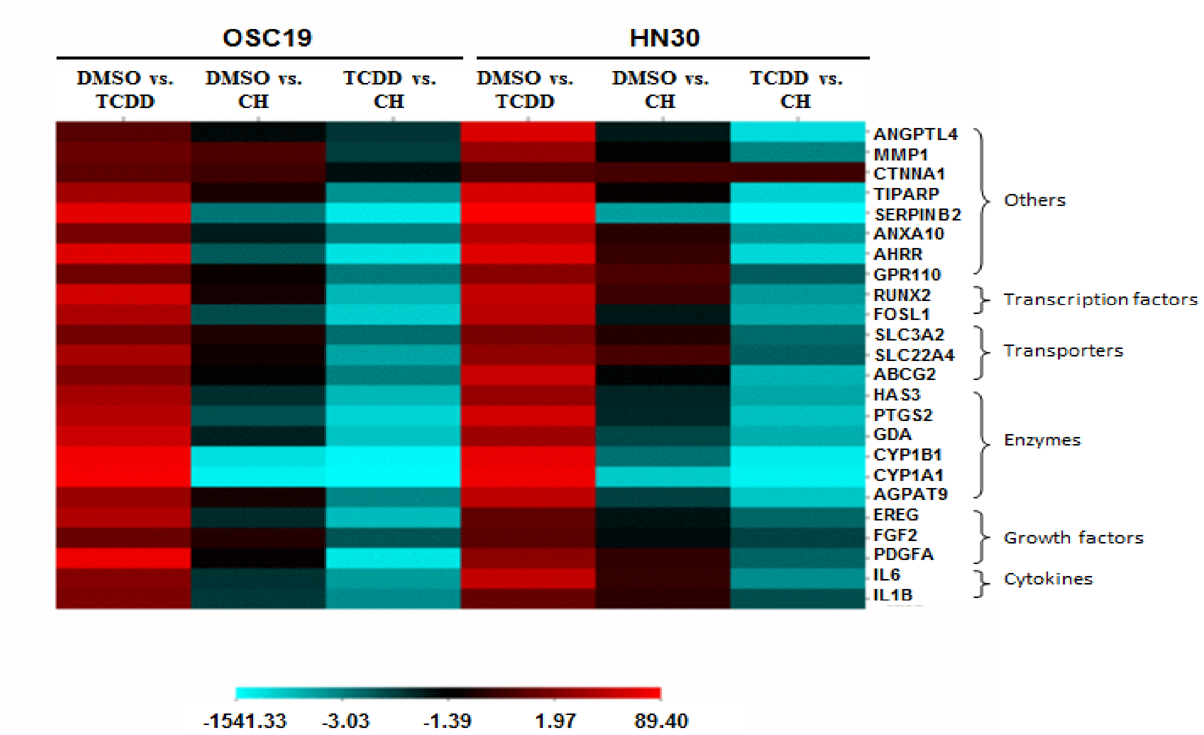
Supplementary Materials and Results

Table S1: Primer sequences for *CYP1A1* and growth factor genes from this study

CYP1A1	5’ -GATTGAGCACTGTCAGGAGAAGC- 3’
	5’ -ATGAGGCTCCAGGAGATAGCAG- 3’
AREG	5’ -GCACCTGGAAGCAGTAACATGC- 3’
	5’ -GGCAGCTATGGCTGCTAATGCA- 3’
EREG	5’ -CTTATCACAGTCGTCGGTTCCAC- 3’
	5’ -GCCATTCAGACTTGCGGCAACT- 3’
FGF2	5’ -AGCGGCTGTACTGCAAAAACGG- 3’
	5’ -CCTTTGATAGACACAACTCCTCTC- 3’
PDGFA	5’ -CAGCGACTCCTGGAGATAGACT- 3’
	5’ -CGATGCTTCTCTTCCTCCGAATG- 3’

