

Table S4. Bioinformatic prediction for Grsf1 and β -catenin co-regulated genes (intersection of Tables S1 and S3)

Probe Set ID	Gene symbol	wt-mut	het-mut	Total matches	Locations	Gene ID	Sequence
99561_f_at	Cldn7	0.6	0.7	1	383	ENSMUSG00000018569.1	GCCCGCACCTGCCGCGCCACCCGCCAGCTCCCTGTG CCGCGCACCCGACGCTGGGGCCCAAGGGCCCGCAT ACTTTCCTGGGGGCCACGCCCTAACGGCCCTCCAC TTCTTTGGGTAGTCTCGGAGCACGCCGTAGGAAC CGCCCGGCTTCGGGGACCGCTTTTGTCTGGAACC AGTCCTTCGGGGCAAGCCGGTTCCTCTGTGTGA GAGTGTGCTTCACCGAGGGGACGATTTGTGT ACCTCGGTAAACAAGATTTGTAGTTACCCGGTCCA AAAAAAATCTTTTCTCCTTTGGGTGACTTAAAT CTCTATCCAAATTTTCTGTGTGTGCTGCCCGG ATTTTGTTTTGTGTGTGTGTGTGTGTGTGTGTGT GTCGCCCTCCCGCGCTCCCGTCTTTTCTGAGAC AAGGAA
94036_at	Cdc42ep4	-0.6	-1	1	286	ENSMUSG00000041598.1	AACAATCGGCGCGGTGCCCCGAGGGGGCGTGT GCGCACAGACTTCTCCATGAATAACCGCTGAGTTC GTCGGTAGTGGTAGAGGGGTGACCGTGTCTCC CGTGTACACACTGCTTTAGGCGCCACCCGGTGT CGCCCGCGGGGAGAAAGGAGGGCAAGAGCCGGC TGGAAGGCAATAGCCTAAAGAGCAAATACTCCCG CCCGTCCGAGCCCTTCTTCTCCCGCCCGCCGC CTCCCTTGAAGACTTGGAGGCAAGGCCGCAAGA GGCGAGGGTGGGGCTGGGCCGAGCTGGCGTCCC TTAGAACTTGGACGAGGCTTTACGCGGGGGGAC CTGCGCGCGCCCGGTACGTCGGAAGCATGGGC TCGAGGCTTTTTCAGGGCGAGTAGGTAGCGTGTG GTTAATGATTTAACCCTGGCTTGGGACGTTGAAG GCTGCGATCCTGATCTCTGGCTCCTCCCATTCCT GGAGCGCCCCAGCCGAGGAACAAATCTGCCCTC CTGTGCTGTGGCGTCTGTGCTGGAGCTGCCTTT CCCTTTGGGGGACCCCTGGTGTGTGTGGCCCTC GATTGCCCTGTCTACCTTTGCATTGTGGACTTC AGATCTGACCCATACTGCTGTGTGTGTGGGAG TGCCAGCTCCCCCGACCCAGCAGCAG
94449_at	protocadherin gamma subfamily B, 1	-0.5	-0.6	2	47,62	ENSMUSG00000024463.1	CCTGTCAGATCACCATCCCATATCGTCAAGTGCAT TCTACTGTCAAAGGGTACAGTGGCTGAGGGTCTGT GCCCTGCTCCACGGCAGCCCCGAATGGTGCAC CATGGCACCCTGATATCTTAGGTTCCTGGGTCCAC CCACAATGCTGCTACTCGTGAACCTCAGTGTGAGT CATTTGGCAAGTCTGGGTCTTCTTCTCCCGAGAG TAATCACACAGAGCGCTCACACTCTCTCCTCTGG GAGCCTGTGTGAGAATTAATTACCAGCACATCCC GAACTGGTGAAGTCTGGCTGTAGGAGAATGTGT GGTGGGATACATCTCCTGGAAGGGACCTGCGGAG TTAGAAATTAAGCGTGGCTGGCGAGCCCTGCACA TTGAGCTGGTTGGGAGAGGGCTACGGATCAGTTGG CTCTGTCTGGAGCCTGTAGAAT
164467_f_at	Gjb3	1.8	0.8	1	20	ENSMUSG00000042367.1	GAGATGCCTCCTTAATGAGTAGGGTAGAAAGGAA AGCATTCAGGGCGGGAGGAATCAAGGCCAGGTCTG AGCAGAGAGAGGCAAGGTGGGCACAGCCCCCGAA CCCTGAGCAGGCACC
97013_f_at	Cyba	0.5	0.5	1	48	ENSMUSG00000006519.1	GACTTGCGAAGTGGGCTGCAGAGTTGGACCGGGCT GCTGCGTGTGCGCAGGGTCCCTCGTC
93941_at	T	-1.4	-1.4	1	95	ENSMUSG00000023865.1	GGCTCCGCAGAGTGACCCTTTTCTTGGAAAAGCG GTGGCGAGAGAAGTGAAGGTGGCTGTTGGGTAGGG AGTCAAGACTCCTGGAAGGTGGAGAGGGTGGCGGG AGG
100009_r_at	Sox2	1.3	1.3	1	318	ENSMUSG00000047245.1	GTGTTTGCAAAAAGGAAAAGTACTTTGTGCTC TTAAGACTAGGGCTGGGAGAAAGAAGAGGAGAGA GAAAGAAAGGAGAGAAAGTTGGAGCCCGAGGCTTA AGCCTTTCCAAAACTAATCACAACAATCGCGGCG GCCCGAGGAGAGAGCGCTGTTTTTCATCCCAA TTGCATTCGCCCGTCTCGAGCTCCGCTTCCCCC AACTATTCTCCGCCAGATCTCCGCGCAGGGCCGTG CACGCCGAGGCCCGCCCGGCCCTGCATCCC GGCCCCGAGCGCGGCCCCACAGTCCCGGCCGGG CCGAGGGTTGGCGGCGCCGCGGGCCGCGCCCGC

