

>A1\_1st\_L  
CGCATATTTGGTGGCTAGGCA  
>A1\_1st\_R  
GAGCATTTAAACCGACAGGG  
>A2\_1st\_L  
AGAATAGCAGATGGCTGCCT  
>A2\_1st\_R  
TGCCGGTTAACATGGAGAAG  
>B1\_1st\_L  
TCAGCGACTTATCTCCCCTA  
>B1\_1st\_R  
AGGAAAGGTTGAGCGTAAGC  
>B2\_1st\_L  
ACAGGGACTTTTCGTCAGGTA  
>B2\_1st\_R  
CCAATCATGAAGAAGCAGCC  
>B3\_1st\_L  
TGTTATATGGGTCCCTTGCC  
>B3\_1st\_R  
TGGTGCTCATGTGCTATCAC  
>B4\_1st\_L  
GGGGCAATTGTCAGCATTCT  
>B4\_1st\_R  
GATTCCATCCACTGGATGTC  
>C\_1st\_L  
CATTACCTGCCCAACTGAAG  
>C\_1st\_R  
CAGTTACAAGTGGACTCTGC  
>D\_1st\_L  
CAAATGTTGGGAGGGGACTT  
>D\_1st\_R  
GGGTGATCATTGGGATGAG  
>E\_1st\_L  
AGCCAGACTCCAACCTCTGAT  
>E\_1st\_R  
GGGTGGAATGGATTGCACTT  
>F\_1st\_L  
ATTTCGACTTTGCGGTTCC  
>F\_1st\_R  
CAGTCACACCACCTTGCAACT  
>G\_1st\_L  
TTCAACAGTCCGAGCCAGTA  
>G\_1st\_R  
TATGTCAGTGTTAGCACCCC  
>H\_1st\_L  
AACCTGGGCGCAAATTGCAT  
>H\_1st\_R  
TCTCTGTCAGCTGAACCTCT  
>I\_1st\_L  
TGAAGTTCCTGCTGCTCTAC  
>I\_1st\_R  
GCTTTTTGCCCTCGTCTATG  
>J\_1st\_L  
AATGTTTCCCACGTCCTCTG  
>J\_1st\_R  
AGGAGGCAAATATGGGTGC  
>K\_1st\_L  
CAGGACCAACATTTCCATGC  
>K\_1st\_R  
TGGGGTTCATGGATGGTAGA  
>L\_1st\_L  
TACTAATGAAGCCGCTTGG  
>L\_1st\_R  
TGGGTATCGGTTGATATGGG

>A1-2nd\_L  
AGGAACAGTAACACCAAAAAATGAAAGTGT  
>A1-2nd\_R  
AGGAACAGTAACACCAAAAAATGAAAGAGC  
>A2-2nd\_LR  
AGGAAAAGTAACACTAAAAWTTTTTWAGWA  
>A2-2nd\_inner  
AGGCTAGGATCGATCAATCGATCGCT  
>B1-2nd\_L  
AGGAGAAGGAAAGGCTAATAAAGAGTTAAT  
>B1-2nd\_R  
AGGAGAAAAGAAAGGTAAAACTAAGTAAGC  
>B2-2nd\_L  
AGGAGAATTAAAGTCATTTTGGCATTTTAC  
>B2-2nd\_inner  
TATAAGGGCTAGACTGCAGGCAGGAAGATA  
>B3-2nd\_LR  
AGGRGAAGGAAAGGCTAAGTCACTTGGGGG  
>B3-2nd\_inner  
TTTTCACTCTACTGCGCATGCGCCGCCGA  
>B4-2nd\_R  
AGGAGAAGGAAAGGGTTTCACTCATTTTTT  
>B4-2nd\_inner  
CATCGCTCTTTTCCAGGACTTGGAGACTTA  
>C-2nd\_L  
AGGAGACATATTGGATAAATGGGAAAACCC  
>C-2nd\_R  
AGGAGACATATCCTATAAAAATTATGAATG  
>D-2nd\_L  
AGGGAAACTACACCCCAGAATGAATACGT  
>D-2nd\_R  
AGGGAAACTATCCCCCAAACAATGTAGGT  
>E-2nd\_L  
AGGGGTGGTTACCTTTAACTTAACATTTA  
>E-2nd\_R  
AGGGGAAGTTCACCTTTGAGTTAACATTTA  
>F-2nd\_L  
AGGAATACTGACATGGGAAAACATGGTTTT  
>F-2nd\_R  
AGGGATACTGTCATGATTTTTATGGGGTAC  
>G-2nd\_L  
AGGGGACCTATCACCCAGACATAAAAAGCT  
>G-2nd\_R  
AGGGGACCTGTCACCCTAAGAAATAACTCC  
>H-2nd\_L  
AGGAGAACTAAAGCCTAACTAAAGAAGTAG  
>H-2nd\_R  
AGGAGAACCAACCCTAAAAATGAATATGG  
>I-2nd\_L  
AGGGGAACTCTTGCTTCTGAACCAAAATTT  
>I-2nd\_R  
AGGGGAACTGCACCCAAACACACAGCTTT  
>J-2nd\_LR  
AGGAACAGTTCAGTGTAATAATKAAACTGG  
>J-2nd\_inner  
GACCTGCGTGCTTACAAACTAACTGAA  
>K-2nd\_L  
AGGAGACATTTTATATAAAGTTCATATTCA  
>K-2nd\_R  
AGGGGATATATAGCATAACATTTTACAATG  
>L-2nd\_L  
AGGGGATATAAACCCCTGCTGCCAGCGCGG  
>L-2nd\_L  
AGGGGATATAAACCCAGCCATGATGCTGCC

>A1\_Full

AGGACAGTAACACCAAAAAATGAAAGTGTATAAAAGTAACTAAAATATAATGTGCTGCTGCCCTGCACTGGTAAAAGTTGTGTGTTACTTTCA  
GAAAGTCTACTATAAATTTATATAAAATAAGCTGCTATGTTAGCCATGGAGGCAGCCATTTCAAAGGAGAAAAGGCACAGGCACATAGCAGATAACA  
GATAAAACACTATTGTATTTTACAGAACTTATCTGTTATCTGCTATGTAACCTGTGCCCTTTTCTCCTTTTTTCCAGCTTGAATGGCTGCCCCCG  
TGGCTACACAGCAGCTTATTATATAAATATAGTAGTGTACTGTAGCAAAACACCAGTTTTTACCCAGTGCAGGGCAACAGTGCATTATATTT  
TTATTACTTTAAAGCTCTTTTCATTTTTTGGTGTACTGTTCCT

>A2\_Arm

AGGCTAGGATCGATCAATCGATCGCTGCATAGTGGATGCTTTCCCTGCATCGGCGTATCGCCTATTTTTCAAATGACTGGAAGCCAAGTTTTAAC  
AGGTATTTTTCTAATAAAGCATTCAAATACTAAATGTTTGCAGGATAGGTAATTTATTTGGGGCAGGGTAGAATAGATTTTTTCTAAAAAAAT  
TTAGTGTACTTTTTCCCT