A


OSC19
HN30
DMSO vs. TCDD
DMSO vs. CH
TCDD vs. CH
DMSO vs. TCDD
DMSO vs. CH
TCDD vs. CH
ANGPTL4
MMP1
CTNNA1
TIPARP
SERPINB2
ANXA10
AHRR
GPR110
RUNX2
FOSL1
SLC3A2
SLC22A4
ABCG2
HAS3
PTGS2
GDA
CYP1B1
CYP1A1
AGPAT9
EREG
FGF2
PDGFA
IL6
IL1B
Others
Transcription factors
Transporters
Enzymes
Growth factors
Cytokines
-1541.33
-3.03
-1.39
1.97
89.40

B

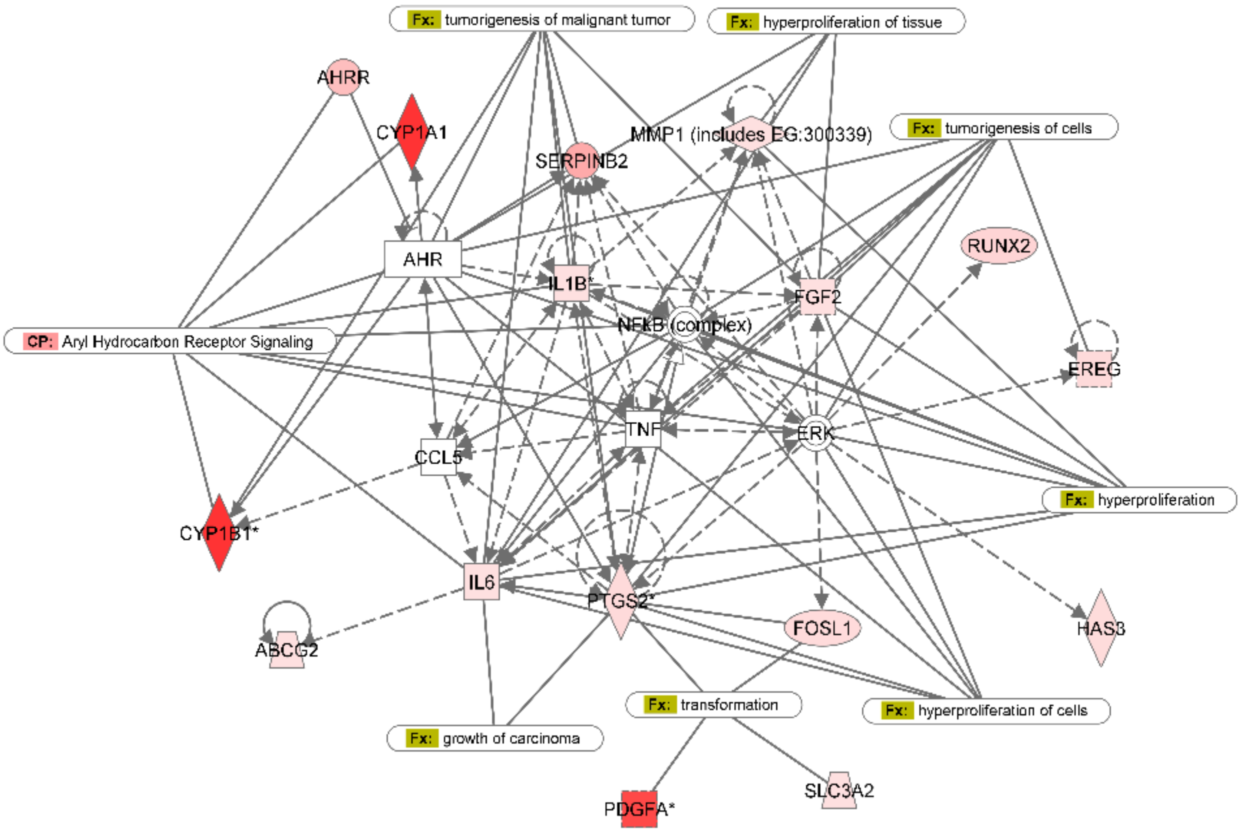

Fx: tumorigenesis of malignant tumor
Fx: hyperproliferation of tissue
AHRR
CYP1A1
MMP1 (includes EG:300339)
Fx: tumorigenesis of cells
SERPINB2
RUNX2
AHR
IL1B*
FGF2
NFkB (complex)
CP: Aryl Hydrocarbon Receptor Signaling
EREG
TNF
ERK
CCL5
Fx: hyperproliferation
CYP1B1*
IL6
PTGS2*
FOSL1
HAS3
ABCG2
Fx: transformation
Fx: hyperproliferation of cells
Fx: growth of carcinoma
SLC3A2
PDGFA*

