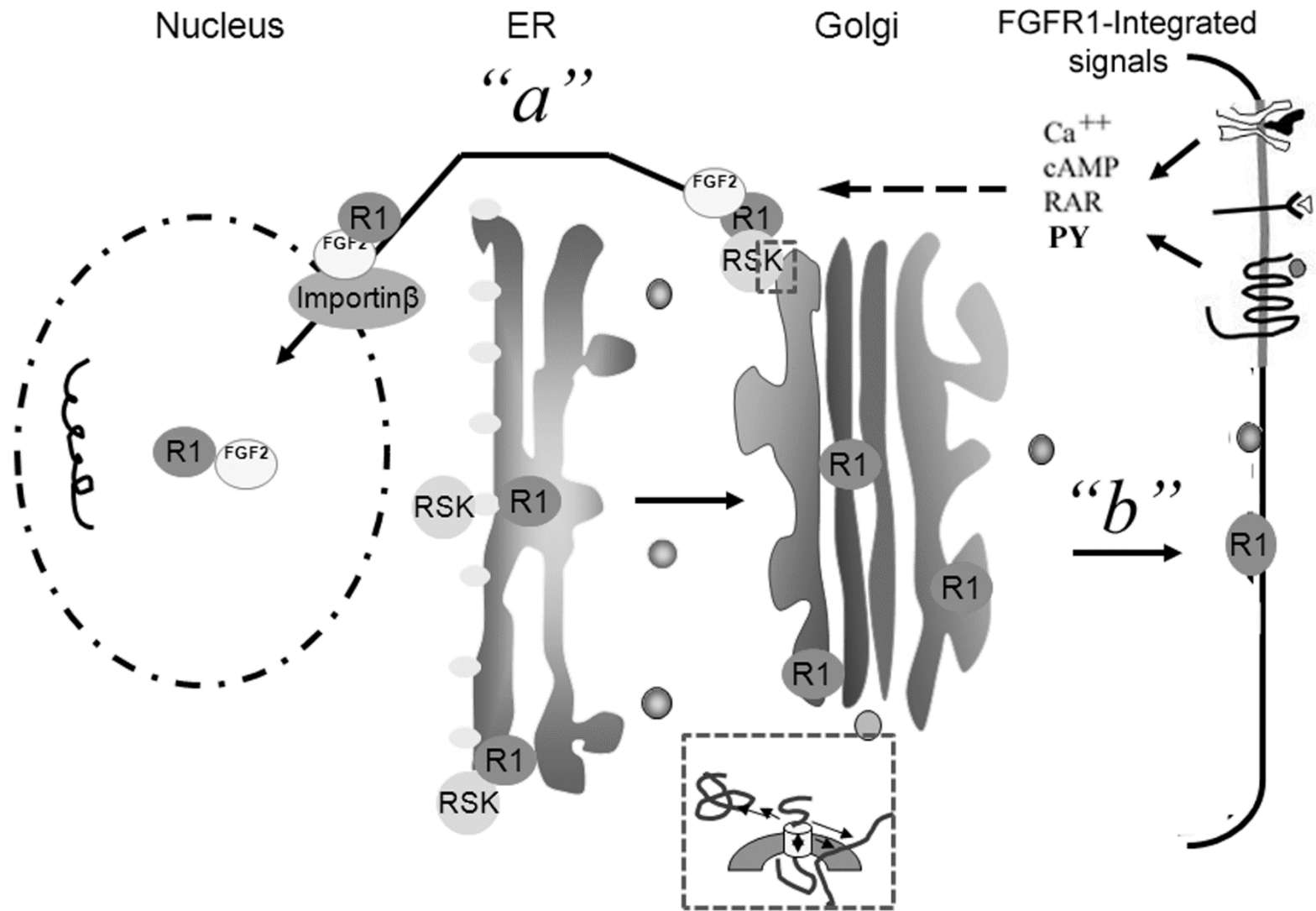


nuclear FGFR1 (R1) trafficking by RSK1, FGF & Importin

- Integrative Signaling Mechanism

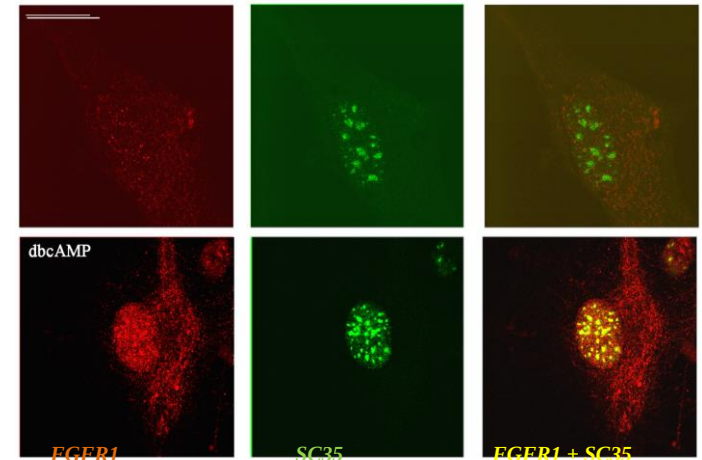
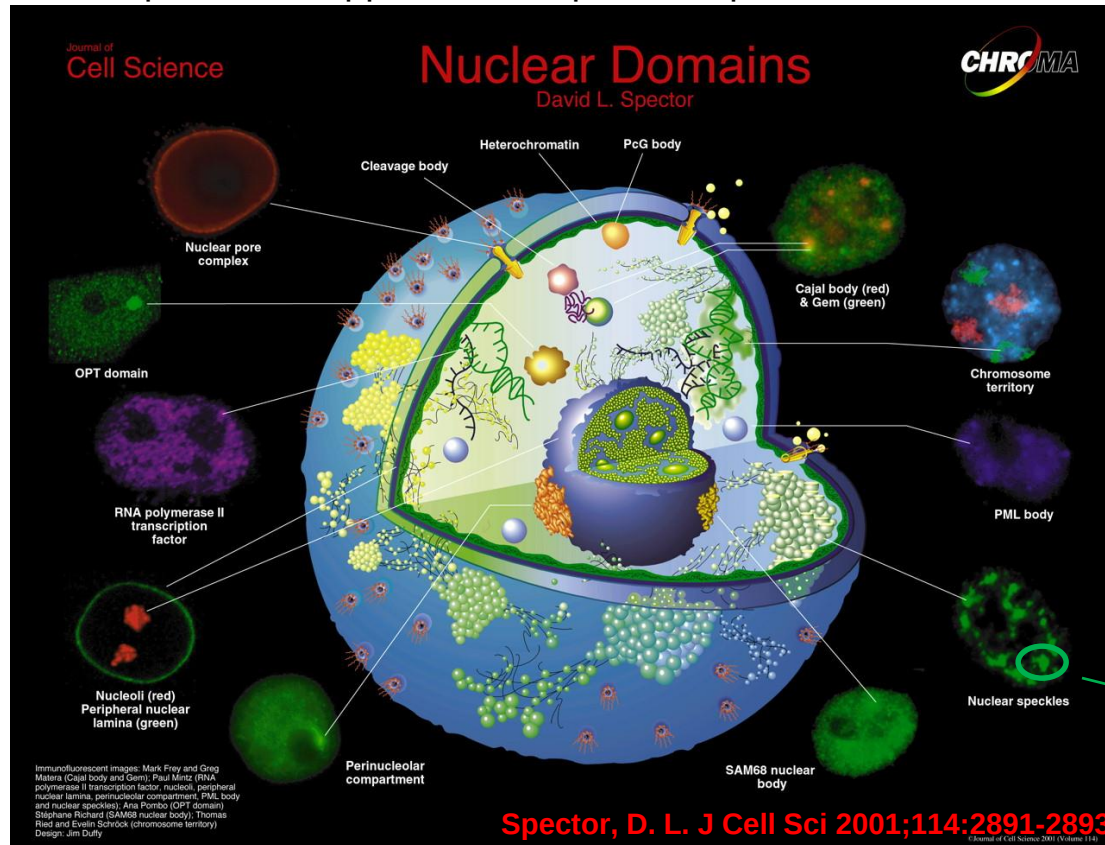


INFS – Global Genome Programmer

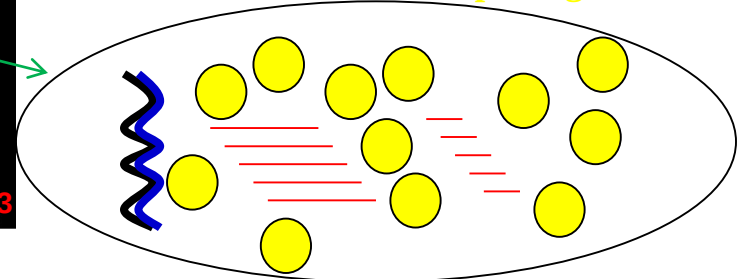
Lecture 8

FGFR1 concentrates in Nuclear Bodies (“speckles”)

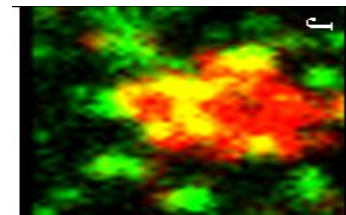
- The cell nucleus contains nearly 30,00 genes and complex machineries for their replication and expression.
- These processes appear to take place in specialized subnuclear domains (diverse nuclear bodies).



DNA transcription and RNA processing co-occur in nuclear domains rich in **splicing factors**.



RNA PolII

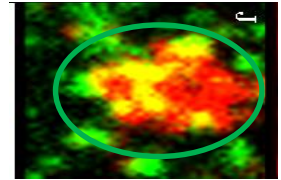
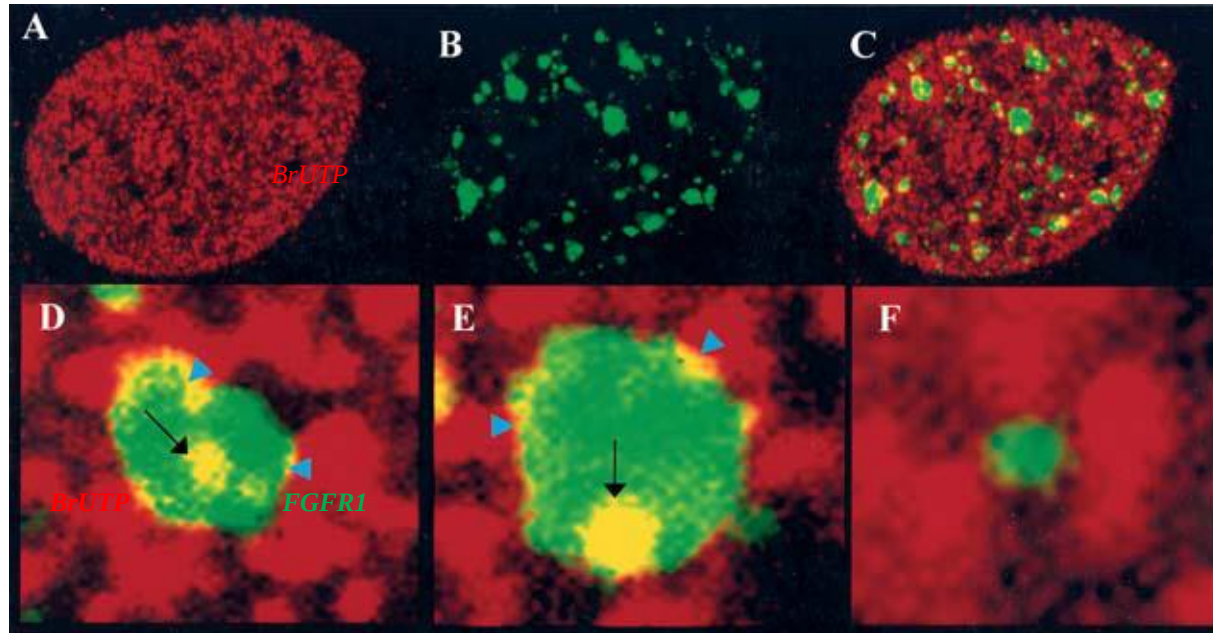


FGFR1

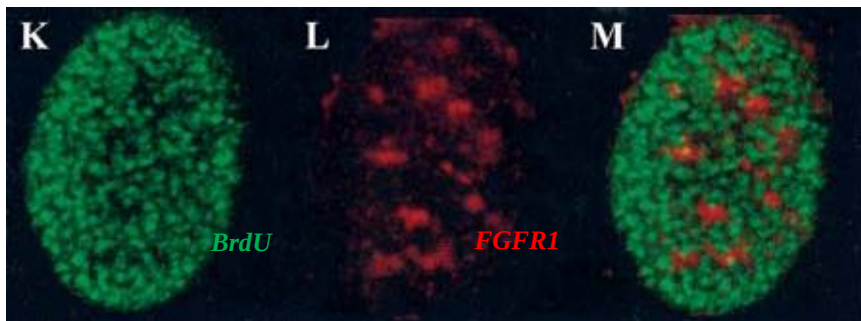
Does nuclear FGFR1 signal directly to genome?

FGFR1 colocalizes with transcription sites:

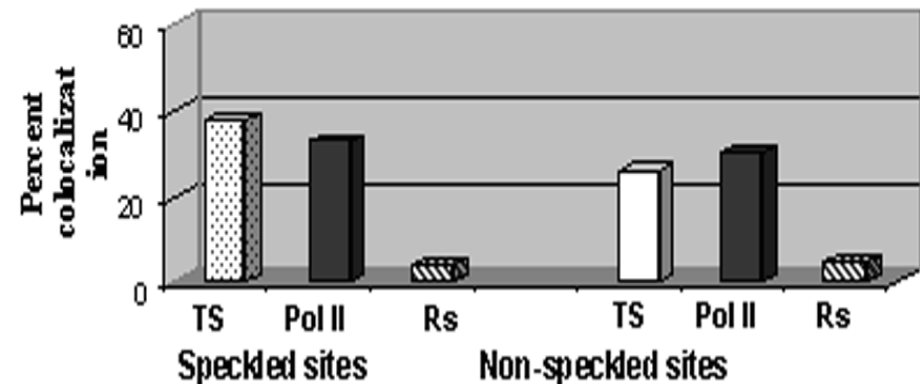
FGFR1, RNA Pol II



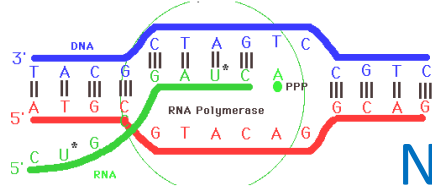
...but not with replication sites:



Colocalization of FGFR-1 sites with Transcription (Ts) and Replication (Rs) Sites

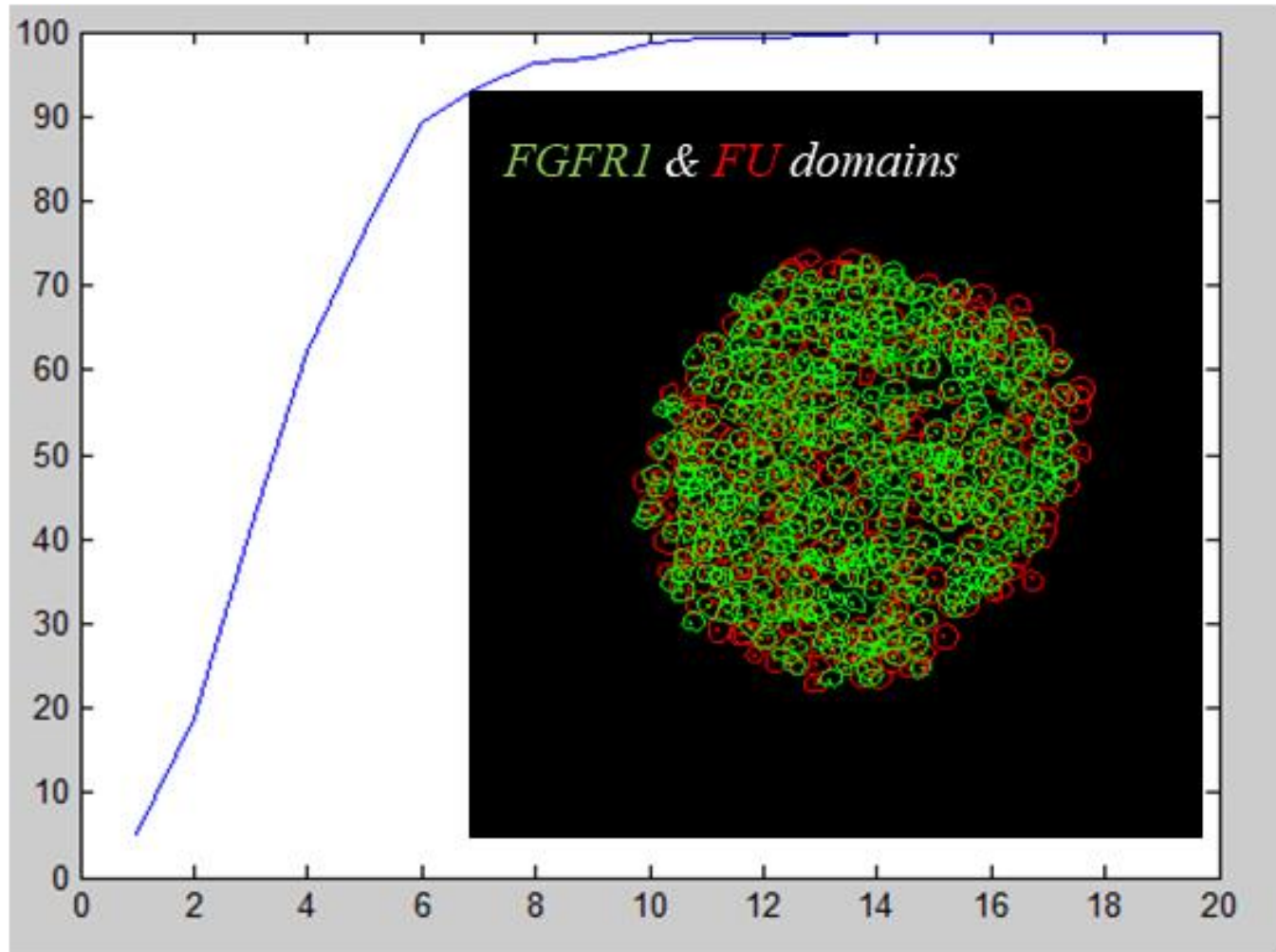


* Fluor- or Deuterium-labeled ribosyl-Uridine substitutes for Uridine (U) in newly synthesized RNA



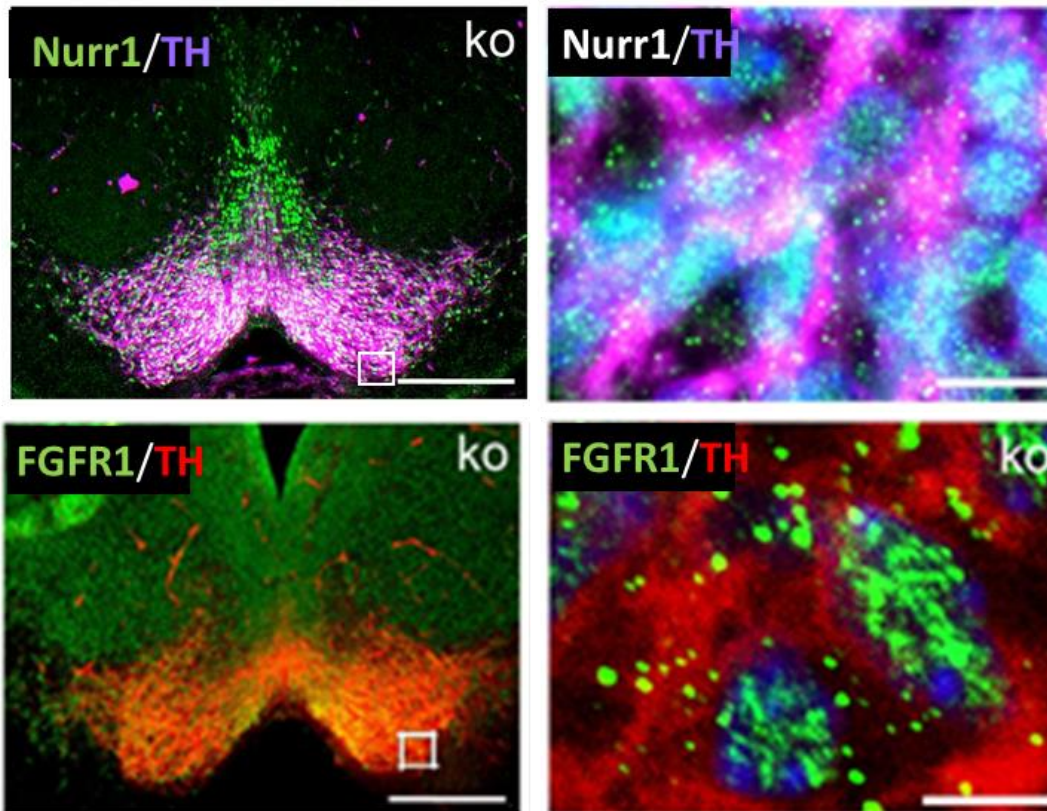
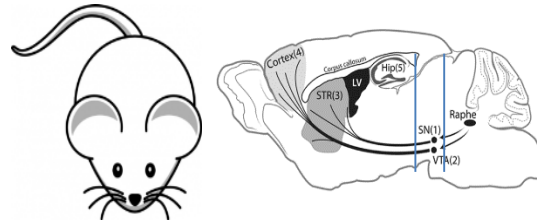
Nuclear FGFR1 colocalizes with RNA transcription sites

% of total domain population

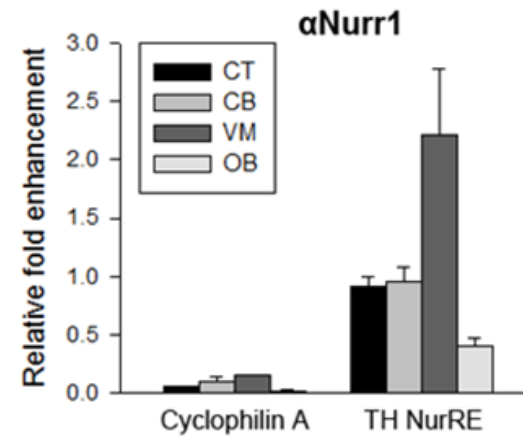
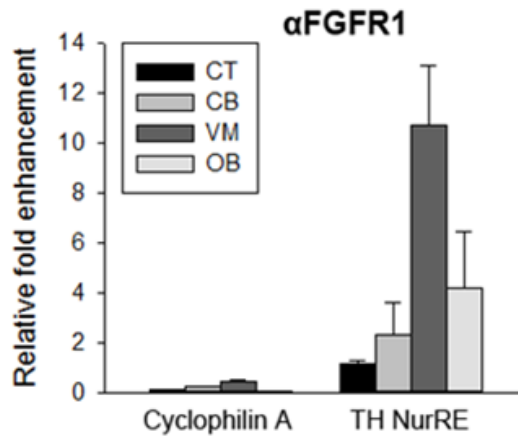
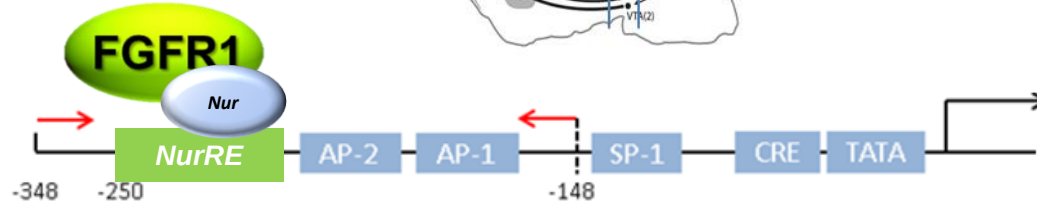
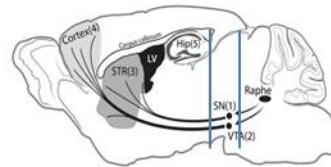
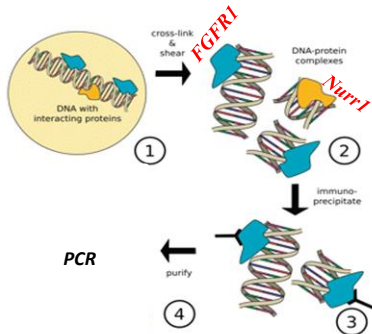


Centroid distance (pixels)

FGFR1 and Nurr1 bind to tyrosine hydroxylase (TH) gene in ventral midbrain

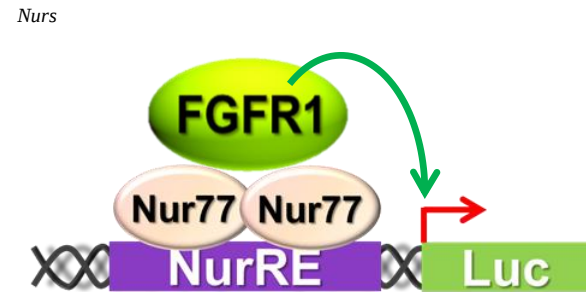
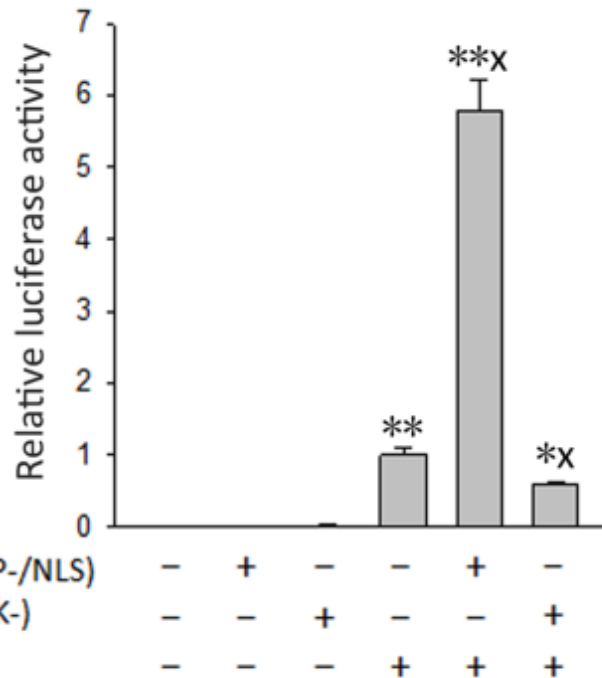


FGFR1 and Nur binding to TH gene in rat brain (ChIP)

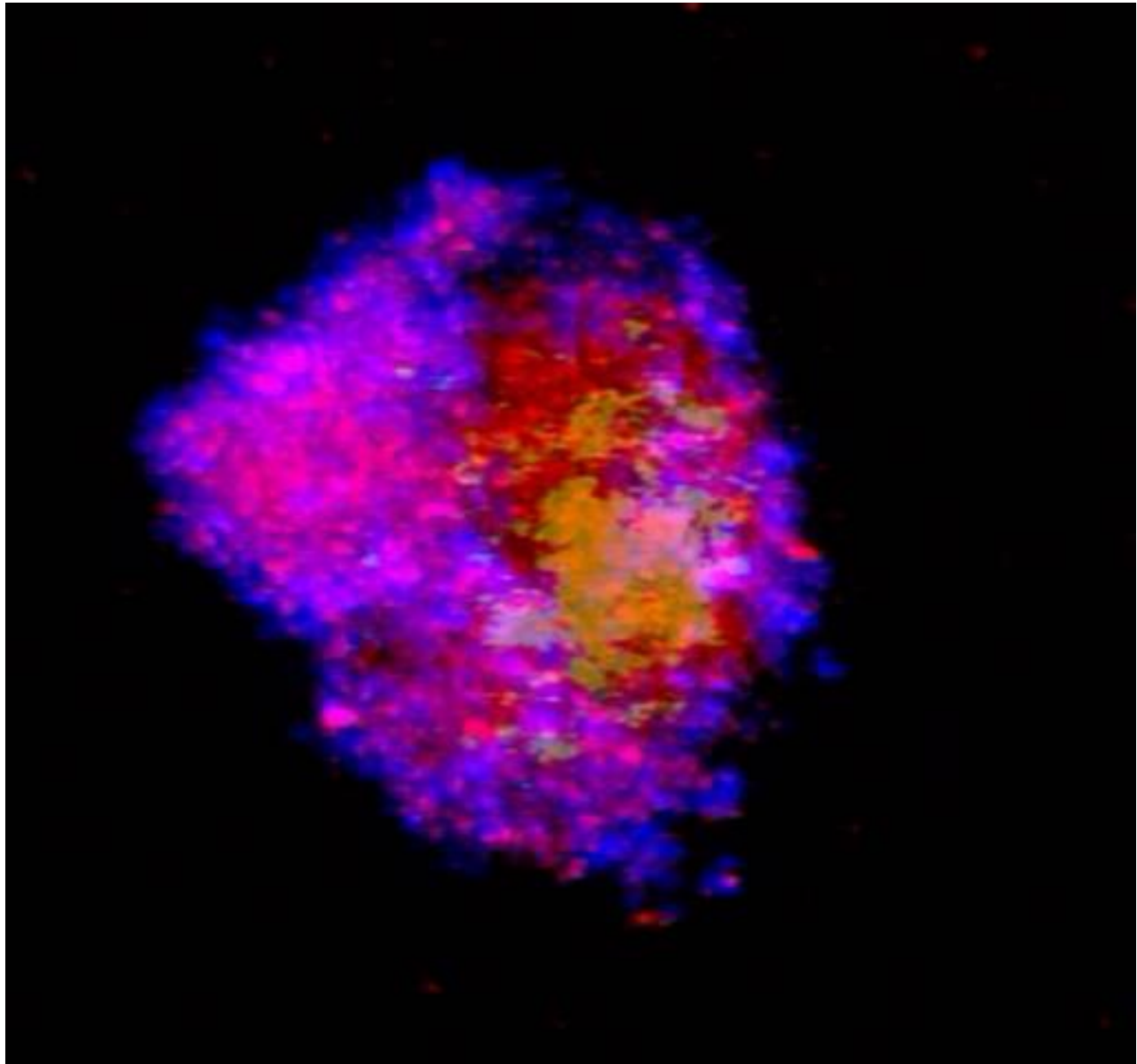


O. Baron, B. Foerthmann, Y-W. Lee, C. Terranova, A. Ratzka, E. K. Stachowiak, C. Grothe, P. Claus and M.K. Stachowiak (2012) Cooperation of nuclear FGFR1 and Nurr1 offers a new interactive mechanism in postmitotic development of mesencephalic dopaminergic neurons. *J. Biol. Chem.* 287, 19827-19840

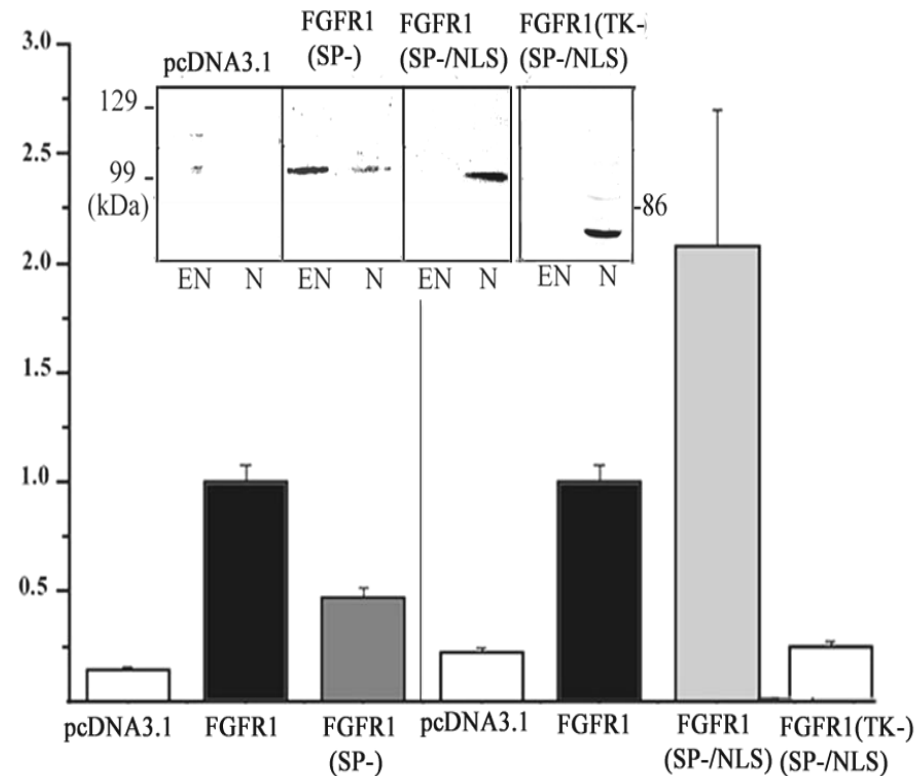
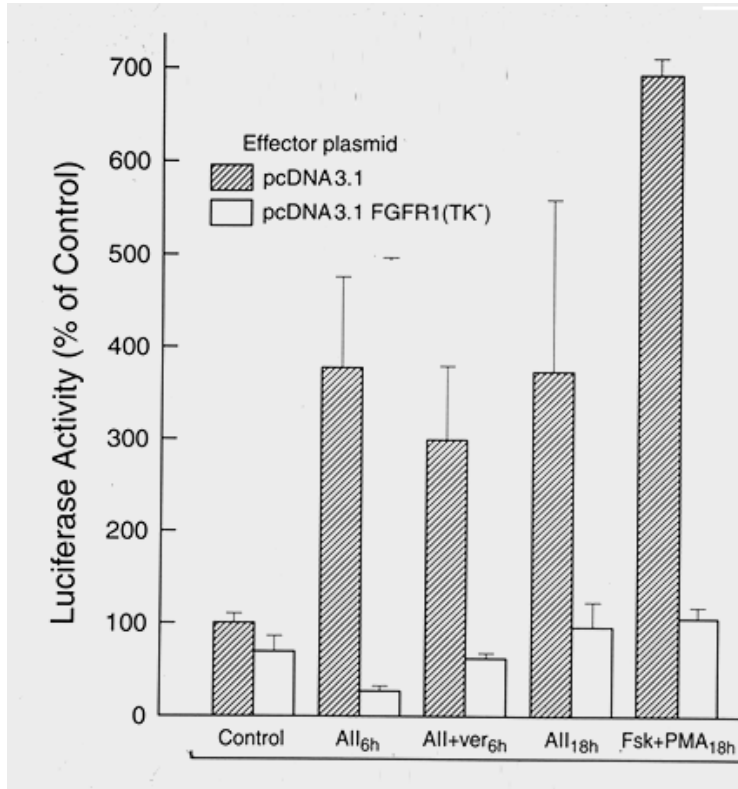
Nuclear FGFR1 Augments the TH gene transcription through NurRE



