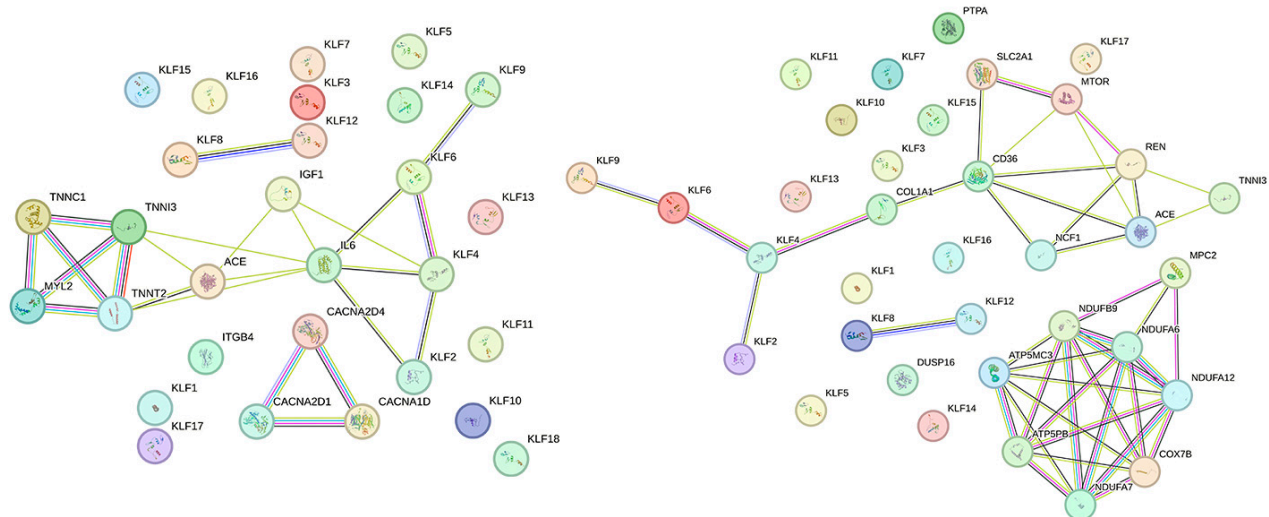


Supplementary Figure S1. CACCC-box binding partners (Non-KLFs).



**Supplementary Figure S2.** KLF and CACCC-box gene interactions: (Left) Hypertrophic cardiomyopathy, (Right) Diabetic cardiomyopathy

**Supplemental Table S1.** Python analysis results of 3044hits from Signal Search Analysis Server resulted in 40 representative sequences.

Region	Sequence
FP001062	CAGTTAG- <u>GGGTG</u> -CGCTGGAGA- <u>GGGTG</u> -GGGCCCCACTCCGCCA- <u>CACCC</u> - CAACGGTCCTTCCCCCTCCTCACTACTCCCGCCCC- <u>CACCC</u> - CCAATGGATCTGGGACTGCCCCTTTAAGAGTAGTGGCCCCTCCTCCCTTCAGAGGAGGACCTATTAGAGC CTTTGCCCCGGCGTCGGTGAAGTCTGCGGGAGCGCCGACCTACACCAGCCAACCCAGATCCCCG AGGTCCGACAGCGCCCGGCCAGATCCCCACGCCTGCCAGGAGCAAGCCGAGAGCCAGCCGGCCGGCG CACTCCGACTCCGAGCAGTCTCTGTCTTCGACCCGAGCCCCGCGCCCTTTCCGGGACCCCTGCCCCGCG GGCAGCGCTGCCAACCTGCCGGCCATGGAGACCCCGTCCAGCGGCGCGC- <u>CACCC</u> - GCAGCGGGGCGCAGGCCAGTCCACTCCGCTG
FP001404	AGCCGAGGTTCTGCTACTCCAGGAGCCGAGGTTCTAACGTGGTCTGCGTCCAGCGCCCC- <u>CACCC</u> - CTACTCC- <u>CACCC</u> -CTACCCC- <u>CACCC</u> -C- <u>CACCC</u> -TTCAACCCGCCCCCTACCCCAAGC- <u>CACCC</u> - CGTGGCCGCGAGCCAAGAGGTCCCTTTAAAGGCGCGAGTCCCGCCCCACTGCTCATTAGGGCTTTCGAT TGGCGGCTCCTGGGCGGGCGGGGCCCGGCTGGGCTCGGGGCTGGCTCGGGGCGGGCTCGGGGCCGGA TCGGCCCCCGCCCCCTTTGTTCGCGCTGCGGCGGGAGGTGGTGCC- <u>GGGTG</u> - GGAGGTGTGTGCGCTGTGCCGCGCCGTAGGGAGCGGGGTCGCGCCGCGGGCTGTGAGCTAGCTCCG CGCCGCGCCCGATGGCGCGAGGAGGCGCGGGGCCAGCCCCGGGGGGCGGGCGC- <u>GGGTG</u> - AGCCCC
FP006896	ACCCCTCGGTAATCCCGTACTCCCTTAGCGGGCGGGCCACTGCAGCGTGCCACCGCCCC- <u>CACCC</u> - CCATCCCCCATCCCCG- <u>CACCC</u> -CCCTC- <u>CACCC</u> - CCTAGCCCGCGGAGCAGCTGGGATTTGGCGCCCCCTCCTCGGTGCAACCTATATAAGGCTCACAGTCT GCGCTCCTGGTACACGCGCTTCAACTTCGGTTGGTGTGTGTCGAAGAACTGACTGCGCCCTGAGGAGA ACAGCGGAGAAGGTCCACCGAGCCTGGCGAAAGTCCGCTGAGCGGGCTGCTGTCGGAGCCACTCCG GGCTGCGGAG- <u>CACCC</u> - AGTGGAGACCGCGCTGGCTCAGGTGTGGGACCCCATCCTTCCTGTCTTCGAGAGGAGTCTCGCGTGG TGAGTATGCGGTGAGGACGTTTTTTTTTAAAGATACGTTTCATTCCCCGTGCTTATCGGG
FP009159	GTCCCAACTGGGAGGGGCCCTGGCAGCATGAAACCCC- <u>CACCC</u> - CCACTCTCTGCGACGGCCAGATGGAGGGCAGGAGGAACAGCGGTTACGCCCTGGCTGGGGCTGCAGG GGCTG- <u>GGGTG</u> - TGTTACTCACTGGCAGCATGGAGAACTGCATGAAGAGGCAGGTAAGTTCTGTGGCGGCCAGCACGTAGG TAAGCAAGATGACCGAGGACCGGCCCTAGAGCGCTCATCTGCCGGGGACCGGCCCTGGTCCCTGGGAG CCCAGCTCCCTGCATCCTGGACAGGCGCAGCAGGAGACCCAGGAGAGATCCAAGCAGGAGGCTGGC GGAGCAGGGGGCAAAAGTCCAGTTGATCCGGGCGAG- <u>GGGTG</u> -CTGAGTCACTGGGTCCAGGCAG- <u>CACCC</u> -GCCTGGCCTTGCTGCAAGAGAGGACAGCACTGCAGGACCCCTCCCCAGTGGAGCT