Figure S1: Whole genome expression analysis of head and neck tumor cell lines following treatment with an AHR agonist and antagonist reveals putative AHR target genes altered in head and neck cancers
(A) Gene expression patterns of 24 genes up-regulated following treatment with TCDD and significantly down-regulation by the AHR antagonist, CH223191, relative to cells treated with TCDD alone (B) Network mapping of these genes revealed seven genes to be unconnected to the network (not shown here). Among the remaining connected genes three were growth factor regulators whose expression was up-regulated by TCDD and subsequently down-regulated by CH223191 and hence considered for further analysis. AREG though absent in this gene-set was considered based on previous unpublished results from this lab. The legend to the different types of designations and interactions can be found in the Supplementary Figure S3.

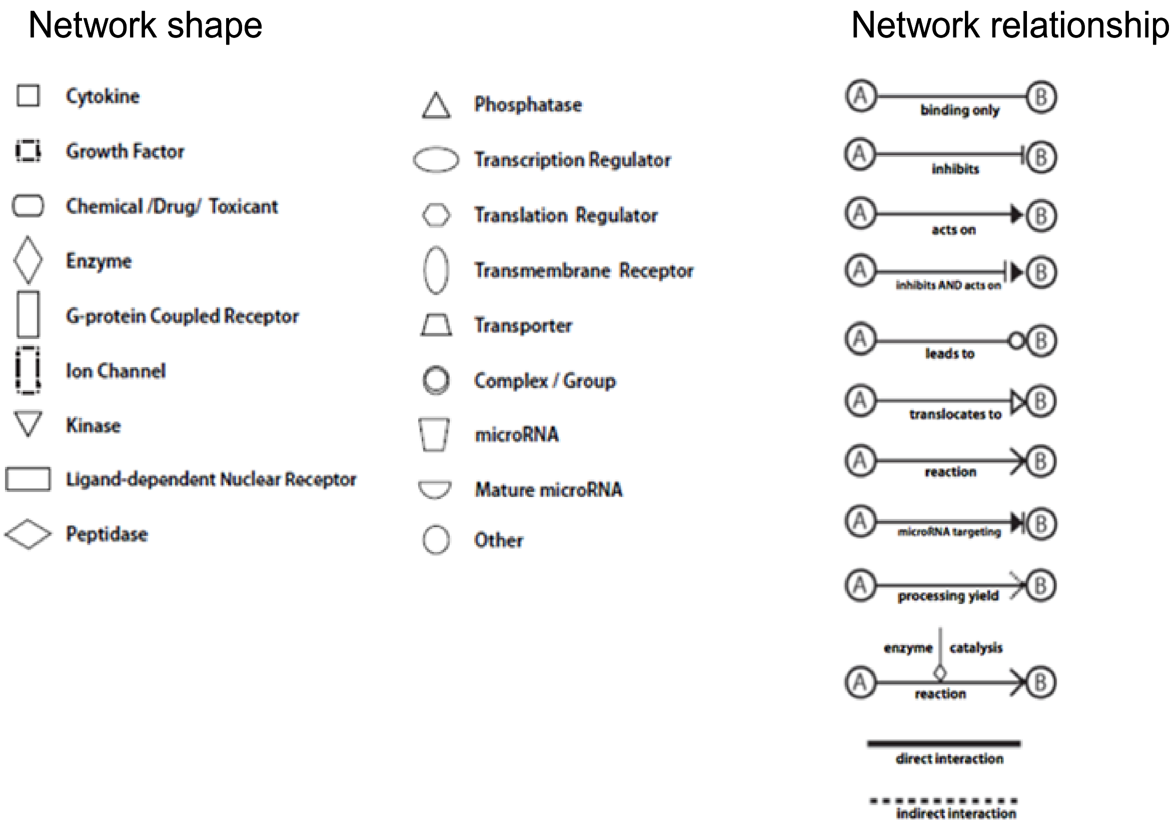


Figure S2: Legend to different designations and relationships used in the network analysis depicted in Figure S2

