

Supplementary figure 1. RNAseq identified fusions.

CIITA-DEXI (bp1)

Tile 1: chr16:10924643-10924683
Tile 2: chr16:10942544-10942584

CTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCC
CGGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGA
GCCTGAGATGATCCCAGCTGTGCTCTGGACATG	GACAAGCGAGAATCCC
ACTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCC
AGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAA
TCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAA
GGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAG
TGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGC
GATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAA
GCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCA
CGGCCTGAGATGACCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATC
TGTGCNCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCATC
ATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCA
TGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCA
CTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCAT
GCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCATCATC
GATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAAT
ACGGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAG
TGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCATCATCA
GATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAA
CCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGT
GAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAA
TCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCA
CTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCATCATCAAG
AGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCAT
AGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCA
ATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCC
ACGGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	GACAAGCGAGAATCCCCCAAAGCCAAGGTCATCATCAAGC

CIITA-DEXI (bp2)

Tile 1: chr16:10924643-10924683
Tile 2: chr16:10936473-10936513

GCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCT
CGGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAA
GCAGCCGGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGA
CAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAG
TCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCTGAGGTGT
GATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGA
CTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTT
ATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAG
CTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCTGAGGTGTT
GATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGA
GGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGC
AGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCTG
AGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCT
CCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTA
AGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAG
TGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATG
TGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGG
CTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCTGAG
GAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGA
ATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGAA
CCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTC
CCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGAGAAGA
ACGGATCAGCCTGAGATGATCCCAGCTGTGCTCTGGACAGG	AGAAGGAAACCGAGGCTTAGGAGATGAAGTCTGAGGTGTTG

FAM65B-BC070382

Tile 1: chr6:24983983-24984024

Tile 2: chr6:25150057-25150098

CGGGAGTCTGGTCGGTAGTC	GGTTGCGCTGGCGCCTCCGGATCCTGTCCCT
CCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCC
CTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCT
TTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCT
ATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGT
ACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGA
TACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCT
GTCCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCTCCATG
CATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGAT
CAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCG
CGATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTG
GTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCTCCATGGCCTG
GAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGCCCTCCA
ATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATC
CAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCG
CCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCC
TACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCT
ATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGC
GGATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCTCCATGGCCTG
TTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGT
GATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCT
ACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGA
AACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGG
CCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGC
TCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCC
ATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGT
CATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGAT
CTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCT
CCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCC
TTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCT
CGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCT
CCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCC
ATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATC
CCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCC
CATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGAT
TTCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGC
CGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCT
CCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCC
TCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCC
TTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCT
GATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCT
ACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGA
CCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGC
GGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCTCC
CCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCTCC
TCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCG
ATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGT
ATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGC
CGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCT
ACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGA
CTGCCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCT
GGATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTG
GGATCCTACCAACATGATTTCCGGGAGTCTGGTCGGTAGTC	GGTTGAGCTGGCGCCTCCGGATCCTGTCCCTCCATGGCCTG

ARL13A-TRMT2B

Tile 1: chrX:100115327-100115366

Tile 2: chrX:100152166-100152205

GCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTAACAAATAGCCT
TCCGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTC
CGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAG
GGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGC
ATGAATCATGTTCCGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTT
CCGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGC
CTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTA
TCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTAACAAATAGC
CTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTAACAAATA
TTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTAA
TTCCGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCA
ATGAATCATGTTCCGGCTTTTGTCTCCTGCTGCTCTTG	CCTGAAAGTTTCTGAAACTTCAGCCTTAACAAATAGCCT

G3BP2-AK311578

Tile 1: chr4:76806216-76806257

Tile 2: chr4:76868483-76868524

CTTCTCCATAACCATTCTTTGCTGCACAATGTCAAATG	CTGTCACGTTGG
GGCTTCTCCATAACCATTCTTTGCTGCACAATGTCAAATG	CTGTCACGTT
CTTTGCTGCACAATGTCAAATG	CTGTCACGTTGGCCAAAGGAAAATTTAC
CTCCATAACCATTCTTTGCTGCACAATGTCAAATG	CTGTCACGTTGGCCA
CATAACCATTCTTTGCTGCACAATGTCAAATG	CTGTCACGTTGGCCAAAG
ATTTCTTTGCTGCACAATGTCAAATG	CTGGTGTTTAGATCTAGGAATTCCT
GGCTTCTCCATAACCATTCTTTGCTGCACAATGTCAAATG	CTGGTGTTTAGATCTAGGAATTCCTTTTCAGCAGGTTTGAAG