Induction of **TH** in **Adrenal Medullary Cell** by **Angiotensin II**
is accompanied by nuclear accumulation of **FGFR1**

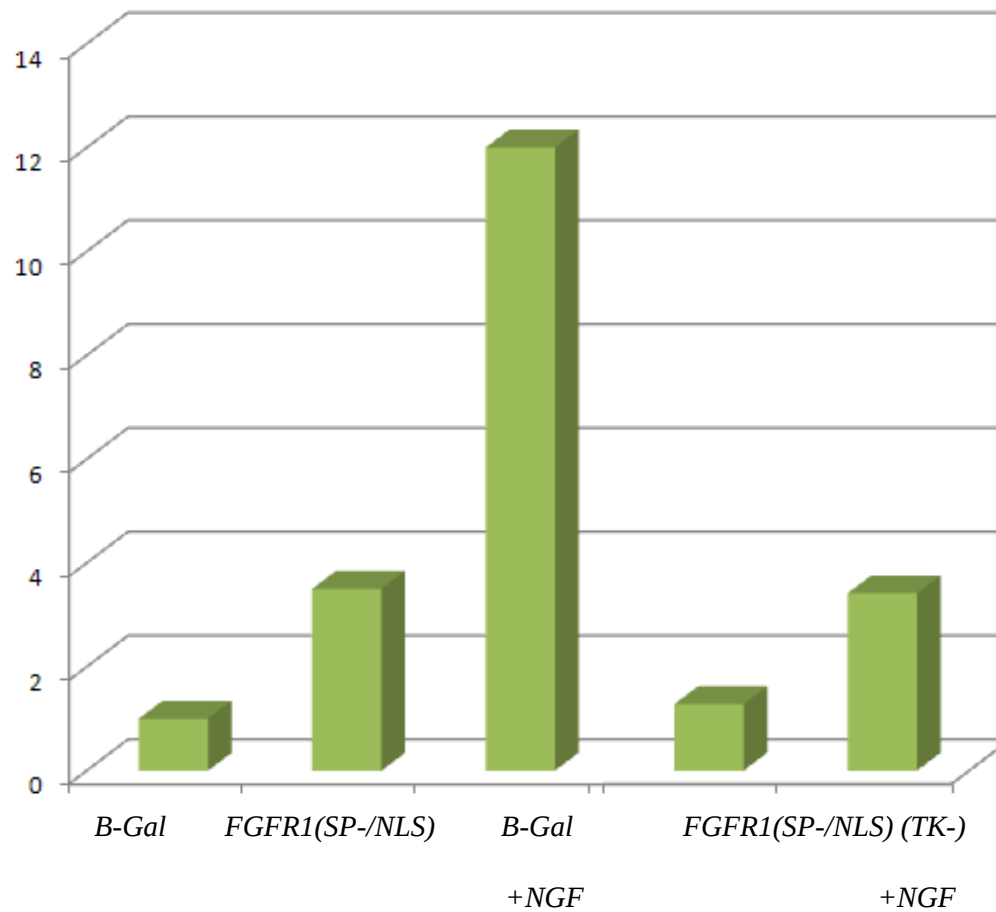


Nuclear FGFR1 is essential and sufficient to stimulate Tyrosine Hydroxylase Gene promoter

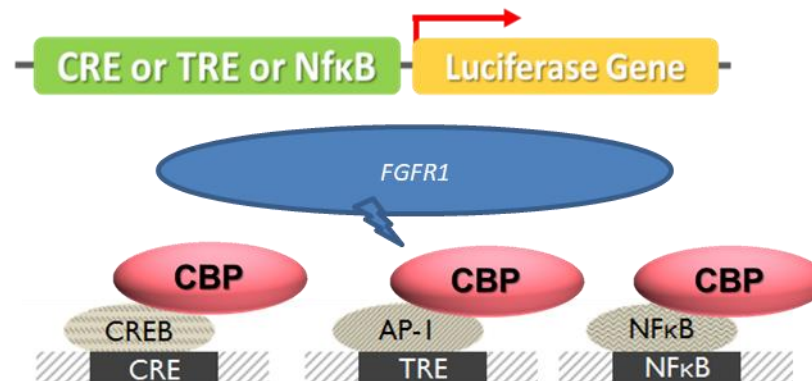
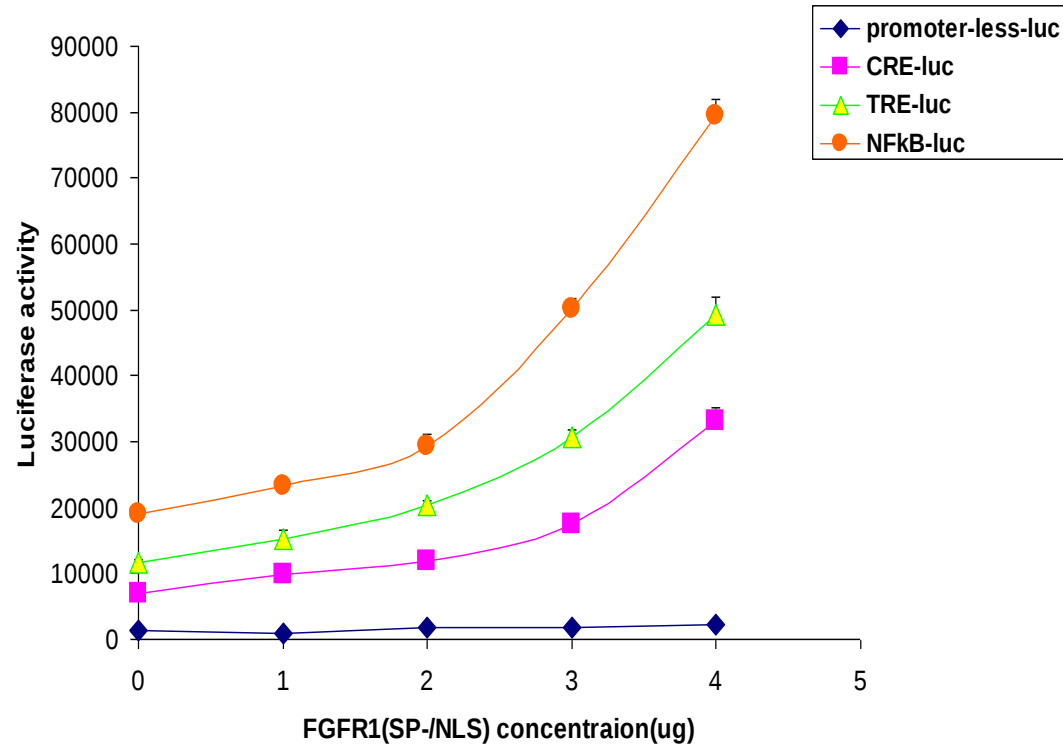


Genes activated by nuclear FGFR1 include: NfL, FGF-2, NSE, TH, DCX, MAP2

Induction of Doublecortin gene by NGF involves nuclear FGFR1

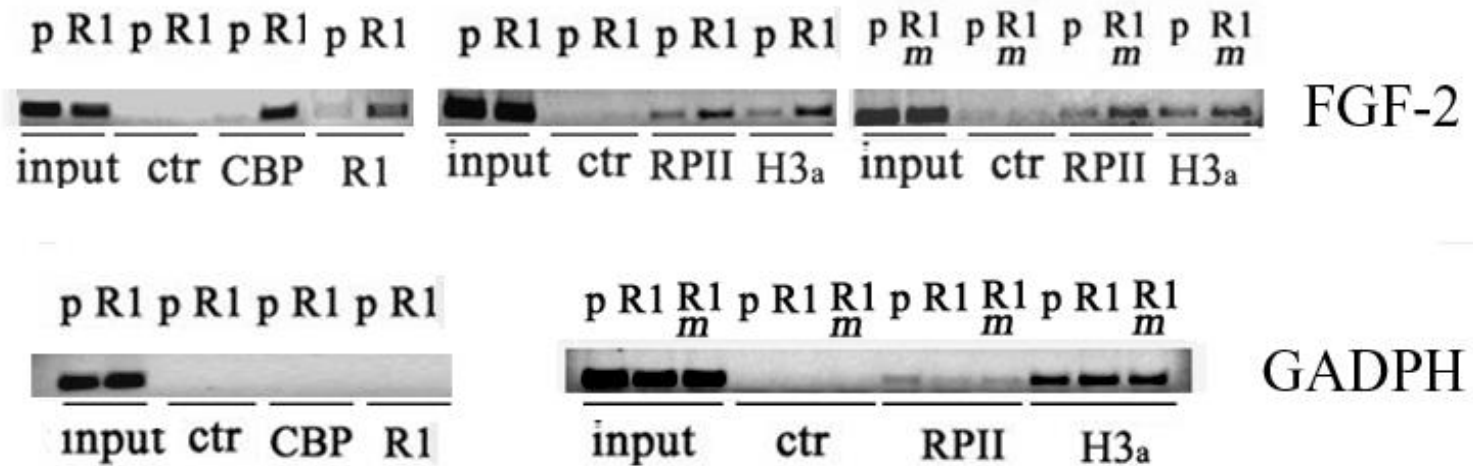


Nuclear FGFR1 Activates CRE and other CREB Binding Protein (CBP) - dependent Enhancers



FGFR1 associates with gene promoter, increases binding of CBP, RNA Pol II and acetylation of Histone H3.

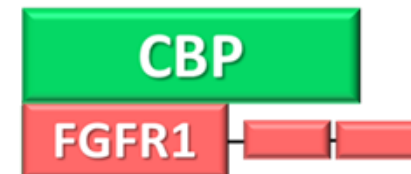
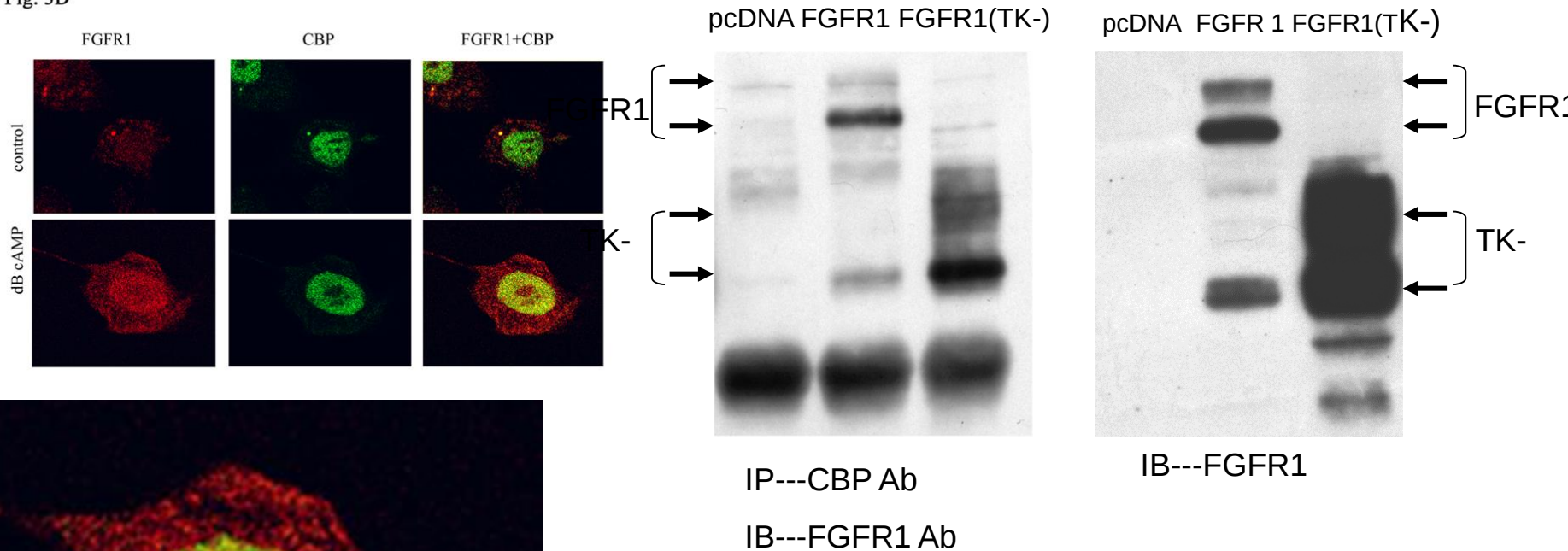
p – pcDNA, - R1 – FGFR1, R1m – kinase inactive R1



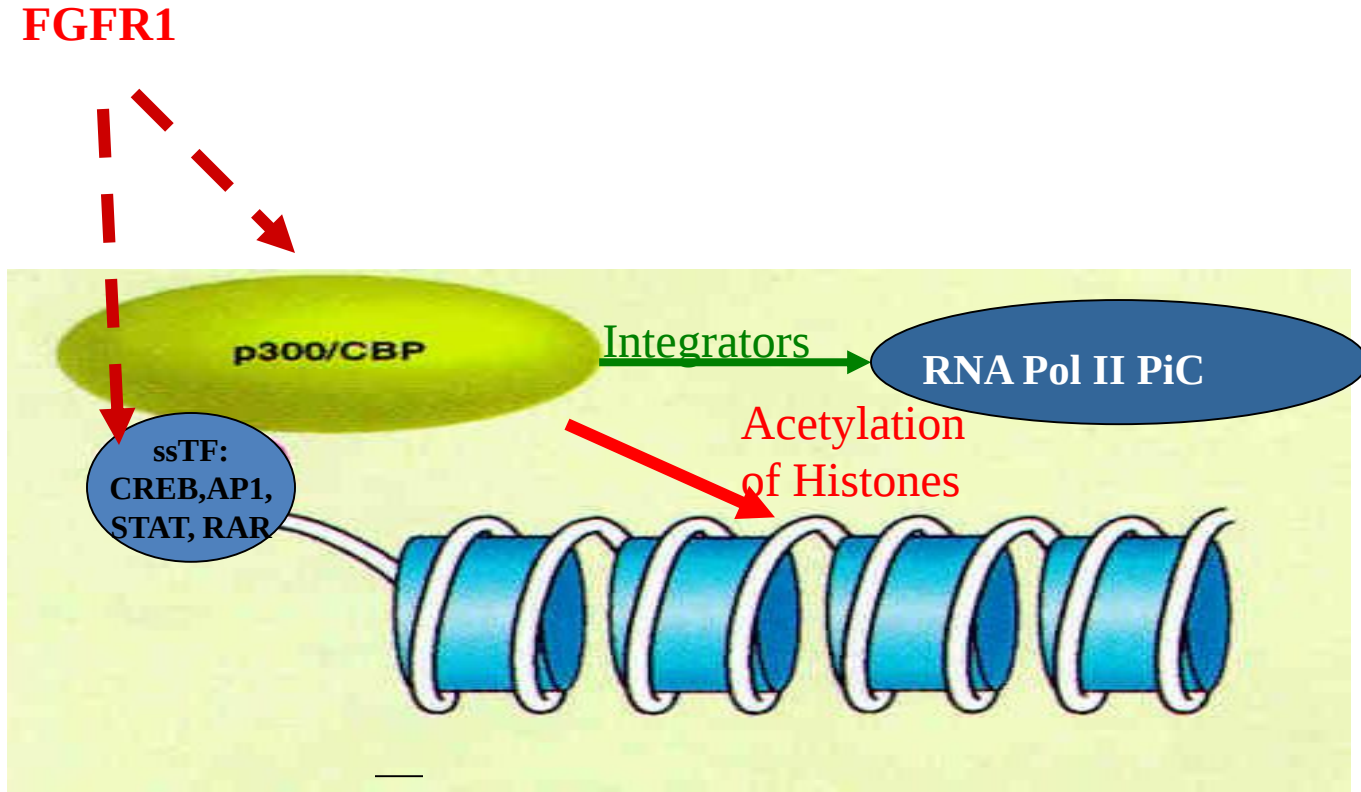
Chromatin immunoprecipitation - FGF-2 and GADPH genes

N-terminal part of nuclear FGFR1 interacts with CREB Binding Protein - CBP

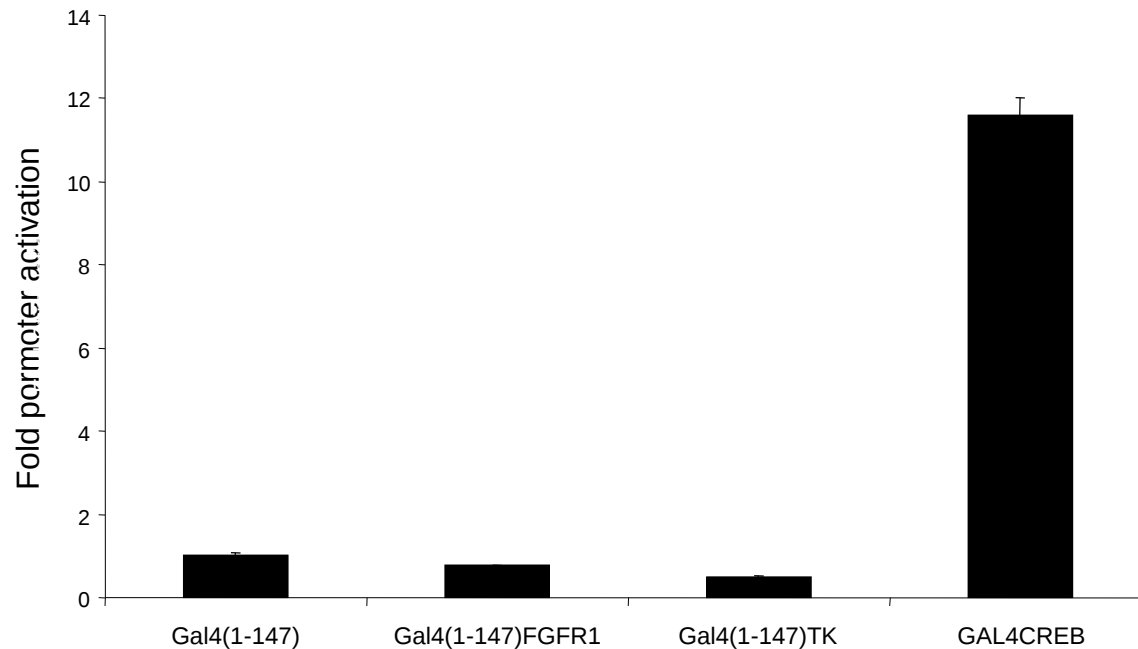
Fig. 3D



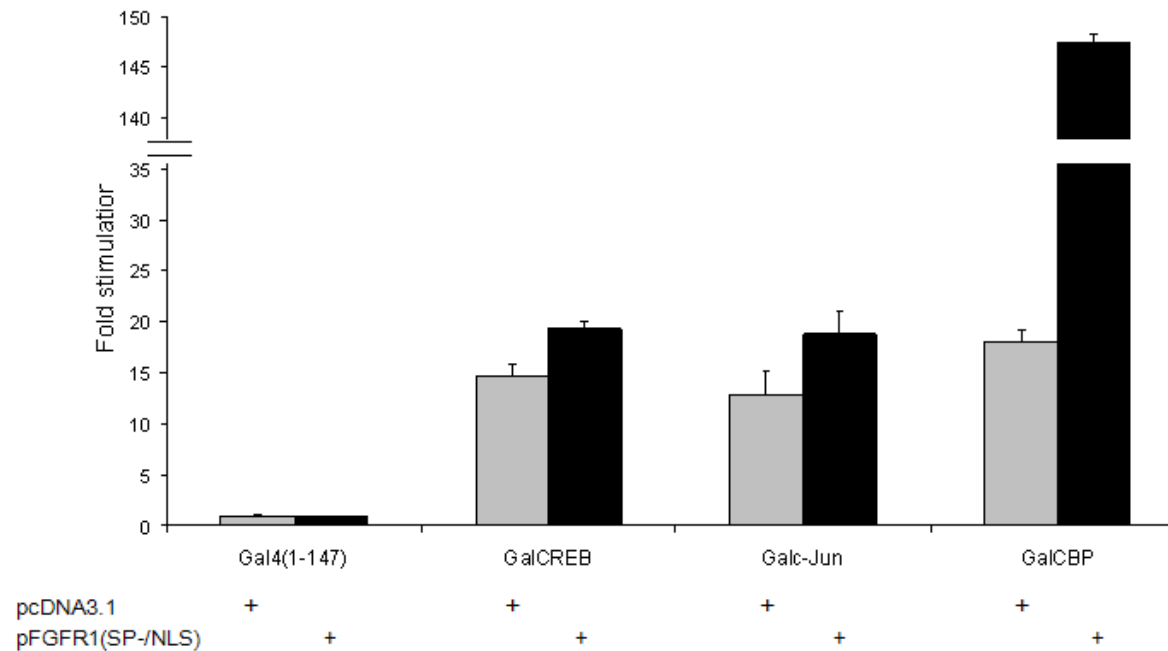
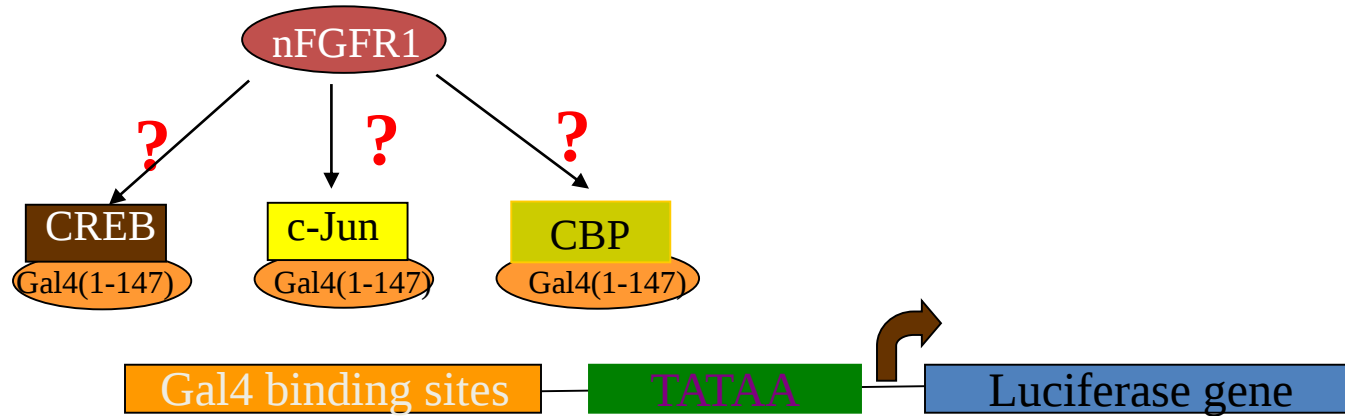
How could nuclear FGFR1 activate transcription::



FGFR1 lacks autonomous transactivating function.



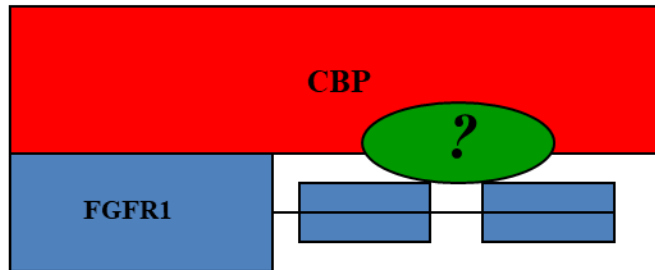
Nuclear FGFR1 increases transcription by via CBP.



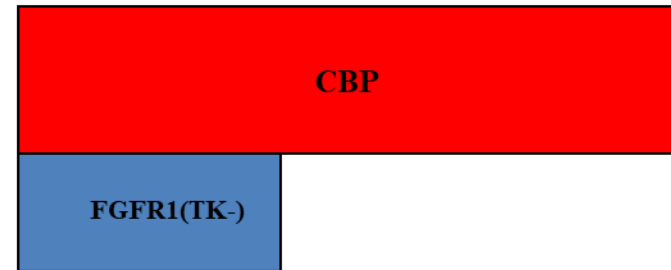
Nuclear FGFR1 stimulation of CBP-mediated transcription requires both TK and NT domains but not tyrosine kinase activity.

FGFR1 - a scaffold for CBP-regulating protein?

Active:



Inactive:



Yeast 2-hybrid assay

FGFR1 binds to the central region of RSK1

Fig. 1A

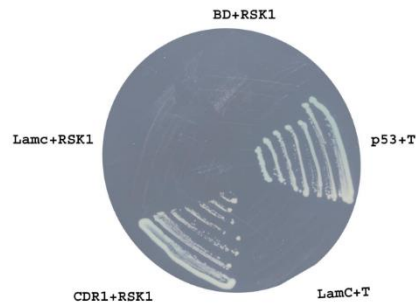
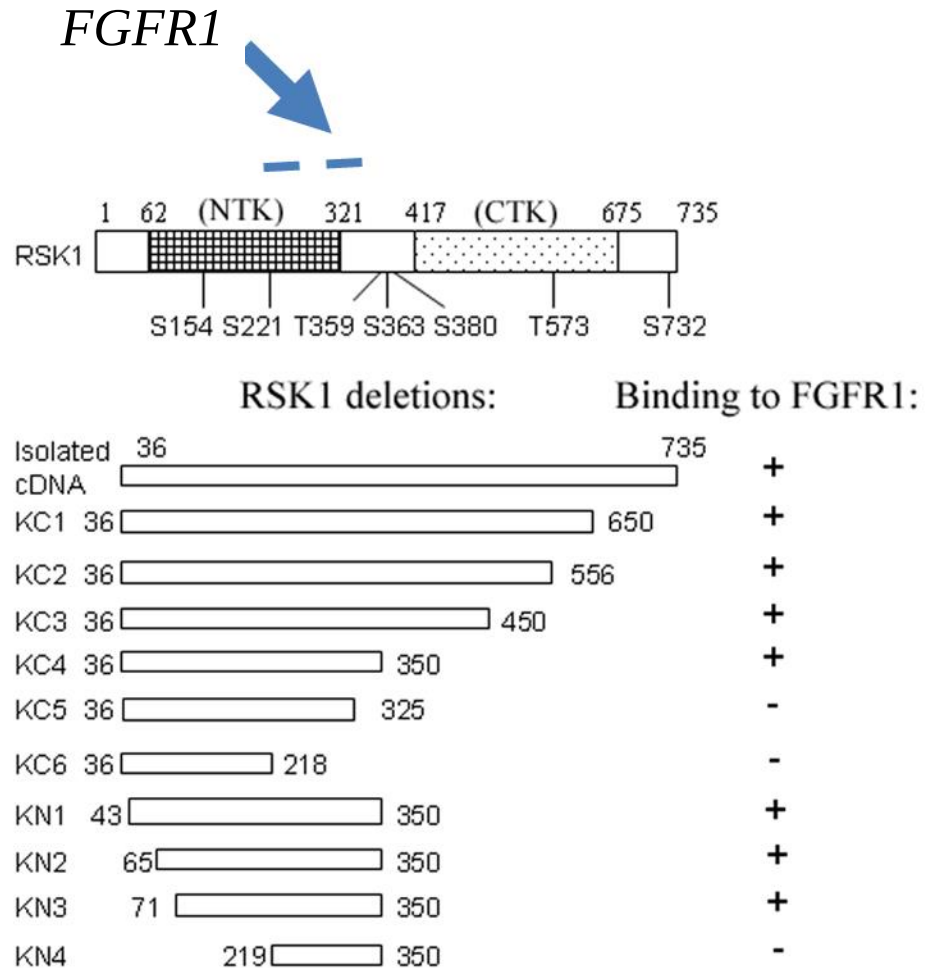
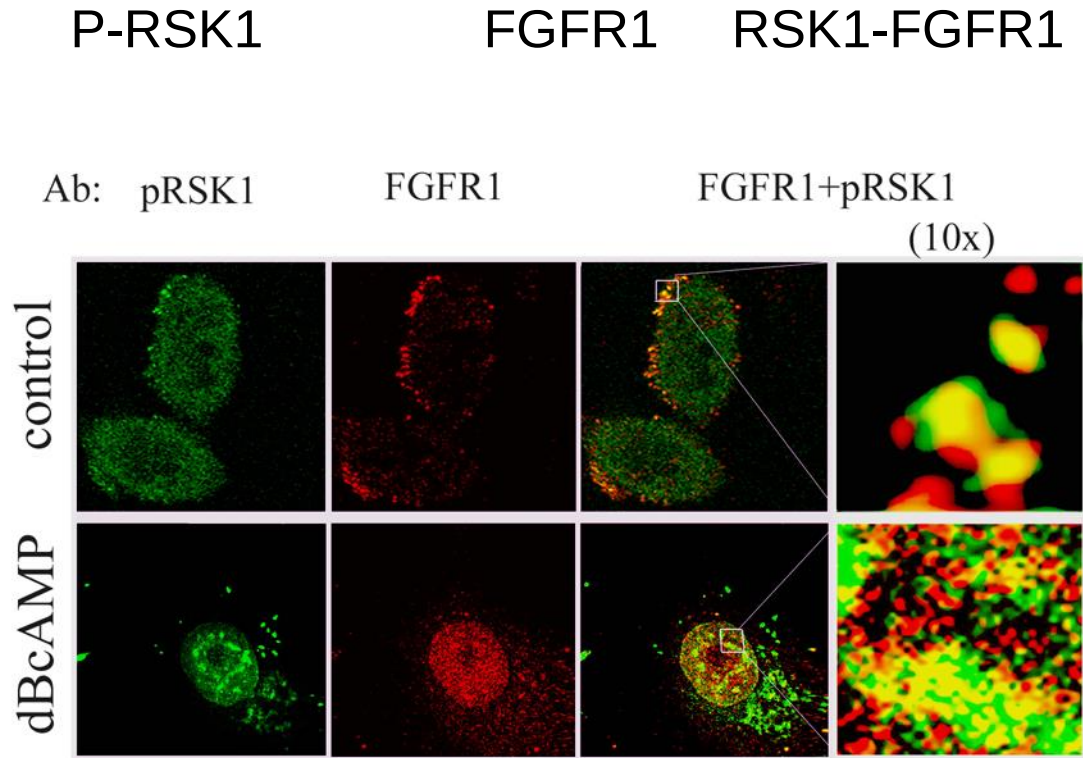


Fig. 1B



FGFR1-RSK1 Interaction



GST-CBP (fragments) pull down of transfected FGFR1 or endogenous RSK1



Fig. 5A

single images: merged images:

RSK1 CBP R1 Rsk1(red), CBP (green) RSK1 (blue), R1 (red) R1(red),CBP (green)

I

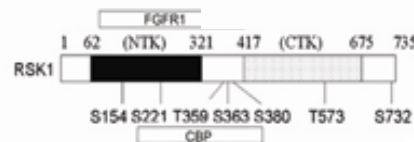
r

Control

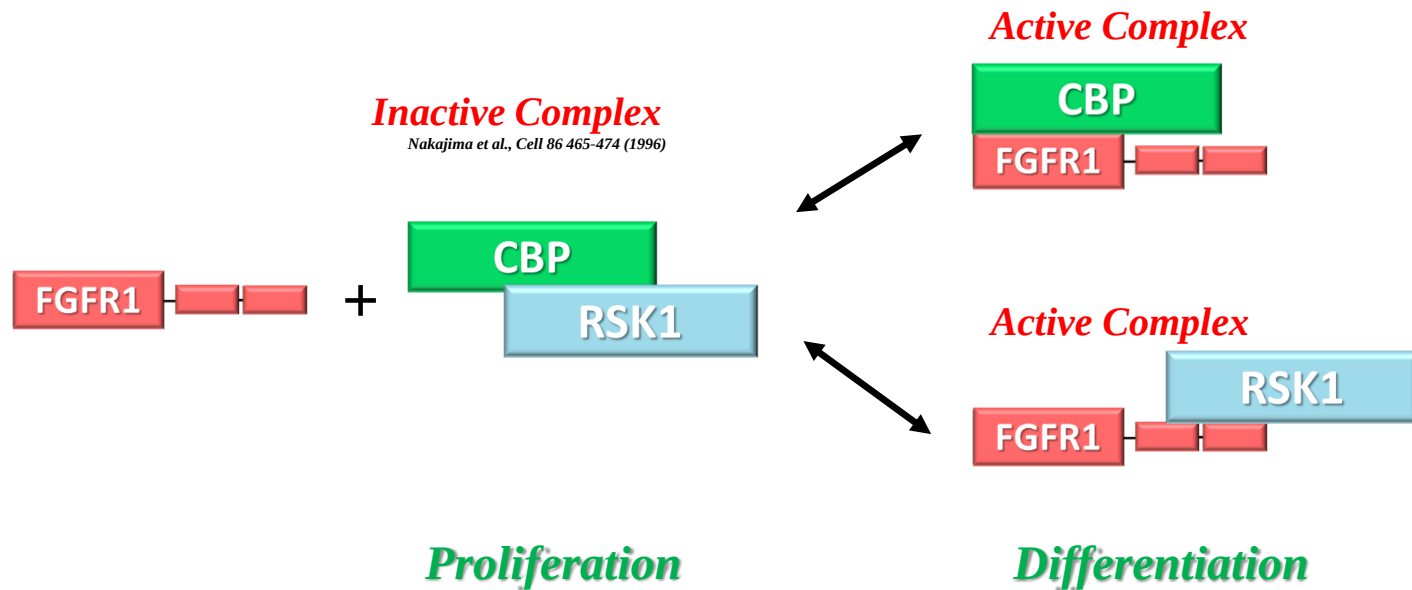
dB cAMP

The figure displays fluorescence microscopy images of cells treated with either Control or dB cAMP. The images are arranged in a 2x6 grid. The columns represent different channels: RSK1 (red), CBP (green), R1 (red), a merge of Rsk1 (red) and CBP (green), a merge of RSK1 (blue) and R1 (red), and a merge of R1 (red) and CBP (green). The rows represent the treatment conditions: Control and dB cAMP. The 'Control' row shows a cell with a distinct nucleus and some peripheral staining. The 'dB cAMP' row shows a more elongated cell with more diffuse staining. The labels 'I' and 'r' are on the far left, with 'I' above 'r'.