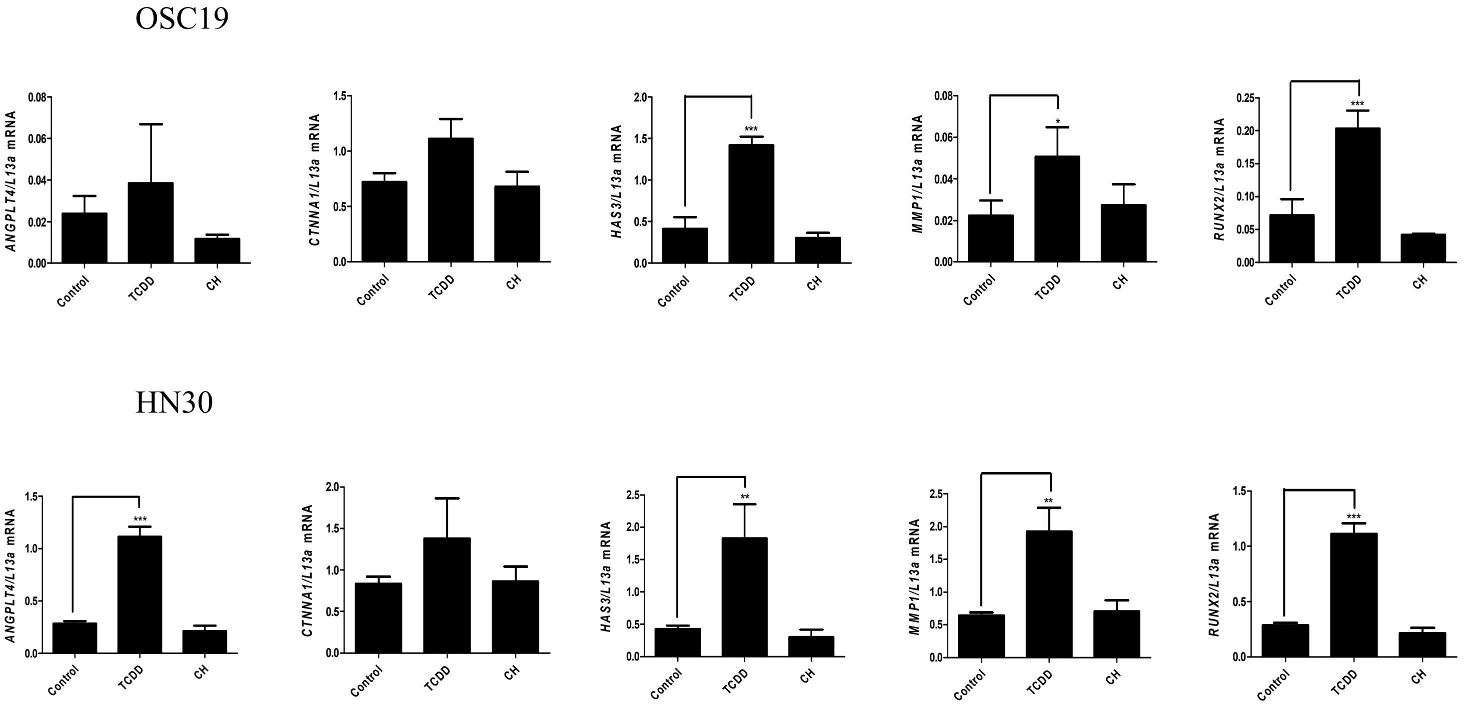


Figure S3: Validation of microarray gene expression patterns, for select genes, by qPCR analysis.