100479_at	Dnmt3a	0.7	0.8	1	62	ENSMUSG00000020661.1	<p>CCAGCGCCCGC</p> <p>CCACAGGCAGAGCCGCCTGAAGCCCAGCGCTGAGG CTGCACCTTTCCGAGGGCTTGACATCAGGGTCTAT GTTTAAGTCTTAGCTCTTGCTTACAAAGACCACGG CAATTCCCTCTCTGAAGCCCTCGCAGCCCCACAGC GCCCTCGCAGCCCCAGCCTGCCGCCTACTGCCAG CA</p>
104672_at	Frzb	-1.1	-1	2	10,105	ENSMUSG00000027004.1	<p>GTGGGGACCAAGGGTTCGTCTATGGATCCAGAGCC GGGGTGGAGTGGGAAAGGTGTGCGGCTCCTGTG GGGAGCTGCCTGGGGCTACAGCATCACAGATAGAC AGGGTCTCACACTCCAGTCCCCGAAAACCTCAAAG CCTTCTCGGAAGGAGGAGCCGGAGGGCAGGGGACC GCCGGGCGGAGCTCTTGTCGGCCGAGGTGGGAAGG CGCAGCTGCGAGCCAAGGCGCTGACCTCCTCTGAG CTCCTCTGGCCGCTCGCAGGATCTCCCGACCCTG CAGGACTTGGCAAACCTCCACCTCCCGTCCCATA GTCTCCACCCCCACAAATCTCCTCCTCGGAG GTCCCTATCCATCTCACTTTGCAGAATTTATCGC TTCTTCCAACACCTTTTGGCAACCCCCAGAATC CGAGTCCCTAACTGAATTTGACTTTTGTTTTAT TTCTCTCTGGCTTCCTCTCTGCCCTCATCTGA TTGATGTGCTAAGGCTGATGTCTCTGCCAGAGCGA GAGGAATAAATAGATGCTGCCCTAGAGGCTT AGACGCTTGGGAAGAGCAGCCGGCCGAGCAGGCA CCGGGCTCCGCCAAGCTAGTGGACCGACCTGGGA GCACTTGGATCCAAGAGAATGTGATTTGCCAGG GGTGGGGCAGCTCCCCAGGTCGTGGGATCACCC CTCGGAACCGCAGGGGGAGACTTCGGAACGAAAGT GTCTCCCGCTCCGTCGCTCGGCTGCGCCCTGCC CATCTGTGGGACC</p>
93543_f_at	Gstm1	0.7	0.7	2	14,72	ENSMUSG00000004038.1	<p>CTGCCTTCCGCTTTAGGGTCTGCTGCTCTGGTTAC AGACCTAGGAAGGGAGTGCCTAATTGGGATTGGT GCAGGGTGGGAGGGACCCGCTGTTTTGTCTCTGCC CACGTTTTCTTAGTAGTCTGTATAAAGTCACAACT CCAAACACACAGGTCAGTCTGCTGAAGCCAGTTT GAGAAGACCACAGCACCAGCACC</p>
93888_at	Hoxb1	-1.7	-1.8	1	31	ENSMUSG00000018973.1	<p>TGACATACTGCCGAAAGGTTGTAGGGCAAGAGGGT GTCTCCCCAAACGGCCCGACCCTCCTTCGGCCCTC TAC</p>
98419_at	Meox1	-1	-0.7	1	14	ENSMUSG00000001493.1	<p>CACTCATCACTCAGGGTCCCCGGGAAGGGCTTGT CAGTATGGGTGGGTCCAAGGTAGGACAGTCAAAT GTTTCAGCATGGTAGGAACAACCTCCGTGCCCGATA GTCAGCGTGTGTCGGGGCAGGAAGGCAGACGTGA AGCCTAGACAGGTGTGGACACGCACATGTGTGTTC CTGGCCACGTGTTGTGGAATTTGAGGCAAAATTT TTGTTTTGGTTCCTGGGGTAAAGTTTCCATTCAAC AATTTCCCTACTGTTAATTTTCTTTAATTTT AAATTACAAAACCTGACTAGAAAAAGCGCAATAC CTTTGAAAGGACTGGGGCAGGCAGTGGACAGCAG</p>
93953_at	Prss12	0.7	0.6	1	2	ENSMUSG00000027978.1	<p>CGAGGGTGGGGTGGAGTCCGGACTCCGGGCTACAG AGCTCCTGGCGCTCATCGCCTCTGGCGCTCCAGCC TTTGTCTCGCGGGCTGACCCTTTGGGTCCCGGTG TGA</p>
98427_s_at	Nfkb1	-1.3	-1.1	2	206,229	ENSMUSG00000028163.1	<p>CGCGGGCCGGTTCCTAGCAGCGCAGGCCGGAGCTCA GGCCCCCGCCGCGCCCGCCCGCCCGCGCTTCTC CGCCCGCGCCGAGCCATGGCGCGCCGCTGAGCCG CCGCCCCCGCCCGCCGCGCCCGACCCGGCTCGGG CTCCCGCCGGTCCGCGCCGCTCCGCAGCGGGAGCC CGCAGGCAGGAGAGGCGCGCCGATCTCCAGGG TACCCTCAGAGGCCAGAAGAGGGTGTCTCAGAGCCCT GTAACTGGAGTTTGACGGTCTGAGCTGCGCATC TTCACC</p>
103818_at	Slc7a7	0.6	0.6	2	43,187	ENSMUSG00000000958.1	<p>AGCAAATCAGCAAAAAGAGGATCTAGCGAATCAGT TGGTTTCAGGGTTGGTTCTCATACAGGCATCTCA GCGCAGGGACATTTGAAACTGAAATCAGAGGGGAG AGACTTTGGGGGTCAGGGGGAGGCAGAAAAAGTT TTACCAAACCTGCCTCATTCATGCCTGTCTGTGTC ATAACAGGTTGAGGGTTCAGCTGTCTGATAAATAA GAGGGCAATGCGAGCAAGCTGGTGAAGGTCTTCTT TCTTTCGCC</p>