FGFR1 disrupts RSK1-CBP complex:



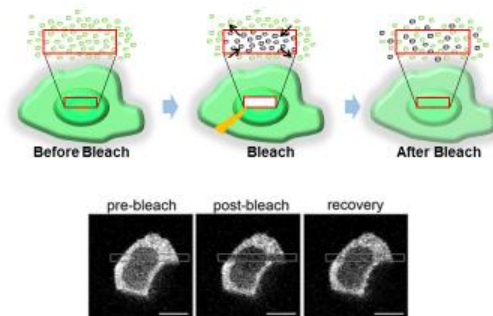
FGFR1 – a molecular switch for CBP-RSK1:



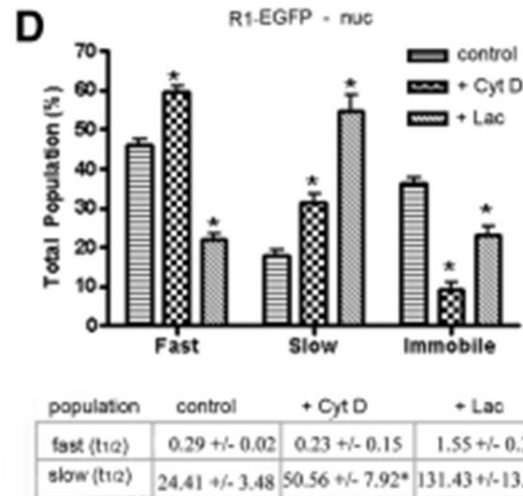
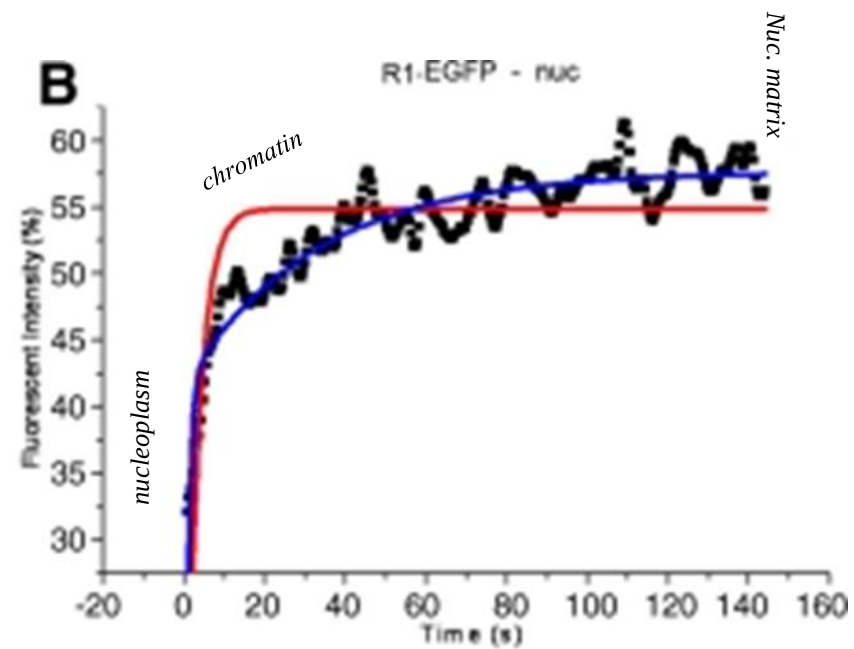
Yafang Hu, Xiaohong Fang, Star M. Duham, Claudia Prada, Ewa K. Stachowiak, Michal K. Stachowiak. (2004) RSK1 is a direct target for the nuclear fibroblast growth factor receptor (FGFR1) – role in FGFR1 signaling. *J. Biol. Chem.*, 279, 29325-29335.

Fang X, Stachowiak EK, Dubham-Ems S, Klejbor I, Stachowiak MK (2005) Control of CBP signaling by nuclear Fibroblast Growth factor receptor-1 (FGFR1) – a novel mechanism of gene regulation. *J. Biol. Chem.* – 280(31):28451-62.

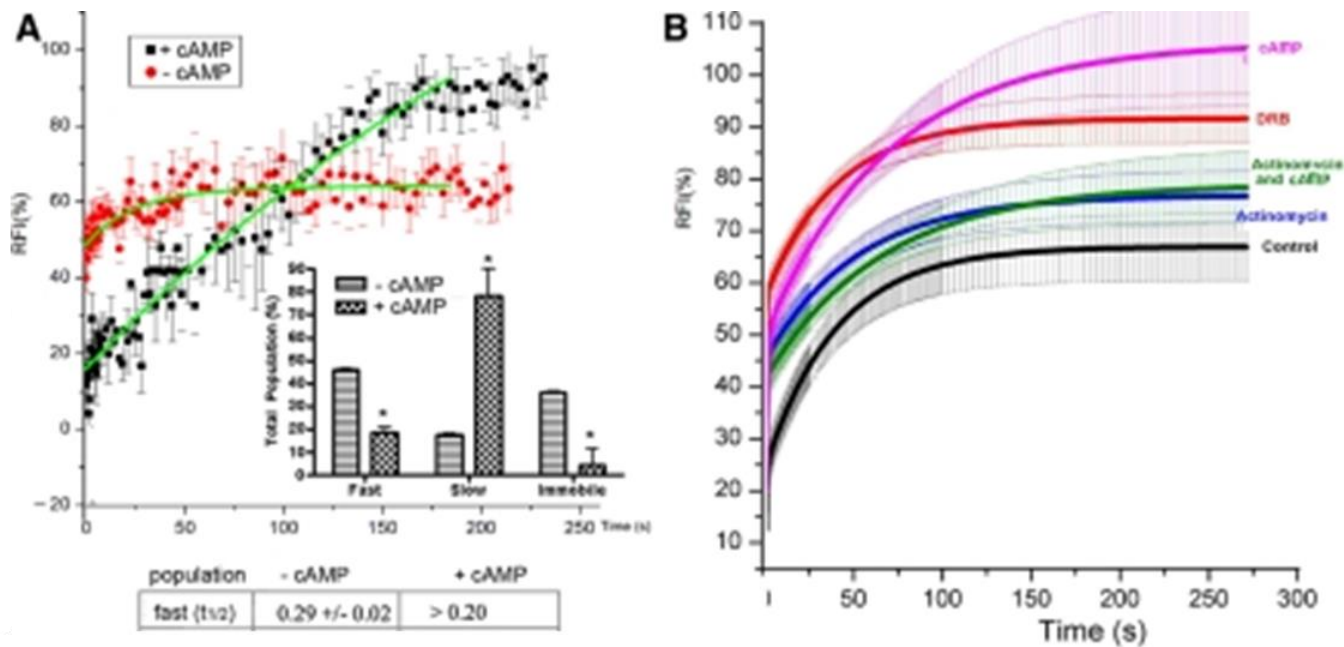
Fluorescence Recovery After Photobleaching (FRAP) of FGFR1-EGFP - kinetic model of gene regulation by nuclear FGFR1



© 2006 The Authors
Journal compilation © 2006 Blackwell Publishing Ltd
Journal of Cellular Biochemistry 100: 2229–2235, 2006
DOI 10.1002/jcb.21225

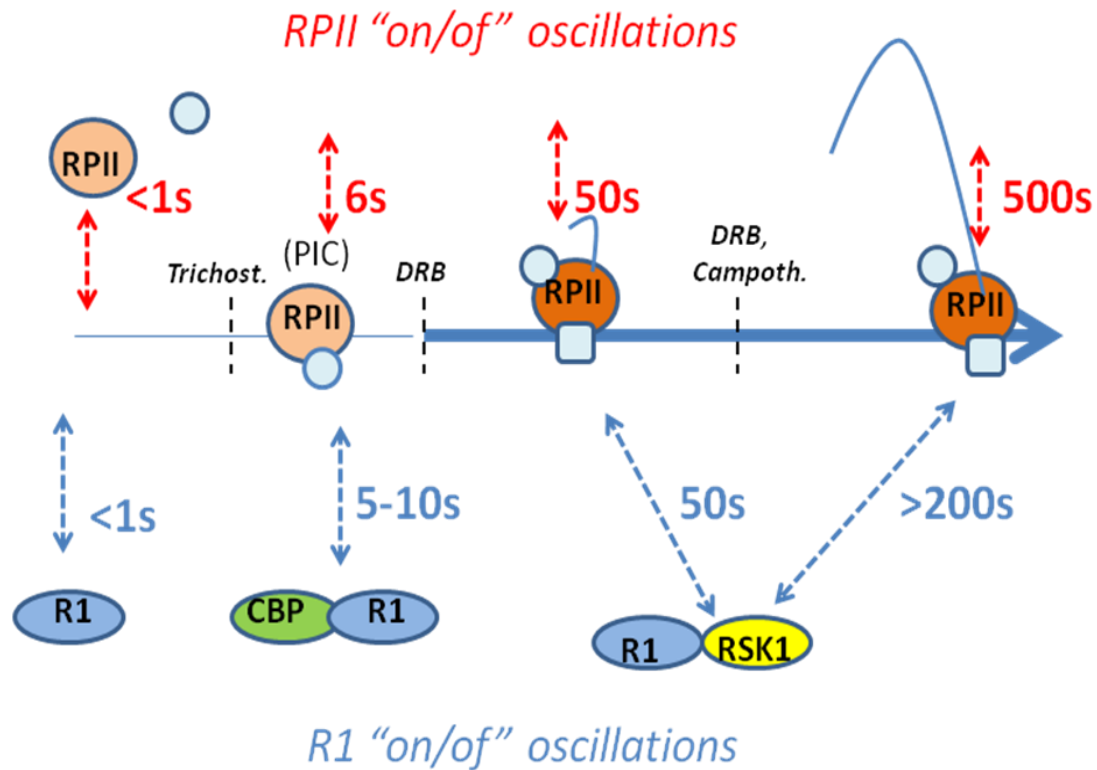


Changes in nFGFR1 mobility during transcription activation and inhibition reflect chromatin-matrix distribution



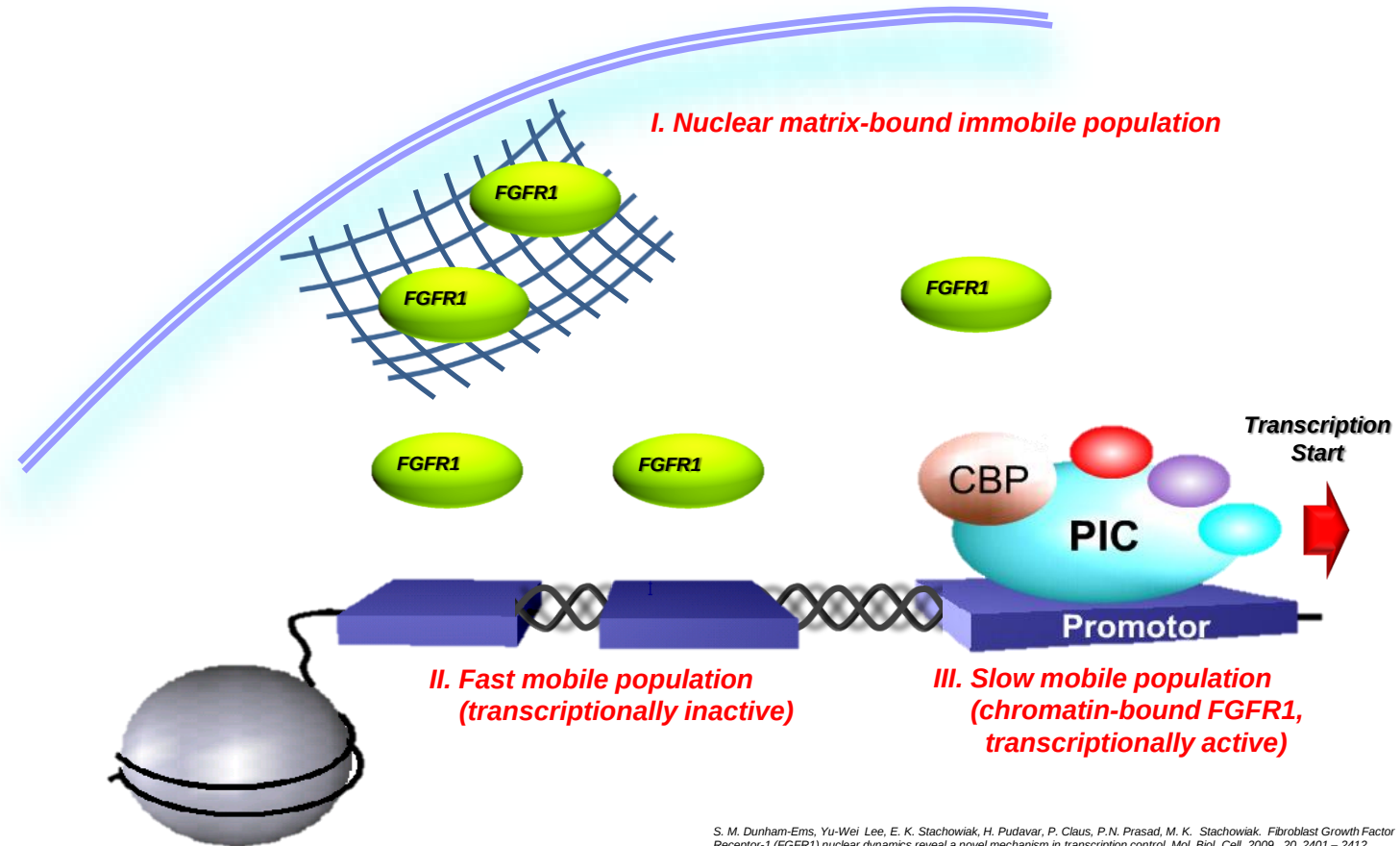
Nuclear FGFR1 movement is affected by its binding partners CBP and RSK1

Transfected plasmids	Fast half-time	Slow half-time	Fast mobility (%)	Slow mobility (%)
R1-EGFP	0.29 $\pm$ 0.02	24.41 $\pm$ 3.48	46.14 $\pm$ 1.57	17.68 $\pm$ 1.52
R1-EGFP + CBP	0.55 $\pm$ 0.26	133.3 $\pm$ 14.91*	25.35 $\pm$ 2.22*	75.12 $\pm$ 5.53*
R1-EGFP + CBP (451-689)	0.44 $\pm$ 0.02	87.45 $\pm$ 12.56*	35.25 $\pm$ 2.03*	49.02 $\pm$ 2.0*
R1-EGFP + CBP (1678-2441)	0.36 $\pm$ 0.10	33.71 $\pm$ 0.65	38.96 $\pm$ 1.78*	0.92 $\pm$ 2.89*



.Fig. 6 . Kinetics of RNA Polymerase II (RPII) "on/off" gene oscillations at different phases of transcription are based on ("PIC"- preinitiation complex). Kinetic model of INFS (R1, CBP, RSK1) gene activation is based on our hetherto findings using FRAP R1 kinetics on bulk chromatin, its regulation by CBP and RSK1 and by the demonstrated static interaction among these proteins.

Three Different Population of FGFR1-EGFP in the Nucleus



Integrative Nuclear FGFR1 Signaling (INFS) pathway forms common modules that control diverse gene programs.

Generic
“Feed-Forward”
“And” gate module

neurotransmitters, hormones, growth factors, contact receptors

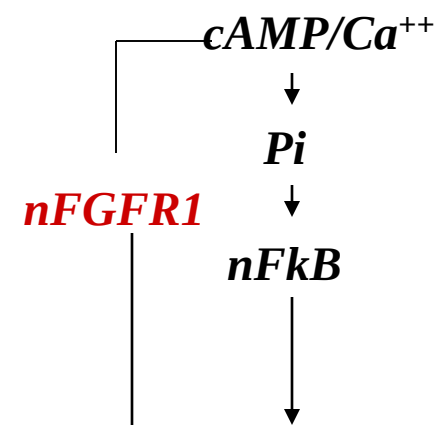
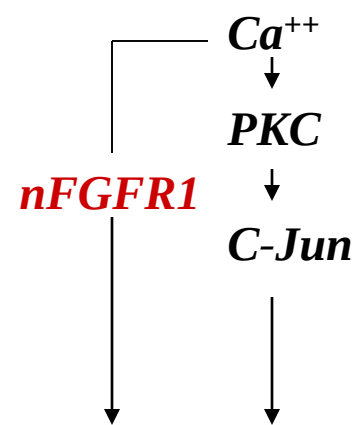
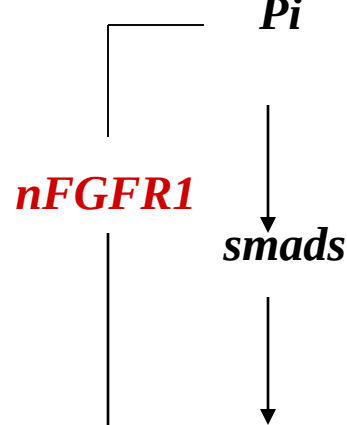
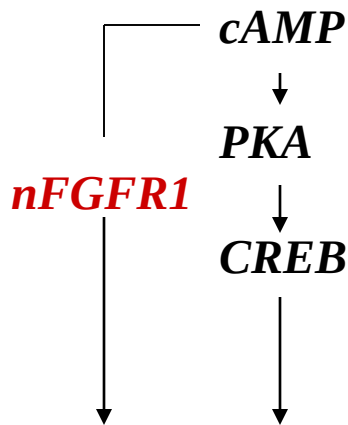
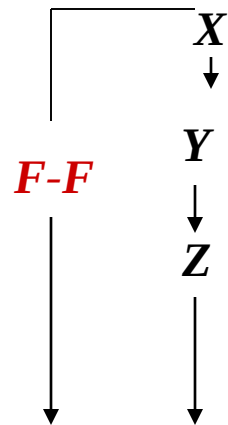


BMP7

Pi

Ca⁺⁺

cAMP/Ca⁺⁺



And

CBP

CBP

CBP

CBP

Output

transcription

transcription

transcription

transcription

***growth/
differentiation***

differentiation

proliferation

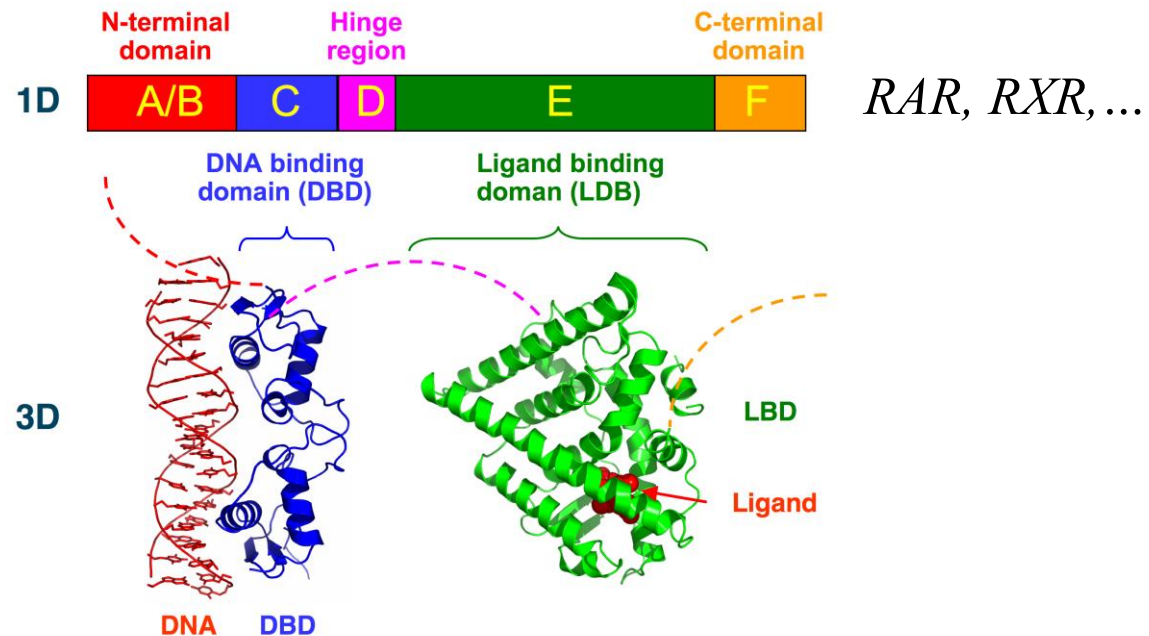
survival

Nuclear FGFR1 in Embryonic Stem Cells

RAR/RXR & Nur partners

ONTOGENIC REGULATORS - DUAL FUNCTION PROTEINS: RECEPTORS AND TRANSCRIPTIONAL FACTORS

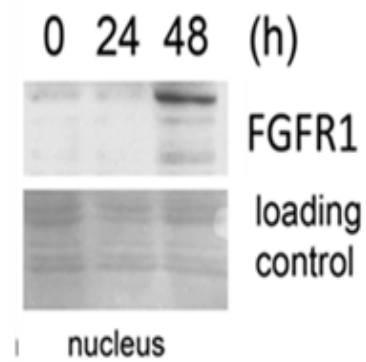
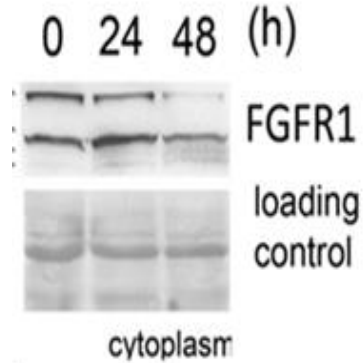
Structural Organization of Nuclear Receptors



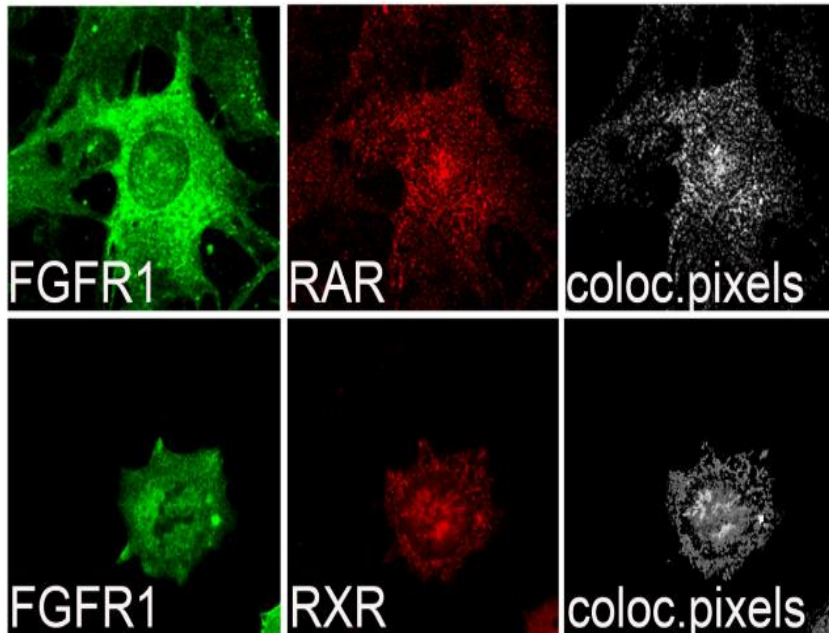
Orphan Nuclear Receptors lack ligand binding domain: Nur77, Nurr1

Interaction of *FGFR1* with *RXR* and *RAR*:

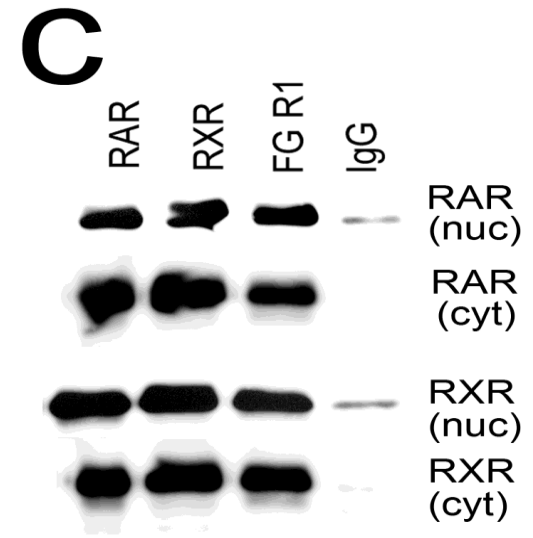
RA:



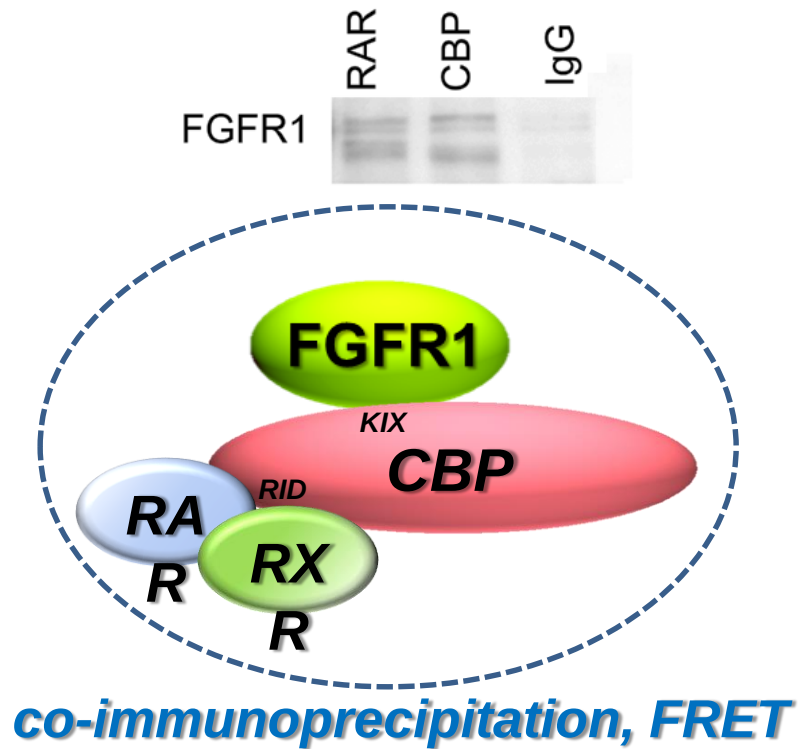
a *Confocal microscopy:*



Coimmunoprecipitation:



The mutual interaction between nuclear FGFR1 and RAR/RXR may via CBP



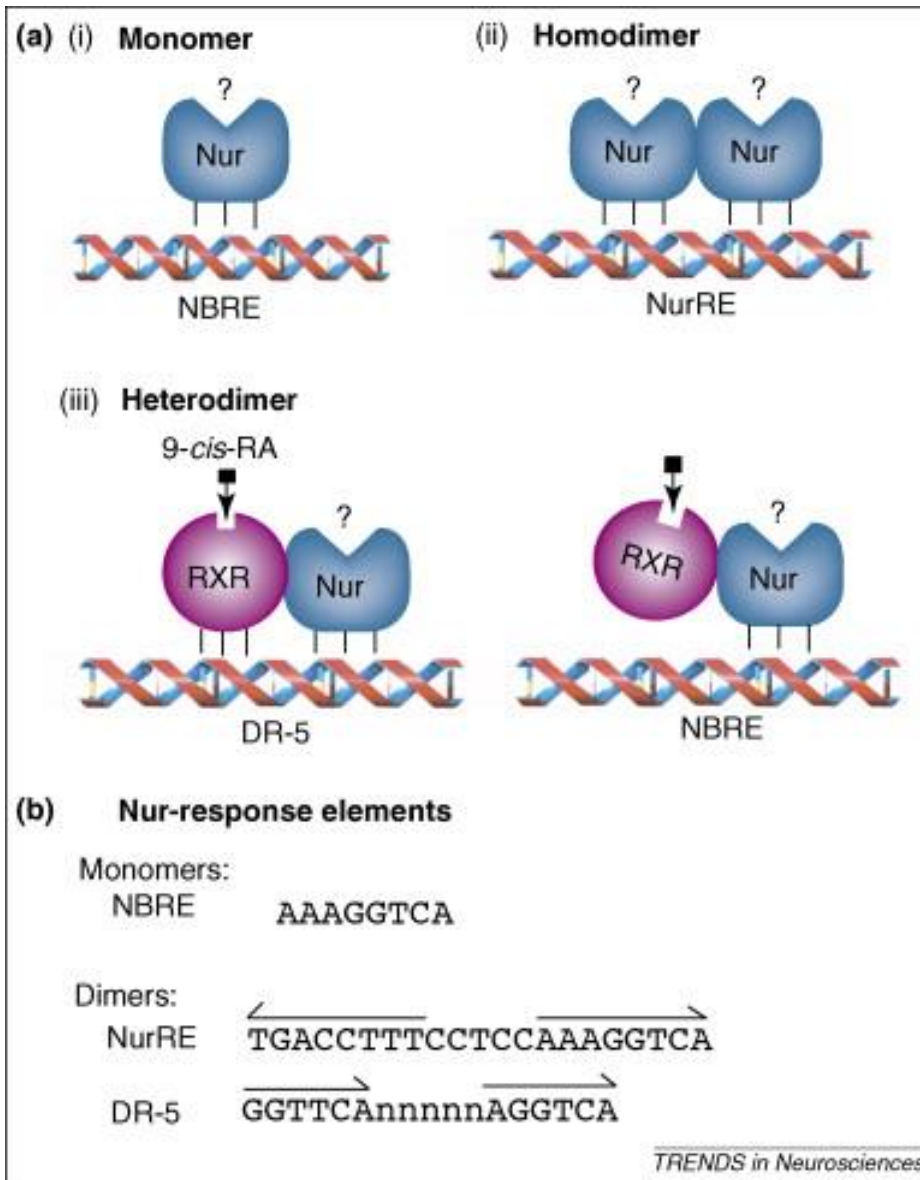
Fang X, Stachowiak EK, Dubham-Ems S, Klejbor I, Stachowiak MK (2005) *J. Biol. Chem.* – 280(31):28451-62.