FP009252	GGTGAGTGTAGGCCGGCGGGGCCAGCGACGCGATCCCGCG- <u>CACCC</u> -CGTCGGGGGCCGTTAG- <u>CACCC</u> - TCGCGGGCGCTGCGCCCCTGCCGCCGCCCCGGGGCAACCCGGCCGCCGAAGAACCCTGCCCCGACGTGC CCGCTGCCGGCCTTAAAGGGCCCGTGACCGCTCCCTGCCCC- <u>CACCC</u> - GGGCCGTGGGGAGGCTGCGCCCCTTAAAGGCGCCGCGCCCTCCGCCCCATCCTCCTCGCGGGGGCTG CCGCTGCGGGCTAGGGCAGGCAGAGGTGCTGCAGGAGCCCTTAAAGGGGCCGGGAAAGTGTTCGCTGG AGTACCCACCGCCCTCCGCGGGCATCGTACCTGGCGGGGGGAGGGGGCAGCTAGCTGCCTCTTAAAG GGATAGCTCTGCCCTTGGGGGCACTGACTCGGCCGAAGAGGACTCCTAGATGTGTCCCCGGG
FP010074	GGCTGGGACTGGGGTCCAGGAGGCCCTACCCC- <u>CACCC</u> -TGTGAGAGGTAG- <u>GGGTG</u> - TGGGGAAGGCAGCAGGGGAGGATGGCAATAAGAGGGAGGCTGGGATGAGATCTCAAGCTCTGGGGTCG

	GTACTTCAGAGGGAAAGGAAGAGATTATAAAGGAAGGAAAGAGTAGGGAAGAGAAGAAAATGAGAAT TCCTATGTAGCAGGCTCTGTGCTGGGCACTGCACCTGCAGTCCGTTTTTTTTTGTGTGTGTGTAGAGTCTT GCTCGGTCGTCCAGATGGAGTACAGTGGCACCATCTCCACTCACTGCAGCCTAGACCTCCCGGGTTCGAG AGATTCTCGTGCCTCAGCCTCCTGAGTAGCTGGAATCACAGGCATGCACCACCACGCCCAGCCTGTCATT GATTTTTACCAAAATTTTCCACCGTTGGAAGGGACATTAGGCTTGGCGA
FP017185	AGACGGGTTTTAACCATGTTGGCGAGGATGGTCTCGATCTCTTGCCACATGATC- <u>CACCC</u> - GCCTCCGCCCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGTCATGGAGTGAGTTTTGA AGGCTGACTTTATTTGAGGTATTTGAGTCTGGTGGGGGGGAACCCACACACAGAGAGGAGGGATTCCA AAGTCGTTAATGGGGACCTGGGAAGGAGCATAGGACAGGGCAAGGCGGGATAAGGAGGGGCACCACA GCCCTTAAGGCACGAGGGAACCTCACTGCGCATGCTCTTTGGTGCCACCTCAGTGCGCATGTTCACTG GGCGTCTTCCCATCGGCCCCCTTCGCCAGTGTGGGGAACGCGGCGGAGCTGTGAGCCGGCGACTCGGGTC CCTGAGGTCTGGATTCTTTCTCCGCTACTGAGACACGGCGGGTAGGT
FP013339	GCCCTTCCTGCCTTCTTGCCGGGAGGAAGTAGTGAGCCCCAAAATCAGAGGCC- <u>CACCC</u> - AGCGCCCCAGAGGGCCTGGTCAGAGGTCTCCCTGCTCCCCAGGAGGGCAGGCGCCCCAGATCCTCTCC CCTCCTTCTCGCTGGCCGAGATAAGCCCCAGGGCCCCAGCCTGGCACAGACTGTGGGCACCAGTGGC TTCTGTGCAAGGACTGAAGT- <u>CACCC</u> - AGCAGGCTGCCCTTCCACAGGCGAGATCACCAGGTTCTGTGGCCAAAGAGGTGGAGCTGCTGCTGAA AACCTGGCTACCGGGGA- <u>GGGTG</u> - CTGTGCAAAACCATGTCTGGTATGGGGCAGGGACAGAGCCGGGAGGCGGCTGTGGCCCCACAGAA AGAGCCTCTTGCTCTGCCAGGATATCAGACTGTCTTTCCCCAGGCACTGCTACGATGGAGAGCCTAC
FP016445	GGCCAGCTCAGGGCACCGA- <u>GGGTG</u> -GCCGGGTCTGCTGTCAAGGTGAGGAGCT- <u>GGGTG</u> - CCTCTGCCGGGGCCCTGGCCCAAGGAGAGTGTACGGGGAAGGCTGCAGCATGGCC- <u>CACCC</u> - AGGACTTCTGGGGATGAGTCTTGTTTTCTGTTTTATAGAAACACAGATCTTTGTCCTAACACAAGGTTT CCCTTTGGTTTATGTGGTTTCTCTGGTTCTGCCACCACCACCTCCCCAGGCCGGGGCCTTCCCATCCCTG CCCAGTGGGGAGTGGGAGGAAGAGCCTGGGACAGTGGCCATACGTCCCGGGCTGATTTCTGGATTGGGG GTTCTGGGGACCAGGGAGGTGCAGGTGTCTGCAGTGTGAGAGAGCCGCTGGGCTCGCCAGGTGTTGC CTGAAGCCCTCCGTGGCCTCTTGCCCTTGGA CTCTGACAGGAGGGACACC
FP000345	CGTTTT- <u>CACCC</u> - TGGAAGGAGTTTGGGTTTCAAGTGTGACGAGGCGCTATTAAAGAGTTTAAACATGGAAATTACTCGA TCTGATGTTGTGTAGTGTCTGTTTGTAGTCATCTTTCCAACTATAATACATTTTTTTTTTCTAAAAA TGGTCGTTAAAGCAGCCTAGGACTTAGGTCAATTGCGGTGGTCACTTGACCGCCTGTGAGGAGCGGCCG GTG- <u>GGGTG</u> -GATCGGACTGGGCGTGGCGGGGGCTCAGGAAGGA- <u>GGGTG</u> - GCCCTACCCAGCGGGCTCGGCTCGGGGCCTCCGCGCAGTTGCGGGTCTT- <u>CACCC</u> - GCCGGCTCCAGGTAGGCTACTCCTCAGGTAAGCCCCGCCGCCAGCCGCGACGTCGTCGAGACAGGCAC CGCCCCCACTCGTGGCGCGAGTAGTCCTGCCCTCCGCGTTGTCTCCGGCCG
