

The Impact of Altered Metabolism on the Regulation of IGF-II/H19 Imprinting Status in Prostate Cancer.

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Abstract

Background: Prostate cancer is the most frequently diagnosed cancer type and the second major cause of cancer deaths amongst men. A link exists between obesity, type 2 diabetes, and cancer risk. Insulin-like growth factor II (IGF-II) plays a role in numerous cellular events, including proliferation and survival. The IGF-II gene shares its locus with the lncRNA, H19. IGF-II/H19 was also the first gene to be identified as being 'imprinted' – where the paternal copy is not transcribed. This silencing phenomenon is lost in many cancer types.

Methods: We disrupted imprinting behaviour *in vitro* through the alteration of metabolic conditions and quantified it using RFLP, qPCR and pyrosequencing; changes to peptide were measured using RIA. Prostate tissue samples were analysed using ddPCR, pyrosequencing and IHC. We then compared with *in silico* data, provided by TGCA on the cBIO Portal.

Results: Disruption of imprinting behaviour, *in vitro*, occurs at the molecular level with no changes to peptide. *In vivo*, most specimens primarily retained imprinting status, apart from a small subset which showed reduced imprinting. A positive correlation was seen between IGF-II and H19 mRNA expression, which concurred with findings of larger Cancer Genome Atlas (TGCA) cohorts. This positive correlation did not affect IGF-II peptide.

Conclusions: Type 2 diabetes and / or obesity directly affect regulation growth factors involved in carcinogenesis.

Trial registration: Prostate Cancer Evidence of Exercise and Nutrition Trial: nutritional and physical activity interventions for men with localised prostate cancer – feasibility study (ISRCTN99048944). Registered on 17 November 2014

Background

Prostate cancer (PCa) is the most frequently diagnosed cancer type and the second major cause of cancer deaths amongst men [1]. Several factors have been found to contribute to disease susceptibility, progression, and prognosis including familial history and genetics [2], obesity [3], aging [4] and ethnicity [5].

It is clear that a link exists between obesity and cancer risk [6]. The increased adipose tissue, associated with obesity, produces over 20 hormones and cytokines that can disturb the delicate balance of the cellular environment [7].

Obesity also increases susceptibility to type 2 diabetes (T2D) [8]. One key characteristic associated with T2D is hyperglycaemia. As glucose is the main energy source for cells, an increase in its supply can cause increased proliferative potential [9].

Insulin-like growth factor II (IGF-II) is a growth factor expressed in high quantities during early embryonic development [10]. Expression continues throughout adulthood, with the liver being the primary site of synthesis [11]. IGF-II plays a critical role in a number of cellular events, including proliferation and survival [12].

In obese subjects, circulating serum levels of IGF-II are elevated and show a positive correlation with increased body mass index (BMI) [13]. Conversely, after weight loss, circulating levels of IGF-II have been shown to drop [14].

The IGF-II/H19 gene is located on the short arm of chromosome 11p. 15.5 [15]. It is composed of 10 exons and contains 5 promoters. Exons 1–4 and 6 are non-coding. Control of expression takes place from promoters 0 to 4 and is strictly regulated. 128 kb downstream from IGF-II is a long non-coding RNA, H19, which is linked to IGF-II by an imprinting control region (ICR) [16],

IGF-II was the first gene identified to be 'imprinted' [17]. This is a heritable epigenetic event whereby, through changes to the DNA structure (such as methylation or histone modification) one parental copy will be silenced or imprinted [18]. The loss of this natural silencing phenomenon (loss of imprinting – LOI) has been identified across a number of cancers, including prostate [19], breast [20], colorectal [21] and lung [22].

Models for the imprinting mechanism have been proposed, with the most widely accepted being the 'enhancer competition model' [23], in which the presence of a CCCTC-binding factor (CTCF) – a multi-zinc finger protein (and a transcriptional repressor) - is able to bind to the unmethylated imprint control region (ICR) embedded within the maternal IGF-II / H19 allele. This impedes IGF-II transcription. Conversely, on the paternal allele, the ICR is hypermethylated. This blocks CTCF from binding, which permits IGF-II to be transcribed. LOI occurs when both parental copies of IGF-II / H19 are hypermethylated at the ICR, resulting in the bi-allelic expression of IGF-II [24].

The function of H19 is unclear. In some cancers it is oncogenic: in gastric cancer, H19 and an embedded micro-RNA (miRNA-675) within its first exon, were found to be increased in tissue and cell lines. This over-expression led to increased cell proliferation and the inhibition of apoptosis [25]. In non-small-cell lung cancer, H19 expression was significantly higher in malignant lung tissue compared with normal, being at its highest in those from stage III and IV tumours [26]. In contrast, H19 behaves as a tumour suppressor in some cancer types, such as colorectal [27] and prostate [28]. The mechanism that dictates H19 behaviour differs between cancer types.

One study, published in 2012, analysed circulating IGF-II protein levels [29] in patients with a history of PCa. Of 106 (41 patients - radical prostatectomised (RPE) - and 65 controls) IGF-II levels were significantly elevated in the RPE cohort. LOI was also significantly higher in the RPE group (39%) compared to the control (20%). Despite the link between LOI and elevated serum IGF-II in the RPE group, the two were found to be uncoupled. Of the control cohort with LOI (20%), circulating IGF-II levels were

found to be very similar to those of the RPE cohort with LOI (39%). The authors suggested that, under normal conditions, only approximately 35% of the total serum IGF-II is regulated by imprinting [29].

A previous report focused on promoter methylation as a factor contributing to IGF-II transcription [30]. IGF-II mRNA and peptide levels were decreased in 80% of PCa, compared to non-neoplastic adjacent prostate and were independent of LOI status. IGF-II expression in both tumour and adjacent tissue depended on usage of the IGF-II promoters P3 and P4; decreased IGF-II expression in tumour tissue was strongly related to hypermethylation of these two promoters. The cause of hyper-methylation in this cohort was attributed to cumulative DNA damage, due to aging.

In this study we examined, *in vitro*, the effects of altering metabolic conditions on IGF-II imprinting status (IS), IGF-II / H19 mRNA, and IGF-II peptide levels in the PC3 PCa cell line. In addition, a clinical cohort of PCa tissue was analysed for expression of IGF-II and H19 mRNA using digital droplet polymerase chain reaction (ddPCR) and compared with two larger publicly available patient cohorts from the Cancer Genome Atlas (TCGA). IGF-II IS status was also analysed, using pyrosequencing, along with IGF-II localisation and abundance using immunohistochemistry (IHC).

Methods

Prostate cell lines

PCa cell lines PC3, LNCaP, DU145 and VCaP, and a normal prostate epithelial cell line – PNT2, were purchased from the American Type Culture Collection (ATCC, Manassas, Virginia, USA). PC3, VCaP and DU145 were cultured in Dulbecco's modified Eagles Medium (DMEM, BioWittaker, Verviers, Belgium) supplemented with 10% foetal bovine serum (FBS, Gibco, Paisley, UK) and 1% L-glutamine solution (2 mM; Sigma, Dorset, UK). LNCaP and PNT2 cell lines were cultured in Roswell Park Memorial Institute (RPMI-1640, BioWittaker, Verviers, Belgium) growth medium supplemented with 10% FBS and 1% L-glutamine solution, as before. Cells were incubated at 37 °C, in a humidified 5% carbon dioxide environment.

