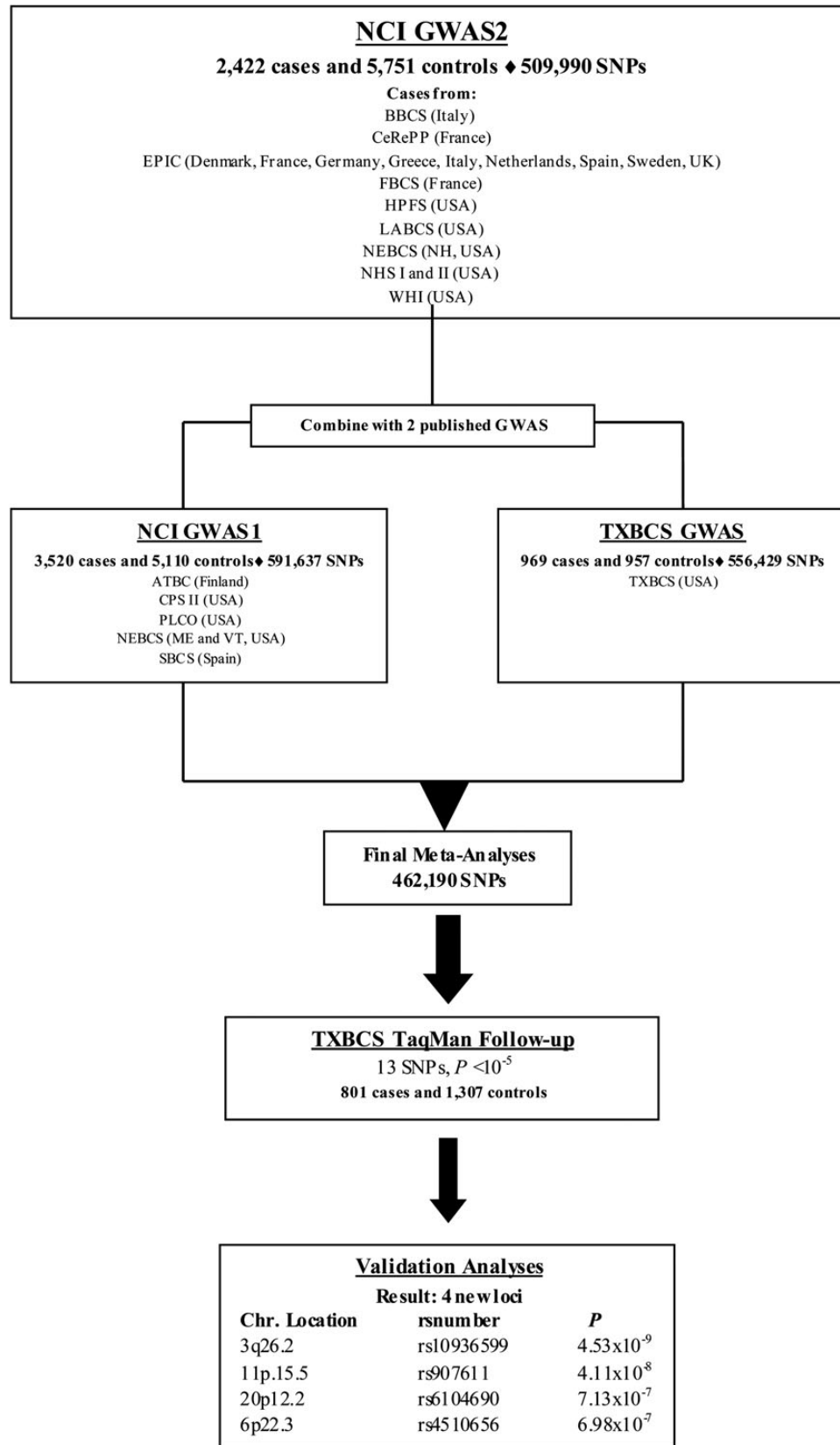


Figure 1. See Supplementary Material, Table S1 for details of study designs and sample sizes. The New England Bladder Cancer Study (NEBCS) represents a single study comprises Maine (ME) and Vermont (VT) components genotyped in NCI-GWAS1, and the New Hampshire (NH) component genotyped in NCI-GWAS2.