C2orf56-PRKD3

Tile 1: chr2:37329032-37329073

Tile 2: chr2:37333732-37333773

TCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGTTACACAG
AGGAAACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAA
CAAGAAATCAAATAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGTTACACAGCAA
TATACTGCAG	CACTGCAGATGACAACCTACGAAGAACAAGTTACACAGCAA
ATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGTTACACAGCA
CACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGTT
ACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGT
TAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAA
AATCAAATAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATGACAA
AGAAATCAAATAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATGA
AACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAG
AAGAAATCAAATAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATG
GAAACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACA
CAAGAAATCAAATAAAGGAAACACATTTTCATATACTGCAG	CACTGCAGATGACAATCTACGAAGAACAAGTTACACAGCAA

BC042152-AK024119

Tile 1: chr19:47328979-47329020

Tile 2: chr19:47351698-47351739

ATCAAGCAAGCCCTGCGCCTATCTGCAG	GCCGGATCTCTGGATCTCCCCAG
CGCAAGCCCTGCGCCTATCTGCAG	GCCGGATCTCTGGATCTCCCCAGCCTC
GGAAGATCAAGCAAGCCCTGCGCCTATCTGCAG	GCCGGATCTCTGGATCTC
CGCGGCAGGGAAGATCAAGCAAGCCCTGCGCCTATCTGCAG	GCCGGATCTCTGGATCTCCCCAGCCTCCAGATCTCAGTGTG

BC067907-MSN

Tile 1: chrX:64725176-64725217
Tile 2: chrX:64853404-64853445

GCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGA
ACCATGCAAAACACCCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAG
CTTAACTGCCAGTGTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGT
CCCTTAACTGCCAGTGTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGAGTT
C AAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGAG
CCCTTAACTGCCAGTGTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGAGTT
GGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAG
GTTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGG
ACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAG
CGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATG
CCAGTGTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCAC
C AAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGAG
CCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGC
TTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGA
TGTTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATG
CCCTTAACTGCCAGTGTTCGTGGACCATGCAAAACAACCAA	ATCAGTGTGCGTGTGACCACCATGGATGCAGAGCTGGAGTT

KIAA1267-ARL17

Tile 1: chr17:41786010-41786051
Tile 2: chr17:41527741-41527782

TCTCCACACAGAAA	CCTTATTAGCACGTATCTGTTTGTAAATGTCTGTTTG
TATATTCTACTGTCTCCACACAGAAA	CCTTATTAGCACGTATCTGTTTGTAA
TTTTATTTCTACTGTCTCCACACAGAAA	CCTTATTAGCACGTATCTGTTTG
CGAAGGTGTTATTTTTATTTCTACTGTCTCCACACAGAAA	CCTTATTAGC
ACTGTCTCCACACAGAAA	CCTTATTAGCACGTATCTGTTTGTAAATGTCTG
GAAGGTGTTATTTTTATTTCTACTGTCTCCACACAGAAA	CCTTATTAGCA
CGAAGGTGTTATTTTTATTTCTACTGTCTCCACACAGAAA	CCTTATTAGCACGTATCTGTTTGTAAATGTCTGTTTGCTGA

HARS2-ZMAT2

Tile 1: chr5:140058558-140058599
Tile 2: chr5:140060586-140060627

ATTTGAAGTGCCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGC
ACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGCCGAAAGTGGGAC
CCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGCCGAAAGTGGG
GCCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGCCGAAAGTGG
GGCAAATTTGAAGTGCCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACT
AGTGCCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGCCGAAAG
CTGCAGAGGCAAATTTGAAGTGCCACGGAACGTTGTCAAGA	GACAAAAAACTTGGACTTTCGCCGAAAGTGGGACAAAGATG

