

Supplemental Table 1

Key Genes				
GeneName	GeneSymbol	EntrezGeneID	regulation	p-value
Key genes selectively regulated in Sox9-EGFP^{Low} cells in uninjured intestine by IGF1				
inhibitor of growth family, member 3	Ing3	71777	down	1.22E-02
junction-mediating and regulatory protein	Jmy	57748	down	1.50E-02
DNA-damage regulated autophagy modulator 1	Dram1	71712	down	4.71E-02
ataxia telangiectasia mutated homolog (human)	Atm	11920	down	4.93E-02
ephrin B3	Efnb3	13643	down	3.46E-02
Indian hedgehog	lhh	16147	up	1.28E-02
frizzled homolog 10 (Drosophila)	Fzd10	93897	down	2.40E-02
MAD homolog 4 (Drosophila)	Smad4	17128	down	1.55E-02
bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	12168	down	2.16E-02
Key genes selectively regulated in Sox9-EGFP^{High} cells in uninjured intestine by IGF1				
RAD21 homolog (S. pombe)	Rad21	19357	up	4.44E-02
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Atp5j	11957	down	4.80E-02
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	Atp5j2	57423	down	1.76E-02
ATPase, H+ transporting, lysosomal V0 subunit D2	Atp6v0d2	242341	down	8.62E-03
cytochrome c oxidase subunit IV isoform 2	Cox4i2	84682	down	7.90E-03
cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	110323	down	2.91E-02
cytochrome c oxidase, subunit VIIa 1	Cox7a1	12865	down	1.45E-03
cytochrome c oxidase, subunit VIIa 2	Cox7a2	12866	down	1.38E-02
cytochrome c oxidase subunit VIIb	Cox7b	66142	down	3.72E-02
cytochrome c oxidase, subunit VIIa	Cox8a	12868	down	4.28E-02
cytochrome c oxidase, subunit VIIb	Cox8b	12869	up	3.81E-02
NADH dehydrogenase subunit 3	ND3	17718	down	1.74E-02
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	Ndufa12	66414	down	2.17E-02
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	Ndufa2	17991	down	1.18E-02
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	Ndufa5	68202	down	5.75E-03
NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	Ndufab1	70316	down	2.12E-02
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	Ndufb3	66495	down	1.31E-02
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	Ndufb9	66218	down	4.25E-02
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	17993	down	1.85E-02
ubiquinol-cytochrome c reductase, complex III subunit X	Uqcr10	66152	down	2.45E-02
ubiquinol-cytochrome c reductase binding protein	Uqcrb	67530	down	3.94E-03
ubiquinol-cytochrome c reductase hinge protein	Uqcrh	66576	down	2.78E-02
Key genes selectively regulated in Sox9-EGFP^{Low} cells in regenerating intestine by IGF1				
family with sequence similarity 175, member A	Fam175a	70681	down	4.16E-02
meiotic recombination 11 homolog A (S. cerevisiae)	Mre11a	17535	down	3.47E-02
E2F transcription factor 6	E2f6	50496	down	3.87E-02
retinoblastoma-like 2	Rbl2	19651	up	2.44E-02
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	Smarcd2	83796	up	4.51E-02
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	Smarcd3	66993	up	1.36E-02
Kruppel-like factor 5	Klf5	12224	up	3.22E-04
BCL2-associated athanogene 5	Bag5	70369	down	2.03E-02
baculoviral IAP repeat-containing 3	Birc3	11796	up	1.14E-02
Key genes selectively regulated in Sox9-EGFP^{High} cells in regenerating intestine by IGF1				
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	Atp5j2	57423	down	2.67E-02
ATPase, H+ transporting, lysosomal V1 subunit E2	Atp6v1e2	74915	down	3.92E-02
ATPase, H+ transporting, lysosomal V1 subunit G2	Atp6v1g2	66237	up	2.26E-02
ubiquinol-cytochrome c reductase, complex III subunit VII	Uqcrq	22272	down	2.55E-02
hemopoietic cell kinase	Hck	15162	up	3.06E-02
snail homolog 2 (Drosophila)	Snai2	20583	up	6.23E-03
Spi-B transcription factor (Spi-1/PU.1 related)	Spib	272382	up	3.28E-02

Supplemental Table 1: Key genes regulated by IGF1 exclusively in Sox9-EGFP^{Low} or Sox9-EGFP^{High} cell populations in uninjured or regenerating intestines. Selected genes significantly and selectively regulated by IGF1 in Sox9-EGFP^{Low} or Sox9-EGFP^{High} cell population isolated from uninjured small intestine or at day 5 post-radiation.