Table 1. Associations for rs10936599 at 3q26.2, rs907611 at 11p15.5, rs6104690 at 20p12.2 and rs4510656 at 6p22.3 with bladder cancer risk

| SNP | Cytoband | Alleles | Minor allele | MAF | Cases | Controls | Group | OR _{adj} | (95% CI) | P _{trend} | | |
|------------|----------|---------|--------------|------|-------|----------|--------------|-------------------|-----------|-------------------------|-------------------------|-------------------------|
| rs10936599 | 3q26.2 | T/C | T | 0.24 | 2415 | 5751 | NCI-GWAS2 | 0.81 | 0.73 0.89 | 4.53 × 10 ⁻⁹ | | |
| | | | | 0.24 | 3517 | 5107 | NCI-GWAS1 | 0.88 | 0.81 0.94 | | | |
| | | | | 0.24 | 969 | 957 | TXBCS-GWAS | 0.84 | 0.72 0.98 | | | |
| | | | | 0.25 | 790 | 1293 | TXBCS-TaqMan | 0.90 | 0.77 1.05 | | | |
| rs907611 | 11p15.5 | G/A | A | 0.31 | 7691 | 13 108 | Combined | 0.85 | 0.81 0.90 | | | |
| | | | | 0.31 | 2379 | 5720 | NCI-GWAS2 | 1.25 | 1.14 1.36 | | | |
| | | | | 0.33 | 2757 | 4314 | NCI-GWAS1 | 1.12 | 1.04 1.2 | | | |
| | | | | 0.32 | 968 | 955 | TXBCS-GWAS | 1.20 | 1.04 1.39 | | | |
| rs6104690 | 20p12.2 | G/A | G | 0.31 | 797 | 1291 | TXBCS-TaqMan | 0.97 | 0.84 1.12 | | 4.11 × 10 ⁻⁸ | |
| | | | | 0.44 | 2409 | 5747 | NCI-GWAS2 | 0.89 | 0.82 0.96 | | | |
| | | | | 0.44 | 3510 | 5097 | NCI-GWAS1 | 0.89 | 0.84 0.95 | | | |
| | | | | 0.45 | 969 | 957 | TXBCS-GWAS | 0.91 | 0.79 1.04 | | | |
| rs4510656 | 6p22.3 | C/A | A | 0.46 | 790 | 1287 | TXBCS-TaqMan | 0.89 | 0.78 1.02 | 7.13 × 10 ⁻⁷ | | |
| | | | | 0.45 | 2416 | 5747 | NCI-GWAS2 | 0.87 | 0.8 0.95 | | | |
| | | | | 0.43 | 3515 | 5106 | NCI-GWAS1 | 0.91 | 0.85 0.97 | | | |
| | | | | 0.45 | 968 | 957 | TXBCS-GWAS | 0.88 | 0.77 1.01 | | | |
| | | | | 0.46 | 798 | 1300 | TXBCS-TaqMan | 0.90 | 0.79 1.03 | | | 6.98 × 10 ⁻⁷ |
| | | | | 0.46 | 7678 | 13 088 | Combined | 0.89 | 0.85 0.93 | | | |
| | | | | 0.46 | 7697 | 13 110 | Combined | 0.89 | 0.85 0.93 | | | |
| | | | | | | | | | | | | |

OR adjusted for age, study group, smoking status and gender. Fixed-effects meta-analysis by stage was used to calculate the combined OR, 95% CI and P-trend.

the set of bladder tissues showed comparable expression of *LSP1* and *mir-4298* in relation to sample status (normal or tumor) and rs907611 genotypes (Supplementary Material, Fig. S5). *LSP1*, *mir-4298* expression levels did not show significant differences in relation to rs907611 genotypes (Supplementary Material, Fig. S5).