>B1\_Full

AGGAGAAGGAAAGGCTAATAAAGAGTTAATCTCAAGATGCAGGCATACCTTCAGTTGTCTCAATAGTGCCTTAAAGTCTCCCATATTGCACCT  
GTTTCAGATGATCAGAAGCCAAACAGGAAGAAAAACGCTTAGCTGTGTAAGAAAGTTCCATAATGCCCTCACTCCTGCACAGACACCCAGACC  
AAGTGAACATGCTCAGTTAGTAAAACATGAGTCAGCTTCCCTGCTGATTGGCTCAGATCCACATTCCCTAAGGGGGGAGTGAGTTCTTAGCATT  
CTTGAGGGAGGGGGGAGCAGGAGAGGGGAGGAGAGCAGAGAGCTGCGTGTCTCTGGCACATGAATTACAGACACAAGAAATCTTTTGACAG  
AGAAGTCAGTGCAGCATTTCTGTGAGTGTCTATGGCTGTATTTACATAGACCTTTCTGTATAAAGCTTACTTAGTTTTTACCTTTCTTTCTCCT

>B2\_Arm

AGGAGAATTAAGTCATTTTTGGCATTTTACTGCCAATAGATTTGCCACATTAGTGCACCTAGAACACAATATTTATTTCTGCAGAAACCATTAC  
CATACTGAGTAAACAGCTTTAGAAGCTTTCTCCATTTGCTTAAGATAGCAGCTGCCATTTAAGTATCTTCTGCCTGCAGTCTAGCCCTTAT  
A

>B3\_Arm

AGGGGAAGGAAAGGCTAAGTCACTTGGGGGTGCCAAAATGTTAGGCACCCCAAGTGAAGTACTTAGATCACTTACCTTGTACCCTGGGCTGGTGCCC  
CTGTTTAGGAGAAAAAGCACCAGCCGGGGTACCTGTAGGAAGCGCTGCCCTCCTTCTTCTTTTTGCCGGCGAAATCCGTCGGCCGGCGCAT  
GCGCAGTAGAGTAAA

>B4\_Arm

AGGAGAAGGAAAGGTTTCACTCATTTTTTAGTATGTAATAGAGGGCCCTGCCCTACCTGAACGCTGAAATCATTTCTTCTAAAAATGCTCC  
TTTTGCCAGTACGGTCTCCCGATGTACACACTATTTCTCCTTGTCTGCGCCGCGATGTTTTAAACATGGCGCTCCACTAAGTCTCCCTGCTTGC  
CTCTCCCTCCAGCACCTGTGAGTGTACCGTTCCTCACCCCTCCCTCCCTGCGTCTTTTCATCCCTGCTCCTCTCCCGCTTGCCTCTCC  
GCCCCAGCACCTGTTAGCCGACACCTGTGAGTCTCACCGCTCCCTCCCTGCACCTGTGTCTCTTGTCCCGCTCGCCTCTCCGCCCCAGCAC  
CTGTGACCCGACACGTTCTCACCCCTGTGACCTCTCCCTCCCTGCGCTGTGTCTCTGGTCCCGCTCGCCTCTCCGCTCCAGTACCCG  
CAGCCGACAGTTCCTCACCCCTGTGACCTCTCCCTCCCTGCGCTGTGTCTCTGGTCCCGCTCCTCGCTTGCCTCTCCGCTCTGCAC  
CTGCCGGCTGCGTCTGTAATGGCCCCAGCTGCTGCTTCTAATGGCAAATAGCGTCTCATAACCAGACGCTAGGGGGAGCGCCTGCTTGTGC  
GCATGCGCCGCTTTAATAGTAAGTCTCCAAGTCTGGAAAAGAGCGATG

>C\_Full

AGGAGACATATCCTATAAAAAATTGAATGTGCCAGGGAATTATACTCCTCTAGATATAGAAGGATTGTGCTTAAAAAGTTGTGTTTCTGACTG  
ATTTATTTGAGAAATTCACAAAAAACCCTACTAGCCCCGCCATCTGTGCCACTTCTGTGGCTGAATTTCTCTGGATGAGCTGGGGAGCCGGC  
GGCCTCCGTACCTGCATGTAGGATAGGAACCAATCAGCAGCTAGGCTGACCTGATAGGGAAGTGAAGCTGTCTGTGCTTGTGTGACTGCA  
GGCTGTGATTGGCTCTCCCTCCTACTGTGCTTCTGGCAGGACCGTTAGGACACGCCACTCTCCATTTCAAACCTCTGACAGAGAAGAGAT  
AGGATCTATAGGGAGCTCCAATAAAGGGGCCATTGTTACAGACAGGATTAATGTTTAGCCCAAAGGAAACCAGCACCGTATATTATTCATAAT  
TGCCTACAAAATTAGGGTTTTCCCATTTATCCAATATGTC

>D\_Full

AGGGAACTACACCCCGAATGAATACGTAACCAACAGACAGTTTATATTTATGTTAAGTGGCCTATTAAGAATCTCCCAAACTGGAATATA  
TATATCAGTAAATATTGCCCTTTTACATCCTTTCCCTTGGAGCCGATTTAGTGTAGGGCTGTGTGCTCCCTCAGAGATCAGCTGACAGGAAGT  
GATGACGCTCTAATTTGAACAGGAAGTAGTGTGGGAGCAAAAGGCAGAACTCTGCCATTCATTGGCTGATGGGGCTAGCATGTATGTGTGCC  
TTGGCTTGTGTTGTGTGACTGTGACTCCTATGATCCAGGGGGCGGCCCTTAGTACTTAAAAATGGCAGTTTCTTATTTAGGATACCCAATGGC  
ACATACTGTAAAAAAGTATATTTATATGAAAATGTTTATTTAGATGAAGCAGGGTTTTACATATGAGCTGTTTATGCAATACAGTATATTTT  
TATAGAGACCTACATTTGTTGGGGGAATAGTTCCCT

>E\_Full

AGGGGTGGTTACCTTTAACTTAAACATTTAGTATGTTATAGAATGGCCTATTCTAAGCAACTTTTTAATTGGTCTTCATTAATTTATAGTTATTT  
AATTAATTTGCTTTCTTCTTAAACACTTTGACGCTTTCAAACAGGGGTCACTGACCCCGCAGCCAAAAACTATTGCTCTGTTAGGCTCCAGTT  
TTATTTGTTACTTTTTTATTAATCTATTTTCTATTCAGCTCCTCCCTATTTCATATATCAGTCTTTTATTTCAAACACTCCTGGTTGCTAAGGTA  
ATTTGGACCCTAGCAACCAGATAGCTGCTGAAACTCCAACTGGAGAGCTGCTGAACAAAAACTGAATTAATTAAAAAAACTACAAATAATTA  
AAAAGTGAAGACCAATGCAAAATGCTCTCAGAATATCCCTCTCTACATCATACTAAATGTTAACTCAAAGGTGAACCTTCCCT

>F\_Full

AGGGTACTGTGATGATTTTTATGGGGTACTTTTTATTTCTAAATTACACTGTTTATATAGCAAATAATCACTCTACCATTAAAATGTTGTT  
CTTGAGCCAACAAATGATTTTTTTAGCTGTAATATTGGTGTGTAGGCGCCATCTTAGTGCATTGTGCCCTGAGTCTGAGCTTTCAGAAGGAGCC  
AGCGTACACATTAGAAGTCTTTCAGGTAACCTATTGTTTCTCCTACTCCCATGTAAGTGGAGAGTCCCAAGCCGGACTTGGATTTCTTACT  
ATTTGAGTTCTATTCTGATACCTACTGGAAGCTGCTATCTTGTCCCTTCCCATTTGTTCTGCTGATCGGCTGCTGGGAGGGGGATATCACTCCAA  
CTTGACAGCGCAGCAGTAAAGTGTGACTGAAGTTTATCAGAGCACAGGTCACATGGCTGTGGCACCTGGGAAATGAAGAATATGGCTAGCCCAT  
GTGACATTTCAAATGAAATGTAAAAAAATCTGTGTTTTGAAAAACAGATTACAATGCAGGATTTCTGCTGGAGAAGCTCTAGTAACTGATGGG  
TTTTGAAAAACCATGTTTCCCATGTGACTATTCCCT