Prostate Tissue

Formalin fixed paraffin-embedded (FFPE) prostate tissue from a large clinical cohort, previously collected for the UK-based PrEvENT study (ISRCTN reference number ISRCTN99048944) [31] was used. 84 patients from the PrEvENT cohort had representative paired samples of benign and malignant tissue.

Isolation of nucleic acids

For cultured cell lines DNA and total RNA were isolated using DNAzol® and RNAzol® (Invitrogen, Thermo Fisher Scientific, Paisley, UK) reagents respectively, according to the manufacturer's instructions. DNA was resuspended in 40 mM NaOH (Merck Life Science, Dorset, UK) and RNA was resuspended in RNase-free water; both were quantified using a NanoPhotometer™ (Implen, München, Germany). For clinical

specimens, total RNA was extracted from formalin-fixed paraffin-embedded (FFPE) using the RecoverAll™ Total Nucleic Acid Isolation Kit for FFPE (Invitrogen). Extracts were stored at -80 °C.

Preparation of cDNA.

RNA was treated with DNase I (Sigma-Aldrich, Gillingham, UK) prior to cDNA conversion, using the High Capacity RNA-to-cDNA Kit® (Applied Biosystems, Foster City, California, USA).

Genotyping of cell lines, using restriction fragment length polymorphism (RFLP) analysis

Cell DNA and RNA (cDNA) was genotyped using the single nucleotide polymorphism (SNP) in exon 7 of IGF-II, at restriction site 680 (APA1). The RFLP process was conducted in two stages: The first amplified IGF-II product via PCR, using the following primer sequences: F *cttggactttgagtcaaattgg* and R *ggctcgtgcccaattacatttca* (Sigma-Aldrich). The second stage used an APA1 digestion enzyme (catalogue no. FD1414, Thermo Fisher Scientific), as per kit protocol, to digest product from stage 1 and “cut” at rs680. The resulting products were run on a 2% agarose (Bio-Rad, Hercules, California, USA) gel and visualised using a trans-illuminator (Bio-Rad).

Dosing experiments

For all experiments, cells were seeded at a density of 1×10^6 million cells per T25 flask (Greiner Bio-one, Gloucestershire, UK) in normal glucose-containing medium (1 000 mg/L – 5 mM). After 24 hours, media was exchanged for serum-free media (SFM) supplemented with sodium bicarbonate (1 mg/ml) (Sigma-Aldrich), bovine serum albumin (0.2 mg/ml – Sigma-Aldrich) and apo-transferrin (0.01 mg/ml) (Sigma-Aldrich), with normal glucose (5 mM), moderate glucose (9 mM) and high glucose SFM (25 mM).

At 6 -, 24 - and 48 - hour intervals, a flask from each different glucose concentration was removed and processed for RNA extraction. At the end of each time point, there were 3 flasks containing 5 mM, 9 mM and 25 mM SFM.

For TNF α dosing, cells were seeded in 5 mM glucose containing DMEM. After 24 hours, media was replaced with 5 mM and 25 mM glucose SFM. 24 hours later, cells were dosed with or without TNF α at 1-, 5- and 10 ng/ml, respectively. Cells were processed for RNA and DNA extraction.

Quantitative PCR (qPCR)

qPCR was performed using SYBR Green (Applied Biosystems) on a StepOne Real-Time PCR machine (Thermo Fisher Scientific). GAPDH was used as an internal control. Primer sequences were as follows: GAPDH *F-CATCTTCTTTTTCGTCGCCA* and *R-TTAAAAGCAGCCCTGGTGACC*, IGF-II *F-GAGCTCGAGGCGTTCAGG* and *R-GTCTTGGGTGGGTAGAGCAATC* and H19 *F-CGGAACATTGGACAGAAG* and *R-GGCGAGGCAGAATATAAC* (Sigma-Aldrich). Quantitation of product was conducted using the Quantitation Comparative CT function within StepOne software (ThermoFisher Scientific). Relative expression was calculated using the Pfaffl method [32].

Pyrosequencing

Pyrosequencing for imprinted allele expression (PIE) was conducted as previously described [33], with the nested PCR step scaled up four-fold to yield 40 μ l product – as per assay requirements defined by the Qiagen Pyromark Q96 protocol. Primers were purchased from Eurofins (Eurofins Genomics, Ebersberg, Germany). PCR product was prepared for pyrosequencing using Qiagen PyroMark Gold Q96 reagents and buffers (Qiagen, Manchester, UK) and sequenced on a PyroMark Q96 machine (Qiagen) by kind permission of Cardiff University Hospital, Cardiff, Wales – UK and North Bristol NHS Trust, Department of Pathology, Southmead Hospital, Bristol - UK. Peak heights and genotypes were quantified by the Qiagen Pyromark software SNP application; peak heights at the rs680 A/G SNP were converted to imprinting percentages using the following formulae: Where $A > 50\%$: $2(A-50)$. Where $A < 50\%$: $2(50-A)$. Tissue was typed as either 'MOI' or 'LOI'

Radioimmunoassay (RIA)

Concentration of IGF-II peptide in cell supernatants was quantified in-house, using radioimmunoassay (RIA) as previously described [34]. This method quantifies all forms of IGF-II peptide, including those that have undergone fragmentation.

Immunohistochemistry (IHC)

Using a microtome (Leica Biosystems, Nussloch, Germany), 8 μ m thick slices were taken from formalin fixed paraffin embedded (FFPE) prostate tissue blocks and mounted on Tomo microscope slides (Matsunami, Bellingham, Washington, USA). Slides were stained for IGF-II peptide using an IGF-II antibody (AbCam, Cambridge, UK) at a dilution of 1:600, on a Ventana BenchMark ULTRA™ machine (Roche, Oro Valley, Arizona, USA). Slides were scored first by a pathologist and second, in-house, using a modified version of the Allred system, combining the proportion of tissue stained (a scale of 1–5) with the stain intensity (a scale of 1–3) to give a score out of 8 [35]. Currently, there is no standardised method of scoring prostate tissue.

