SCIENTIFIC REPORTS

Received: 07 July 2016 Accepted: 06 January 2017 Published: 08 February 2017

OPEN *ISL1* is a major susceptibility gene for classic bladder exstrophy and a regulator of urinary tract development

Rong Zhang^{1,2,*}, Michael Knapp^{3,*}, Kentaro Suzuki⁴, Daiki Kajioka⁴, Johanna M. Schmidt^{1,5}, Jonas Winkler⁵, Öznur Yilmaz⁵, Michael Pleschka⁵, Jia Cao⁶, Christina Clementson Kockum⁷, Gillian Barker⁸, Gundela Holmdahl⁹, Glenda Beaman¹⁰, David Keene¹¹, Adrian S. Woolf^{12,13}, Raimondo M. Cervellione¹¹, Wei Cheng^{14,15,16}, Simon Wilkins^{17,18}, John P. Gearhart¹⁹, Fabio Sirchia²⁰, Massimo Di Grazia²¹, Anne-Karolin Ebert²², Wolfgang Rösch²³, Jörg Ellinger²⁴, Ekkehart Jenetzky^{25,26}, Nadine Zwink²⁵, Wout F. Feitz²⁷, Carlo Marcelis²⁸, Johannes Schumacher¹, Federico Martinón-Torres^{29,30}, Martin Lloyd Hibberd³¹, Chiea Chuen Khor³², Stefanie Heilmann-Heimbach^{1,2}, Sandra Barth^{1,2}, Simeon A. Boyadjiev³², Alfredo Brusco²⁰, Michael Ludwig³³, William Newman³⁴, Agneta Nordenskjöld^{6,35}, Gen Yamada⁴, Benjamin Odermatt⁵ & Heiko Reutter^{1,36}

¹Institute of Human Genetics, University of Bonn, Bonn, Germany. ²Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany. ³Institute of Medical Biometry, Informatics, and Epidemiology, University of Bonn, Bonn, Germany. ⁴Developmental Genetics, Institute of Advanced Medicine, Wakayama Medical University, Japan. ⁵Institute of Anatomy, University of Bonn, Bonn, Germany. ⁶Department of Women's and Children's Health and Center for Molecular Medicine, Karolinska Institutet, Stockholm, Sweden. ⁷Department of Pediatric Surgery, University Hospital Lund, Lund, Sweden. ⁸Department of Women's and Children's Health, Uppsala Academic Children Hospital, Uppsala, Sweden. ⁹Department of Pediatric Surgery, Queen Silvias Children's Hospital, Gothenburg, Sweden. ¹⁰Centre for Genomic Medicine, University of Manchester, Manchester, UK. ¹¹Paediatric Urology, Royal Manchester Children's Hospital, Central Manchester University Hospitals NHS Foundation Trust, Manchester, UK. ¹²Institute of Human Development, University of Manchester, Manchester Academic Health Science, Centre, Manchester, UK. ¹³Royal Manchester Children's Hospital, Manchester, Manchester, UK. ¹⁴Department of Pediatric Surgery, Capital Institute of Pediatrics, Beijing, People's Republic of China. ¹⁵Department of Paediatrics and Department of Surgery, Southern Medical School, Faculty of Medicine, Nursing and Health Sciences, Monash University, Clayton, VIC, Australia. ¹⁶Department of Surgery, Beijing United Family Hospital, Beijing, People's Republic of China.¹⁷Cabrini Monash University Department of Surgery, Cabrini Hospital, Melbourne, Australia.¹⁸Department of Epidemiology and Preventive Medicine, School of Public Health and Preventive Medicine, Monash University, Australia. ¹⁹Division of Pediatric Urology, Johns Hopkins School of Medicine, Baltimore, MD, USA. ²⁰Department of Medical Sciences and Medical Genetics Unit, Città della Salute e della Scienza University Hospital, University of Torino, Torino, Italy. ²¹Institute for Maternal and Child Health, IRCCS Burlo Garofalo, Trieste, Italy. ²²Department of Urology and Pediatric Urology, University Hospital of Ulm, Germany. ²³Department of Pediatric Urology, St. Hedwig Hospital Barmherzige Brüder, Regensburg, Germany. ²⁴Department of Urology, University Hospital Bonn, Bonn, Germany. ²⁵Division of Clinical Epidemiology and Aging Research, German Cancer Research Center, Heidelberg, Germany. ²⁶Department of Child and Adolescent Psychiatry and Psychotherapy, Johannes-Gutenberg University, Mainz, Germany. ²⁷Department of Urology, Pediatric Urology Center, Radboud University Nijmegen Medical Center, Nijmegen, The Netherlands. ²⁸Department of Genetics, Radboud University Nijmegen Medical Center, Nijmegen, The Netherlands.²⁹Translational Pediatrics and Infectious Diseases, Hospital Clínico Universitario de Santiago, Santiago de Compostela, Spain. ³⁰GENVIP Research Group (www.genvip.org), Instituto de Investigación Sanitaria de Santiago, Galicia, Spain. ³¹Genome Institute of Singapore, Singapore. ³²Division of Genomic Medicine, Department of Pediatrics, University of California Davis Medical Center, Sacramento, CA, USA. ³³Department of Clinical Chemistry and Clinical Pharmacology, University of Bonn, Bonn, Germany. ³⁴Centre for Genomic Medicine, University of Manchester, Manchester, UK. ³⁵Pediatric Surgery, Astrid Lindgren Children Hospital, Karolinska University Hospital, Stockholm, Sweden. ³⁶Department of Neonatology