>G\_Full

AGGGGACCTATCACCCAGACATAAAAAAGCTGTATAATAAAAGTCTTTTTCAAATAAAACGTGAAACCCAAATTAATTTTTTATATTAACACATCC  
AAACCTATTATAAAGGCATTTAAAAATCCAGCTGTCAATCATATATGCTTGGCCCACTCTATGCCCTTAGGCATAGAGGTGGGGCAGACAAT  
AACTTTAGCTTTCCATTCAGCACTTCTTAGATGTCACTGCACATCTCACTTTTTCCCTCCCTCCTCCTCATCATCTAACTGTGTAGCCAGTGC  
TGGGTATAGGCATATGGTCCCGTCTGGCACATAACAAGATTTTGGCATGATACAAAGCTTGCCTTAATAACAGTGTCCACAAAATGGTGC

CTGCCTGTTTGCTTTGATTGAGTAATTC AAGATGGAAGGAAACAAGATTTATATTATTTATATAGAGTAAATAAAGTTTATTTTGCTCAACTA  
ACAATATAGAAAATAATTTGGAGTTATTTCTTAGGGTGACAGGTCCCT  
>H\_Full  
AGGAGAACCACAAACCTAAAAATGAATATGGCTAGAAATGCCATATTTTATATTATAAACTGACAGCACTTCCTTAAAGTTTCAGAATCTCTATA  
GTAGTAATGATATAGGTTGTGACAGTTGTACAGGAGCTCCCATCTGGATTCTGTTAAAACTGTCTGGACAGTGCACATGCTCAGTGAGCT  
CTGGGACAGCTGTTAAGAAGCTAAGTTTAGGGTTGCTGCAAAATTATCAAGCTGAAAATGAGGTTTGTCTGTCATATAAGCTGATGCTACAGGGC  
TAATTATTCAATTCCTGATGCAAATGCTCTGGTTTTAGATCTGTCTGATGTAGTGTGAATCTGAATGAGTTACTAATCAGCTTTTACTGTTACATT  
TATATTCTATATATACAGTATATTGTGAGTCACTCCCTAAGCGCAGTAACTGAGAGCAGCACAGAGCATGTGCAGTGAATGAGCAGATAAGAAG  
ATGGGAGACTACTGGGCATCTTTGGAGGCACAAATCTCCCTGTTAAAGGGCTGTGGTTGCCTTGGGCTGATACAGAAGCCAAAACATAATG  
TATAACAGTTATGCCCTACTTCTTTAGTTAGGCTTTAGTTCTCTCT  
>I\_Full  
AGGGGAAGTGCACCCAAACACACAAGCTTTTTGAAAAGGAAACATAATTTCAAGCAACTTTGCAATATACATCAGTTGAAAAATATGCAGCCTT  
TTCATGATATTTAATGAATAATCTGGTTTGGAAACAGTTCCCTAAGCCCCGCCCTGTTCCCTGCTGATCTGGCTGACTACTTTGTCACCTCA  
AATAAAATGTAACAGTAGTCGCCTGTCCCTCAGCCTGCCATCAGCCTGCCTCCCAATCCCAACAATCCCTGCTGCACACGTGATGTCAATA  
AGGAAAGGAACATCCAGTGCAATGCATTTGTGGTTATGTAGTTCCCTGCATGCTGTCTCTAAACTGTGGAGAAGTTGTTACAATCTGTAACATC  
AGTGTTTTAGTCCCTCCTCCCTTGCCAGGATTTCAAATGATGCAGAAAGAGAAGAGCTGTTTTGCAGCTGGATTTAGCATATAAAAAATGGTAT  
TTATTCCTACTGTTTGAAGGAACAGATTACAGGGATAGGGATATTAGGGGTTTCTGTGATGTGTGGGGCTCTTAAACAAATTTTGGTTCAGAAG  
CAAGAGTTCCCT  
>J\_Arm  
AGGAACAGTTTCAAGTGTAAAAATTAAGTGGGTAAAATAGACAGACTGTGCAAAATAAAAAAATATTTGTAATATAGTTAGTTAGGCAGAAATG  
TAATCTATAAAGGCTGGAGTGAGAAGATGTCTAACATAATAGCCAGAACACTACTTCCCTGCTTTTCCAGCTCTCTAACCTCTTAGTTAGTCAGTGC  
CTTTACGAGGGGGGACACAAGGGACATAAATGTTTCAAGTTAGTTTGTAAAGCACGCAGGTC  
>K\_Full  
AGGAGACATTTTATATAAAGTTCATATTCAGTTATAATATTCATCCTCCCTCAAAATGTGAAATGATGCAGAAAGAAAGAAGTTTGAAGCAT  
TTTACCTCCTAAAACAGCATTATATGAGAGCTGCAGAGACAACCGCTCAAGTCTGAAGCCAGAGCAAAATGAGACATGGCAGTGTCTTCAAT  
CTCCACAGGAAAAGGTCACAGCACTGACTGACAGGCTTTACTCAGCAGCAGCAGGGAAAACCCCTCCCTCCTTCTGTGTCTCTCTGCTTATGC  
TGCTGCCAGGGGGGAGGGGAGGGGAGGGGGGAGAGGAGTGAGTAGAGCAGGAAAGGACTGTCTGTGAGCTCGCTAAGCCCGCCACTCTAT  
GAATATTTCTTCACTTTAAGTAGGTGAGGGGTGTCATAGAAGTCTATGAGGGCCGGGGCTCTGAGCCATATACTGAAGAGTCTAAACCGGA  
AGCTGGCATAAGGCTGGGTAGAGCACAGTTTTCAAGCAGTTATGGACATATTTGAACCCAAAGGTATTAATAAAGCACTTCTTCTATTT  
TACAGTTTTTTTACATGGCTTAGTGCAATGTAAAAATGTATGCTATATATCCCT  
>L\_Full  
AGGGGATATAAACCCTGCTGCCAGCGGGCTCAACCAACGTTACTCAGTTGTTACTGGGCTACAAATCCCAACAATAATGTAACATATAATGA  
AGCTTGGGGCATGCTGGGAGCTGTAGTCCAGCAACATCAGGGCTGTATTTCTTAAAGCAATATTGCCCAATAAACTTTCCCCCAAAATCCCCACA  
GCCAGCGACTGCTTTAACATGCAAAAAATCCTCCAATGAGAATCCCAGCTGATGTGAGTAAATCCGGCTCCCTGTTCTCTGTTCCTGCAATTGG  
AGTTGGGAGCAATAAGCACAGTTTCCAGCACTGAACAAGTCTGTCCCTTTATCCCCATGTCTGATTCCCTGTGCCATATAATGAGGGGAGAAAA  
TGCCATCATTATCTCTATATGTAAGGTACCAGCAAGGGCCTGACACAGTGTGGAAATCAGCATTCTCACTGGGCAGTTCTTTTGCATTTATA  
ATCAACTATTTTATCAGTACAATTTCTATTGGGGAATTTCTTGCATCTATAATGATGGTTTTTGGCAACTTCTATAGCAAACTAGGGGGCGC  
CGTGGGGCAGCATCATGGCTGGTTTTATATCCCT