Yafang Hu, Xiaohong Fang, Star M. Duham, Claudia Prada, Ewa K. Stachowiak, Michal K. Stachowiak. (2004) *J. Biol. Chem.*, 279, 29325-29335

Lee, Y-W., Terranova, C., Birkaya, B., Narla, S., Kehoe, D., Parikh, P., Dong, S., Ratzka, A., Brinkmann, H., Aletta, J., Tzanakakis, E., Stachowiak, E.K., Claus, P., and Stachowiak, M.K. (2012). *J. Cell. Biochem.*, 113, 2920-2930

O. Baron, B. Foerthmann, Y-W. Lee, C. Terranova, A. Ratzka, E. K. Stachowiak, C. Grothe, P. Claus and M.K. Stachowiak (2012). *J. Biol. Chem.* 287, 19827-19840

Orphan Nuclear Receptors - Nurs

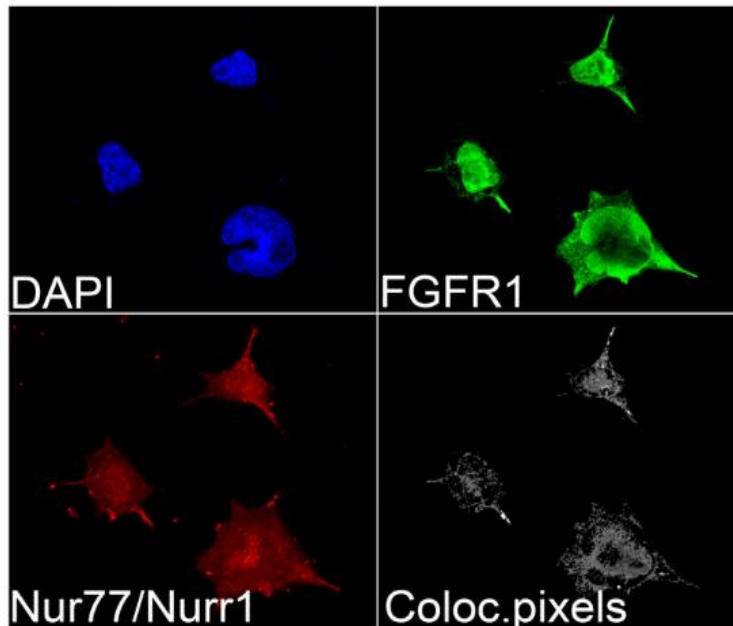


Interaction of *FGFR1* with *RXR*

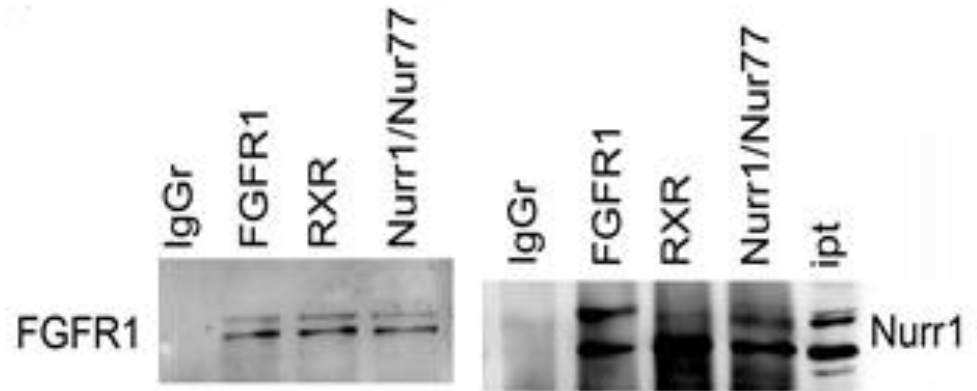
Partners - orphan (Nur) receptors:

Confocal microscopy:

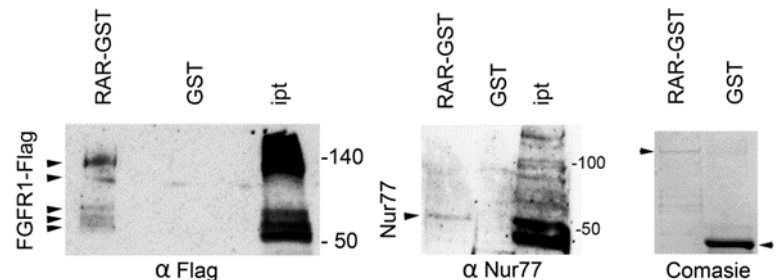
a



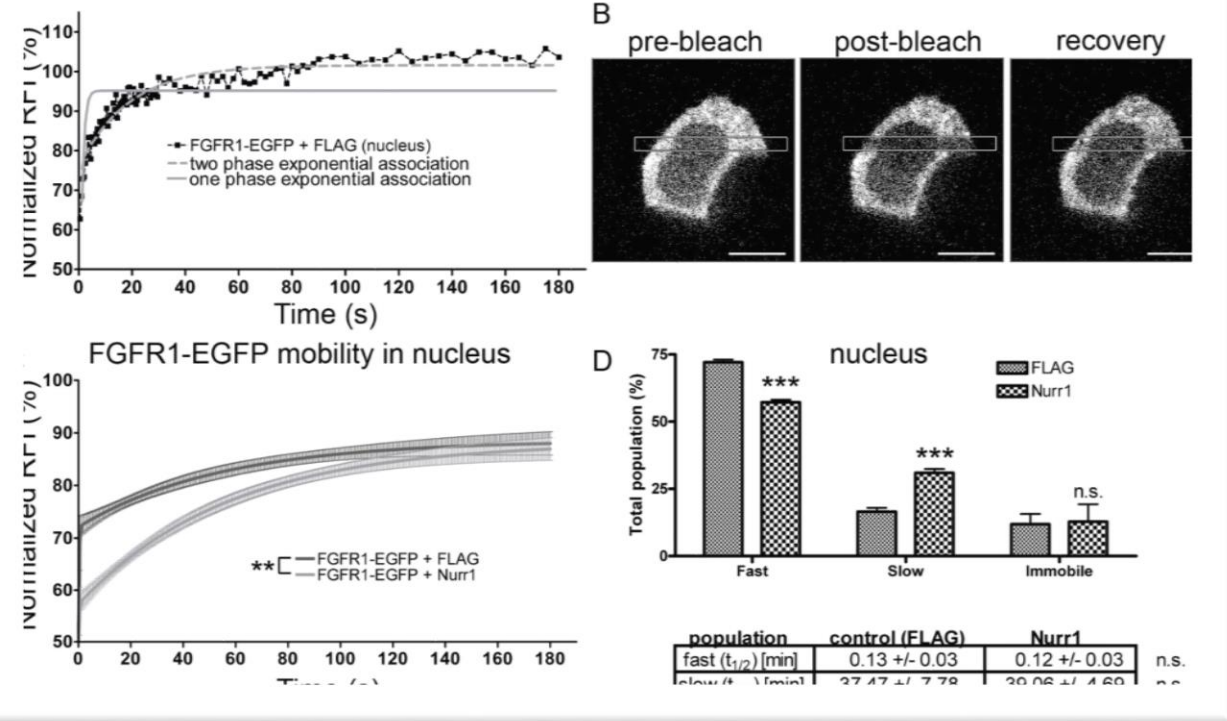
Immunoprecipitation:



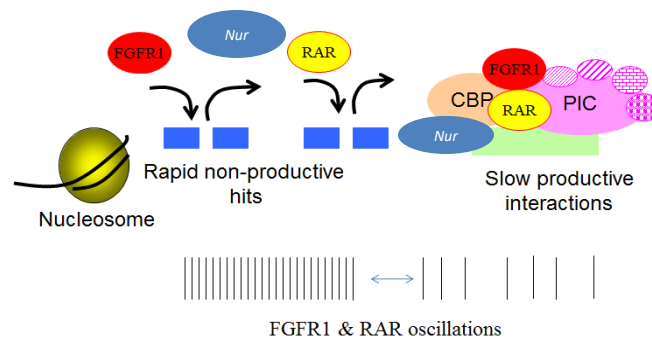
GST-RAR



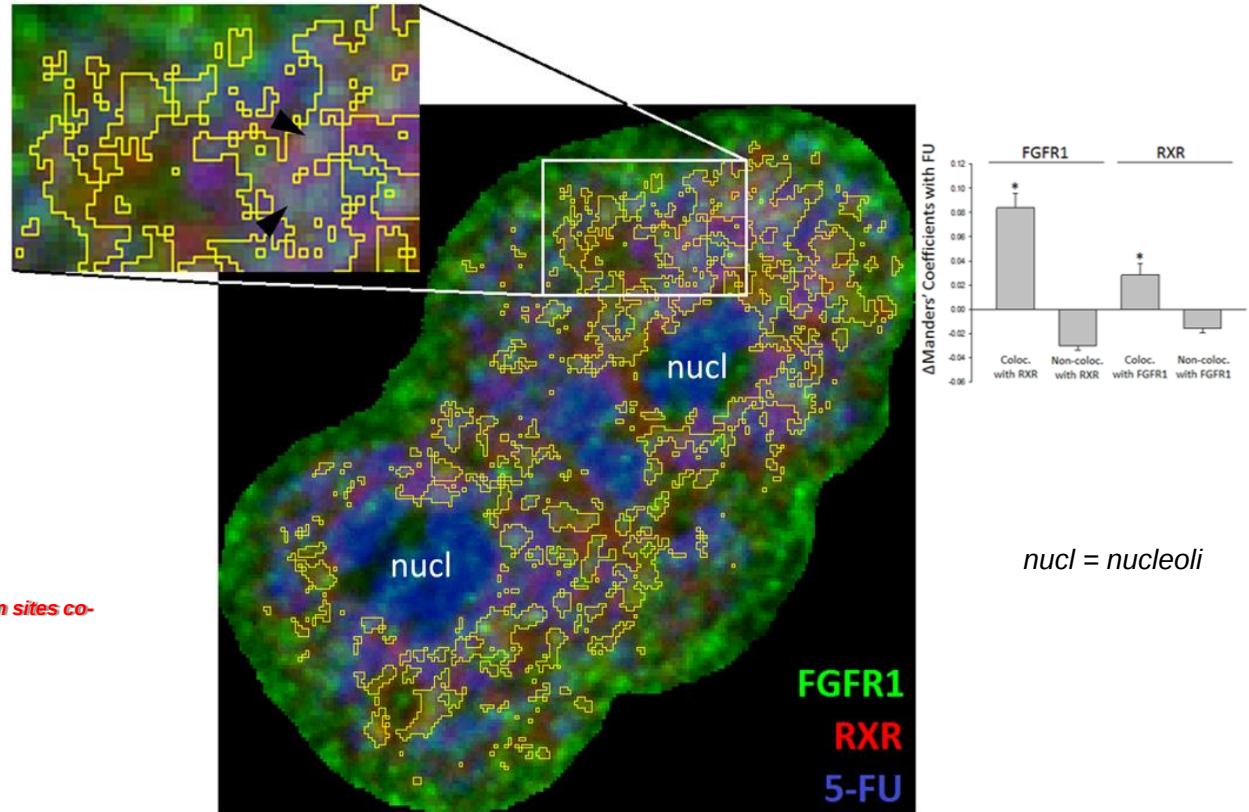
FGFR1 nuclear mobility is reduced by conditions that promote Nur & RXR binding



R1-EGFP nuclear population	- RA	+RA
fast ($t_{1/2}$)	0.4 sec	1.0 sec
% population	17%	21%
slow ($t_{1/2}$)	24.8 sec	224.4 sec
% population	16.0%	32.2%
immobile	67%	46.8%
% population		



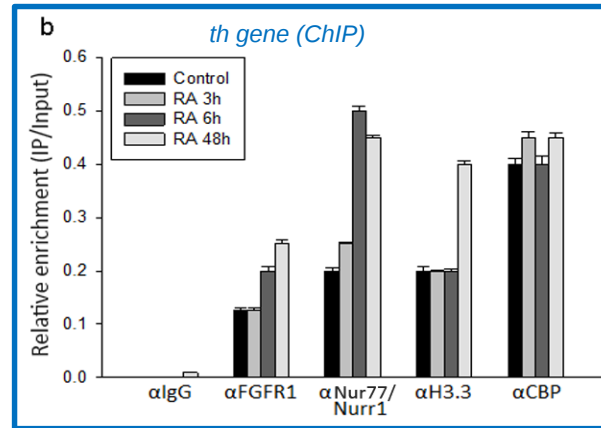
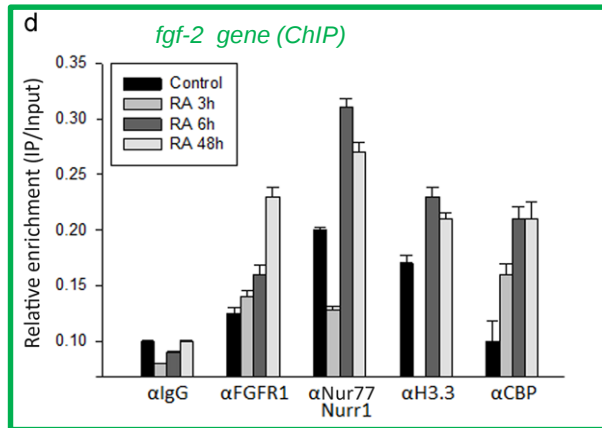
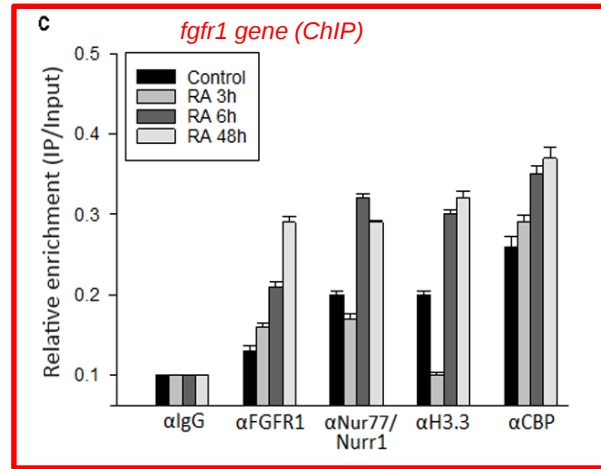
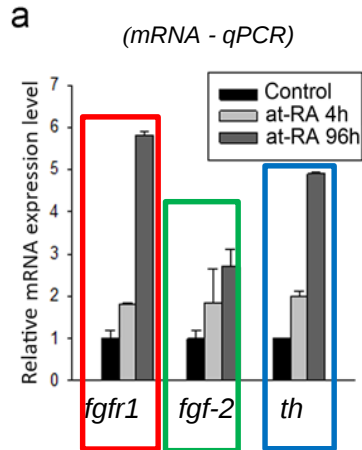
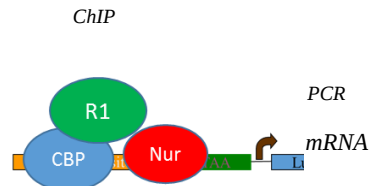
Co-distribution of FGFR1, RXR and Transcriptional Domains (5'-FU) in the nucleus



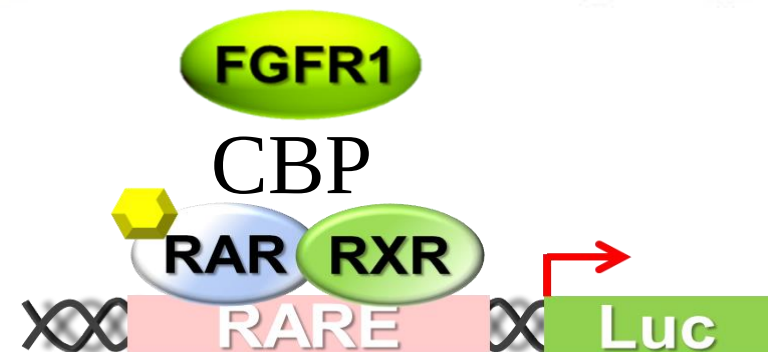
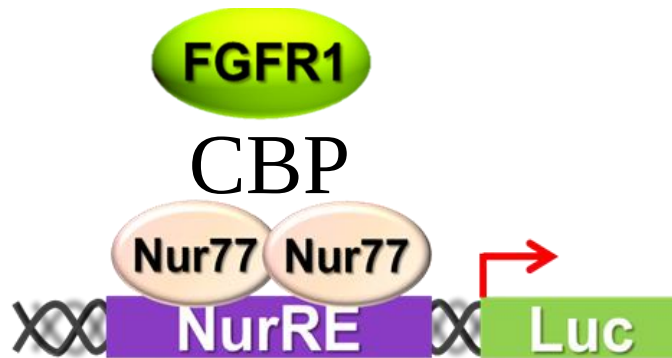
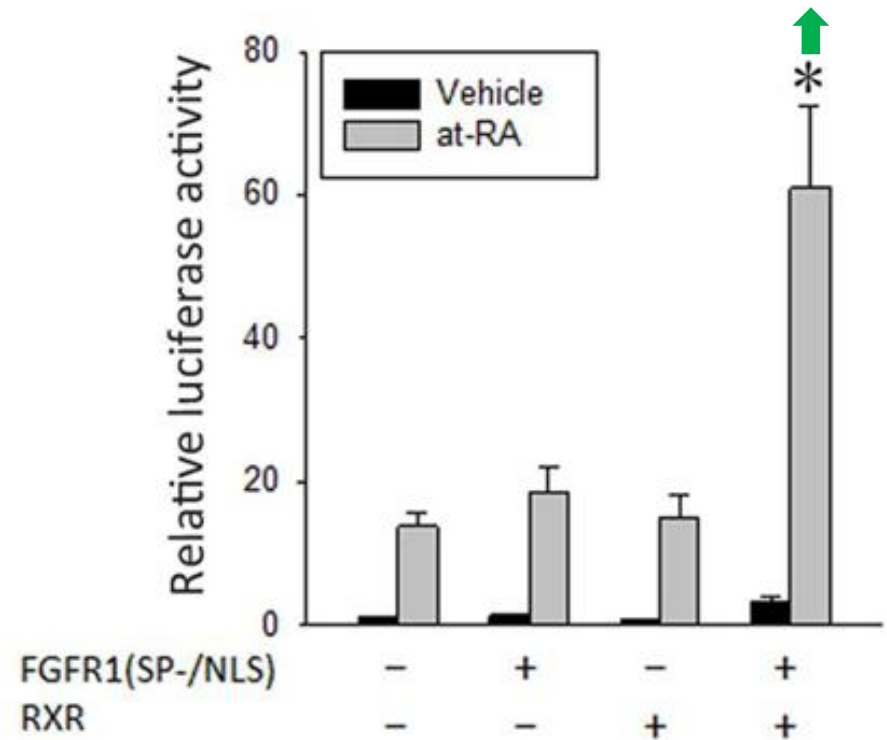
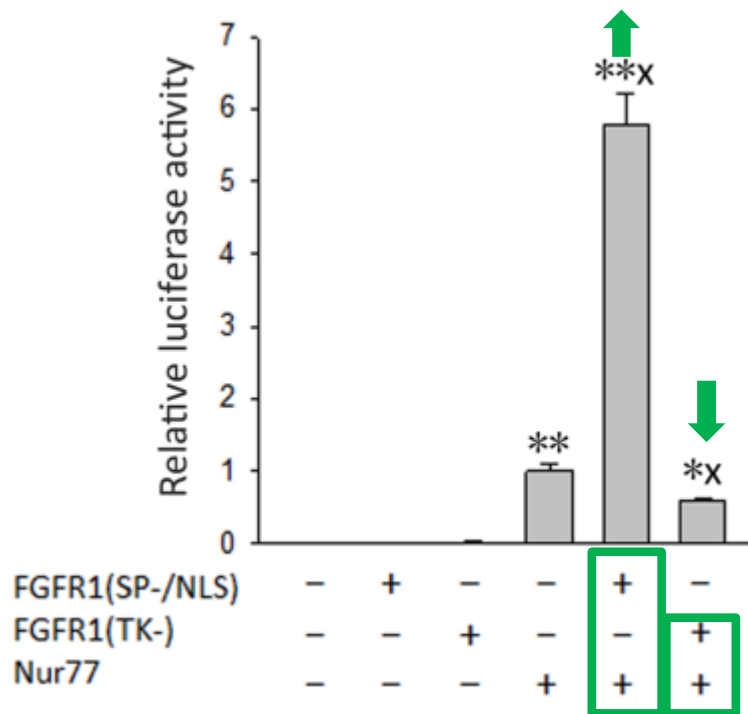
The probability of active transcription increases in sites co-inhabited by both RXR and FGFR1

Lee, Y-W., Terranova, C., Birkaya, B., Narla, S., Kehoe, D., Parikh, P., Dong, S., Ratzka, A., Brinkmann, H., Aletta, J., Tzanakakis, E., Stachowiak, E.K., Claus, P., and Stachowiak, M.K. (2012). A novel nuclear FGF Receptor-1 partnership with retinoid and Nur receptors during developmental gene programming of embryonic stem cells *J. Cell. Biochem.*, 113, 2920-2930

FGFR1 binds to RA-activated genes: *fgfr1*, *fgf-2* & *th*



Nuclear FGFR1 activates genomic enhancers ..

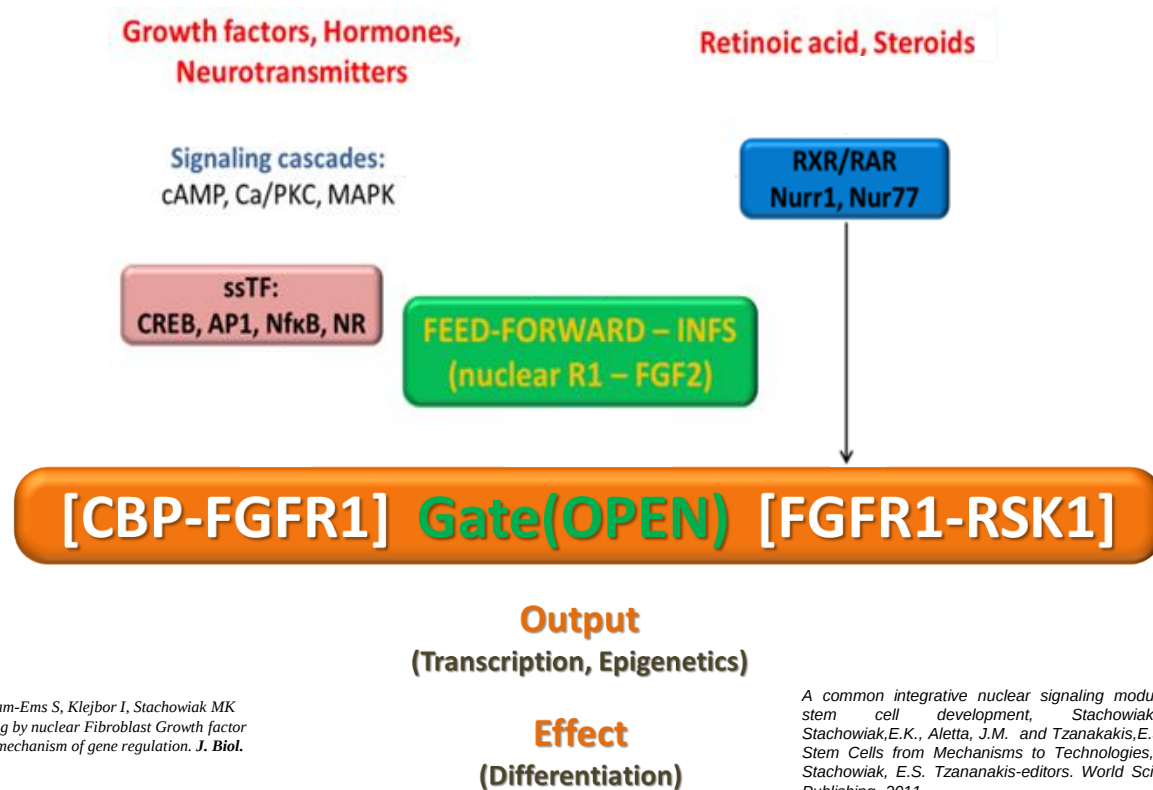


Lee, Y-W., Terranova, C., Birkaya, B., Narla, S., Kehoe, D., Parikh, P., Dong, S., Ratzka, A., Brinkmann, H., Aletta, J., Tzanakakis, E., Stachowiak, E.K., Claus, P., and Stachowiak, M.K. (2012). *J. Cell. Biochem.*, 113, 2920-2930; Baron et al., *J. Biol. Chem.* 2013.....

Y-W.Lee, E. K. Stachowiak, B. Birkaya, C. Terranova, M. Capacchietti, P. Claus, J. M. Aletta, M.K. Stachowiak PLOS ONE, in press (2013).

INFS act through Feed-Forward- And-Gate Module

EXTRACELLULAR STIMULI

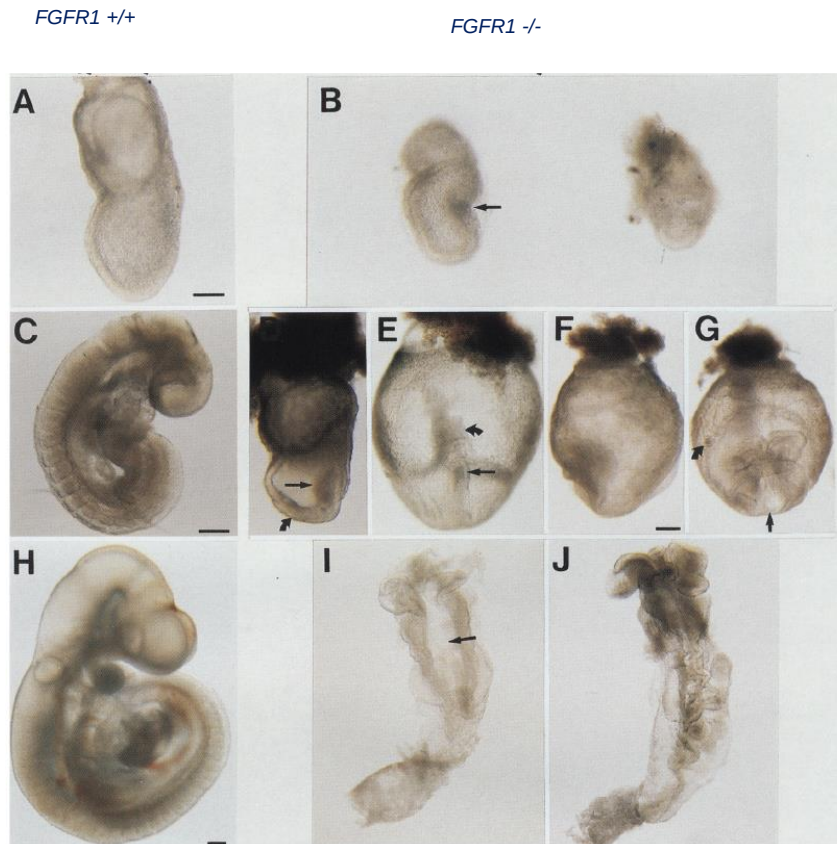


Fang X, Stachowiak EK, Dubham-Ems S, Klejbor I, Stachowiak MK (2005) Control of CBP signaling by nuclear Fibroblast Growth factor receptor-1 (FGFR1) – a novel mechanism of gene regulation. *J. Biol. Chem.* – 280(31):28451-62.

A common integrative nuclear signaling module for stem cell development, Stachowiak, M.K., Stachowiak, E.K., Aletta, J.M. and Tzanakakis, E.S.; In: *Stem Cells from Mechanisms to Technologies*, M.K. Stachowiak, E.S. Tzanakakis-editors. World Scientific Publishing, 2011

Global genomics

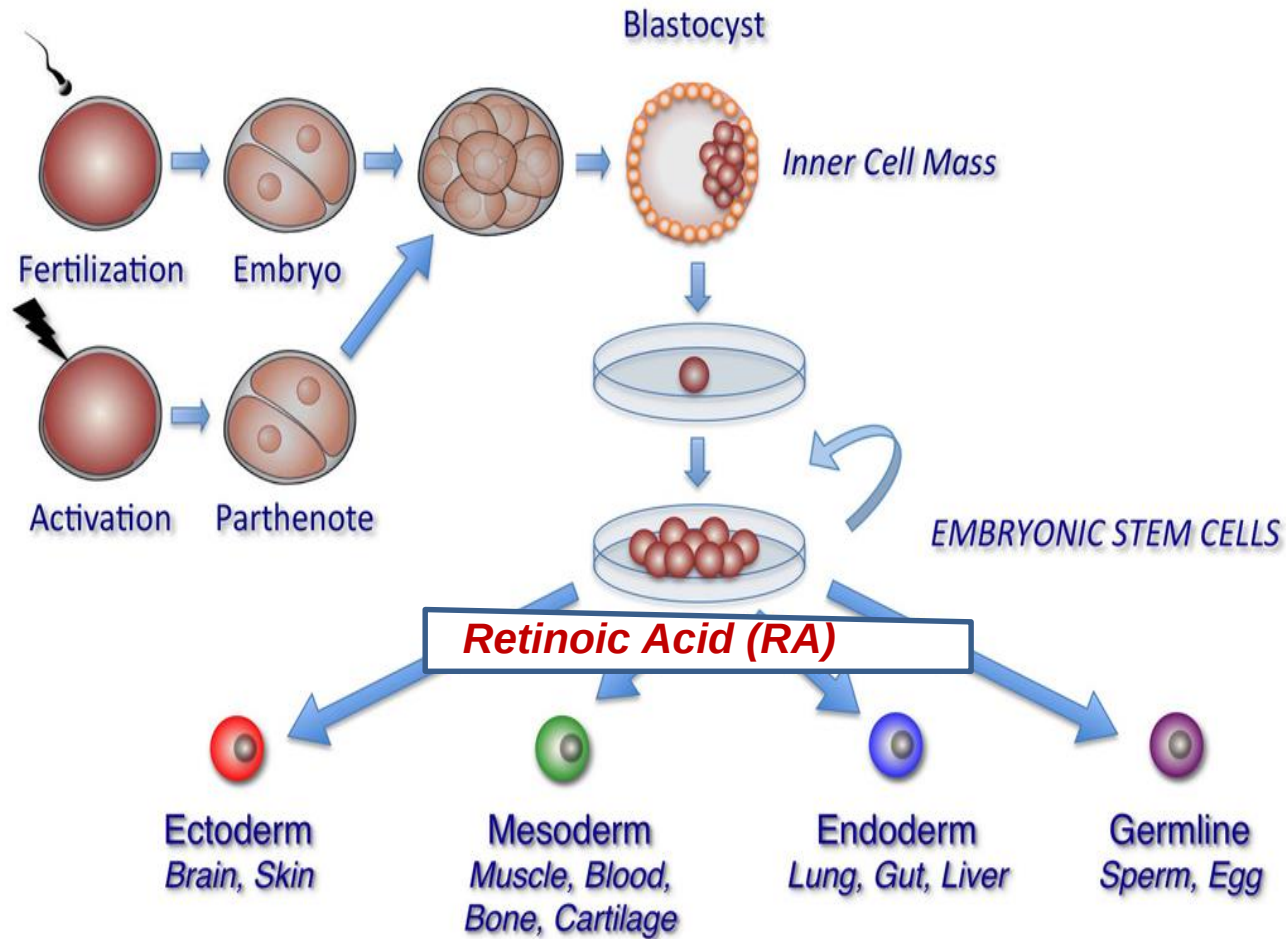
FGFR1 is indispensable for ontogeny



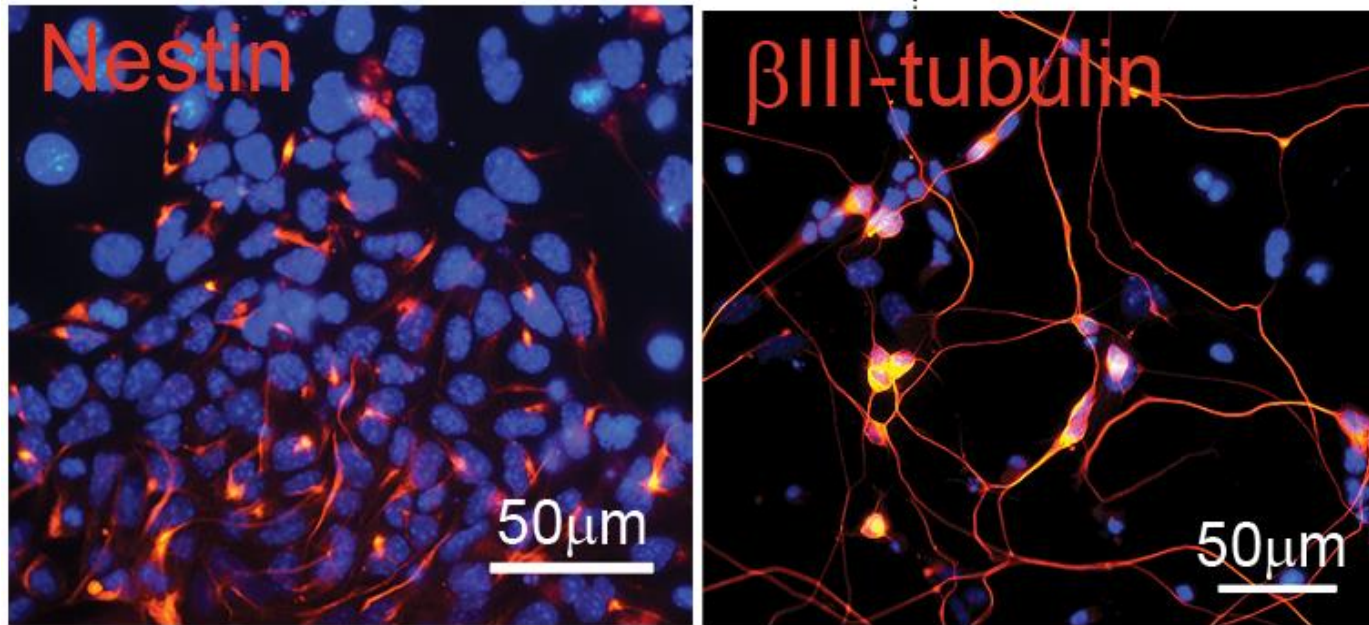
Masashiro Murakami
& Michael Simons

(*Gene @ Dev.*, 8, 3045-57, 1994)