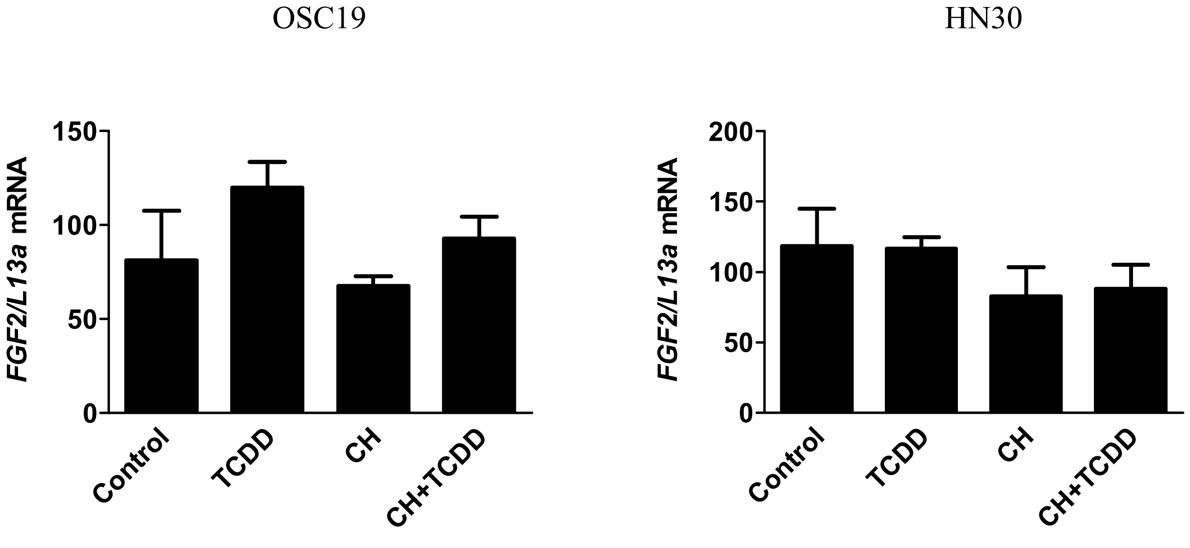


Figure S4: CH223191 fails to significantly attenuate basal and TCDD induced expression of *FGF2* in OSC19 and HN30 cells.

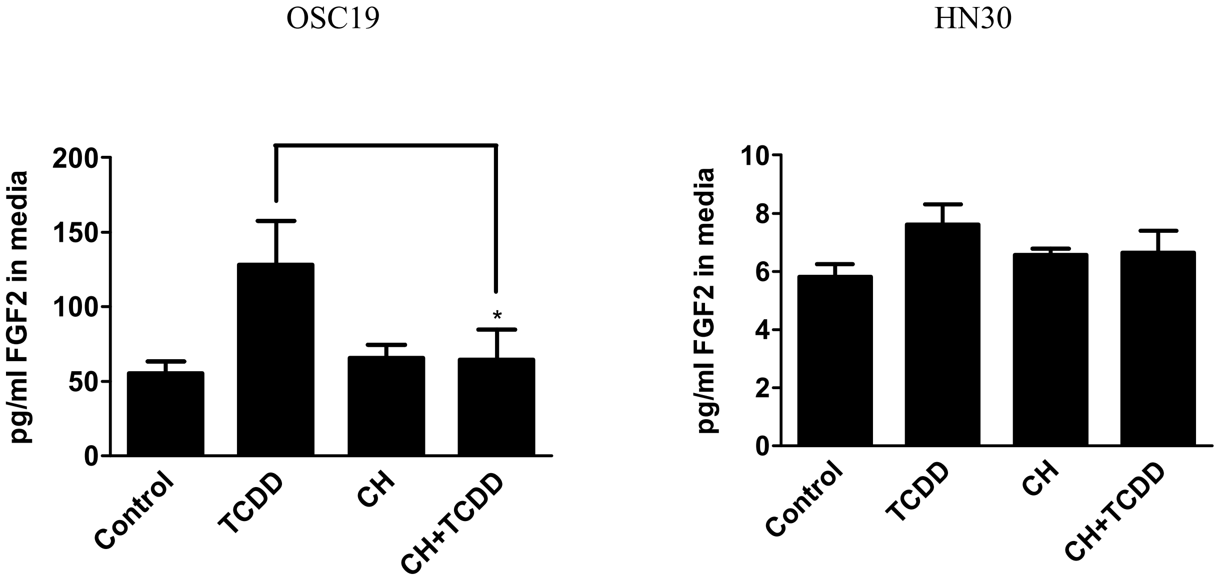
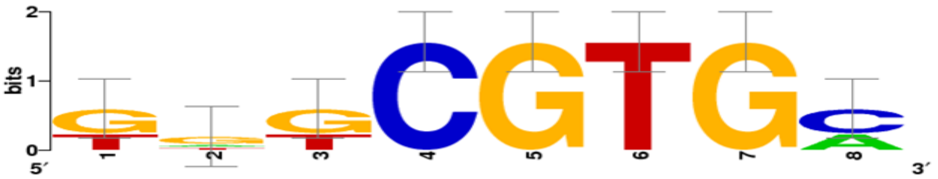