In the analysis, there were also two notable regions that approached genome-wide significance. The first observed signal was marked by rs6104690 at 20p12.2, a non-genic region (OR_{adj} per G allele = 0.89, 95% CI 0.85–0.93, $P = 7.13 \times 10^{-7}$) (Fig. 2c, Supplementary Material, Fig. S4c). Imputation analysis did not yield any signals with a stronger association (Fig. 2c). There was some suggestion of potential heterogeneity by study group for rs6104690 with an I^2 value of 36.3 and $P = 0.09$ (Supplementary Material, Fig. S3). The study heterogeneity was driven by the Italy group composed of Environment and Genetics in Lung cancer Etiology Study (EAGLE) controls and BRESCIA cases, since when we removed this group the $I^2 = 0.0$, $P = 0.48$. The 7 kb LD block includes seven SNPs with $r^2 > 0.8$ with rs6104960 (based on 1000 Genomes CEU). HaploReg data for rs6104690 and seven linked SNPs shows that these variants are located within predicted enhancers, DNase I hypersensitivity sites, and transcription factor binding sites (Supplementary Material, Table S4). The second observed signal was marked by rs4510656 at 6p22.3 (OR_{adj} per A allele = 0.89, 95% CI 0.85–0.93, $P = 6.98 \times 10^{-7}$), which maps to the intronic region of *CDKALI* (Figure 2d). The 17 kb LD block at 6p22.3 includes 22 SNPs highly correlated ($r^2 > 0.8$) with rs4510656 (based on 1000 Genomes CEU), all located within the *CDKALI* gene (Supplementary Material, Fig. S4d). Imputation analysis did not yield any signals with a stronger association (Fig. 2d). TaqMan expression analysis in the set of bladder tissues showed significantly higher levels of *CDKALI* expression in tumors compared with normal tissue ($P = 6.98 \times 10^{-4}$), but did not show significant differences by rs4510656 genotypes (Supplementary Material, Fig. S5).

Within the combined NCI-GWAS1 and GWAS2 datasets, we tested for multiplicative and additive interactions and smoking status (ever/never) for all bladder cancer susceptibility SNPs. We found evidence of significant interaction with smoking on the multiplicative scale for the SNP rs1495741 at *NAT2*, while 11 of the 14 bladder susceptibility SNPs showed evidence of additive interactions in NCI-GWAS2 and NCI-GWAS1 datasets, including rs10936599 and rs4510656, Supplementary Material, Table S5. Analyses of SNP–SNP interactions for the 14 identified bladder cancer susceptibility loci did not suggest evidence for interaction after adjustment for multiple comparisons (data not shown). Analysis of SNP associations by tumor stage and grade suggested a stronger association between rs907611 and rs10936599 and lower grade tumors, Supplementary Material, Table S6.

DISCUSSION

Using our new NCI-GWAS2 data combined with two published bladder cancer GWAS (9,10) and follow-up TaqMan data from for 13 SNPs, we report two new susceptibility regions on 3q26.2 and 11p15.5, plus two suggestive regions on 20p12.2 and 6q22.3 that need further confirmation. As suggested by the Park model, the larger sample size led to the discovery of additional susceptibility regions marked by common, low-penetrance variants (15). Further, using the largest dataset of bladder cancer cases to date, we have refined the risk estimates for previously published loci and provide further support for additive interactions with smoking as noted previously (25). Imputation analysis in all four regions did not yield any signals with a stronger association.

Our strongest signal was for the rs10936599 SNP within 3q26.2, which has been associated in a GWAS of colorectal cancer (26) and approached genome-wide significance in a GWAS of multiple sclerosis (27). The rs10936599 SNP is in complete LD ($r^2 = 1.0$ in 1000 Genomes, CEU) with SNP