INFS in Pluripotent Embryonic Stem Cells



all-trans Retinoic Acid (RA) induced neuronal differentiation of pluripotent ESC

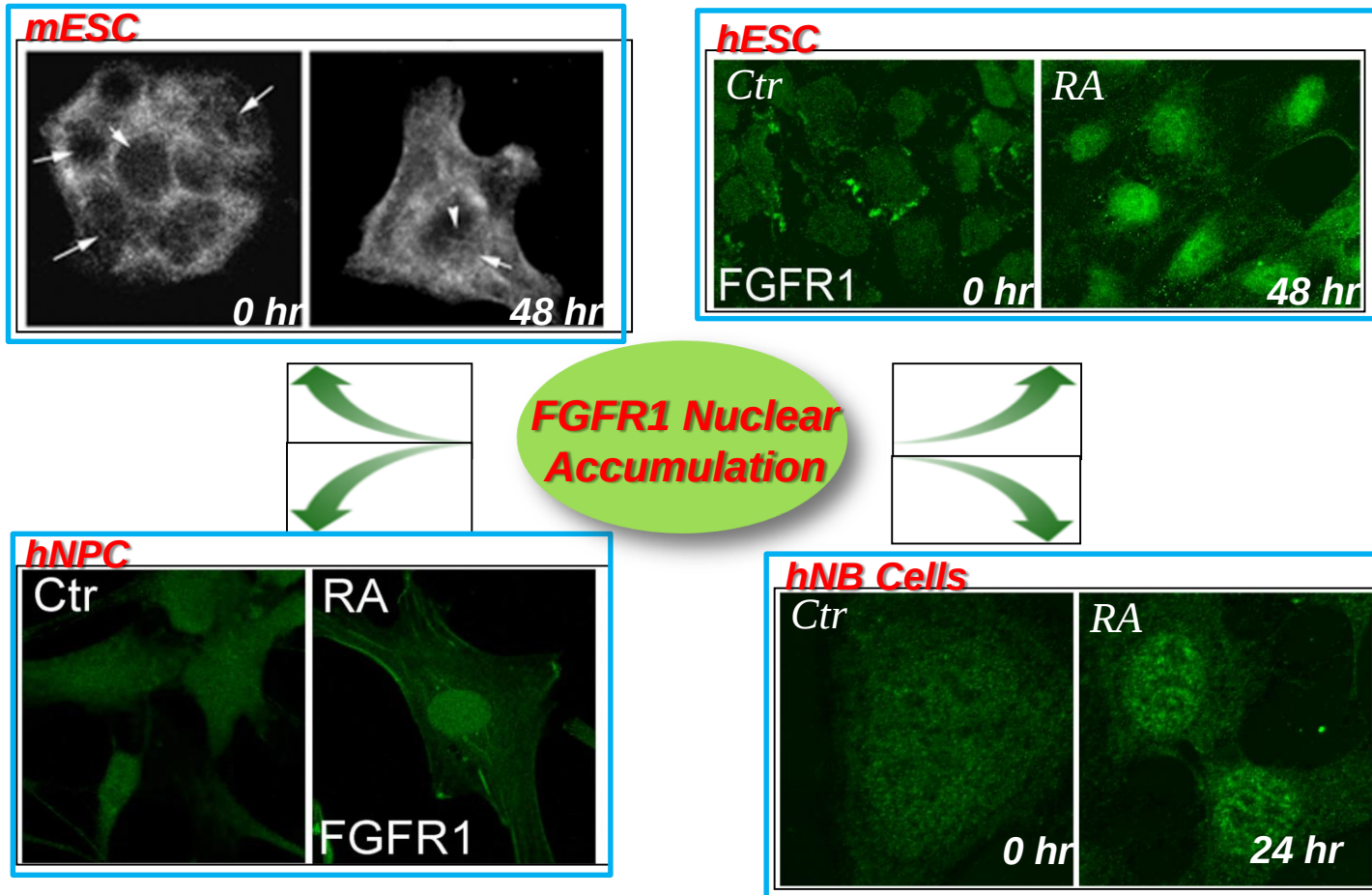


Pluripotent ESC

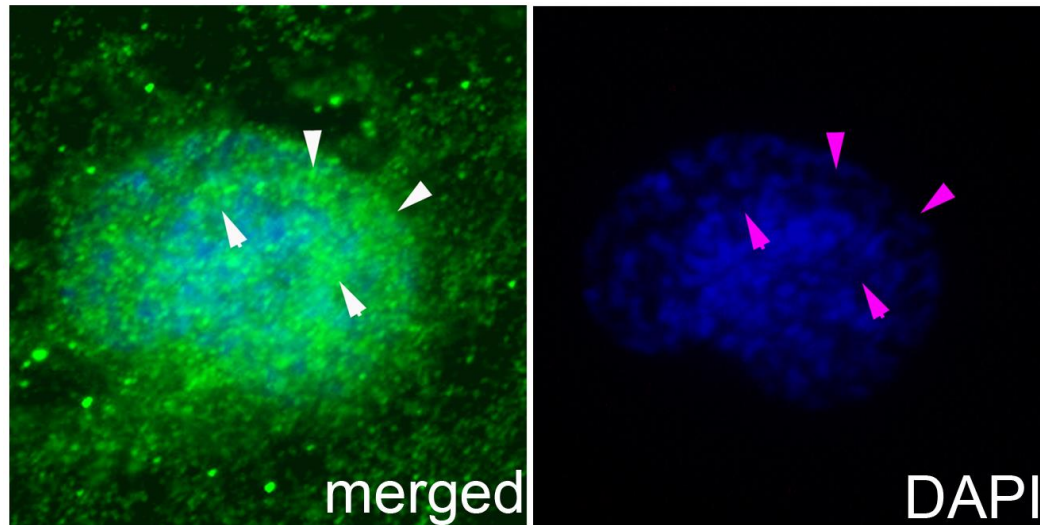


4d at-RA treatment

Nuclear Accumulation of FGFR1 is a common response to Retinoic Acid (RA) in Various Cells

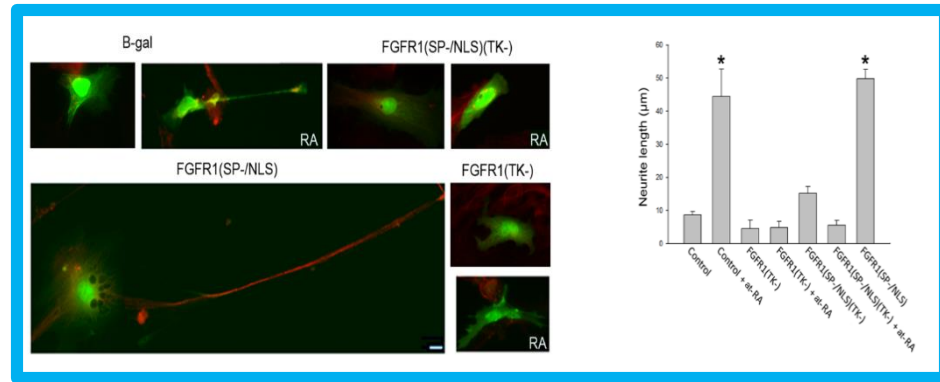
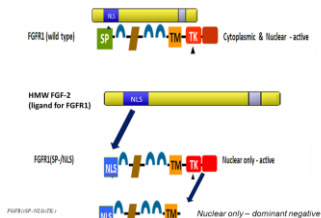


Nuclear FGFR1 is Excluded from Condensed Heterochromatin but enriched in Euchromatin.



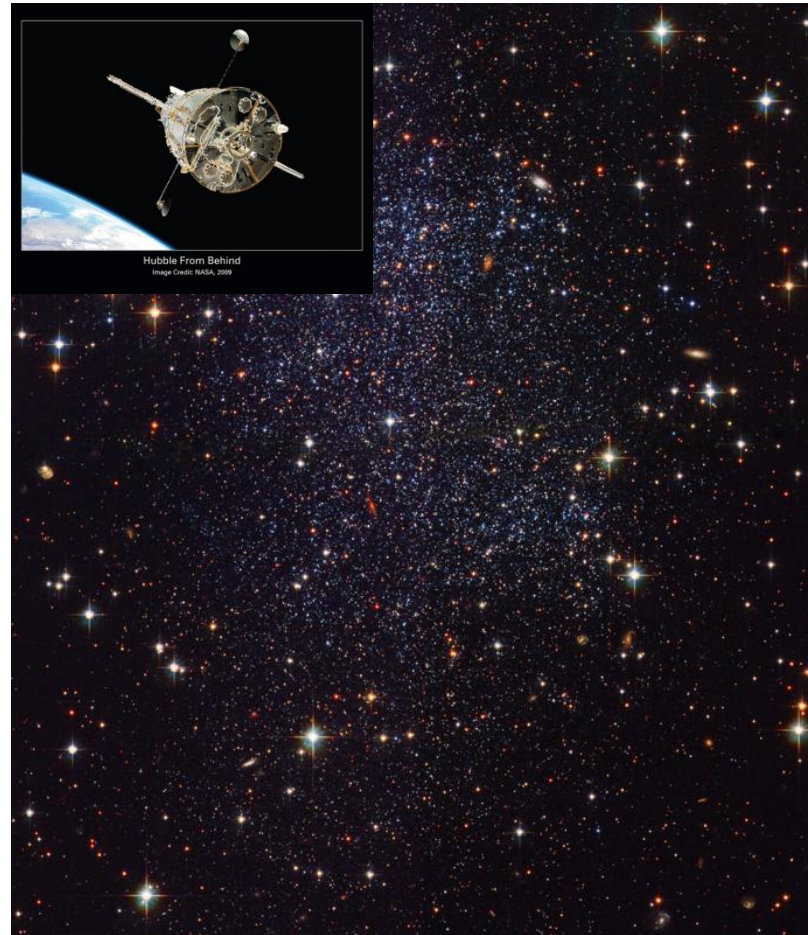
Lee, Y-W., Terranova, C., Birkaya, B., Naria, S., Kehoe, D., Parikh, P., Dong, S., Ratzka, A., Brinkmann, H., Aletta, J., Tzanakakis, E., Stachowiak, E.K., Claus, P., and Stachowiak, M.K. (2012). A novel nuclear FGF Receptor-1 partnership with retinoid and Nur receptors during developmental gene programming of embryonic stem cells J. Cell. Biochem., 113, 2920-2930

Nuclear FGFR1 mediates RA-induced neuronal differentiation of pluripotent mESC

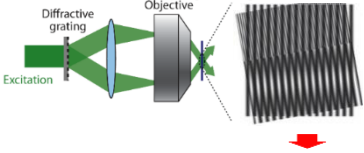


Lee, Y-Wet et al., (2012). A novel nuclear FGF Receptor-1 partnership with retinoid and Nur receptors during developmental gene programming of embryonic stem cells *J. Cell. Biochem.*, 113, 2920-2930

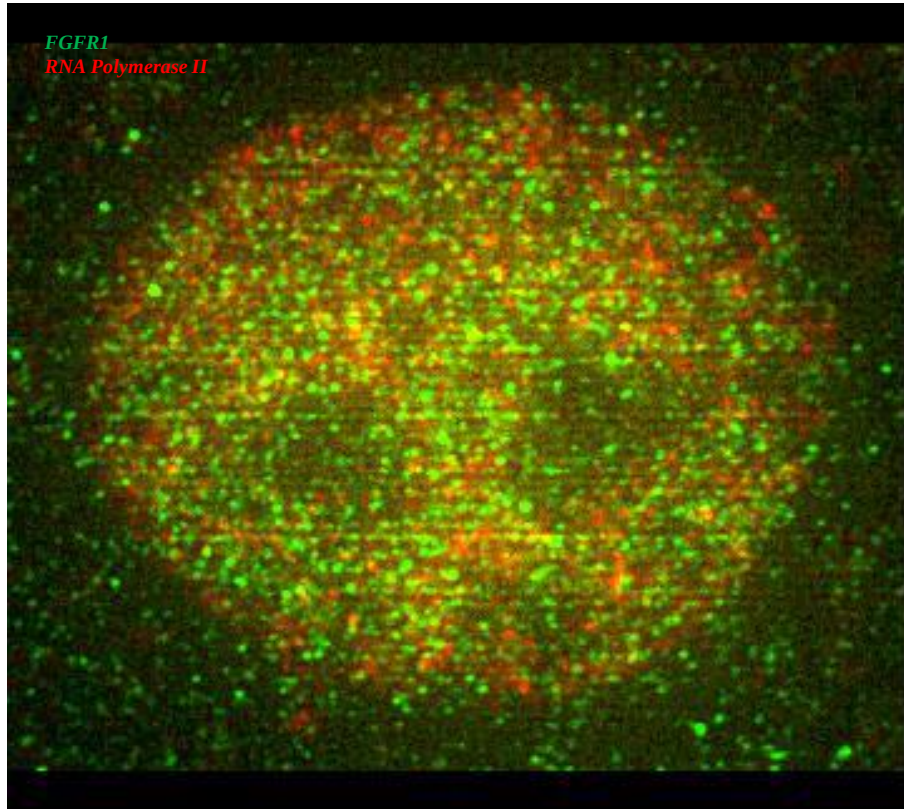
To infinity and beyond...



Structured-Illumination Microscopy (SIM)



FGFR1 localizes within transcription domains



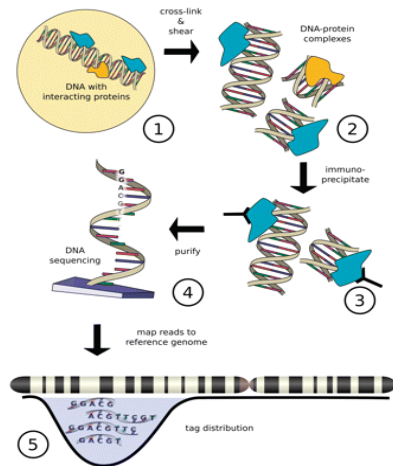
Hypothesis:

*nGFR1 and NR partners mediate neural
programming by:*

- targeting "master developmental" genes*
- targeting multiple gene subsets in diverse
development pathways.*
- organizing chromatin topological domains.*

Insight into the whole genome !

**Cross-linked Chromatin Immunoprecipitation,
DNA sequencing (ChIPseq)**



**RNA and small RNA sequencing
(RNAseq)**

RNA



cDNA synthesis

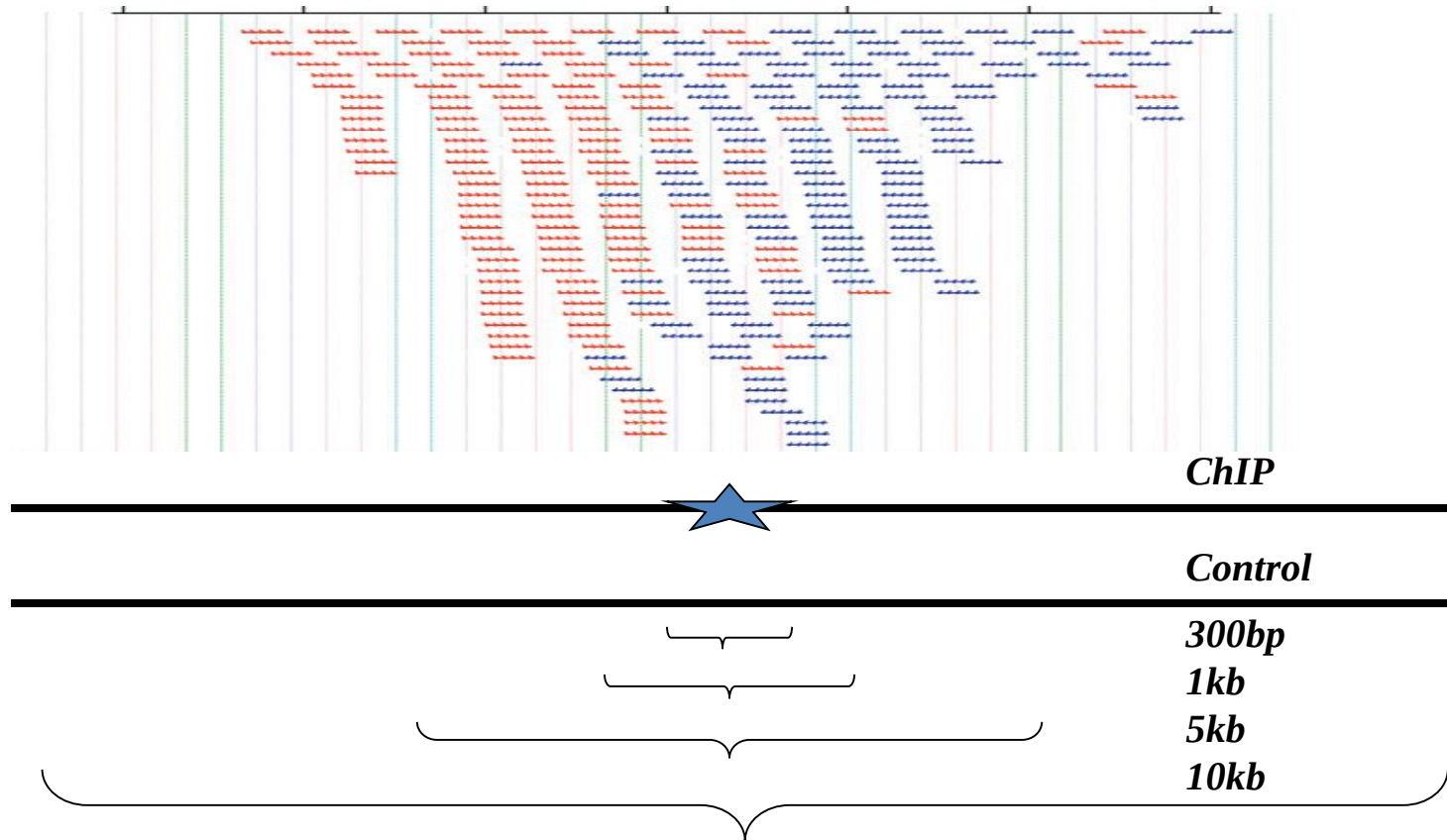
sequencing



Illumina HiSeq 2000

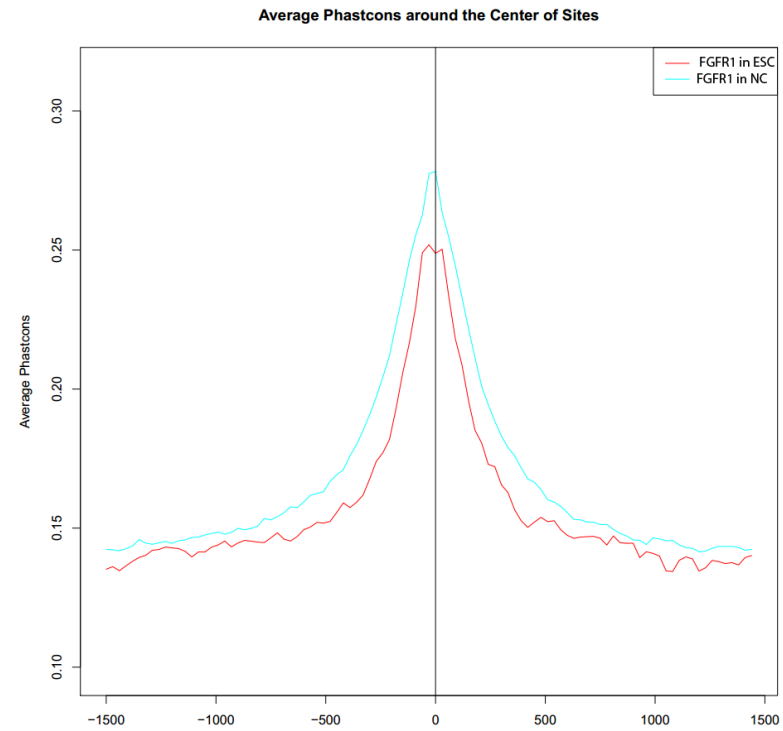
C.Terranova, S. Narla, Yu-Wei Lee, J. Bard, A. Parikh, E.K. Stachowiak, E. S. Tzanakakis, M.J. Buck, B. Birkaya, M.K. Stachowiak, Global developmental gene programming in the form of Fibroblast Growth Factor Receptor-1 (FGFR1). 2015, PLOS One

Call *FGFR1*, *RXR* and *Nur77* peaks (identify binding sites) using Model Based Analysis for ChIP-seq (MACS2)





Sequences of nFGFR1 targeted sites are conserved among different species

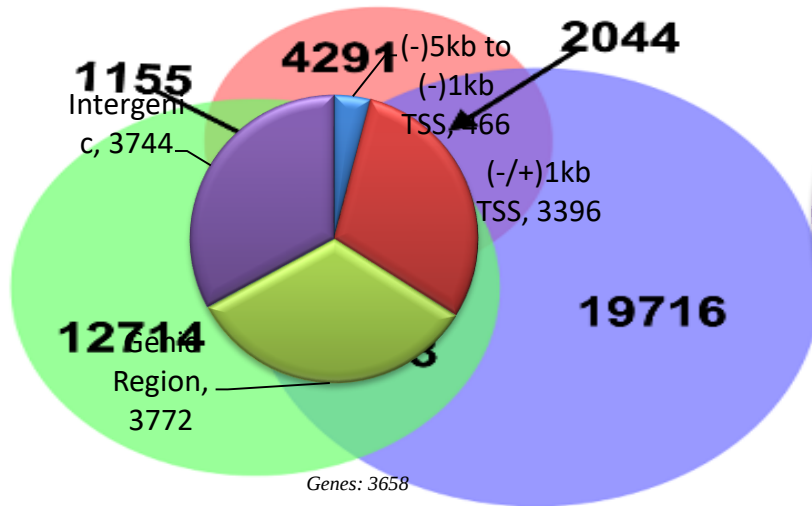


Lessons from ChIPseq:

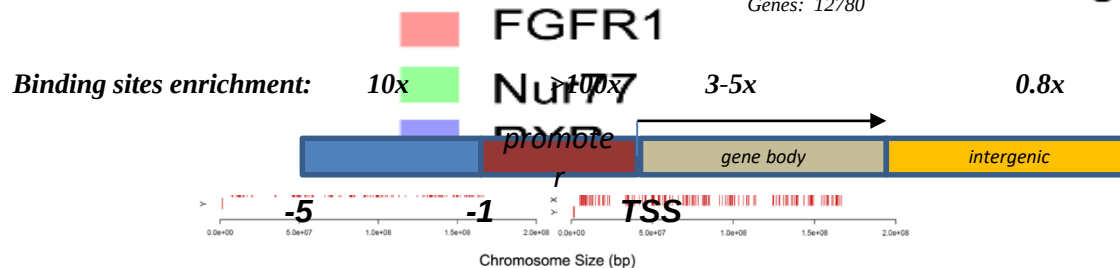
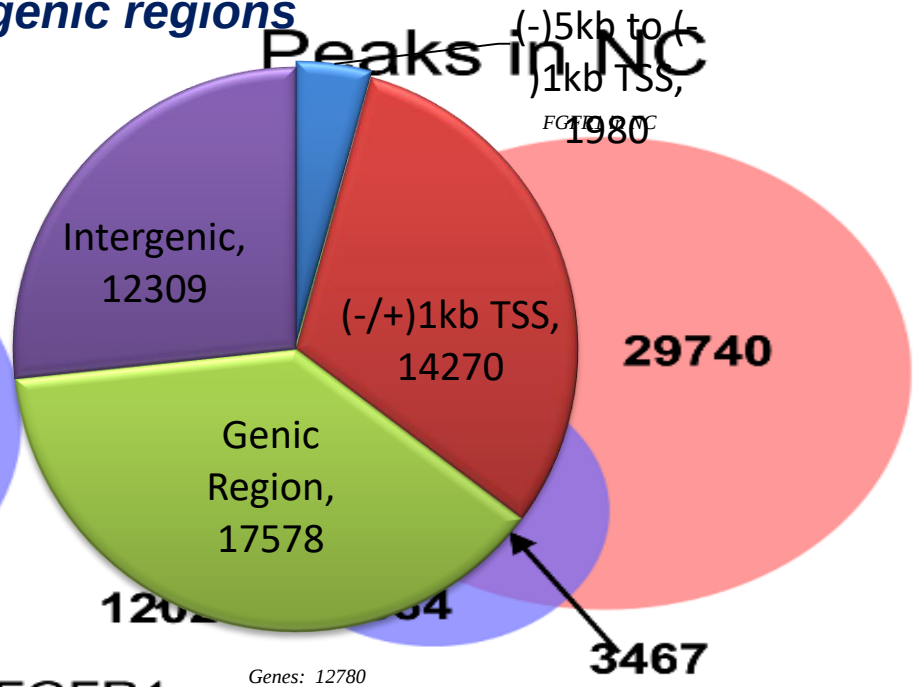
(1) (3) (4) (5) (6) (7) (8) (9) (10) (11) (12) (13) (14) (15) (16) (17) (18) (19) (20) (21) (22) (23) (24) (25) (26) (27) (28) (29) (30) (31) (32) (33) (34) (35) (36) (37) (38) (39) (40) (41) (42) (43) (44) (45) (46) (47) (48) (49) (50) (51) (52) (53) (54) (55) (56) (57) (58) (59) (60) (61) (62) (63) (64) (65) (66) (67) (68) (69) (70) (71) (72) (73) (74) (75) (76) (77) (78) (79) (80) (81) (82) (83) (84) (85) (86) (87) (88) (89) (90) (91) (92) (93) (94) (95) (96) (97) (98) (99) (100)

and genic regions

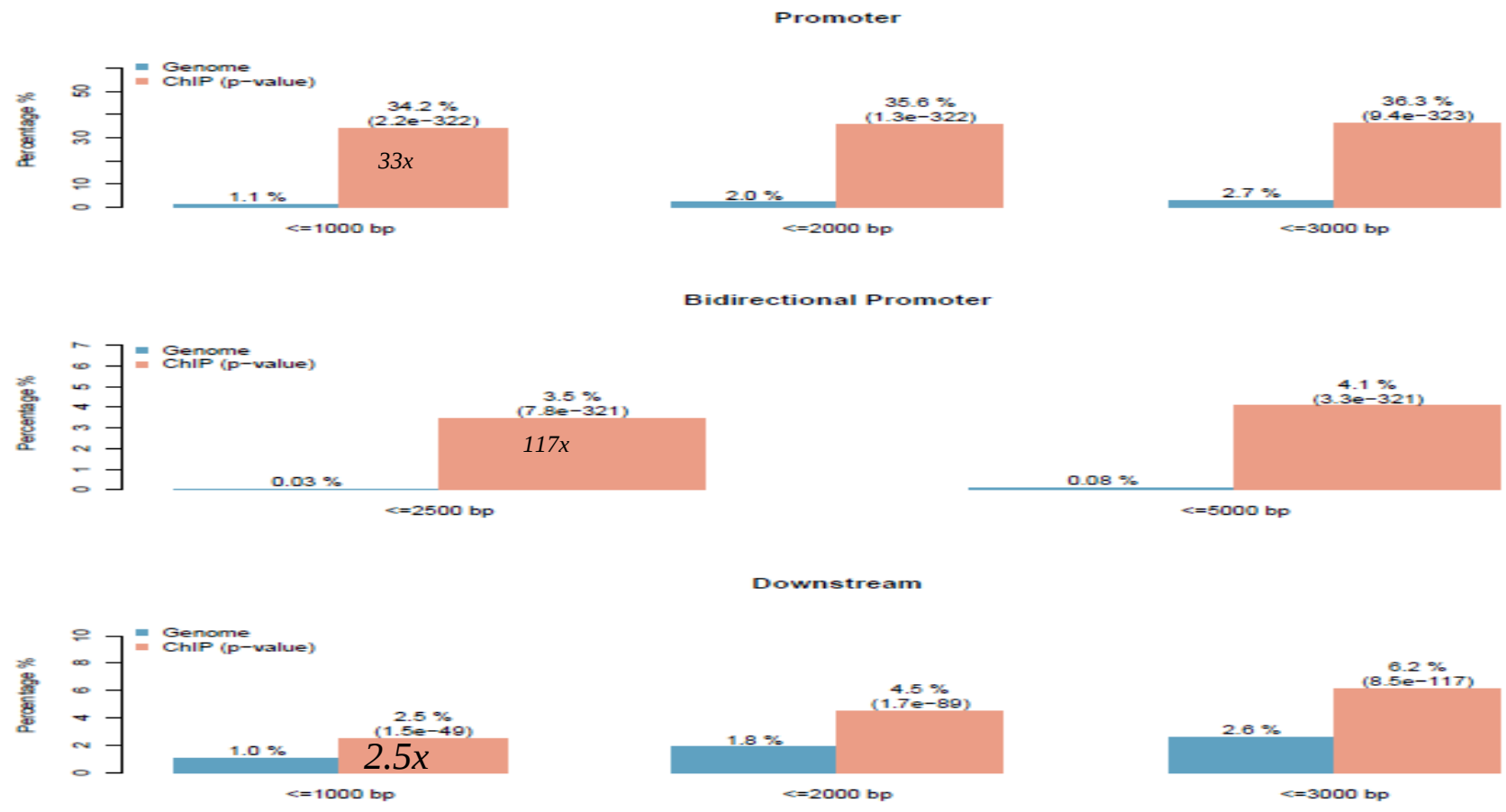
Peaks in ESC



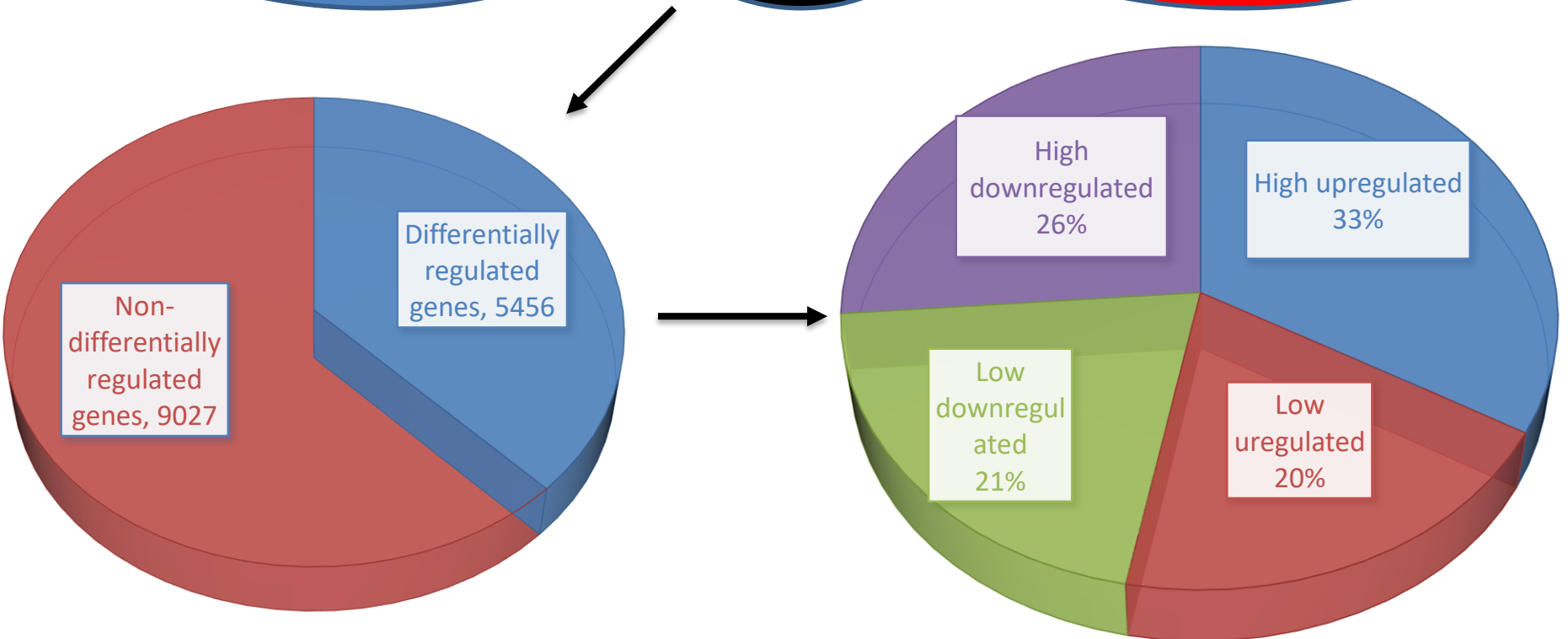
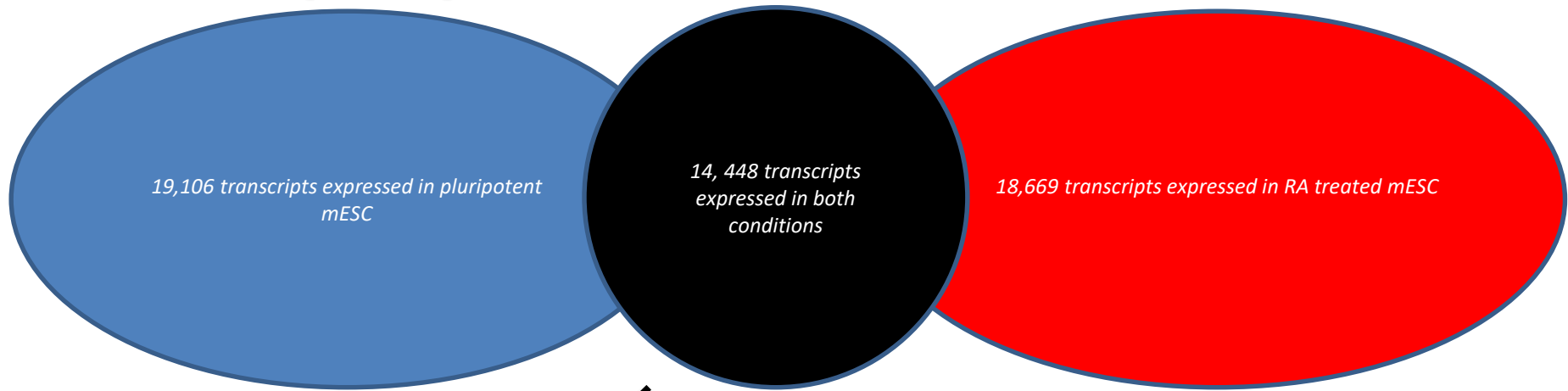
Peaks in NC