Figure S5: CH223191 significantly attenuated TCDD induced protein levels of FGF2 in OSC19 cells, but not in HN30 cells.

G/T N T/G CGTG A/C



C/A N A/C GCAC T/G

A/C GTGC T/G N T/G

T/G CACG A/C N A/C

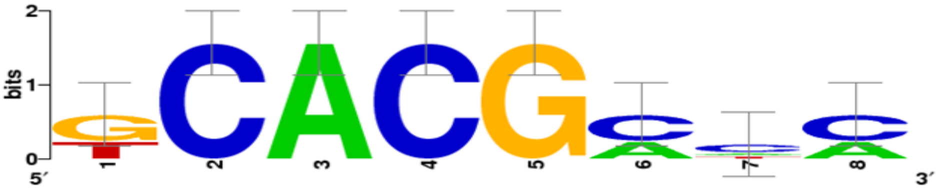


Figure S6: Sequence logos obtained following a scan of the promoter region (2500 bp upstream of transcription start site) of multiple growth factors for the presence of DRE-like sequences (G/T N T/G CGTG A/C), in all possible orientations, on both the plus and minus strand's of DNA. The various orientations of the DRE-like elements used for the searches are displayed above the respective logos. The March 2006 (NCBII36/hg18) assembly of the human genome was used for analysis.

Table S2: Location of the DRE-like consensus sequence (G/T N T/G CGTG A/C), **i**n all possible orientations, in multiple growth factor genes examined in this study. 2500 bp upstream of the transcription start site was scanned *in silico* for the presence of these DRE-like elements. The various orientations of the DRE-like elements used for the searches are displayed above each table. The March 2006 (NCBII36/hg18) assembly of the human genome was used for analysis.

G/T N T/G CGTG A/C

Site	Strand	Location	Gene
gggcgtga	-	-1423 to -1430	AREG
tggcgtga	-	-1547 to -1554	EREG
gatcgtgc	+	-1276 to -1269	FGF2
tggcgtgc	-	-1520 to -1527	PDGFA
gttcgtgc	-	-582 to -589	PDGFA

C/A N A/C GCAC T/G

Site	Strand	Location	Gene
ccagcact	-	-1311 to -1318	AREG
agagcact	+	-1013 to -1006	AREG
ccagcact	-	-1384 to -1391	EREG
acagcact	+	-962 to -955	FGF2
acagcacg	+	-1530 to -1523	PDGFA

A/C GTGC T/G N T/G

Site	Strand	Location	Gene
agtgctgg	+	-1318 to -1311	AREG
agtgctct	-	-1006 to -1013	AREG
agtgctgg	+	-1391 to -1384	EREG
agtgctgt	-	-955 to -962	FGF2
cgtgctgt	-	-1523 to -1530	PDGFA

T/G CACG A/C N A/C

Site	Strand	Location	Gene
tcacgccc	+	-1430 to -1423	AREG
tcacgcca	+	-1554 to -1547	EREG
gcacgatc	-	-1269 to -1276	FGF2
gcacgcca	+	-1527 to -1520	PDGFA
gcacgaac	+	-589 to -582	PDGFA