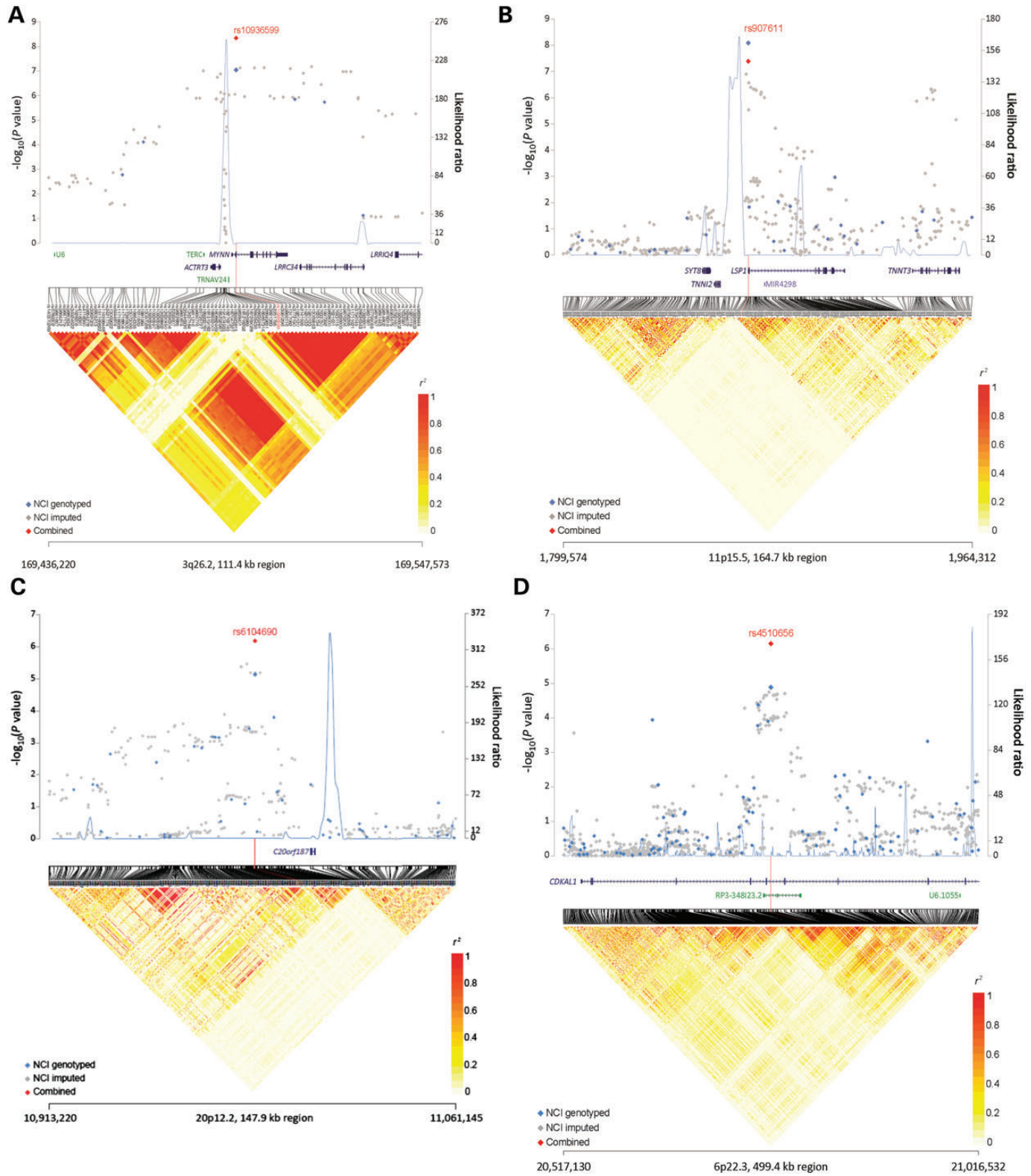


Figure 2. (A–D) The $-\log_{10}(P\text{-value})$ (Y-axis) for NCI-GWAS1 and NCI-GWAS2 genotyped SNPs (blue) and imputed SNPs (gray) was plotted on the genomic coordinates (X-axis; NCBI genome build 37). The combined data for NCI-GWAS1, NCI-GWAS2, TXBCS-GWAS and TXBCS-TaqMan for four novel regions rs10936599 (3q16.2), rs907611 (11p15.5), rs6104690 (20p12.2) and rs4510656 (6p22.3) are shown in red.

rs2293607 located upstream of the *TERC* transcript, which has been shown to affect mRNA folding and telomere length in functional studies (28,29). The *telomerase RNA component (TERC)* gene located within this region is a strong candidate for the association with bladder cancer. *TERC* serves as a template for extension of telomeres by the telomerase reverse transcriptase (*TERT*) and the ability of cells to maintain long telomeres is proposed as a mechanism associated with cell proliferation and cancer (30). Interestingly, a genetic variant within the *TERT* region has been associated with increased risk of bladder cancer in two GWAS (9,14). We found significantly higher *TERC* mRNA expression in muscle-invasive bladder tumors compared with adjacent normal bladder tissues, and a previous report showed significantly higher *TERC* mRNA expression in muscle-invasive compared with superficial bladder tumors (31). Cumulatively, these data suggest that *TERC* may have functional relevance for bladder cancer susceptibility through its function in bladder tissue. However, the possible functional effects of other genes (*MYNN* and *ACTRT3*) in the associated LD block cannot be excluded as a molecular cause of this association.