Digital droplet PCR (ddPCR)

Primers and Taqman probes were purchased from Bio-Rad and Thermo Fisher Scientific; to optimize the detection of total IGF-II and H19 transcript expression with ddPCR, we initially performed an annealing temperature gradient test for our assay using the PCa cell line PNT2 total RNA. At 55 °C, annealing temperature for ddPCR reactions total IGF-II and H19 amplicon-containing droplets showed the best separation between positive and negative clusters. DDPCR samples for total IGF-II and H19 were set up with 16 ng cDNA samples from individual patients; a stock mix was prepared which contained 10 μ L ddPCR Supermix for Probes, no dUTP (Bio-Rad), 500 nM of each forward and reverse primer (FP and RP) and 250 nM probe (FAM and HEX). Each reaction volume totaled 20 μ L. Droplets were generated with 70 μ L oil using a QX200 droplet generator (Bio-Rad). Amplification was performed at 95 °C, 10 min; followed by 40 cycles of 94 °C, 30 s and 55 °C, 1 min using a C1000 Touch thermocycler (Bio-Rad). After amplification, the droplets were read on a QX200 droplet reader (Bio-Rad) and analyzed with QuantaSoft

software V1.7.4 (Bio-Rad), which converted droplets to copies/ng RNA based on the RNA concentration and the total volume added to the reaction dependent on Poisson distribution. For normalized expression, we used the ratio of IGF-II/H19 concentration to an internal / housekeeping control G2E3 concentration. Raw fluorescence amplitude data was extracted from the droplet reader. We excluded/repeat samples which had too many positive or negative droplets or less than 10,000 droplets.

Use of cBioPortal for Cancer Genomics to examine co-expression of IGF-II & H19 mRNA

The cBio Cancer Genomics Portal [36] and [37] was used to explore co-expression of IGF-II and H19 mRNA; one representative Cancer Genome Atlas cohort was selected from the list of breast and PCa studies. Each cohort was assessed for availability of IGF-II and H19 mRNA co-expression data, which had been gathered using the Illumina HiSeq sequencing system.

Statistical Analysis

Analysis of variance (ANOVA) was used for *in vitro* data, where comparative control experiments were conducted; error bars show the standard error of the mean. A two-tailed *t* test was used for *in vivo* data, to compare the differences between two groups. For correlation analyses, the Pearson correlation coefficient was calculated, with results being expressed as an R value.

Results

Identification of prostate cell line suitability.

DNA was extracted from 4 immortalised PCa cell lines: PC3, LNCaP, DU145, VCaP, and 1 normal prostate cell line: PNT2. These were genotyped using restriction fragment length polymorphism (RFLP) digestion at the APA1 restriction site (rs680); VCaP and PC3 cells were found to be heterozygous, presenting with 2 bands of sizes 292 bp and 229 bp, respectively (Fig. 1.A). These cell lines were classified as informative and would be suitable for further assessment of IS. Cell lines DU145, PNT2 and LNCaP were found to be homozygous for the SNP at rs680 (i.e. the same snp base at the same location, on both copies of the gene), resulting in a single band pattern and, as such, were deemed non-informative.

Confirmation of IGF-II IS in the PC3 and VCaP cell lines

The VCaP cell line produced two bands of sizes 292- and 229 bp, confirming bi-allelic expression of IGF-II (IGF-II mRNA transcribed from 2 alleles: maternal and paternal) and, therefore, loss of imprinting (LOI) (Fig. 1.B). The PC3 cell line, produced a single band of size 292 bp, indicating mono-allelic expression of IGF-II (IGF-II mRNA transcribed from a single allele) and hence maintenance of imprinting (MOI) status and, therefore, was considered to be the most suitable cell line for experiments examining induced LOI.

The impact of altered levels of glucose on IGF-II IS

PC3 cells were cultured in 5-, 9- and 25 mM glucose media for 6-, 24- and 48 hours. After 48-hours, cells exposed to 9- and 25 mM glucose-containing media, showed two bands of 229 and 292 bp. This indicated a change from mono- to biallelic IGF-II expression and, therefore, (LOI) (Fig. 1.C).

The impact of altered levels of glucose on IGF-II imprinting percentage

Using the SNP assay facility, within the Qiagen Pyromark Q96 software, it was possible to genotype and calculate imprinting loss using the A/G SNP at rs680. We applied the formula: $2(A-50)$, where $A > 50$, or $2(50 - A)$, where $A < 50$. After 6 hours, cells cultured in 25 mM glucose showed a significant ($P < .001$) decrease in imprinting percentage, compared to those cultured in 5 mM glucose. After 24 hours, cells cultured in both 9- and 25 mM glucose showed significant decreases in imprinting percentage ($P < .01$ and $.001$ respectively), compared to those cultured in 5 mM glucose; the effects of 9- and 25 mM glucose were enhanced further after 48 hours ($P < .001$ and $.001$ respectively), when compared to those cultured in 5 mM glucose (Fig. 1.D).

The impact of altered levels of glucose on IGF-II mRNA expression

After 6 hours, there was a significant decrease in IGF-II mRNA (Fig. 1.E*i*) in cells cultured in 9 mM - and 25 mM glucose media ($P < .01$ and $.001$ respectively), when compared with the control (5 mM glucose). There were no significant changes to H19 mRNA (Fig. 1.E*ii*) expression. The same pattern of IGF-II expression was observed after 24 hours ($P < .001$ and $.001$ respectively), when compared with the control and similarly there were no significant changes in H19 mRNA expression. After 48 hours, however, there was a significant increase in IGF-II mRNA in cells cultured 25 mM glucose media ($P < .01$), when compared with the control. Conversely, a significant decrease in H19 mRNA expression was observed, in cells cultured in 9 mM -and 25 mM glucose media ($P < .001$ and $.001$ respectively).

Effects of tumour necrosis factor (TNF α) on IGF-II IS

PC3 cells were cultured in 5- and 25 mM glucose media and exposed to increasing doses (0- to 10 ng/ml) of TNF α for 24 hours. Cells cultured in 5 mM glucose and dosed with 10 ng TNF α showed two bands sized 229- and 292 bp – which indicated a change from mono- to biallelic IGF-II expression - suggesting LOI (Fig. 2.A*i*). Cells cultured in 25 mM glucose-containing media and dosed with 1-, 5- and 10 ng/ml ng TNF α showed two bands sized 229- and 292 bp. This indicated a change from mono- to biallelic IGF-II expression, suggesting LOI. Untreated cells, cultured in 25 mM glucose, also showed two bands of 229 and 292 bp, confirming LOI with raised glucose (Fig. 2.A*ii*).

Effects of high dose TNF α on the degree of IGF-II imprinting in cells cultured in normal (5 mM) glucose media

Cells cultured in 5 mM glucose (2.B*i*) and dosed with 1-, 5- and 10 ng/ml all showed significant ($P < .001$) decreases in imprinting percentage, compared to controls. Cells cultured in 25 mM glucose (Fig. 2.B*ii*)

and dosed with 5- and 10 ng/ml TNF α both showed highly significant decreases in imprinting percentage ($P < .001$ respectively), when compared to controls.

Effects of TNF α on IGF-II mRNA expression in cells cultured in normal (5 mM) glucose media.

Cells cultured in 5 mM glucose media showed a significant decrease in IGF-II mRNA expression when dosed with 1- and 5 ng/ml TNF α ($P < .01$ and $.05$ respectively), compared with the untreated control. In contrast, cells treated with 10 ng/ml TNF α showed a significant ($P < .01$) increase in IGF-II mRNA expression, when compared with the control. No significant fold changes in H19 mRNA expression were recorded (Fig. 2.C*i*).