92997_g_at	Sox17	-0.8	-0.7	2	733,1020	ENSMUSG00000025902.1	<p>CCCATTTAGTGAAGAACTGAAATATGGCCCACTC ACACTGCTGGCGGGTCTGAAGTGCGGTTGGCCCA ACACTCCTCCCAAAGTATCTATCAAGAGAATGGTC AGCAGAAGTTAGATCTAGTTTTTTAGAGAAATCAAC CAAGACAGGGAAGACAGAGAAAATGCATTCTGGAC CCGCTACTGTTTTCAATCGTCAATTCAAACAAAAC CCGTAGTTTTATTTAAAAAAAAAAAAACCGGAAA GAGAAAATTAGGCCCTGAGATCTTTGAAAAGATGC CCATTACTAGATACAAAAGAGAAGAGTCACTGTGG AGGTGAGGGACTGCGTCCCTGCTTCTGAGAGGCAG GAGAGCTACATGGGGAGACTGTCTCAAACTAACA ACAGAAGAGATAGAATTTTTTTTTCTTAAAGAGC ACCTGGCTAGAGAATCGATTTGTAAAAATTGCTATT TCTACCCCTAGAGTTTTCCCTTGATTAACATCTGAA ATGCATTTTTTTGTTTTACTTTCAAGCTAATGTT TTTCAGAAAAAATAAAAAGCTTTGAGGAAAAGCA CATTATCAGTTAGATTTAAGACCAATTGCTTTTAA ATTACCAATTTAAAATAATCATTTTTTTTATTCTTT AAAGCAGATTTAATTTTACCCCTTTGTATGAATC TTACAGACCTGGAGTTTTAACTACTATCACTGATC TCTACACACAACCTCCAGCTTTAAATGGGAGGGAG GGTCACCACTGCTTTATAACATAACAAATTAGAGA AAAGCTGGCTTCTGTATGAGTTCTTTGGAGACAAA GTAGCTCCAGAACTGCAGACCAGAAGCTATCAAAA ATCTCTGTGCTTTTTTGGAACTCCAGTAAGCCAG ATTTGGTCTCTGAAATAATACAGGAAAACCTCAGC ATGTCACCTCATGGATACAATGAGCAGCACCTCCA GACATCTGAATTCAGCCTTCTATTTCCCAAGA GGTCTTGGCGCCAGCGCCGGCTCCAGCCAGi</p>
96771_at	ErbB3	1	0.8	1	57	ENSMUSG00000018166.1	<p>GCACCGTGAGACTGGGACCACAGCTGCTGCTCA ACTGGGGAGTACAAATTGCCAAGGGTATGTATTAC CTCGAGGAACACAGCATGGTG</p>

Highlighted are those transcripts that showed a significant β -catenin-dependent deregulation and contained a *Grsf1* consensus-binding site in the 5' UTR.