The LD block rs907611 SNP at 11p15.5 and its associated LD block includes a part of the *LSP1* gene and *miRNA-4298*. *LSP1* is an intracellular F-actin binding protein, which in mouse models is important for regulation of leukocyte recruitment to inflamed sites (32). Chronic inflammation is an important factor in bladder cancer initiation and development, as evidenced by the role of infection with schistosomiasis, a urinary parasite associated with bladder cancer risk primarily in Northern Africa (33). The rs907611 SNP has also been associated with ulcerative colitis, one of the major types of inflammatory bowel disease (34), and an independent marker in this region has also been associated with breast cancer risk (35). *miRNA-4298*, found to be expressed both in normal and tumor bladder tissue, is also an interesting candidate for this association signal since miRNAs have documented importance for carcinogenesis (36). Genetic variants within miRNAs might affect the level of miRNA expression, secondary structure, stability and the efficiency of interaction with their targets (37).

The rs6104690 SNP lies within a region of chromosome 20p12.2 with no known genes and there is little data suggesting any functional mechanisms. The associated LD block at 6p22.3 maps within the *CDKAL1* gene and we showed differences in expression for *CDKAL1* with higher levels found in tumors compared with normal bladder tissues. *CDKAL1* variants have been previously associated with insulin secretion and type 2 diabetes risks as well as Crohn's disease (38–41); however, the rs4510656 SNP associated with bladder cancer seems to be an independent signal from these variants based on low LD ($r^2 < 0.20$).

In summary, we refined risk estimates for 11 previously identified bladder cancer susceptibility loci and report up to four new susceptibility loci. We present functional data for three of the new bladder cancer susceptibility regions (3q26.2 and 11p15.5, and 6q22.3), supporting their potential relevance to bladder carcinogenesis. Interestingly, the 3q26.2 and 11p15.5, and 6q22.3 regions associated with bladder cancer have been identified in GWAS studies of other diseases, suggesting pleiotropy for these genetic effects (42). These new observations raise questions and provide new avenues for investigation that

could shed light on shared mechanisms between cancers and other diseases. At the same time, we recognize that each of the four susceptibility regions will need to be carefully mapped to determine the optimal variants for estimating risk. Identification of bladder cancer susceptibility variants as described here provide a foundation to improve risk prediction and explore the complex interplay of genes and environmental exposures involved in bladder carcinogenesis.

MATERIALS AND METHODS

Study participants

The samples and studies for the NCI-GWAS2 are listed in Supplementary Material, Table S1. Cases and controls were non-Hispanic Caucasians of European origin. Cases were defined as histologically confirmed primary carcinoma of the urinary bladder including carcinoma *in situ* (ICD-0-2 topography codes C67.0-C67.9 or ICD9 codes 188.1–188.9). Each participating study obtained informed consent from study participants and approval from the corresponding Institutional Review Boards. Participating studies obtained institutional certification permitting data sharing in accordance with the NIH policy for sharing of data obtained in NIH supported or conducted GWAS.

Genotyping and quality control

For NCI-GWAS2, we performed genotyping on cases and controls for the New Hampshire component of the New England Bladder Cancer Study (NEBCS-NH). Samples from the other two study centers (Maine and Vermont) in the NEBCS were genotyped in NCI-GWAS1 with a dense SNP array as reported previously ((9), Supplementary Material, Table S1). We genotyped cases and used existing control data for four cohort studies already subjected to rigorous quality control metrics: the European Prospective Investigation Into Cancer and Nutrition Study (EPIC), Women's Health Initiative (WHI), Health Professionals Follow-up Study (HPFS) and Nurses' Health Study I and II (NHS I and II), which have been a part of Cancer Genetic Markers of Susceptibility (CGEMS) (Supplementary Material, Table S1). We genotyped cases for four case-control studies, the Los Angeles Bladder Cancer Study (LABCS), the French Center for Research on Prostate Diseases (CeRePP), the French Bladder Study (FBCS) and the Brescia Bladder Cancer Study (BBCS). For LABCS, CeRePP, FBCS and BBCS studies where we genotyped cases only, we created *in silico* study groups based on comparable geographic/demographic parameters, which resulted in three new 'study groups', specifically, Europe (which comprises data from EPIC, CeRePP, and FBCS), Multiethnic Cohort (MEC)/LA (which comprises cases from LABCS and controls from the MEC) and Italy (which comprises cases from BBCS and controls from the EAGLE).