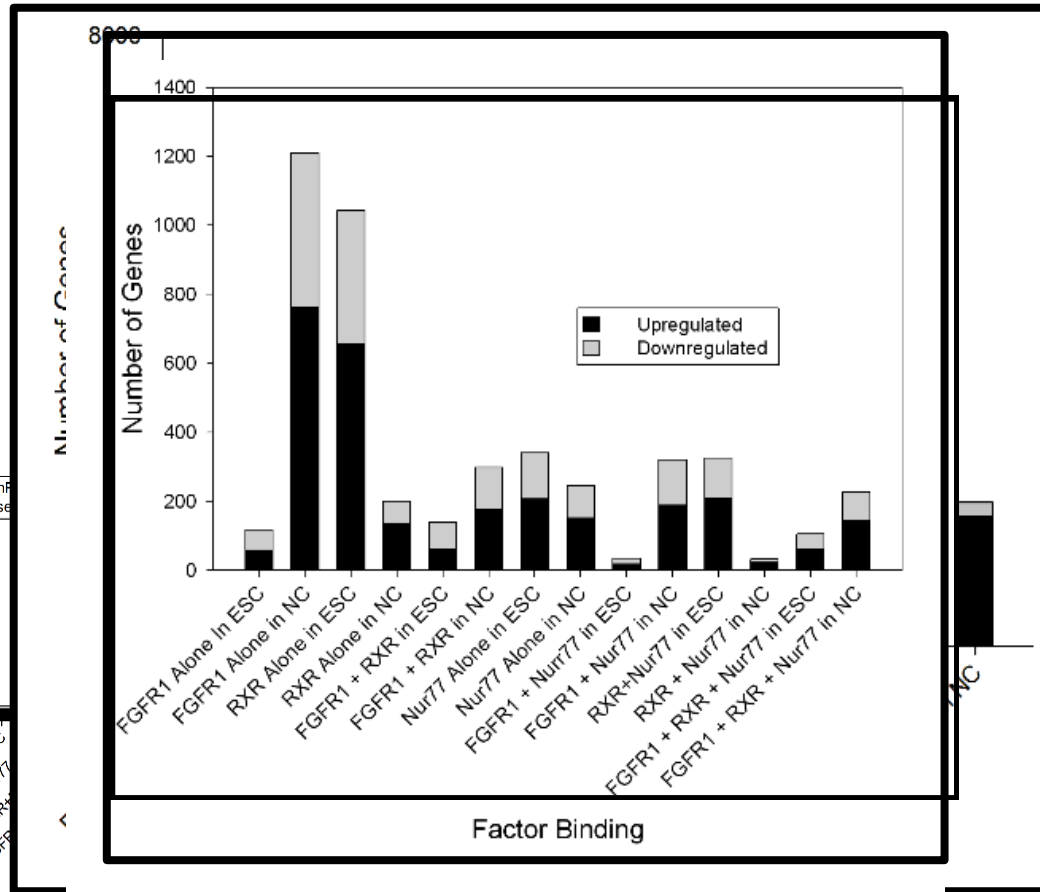
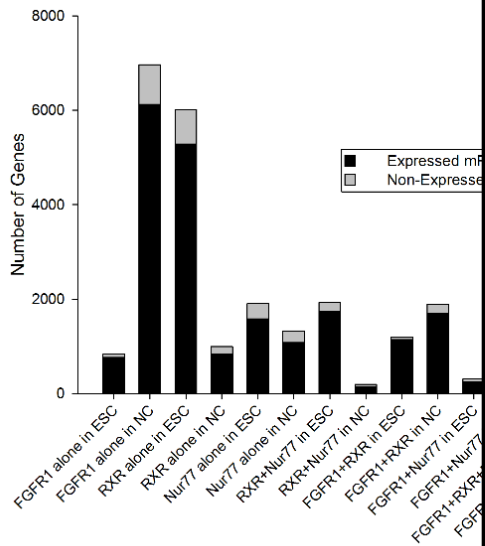
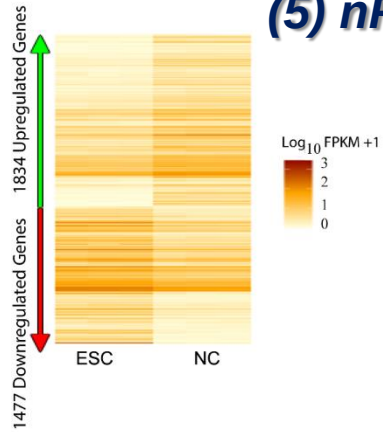
Promoter enrichment of FGFR1 peaks in differentiating mESC (+RA)



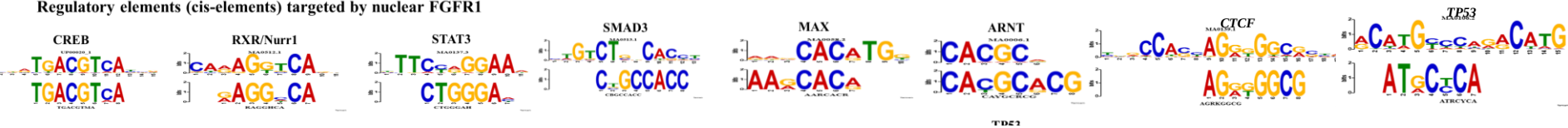
RNA-seq: differential analysis of gene expression in pluripotent and RA treated mESC



(5) *nFGFR1*, *RXR* and *Nur77* bind predominantly to proximal promoters of expressed genes
(ChIPseq+RNAseq)

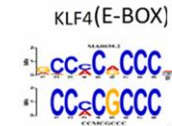
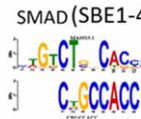
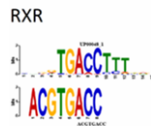


Regulatory elements (cis-elements) targeted by nuclear FGFR1

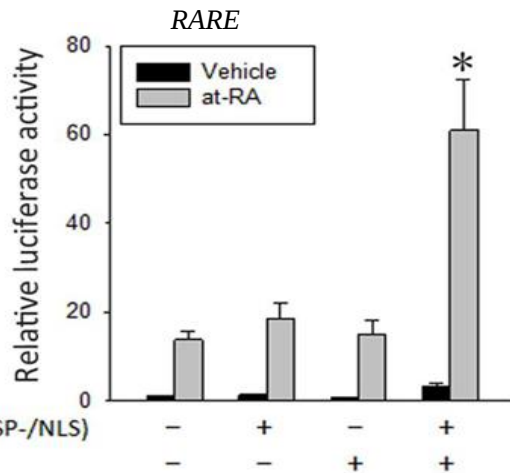


Factor	MOTIF (BOLD are unique to factor)
FGFR1	ARNT, ATF1, CTCF, ERG/ELK4, KLF4, MAX, MZF1, NRF1, Nurr1, Pou2f3 , Pou5f1:Sox2 , RAR α , RFX1, RXR α , SMAD , Sox8, SP1, STAT, TCF3, TP53, YY1, ZBTB33, ZFP161
RXR	ATF1, CTCF, Irx4 , mycn, MZF1, Nurr1, Nr1h3:RXR α , Pitx2 , Pou3f3 , PPARG, Prrx2, RAR α , RFX1, RXR α , Sox8, SP1, YY1, ZEB1 , ZFP161
Nur77	ATF1, CTCF, Hic1 , MAX, mycn, NRF1, Nurr1, Pax6 , Prrx2, Six6 , SP1, STAT, RXR α , YY1, ZFP161

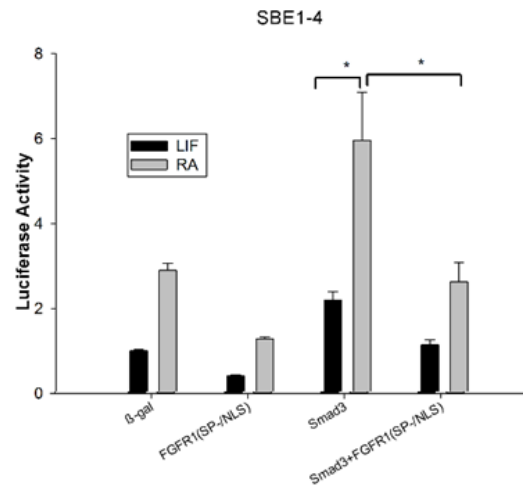
Nuclear FGFR1 activates RARE, E-Box and inhibits SBE



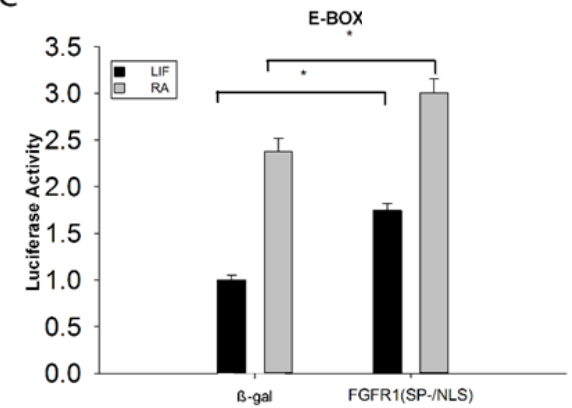
A



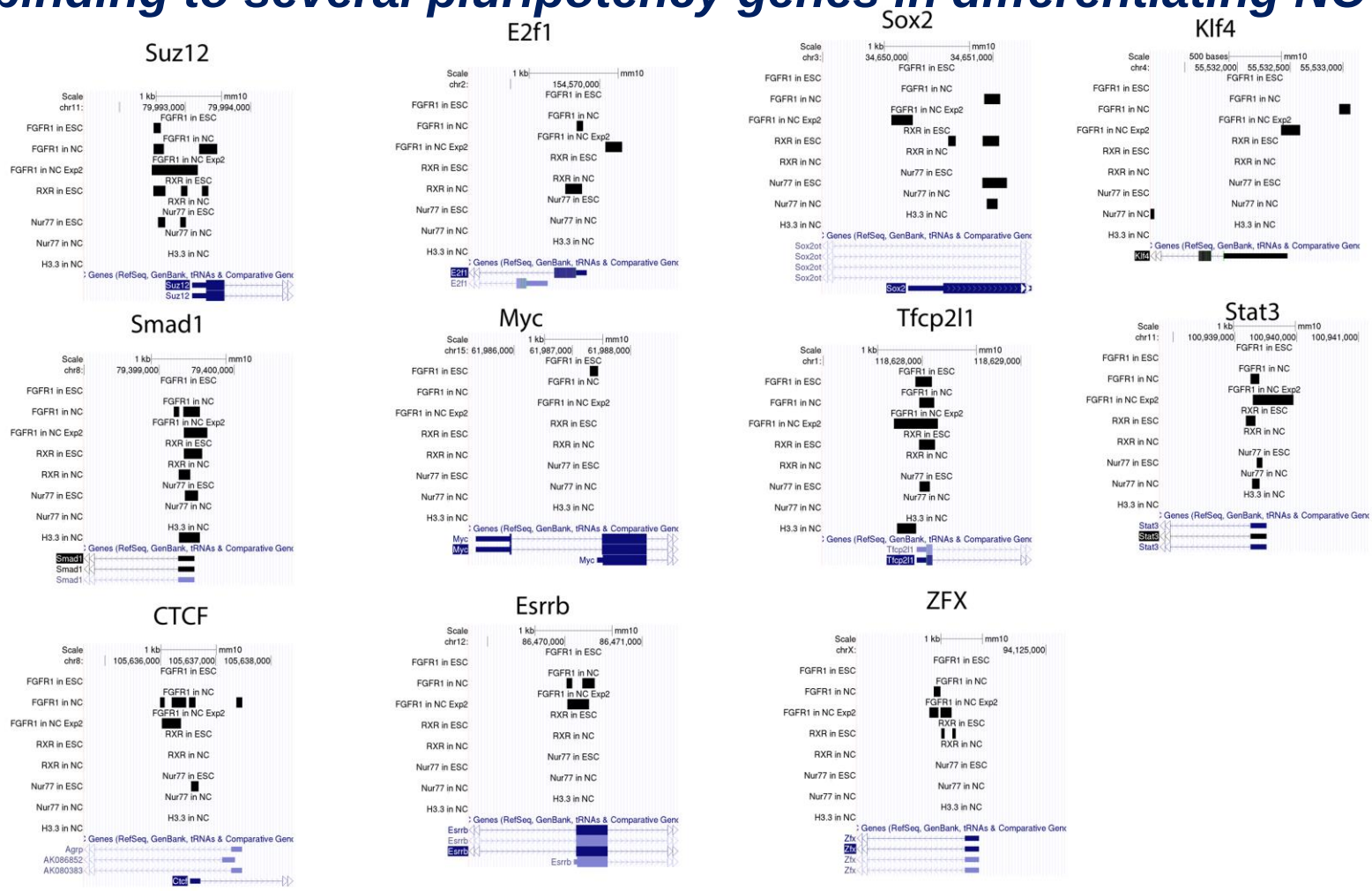
B



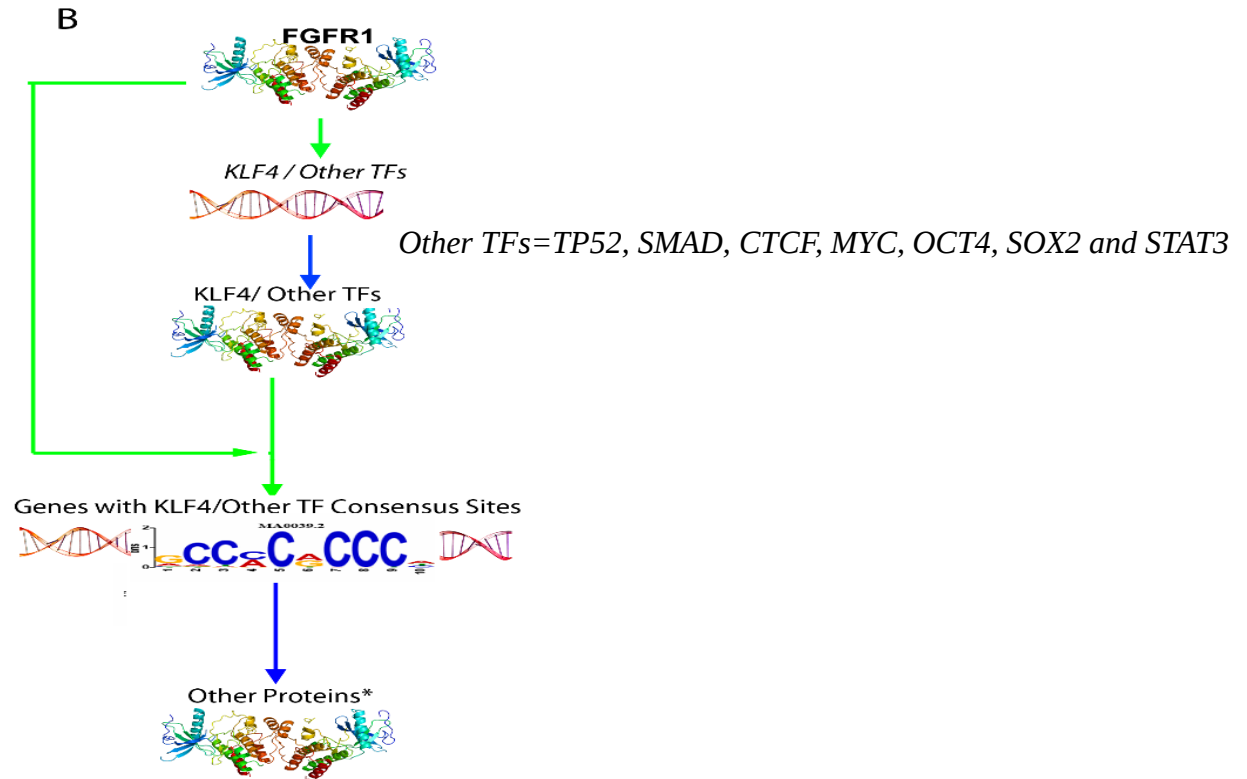
C



FGFR1 binding to several pluripotency genes in differentiating NC



nFGFR1 2-levels of gene control



Global developmental gene programming involves a nuclear form of Fibroblast Growth Factor Receptor-1 (FGFR1). 2015, PLOS One, in press

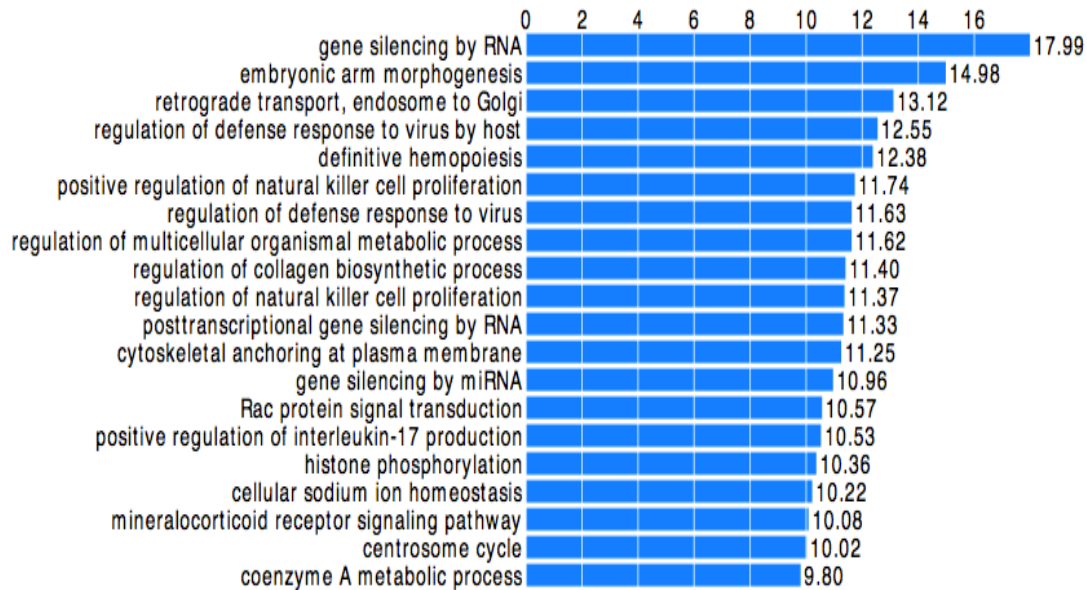
FGFR1-binding gene ontology

bb ID: 20120522-public-1061IZ
Display name: ct_R1MACS_7624

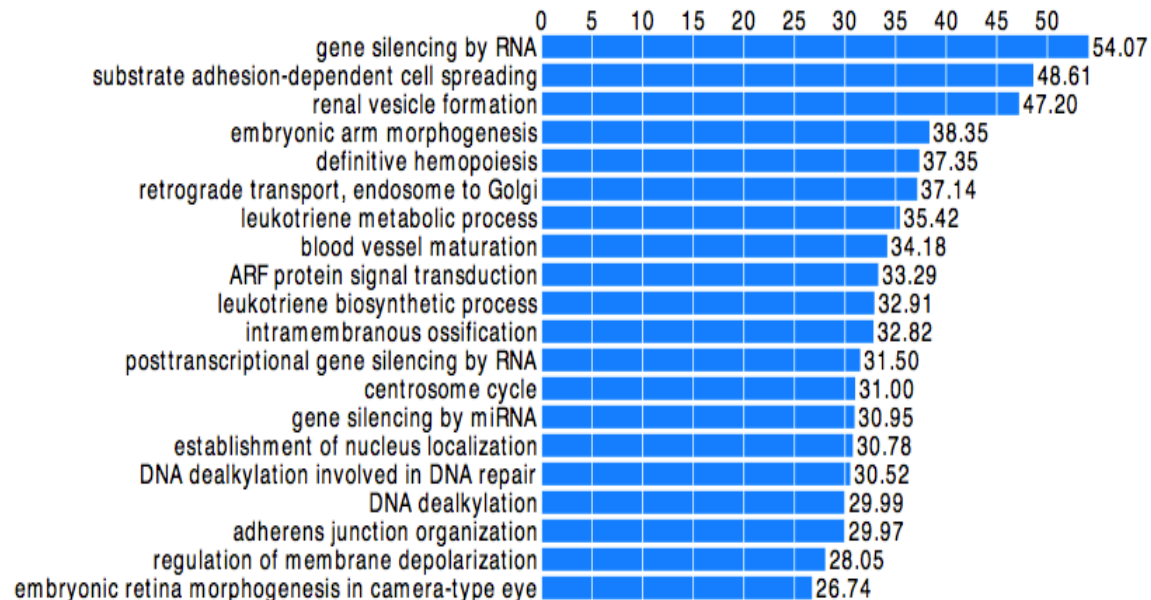
GO Biological Process

-log₁₀(Binomial p value)

- RA



- +RA

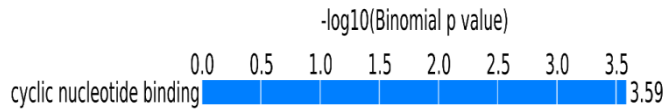


GREAT Gene Ontology based on FGFR1 binding sites

Pluripotent mESC

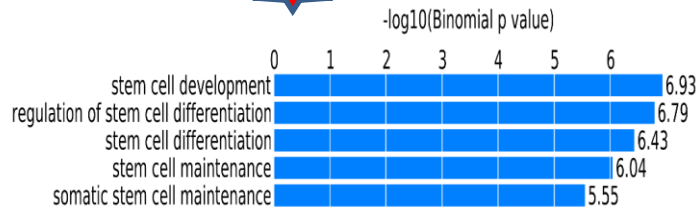
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GO Molecular Function



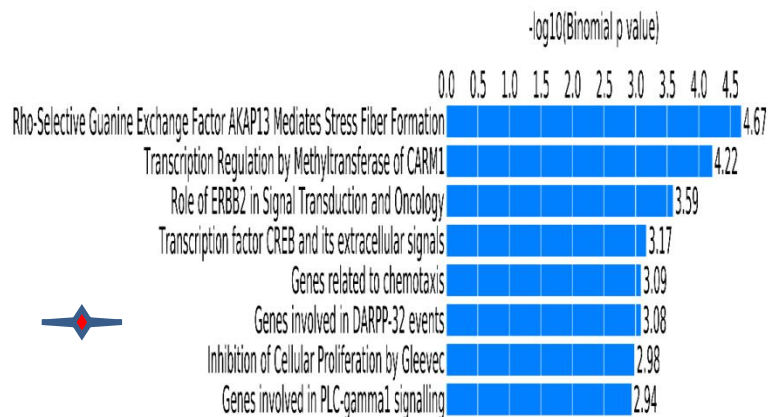
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GO Biological Process



Display name: user-provided data

MSigDB Pathway

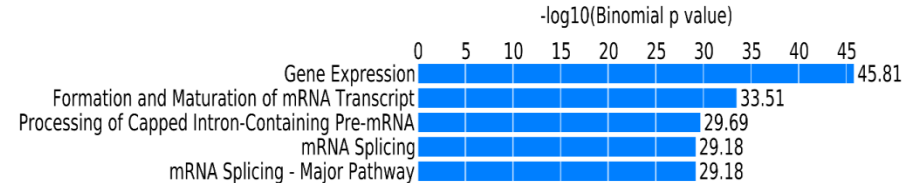


48h at-RA treated mESC

Display name: user-provided data

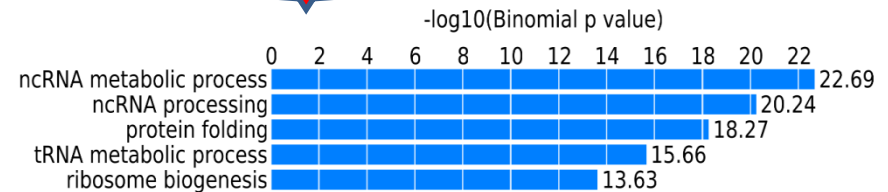


Pathway Commons



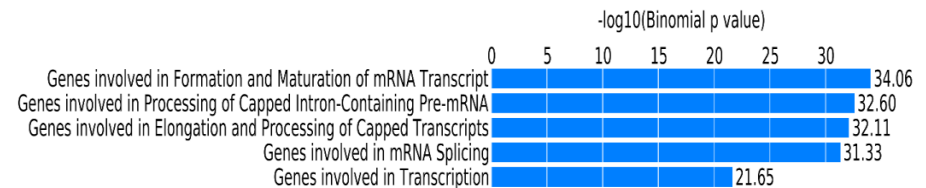
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GO Biological Process



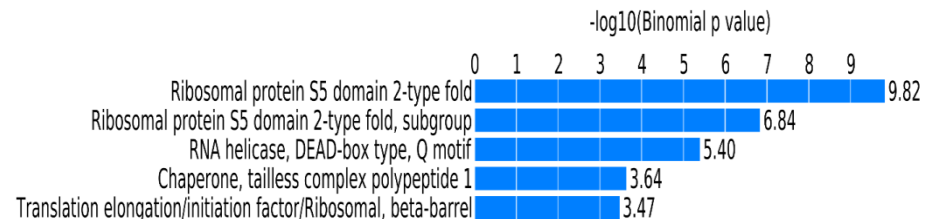
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MSigDB Pathway



Display name: user-provided data

InterPro



Ingenuity Pathway Analysis (IPA)

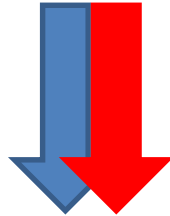
Enriched pathways:

FGFR1



- Pluripotency
- Axonal guidance**
- Wnt/ β -catenin**
- ESC pluripotency**
- Cardiogenesis**
- Osteonegenesis
- cancer**
- Hair and Skin Development and Function

FGFR1
+RXR



- Pluripotency
- Nervous system developmnet
- Axonal guidance
- Wnt/ β -catenin
- ESC pluripotency
- Cardiogenesis
- Basal cells carcinoma**
- myogenic developmnet**

FGFR1
+Nur



- Axonal guidance
- Wnt/ β -catenin
- ESC pluripotency
- Nitric Ox. Signaling**
- Dopamine-DARF signaling**
- G protein receptor signaling**

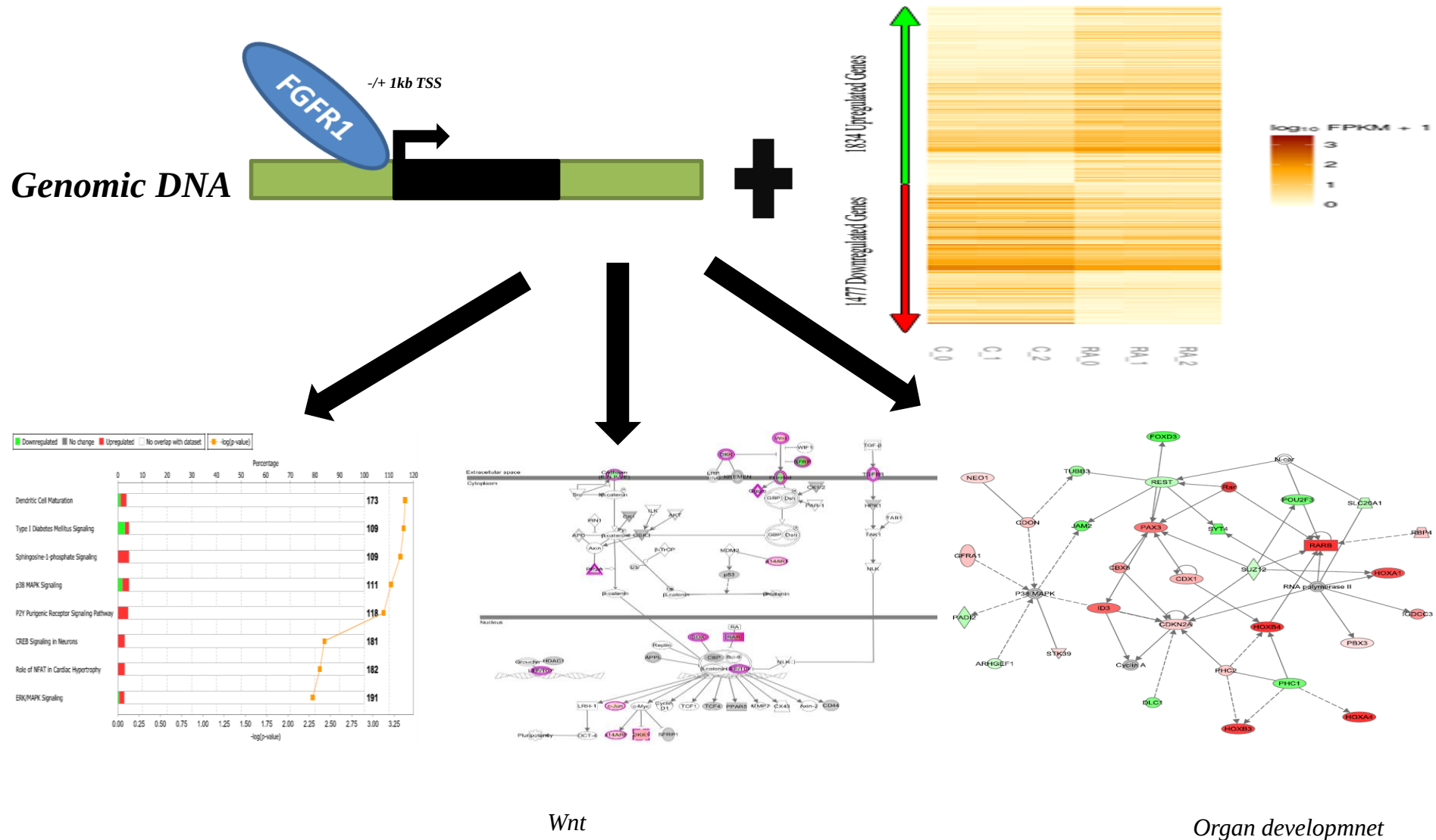
FGFR1
+RXR
+Nur



Metabolism:

- glucose**
- glycogene**
- folate**
- histidine**

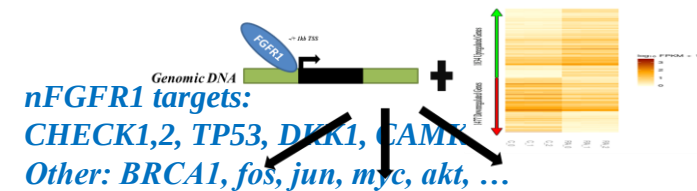
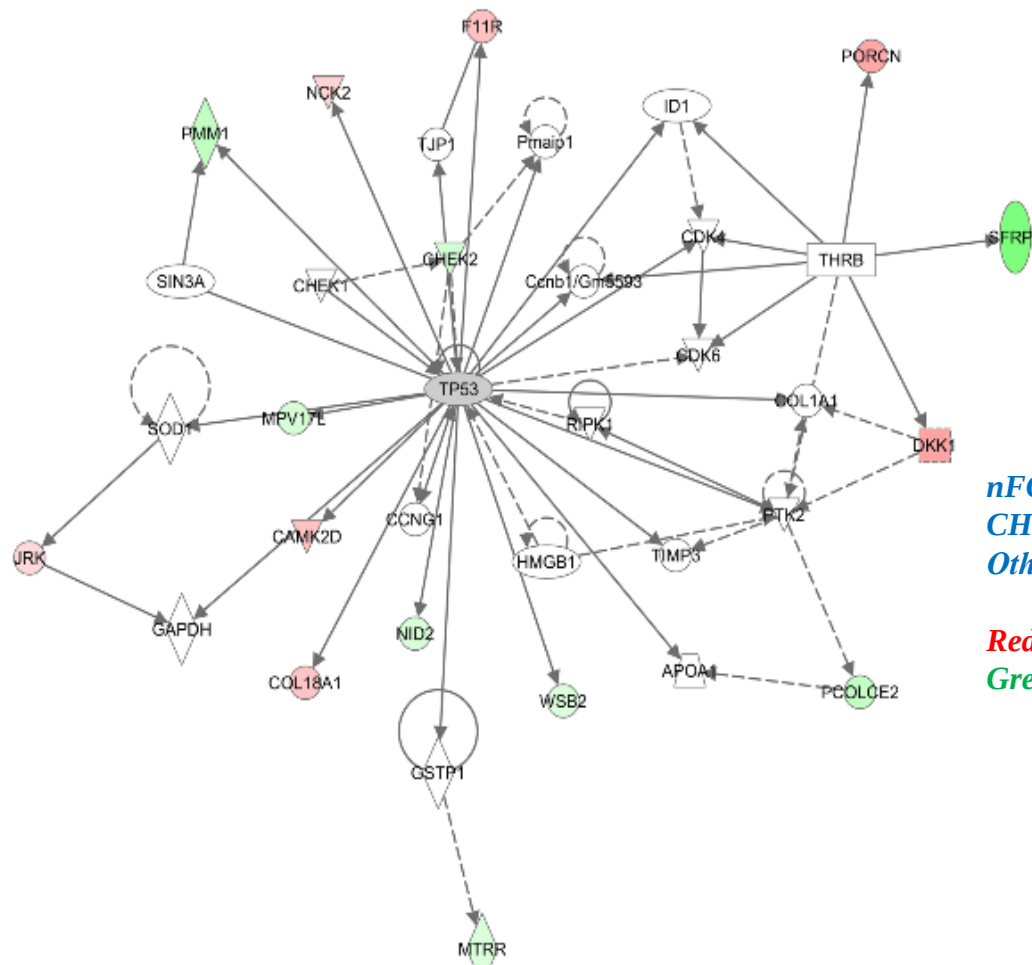
Ingenuity Pathway Analysis (IPA): Combination of ChIP- and RNA-seq



***Ingenuity Pathway Analysis (IPA): Combination of ChIP- and RNA-seq
nFGFR1 alone targets regulated genes of cell proliferation and survival pathways***