FP010429	CTGCAGGAGAGTGGCTTTTATTAAAGCTCTTTTGCTTCTTAGAGAATGTTATCACCACTTAACATCCTCTG CCTCCAATTTAGTGCACTTTAAGTCCAGAAA- <u>CACCC</u> - AGAGTAAGTGGCTTTTCTGTCTCCCTGTTCTGGGAAGTATGAAGGACTGCCCCGAAAAGAGTACAGGG AGGGGGGGATTCTTGATCCATGCACAGCGATGTGAGCTGAGGTGCAGGCACCAGACCTAGGAATTCTTA GAAAAATAGTCAGGAAGCATTAGACACATCAAATGTTAAACGAGTCCTGATTATGATGATAATGATGA TGATTTTGGTGGTTGCAATAGCAAAGCCTTAAGTATGAAGGAGACTTGCCAGCTGGAATACAGGTCCGT AGCAGCATTAAAGTATCTAGAGGAGCTGCAAATATTATTTTTTGTGTGCTATTTTATTTCTTT
FP009059	ATGCAGATTTCTCTGAGCTCTTAGCGCCCCGAGAAGGGGGAGAAAAACAGGATATTTAGGCAAACAA ATGAAAGAAGTGCTGCCCTGAAAGG- <u>GGGTG</u> -GTGGTGGGGAG- <u>CACCC</u> - CCAAGCTGCTCGCAAGTTCTGATTGGACGCAAGCATTAAACCGGAGGGCTTTGTGGTCTGGGTCACTG TGTGTTTTTGTAGATTCAATTTGTTGAGGAATTTCCCCTAGCCTTGACCCCTTGACAGCTCCCGCTCCTA CTCAGTGTGGGGAGAAGTAGGGAGGCCTTAAGCGAAGAGATGGGTCTGCATTTGGAGGAGCCGGAC

	ACTGTTGACTTTCCTGATGTGAAATCTACCCAGGAACAAAACACCAGGTGATCCCAGTGGCCGAGCCAG CAGTGGACAGAT- <u>CACCC</u> -CTTAGGTGGAAGCCCAAAGCGGAGGGCACTGTATTGGTCT
FP005350	CTCAGAGCTGAGGTGGGAGATCTGCTCTTCCAGCCCGCCTCTCCTCCTCCAGCTCCCCAGCTCCACTCAA ATTCAGTCCCCCTCCCCCTGCC- <u>CACCC</u> - CCGCCACTCGGTGACTAAGAACTGCTGCAAGCAGGCAAACCTCCGAGCAGTTTTTAAGAGGCTGGAAGG AGACATAAGAGACTTCAGCTGCTGCATTCCAAGCCCTGGGTCTACCTTGGAGACAGGACAGCACAGACT TACTCTCCACAAAGGGACTTCTGGGTCATGGGGCCCAAGACACTCCCACAGCTCGCTGGGAAATGGCAA GTGCTGTGCATGTTGTCTTGTGCTGCTGGGGCT- <u>GGGTG</u> - TCTGGGCAGCTTCGTTACTCAGTGGTGGAGGAGTCTGAGCCGGGGACGCTGGTGGGGAATGTTGCTCAGG ATCTGGGCTTAAAGATGACAGATCTGTTGAGCCGGCG
FP008185	GATTTGAGGCATTGTCATCCCCCG- <u>CACCC</u> - CTCCCCACGTGGCCTTCTGGCACGAGCCGCTGGCTCGCCGCCTCATTTACATCAGAAAGC- <u>GGGTG</u> - CCGGCCAATAGGCGCGCAGCCTCGCGCCAGCTGGCGGCGCCG- <u>CACCC</u> - ACCAGCCTATATAAGGGCGCGCAGCGTAGTAGGGGCGCACTCGCTGGTGGTGGCGCGCCGTGCTGAGC TCTGGCTGTCACTGTGTTCTGCCCGCTCCCTCCGCGCTCTCCGCTTGTGGATAACTAGTGTCTGGTTGAT CGCACTATGACTCTGGAAGAAGTCCGCGGCCAGGACACAGTTCCGAAAGCACAGCCAGGTGGGTTTCA GGGCGCTGAGAAAGCCGCTGGTGGTCCGCGACCGTCAGGGTTTTCCA- <u>GGGTG</u> - GGAATCCGCGGGGTAGGAGGGGAGCGCGGGGTCCGGCGCCAGATCC
FP009599	CCACAGGACCTGGGCACTGGACCTTATGATGTGCTTCTCTGGAGTGAAGACTGGCTGTACCTCAGCCCC CTCTCCTTTCTTCTGCTGCCATATCATTCTTCACATGCCTACCAGCCCCCTGGAATCTGCCCTG- <u>CACCC</u> - TCATCCCTTATATATTTGCAGAGAGCGTTTAGAGGACTGGAAGTGTGGCATGTAATGGTATCTCTGTTTC- <u>CACCC</u> - CGCAGCCACCTTGGGACACCTTGACTCCAAGCCCAGCAGTAAGTCCAACATGATTCTGGGGCCGCAACT CAGCCACCTCTGCTGATGAGCAGCCCCACATTGAAAACCTACCGGCTCCTCAAGACCATTGGCAAGGGTA ATTTTGCCAAGGTGAAGTTGGCCCCGACACATCTGACTGGGAAAGAGGTGAGCACTGGGACTGGGGACA TGGCAGCACCTCCCAGCCCTGTTGACAC