& Pediatric Intensive Care, Children's Hospital; University of Bonn, Bonn, Germany. *These authors contributed equally to this work. Correspondence and requests for materials should be addressed to H.R. (email: reutter@unibonn.de)

Previously genome-wide association methods in patients with classic bladder exstrophy (CBE) found association with *ISL1*, a master control gene expressed in pericloacal mesenchyme. This study sought to further explore the genetics in a larger set of patients following-up on the most promising genomic regions previously reported. Genotypes of 12 markers obtained from 268 CBE patients of Australian, British, German Italian, Spanish and Swedish origin and 1,354 ethnically matched controls and from 92 CBE case-parent trios from North America were analysed. Only marker rs6874700 at the *ISL1* locus showed association ($p = 2.22 \times 10^{-08}$). A meta-analysis of rs6874700 of our previous and present study showed a p value of 9.2×10^{-19} . Developmental biology models were used to clarify the location of ISL1 activity in the forming urinary tract. Genetic lineage analysis of *Isl1*-expressing cells by the lineage tracer mouse model showed *Isl1*-expressing cells in the urinary tract of mouse embryos at E10.5 and distributed in the bladder at E15.5. Expression of *isl1* in zebrafish larvae staged 48 hpf was detected in a small region of the developing pronephros. Our study supports *ISL1* as a major susceptibility gene for CBE and as a regulator of urinary tract development.

The bladder exstrophy-epispadias complex (BEEC; OMIM %600057) represents the severe end of human congenital anomalies of the kidney and urinary tract (CAKUT), and involves the abdominal wall, pelvis, all of the urinary tract, the genitalia, and occasionally the spine and anus. Birth prevalence rates for the most common defect form, classic bladder exstrophy (CBE), range from 1 in 30,000 to 1 in 50,000, varying among North American ethnic groups with the highest prevalence being observed among Native Americans (8 in 100,000) and the lowest among Asians (1 in 100,000)^{1,2}. Vesicoureteral reflux and obstruction of the ureteropelvic junction are observed frequently in both genders, and cryptorchidism is common in males³. Long-term complications are malignancies of the bladder mucosa, with 95% of these malignancies being adenocarcinomas⁴.

To identify susceptibility loci for CBE, we recently performed a genome-wide association study (GWAS) of 110 CBE patients and 1,177 controls of European origin. Here, an association was found with a region of approximately 220 kb on chromosome 5q11.1-q11.2⁵. This region harbors the *ISL1* (ISL LIM homeobox 1) gene. Multiple markers in this region showed evidence for association with CBE, including 84 markers with genome-wide significance. A subsequent meta-analysis using data from a previous GWAS by our group of 98 CBE patients and 526 controls of European origin also implicated the 5q11.1-q11.2 locus in CBE risk^{5,6}. A total of 138 markers at this locus reached genome-wide significance in the meta-analysis. No other locus in the meta-analysis achieved genome-wide significance.

The present association study followed-up on the most promising genomic regions based on the results of our previous meta-analysis defined by a total of 12 independent markers. One of these markers resides in the *ISL1* region and had previously reached genome-wide significance⁵. The other 11 markers had previously reached p values of 10^{-055} . The study sample before quality control (QC) steps of the generated genotypes comprised 274 Australian, British, German, Italian, Spanish, and Swedish CBE patients and 1,365 ethnically matched controls, and 110 case-parent trios from North America of European background. To better understand the role of *ISL1* during genito-urinary tract development, we performed expression studies in mouse embryos and zebrafish larvae (zfl).

Results

Association study. After performance of QC steps for the generated genotypes we had to exclude six CBE patients and 11 of the ethnically matched controls from the case-control study. Hence the analyzed data set for the case-control study comprised 268 CBE patients of Australian (n = 31), British (n = 40), German (n = 7), Italian (n = 39), Spanish (n = 35), and Swedish (n = 116) origin and 1,354 ethnically matched controls. In controls, there was no evidence for deviation from Hardy-Weinberg equilibrium for any of the 12 SNPs (data not shown). Accordingly we had to exclude 18 of the CBE case-parent trios from North America of European from the transmission disequilibrium test (TDT). Hence the analyzed data set for the TDT comprised 92 case-parent trios from North America of European background. Table 1 shows the results of the association analyses for the 268 cases, the ethnically matched 1,354 controls, the 92 case-parent trios, and the combined meta-analysis. A more detailed description of the results of the TDT is shown in the Supplementary (Supplementary Table 1). A significant result was observed for the marker rs6874700 at chromosome 5q11.2, representing the *ISL1* locus ($p = 2.22 \times 10^{-08}$). A meta-analysis for the marker rs6874700 in this meta-analysis was 1.93 (95% CI, 1.67–2.23) (Table 2).