>G

AGGGGACCTATCACCCAGACATAAAAAAGCTGTATAATAAAAAGTCCTTTTCAAATAAAACGTGAAACCCAAATTAATTTTTTATATTAACACATCC  
AAACCTATTATAAAGGCATTTAAAAATCCAGCTGTCAATCATATATTGCTTGCCCCACCTCTATGCCTTAGGCATAGAGGTGGGGCAGACAAAT  
AACTTTAGCTTTCCATTCAGCACCTTCCAGATGTCACTGCACATCTCACCTTTTCCCTCCCTCCTCCTCATCATCTAACTGTGTAGCCAGTGCA  
TGGGTATAGGCATATGGTCCCCCGTTCTGGCACATAAACAAGATTTTGGCATGATACAAAGCTTGCCTTAATAACAGTGTCCACAAAATGGTGC  
CTGCCGTGTTGCTTTGATTGAGTAATTCAGATGGAAGGAAACAAGATTTATATTATTTATATAGAGTAAATAAAGTTTATTTTGCTCAACTA  
ACAATATAGAAAATAATTTGGAGTTATTTCTTAGGGTGACAGGTCCCT

>H

AGGAGAACTAAAGCCTAACTAAAGAAGTAGGGCATAACTGTTATACATTATGTTTTGGGCTTCTGTATCAGCCCAAGGCAACCACAGCCCTTTA  
ACAGGGAAGATTTGTGCCCTCAAAGATGCCCCAGTAGCTCCCCATCTTCTTATCTGCTCATTCAGTGCACATGCTCTGTGTGCTCTCAGTTAC  
TGCGCTTAGGGACTGACTCACAATATACTGTATATATAAGAAATAAAATGTAACAGTAAAAAGCTGATTAGTAACCTCATTCAGATTCACACTACA  
TGACAGATCTAAAACAGGGCATTTCATCAGAATTGAATAATTAGCCCTGTAGCATCAGCTTATATGACAGACAAAACCTCATTTTCAGCTTGA  
TAATTTGCAGCAACCCCTAAACTTAGCTTCTTAAACAGCTGCCAGAGCTCACTGAGCATGTGCACTGTCCAGGACAGTTTAAACAGAATCCAAG  
ATGGGGAGCTCCTGTGACAACCTTATATCATTACTACTATAGAGATTTCTGAAACTTTAAGGAAGTGTCTGTGAGTTTATAATATAAAA  
ATATGGCATTTCAGCCATATTCATTTTATAGGGTTTTGGTTCTCCT

>I

AGGGGAACTCTGGATTCCCAACCAAAATGTGTTAAAGAGCCCCACACAACACAGAAACCCCTAATATACCTATCCCTGTAATCTGTTCCCTCAA  
AAAGTAGGAATAAATACCATTTTTATATGCTGAAATCCAGCTGCAAAACAGATCTTCTCTCTGTCATCATTTGAAATCCTGGCAGGGGAGGAG  
GGACTAAAACATTGATGTTACAAATGTAACAACCTTCCACAGCTTACAGACAGCATGCAGGAACACATAACCCACAATGCATTGCAGTGGG  
ATGTTCCCTTTCTTATGACATCAGTGTGCAGGGAATGTGGGATTGGGAGGATGCAGGCTGAAGGCTGGGGACAGGGACTACTGTTACATTT  
TTATTTGAGTCACAAAAGTAGCCAGCCAAACAGCAGGGGAACAGGGGGCGGGGCTTAGGGAACTGTTCCAAACCATATTTATACATCAAAAATC  
ATGAAAAGGCGGCATATTTTTTAATGATGTATATGGCAAAGTTGCTTGAAATATGTTTACTTTTTGAAAAGTTAGTGGTGTGTTGGGTGGAGT  
TCTCCT

>J

AGGAACAGTTTCAAGTGTAAAAATTAACCTGGGTAATAATAGACAGACTGTGCAAAATAAAAAAATATTTGTAATATAGTTAGTTAGGCAGAAATG  
TAATCTATAAAGGCTGGAGTGAGAAGATGTCTAACATAATAGCCAGAACACTACTTCCCTGCTTTTCAGCTCTCTAACCTCTTAGTTAGTCAGTGC  
CTTTACGAGGGGGGGCACAAGGGACATAAATGTTTCAAGTTAGTTTGTAAAGCAGCAGGTGAGATTCAAATGCAAACTAACTGACAGTTATGTCTT  
ATAAGCCCCCCCCGAAGTCACTGATTGGCTACTGACTGCTAACAGCTTAGAGAGCTGTAAAGCAGGTAGTAGTGTCTGCTGCTATTATGTTTGA  
CATCTGCCACTCCAGCCTTTATAGATGGCATTGTTGCTTAACTAATATATTGAAAACATTTTTTATTTTGCACAGTCTGTCTGTTTTACCCA  
GTTTCATTTTTTACTGAACTGTTCCCT