Cells cultured in 25 mM glucose showed no significant changes in IGF-II mRNA when compared to the untreated control. Conversely, a significant decrease ($P < .01$) in H19 mRNA was observed in cells treated with 1 ng/ml TNF α , compared to the un-dosed control. A significant increase ($P < .001$) in H19 mRNA was observed in cells treated with 10 ng/ml of TNF α , when compared with the un-dosed control (2.C*ii*).

Effects of TNF α on levels of secreted IGF-II peptide

Cells cultured in 5 mM glucose and exposed to increasing doses of TNF α (0-, 1-, 5- and 10 ng/ml) for 24- and 48 hours, showed no significant changes to secreted IGF-II peptide (Fig. 2.D). This was also true of cells cultured in 25 mM glucose, exposed to identical doses of TNF α after identical time points (Fig. 2.D*ii*).

IGF-II IS does not significantly vary between benign and malignant paired prostate tissue samples

Figure 3.A depicts the total cohort with proportional representation of each tissue pairing; out of 84 patients 64 presented with no change of MOI status (in the benign sample compared to its cancer counterpart), 6 presented with a change in status from MOI to LOI, 7 presented with a change in status from LOI to MOI and 7 presented with no change of LOI status. Figure 3.B shows the percentage imprinting within each genotype grouping. The group containing the 6 paired samples, with LOI in the cancer compared with MOI in the benign tissue, showed a significant decrease ($P < .001$) in imprinting percentage. The group containing the 7 paired samples, with MOI in the cancer compared with LOI in the benign tissue showed a significant increase ($P < .001$) in imprinting percentage.

There is a positive correlation between IGF-II and H19 mRNA expression in benign and malignant prostate tissue.

There was no difference in absolute expression of IGF-II or H19 between benign and malignant tissue. However, we did observe a positive correlation between IGF-II and H19 expression; with a significant weak positive correlation (Pearson: $R = 0.28$, $P < 0.01$) in the benign tissue (Fig. 4.A*i*) and a stronger positive correlation in malignant prostate tissue ($R = 0.67$, $P < 0.001$) (Fig. 4. A*ii*).

After quantifying IGF-II and H19 mRNA expression in the 'Prostate Cancer - Evidence of Exercise and Nutrition Trial' (PrEvENT) cohort, we utilised the cBioPortal for Cancer Genomics website to assess whether co-expression of IGF-II and H19 mRNA existed, in a larger PCa cohort, as well as another hormone-responsive cancer type: breast.

In the prostate cohort - provided by the Cancer Genome Atlas (TCGA) - a strong positive correlation (Pearson: 0.6) was seen in the co-expression of H19 and IGF-II ($p = 1.37e - 49$) with 489 patients (Fig. 4.B*i*). Similarly, in the TCGA breast cancer cohort (Fig. 4.B*ii*), a strong positive correlation (Pearson: 0.64) was also seen in the co-expression of H19 and IGF-II ($p = 1.11e - 115$) with 994 patients.

There is a positive correlation between IGF-II mRNA and the degree of imprinting in benign and malignant prostate tissue.

A significant ($P < .05$) positive correlation ($R = 0.328$) was found between IGF-II mRNA and the degree of imprinting in benign prostate tissue (Fig. 4.C*i*), which was marginally weaker in malignant tissue ($P < .05$ and $R = 0.224$) (Fig. 4.C*ii*).

Levels of IGF-II peptide do not differ between benign and malignant prostate tissue.

The modified Allred scores of IGF-II peptide abundance in benign and cancerous prostate tissue ($n = 94$) showed no significant differences in stain intensity and proportion (Fig. 5.A). Micrograph images (Fig. 5.B) illustrate strong IGF-II peptide staining in cancer (image A) and benign (image D) tissues, and weak staining in cancer (C) and benign (B) tissues.

Discussion

LOI in IGF-II is a phenomenon common to many different cancer types [38]. The causes and consequences remain unclear. If modifiable behaviours can be shown to influence its occurrence, this could have important implications for understanding the development and progression of cancers.

In this study we have demonstrated that under either hyperglycaemic or inflammatory metabolic conditions, loss of IGF-II imprinting can be induced *in vitro*. In high glucose (i.e. above the healthy range of 4- to 5.9 mM/L for an adult – according to NICE guidelines, (The National Institute for Health and Care Excellence, 2012) or increased inflammatory (TNF α 10 ng/ml $>$) conditions, IGF-II loses imprinting with the introduction of gradual expression of the silenced copy. However, the marked increase in mRNA did not translate into increased expression of IGF-II peptide.

Whilst the exact mechanism of imprinting loss is unclear it may be hypothesised that exposure to elevated glucose conditions and / or inflammatory cytokines may cause disruption to the methylation patterns in and around the IGF-II / H19 locus. Our *in vitro* data indicated that LOI was accompanied by an increase in expression of IGF-II and a reciprocal reduction in expression of H19 consistent with the 'enhancer competition model', first posited in 1993 [23]. Further pyrosequencing to analyse methylation

patterns may provide further clarification. Oxidative stress can also induce LOI, in both benign and malignant prostate tissue, by disrupting the expression of CTCF and its binding to H19 and the ICR [39].

In the PrEvENT cohort, most matched benign and malignant specimens showed no change in imprinting status, with MOI being most prevalent in both tissue types. This disagrees with findings that have shown LOI to be more common in prostates associated with cancer [40], however our results were limited by the relatively small cohort size.

Contrary to our *in vitro* findings, we demonstrated a positive correlation between IGF-II and H19 mRNA expression in the prostate tissue; whilst this was weaker in benign tissue, the stronger positive correlation - seen in malignant tissue - concurred with that of the larger TGCA cancer cohorts.

Our *in vitro* findings may be explained by the use of the PC3 cell line – a cultured monolayer of cells, of a single cell type – compared to the use of clinical tissue specimens -which conversely, are greatly heterogeneous in nature – as shown by Küffer *et al.* [30].

Interestingly, IGF-II / H19 LOI is also found in normal tissue and not just cancer, where frequently it is also not related to expression levels. For example, 22% of normal infants have IGF-II LOI with no changes in expression levels in the majority [41]. We suggest that imprinting is only one factor involved in regulating expression and may not be essential in human tissues; IGF-II and H19 share a common enhancer 3'-downstream from H19 [42] that could be a more important determinant of expression of both, rather than imprinting controls.

The key finding that bridges our *in vitro* with *in vivo* findings is that there was no measurable change in IGF-II peptide. The lack of correlative findings may be explained by a deficiency of RNA binding proteins such as the insulin-like growth factor 2 messenger-RNA binding proteins (IMPs). These affect the processing of IGF-II mRNA at multiple levels - including translation. Of the three IMPs (IMP1, IMP2 and IMP3) identified [43], IMP3 has been shown to activate translation of mRNA by binding to the coding regions of IGF-II [44]. Under our simulated *in vitro* conditions, inhibition or insufficient synthesis of IMP3 may have occurred and further quantification of IMP3 would address this issue.

