

Supplemental Table S1. Sequences for oligonucleotides

For expression vector construction

ETV4 full	F	GAATTCATGGAGCGGAGGATGAAAGGC
	R	GCGGCCGCTAGTAAGAATATCCACCTCT
ETV5 full	F	CTCGAGATGGATGGGTTTTGTGATCAG
	R	GCGGCCGCTTAGTAAGCGAAGCCTTCGG

For reporter plasmid construction

ETV4 promoter (-2486/-2019)	F	CTCGAGCTTCAGAGCCAGCTTGCCAG
	R	AGATCTGTGACATTGAAGCATCCAGCC
ETV4 mutated Oct3/4 binding site	F	CTAAAGTCCACGACGTGGGTTTATAATTTA
	R	TAAATTATAAACCCACGTCGTGGACTTTAG
ETV5 intron 6 region	F	CTCGAGGAAACCGGAAGCAGAAGCTA
	R	AGATCTACTGGCTTTCAGGCATCATC
ETV5 mutated Oct3/4 binding site	F	TGGTTACTGTGCCGCTGCCTCCCTG
	R	CAGGGAGGCAGCGGCACAGTAACCA

For EMSA assay

ETV5 Oct3/4 binding site	F	TGGTTACTATGCAAATGCCTCCCTG
	R	CAGGGAGGCATTTGCATAGTAACCA
ETV5 mutated Oct3/4 binding site	F	TGGTTACTGTGCCGCTGCCTCCCTG
	R	CAGGGAGGCAGCGGCACAGTAACCA

For biotin-labeled DNA pulldown assay

ETV4 Oct3/4 binding site	F	CTAAAGTCCACATTTGCATTTTATAATTTA
	R	TAAATTATAAAATGCAAATGTGGACTTTAG
ETV4 mutated Oct3/4 binding site	F	CTAAAGTCCACGACGTGGGTTTATAATTTA
	R	TAAATTATAAACCCACGTCGTGGACTTTAG
Gbx2 ETV4/5 binding site	F	AGCCAGAGCTCTTCCGGGTGAACTGA
	R	TCAGTTCACCCGGAAGAGCTCTGGCT
Gbx2 mutated ETV4/5 binding site	F	AGCCAGAGTTAGCATTTGTGAACTGA
	R	TCAGTTCACAAATGCTAACTCTGGCT

For expression analysis

ETV5	F	AGCCACCATGTATCGAGAG
	R	TGCATGATGCCCTTTTCATA
ETV4	F	CCACCAGGATCAAGAAGGAA

	R	CCCTGAGGAGATGTGAAGGA
Gata6	F	GCGCCTCCTCTCTCCTTTTT
	R	GCGCTACTCCAACCTGACTT
Fkl1	F	GGCGGTGGTGACAGTATCTT
	R	GTCACTGACAGAGGCGATGA
Tbx5	F	GGACCCAGTCCCTTGAATGG
	R	TCCAGGCTGAGGAGTTCTAGGC
Sox1	F	AGGGCCCAAGAGTAAGGAAA
	R	ACTGAGCACAACCCATCCTC
Pax3	F	ATAAGCCCAGGACACAGAGTTGTG
	R	GTCTAGTCTGTGGAGGCCGAAAC
p16/p19	F	AGAGCGGGGACATCAAGAC
	R	AGAAAAAGGCGGGCTGAG
p15	F	AAGGACCATTTCTGCCACAG
	R	TCGTGCACAGGTCTGGTAAG
p57	F	GTACCTCCGCAGCAGAACAG
	R	ACAGACTCGCTGTCCACCTC
Tcf15	F	CAGCTGCTTGAAAGTGAGGG
	R	TCCTCCGGTCCTTACACAAC
Gbx2	F	AGACGGCAAAGCCTTCTTG
	R	AGCAGTCTGACCAGGCAAAT
LRH1	F	GAGCAGAGTAACCGAAACAGG
	R	TGAACAGCACCAGGAACTTG
Zic3	F	CCATGCATGAGTTGGTTACG
	R	TATAGGGCTTGTCCGAGGTG
Baf60c	F	GGACCCATCAGACCAGAAGA
	R	TGCCACATCTGTCATCACCT

Supplemental Table S2. Pathway analysis

MAPP Name

PE 15-2/PE 9 (ratio > 2.0)

- 1 Mm_Striated_Muscle_Contraction_WP216_33380
- 2 Mm_Prostaglandin_Synthesis_and_Regulation_WP374_33046
- 3 Mm_Statin_Pathway(PharmGKB)_WP1_35542
- 4 Mm_Regulation_of_Actin_Cytoskeleton_WP523_34401
- 5 Mm_Myometrial_Relaxation_and_Contraction_Pathways_WP385_35258
- 6 Mm_Hypertrophy_Model_WP202_32968
- 7 Mm_EGFR1_Signaling_Pathway_WP572_35717
- 8 Mm_Methane_metabolism
- 9 Mm_O_Glycans_biosynthesis
- 10 Mm_Focal_Adhesion_WP85_35638
- 11 Mm_Glycerolipid_metabolism
- 12 Mm_Ovarian_Infertility_Genes_WP273_32715

PE 15-2/PE 9 (ratio > 0.5)

- 1 Mm_Cytoplasmic_Ribosomal_Proteins_WP163_34552
 - 2 Mm_Nitrogen_metabolism
 - 3 Mm_Phenylalanine_tyrosine_and_tryptophan_biosynthesis
 - 4 Mm_Non-homologous_end_joining_WP1242_35403
 - 5 Mm_Proteasome_Degradation_WP519_33047
 - 6 Mm_Glutathione_metabolism
 - 7 Mm_Glycine_serine_and_threonine_metabolism
 - 8 Mm_Thiamine_metabolism
 - 9 Mm_Polyol_pathway_WP1265_32726
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