Lineage analysis of *Isl1*-expressing cells in mouse embryos. Lineage tracing provides a powerful means of understanding tissue development, homeostasis, and disease, especially when it is combined with experimental manipulation of signals regulating cell fate decisions. In order to address the contribution of Isl1-expressing cells in the developing early genito-urinary tract, we used the Isl1-mER-Cre-mER allele in which sequences encoding a tamoxifen dependent Cre recombinase were inserted into the Isl1 locus⁷. Here Isl1-expressing cells were observed in the early genito-urinary tract of mouse embryo at E10.5 (Fig. 1A, arrow). Isl1-expressing cells later distributed in the bladder at E15.5 (Fig. 1B). To further analyze the involvement of

SNP	Chromosome/ Region	Position	Risk/ other allele	Meta-analysis Cases (n = 268) vs. controls (n = 1,354) (AUS/GB/DE/ IT/ES/SE) RR (95% CI)	TDT Case-parent trios (n = 92) (North America) RR (95% CI)	Meta-analysis Cases (n = 268), Controls (n = 1,354), Case- parent trios (n = 92) RR (95% CI) p values	
rs1475601	1q31.3	194,721,655	G/A	1.11 (0.60-2.05)	0.88 (0.32-2.41)	1.04 (0.61–1.76)	0.884
rs72748303	1q32.2	208,973,633	A/G	1.54 (0.95-2.52)	0.71 (0.23-2.25)	1.37 (0.87-2.15)	0.170
rs79145914	4p14	39,490,706	G/A	1.26 (0.74–2.14)	1.75 (0.51-5.98)	1.33 (0.82-2.15)	0.254
rs7689350	4q13.3	76,207,570	A/C	0.98 (0.70-1.38)	2.13 (0.92-4.92)	1.10 (0.80–1.51)	0.568
rs6874700	5q11.2	50,701,750	A/T	1.80 (1.44-2.25)	1.61 (1.07-2.41)	1.75 (1.44-2.13)	$2.2 imes10^{-08}$
rs1514351	6q12	68,694,074	C/T	1.20 (0.96–1.50)	0.91 (0.60-1.39)	1.13 (0.92–1.37)	0.239
rs117622209	6q22.1	118,108,159	C/T	1.12 (0.64–1.96)	1.20 (0.37-3.93)	1.13 (0.69–1.88)	0.623
rs56189125	7p14.3	28,855,348	G/A	1.05 (0.09-11.78)	1.67 (0.61-4.59)	1.56 (0.61-3.96)	0.353
rs57086087	8p11.21	40,301,811	T/C	1.07 (0.80–1.44)	1.42 (0.84-2.39)	1.15 (0.89–1.48)	0.301
rs10119066	9p24.1	7,509,895	T/G	0.99 (0.66–1.50)	1.60 (0.52-4.89)	1.05 (0.71–1.55)	0.806
rs16917077	9p21.1	31,532,212	C/T	1.39 (0.74–2.59)	1.38 (0.55-3.42)	1.38 (0.83-2.32)	0.215
rs1514921	12q21.2	79,481,756	C/T	1.21 (0.89-1.64)	1.35 (0.72-2.53)	1.23 (0.94-1.62)	0.136

Table 1. Results of the association analyses for cases and controls, the case-parent trios, and the combined meta-analysis.

.....

SNP	Chromosome/ Region	Position	Risk/other allele	Previous meta-analysis Draaken <i>et al.</i> ⁵ RR (95% CI)	Replication RR (95% CI)	Present meta-analysis RR (95% CI) p values	
rs6874700	5q11.2	50,701,750	A/T	2.17 (1.75–2.70)	1.75 (1.44–2.13)	1.93 (1.67–2.23)	9.2×10^{-19}

 Table 2. Results of our previous meta-analysis and the presently tested sample for the marker rs6874700.

.....

Isl1- expressing cells for the bladder formation, we performed detailed cell lineage analysis by conducting several timing of tamoxifen treatments. An increasing number of Isl1-expressing cells at E7.5 were detected in the early genito-urinary tract and bladder region (Fig. 1C,F). Of note, a large number of Isl1-expressing cells were observed in such regions after the treatment of tamoxifen at E8.5 and E9.5 (Fig. 1D,E,G,H). In addition to the bladder, Isl1-expressing cells also contributed to the genital tubercle region (Fig. 1F–H, arrowheads). To further investigate the contribution of Isl1-expressing cells for caudal body formation, we analyzed the Hoxa3-IRESCre; Isl1Flox/Flox mutant embryos (*Isl1* cKO). Hoxa3 Cre driver mouse line possesses Cre activity in the caudal body regions⁸. *Isl1* cKO showed the hypoplasia of GT (Fig. 1I–L, red arrows) as well as bladder (Fig. 1K,L, circle). The embryonic time dependent Isl1 positive mesenchymal cell population was thus discussed further in Discussion.