In vivo, a deficiency of RNA binding proteins may be also contributory, but an additional factor may be that circulating IGF-II peptide is unstable and may be susceptible to degradation [45]. To combat this, it binds with specific binding proteins – insulin-like growth factor binding proteins (IGFBPs). There are six IGFBPs: IGFBP1-6 and they bind to IGF-I and -II with high affinity [46]. More specifically, IGFBP2 binds to IGF-II with very high affinity [47]. Therefore, the inconsistency of IGF-II staining is likely due to the presence of peptide bound to IGFBP-2.

Conclusion

To summarise, our study illustrated that an artificially simulated inflammatory environment does induce LOI in IGF-II, causing upregulation of IGF-II and downregulation of H19 mRNA. The potential cause may

be due to disruption of methylation patterns throughout both copies of the gene, inducing partial expression of the usually silenced paternal copy. The increase in IGF-II mRNA did not equate to elevated protein expression – which may be due to impaired RNA-binding protein synthesis. Matched benign and malignant specimens from the PrEvENT cohort primarily retained IS, although a small subset with LOI did exhibit reduced imprinting. A positive correlation was seen between IGF-II and H19 mRNA expression, which concurred with findings of larger TCGA cohorts and other hormone-responsive cancer types (breast). This positive correlation did not affect IGF-II peptide. Our *in vitro* findings are of utmost relevance to indicate that type 2 diabetes and / or obesity directly affect the regulation of growth factors involved in carcinogenesis. Furthermore, our data suggest that LOI does not necessarily coincide with the development of cancer or translate into more IGF-II peptide, but its actual consequences may only be fully understood when the complex interactions between all the products of the gene locus, including long non-coding RNA, microRNA and antisense transcripts, are fully characterised.

Abbreviations

ANOVA

Analysis of variance

B

Benign

BMI

Body mass index

C

Cancer

cDNA

Complementary DNA

CTCF

CCCTC-binding factor

ddPCR

Digital droplet PCR

DMEM

Dulbecco's modified Eagles Medium

FBS

Foetal bovine serum

FFPE

Formalin fixed paraffin embedded

FP

Forward primer

ICR

Imprinting control region

IGF-II

Insulin-like growth factor 2
IGFBPs
Insulin-like growth factor binding proteins
IHC
Immunohistochemistry
IMPs
insulin-like growth factor 2 messenger-RNA binding proteins
IS
Imprinting status
lncRNA
Long non-coding RNA
LOI
Loss of imprinting
miRNA
Micro-RNA
MOI
Maintenance of imprinting
NICE
The National Institute for Health and Care Excellence
PCa
Prostate cancer
PIE
Pyrosequencing for imprinted allele expression
PrEvENT
Prostate cancer - evidence of exercise and nutrition trial
qPCR
Quantitative PCR
RFLP
Restriction fragment length polymorphism
RIA
Radioimmunoassay
RP
Reverse primer
RPE
Radical prostatectomised
RPMI-1640
Roswell Park Memorial Institute 1640
Rs680
Restriction site 680
SFM

Serum free media
SNP
Single nucleotide polymorphism
T2D
Type 2 diabetes
TGCA
The Cancer Genome Atlas
TNF α
Tumour necrosis factor alpha

Declarations

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Author's contributions

GK and KB conducted the majority of experiments and analysed data; AS, PG, RB and HZ assisted with IHC; AG assisted with pyrosequencing and KM, RMM, JAL, LM, AK, ER and JO participated in the PrEvENT study. GK wrote the paper. JH and CP revised and edited the paper and acquired funding. All authors read and approved the final manuscript.

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Availability of data and materials

The data used throughout the study are available on request from the corresponding author.

Ethics approval and consent to participate

The PrEvENT study was approved by the NRES Committee South West – Cornwall & Plymouth, on 9th September 2014 (reference number: 14/SW/0056) and was registered with the ISRCTN registry on 17th November 2014 (ISRCTN99048944)

Consent for publication

N.A

Competing interests

The authors declare no competing interests in relation to the work described.

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Figures

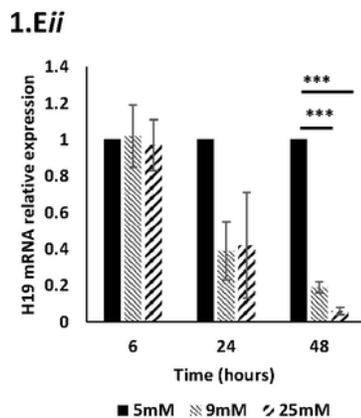
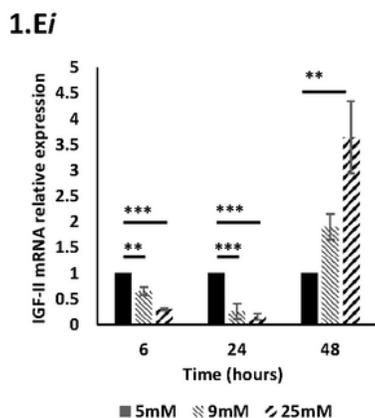
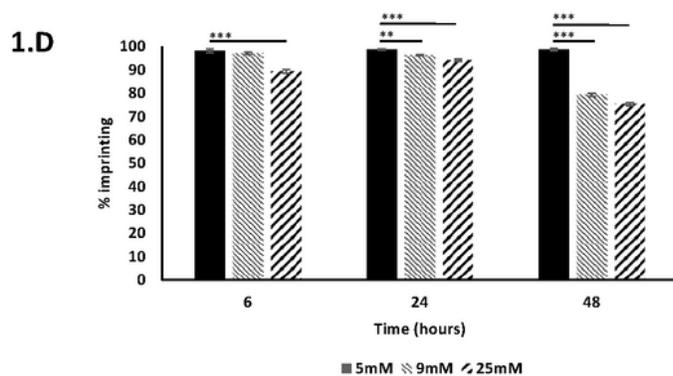
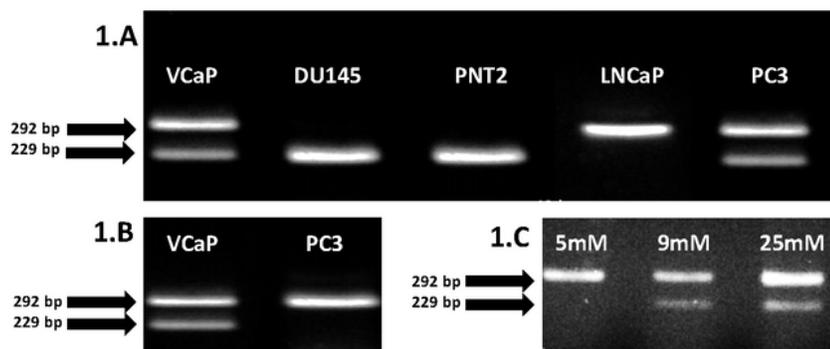