FP003211	TGGACTGTTACAATATTCAGTGGCCTATCAGAAGAGGTGAGTTAAATATT- <u>CACCC</u> - AGGCCCTGGGGGCTCTTTACAGCTGTTCTGGCAGATATTGAAGTAATATGGTCTCATGCGATACAAAA TACTTGGAATCCCACTGAAAGATTTAAAGGTGAGCTAAAATCCTCAGTTATTTGGATTGTTTTTAAGATT CTTGGTCAATGAAAGTACACGTTACCGAGTTGTTTGTAAATATAGTGTCTTCTTGAACATTCTTGACCT CA- <u>GGGTG</u> - AGGATTCTTGGTGGCATGAGGATGTCTTTCTTCTTCACTTAATTCCCTTCTGGTGCTTTTTTCTTCTCTGT TTCTTTGGTGTCTTATTACTCGAATCAGCAAGCTTGCTCATTTTTGTCTTCTTTGGACCTTACTGACACA TCAGTTGTCTTATTTTGTATTTTACAAGTT
FP003847	CTTCTTAAAGGAGGAGCTTTCTCCTCTCACCTCAAGGACTGTTATTTATTTGTCTGCGCTACTCTTTCGAC GTTTCCATTCTCTTGGTCTCAAGATGTGAAT- <u>CACCC</u> - ATTTTTCCGTAGGGGGGAAGACGGCGTATCTCTGGCCCTTTAAATAGGGGCGTGGTGAAGAGGCGCGG ACCGCCCAGGAGGGGGAGCAGTGCGAGGAGGAAAGCGGAAGCGCTGCCCGCAGTGGTAGGTAGTGCGC GTGCGTAGGGCTAGAGCAGT- <u>GGGTG</u> - CGGTACGTGGGCCGGCGGTCCACGGCCGGAATGGCAGCAAGCTCAGGTAACGAGTTTCCAGAGAGCG GGCCCGTGAAGGAGACAGGATTGAGGGGCCGTATTAGGGTAGGAGGAGCGCGCGACAGGTCTCT GAGCCTCGGCGTCTCTCCCCGCGGACAGCGGGGACCTCGG
FP014009	CCGGGTTTCTGGGCTACTACGATGGCGATGAGTTTCAGTGGCCGTGGCAGTATCGCTTCC- <u>CACCC</u> - TTCTTTACGTGAGGCTCAGACCCCAAGAAGCACCGCTGTGCCTCCCTCCCCTCCCCCGACCCTGGGCTC AGCCCTGATGCTTCATATGGGGAGGGGGAGAAAAGACCCGTCGGCCAA- <u>CACCC</u> - TCAGTCCCTTACTTTCTCTGAAATGCGTCCCGGGCAAGTGTGCTCCCGCCCTCTAATTCTGCGCCCC ACTCCCTT- <u>CACCC</u> -

	GGCAGGTTACAACCGAATGTGGACACTCGGCAGAAGCAGCTGGCCGCTGGTGCTCGCTGGTCCTGTCTCTGCGCGCTGCACAAACAGTCCAGCATGACGGTGATGGAAGCTCAGGAGAGCCCGCTCTTCAACAACGTC AAGCTACAGCGTATCCTCCCTCAGGCTCTTCCACAG
FP007067	ATGGGGAGTGTAAGAGGCACTAGCAAAGTCCGAGATGAATGTGAATATGAAGTATCAGCTTCCCAACTTCACCGCGGAAA- <u>CACCC-</u> ATCCAGAATGTCATTCTACATGAGCATCACATTTTCCTTGGTGCCACTAACTACATTTATGTTTTAAATGAGGAAGACCTTCAGAAGGTTGCTGAGTACAAGACTGGGCCTGTGCTGGAA- <u>CACCC-</u> AGATTGTTTTCCCATGTCAGGACTGCAGCAGCAAAGCCAATTTATCAGGAGGTGTTTGGAAAGATAACATCAACATGGCTCTAGTTGTCGACACCTACTATGATGATCAACTCATTAGCTGTGGCAGCGTCAACAGAGGGA CCTGCCAGCGACATGTCTTTCCCCACAATCATACTGCTGACATACAGTCGGAGGTTCACTGCATATTCTCC CCACAGATAGAAGAGCCAGCCAGTGTC
FP002937	GTTGAGTTCTCTACAGATTGCTCTTGGGTTATTATCTGCCCCCTC- <u>CACCC-CTGA-GGGTG-</u> TCAGTGCTGTGAGGACGCTGGGAACCTGTCTTGCTGGCTGATAAACCCCTGGTTCCTAGAGGGGCT- <u>GGGTG-</u> CAGAGGAGGCGTTCCTTTAGAAATGGGGCAGGCTTGGGGACCACTGCTGTGGTAACGAGTCTGCTGTCC CTCTGTCACTGCCCTATGGGGCTGCGCTTTAGGCTGGGAGTCGGAGAAGGAGCTCTTGCTGTGACTTTG GGGAGCACGCTGTCTATAAGAGTCAGGTACGGCCACTGGGTCACAAGTGGGGCTACAGGCACTGGGGA CTTGGGCCA- <u>GGGTG-</u> GAGGAGGGAGGAGGCATGAGGACTGGTGAGAAGGTGGCATTGAGTGGCTGTGCAAGATGAGAGGGG AGAAGAGCCCTTGGGGGAGTTCAGGCCTAA
FP013104	CCGT- <u>CACCC-CCC</u> ATCATACCTCC- <u>CACCC-</u> CCTCCGGGAAGGGAAATTACATTTCCCCATTTTAGCAAG- <u>GGGTG-</u> GCGAGAGGGAAGAATGAGTGAACACAAAGCTGAAAGTACAAGCAGGACGGAAAGTGAAACCGGGCAC AGCCCCAGTATAAGACCCCCCTACCCAGGAGATGGCTGACCAAAGAGGCTGGGCCCGCCATGGGC CAGACGGCAGGCGACCTTGGCTGGCGTGAGTTGAAGCCAG- <u>GGGTG-</u> GGGGGCTTGTTGAGTTGGGCAGAGAATGGACGAGCTTGGCTGGTGAGATGGGGGGTCGAGAGCTGA GAGCAGCAACTTGGCCAAGACTGAGGATTGCGCTGGCTGCTGCATGGGAAGGGAGGCTGGCATGACT- <u>GGGTG-</u> GGGGCCTGGGGCAGTG- <u>GGGTG-</u> GTGGTCTGACCCAGGGCTGGGCAGAGGATGAGAAGG