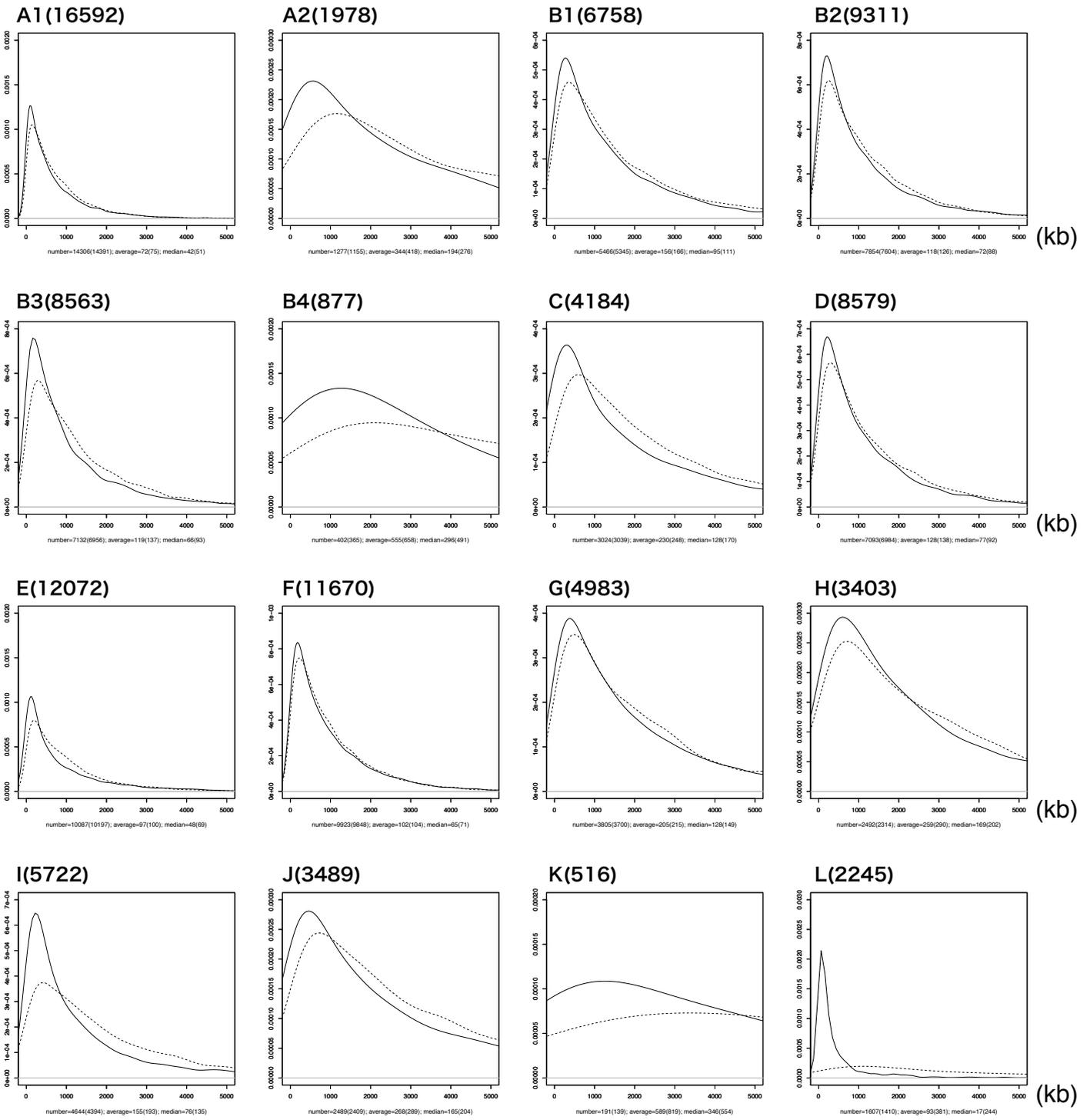
>K

AGGAGACATTTTATATAAAGTTTATATTCAGTTATAATATTCATCCTCCCTCAAATGTGAAATGATGCAGAAAGAAAGATGTTTTGAAAGCAT  
TTTACCTCCTAAAACCTGCCATTATATGAGAGCTGCAGAGACAACCACTCAAGTCTGAAGCCAGAGTAAATGAGACATGGGAGTGTCTTTCAGT  
CTCCACAGGAAGTGGTCACAGCACTGACTGACAGGCTTTACTCAGCAGCAGCAGGGAAAACCCCTCCCTCCTTCTGTGTCTCTCTGTTTTGTGC  
TGCTGCCAGGGGAGGGGGGAGAGGAGCGAGTAGAGCAGGAACGGACTGTCTGTGAGCTCGCTAAGCCCCGCCACTCTAAGAAATATTCACCTC  
ACTTTAAGTGGGTGAGGAGGGTGTCTATAGAAGTCTATGAGGGTGGGGGCTCTGAGCCCTATACTGAAGAGTCTAAACCGGAAGCTGGCATAAG  
GTCTGGGTAGAGCACAGTTTTCAAGCAGTTATGGACATATTTGAACCCAAAGGTATTTAAATAAAAGCACTTCTTCTATTTTACAGTTTTTTA  
CATGTTGAGTGCATTGTAAAAATGTATGCTATATATCCCT

>L

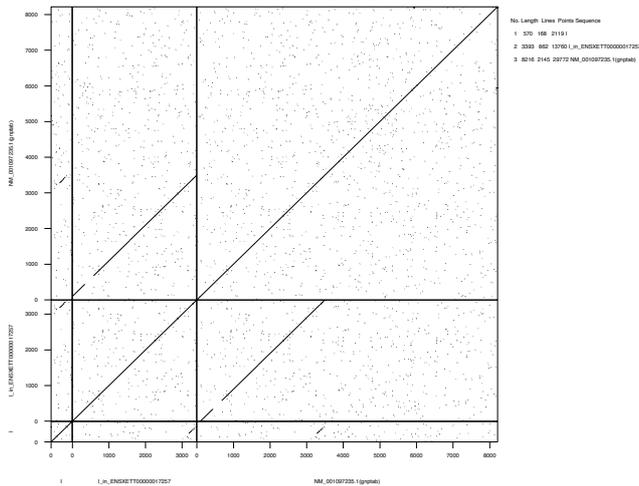
AGGGGATATAAACCACCAACATAACGCTGTCCACTGCGCCCCCTAGTTTTGCTATAGAAGTTGTGCAAAAAACATAATTATAGATGCAAGGAAAT  
TCCCCAATGAGAATTTACTGAGCAACAATCTGATTATAAGTGCAAGAGAAGTGACCAATGAGAATGCTGATTCCAGCACTGTGTGAGGCCCC  
TTGCTGGTACCTTACATATAGAGATAATGATGGCATTTCCTCGTCATTATATGGCACAGGAATCAGACATGGGGATAAAGGGACAGACTTGTTC  
AGTGTGGGAAACTGTGCTTATTGCTCCCAACTCCAATTCAGGAACAGAGAACAGGGAGCCGATTTACTCACATCAGCTGGGATTCTCATTG  
GGGATTTCTTGCATTTAATGGGGATTTGGGGGAAAGTTTTTTAGTGCATATTGCTTTAAGAATACAACCTGATGTTACTGGACTACAGCT  
CCCAGCATGCCTCACCTTTATTATATGTTACATTATCTGGGATTTGTAGTCCAGCAACAACCTGAGTAACGTTTGGTTGAGCCGCGCTGTGCA  
GCAGGGTTTAGTTCCCT