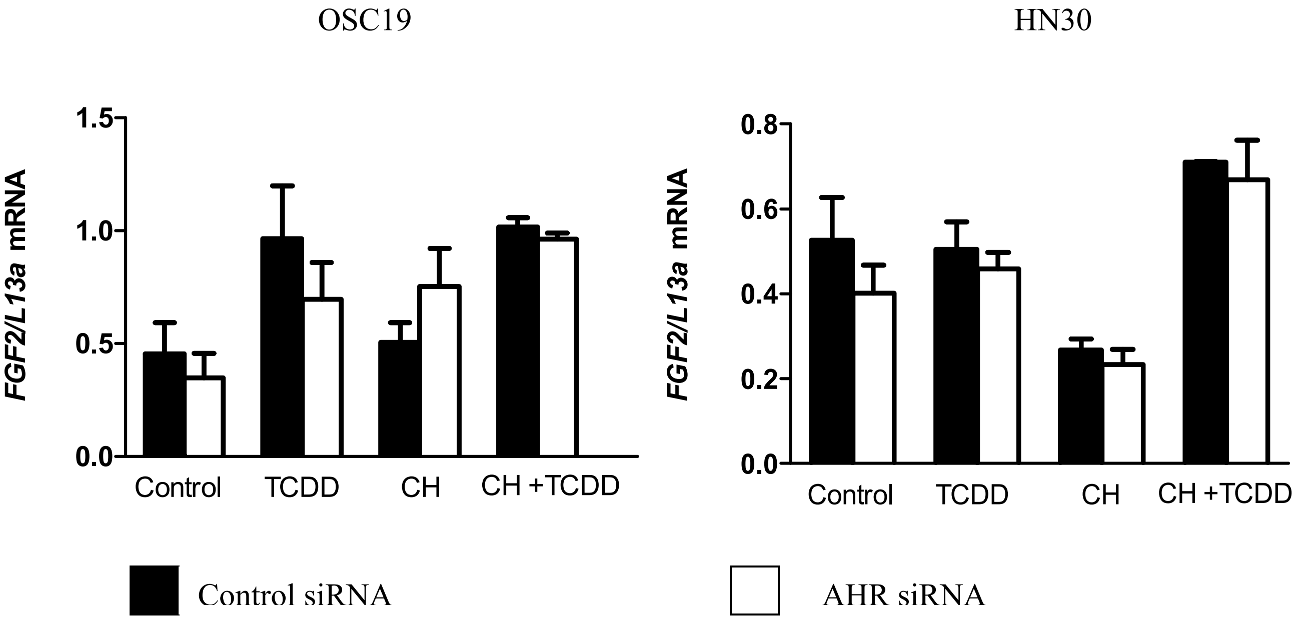


Figure S7: siRNA mediated knock down of AHR failed to mitigate both basal and TCDD induced expression of *FGF2* in OSC19 and HN30 cells.