FP000529	GGAAGTGGCGGAGGCGCGAGGGAGGGAGCAGCAGCAGGAGGCACGCGCCCGCCGGTCCG- <u>CACCC-</u> GGCCCCCGCAGCCGCGCCCGCTGCGCGTCGCGCAGCAGCCATGGCCGAGCGCCGCGCCTTCGCCC AGAAGATCAGCAGGTAAATATCCGGCTGCGGGCGCGCCGCGCCCGCCGAGAAAGAGCCGCGGAG TCCTCCCAGGCCTGGCCTAGGAGGC- <u>GGGTG-</u> GGTGTGGCGGGGCCGGCACCGGATCCCGCGGCCTGGCTCGCGCGGGGCGGAAGGGGTTTCG- <u>GGGTG-</u> GCTGAGGGGGTAGCGGAGGCCTCGCGCCGCCCTCGAACCCCGCCTTCAGCCCGCGCCCGCCGCTGAGC CTCGGCAGGGAGCGGAGAGGGCCGCGGACTCCAGCGCGCCCGCCTCCTCTGCTCCTCGGCGCCCGGG CCTGGACTTCTGCG
FP004135	GCGGGTCTCCATCCGTGGCGCCTCGCCAGCTGCAGGACGACGCGGGCTCTTGAGGGGCAGAGCAGCGCA TCATGCAGGTGAGGGTCGGGACCTGCCGAGC- <u>CACCC-TGGAA-CACCC-</u> AGTGGGTCTCCAGCTGGGCCCCGAAGCCAAGGGACACAAATGGGGAGGGCGGACACAGGAGGTAGGCTC TAACATTTGTTCTTGAAAGTGCTAAATTTTGGCTGCTTCTGTCTAGTTTTGAGAAAAATCCTCTAGGA GAACGCCATTTTTTCAGCCTTTAAGACTTGTGTCTGTGCTGGAGAAAACGTTAAAAAGATTGTTACGTAT TGTGTTTCACACCAAAATCATAGAAATCTTACTGCTGAATACTATTTTGACTTAATAGAGCGGCAACGTT AGCCCAAGTGTAATTCAATTTGGTTGCTCCTCCACTACCTAAAAAATAAGAA
FP017366	ATTGGTCTCTGTTTTTGTGAATCCCTGTAGGTAGATCTGTCCCCAGGTCTGTGGAAGTGTGAGTTGTGAAGT TTTGTAAAATGGT- <u>CACCC-</u> AACTTAAACTAGGAAATTACGAAGAAGAGAAAAATTGCCCTGTATCTGTTAAGGTTGGTGTAAGGTAC AGGGACAGGGGGGCAACTTCGACTAGAGAAATCCATCTCTCTGTTTTGTCATTTACCAATTATCCCAT

	CTGCCC- <u>CACCC</u> - CCTGCTGCTGCTGATTTAGTTGGGAGTCTTGGAAGTTGTGGGGGTACAGAATGCTAAGCTGCCTTTCCCA CTCTCCACTGCTTGTCTGCTCTCACGCTTGAACCTAGTCTAATCTGAACGAGGGACATTCTAGGGCAATC ACTGAAGAGGAAGATGGTGGGCAATAGGAAGGAGGAGGAGTAGCCCTGAAACAAAGCAGTGGGG G
FP003318	GTTCCCCCATCCCAG- <u>CACCC</u> - TCCCTCGCCACCTCGGCCGCGTCCAGAAGCGTCTCATTACAGATAGAGGTACCCAGCCGGGCCCCAGGTCT CACCTGGGTCAGCATTGTCCCGCTGAGAGCTTTCAAACAACAGGTGTACGCGAATCAGTATCAAAAAGC CTCCAGGGAAGTGAACAAAACAGTCTGACTTCCGGGATTTCGCGGCATCCACTTTTATTCTCACGTTTCC TCTTAATTTCTCGCGAGATACTGATTTGCTCGCGCTATAGAATCTTGTCTGAAGAGGCTTAGCTCCCGCG GGAGATTTCTGTGCGCAGTTACTTCCGGTAGCTGGTAAAGGCTGATACTTCCCAGGACGCGGAGGTAACG GGCCAGGGCCAAAGCGACTTTCGCTACTTGGATTGGTTCGGCGTAGCTTTGGGCGGCCGACCTTAGAAA GTCACACATCTGC
FP001165	GTCACAAGGTTCC- <u>CACCC</u> - ACTGGAGTCCCTCCCGTGTGCCACCAACCAGCACTTTTGTCTGCTGGGAAAACCTCC- <u>CACCC</u> - AGGCCTTTGCCCTGAGTCCAGGGTCTGTGCCCTAACCCACAGTCACTGAGAGCAACTGGAGGCCACAT AAAACAGACATCTCTTGTTTCCAGATACTACGGGTCATAATCCCTAACTCCAATCACTGGCAACTCCTG AGATCAGAGGAAAACAGCAACAGCGTGGGAGTTGGGGAGAGGCATTCCATACCAGATTCTGTGGCCT GCAGGTGACATGCTGCCTAAGAGAAGCAGGTAGGAAATCTGTTGGGGACCAAGACTAAATGTAATAA AATACAGATAATGCTGGGGGCTAGGCATAGTGGCTCACGTGTGTCATTCCAGCACTTTGGGAGGCCAAG GTGGGGGGATCGCTTGAGCCCAGG