#	length	A1	A2	B1	B2	B3	B4	C	D	E	F	G	H	I	J	K	L	S0	S2	S4	S6	#	length	A1	A2	B1	B2	B3	B4	C	D	E	F	G	H	I	J	K	L	S0	S2	S4	S6	
1	62827	103	13	64	64	53	4	18	37	46	72	39	28	16	20	2	1	36	24	6	1	101	21299	33	7	9	10	23	1	3	14	16	22	5	8	6	5	1	0	9	6	2	0	
2	62330	108	26	61	66	92	16	33	31	34	73	48	22	7	26	4	2	30	17	5	2	102	21299	31	2	20	27	16	0	15	20	21	20	7	9	18	11	2	0	15	2	4	1	
3	55541	82	13	31	52	47	6	19	36	55	65	32	20	39	8	1	3	25	13	10	0	103	21106	31	2	7	20	17	2	5	13	19	15	8	10	14	6	0	0	14	5	2	2	
4	54405	102	8	41	50	65	5	22	37	35	56	24	17	18	25	3	0	35	10	11	2	104	20886	27	7	17	23	23	1	13	19	18	20	12	5	4	1	0	7	8	2	0		
5	52428	111	16	50	48	67	7	21	37	38	55	36	17	11	14	6	1	30	19	3	0	105	20881	37	7	10	34	20	0	7	22	13	30	8	8	8	7	2	1	9	2	0	2	
6	52010	90	14	32	43	52	10	21	36	28	40	30	19	10	17	13	0	26	9	9	3	106	20873	41	3	12	13	17	2	8	5	15	18	8	9	8	10	0	1	15	5	1	1	
7	46758	74	11	26	39	29	3	9	25	17	54	15	17	14	14	1	1	33	10	4	1	107	20862	52	4	15	24	18	0	11	21	33	32	12	15	22	9	1	1	12	8	2	0	
8	46591	97	17	31	44	51	6	17	33	32	37	25	26	15	23	2	1	28	12	1	3	108	20815	13	5	14	18	17	2	5	13	20	15	8	9	1	4	0	0	10	4	3	1	
9	46283	76	3	16	42	41	3	16	39	42	56	20	11	17	18	0	2	21	10	4	3	109	20776	40	1	18	25	11	0	8	21	19	19	13	15	27	9	0	0	13	8	0	0	
10	44111	79	9	24	38	38	5	12	27	20	46	20	19	10	12	2	1	15	15	5	0	110	20648	29	5	10	17	21	2	4	17	12	27	8	7	7	8	0	2	14	7	2	1	
11	43972	76	13	27	42	61	3	15	26	21	49	28	16	10	22	1	3	27	6	3	2	111	20623	30	0	4	10	7	0	5	16	25	30	3	1	13	3	0	3	15	6	2	1	
12	43756	81	5	27	35	43	3	11	36	23	45	24	15	15	14	1	1	14	10	6	4	112	20107	53	2	7	20	13	1	6	21	29	27	10	8	21	5	0	11	7	1	3	1	
13	42981	78	7	32	30	51	3	13	25	20	43	18	18	5	20	8	0	21	10	6	6	113	20015	29	9	18	16	26	2	7	7	9	19	12	5	3	5	0	0	18	4	1	0	
14	42730	42	6	30	68	9	2	13	31	27	50	10	16	39	9	2	1	21	10	4	1	114	19591	37	11	21	27	23	3	7	10	19	16	9	4	3	6	3	0	10	9	2	2	
15	42605	64	4	16	39	37	2	13	37	36	42	16	10	29	10	0	0	29	9	5	2	115	19520	51	7	18	19	22	2	5	15	14	23	15	8	5	3	2	0	10	4	4	0	
16	42535	73	4	29	49	32	2	10	49	43	49	12	13	38	12	2	0	27	8	6	1	116	19230	16	6	11	20	19	2	2	9	5	16	9	4	2	3	2	2	1	0	7	3	2
17	42425	104	9	45	52	49	3	19	27	25	59	21	21	7	19	2	0	19	15	7	0	117	19078	28	5	11	20	19	26	1	4	9	12	34	17	5	1	12	2	0	20	7	1	0
18	40456	62	7	23	39	38	6	12	36	24	49	27	18	13	12	2	3	25	7	8	2	118	18666	33	3	12	17	27	0	4	14	14	15	13	8	7	5	0	0	11	6	1	3	
19	39362	72	9	30	35	33	4	16	22	36	48	27	10	29	14	0	3	20	9	3	1	119	18501	29	5	15	15	20	0	5	15	13	9	8	6	7	2	0	10	3	1	0		
20	38510	64	9	27	38	31	6	16	30	26	30	14	12	11	14	2	17	23	13	1	0	120	18487	34	1	15	16	16	2	4	19	10	12	5	16	8	5	1	1	12	5	3	2	
21	37693	51	8	19	30	32	1	17	29	28	41	19	27	19	14	0	2	36	12	2	0	121	18299	57	2	18	22	16	1	10	19	19	22	15	6	15	4	2	1	8	3	4	2	
22	37689	61	5	22	21	23	5	33	45	40	33	15	18	64	10	0	42	18	18	1	0	122	18151	40	6	17	14	17	2	12	21	28	26	7	3	16	17	1	5	9	5	3	0	
23	36649	59	5	32	43	37	3	13	25	23	39	22	20	16	16	3	3	15	7	3	3	123	18049	28	6	8	22	20	2	7	12	16	24	15	5	16	9	0	1	8	4	2	0	
24	35408	63	10	26	28	41	4	8	16	17	34	15	11	6	12	6	0	27	11	1	2	124	18044	17	3	11	20	21	2	4	16	14	16	8	6	4	10	0	0	10	7	0	0	
25	34389	74	10	28	51	39	6	15	18	33	34	20	16	6	11	3	1	11	11	4	4	125	18012	25	7	25	18	38	6	9	5	11	11	14	1	1	7	4	1	11	4	1	2	
26	34224	57	8	27	24	45	2	12	17	34	39	14	8	10	10	5	0	20	6	3	2	126	18001	44	2	15	12	7	3	9	19	13	17	10	5	13	8	0	0	12	3	2	1	
27	33484	58	10	24	29	42	5	13	23	24	43	31	8	13	11	1	2	17	7	4	0	127	17989	30	0	5	20	7	0	5	28	14	15	10	6	21	13	1	0	5	7	2	1	
28	33121	44	5	20	27	13	3	17	48	35	66	14	3	39	14	0	3	21	10	6	1	128	17872	26	2	9	20	22	1	7	14	22	12	7	10	2	6	0	1	11	2	3	0	
29	32675	59	9	27	38	43	5	19	27	29	32	26	15	2	18	5	0	14	7	2	0	129	17725	46	6	20	24	27	3	6	12	26	17	6	4	7	6	3	0	14	3	2	3	
30	32545	61	4	14	27	25	7	8	22	21	29	19	15	8	17	0	2	12	4	2	0	130	17721	21	0	13	23	9	0	7	33	21	19	12	6	33	7	1	2	8	6	0	0	
31	31759	48	12	22	19	20	4	7	14	15	29	18	5	1	11	3	1	8	9	3	1	131	17622	54	9	10	19	32	1	11	16	18	18	16	10	10	7	1	3	9	3	3	1	
32	31444	49	8	18	14	22	1	11	22	24	14	15	8	4	1	3	20	9	7	1	0	132	17591	24	4	15	13	22	4	4	14	10	15	6	2	4	0	6	3	1	2	0	0	
33	30458	68	22	33	44	54	4	9	18	24	31	25	8	3	29	7	0	21	12	2	1	133	17585	36	2	20	12	16	1	9	12	23	26	6	8	16	3	3	0	9	3	1	0	
34	30419	60	6	40	34	37	7	11	13	34	25	17	9	15	10	3	0	11	8	4	2	134	17420	20	0	5	21	13	1	5	11	7	27	3	3	1	2	0	0	9	4	1	1	
35	30391	83	17	32	41	37	3	15	22	26	32	25	23	4	6	2	1	19	4	5	1	135	17398	30	6	29	24	35	6	7	15	12	15	11	5	4	4	1	1	13	8	1	1	
36	30088	69	9	30	39	32	7	11	14	26	35	20	7	8	14	3	1	22	14	4	0	136	17268	37	8	12	13	17	2	5	16	16	29	8	6	13	7	0	1	8	5	5	0	
37	29897	47	6	25	30	34	3	14	25	18	33	19	14	8	13	1	3	14	3	0	0	137	17194	23	4	14	23	17	1	5	6	12	5	13	2	3	4	1	0	13	4	1	2	
38	29847	51	7	20	24	18	0	11	9	25	27	23	10	11	15	1	0	16	10	1	5	138	17096	31	6	8	5	11	1	7	9	28	17	13	9	16	4	1	0	7	2	2	1	
39	29628	46	1	19	40	10	2	12	60	28	42	10	9	53	11	0	2	12	6	2	0	139	17085	34	4	18	22	18	2	8	11	8	22	7	4	5	3	0	25	11	5	1	2	
40	29218	37	2	16	33	8	0	10	47	27	39	16	8	45	8	2	2	14	6	1	3	140	17070	34	7	9	20	23	3	15	10	11	23	6	8	2	2	0	3	5	6	2	1	
41	28998	37	2	20																																								