Figure 1

Genotyping, IGF-II allelic expression and imprinting behaviour after treatment with glucose, in prostate cancer cell lines using APA1 RFLP, PIE and qPCR analyses. A) Gel image depicting genotype results of cell lines VCaP, DU145, PNT2, LNCaP and PC3. VCaP and PC3 showed two bands, sized 292- and 229bp. This meant that these cells were heterozygous for the SNP at rs680 and, therefore, informative. (n=3) B) Gel image depicting IGF-II allelic expression. The VCaP cell line showed two bands, sized 292 and 229 bp,

signifying bi-allelic expression and, therefore, loss of imprinting of IGF-II. The PC3 cell line showed a single band sized 292 bp, indicating mono-allelic expression of IGF-II and, therefore, a retention of imprinting status. (n=3) C) Gel image depicting the effects of varied glucose concentration on IGF-II allelic expression in the PC3 cell line after 48 hours. Cells cultured in 9- and 25 mM glucose showed two bands sized 229- and 292 bp, indicating a change from mono- to biallelic IGF-II expression and, therefore, loss of imprinting. (n=3) D) Imprinting percentage change of PC3 cells after exposure to glucose for 6-, 24- and 48 hours. After 6 hours, cells cultured in 25mM glucose showed a highly significant ($P < .001$) decrease in imprinting percentage compared to those cultured in 5mM glucose. After 24 hours, cells cultured in 9- and 25mM glucose showed significant decreases in imprinting percentage ($P < .01$ and $.001$ respectively), when compared to those cultured in 5mM glucose. After 48 hours, cells cultured in 9- and 25mM glucose showed highly significant decreases in imprinting percentage ($P < .001$ and $.001$ respectively), when compared to those cultured in 5mM glucose. (n=3) E) IGF-II and H19 mRNA relative expression in the PC3 cell line, after exposure to increased glucose levels; a significant increase in IGF-II mRNA expression (i) was observed after 6-, 24- and 48-hours in 9- and 25mM glucose media. A significant decrease in H19 mRNA expression (ii) was observed after 48-hours in 9- and 25mM glucose media. (n=3)

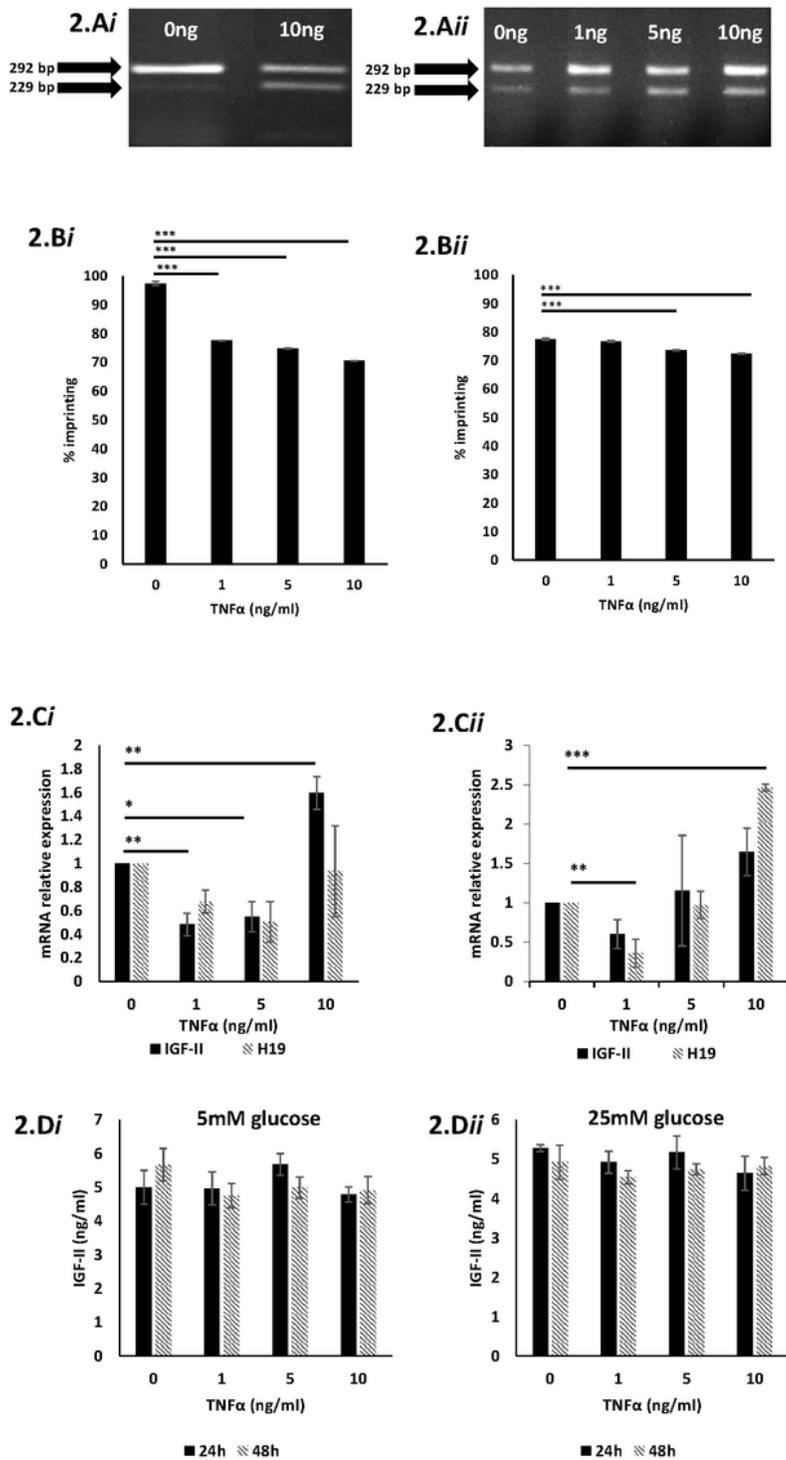
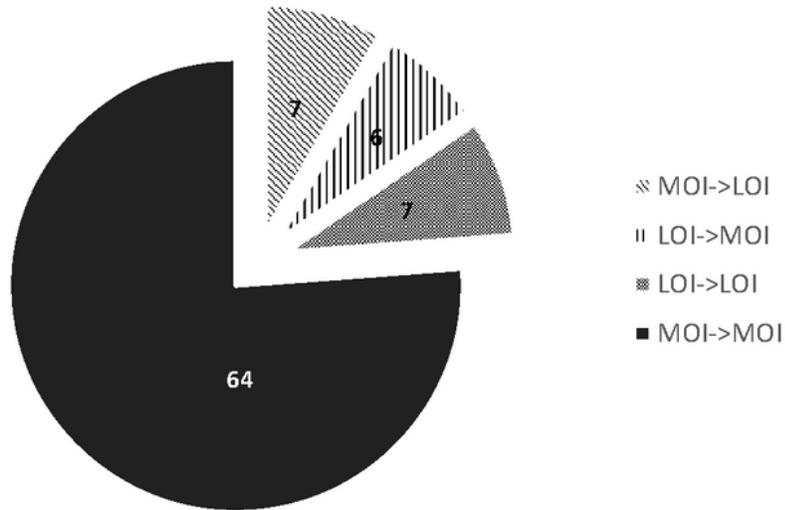