HSP90B1-DKFzP547P055

Tile 1: chr12:102865296-102865337
Tile 2: chr12:102871292-102871333

CAGATGAAGGAGAAGAAACAGCAAA	GATGAGCTGAGCTGGACAACATAAAG
AACAGATGAAGAAGAAGAAACAGCAAA	GATGAGCTGAGCTGGACAACATAA
GGGAACAGATGAAGAAGAAGAAACAGCAAA	GATGAGCTGAGCTGGACAAC
GAAATGGATGTGGGAACAGATGAAGAAGAAGAAACAGCAAA	GATGAGCTGA
GAAATGGATGTGGGAACAGATGAAGAAGAAGAAACAGCAAA	GATGAGCTGAGCTGGACAACATAAAGCACCTGTAGCAGTTC

IL17RB-ACR8

Tile 1: chr3:53874044-53874085
Tile 2: chr3:53877739-53877780

CAGTGTGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAGTGACA
CAACAGTGTGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAGTG
GTCAACAGTGTGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAG
GTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAGTGACATTTCCCT
TGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAGTGACATTTCC
TCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTA	CCAAGAAGCTTG
CGTCAACAGTGTGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCA
CTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTA	CCAAGAAGCTTGTT
CTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTA	CCAAGAAGCTTGTTTTTGGTCTTCGGCAGTGACATTTCCCTC

ANKRD23-CNNM3

Tile 1: chr2:96862966-96863007
Tile 2: chr2:96869463-96869504

CCAGGTGGATCCTCTT	ATCCTGTGCGTTCAGGTGGGCGCCACACTCGATGA
AGAGCAGTGAGGGAGGGTTCATGAACCAGGTGGATCCTCTT	ATCCTGTGCG
AGAGCAGTGAGGGAGGGTTCATGAACCAGGTGGATCCTCTT	ATCCTGTGCGTTCAGGTGGGCGCCACACTCGATGAGGTGCT

PPCS-LOC728621

Tile 1: chr1:42695568-42695609
Tile 2: chr1:42711380-42711421

CATCTGGGGGCCCACTGCAGG	GAAAAGTTCAGTTAGAAGACATACTTCACC
CAAGATCCAGTCATCTGGGGGCCCACTGCAGG	GAAAAGTTCAGTTAGAAGA
ACAAGATCCAGTCATCTGGGGGCCCACTGCAGG	GAAAAGTTCAGTTAGAAG
GCCTGAACACAAGATCCAGTCATCTGGGGGCCCACTGCAGG	GAAAAGTTCAGTTAGAAGACATACTTCACCATCTTGAAAAA

HERC3-FAM13AOS

Tile 1: chr4:89848392-89848433
Tile 2: chr4:89850282-89850323

AAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGACCAGA
AAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGACCAG
AAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGACCAG
GAAAATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACC
AGAAAATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGAC
TAAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGACCG
ATTAAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGAC
ATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATC
AAATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAA
GGAGTAAGAAAATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACA
CTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTT
TACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTA
CATCATGGAGTAAGAAAATTCTACATGATTAAGAATCCAT	CCCTTTACAGAAAACAACACTGACCAATCCTTATGAGACCAGA

PAQR6-SMG5

Tile 1: chr1:154483129-154483170
Tile 2: chr1:154485982-154486023

GGTACCTCCACGTTGA	CCTCAACACTCCAAAAGCCAGCCCCCTTCAGGTCTT
GCTTGAGACTGAGCATGGTGGCCTGGTACCTCCACGTTGA	CCTCAACACTC
TCCACGTTGA	CCTCAACACTCCAAAAGCCAGCCCCCTTCAGGTCTTCAGTCC
TGAGCATGGTGGCCTGGTACCTCCACGTTGA	CCTCAACACTCCAAAAGCCA
GAGCATGGTGGCCTGGTACCTCCACGTTGA	CCTCAACACTCCAAAAGCCAG
AGCTTGAGACTGAGCATGGTGGCCTGGTACCTCCACGTTGA	CCTCAACACTCCAAAAGCCAGCCCCCTTCAGGTCTTCAGTCC