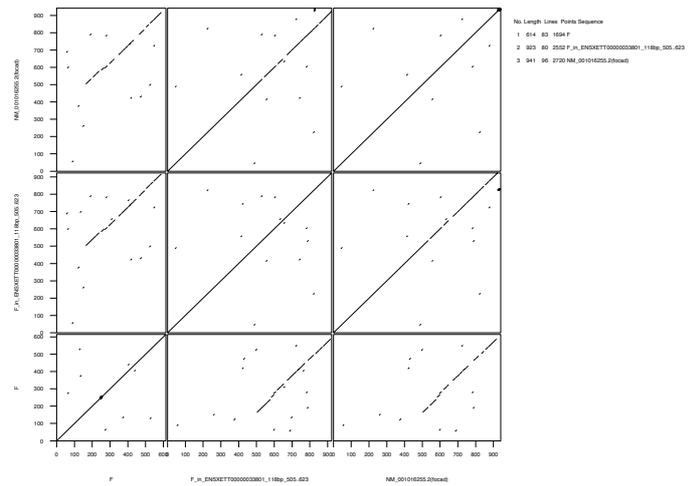


subfamily	scaffold	MDS (blast hap)	CDS	overlap (bp)	gene	gene_name	transcript_id	RefSeq	confirmed by RefSeq?
I	GL172879.1	261531..261933(+)	261674..261884(+)	211	225856..265318(+)	GNPTAB	ENSETT00000017257	NM_001097235.1	Yes
K	GL172875.1	3435261..3435711(+)	3435469..3435603(-)	135	3433943..3454607(-)	ppp2r1b	ENSETT00000022421	NM_001006774.1	No
A1	GL173124.1	823341..823711(+)	823347..823466(-)	120	815780..830227(-)	dhx16	ENSETT000000051925	NM_001123409.3	No
F	GL173413.1	116282..116735(+)	116603..116720(-)	118	33530..137132(+)	kiaa1797	ENSETT000000033801	NM_001016255.2	Yes
A1	GL173088.1	901059..901326(+)	901067..901183(-)	117	876873..912553(-)	lrcc1	ENSETT00000040731	NM_001197231.1	No
F	GL172733.1	1441562..1441885(-)	1441601..1441716(-)	116	1436696..1447770(-)	NP_001027479.2	ENSETT00000017435	NM_001032308.2	No
G	GL172834.1	859221..859588(+)	859317..859429(-)	113	849959..888471(-)	adam33	ENSETT00000005550	NM_001040013.1	No
A1	GL172761.1	344065..344404(-)	344282..344392(+)	111	328399..411668(+)	kidins220	ENSETT00000018144	NM_001126687.1	No
B3	GL173184.1	286838..286942(-)	286834..286966(+)	105	245716..287988(+)	ddx25	ENSETT00000000036	NM_001016345.2	No
A1	GL172692.1	3122405..3122570(-)	3122468..3122604(+)	103	3115645..3125278(-)	c7orf46	ENSETT00000038945	NM_001016728.2	No
D	GL172915.1	373229..373713(+)	373437..373537(-)	101	370579..375892(-)	ncstn	ENSETT00000020345	NM_001130239.1	No
B4	GL173378.1	70528..70853(+)	70548..70645(-)	98	63534..76290(-)	ccdc38	ENSETT00000004674	XM_002941257.1	No
A1	GL173124.1	823341..823711(+)	823565..823661(-)	97	815780..830227(-)	dhx16	ENSETT000000051925	NM_001123409.3	No
F	GL173241.1	500860..501186(+)	500923..501019(+)	97	487714..508657(+)	eif3a	ENSETT00000022578	NM_001102703.1	No
L	GL178349.1	2550..2957(-)	2679..2772(-)	94	30..4446(-)	ldha	ENSETT00000030484	NM_203822.1	No
F	GL173156.1	804319..804781(+)	804511..804602(+)	92	799519..813029(+)	ifl3	ENSETT00000025481	NM_001005648.1	No
B4	GL173194.1	319547..320154(+)	319809..319896(+)	88	295158..331402(+)	otud4	ENSETT00000038234	NM_001079130.1	No
G	GL172832.1	433681..434178(-)	433745..433831(+)	87	289826..480506(+)	grm7	ENSETT000000014740	NM_001113008.1	No
A2	GL173259.1	515994..516193(-)	516005..516089(-)	85	515598..518296(-)	ubiad1	ENSETT00000037881	NM_001016538.2	No
F	GL173417.1	292137..292331(+)	292159..292242(-)	84	290402..295844(-)	rae1	ENSETT00000024601	NM_001017142.2	No
D	GL173861.1	35653..35949(+)	35871..35965(+)	79	17161..37781(+)	XB-GENE-5944458	ENSETT00000035505	NM_001113022.1	No
C	GL172841.1	1404856..1405124(+)	1405043..1405120(+)	78	1403017..1405503(+)		ENSETT00000006289	XM_004911490.1	No
F	GL173241.1	500860..501186(+)	501039..501116(+)	78	487714..508657(+)	eif3a	ENSETT00000022578	NM_001102703.1	No
L	GL173631.1	217462..218049(-)	217940..218017(+)	78	144655..227690(+)	pde2a	ENSETT00000026797	NM_001079139.1	No
F	GL173156.1	804319..804781(+)	804420..804494(+)	75	799519..813029(+)	ifl3	ENSETT00000025481	NM_001005648.1	No
G	GL172699.1	2495226..2495349(-)	2495085..2495300(-)	75	2491536..2502094(-)	kkf5	ENSETT00000034619	NM_001033942.2	No
B3	GL173016.1	422877..423063(+)	422890..422959(-)	70	406036..430325(-)	cnat2	ENSETT00000024867	NM_001113129.1	No
L	GL178349.1	2550..2957(-)	2556..2623(-)	68	30..4446(-)	ldha	ENSETT00000030484	NM_203822.1	No
F	GL172757.1	1800462..1800532(+)	1800467..1800580(+)	66	1791437..1802208(+)	ing3	ENSETT00000049164	NM_001008672.2	No
E	GL173985.1	3111..3233(-)	3102..3174(-)	64	550..45030(-)	spag17	ENSETT00000052139	NM_001130282.1	No
B2	GL173247.1	155864..155782(+)	155885..155747(-)	63	136912..180408(-)	usp15	ENSETT00000046428	NM_001128026.1	No
F	GL173241.1	500860..500812(+)	500671..500728(+)	58	487714..508657(+)	eif3a	ENSETT00000022578	NM_001102703.1	No
G	GL172699.1	2494921..2494986(-)	2494929..2495007(-)	58	2491536..2502094(-)	kkf5	ENSETT00000034619	NM_001033942.2	No
E	GL173076.1	687295..687608(-)	687553..687765(-)	56	665658..696816(-)	acly	ENSETT00000004898	NM_0010000004898	No
A1	GL173124.1	823341..823711(+)	823509..823562(-)	54	815780..830227(-)	dhx16	ENSETT000000051925	NM_001123409.3	No
F	GL172818.1	565107..565380(-)	565282..565335(-)	54	559393..590587(-)	irs2	ENSETT00000005915	NM_0010000005915	No
K	GL172665.1	2113698..2114088(-)	2113778..2113831(+)	54	2112442..2131155(+)	F7D6V4_XENTR	ENSETT00000066405		No
B3	GL172950.1	1007416..1007619(-)	1007426..1007478(+)	53	1005964..1031967(+)	nph3	ENSETT00000057498	NM_0010000057498	No
D	GL172637.1	2000610..2000675(-)	2000612..2000660(+)	49	1991738..2005275(+)	rad54l	ENSETT00000009513	NM_0010000009513	No
A1	GL172721.1	531790..532007(+)	531905..531951(+)	47	521344..536936(+)	sass6.2	ENSETT00000002827	NM_0010000002827	No