DNA samples for cases in NCI-GWAS2 were selected for genotyping based on pre-genotyping quality control measures performed for GWAS at the Cancer Genomics Research Laboratory of the NCI (CGR). 1504 samples were attempted at CGR on the Illumina HumanHap660 chips for NCI-GWAS2. The 1504 bladder cancer case samples, mapped to 1483 unique individuals from seven studies: HPFS, BBCS, FBCS, CeRePP, WHI,

LABCS and NHS I and II. A total of 816 EPIC bladder cases were genotyped in UK and mapped to 772 unique individuals. In addition, 742 samples from NEBCS-NH were genotyped on Illumina HumanHap610 chip at the CGR, mapping to 720 unique individuals. Genotype clusters were estimated with samples by study with preliminary completion rates >98% per individual study (namely, EPIC, WHI, LABCS, NEBCS-NH, CeRePP, FBSC, BBSC, HPFS and NHS I and II). Genotypes for the analytical build were based on study-specific clustering. SNP assays with locus call rates <90% were excluded. The number of SNPs available for association analysis for NCI-GWAS2 was 509 990. After quality control metrics were applied to the full data set, 462 190 SNPs overlapped across the three GWAS datasets. Access to the NCI-GWAS1 and GWAS2 genotypes are available through dbGAP identifier, phs000346.v2, at <http://www.ncbi.nlm.nih.gov/gap>.

Additional participants were excluded based on: (i) completion rates <94–96% ($n = 126$ samples), (ii) heterozygosity of <27% or >33% ($n = 13$), (iii) gender discordant subjects ($n = 26$), (iv) one from each first-degree relative pairs including unexpected duplicates ($n = 33$). Seventy-five expected duplicates were evaluated and yielded an average concordance rate of 99.93%.

Assessment of the population substructure of study participants was performed with Genotyping Library and Utilities (GLU) *struct.admix* module by seeding the analysis with founder genotypes from three HapMap populations (build 26) (43). A set of 12 898 SNPs with extremely low pair-wise correlation ($r^2 < 0.004$) was selected for this analysis (44–46). A total of 79 participants (15 cases and 64 controls) were estimated to have <80% HapMap CEU admixture (Supplementary Material, Fig. S6). Principal component analysis (PCA) of genotyped subjects (excluding one from each inferred closely related pairs) was performed with GLU *struct.pca* module (a similar procedure to EIGENSTRAT) (44,45). We ran a logistic regression model based on studies in NCI GWAS2 or studies in NCI GWAS1, respectively, and the eigenvectors that we adjusted for in the regression model were derived from principal components analysis, which were significantly associated with the case–control status based on each coefficient z statistic with P -value of <0.05, as has been shown previously (47–49). Based on this analysis, we adjusted for EV4 in NCI-GWAS1 and (EV1, 2, 3, 4, 6, 7) for NCI-GWAS2. We also evaluated PCs by each case–control set and adjustment by PCs by this alternate approach yielded similar association results (data not shown).

We estimated the inflation of the test statistic, λ , adjusted to a sample size of 1000 cases/1000 controls as per the method of de Bakker *et al.* λ (corrected) = $1 + (\lambda - 1) \times [n_{\text{case}}^{-1} + n_{\text{cont}}^{-1}] / [2 \times 10^{-3}]$ (50). A quantile–quantile plot of NCI-GWAS2 data showed some enrichment of the test statistics at lower P -values compared with the expected uniform distribution (Supplementary Material, Fig. S7). The corrected estimated λ_{1000} is 1.004, whereas the uncorrected λ is 1.012. For the NCI-GWAS1 and TXBCS-GWAS, genotyping was conducted as previously described (9,10). A quantile–quantile plot of combined meta-analysis data from NCI-GWAS2, NCI-GWAS1 and TXBCS-GWAS showed a $\lambda = 1.016$ and after removal of SNPs 200 kb within the 14 bladder cancer susceptibility regions with tag SNPs $\lambda = 1.015$ (Supplementary Material, Fig. S8).