FP001272	TTTTTAAAAAGAACTCCAAACAGACTTCTGGAAGGTTATTTTCTAAGAATCTTGCTGGCAGCGTGAAGG CAACCCCCCTGTGCACAGCCC- <u>CACCC</u> - AGCCTCACGTGGCCACCTCTGTCTTCCCCATGAAGGGCTGGCTCCCCAGTATATATAAACCTCTCTGGA GCTCGGGCATGAGCCAGCAAGGC- <u>CACCC</u> - ATCCAGGCACCTCTCAGCACAGCAGAGCTTTCCAGAGGAAGCCTACCAAGCCTCTGCAATGAGGTTCTT CTGTGCACGTTGCTGCAGCTTTGGGCCTGAGATGCCAGCTGTCCAGCTGCTGCTTCTGGCCTGCCTGGTGT GGGATGTGGGGGCCAGGACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAGTATACC TTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGCCAG
FP013976	CTCGCCCTTCTTGCCCTGCTTTTCTTACTGTGCTCTGTTCCGTACCACTAGCTCCCTCCCGCGCGGCTCT GAGTCCCGCTTGCCACTAGTTGCTTCTCGGCAGCCCC- <u>CACCC</u> - CTACGCGTGGTCCGCCCCGGCGGCTGGCGCAGGTTATAAAGGTCCCGCCGAGCAGCGGACGGCAGACT CGAGATGCGCCCAAGAGGTTGGGCCGTGCTGCGCGGGGAGCCGGCTCGGACCCGGGGACCCAGCAG CACTCACCTGTGCACCTTCGCCCTCAGCCAGTCCCGCTCCGAGCCCTCTGCGCAGCCGAGGCACGGGG CACTGGACAGAGAGTAGGATCCCAGCCACCTCTGGATCCCAGTTCCTCTCGGAAGCCCGCACCGGAGC TCGCCCCGCCCTCGGAGGCTGGAGCCAAGGCAGGAGCCCCGGCGCCCGTCCGATTCTCGGCC
FP017441	GCTCTCCAGCAGCCCAGCCCTTTCCAGGGCTGGGGCAGGAGATTGCTACATGTAGGCTTATCTGGGGAA AAACCAGAGCCTCACTTTAGTCCCTTCCGGTAATTGACACTACTGGA- <u>CACCC</u> - AGGAGGGGGAGGAGAGAGCTTCTCTTCATAAATGTTCC- <u>CACCC</u> - CTGGGCAAGGTGGTCACTCTGGCAGGTAGGAACAGGGGAGAGTGCACCTGCTACCAGTCAAGCTCAGC CAGACTGCAAGAGGAGGCGAGGCGGAGCCAGCCAGGGAGTGAACCATGGACAAGTTGAAATGCCCG AGTTTCTTCAAGTGCAGGGAGAAGGAGGTAGGGGTCTGGGAGCTGCGGGAGGTGTGGAGGACCTGAGA GTGGAAAACCTTAAGGGGGGTTGCTAGTCTCAGTTTTGTCTTCTGTGGCTGTTCTGTGCTCCACATTCT GTTCAACTAT
FP003053	AGGATTAGAAAGTGGAGCAGCAACCGGAGGCGTCTCTGGGCCGCCCCCAACCCCC- <u>CACCC</u> - CGCCTCGCCCACTC- <u>CACCC</u> - TCACACTGGCGTTGCCACAGTCCCTCCATTCCAGAGGGAATTCCAGAGCGGAATACGGATTCCGATTTTA

	AAATAAGCGCTTCTAAATCTTTCTCCTTGCATCTAAGAC- <u>GGGTG</u> - GGGAAAAGAAAGGGAGAGGAGTTGAGGTCCCAAGGTTCAAGGCCTGGTGATCTCCAGGTCCCAGGCTG GGCGGCTCGGTGCACGGAGAGGGCGAGGGGCGTGTGTGGAGCCTTGGCAAGGCGCTGCTCTTCCTCG CGCCTCGGTTTGCGGTCTGTGAAATGGGGTTGGCAGTGCCTTTCAGGGACGCGGCGAACTCAAGCACCA GCAAGCGGACTCGAACTCAAAGGGTTCA- <u>GGGTG</u> -TAGACGACCAGAGC
FP002378	GTGAGCGACGTCCATT- <u>CACCC</u> -ACCTCGCCGCGACC- <u>CACCC</u> - TGGGATATGTAGTGCCTGACTTCCGAGTGACGCTGCGCCTGCCGGGCATTTTTCTGGTTTGGGGCA AGGTCTCATGGGAAAGGTCATGTCTCTGAAGAAAGTTATAAACCTGAGATATGAGGGTTGGGCGAG ACATCCGAGCCTGTTTCGTTCCGTGTTGGGACCAGGAATAACCCTGACTTCTGAGCTTTCATAACCCAG GATCCTCCAGAAAATTTGCGGCGCGCTGAGGGAAAACCTTGCTGGCAAGTCGGGACTGTGTGGCAGCGG CTATTTTTCTTTCC- <u>CACCC</u> - AGCACGTTTTCGGGCTGGGGACATAGGGTTCAGTTGAGATACGGAGGCTTCCTTCGGGATATTGGGTTCT CTGAAGTGCGGATGGACTAGGGCAGGGCTGAGACCCATTG
FP010292	CAGGTTCTTCCTCAGGAAAAGCCAAGGTCAGGCGCAACTTTGCCAAATCCCTGCCCTCCTCAGGCTG GAGACAC- <u>CACCC</u> - CCAAACTCACCATGCGGGGAGGGAAGAAGTCTGGTAGGGACTCTATTGCAACAGGGCCCCAGCCTTAT AAAAAGCCTGGTAACCCGGCCATTACACATCCTGTCTGTGTGGAGCTGGCTGGAATCTCTCAGCC TCACCTGCCAGACAA- <u>CACCC</u> -CCTCCTCCT- <u>CACCC</u> - TGTCTCTGCATTCTCTGAAACCTTCATCCACACAATGCCTCCAACTCACTGGCTACTACCGCTTTGT CTCGCAGAAGAATGGAGGACTACCTGCAAGCCCTAAGTAATGGCTCGCCCTCCAGACCCCTGTCA CTCCCTTCTCCCTCTCTCCTGCTTCTTGGTCCCATGGAGAAGAGGGAATG