ZNF789-ZNF394

Tile 1: chr7:98922479-98922520
Tile 2: chr7:98934272-98934313

CTCTTACGGTCCATAAACAGTGTC	ACTCGGCGGAAGTGTGCTCCCGGAATC
TTACGGTCCATAAACAGTGTC	ACTCGGCGGAAGTGTGCTCCCGGAATCCTT
TCAGCTCTTACGGTCCATAAACAGTGTC	ACTCGGCGGAAGTGTGCTCCCGG
C TTCAGACAGCGGT CAGCTCTTACGGTCCATAAACAGTGTC	ACTCGGCGGAAGTGTGCTCCCGGAATCCTTCTGCGCACTCT

CLR-CLEC2D

Tile 1: chr12:9700978-9701019
Tile 2: chr12:9724785-9724826

AGCAGCTTCCACCATGCCCTGGAAAACT	GTTGTCTGCATTCAAAAGAGC
ATCAGCAGCAGCTTCCACCATGCCCTGGAAAACT	GTTGTCTGCATTCAA
GTGGAATCAGCAGCAGCTTCCACCATGCCCTGGAAAACT	CAATAAGAGC
GTGGAATCAGCAGCAGCTTCCACCATGCCCTGGAAAACT	CAATAAGAGCTAACTGCCATCAAGAGCCATCAGTATGTCTT

GGCT-BC041636

Tile 1: chr7:30506780-30506821
Tile 2: chr7:30530506-30530547

GGGAATTGCCAAAGTCAAGCTTAAAT	CATCCTCAGGTGAGTGGCAACCAC
TGGGAATTGCCAAAGTCAAGCTTAAAT	CATCCTCAGGTGAGTGGCAACCA
CTTGGGAATTGCCAAAGTCAAGCTTAAAT	CATCCTCAGGTGAGTGGCAAC
ACTTGTTTTGCCTTGGGAATTGCCAAAGTCAAGCTTAAAT	CATCCTCAGGTGAGTGGCAACCACCAGAAGTGGCTGTTTCA

CLN5-FBXL3

Tile 1: chr13:76474145-76474186
Tile 2: chr13:76487545-76487586

TGATGATCAACTGAACACGTTTC	TGCTGGAGAGACATGAGGACAGCTGCTC
CGTCCTTTAAGTATTTGATGATCAACTGAACACGTTTC	TGCTGGAGAGACA
ACTGAACACGTTTC	TGCTGGAGAGACATGAGGACAGCTGCTCATTTTTCAAC
TTGATGATCAACTGAACACGTTTC	TGCTGGAGAGACATGAGGACAGCTGCT
GTATTTGATGATCAACTGAACACGTTTC	TGCTGGAGAGACATGAGGACAGC
CAAGGTCTTTAAGTATTTGATGATCAACTGAACACGTTTC	TGCTGGAGAGACATGAGGACAGCTGCTCATTTTTCAACAGCT

AGK-KIAA1147

Tile 1: chr7:140999111-140999152
Tile 2: chr7:141010440-141010481

GGGAGCTGCAGTTCTTCTGTGATC	AGCACGAAGAGGTCTCTTCAACAAGG
AGCTGCAGTTCTTCTGTGATC	AGCACGAAGAGGTCTCTTCAACAAGGGTTG
GGTGAAACTGCTCCCCAGGAAGCTGCAGTTCTTCTGTGATC	AGCACGAAGAGGTCTCTTCAACAAGGGTTGTAGTCTTCTTC

ZNRF2-DKFZP586I1420

Tile 1: chr7:30372398-30372437
Tile 2: chr7:30377094-30377133

GTCATCTACATAG	GTATTTTCCTGTTAAATAAGATATCAAAAGCATCAATC
CTTAATAGTCATCTACATAG	GTATTTTCCTGTTAAATAAGATATCAAAAGC
ATAGTCATCTACATAG	GTATTTTCCTGTTAAATAAGATATCAAAAGCATCA
CCCTTAATAGTCATCTACATAG	GTATTTTCCTGTTAAATAAGATATCAAAA
TGAAAATGCTGCACATCCCTTAATAGTCATCTACATAG	GTATTTTCCTGTTAAATAAGATATCAAAAGCATCAATCAC