Custom TaqMan genotyping assays (ABI, Foster City, CA, USA) were designed and optimized for 13 SNPs. TaqMan genotyping for the 13 SNPs in TXBCS replication samples were conducted at MD Anderson Cancer Center. For the four SNPs with the most significant associations that achieved or approached genome-wide significance (rs10936599 at 3q26.2, rs907611 at 11p15.5, rs6104690 at 20p12.2 and rs4510656 at 6p22.3), a total of 425 samples were randomly chosen from NCI-GWAS scans for technical validation. One sample was excluded due to its low completion rate (<80%, i.e. no call for more than one assay), and the remaining 424 samples were merged into 376 unique individuals (145 cases and 231 controls). The overall concordance rate for 48 pairs of blind duplicates was 100%. A comparison of the genotypes from the GWAS scan and these TaqMan assays showed 100% concordance among the 376 unique individuals for these four SNPs. The Illumina Infinium cluster plots for the four novel associations, rs10936599 at 3q26.2, rs907611 at 11p15.5, rs6104690 at 20p12.2 and rs4510656 at 6p22.3 are shown in Supplementary Material, Figure S9.

Association analysis

Primary association analyses used logistic regression, adjusted for age (in 5-year categories), sex and study group. Based on the results of the PCA described above (Supplementary Material, Fig. S1), we further adjusted for eigenvectors in NCI GWAS datasets: EV4 for NCI-GWAS1 and (EV1, 2, 3, 4, 6, 7) for NCI-GWAS2. Each SNP genotype was coded as a count of minor alleles, with the exception of X-linked SNPs among men that were coded as 2 if the participant carried the minor allele and 0 if he carried the major allele (51). A score test with one degree of freedom was performed on all genetic parameters in each model to determine statistical significance. We assessed heterogeneity in genetic effects across study groups using the I^2 statistic. Fixed-effects meta-analysis were conducted for the 13 SNPs assessed across the four datasets, using allelic odds ratios adjusted by age, sex, smoking status and study group, and eigenvectors for NCI-GWAS2 and NCI-GWAS1. Adjusted allelic odds ratios did not materially differ from unadjusted allelic odds ratios using genotype counts by case–control status (Table 1 and Supplementary Material, Fig. S3).

Assessment of gene–environment interactions for both additive and multiplicative models tests whether the observed joint effects OR for smoking and the genetic risk are significantly different than the expected joint effects OR. On a multiplicative scale, which evaluates whether the relative risk for smoking varies across levels of genetic risk, the expected joint effects are calculated as $OR_{\text{SNP}} \times OR_{\text{smoking}}$. On an additive scale, which evaluates whether the risk difference for smoking varies across levels of genetic risk, the expected joint effects are calculated as $OR_{\text{SNP}} + OR_{\text{smoking}} - 1$. Because the expected joint effects of the additive model are lower than the multiplicative, except when one of the two ORs for SNP or exposure are equal to 1.0, the observed joint effects were closer to the multiplicative than the additive expected effects, rejection of the null hypothesis for additive more than multiplicative interaction is more frequent.

To conduct a test for gene–environment interaction on the relative risk scale (multiplicative interaction), we used an

Empirical Bayes (EB) model fitting procedure that can gain power by exploiting the assumption of gene–environment independence in the underlying population and yet is immune to bias when the independence assumption is violated (52,53). For gene–environment interaction testing on the additive scale (i.e. risk difference), we conducted a likelihood ratio test comparing an unconstrained and constrained model for joint effects using logistic regression models (54). Under the null hypothesis of an additive model, the OR for the joint effect of a given SNP and smoking status is constrained so that the risk difference associated with one exposure (e.g. smoking) is constant across levels of other exposure (e.g. SNP) and vice versa. All tests for gene–environment interactions were conducted using categorical variables (each SNP was coded as a dichotomous variable indicating the presence of any risk allele) to avoid complex numerical issues in the additive test and to make the additive and multiplicative tests comparable.

Polytomous logistic regression was used to obtain estimates of effect for different tumor subtypes. Case–case analyses with tumor type as an outcome were used to test for differences in effect size across subtypes. Polytomous logistic regression models were also used to test for trends and were calculated by constraining the effect size to increase linearly across levels of tumor grade and stage. SNP–SNP interactions were assessed using logistic regression models adjusted by study center, age sex and smoking status and including interaction terms.