Figure 2

IGF-II allelic expression, imprinting behaviour and peptide expression after treatment with TNFα, in prostate cancer cell lines using APA1 RFLP, PIE, qPCR and RIA analyses. A) Gel image depicting the effects of TNFα upon IGF-II allelic expression in the PC3 cell line, after 24 hours exposure. Cells cultured in 5mM (i) glucose and dosed with 10ng/ml TNFα showed two bands, sized 229 and 292 bp, indicating a change from mono- to biallelic IGF-II expression and, therefore, loss of imprinting. Cells cultured in 25mM

(ii) glucose and dosed with 0-, 1-, 5- and 10ng/ml TNF α showed two bands sized 229 and 292 bp, indicating a change from mono- to biallelic IGF-II expression and, therefore, loss of imprinting. (n=3) B) Imprinting percentage change of PC3 cells after exposure to TNF α for 24 hours in 5mM (i) and 25mM (ii) glucose. Cells cultured in 5mM glucose media (i) and dosed with 1-, 5- and 10ng/ml TNF α all showed highly significant (P<.001) decreases in imprinting percentage; those cultured in 25mM glucose media (ii) and dosed with 5- and 10ng/ml TNF α , also showed highly significant (P<.001) decreases in imprinting percentage when compared with the control. (n=3). C) IGF-II and H19 mRNA relative expression in the PC3 cell line, after treatment with TNF α in 5mM (i) and 25mM (ii) glucose for 24-hours, using qPCR; i) a significant increase in IGF-II was observed in cells dosed with 1, - 5- and 10ng/ml TNF α . No significant fold changes in H19 mRNA were observed (n=3). ii) No significant fold changes in IGF-II mRNA were observed. A significant decrease in H19 was observed in cells dosed with 1ng/ml TNF α , whilst a significant increase was observed in those dosed with 10ng/ml TNF α . D) After 24- and 48 hours exposure to 5- (i) and 25mM (ii) glucose, combined with increasing doses of TNF α , there were no significant changes in the quantities of IGF-II peptide. (n=3)

3.A



3.B

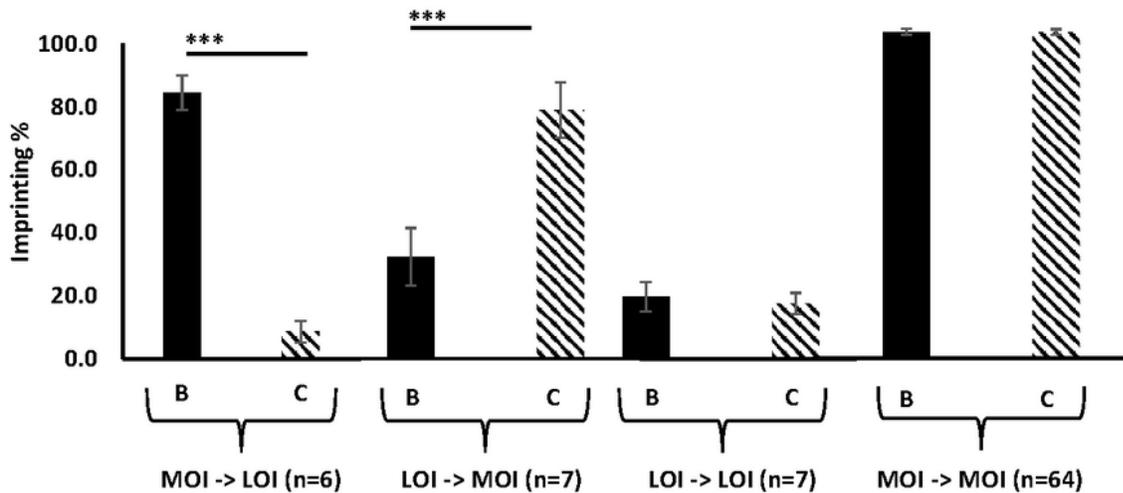


Figure 3

Imprinting status of paired benign and malignant prostate tissue samples from the PrEvENT cohort. A) Cohort divided by imprinting status change, moving from benign to corresponding malignant counterpart. Of the total cohort (84 tissue pairs), 64 showed no change of maintenance of imprinting (MOI) from benign to malignant; 7 showed no change of loss of imprinting (LOI), from benign to malignant; 6 showed a change from LOI to MOI and 7 showed a change from MOI to LOI. B) Imprinting status sub-divisions of

PrEvENT cohort, with changes in imprinting percentage. A significant decrease ($P < .000$) in imprinting percentage was seen in samples where imprinting status changed from MOI to LOI ($n=7$); conversely, significant increase ($P < .000$) in imprinting percentage was seen in samples where imprinting status changed from LOI to MOI ($n=6$).