Whole mount in situ hybridization (WISH) of zebrafish larvae (zfl). In contrast to mammals, in early developmental stages of zfl between 48-96 hours post fertilisation (hpf) the pronephros containing two glomeruli plus nephrons, is already fully functional. In adult fish the subsequently developing mesonephros will yet become the final kidneys. In mammals however only the hereafter developing metanephros will become the final kidney⁹. In the early developing zfl, just after gastrulation (tail-bud stage around 10 hpf) first renal progenitors can be detected in bilateral stripes of intermediate mesoderm (IM), located either side of the embryonic midline in between the paraxial mesoderm (PM) and the lateral plate mesoderm (LPM)¹⁰. These renal progenitor fields give then, from about 10 somite stage, rise to a pair of bilateral nephrons. The pronephros itself is again comprised of a series of discrete cell types, well differentiable approximately from the prim-5 stage on at around 26 hpf^{11,12}. To test for a potential involvement of *isl1* in the above described renal progenitor development in zfl, our first step was to investigate *isl1* expression at these sides during the respective time points by whole mount RNA in situ hybridization (WISH) expression analysis in the early wt zfl between 22 and 60 hpf (corresponding approximately to 26 somite and pec-fin stage). Using an antisense in situ probe comprising an UTR region of zfl isl1 cDNA (see methods section^{13,14}) we could clearly detect isl1 expression in some region of the developing pronephros for all tested time points mentioned above. At 48 hpf we could clearly detect isl1 expression at most anterior regions of the proximal convoluted tubular (PCT) regions (Fig. 2), which we co-localized with a previously described *slc20a1a* in situ marker¹². Long-peg stage zfl at 48 hpf showed *isl1* expression in regions close to the yolk-sac, which have previously been described as the early developing pancreatic region¹⁵, but do also overlap with *slc20a1a* marker expression here in the most anterior developing nephros region (Fig. 2).

Discussion

Following-up on the most promising genomic regions based on the results of our previous meta-analysis in a total of 360 CBE patients, we were able to replicate our findings on the *ISL1* harboring region with the marker rs6874700 ($p = 2.22 \times 10^{-8}$). A meta-analysis for the marker rs6874700 of our previous and present study showed a *p* value of 9.2×10^{-19} . The relative risk (RR) (95% CI) for rs6874700 in this meta-analysis was 1.93 (95% CI, 1.67–2.23).





Isl1 is a transcription factor, containing LIM domains, which has been described as playing essential roles for the regulation of cell lineage commitment in organogenesis. It is essential for development of heart, kidney, neurons and limb^{15,16} however, the role of Isl1 in caudal embryonic region has been left unexplored. The cloaca is the essential embryonic structure to develop the external genitalia and the adjacent mesenchymes (termed as peri-cloacal mesenchyme, PCM)¹⁷. Cloacal epithelia and the surrounding mesenchyme interaction play a major role in caudal embryonic development. The mesenchyme adjacent to the cloaca receives cloacal derived signals and such mesenchyme includes the anterior part of the PCM (aPCM), which locates in the anterior (upper) part of the cloacal field^{17,18}.

Our findings in CBE patients for the ISL1 locus are further supported by lineage analysis of Isl1-expressing cells in mouse embryos and mutant mice analysis of Isl1 cKO embryos. Isl1 marks the aPCM, which has been shown to contribute to the embryonic formation of the bladder, rectum, and the external genitalia¹⁹. As outlined above, many CBE patients present with additional anomalies of the human CAKUT spectrum including vesicoureteral reflux and obstruction of the ureteropelvic junction underlining that CBE affects all of the urinary tract system and not the bladder only. Thus, Isl1 cell lineages match with the organs reflecting various phenotypes of CBE. In the current study, we found that Isl1 is required for the caudal body formation including bladder and GT. The accurate lineage analyses of Isl1-expressing cells suggest that aPCM cells are specified to the bladder and external genitalia around at E7.5. Hence, the current study revealed the presence of the embryonic-time dependent mesenchymal cell population as sensitive for the current set of genetic mutations. The epithelial-mesenchymal interaction between the epithelia and PCM is necessary to form the major parts of the caudal embryo. During such caudal embryonic development, several signaling pathways such as Bone morphogenetic protein (Bmp) and Sonic Hedgehog (Shh) are activated in the aPCM. On note, Defects of Bmp signals cause the body wall closure defects^{20,21}. Another growth factor, Shh, is reported as expressed in the early staged cloacal epithelia affecting the adjacent PCM development¹⁷. It has been also shown that Shh signals relay to modulate mesenchymal Bmp signals²². Hence, the current analyses suggest that the signals including Shh, Bmp possibly affecting Isl1 lineage aPCM cells specified at early embryonic stage such as E7.5. Further analyses are required to understanding the molecular mechanisms for the bladder and body wall formation.

Using WISH analysis in early developmental stages of zfl (22–60 hpf), we were able to detect *isl1* expression close to the proximal region of the developing pronephros for all tested time points. Later during development of zfl, the two nephrons fuse with the caudal end of the intestine, attaching at 96 hpf at the cloaca²³. The pronephros filtrates the blood before delivering the waste to the cloaca for excretion, thus representing very premature structures of an urinary tract¹⁰. Therefore, even though *isl1* could not be detected in the developing more distal cloaca or proctodeum regions in the zfl we analyzed, proximal expression of *isl1* at regions of these early structures of mammalian urinary tract equivalents in zebrafish provides additional evidence for *ISL1* as a regulator for urinary tract development across species.