Data analysis and management were performed with GLU (version 1.0), a suite of tools available as an open-source application for management, storage and analysis of GWAS data, and STATA.

Estimate of recombination hotspots

SequenceLDhot (55) that uses an approximate marginal likelihood method (56) was used to compute likelihood ratio statistics for a set of putative hotspots across the region of interest. We sequentially analyzed subsets of 100 controls of European background (by pooling five controls from each study). We used Phasev2.1 to infer the haplotypes as well as background recombination rates. The analysis was repeated with five non-overlapping sets of 100 pooled controls.

Imputation

Imputation was performed on 5942 cases and 10 861 control samples from NCI-GWAS2 and NCI-GWAS1 for the four newly identified bladder cancer susceptibility regions at 3q26.2, 11p15.5, 20p12.2 and 6p22.3. IMPUTE v2.2.2 (57) was used to impute 2-Mb intervals of Chr3: 168492101–170492101; Chr11: 874072–2874072; Chr20: 9988099–11988099 and Chr6: 19766697–21766697 (GRCh37/hg19) using a 1000 Genomes Phase 1 integrated variant set (release v3) updated on August 26, 2012.

Expression analysis

The full set of bladder tissue samples included 45 muscle-invasive tumors and 44 adjacent normal bladder samples. All tissue samples were purchased from Asterand (Detroit, MI, USA) after exemption #4715 by the National Institutes of

Health (NIH) Office of Human Subjects Research. The samples were not included in GWAS and were genotyped separately for index GWAS markers with TaqMan assays used for GWAS validation studies. RNA-sequencing of tumor ($n = 7$) and adjacent normal ($n = 5$) bladder tissue samples was previously described (58). The high-quality RNA samples (RIN > 8.0) were sequenced with HiSeq 2000 to generate paired reads of 107 bp. Expression studies for individual transcripts were performed in total RNA samples extracted from tissues with MirVana to preserve miRNA fraction (Life Technologies). cDNA samples were synthesized with SuperScript III and random hexamers (Life Technologies). All the TaqMan expression assays were from Life Technologies: Hs00158885_m1 for *LSP1*, Hs00268536_g1 for *TNNI2*, Hs00610931_m1 for *MYNN* and Hs00214949_m1 for *CDKAL1*. Endogenous controls beta-2-microglobulin (*B2M*, assay Hs00187842_m1) and beta-actin (*ACTB*, assay 4352935) were used for normalization of expression.

Expression of mRNA and miRNA transcripts was analyzed according to relative quantification method and the differences were presented on log₂ scale as $dCt = Ct(\text{control}) - Ct(\text{target})$. dCt values can be converted to fold differences as $\text{fold} = 2^{dCt}$. For all assays, reactions with water and 10 ng of genomic DNA were used as negative controls. The expression detection was performed on the ABI PRISM 7900HT SDS with cDNA prepared from ~10 ng of total RNA, 0.25 μl of 20 \times TaqMan gene expression assays and 2.5 μl of 2 \times Gene Expression Master Mix in 5 μl reaction volume. The expression was measured in four technical replicates and average values were used for the analysis. An unpaired two-tailed *t*-test was applied when comparing expression of tumor and normal samples. Association between genotypes and expression of transcripts was analyzed by linear regression (*P*-trend) implemented in PLINK.

Data access

The CGEMS data portal provides access to individual level data for investigators from certified scientific institutions after approval of a submitted Data Access Request.

URLs

CGEMS portal, <http://cgems.cancer.gov/>; Cancer Genomics Research Laboratory, CGR, <http://cgf.nci.nih.gov/>; GLU, <http://code.google.com/p/glu-genetics/>; EIGENSTRAT, <http://genepath.med.harvard.edu/~reich/EIGENSTRAT.htm>; SNP 500Cancer, <http://snp500cancer.nci.nih.gov/>; STRUCTURE, <http://pritch.bsd.uchicago.edu/structure.html>; STATA, <http://www.stata.com/>; <http://www.ncbi.nlm.nih.gov/gap>.

SUPPLEMENTARY MATERIAL

Supplementary Material is available at *HMG* online.

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