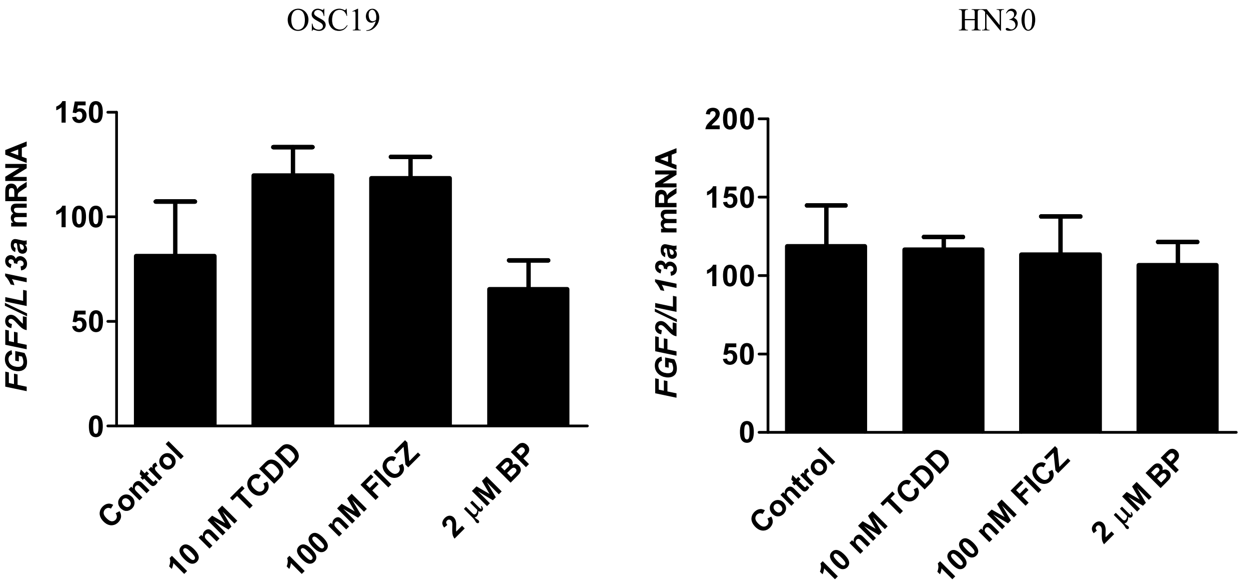


Figure S8: Effect of three prototypic AHR agonist on *FGF2* expression.

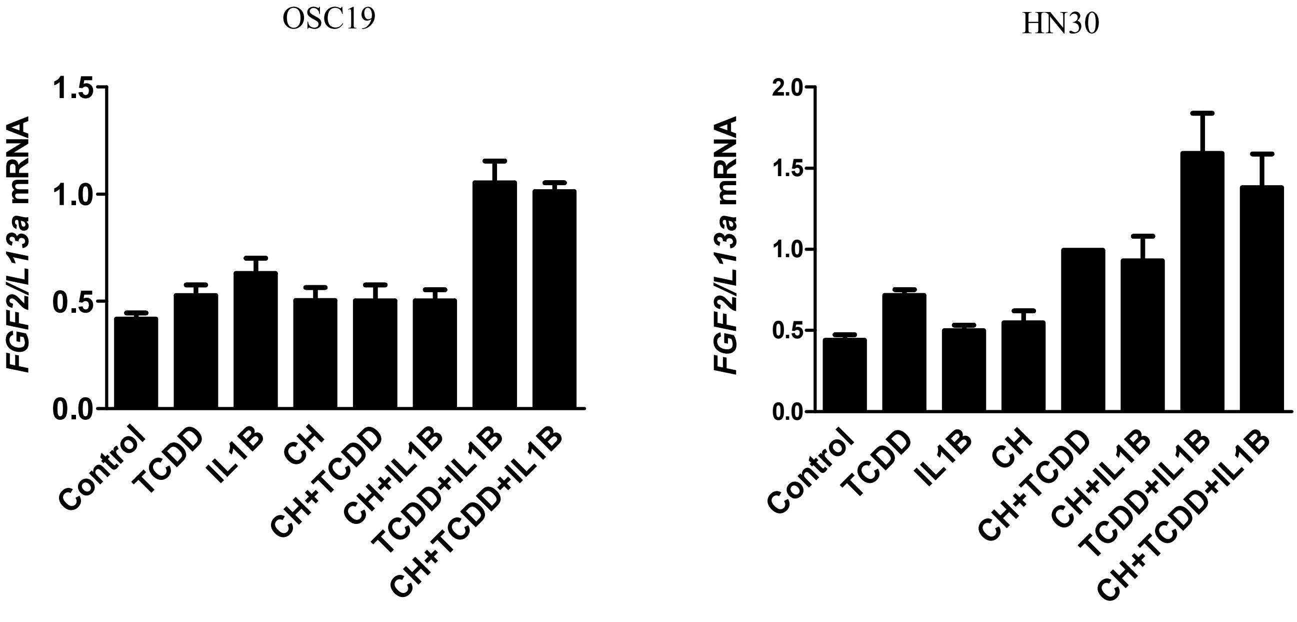


Figure S9: TCDD and IL1B in combination significantly induced the expression of *FGF2* in both OSC19 and HN30 cells and CH223191 failed to block TCDD and IL1B mediated induction of *FGF2*.