FP001502	CTGTGTGGGGTAGGGCAGGGTCCACACTCCTTCCCATCCATTTAGAGGAGGAAGCTGGAGTCTGGGAA GGGATGGGATTTTCCAGGG- <u>CACCC</u> - TGTGAGTCACATGCCACTTGAGACAAGGGTCTAGAGCTCCAGCATTTTCCAAGCTACAAATGTATCTGCT GCTCCAAGTGTCTAGATCAGGACCCTAGGTAAAGACTTCTGAAAAATACTTGAGTCTAGAAACAGAAA AGAAAAAGGGTAGTGTGCTCTAGGGGTTTGCACTGTTGTACCCAGTTTGCTTGTGCTCTAGGAAA GGTCCTTTCTGGGGAT- <u>CACCC</u> - CATTGGCTGAAGATGAGACCATTCTCCTCTTGTGTTTTGGTAAGTACCCCTTCCCATCCTTCCAGGCCCTG TTATATGGCAGGGAGGCAACAGCCACAGGGAGAAGGAGAGTTTACCAAAGTGTTG
FP011777	TCTGGGCTGAATAGGTGGTCCACTCTGAGTCATCAGCTGT- <u>GGGTG</u> - ATGATGTGGTCACTGCATGATTCTACACAAG- <u>CACCC</u> -AGAGGACGTCATCAGGCAGAGGCAGTGG- <u>GGGTG</u> - GGCAGCATTTACAGAAAATCTGTGATGAGACACCACAAAACCAGAGGGGAACATGAAGTCACTGAGCC TGCTCCACCTCTTCTCTCCCAAGAGCTAAAAGAGAGCAAGGAGGAAACAACAGCAGCTCCAACCAGG GCAGCCTTCTGAGAAGATGCAACCAATCCTGCTTCTGCTGGCCTTCTCTGCTGCCAGGGCAGATGC AGGTGAGTGACCGTCTC- <u>CACCC</u> - TCGGGGGGCCCAACCCATCCACAGGTCTCCTGCCCTTCTCCACATTCTGATCCATCTATCTACCAGGA ATGTTCTGAACTCCAGCTCCATTCTACCAAGACCC
FP010713	CATACGAATCTAGCCCGGGAACCGAGTTGCGGGAGTGCGGTCTGTGCCGTTCCGGCCAGGAGTTTGCCG ACTGCAGACGTCTGCGAACCGGCAAGATGTGCTCTCTGGGGTTGTTCCTCTCCACCGCCTCGGGGTC AAGT- <u>CACCC</u> - TATATGAGCACAATAACGAGCTGGTGACGGGCAGTAGCTATGAGAGCCCCGCCCCCGACTTCCGGGGCC AGGTGGCCAGGGCGAGGAGGGAGGGGACCTACAGGCATGGGGGCGGAGTCGGGGACTACTGGGGA GGAGGCAGTGTGACAGGGGCGAGGGTCACAGAGTCTGGCGGAGTGGAACAGCTTGGCCCCGGCAGGAG GCTAGAAGGGCTGGAATCTGTTTTAGGACTGGGATTGGAGTATAACGGGGGAACGGTTAAGGAGCTGTG GAGGAGCCTAGAGGGAATGGAGAGAATGA



FP015337	AGGTAGGGAGAGAGAGCTGAGGCCCCAGATCAGCGGCCGCGGGCAAGGTCGCTCAGCGGG- <u>CACCC</u> -GGCCTGGGTATCGGGGCGCGGGTCGGGGGCGGGGCCGGGGCTCAG- <u>GGGTG</u> -GGGCCGGGCGCGGGCCGGGCGGGCGCCTGCGCCATAAAGGCCGCCGCGCGCCACGCGCCTCGCTTGCTGCGCGCTGCCGGCGCTCCTTCCTCCTCGGCTCGCGTCTCACTCAGTGTAACCTTCTAGTCCCGCCATGGCCGCTCT- <u>CACCC</u> -GGGACCCCCAGTTCAGAAAGCTGCAGCAATGGTACC GCGAGCACCGCTCCGAGCTGAACCTGCGCCGCCCTTCGATGCCAACAAAGGACCGCTTCAACCACTTCAGGTGCGGGCGGGCCGGAGGCGGGGGCTGCCACGCGCGCGCCCGGAACCGGGCACGCGGGCCTGGGGTCTGGAGGCGGGGG
FP000316	GGCTCCGGGGGAGAAGACTACAGTAAGGGCGAGCAGAGCTGAATGCTTTATGTCGGAATCGACCAATGGGATGGCGG- <u>CACCC</u> -GGTTGCCAGGGCTACGGCCAAGCGGAGGTAGGGCCTCGGCACTATGGGCGGGGCTGGGCGGGGTATATAAGCCAGCGGCGGGCGGAAGGCGGGGCGTGGGGGTCTGTGGCTGCTGGGCTGGCGGGGCGCAGGCCGCGGACCCGAGCCCGGGGAAGCGAGAGAGCGGAGGCGCCGAGGATCCGATTCACTCCCTGGGGAGACCTATGGGCCGAAGCCGTGTAAATGCGTTTTAAGGCGAGTGCGGAAAGTGGCCTGGGGAGCCTCGGGGAGCGGACGCCCTCCGCCCTGGTGCTGACCTGCCTCCCTGCCCCCTTCTGCCTCCTGTACGAGAGGCCTCGGCTCAGCAACTGCCACTCCTCCTCGG