We were not able to replicate any of the other 11 regions tested in our single-marker analysis. While we cannot exclude, that the inability to find further evidence for association for these 11 regions is based on a lack in statistical power of our present study, it is more likely, that these regions, respectively markers within these regions, had a higher effect in our previous meta-analysis ('winner's curse') (208 CBE patients in total) than in our extended replication sample (268 CBE patients in total in our case-control study and 92 case-parent trios in our TDT).



Figure 2. WISH against *isl1* (antisense 3'-untranslated region-probe; upper row), *slc20a1a* (middle row) and both probes combined (lower row) on wild-type zfl at 48 hpf. 48 hpf long-pec stage zfl in lateral (left column) and dorsal view (middle column; same fish; scale bar = $500 \,\mu$ m) in the top row are showing *isl1* expression amongst other previous described regions also at most anterior regions of the proximal convoluted tubular (PCT; arrows). 25 μ m transversal slices sections of the same fish are shown in the right column (scale bar = $150 \,\mu$ m). The orientation of sections is shown with red dashed lines in the corresponding whole mount images. The zfl show a clear *isl1* staining in what has previously been described as the developing pancreatic region, and which might well be overlapping with an anterior region of the *slc20a1a* labeled PCT (black arrow heads). The overlap of *isl1* and *slc20a1a* expression at this region is further supported by the fact that no additional stained area could be found there, when we used both *in situ* probes simultaneously for staining. *Isl1* expression could not be detected in the developing cloaca or proctodeum region (not shown).

Alternatively, these regions might have been false positive signals in our previous meta-analysis, which were unrelated to CBE, or only show association with CBE patients of central European origin but not in CBE patient cohorts of different ethnicity. Finally, and most likely, our previous meta-analysis may have failed to identify the possible relevance of other markers and regions, that are actually involved in human CBE formation but were not considered for replication in our follow-up step since they might have obtained *p* values which were not considered worthy of note (e.g. *p* values $> 10^{-5})^5$. It is therefore warranted, in order to identify additional markers and regions that might actually be involved in human CBE formation that we perform genome-wide genotyping of the present sample in a separate analysis. It is therefore warranted, in order to identify additional markers and regions that are actually involved in human CBE formation to perform genome-wide genotyping of the present sample in a separate analysis.

Within our replicated region of genome-wide significance and with an achieved p value of 1.14×10^{-10} in our previous meta-analysis the marker rs2303751 in exon 4 of *ISL1* reaches a score of 2b (scale 1a–6) in "RegulomeDB" (http://regulomedb.org) indicating that rs2303751 resides in a functional region. The marker rs2303751 alters 17 DNA binding motifs according to HaploReg v4.1, including alteration of the position-weight matrix for SMAD4, an essential downstream transcriptional regulator of the TGF beta signaling pathway²⁴. In addition, the genomic region encompassing rs2303751 is occupied by EZH2 (enhancer of zeste 2), the major component of the genome regulating Polycomb Repressive Complex 2 (PRC2) and a therapeutic target in human bladder cancer²⁵. With EZH2 being involved in human bladder cancer and with SMAD4 playing an essential role for initiating the smooth muscle cell differentiation program during ureter development, further analysis of the rs2303751 comprising region enclosing *ISL1* is warranted^{24,25}.

In addition, Kitchen *et al.*, looking at methylation in low/intermediate grade non-muscle invasive bladder cancer, showed that the *ISL1* genes' promoter-associated island was more frequently methylated in recurrent and progressive high-grade tumors than their non-recurrent counterparts²⁶. Since, Kolarova *et al.*, were just recently able to provide certain lines of evidence, that imprinting might play a role in BEEC formation, further studies regarding differences in methylation of the *ISL1* region in CBE patients compared to matched controls are also warranted²⁷.

Conclusion

Our present association study in CBE patients together with functional studies in mouse embryos and zebrafish larvae suggest *ISL1* as a regulator of urinary tract development.

Materials and Methods

Ethics statement and subjects. This study was approved by each participating center's institutional ethics committee. All methods were carried out in accordance with relevant guidelines and regulations. All experimental protocols were approved by the institutional committee of the University of Bonn. Furthermore the study was conducted according to Declaration of Helsinki principles. Written informed consent was obtained from all patients, parents/guardians and the normal controls. Demographic information was collected from both, patients and controls, through a structured questionnaire. Experienced physicians trained in the diagnosis of the BEEC personally recruited all BEEC patients included in this study.

The study sample comprised 274 Australian (n = 36), British (n = 40), German (n = 7), Italian (n = 40), Spanish (n = 35), and Swedish (n = 116) CBE patients and 1,365 ethnically matched controls, and 110 case-parent trios from North America of European background. Peripheral venous blood samples, saliva samples or buccal swab samples were obtained from patients and controls for DNA extraction. More details about the recruitment process for patients and population based respectively phenotype unrelated controls can be found elsewhere and in the Supplementary 'Materials, Methods'^{5,6,27–30}.