BC016361-EREG

Tile 1: chr4:75414846-75414885
Tile 2: chr4:75449731-75449770

AAAGGGAGACCTCATCT CTGATATTTCCAGTGTGACAGGGACACAGCCA
TGGGCAACAAGGGAGACCTCATCT CTGATATTTCCAGTGTGACAGGGA
AATTCAGACCAGCTGGGCAACAAGGGAGACCTCATCT CTGATATTTCCAGTGTGACAGGGACACAGCCAACGTGGG

NFATC3-PLA2G15

Tile 1: chr16:66783137-66783178
Tile 2: chr16:66840692-66840733

TTTAGATGAT GTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGA
CATCACTTTAGATGAT GTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAA
ACTTTGCAACCATTGGTCTGCAGGACATCACTTTAGATGAT GTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGA

LY6G5C-ABHD16A

Tile 1: chr6:31759055-31759096
Tile 2: chr6:31762934-31762975

GAGTGCTCCTA CCCCATTCTTCCATAATGAGTCCCAGTTGGTCCCTAGAGG
ACGGTGCTCCCTTCTGAGTGCTCCTA CCCCATTCTTCCATAATGAGTCCCAG
ATGACGGTGCTCCCTTCTGAGTGCTCCTA CCCCATTCTTCCATAATGAGTCC
GCGACAGCAGCAGATGACGGTGCTCCCTTCTGAGTGCTCCTA CCCCATTCTTCCATAATGAGTCCCAGTTGGTCCCTAGAGGT

PLD4-AHNAK2

Tile 1: chr14:104469693-104469734
Tile 2: chr14:104474544-104474585

GCAAGTTCATGGTCACGGAGAAGGCAGCCTACA TAGAGCTGCTTAGTAGAG
ATGGTCACGGAGAAGGCAGCCTACA TAGAGCTGCTTAGTAGAGACCAGGAG
GTTTCATGGTCACGGAGAAGGCAGCCTACA TAGAGCTGCTTAGTAGAGACCA
CACCACAGCAAGTTCATGGTCACGGAGAAGGCAGCCTACA TAGAGCTGCTT
GAACCACAGCAAGTTCATGGTCACGGAGAAGGCAGCCTACA TAGAGCTGCTTAGTAGAGACCAGGAGTGTGTGGGAGGAAAG

DHX8-ETV4

Tile 1: chr17:38957039-38957080
Tile 2: chr17:38969306-38969347

CTTGTGCAGGACATGG GACCTCTACTCACGGTTTTCTGAATGGAATCAG
GTGGGTGAGCATCTTGTGCAGGACATGG GACCTCTACTCACGGTTTTCTG
TGGGAAGGTGGAGTGGGTGAGCATCTTGTGCAGGACATGG GACCTCTACTCACGGTTTTCTGAATGGAATCAGGAACAAA

ATP5I-MFSD7

Tile 1: chr4:657152-657193
Tile 2: chr4:666572-666613

AGGTAATCTG TCCAGTCAAGTGGATCCTCCCCCTGCTGGCAGGTGGACAAG
TAGGTAATCTG TCCAGTCAAGTGGATCCTCCCCCTGCTGGCAGGTGGACAA
TATCCTCCTCCTCTTCTGCCGAGGTTTTAGGTAATCTG TCCAGTCAAGTGGATCCTCCCCCTGCTGGCAGGTGGACAAG

NUMB-AK055876

Tile 1: chr14:72999086-72999127
Tile 2: chr14:72892088-72892129

CCAAGGTACT TAACCGGGAAGCTACATTTTCCGGTGCGAACGCCTTCTTCA
GGCCAAGGTACT TAACCGGGAAGCTACATTTTCCGGTGCGAACGCCTTCTT
CGGGAAGTGCCACGCTGCTTCCACGCTGGAACAAGGTACT TAACCGGGAAGCTACATTTTCCGGTGCGAACGCCTTCTTCA