

SUPPLEMENTARY ONLINE DATA

Neuregulin-1 β induces embryonic stem cell cardiomyogenesis via ErbB3/ErbB2 receptors

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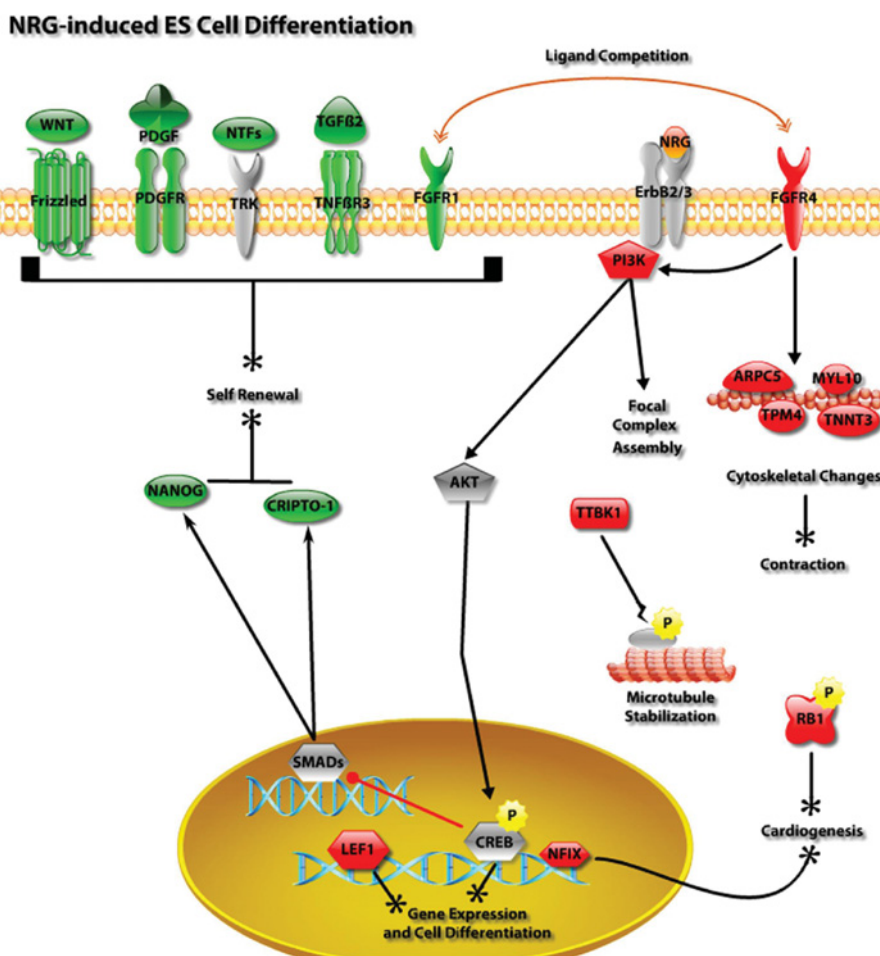


Figure S1 Inferred signalling pathway based on gene expression analysis, laboratory evidence and literature searches

Gene expression changes induced by NRG-1 β from day 0 to 2 in mESCs were used to build an inference pathway using known signalling events as provided by various online databases, including Protein Lounge (<http://www.proteinlounge.com>), the Kyoto Encyclopedia of Genes and Genomes (KEGG; <http://www.genome.jp/kegg>) and literature searches. NRG-1 β is shown in orange, bound to the ErbB2–ErbB3 heterodimer, the latter of which as inferred was on the basis of qPCR and siRNA experiments. Proteins that were presumably down-regulated in response to NRG-1 β treatment as defined by a lower gene expression are shown in green and those most probably induced are shown in red. Molecules coloured grey were not identified as differential by microarray analysis, but were either inferred to be so based on literature or, in the case of CREB activation, inferred from Western blot analysis or other traditional laboratory techniques. As shown, genes associated with cellular self-renewal were down-regulated, and genes involved in cardiomyogenesis, focal complex assembly, microtubule stabilization and cytoskeletal changes associated with contraction were up-regulated.

Received 19 June 2013/20 December 2013; accepted 24 December 2013
 Published as BJ Immediate Publication 24 December 2013, doi:10.1042/BJ20130818

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