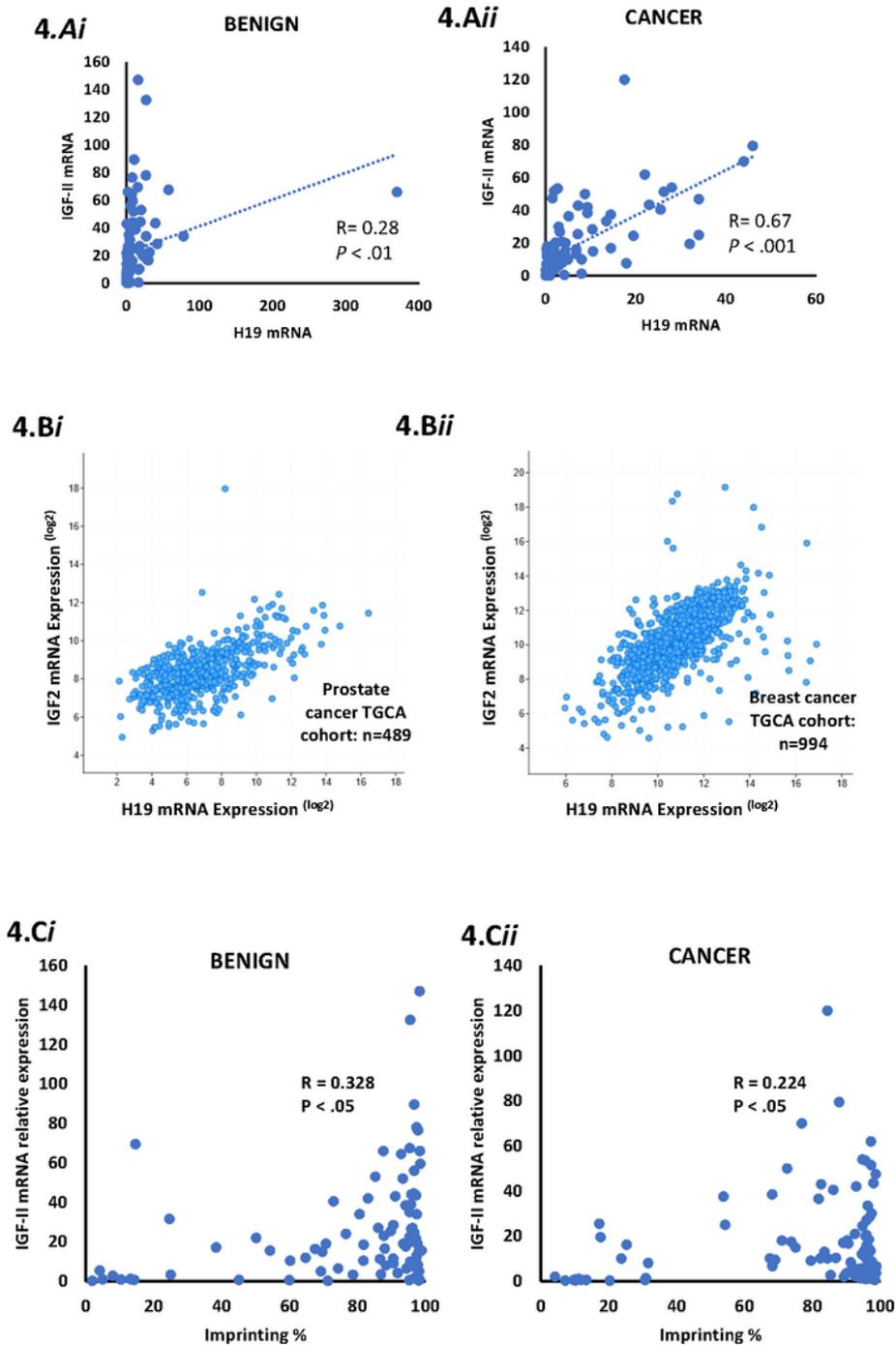
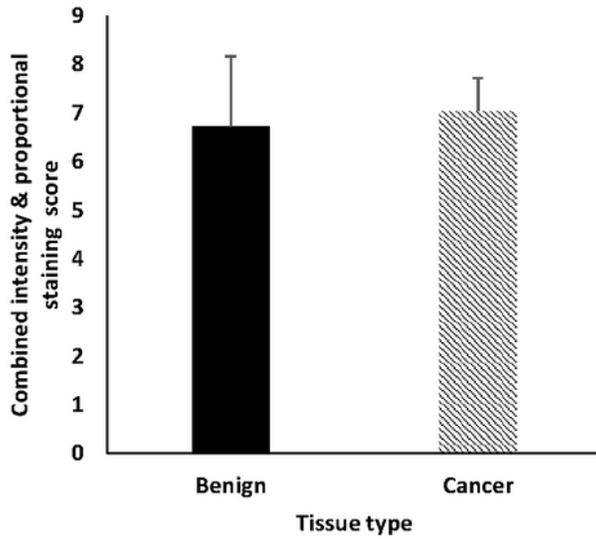


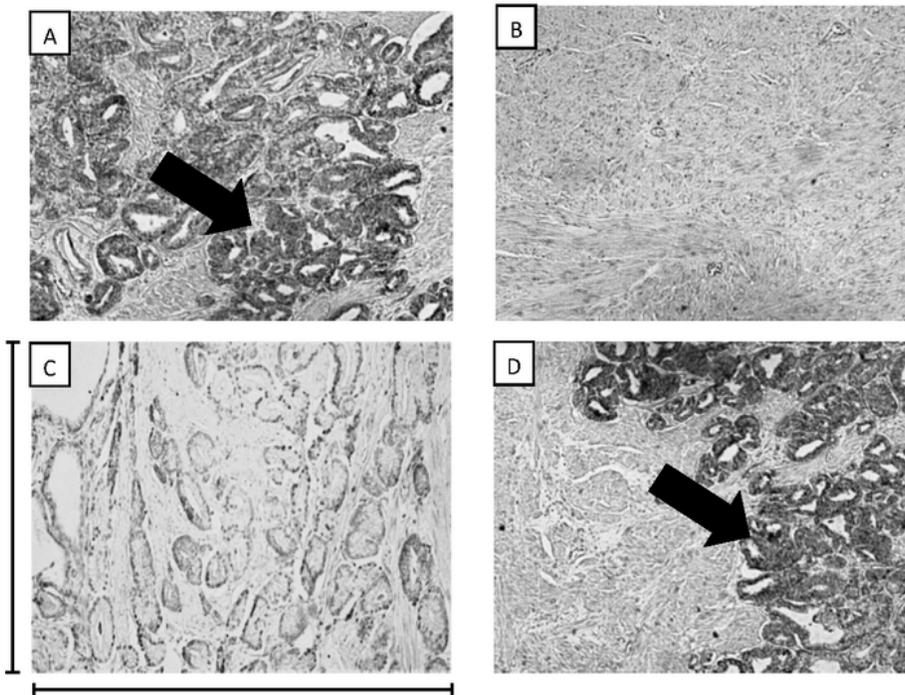
Figure 4

Co-expression of IGF-II & H19 mRNA and IGF-II & imprinting percentage in benign and prostate cancer tissue sections. A) Co-expression of H19 & IGF-II mRNA in benign (i) and cancer (ii) derived from FFPE prostate tissue from the PrEvENT cohort. Pearson's correlation coefficient analysis found a significant ($P < .01$) weak positive ($R=0.28$) correlation between H19 and IGF-II mRNA expression in benign prostate tissue; a significant ($P < .001$) stronger ($R=0.67$) positive correlation was found in cancer tissue ($N=95$) B) Metabarc data from The Cancer Genome Atlas (TCGA) showed strong positive correlations between co-expression of H19 & IGF-II mRNA in (i) prostate ($R = 0.6, p= 1.37e - 49$) (i) and (ii) breast ($R = 0.64, p = 1.11e -115$) cancer. C) Imprinting percentage of IGF-II gene plotted against IGF-II mRNA in i) benign and ii) cancer prostate tissue. A significant negative correlation was seen between IGF-II imprinting percentage and mRNA expression in both tissue types. ($n=84$)

5.A



5.B



Scale: 1x1 mm, at 20x magnification.

Figure 5

IHC staining of IGF-II peptide in benign and malignant prostate tumour tissue. A) IHC staining of IGF-II peptide in FFPE prostate tumour tissue using the Ventana Benchmark Ultra machine. There were no significant differences in staining scores between malignant and benign prostate tissue. B) Patterns of IGF-II cytoplasmic IHC staining in paired tissue samples from 2 patients. Strong IGF-II peptide staining

was observed in both cancer (A) and benign (D) tissue, as was weak staining (B / benign & C / cancer).
Scale is 1x1 mm, at 20x magnification.