Genotyping. For SNP-marker genotyping, we used the Sequenom MALDI-TOF mass-spectrometer (MassArray system), TaqMan[®] SNP genotyping assays (Life Technologies Europe BV, Netherlands) and conventional Sanger sequencing. Sequenom data were analyzed using the Spectrodesigner Software package (Sequenom, San Diego, CA) and allele peaks were analyzed with the Sequenom Typer Analysis software. TaqMan generated data were analyzed using the ABI 7900HT instrument and the SDS software (v2.4, Applied Biosystems). Sanger sequencing generated data were analyzed using CodonCode Aligner software package (CodonCode Corporation, MA, USA).

Statistical analysis. Statistical analysis was performed using SAS software (version 9.1). The standard chi-square test was used to test for deviations from Hardy-Weinberg equilibrium. The two-sided Armitage's trend test was used to compare genotype distributions between cases and controls separately in each case-control sub-sample. In order to test for association of the risk alleles with CBE in trios from North America, we applied the transmission/disequilibrium test (TDT)³¹. Fixed effects meta-analysis was used to combine samples³².

Embryo collections for lineage analysis of *Isl1*-expressing cells and analysis of knockout mouse embryos. All experimental procedures and protocols were approved by the Committees on Animal Research at Wakayama Medical University and the experiments were carried out in accordance with the approved guidelines. Each mouse strain used in this study Isl1flox/flox conditional mutant allele, Hoxa3-IRESCre, Isl1-mER-Cre-mERm and R26R-LacZ indicator strain was described previously^{7,8,33-35}. The tamoxifen (TM)-inducible Cre recombinase system removes the floxed sequence from the target genome³¹. TM (Sigma, St Louis, MO, USA) was dissolved in sesame oil at 10 mg/ml and injected into pregrant female by oral administration at a dose of 0.05 mg/g of body weight. The mice for Isl1 positive-lineage analyses used in this study were Isl1-mER-Cre-mER and R26R-LacZ indicator strains. These mice strains were generated as described previously^{7,34}. TM was administrated from embryonic days (E) 7.5 to E9.5 and the embryos were harvested at E10.5, E12.5 and E15.5, respectively. X-gal staining for the detection of Isl1-expressing cells was performed as previously described^{33,36}. Briefly, freshly dissected embryos were fixed 1 hour in a solution composed of 1% formaldehyde and 0.2% glutaraldehyde at 4 °C. The embryos were washed with PBS and color development was performed with the developing solution. For histological analysis of the Isl1-expressing cells, the X-gal stained specimens were refixed overnight in 4% paraformaldehyde (PFA)/PBS, dehydrated in methanol and embedded in paraffin. 10 µm serial sections were prepared and stained by Eosin.

For analysis of Hoxa3-IRESCre; Isl1 mutant embryos (hereafter described as Isl1 cKO), we mated Hoxa3-IRESCre; Isl1Flox/+ with Isl1Flox/Flox, and subsequently harvested at E13.5. Embryonic specimens were fixed overnight in 4% paraformaldehyde (PFA)/PBS, dehydrated in methanol, and embedded in paraffin. Serial sections (6-µm thick) were prepared for hematoxylin/eosin (H&E) staining.

Whole mount in situ hybridization (WISH) of zebrafish larvae (zfl). All experimental procedures and protocols were carried out in accordance with the approved national guidelines. Zfl for the presented experiments were maintained and staged as described elsewhere^{14,37}. Mixed Tübingen long fin (TL) and Ekkwill (EK) strain wild-type (wt) embryos were used for all experiments. All embryos were gained by natural fish spawning set up in the mornings and raised at 28 °C in Danieau (30%) medium, following local and international animal procedure standards. To analyse isl1-expression in zfl mRNA WISH was performed in embryos of different ages (22 hpf, 48 hpf and 60 hpf). We mainly followed a WISH standard protocol using an anti-Dig Ab-dilution of 1:10:000³⁷. The RNA *in-situ* probe was designed for binding at the 5' untranslated (UTR) region of zf *isl1* using the following forward primer (CATCATctcgagAGAGTGACATCGACCAGCCTGCTTTCC) and the reverse primer (CATCATggatccGAAATTCCCACACAGCTTGTGGC) on cDNA of 1 dpf whole zfl. The resulting amplified PCR product of the probe was then cloned into SK(-)pBluescript[®] using BamHI and XhoI sites and sequenced. We used the DIG RNA Labeling Kit (SP6/T7) (Roche; product number: 11175025910) to transcribe an antisense (T3) and a sense probe (T7) as negative control (not shown) from the above plasmid. Final imaging of the WISH stained larvae fish was performed using an Eclipse upright microscope (Nikon) equipped with a 10x and 40x objectives (NA = 0.25 and 0.65 respectively) and a DS-Vi1 digital colour camera run by NIS-Element software (Nikon).