FP002584	CCCTCCCCTGGGTGCTCCCC- <u>CACCC</u> -ATTTCCCGCTTGCTTTCTCTCTTCTCTCTCCCTCCTCCCTGCGGAAGCGGAAGTGACGCGAGGCGTAGCGGAAGTTACTGCAGCCGCGGTGTTGTGCTGTGGGGAAGGGAGAAGGATTGTAAACCCCGGAGCGAGGTTCTGCTTACCCGAGGCCGCTGCTGTGCGGAGACCCCC- <u>GGGTG</u> -AAGCCACCGTCATCATGTCTGACCAGGTACCGGGCTGGGAGCCATCCAACGGCGGTGGCCAGGGCCTTCCTGCAGGTCTGCCTGCCGCTAGGCTGGGGTCGGGGATGGAGGCGCGGGGAGGGGAGCGCGGAATGGGGAGGGGGCGGCCGTGGGGACTAGGCAGGCGAGGGAGAGGAGCCGACTACGGCCGAGGTGCCGGGCCTGCTGCGGGGCTCCCGAGCCGCCGCCCT
FP006713	GGGCAAGCCTGGCAGGGCAGAGGGAGCCCCGGCTCCGAGGTTGCTCTTCG- <u>CACCC</u> -GAGGATCAGTCTTGCCCCCAAAGCGCGACGCACAAATCCACGTGAGTGTTTTCAAATTGAATTTCAATAGAAAACTTGGGGTAACTGGTGAATTTAAAAAAAAAAAAACACAGTAAAGAAAAAGCGGTAAGGTTGGTAGACCTGGTGTCGCTCAGGTCCGCCTCTCTTTCTGAGGACAGTGAGAGAGTTCACTTCTGTCAAGCGTCTGTTGCTCTGCACTGTGCCAGCAGGTGCAGGACCAGGCCGACATGGGACACTTCTGAGCAGCCCCGCTGTCAACAGGAGAGGAGTTCTAGCTCCCAACCATATTTAAATTTATGTAGACCTACATATACCCACGGAAGTACGCTTTATAAAGTCGTGTGTAAGAGTTTTTCCTATATTGAGCCGG
FP016947	CAGCCAATTAGAGCCCGGCCAGACACCGCGACCCCTCCCC- <u>CACCC</u> -GCCCCACTCTGCCCCACTGGCGATTGGGTGCGGGACGCGCGGGGCGGGGCTTCCGGGCGGGGAGGCTGGCTTCCGGCGGGAGCGGGGCCGCGGATGGCCGTATACAGGGCAGCGCTCGGGGCTTCGCTCGCGGCTGCCGACTCTTGCCCCCTCGGTGCTGTTCCCCGTGCGCGGCGCCCCGCTCTACGTTGTGCGGCGCCGCCATGAGCCCCGCGCCTCGCTGGCTGGCGGGGCTGCGCTTCGACAACCGCGCCCTGCGCGCCCTGCCCGTGGAGGCGCCGCGGCCGGTCCCGAGGGCGCCCCGTCCGCGCCGCGGCCCTGCCCGGGGCTGCTT- <u>CACCC</u> -GCGTGACCC- <u>CACCC</u> -CGCTGCGGCAGCCGCGCCTCGTGGCGCTGTACAGACCCGCGCTG

**Supplemental Table S2.** Transcription factors interactions according to the STRING database. The table shows direct interactions between non-members of the KLF family and their target genes.

Transcription factor family	Gene	Direct interaction
SP	SP1	COL1A1, NR3C1, TBPL1, TBPL2 MYOD1, HBZ, MDM2, EPAS1, ICAM1, LEF1, RB1, NCOR1, MBNL1, FASN, FOS, HCFC1, PRKACA, DHFR2, HNF1A, MEF2C, IL6, DMPK, MTOR, FHL2, TFDP2, NF1, FDFT1, NCOA1, TFAP2A, ESR1
SP	SP2	FHL2
SP	SP3	SLC20A1, NF1, SUMO1, DYRK1A, ESR1
SP	SP4	NRL, GJA5
SP	SP5	PEX11B
SP	SP6	HHEX, JAZF1, FHL2, CA1, CAMK1D, TCF7L2
*SP	SP7	ACP5, STUB1, COL1A1, SOX9, CD68, LEF1, FGF18, PLOD2, TNFRSF11B, SOST, FOS, FGF3, MEF2C, DMP1, ADAMTS4, NES, DKK1, IFITM5, IGF1, MEPE, CCK, IL6, ACAN, CD44, FGF16, ESR1, DLX5
SP	SP8	PVALB, LEF1, GAD1, BAG3, TBR1, LHX6, DLX5, ENO1, PAX6
SP	SP9	LHX6
WT	WT1	IL2, IFNG, MLH1, FLT3, SOX9, MYOD1, KRT5, THAP1, MDM2, SULF1, PAX8, EPCAM, LEF1, STAR, ATM, WNT9B, RAD21, MN1, TBX5, NKX2-5, GATA2, NF1, NUP214, RBMX, NFIA, CSF3R, AMER1, VIM, PBX1, TNNT2, CD44, FBXW7, PMEL, CITED1, CD8A, MYH11, IDH1, ESR1, PAX6, IGF2, TET2
PATZ	PATZ1	SNRPC, ESR1, CD8A, NR4A3, NCOR1
SALL4	SALL4	TBX3, LEFTY2, ADAMTS18, SOX15, TBR1, EPCAM, PAX8, ALPP, GJA5, KDM2B, EPAS1, TET2, TBX6, PBX1, EED, NKX2-5, TBX5