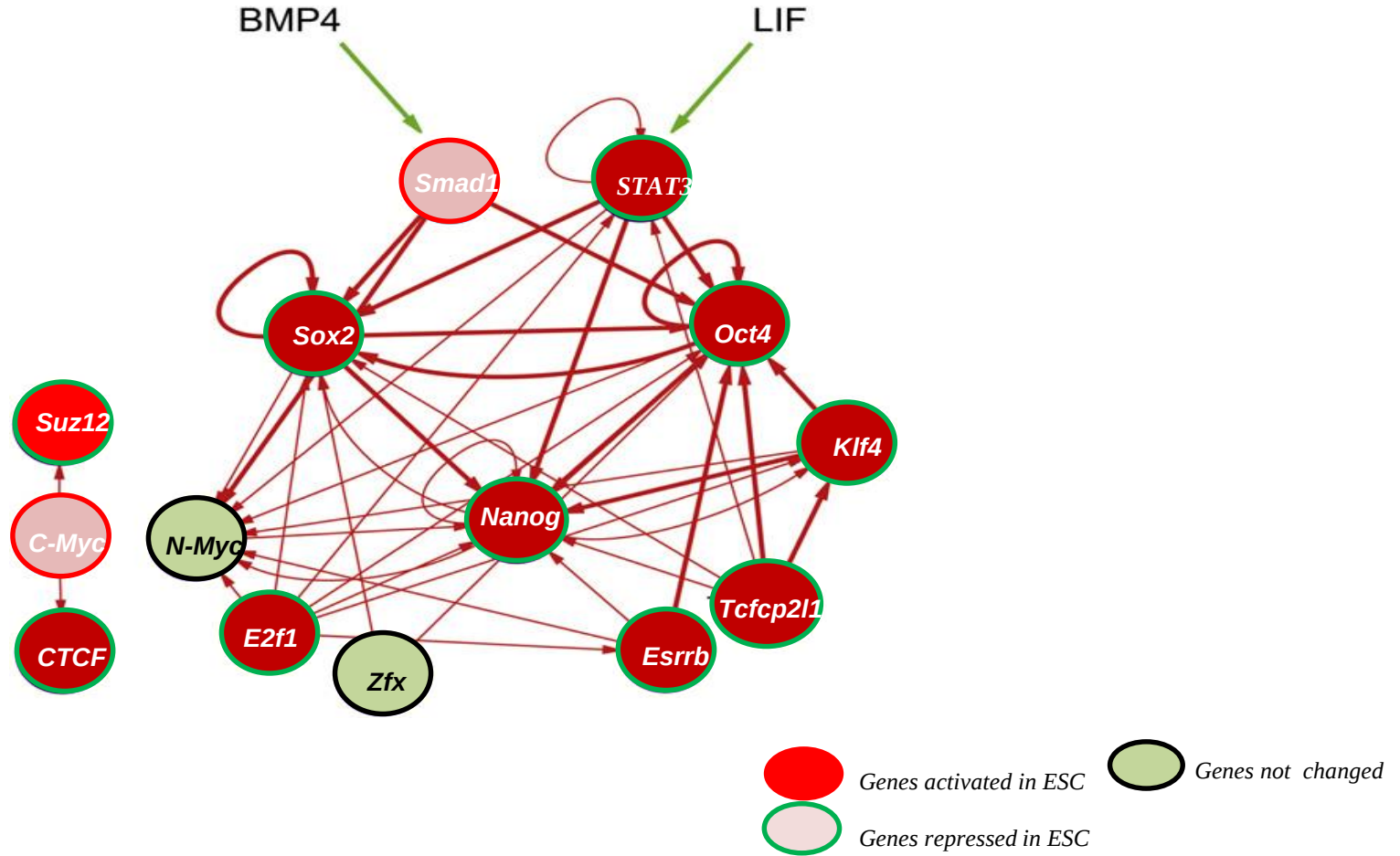
Top network controlling cell proliferation and survival:

B

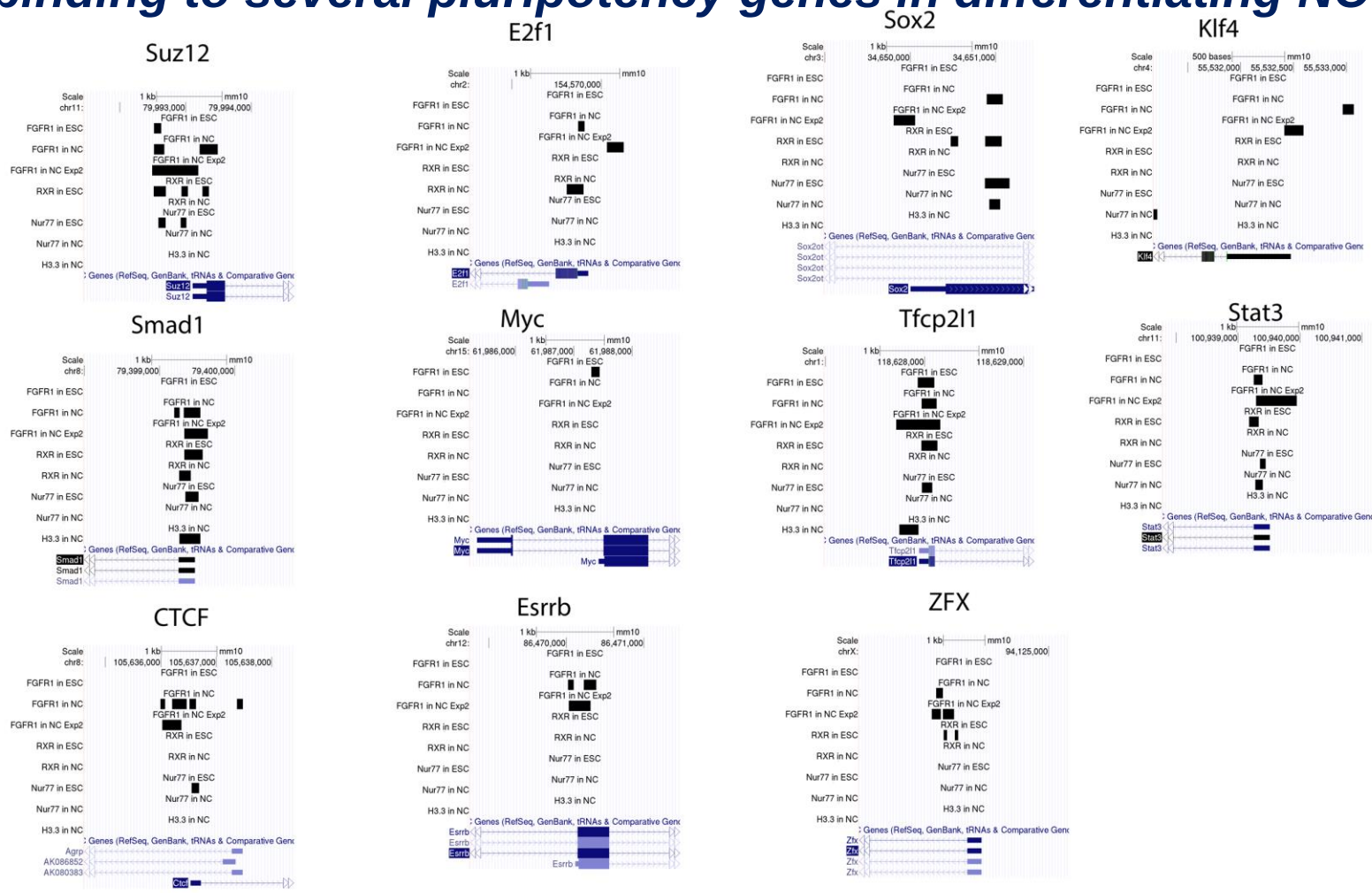


Red – activated genes
Green – inhibited genes

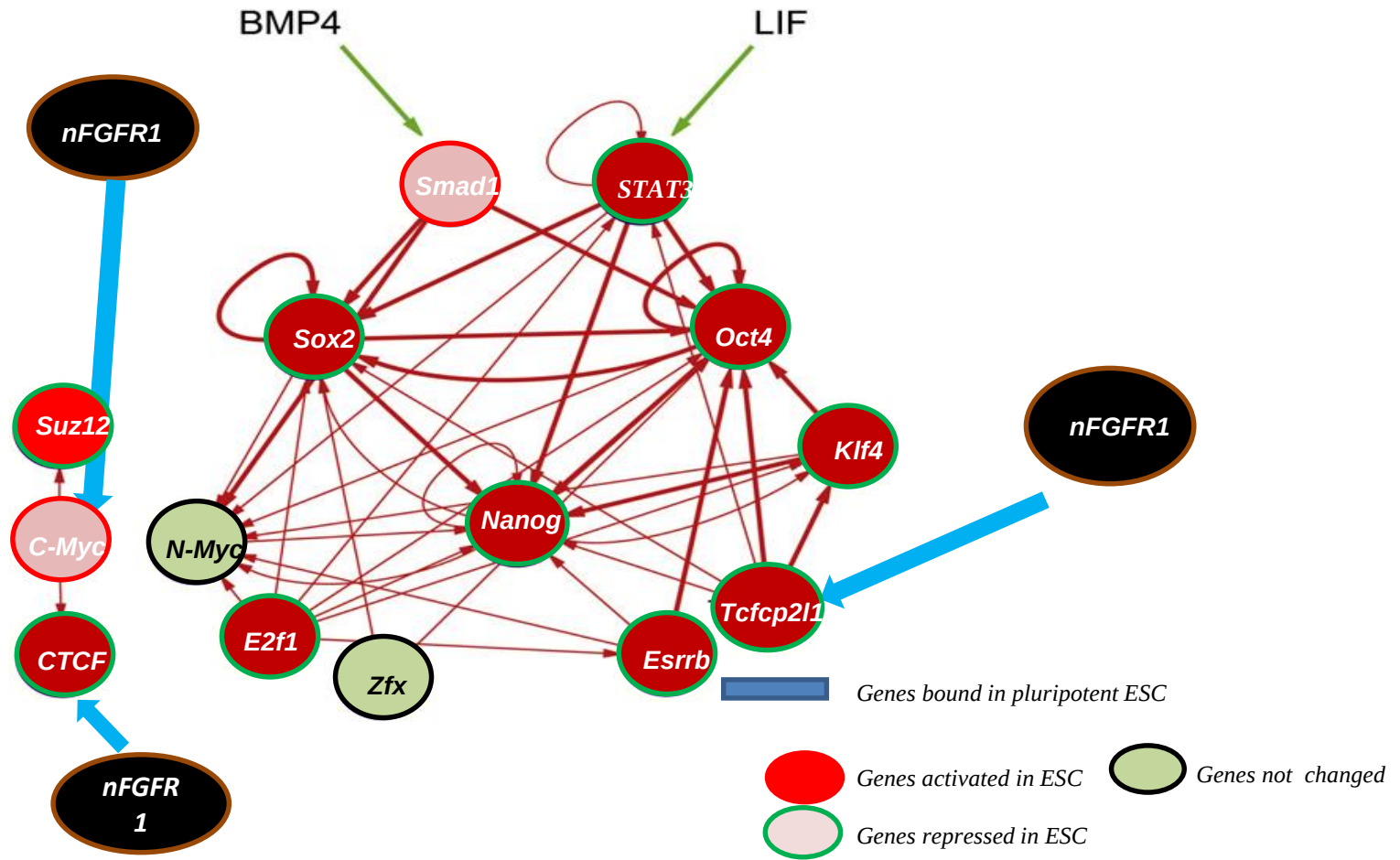
Active pluripotency network in ESC



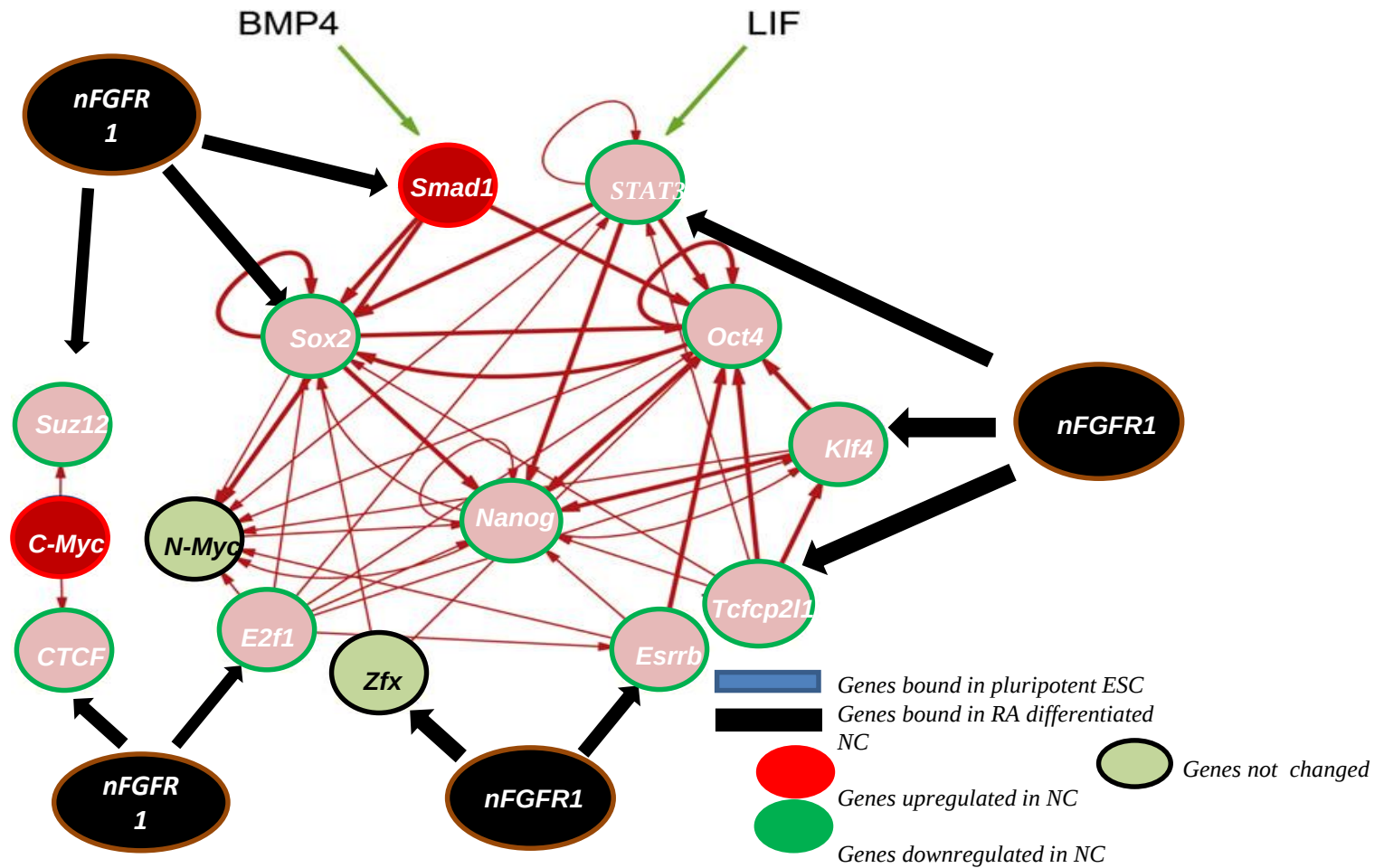
FGFR1 binding to several pluripotency genes in differentiating NC



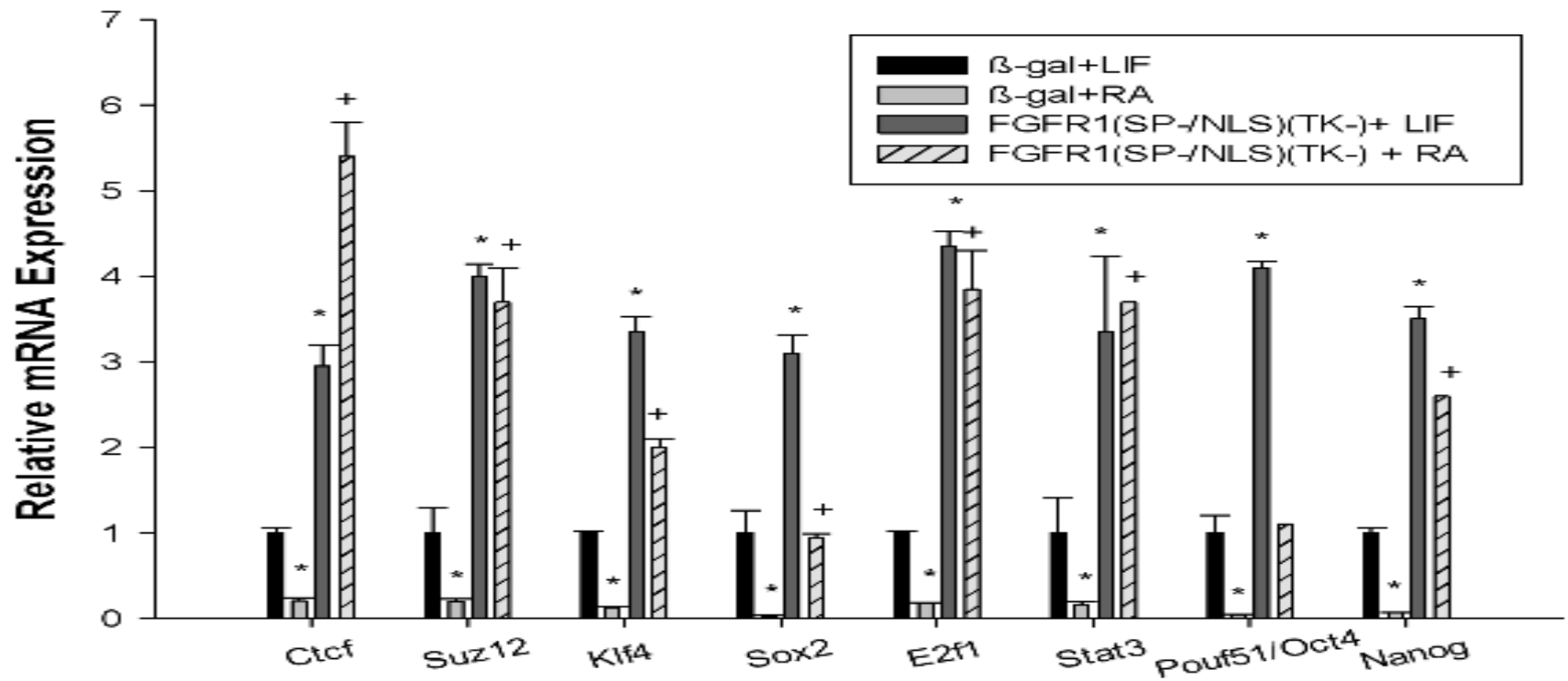
Active pluripotency network in ESC - nFGFR1 targets few genes



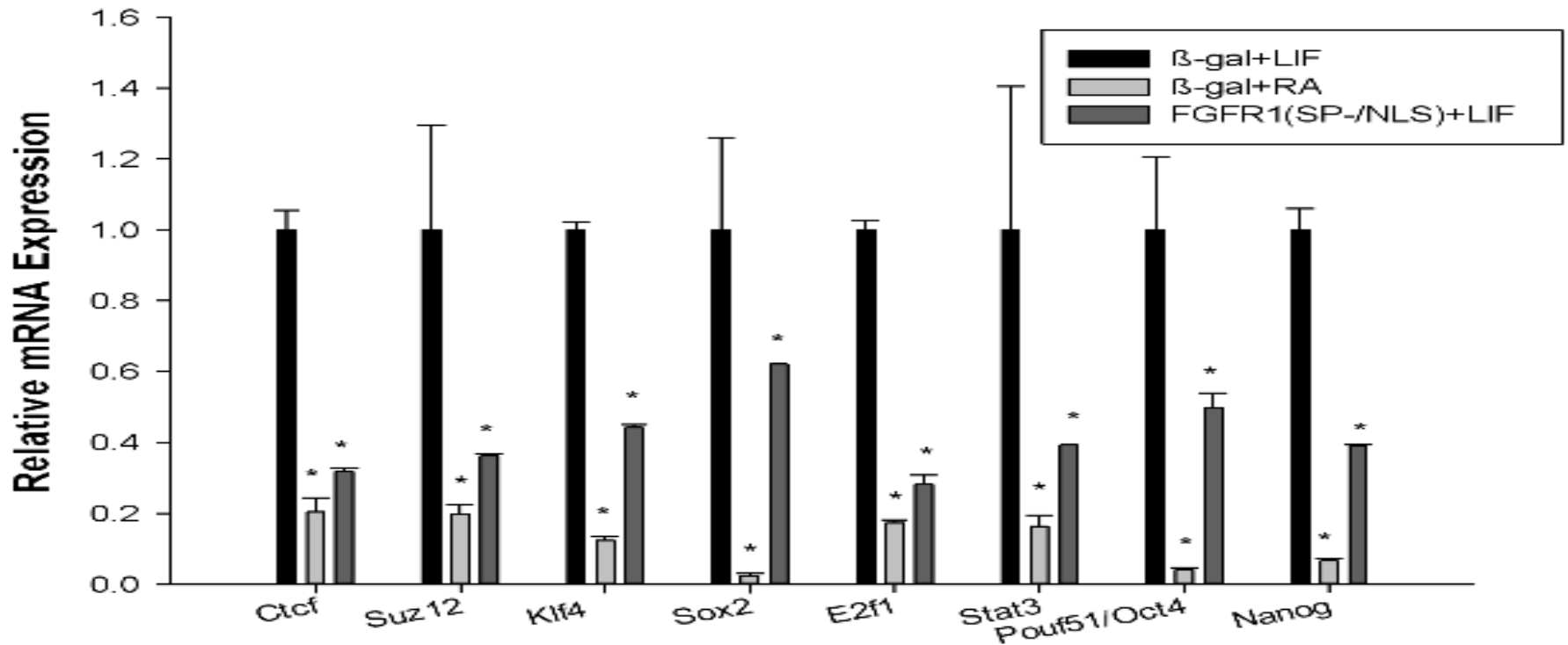
nFGFR1 turns off pluripotency network in differentiated ESC (NC)



nFGFR1 represses pluripotency genes during neuronal programming

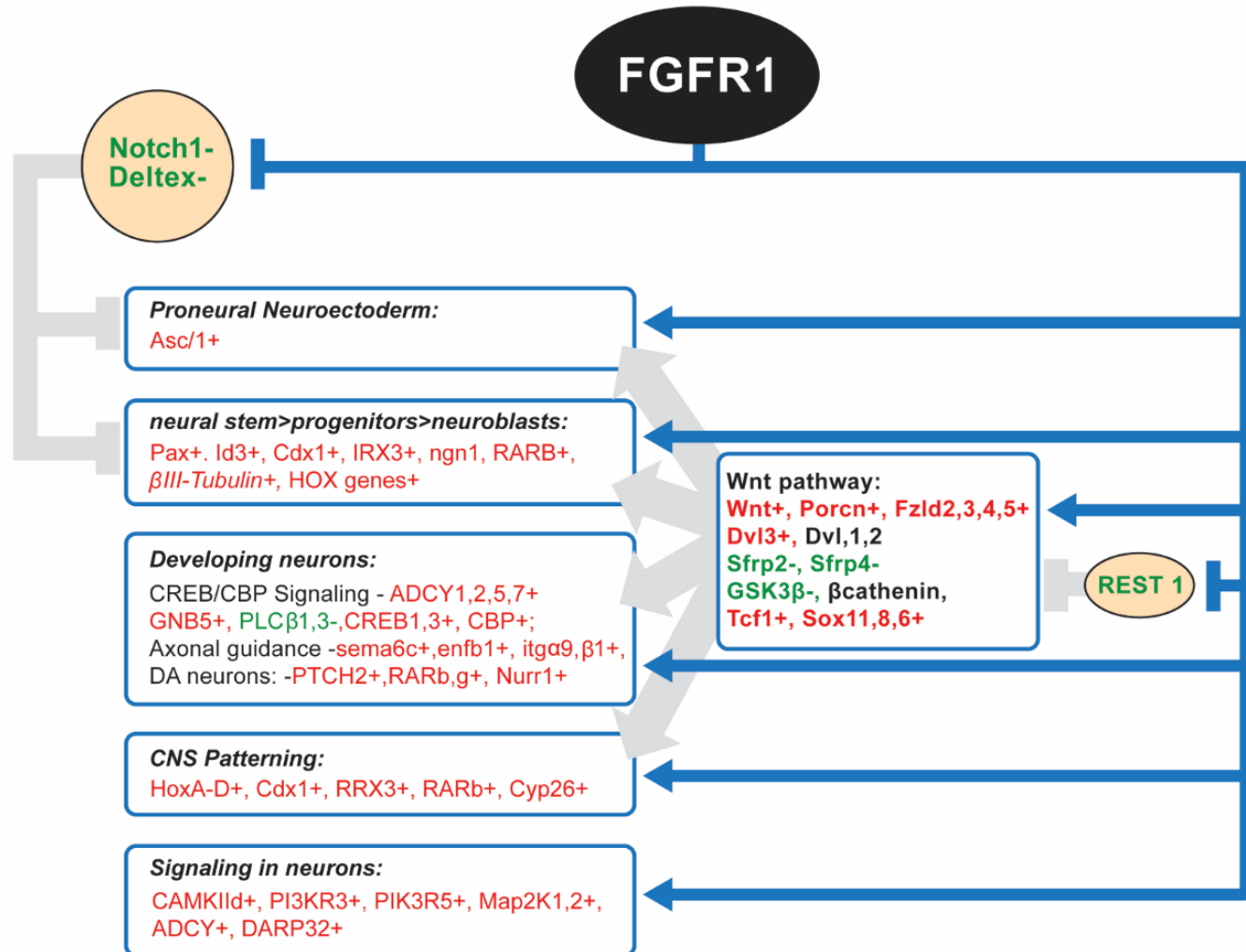


Nuclear active FGFR1 (NLS) downregulates core pluripotency genes in the absence of RA



nFGFR1 controls multiple stages in neural development (Terranova et al., 2015) and linked database).

6

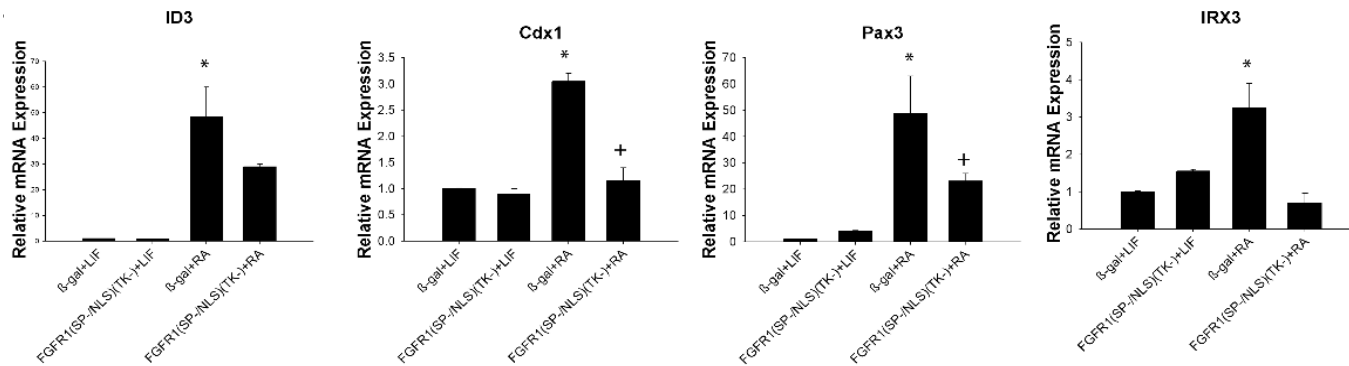


Decisions – brains or muscles?

*n*FGFR1 upregulates **neuronal** and downregulates **mesodermal** genes:

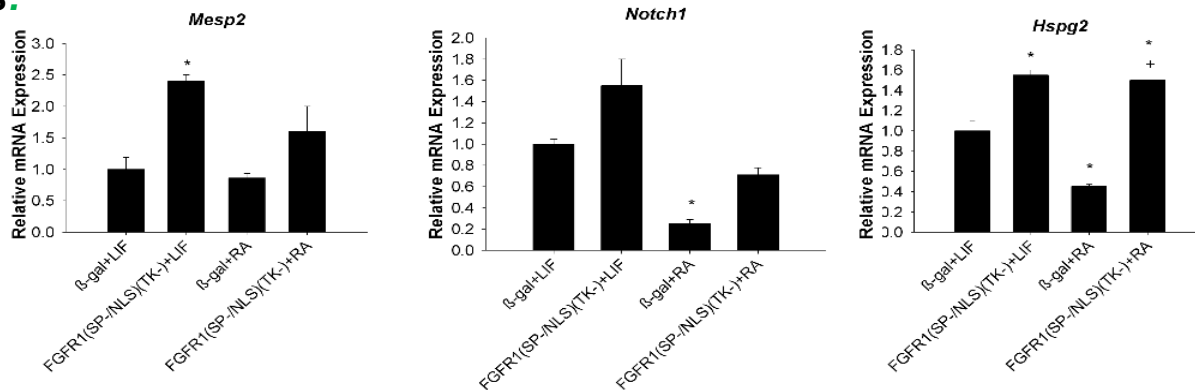
Neuronal genes:

Id3
Cdx1,
Pax3
IRX3
Res, *Pouf3*
Foxd3



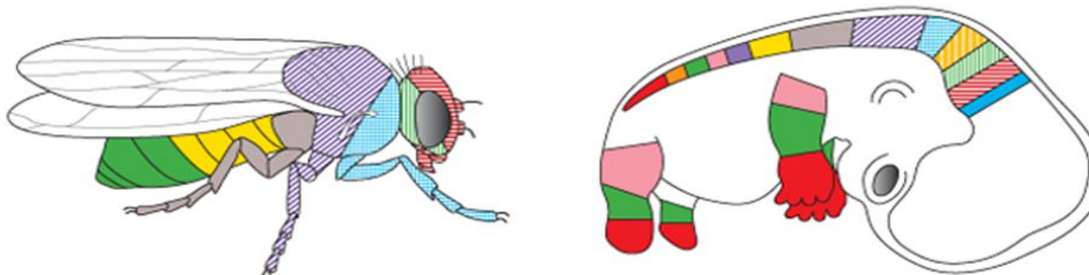
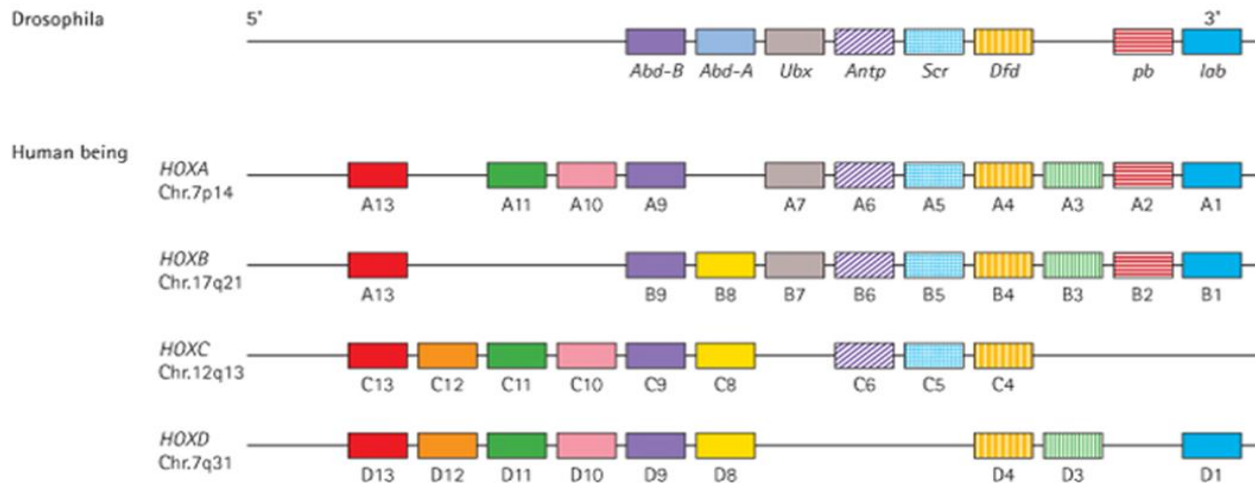
Mesodermal genes:

Mesp2
Ntoch1
Hespg2 (Perlecan)
DUSP6
Ifng,
Porcn
Ndk1
FGF23/FGF23

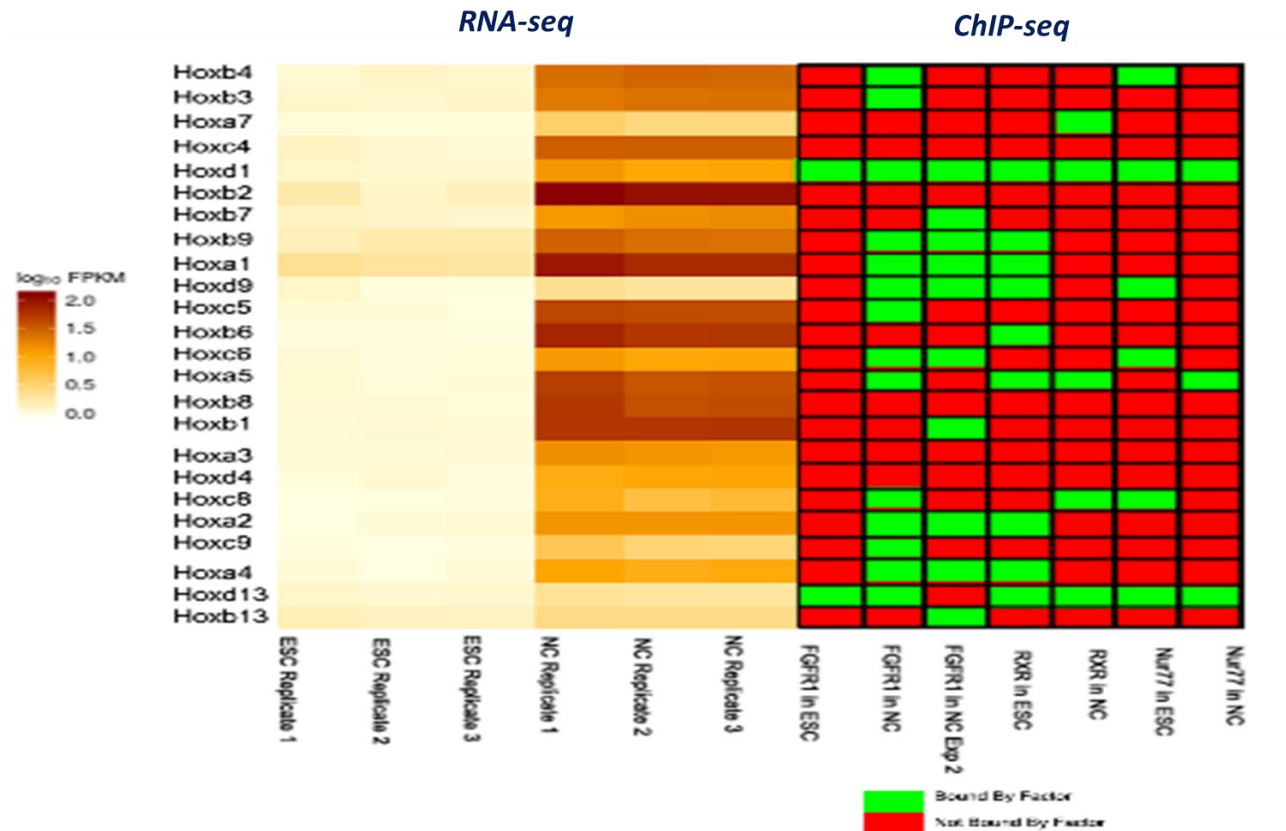


Building body parts and axes

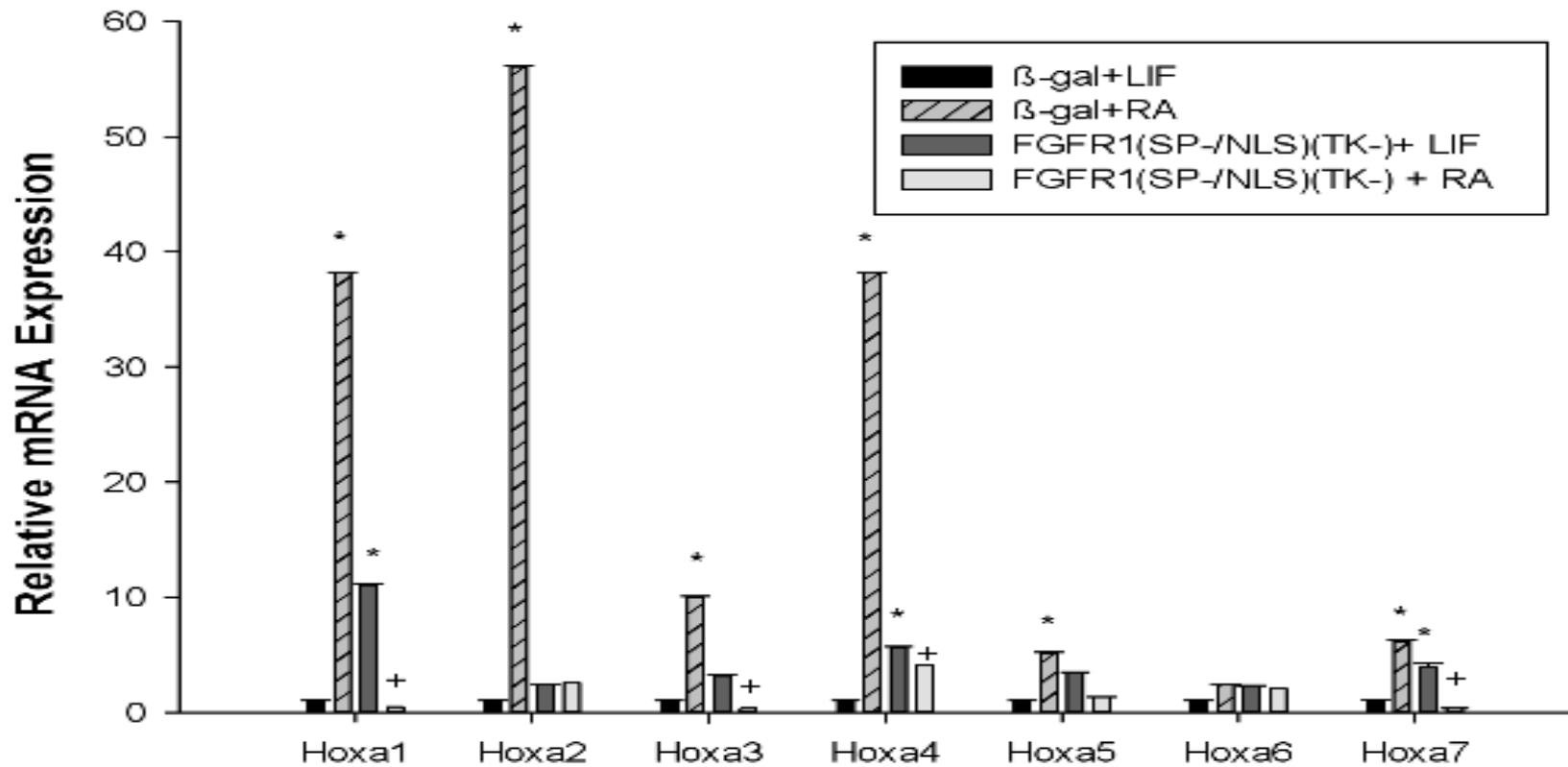
Hox genes - architects of body axes, segmentation, limbs, nervous system, musculature and skeletal system



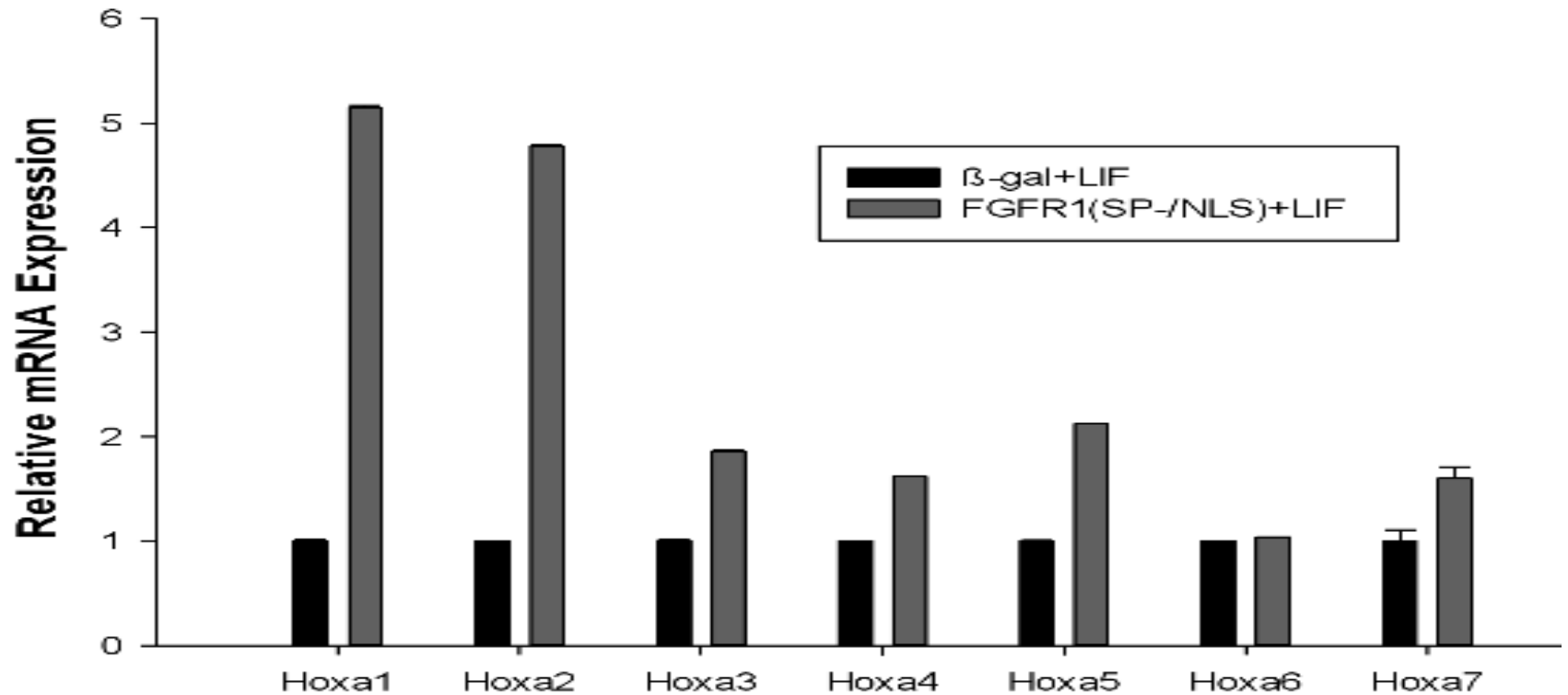
Nuclear FGFR1, RXR and Nur77 binding and gene activities in the Hox clusters in ESC and NC



Dominant negative nuclear FGFR1 (NLSTK-) blocks RA upregulation of core 3' Hoxa genes



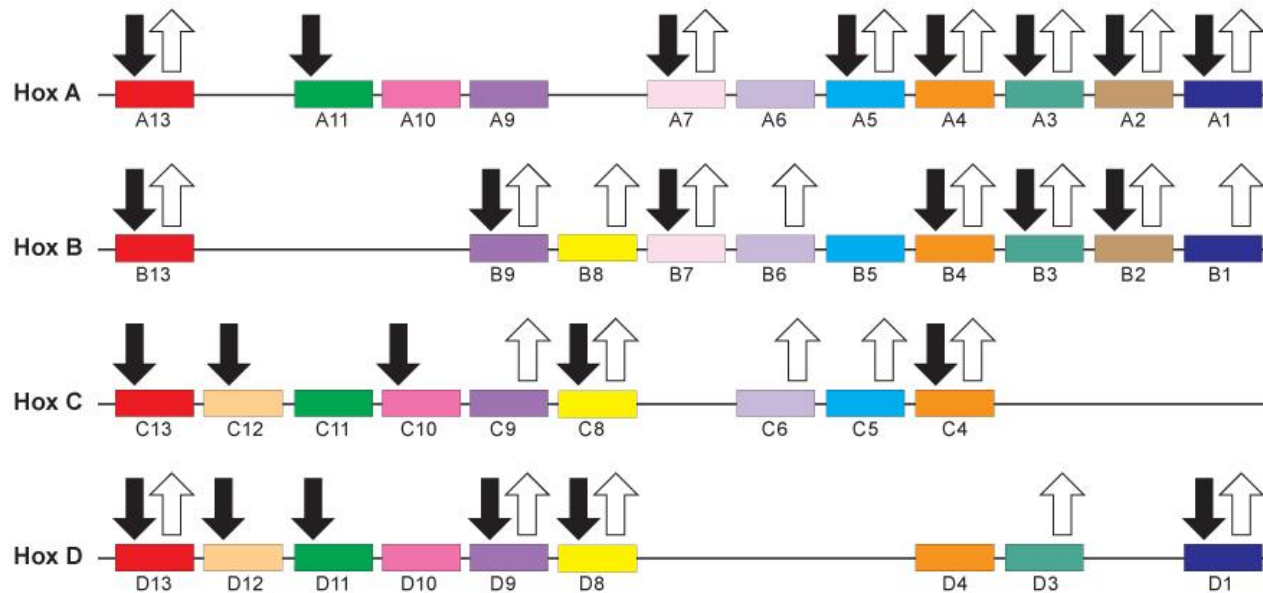
***Nuclear active nuclear FGFR1 (NLS) upregulates core 3' Hoxa genes
in the absence of RA***



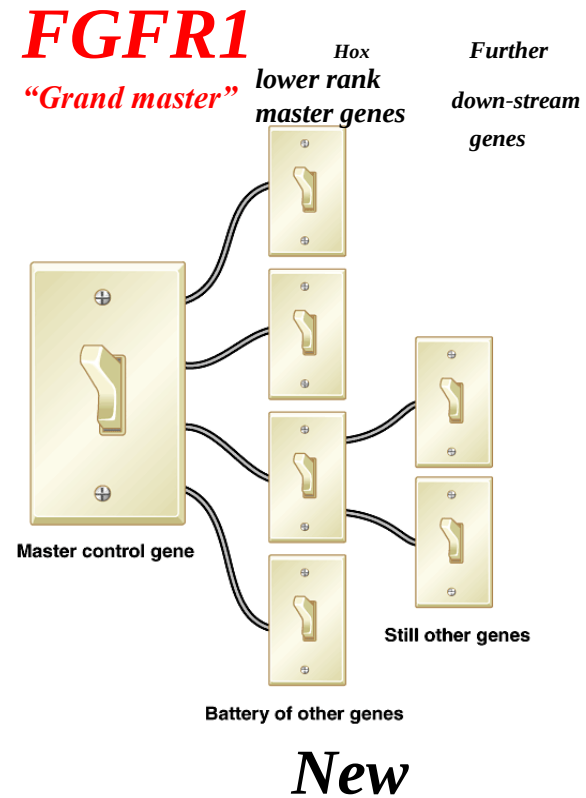
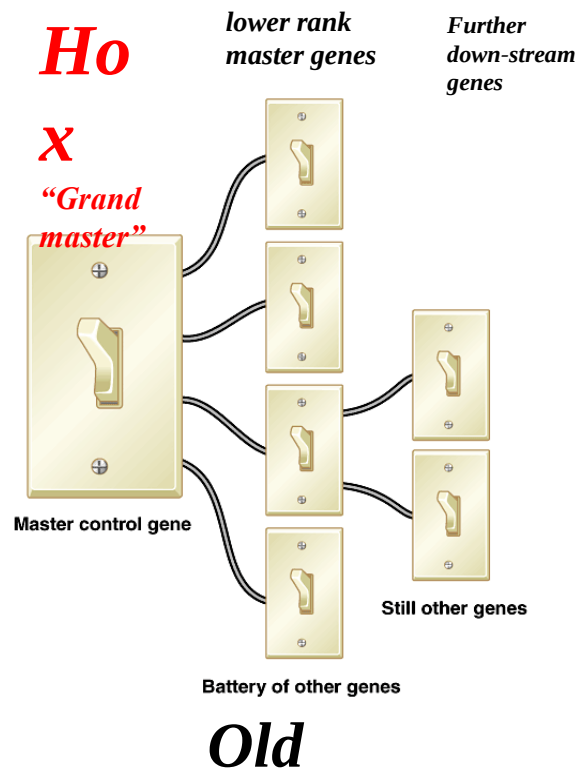
nFGFR1 directly upregulates Homeobox (Hox) genes in NC

↓ nFGFR1 binding to promoter

↑ Upregulation of Hox mRNA



Change in the Hierarchy of Master Genes



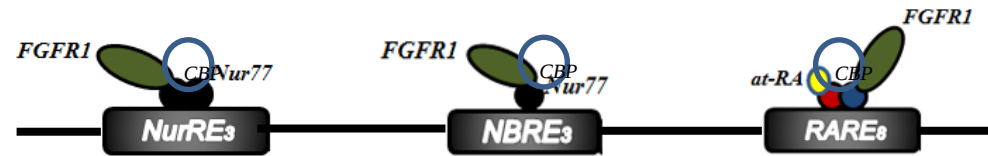
3C

Chromatin Structure

Brandon Decker

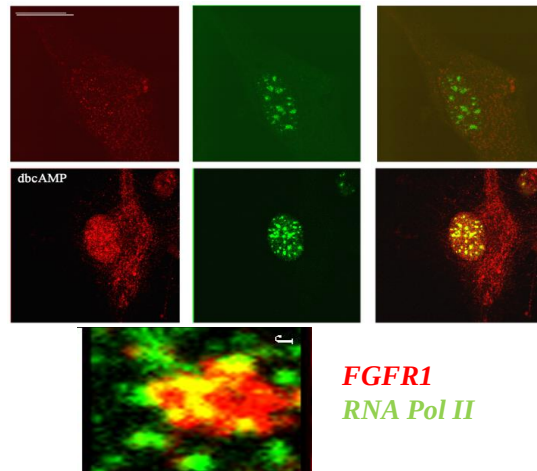
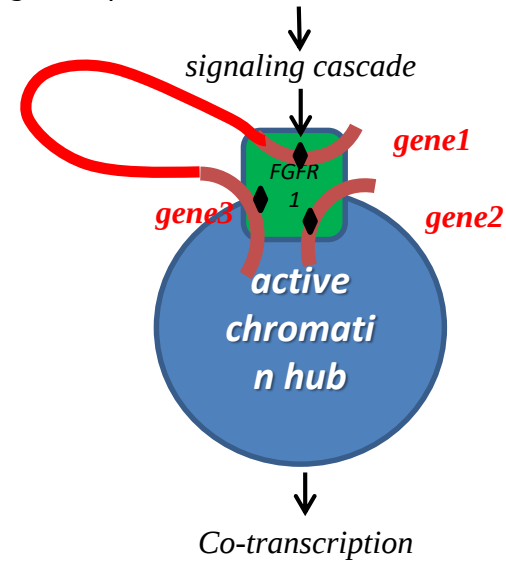
How to coordinate regulation of the thousands of genes?

"Cis" model

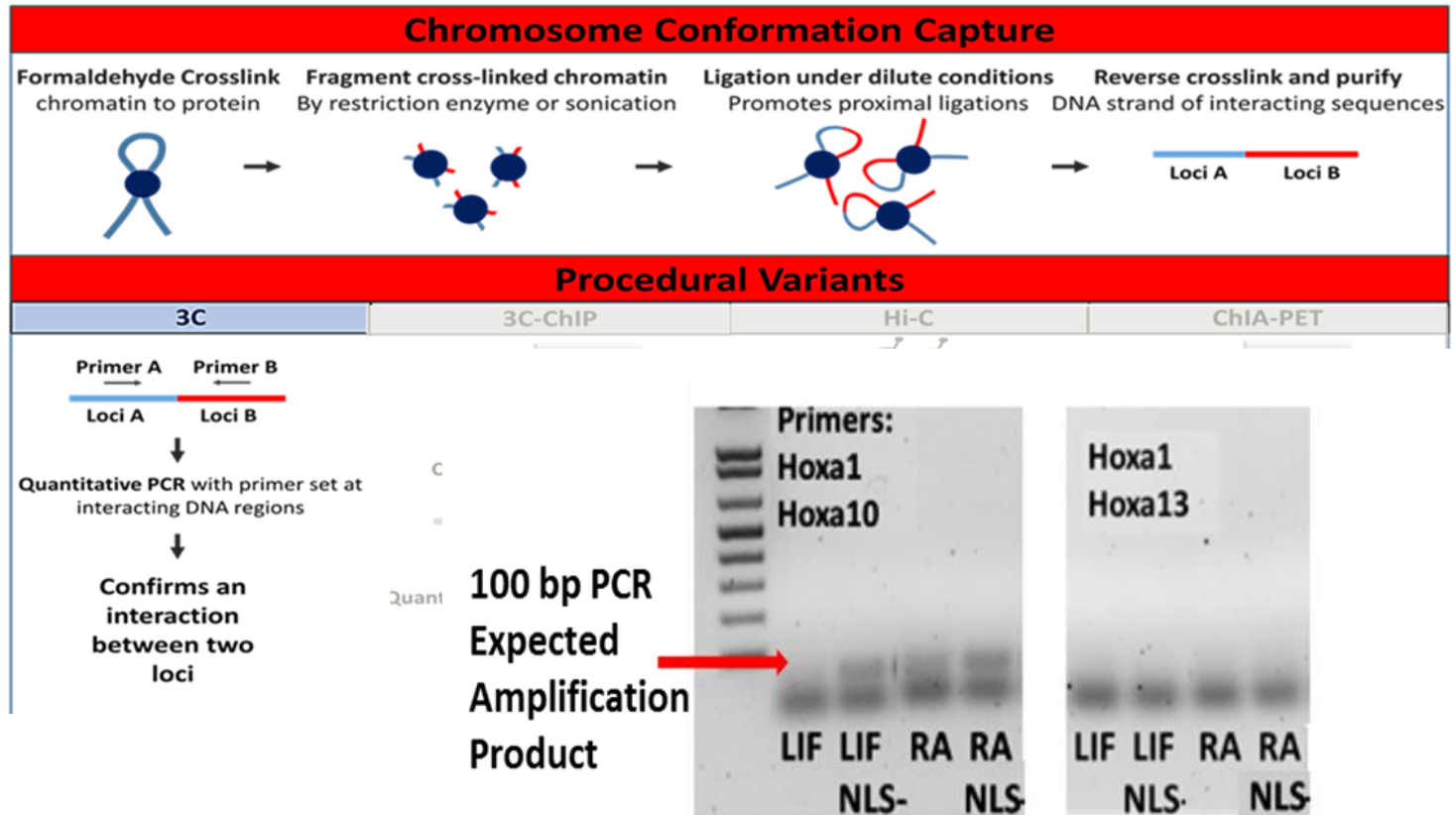


"Trans" model

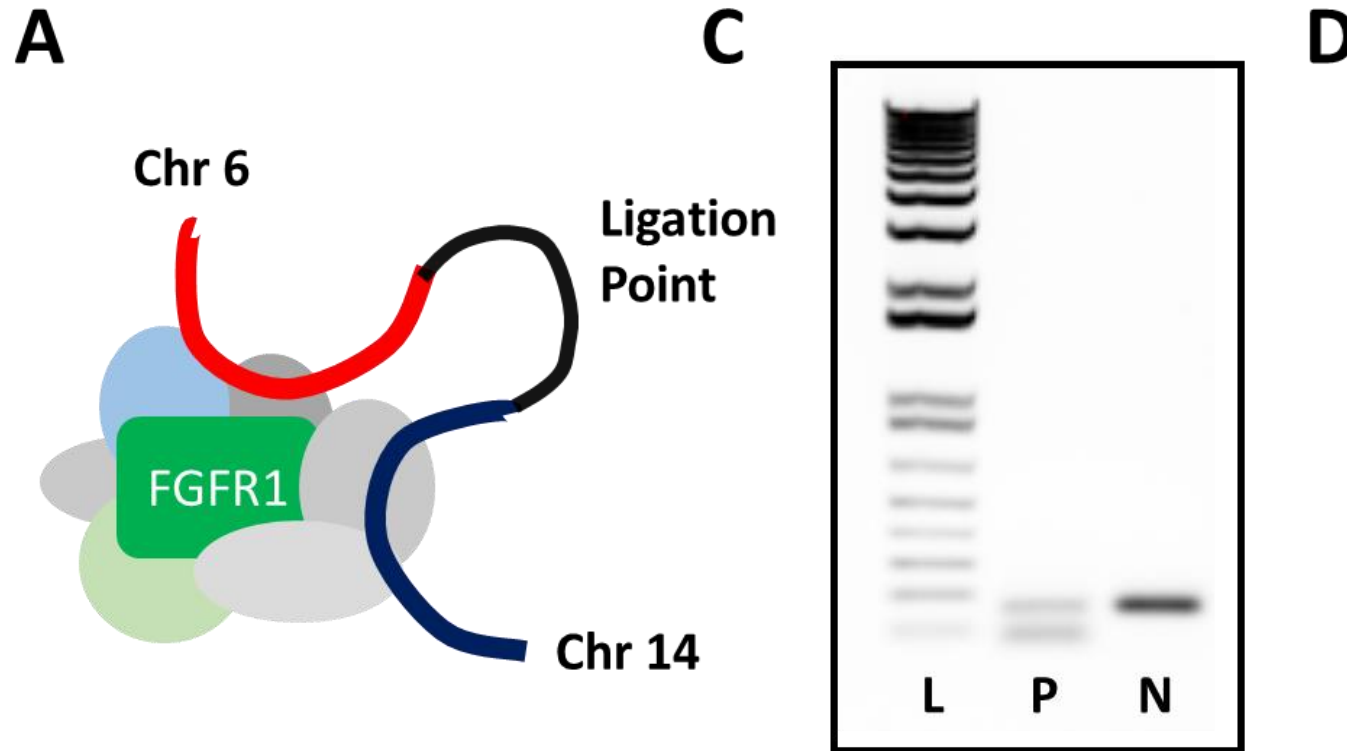
growth factors, hormones, neurotransmitters



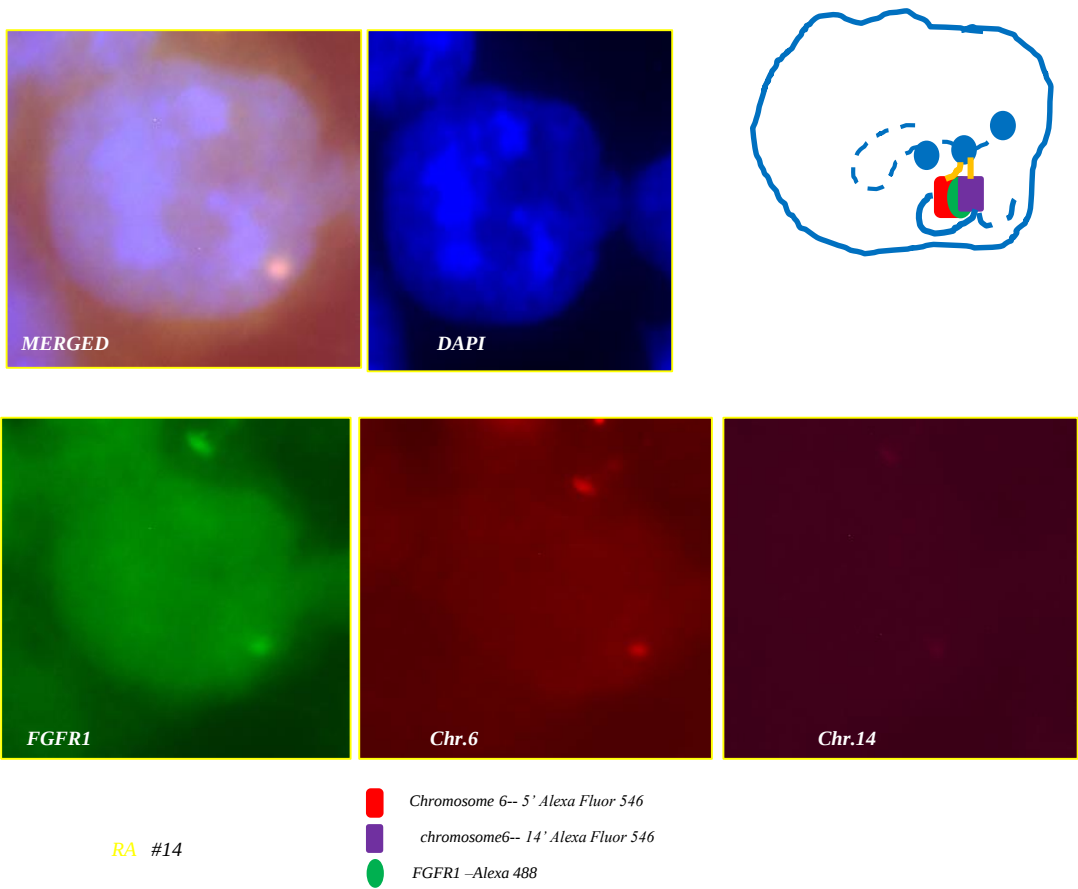
FGFR1
RNA Pol II



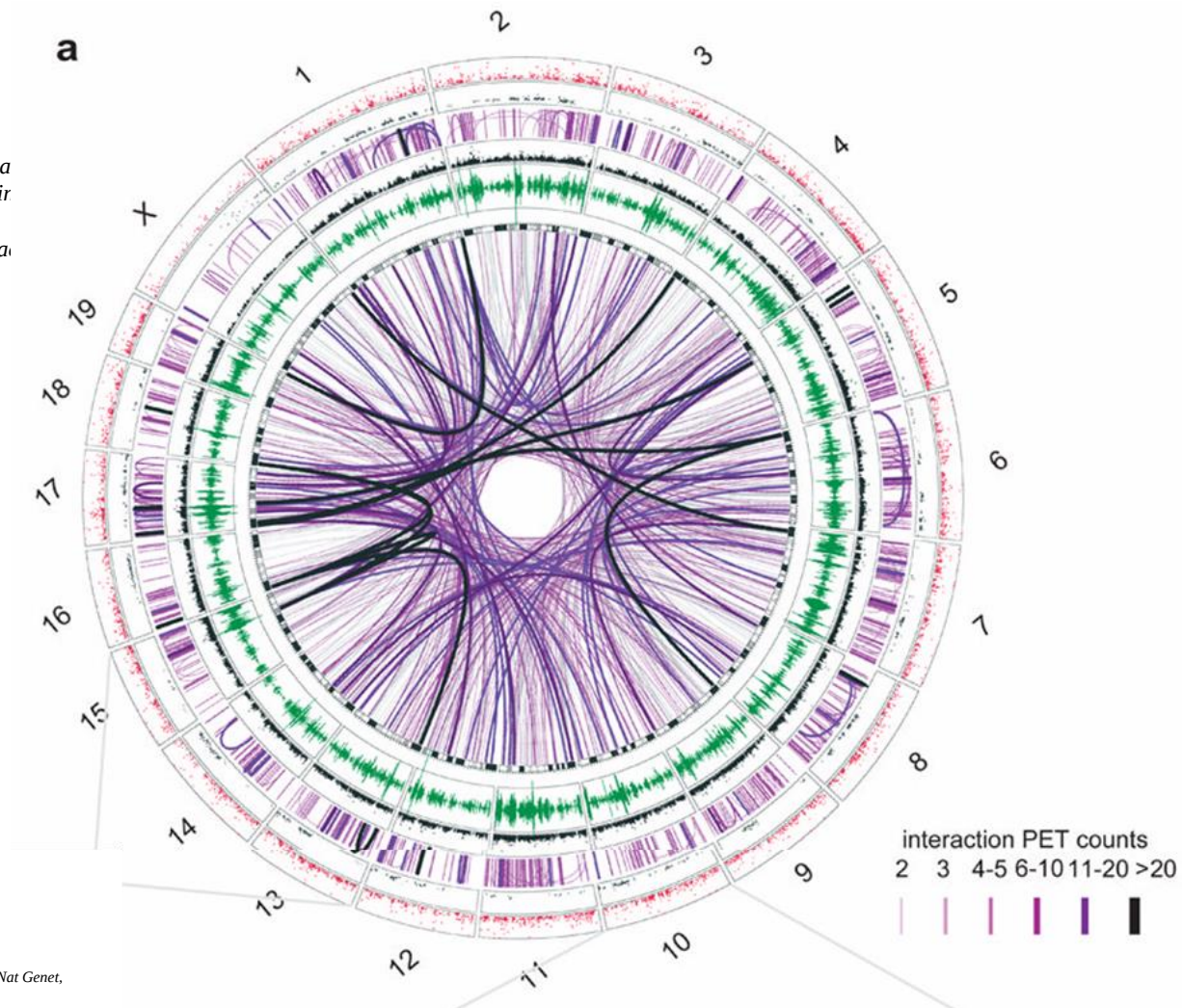
Chromatin Conformation Capture – 3C



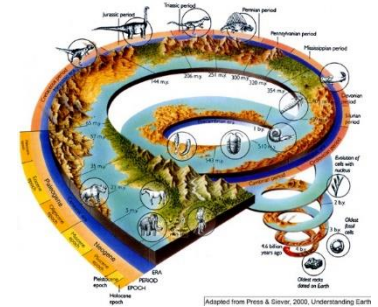
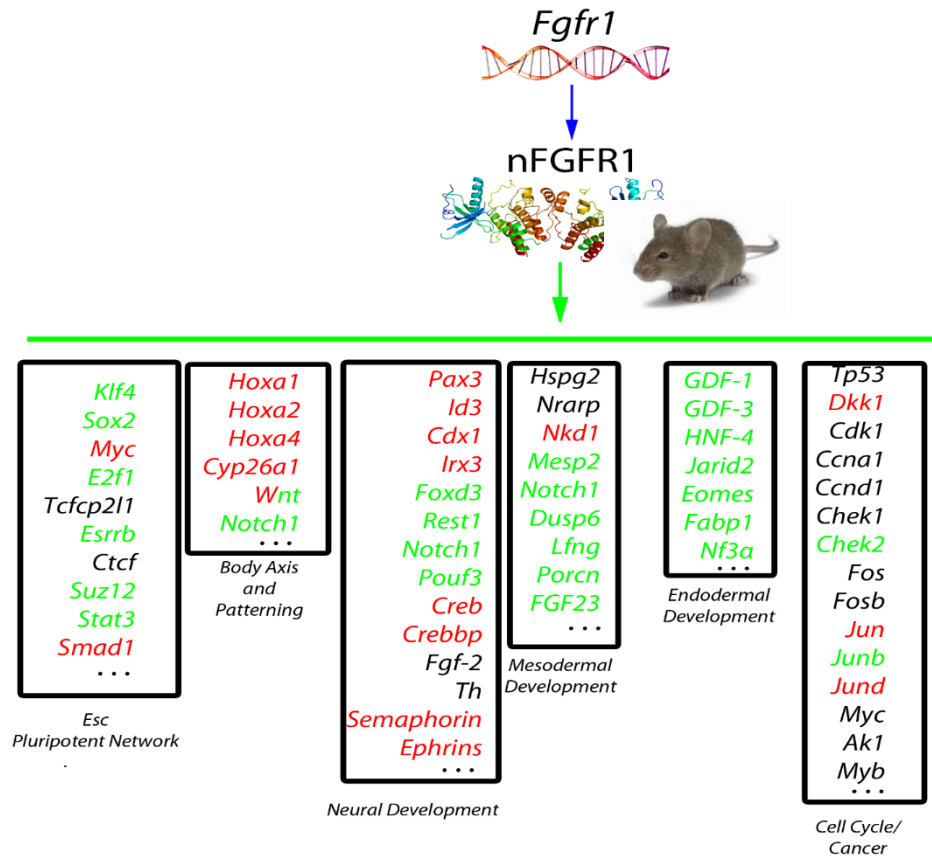
In Situ Hybridization/Immunocytochemistry verifies interchromosomal interactions involving nFGFR1



Track I : **ChIP-seq p300** – genome-wide p300 binding
 Track II: **ChIP-seq LAD** – genome-wide LAD binding
 Track III: **ChIA-PET CTCF** – Intrachromosomal intera
 Track IV: **ChIP-seq CTCF** – genome-wide CTCF bindir
 Track V: **RNA-seq** – Genome-wide gene expression
 Track VI: **ChIA-PET CTCF** – Interchromosomal intera



Evidence based theory of ontogeny – Nuclear FGFR1 a new type master regulator of ancient and new genes



Global developmental gene programming involves a nuclear form of Fibroblast Growth Factor Receptor-1 (FGFR1). 2015, PLOS One

New Theory of Ontogeny

The End