References

- Caton A. R. et al. Epidemiology of bladder and cloacal exstrophies in New York State, 1983–1999. Birth Defects Res A Clin Mol Teratol. 79, 781–787 (2007).
- 2. International Clearinghouse for Birth Defects Monitoring Systems. Epidemiology of bladder exstrophy and epispadias: a communication from the International Clearinghouse for Birth Defects Monitoring Systems. *Teratology*. **36**, 221–227 (1987).
- Gearhart, J. P. & Mathews, R. I. Exstrophy-Epispadias Complex In Campbell-Walsh Urology 11th ed. (eds Wein, A. J., Kavoussi, L. R., Partin, A. W., Peters, C. A.) 3182–3233 (Elsevier, 2016).
- 4. de Riese, W. & Warmbold, H. Adenocarcinoma in extrophy of the bladder. A case report and review of the literature. *Int Urol Nephrol.* **18**, 159–162 (1986).
- Draaken, M. et al. Genome-wide Association Study and Meta-Analysis Identify ISL1 as Genome-wide Significant Susceptibility Gene for Bladder Exstrophy. PLoS Genet. 11, e1005024 (2015).
- 6. Reutter, H. *et al.* Genome-wide association study and mouse expression data identify a highly conserved 32 kb intergenic region between *WNT3* and *WNT9b* as possible susceptibility locus for isolated classic exstrophy of the bladder. *Hum Mol Genet.* **23**, 5536–5544 (2014).
- 7. Laugwitz, K. L. et al. Postnatal isl1+ cardioblasts enter fully differentiated cardiomyocyte lineages. Nature. 433, 647-653 (2005).
- Macatee, T. L. et al. Ablation of specific expression domains reveals discrete functions of ectoderm- and endoderm-derived FGF8 during cardiovascular and pharyngeal development. Development. 130, 6361–6374 (2003).
- 9. Marra, A. N. & Wingert, R. A. Roles of Iroquois transcription factors in kidney development. Cell Dev Biol. 3, 1000131 (2014).
- Drummond, I. A. *et al.* Early development of the zebrafish pronephros and analysis of mutations affecting pronephric function. *Development.* 125, 4655–4667 (1998).
- 11. Perner, B., Englert, C. & Bollig, F. The Wilms tumor genes *wt1a* and *wt1b* control different steps during formation of the zebrafish pronephros. *Dev Biol.* **309**, 87–96 (2007).
- 12. Wingert, R. A. *et al.* The cdx genes and retinoic acid control the positioning and segmentation of the zebrafish pronephros. *PLoS Genet.* **3**, 1922–1938 (2007).
- 13. Thisse, C. & Thisse, B. High-resolution in situ hybridization to whole-mount zebrafish embryos. Nat Protoc. 3, 59–69 (2008).
- 14. Thisse, C. & Thisse, B. High Throughput Expression Analysis of ZF-Models Consortium Clones. ZFIN Direct Data Submission http://zfin.org/ZDB-PUB-051025-1 (2005).
- 15. Biemar, F. *et al.* Pancreas development in zebrafish: early dispersed appearance of endocrine hormone expressing cells and their convergence to form the definitive islet. *Dev Biol.* 230, 189–203 (2001).
- Cai, C. L. et al. Isl1 identifies a cardiac progenitor population that proliferates prior to differentiation and contributes a majority of cells to the heart. Dev Cell. 5, 877–889 (2003).
- 17. Caku, Y. et al. Islet1 deletion causes kidney agenesis and hydroureter resembling CAKUT. J Am Soc Nephrol. 24, 1242–1249 (2013).
- Haraguchi, R. *et al.* Molecular analysis of coordinated bladder and urogenital organ formation by Hedgehog signaling. *Development.* 134, 525–533 (2007).
- 19. Suzuki, K. *et al.* Reduced BMP signaling results in hindlimb fusion with lethal pelvic/urogenital organ aplasia: a new mouse model of sirenomelia. *PLoS One.* 7, e43453 (2012).
- Sun, J. et al. Deficient Alk3-mediated BMP signaling causes prenatal omphalocele-like defect. Biochem Biophys Res Commun. 360, 238–243 (2007).
- 21. Uchimura, T. *et al.* Bmp2 and Bmp4 genetically interact to support multiple aspects of mouse development including functional heart development. *Genesis.* **47**, 374–384 (2009).
- 22. Haraguchi, R. *et al.* Unique functions of Sonic hedgehog signaling during external genitalia development. **128**, 4241–4250 (2001).
- 23. Pyati, U. J. et al. Sustained Bmp signaling is essential for cloaca development in zebrafish. Development. 133, 2275-2284 (2006).
- Yan, J. *et al.* Smad4 regulates ureteral smooth muscle cell differentiation during mouse embryogenesis. *PLoS One.* 9, e104503 (2014).
 Martínez-Fernández, M. *et al.* EZH2 in bladder cancer, a promising therapeutic target. *Int J Mol Sci.* 16, 27107–27032 (2015).
- Kitchen, M. O. et al. Methylation of HOXA9 and ISL1 predicts patient outcome in high-grade non-invasive bladder cancer. PLoS One. 10, e0137003 (2015).
- Kolarova, J. et al. PLAGL1 epimutation and bladder exstrophy: Coincidence or concurrent etiology? Birth Defects Res A Clin Mol Teratol. in press, doi: 10.1002/bdra.23521 (2016).
- Wilkins, S. et al. Insertion/deletion polymorphisms in the ΔNp63 promoter are a risk factor for bladder exstrophy epispadias complex. PLoS Genet. 8, e1003070 (2012).
- 29. Baranowska Körberg, I. *et al.* WNT3 involvement in human bladder exstrophy and cloaca development in zebrafish. *Hum Mol Genet.* 24, 5069–5078 (2015).
- 30. von Lowtzow, C. et al. CNV analysis in 169 patients with bladder exstrophy-epispadias complex. BMC Med Genet. 17, 35 (2016).
- Spielman, R. S., McGinnis, R. E. & Ewens, W. J. Transmission test for linkage disequilibrium: the insulin gene region and insulindependent diabetes mellitus (IDDM). *Am J Hum Genet.* 52, 506–516 (1993).
- 32. Willer, C. J., Li, Y. & Abecasis, G. R. METAL: fast and efficient meta-analysis of genomewide association scans. *Bioinformatics*. 26, 2190–2191 (2010).
- Sun, Y. et al. A central role for Islet1 in sensory neuron development linking sensory and spinal gene regulatory programs. Nat Neurosci. 11, 1283–1293 (2008).
- 34. Soriano, P. Generalized lacZ expression with the ROSA26 Cre reporter strain. Nat Genet. 21, 70-71 (1999).
- Feil, R., Wagner, J., Metzger, D. & Chambon, P. Regulation of Cre recombinase activity by mutated estrogen receptor ligand-binding domains. *Biochem Biophys Res Commun.* 237, 752–757 (1997).
- Ipulan, L. A. et al. Nonmyocytic androgen receptor regulates the sexually dimorphic development of the embryonic bulbocavernosus muscle. Endocrinology. 155, 2467–2479 (2014).
- Westerfield, M. THE ZEBRAFISH BOOK, 5th Edition; A guide for the laboratory use of zebrafish (Danio rerio), Eugene, University of Oregon Press. Paperback (2007).

Acknowledgements

We acknowledge the assistance of the German (www.blasenekstrophie.de), Spanish (www.extrofia.info/ asafex), and Italian (www.estrofiavescicale.it) self-help organizations in the recruitment of patients with CBE. A.-K.E., W.R., E.J., N.Z., M.L., and H.R. are members of the "Network for the Systematic Investigation of the Molecular Causes, Clinical Implications, and Psychosocial Outcome of Congenital Uro-Rectal Malformations (CURE-Net)". H.R. is supported by grant RE 1723/1-1 from the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG). J.M.S. is supported by the BONFOR program of the University of Bonn (grant number O-149.0112). E.J. is supported by grant JE 681/3-1 from the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG). A.S.W. is supported by a grant from the Medical Research Council (MR/ L002744/1), Kids Kidney Research, Newlife Foundation and Kidneys for Life. F.M.-T. has received support from Consellería de Sanidade, Xunta de Galicia (RHI07/2-intensificación actividad investigadora, PS09749 and 10PXIB918184PR), Instituto Carlos III (Intensificación de la actividad investigadora 2007–2012), Convenio de colaboración de investigación (Wyeth España-Fundación IDICHUS 2007–2011), Convenio de colaboración de investigación (Novartis España-Fundación IDICHUS 2010-2011), Fondo de Investigación Sanitaria (FIS; PI070069/PI1000540) del plan nacional de I + D + I and 'fondos FEDER' (F.M.T.). More information at: www. esigem.org/www.genvip.org. S.A.B. was partially funded by the grant and Endowed Chair from the Children's Miracle Network. W.C. and S.W. were supported by grants from Jack Brockhoff Foundation (#3095, 2010), the Helen Macpherson Smith Trust (#6940, 2010), and the Marian and E.H. Flack Trust.

Author Contributions

H.R., M.K., B.O., G.Y., A.N. and M.L. conceived and designed the experiments, supervised the project and wrote the manuscript. M.K. and A.N. performed statistical analyses. R.Z., K.S., D.K., J.M.S., J.W., Ö.Y., M.P., J.C., S.H.-H. and S.B. performed the experiments and analyzed the data. H.R., A.N., C.C.K., G.B., G.H., G.B., D.K., A.S.W., R.M.C., W.C., S.W., J.P.G., F.S., M.D.G., A.-K.E., W.R., J.E., E.J., N.Z., W.F.F, C.M., J.S., F.M.-T., M.L.H., C.C.K., S.A.B., A.B. and W.N. recruited patients, collected all samples and provided clinical data. All authors discussed the results and interpretations and read and approved the manuscript.

Additional Information

Supplementary information accompanies this paper at http://www.nature.com/srep

Competing financial interests: The authors declare no competing financial interests.

How to cite this article: Zhang, R. *et al. ISL1* is a major susceptibility gene for classic bladder exstrophy and a regulator of urinary tract development. *Sci. Rep.* **7**, 42170; doi: 10.1038/srep42170 (2017).

Publisher's note: Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

This work is licensed under a Creative Commons Attribution 4.0 International License. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in the credit line; if the material is not included under the Creative Commons license, users will need to obtain permission from the license holder to reproduce the material. To view a copy of this license, visit http://creativecommons.org/licenses/by/4.0/

© The Author(s) 2017