A1	GL173053.1	310205..310530(+)	310406..310452(+)	47	296293..327722(+)	csnk1g1	ENSETT000000014106	NM_00100000014106	No
G	GL172699.1	2495226..2495349(-)	2495303..2495372(-)	47	2491536..2502094(-)	kkf5	ENSETT00000034619	NM_001033942.2	No
K	GL172888.1	725962..726202(+)	726069..726113(-)	45	716489..732583(-)	TDRD5	ENSETT000000063785	NM_00100000063785	No
B2	GL172854.1	481922..481971(-)	481920..481965(+)	44	455077..489979(+)	abi2	ENSETT00000009002	NM_0010000009002	No
B4	GL173388.1	119248..119325(-)	119250..119293(+)	44	108207..128102(+)	bag6	ENSETT00000005323	NM_0010000005323	No
F	GL172733.1	1441338..1441511(-)	1441390..1441433(+)	44	1436696..1447770(-)	NP_001027479.2	ENSETT00000017435	NM_001032308.2	No
B2	GL172677.1	2491833..2491874(+)	2491802..2491898(+)	42	2467602..2504567(+)	ahcy1l	ENSETT00000032638	NM_0010000032638	No
B2	GL172961.1	236838..236899(-)	236746..236879(+)	42	228909..238059(+)		ENSETT00000015926	NM_0010000015926	No
D	GL172971.1	312282..312723(-)	312434..312475(-)	42	268235..341061(-)	ppf1bp2	ENSETT00000019847	NM_0010000019847	No
J	GL172648.1	4945779..4945938(+)	4945897..4945949(-)	42	4944813..4948407(-)	snrpd3	ENSETT00000035564	NM_0010000035564	No
K	GL172719.1	2644669..2645068(-)	2644491..2644982(+)	42	2641378..2671639(+)	lyn	ENSETT000000065618	NM_00100000065618	No
A1	GL172692.1	2572738..2572884(-)	2572834..2572874(+)	41	2501109..2579685(+)	osbp3l	ENSETT000000062912	NM_00100000062912	No
F	GL172733.1	1441562..1441885(-)	1441793..1441833(-)	41	1436696..1447770(-)	NP_001027479.2	ENSETT000000051925	NM_001032308.2	No
E	GL173718.1	4917..4981(+)	4908..4956(-)	40	3586..16432(-)	c9orf86	ENSETT00000008555	NM_0010000008555	No
I	GL173266.1	275103..275541(+)	275159..275198(-)	40	247694..275775(-)	c3orf84	ENSETT00000035246	NM_0010000035246	No
K	GL172675.1	3435261..3435711(+)	3435529..3435566(-)	38	3433943..3454607(-)	ppp2r1b	ENSETT0000004582	NM_001006774.1	No
K	GL172888.1	725962..726202(+)	726166..726220(-)	37	716489..732583(-)	TDRD5	ENSETT000000063785	NM_00100000063785	No
K	GL173622.1	128150..128744(+)	128417..128451(-)	35	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
K	GL173622.1	127008..127602(+)	127274..127308(-)	35	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
K	GL173210.1	85352..85914(-)	85646..85679(+)	34	23894..102289(+)		ENSETT00000042208	NM_0010000042208	No
B3	GL172669.1	965637..965862(-)	965831..965887(+)	32	959419..969380(-)	pak1ip1	ENSETT00000002331	NM_0010000002331	No
B4	GL173388.1	119248..119325(-)	119294..119383(+)	32	108207..128102(+)	bag6	ENSETT00000005320	NM_0010000005320	No
E	GL172871.1	134813..135136(-)	134774..134844(+)	32	134509..140013(+)	tmem41b	ENSETT000000052225	NM_00100000052225	No
A1	GL172842.1	399298..399429(+)	399330..399360(+)	31	397199..414974(+)	C6orf97	ENSETT00000031912	NM_0010000031912	No
B1	GL172771.1	2072861..2073114(-)	2072859..2072891(-)	31	2049695..2079965(-)	SBNO1	ENSETT000000063499	NM_00100000063499	No
F	GL172818.1	565420..565526(-)	565493..565523(-)	31	559393..590587(-)	irs2	ENSETT00000005915	NM_0010000005915	No
K	GL173622.1	135770..136365(+)	136039..136069(-)	31	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
B1	GL173046.1	113291..113396(-)	113309..113338(-)	30	101711..122392(-)	E2IFV0_XENTR	ENSETT000000064398	NM_00100000064398	No
B2	GL173046.1	113293..113396(-)	113309..113338(-)	30	101711..122392(-)	E2IFV0_XENTR	ENSETT000000064398	NM_00100000064398	No
E	GL173718.1	9096..9144(-)	9091..9125(-)	30	3586..16432(-)	c9orf86	ENSETT00000008555	NM_0010000008555	No
K	GL173622.1	134090..134686(+)	134361..134390(-)	30	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
K	GL173622.1	131274..131866(+)	131545..131573(-)	29	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
K	GL173622.1	137447..138034(+)	137717..137745(-)	29	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
A1	GL173076.1	688862..689278(+)	689251..689284(-)	28	665658..696816(-)	acly	ENSETT00000004898	NM_0010000004898	No
A1	GL173088.1	901059..901326(+)	901244..901271(-)	28	876873..912553(-)	lrcc1	ENSETT00000040731	NM_001197231.1	No
K	GL173622.1	124142..124738(+)	124414..124441(-)	28	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
K	GL173622.1	132952..133496(+)	133223..133250(-)	28	104164..180986(-)		ENSETT00000013455	XM_002942482.2	No
F	GL172801.1	1935177..1935276(+)	1935241..1935267(+)	27	1920841..1937615(+)	nxph3	ENSETT000000063146	NM_00100000063146	No
G	GL172654.1	4272619..4272723(-)	4272697..4272742(-)	27	4260489..4315746(-)	arc3	ENSETT000000049117	NM_00100000049117	No
J	GL172648.1	4945779..4945938(+)	4945837..4945863(-)	27	4944813..4948407(-)	snrpd3	ENSETT00000035564	NM_0010000035564	No
K	GL173622.1	122469..123059(+)	122740..12						

(A) I : ENSXETT00000017257 : RefSeq(gnptab)



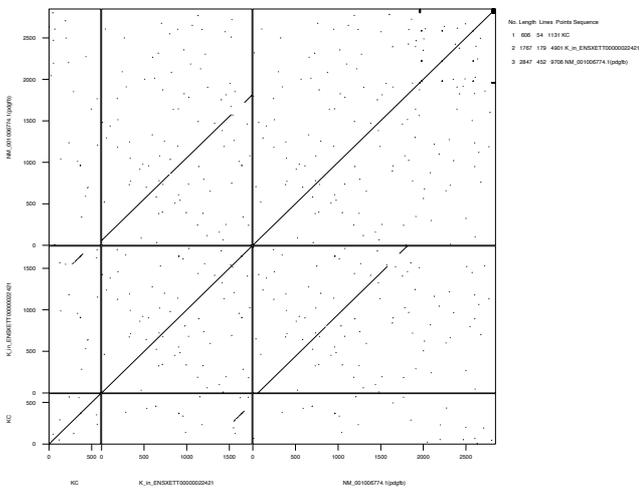
(B) F : ENSXETT00000033801 : RefSeq(focad)



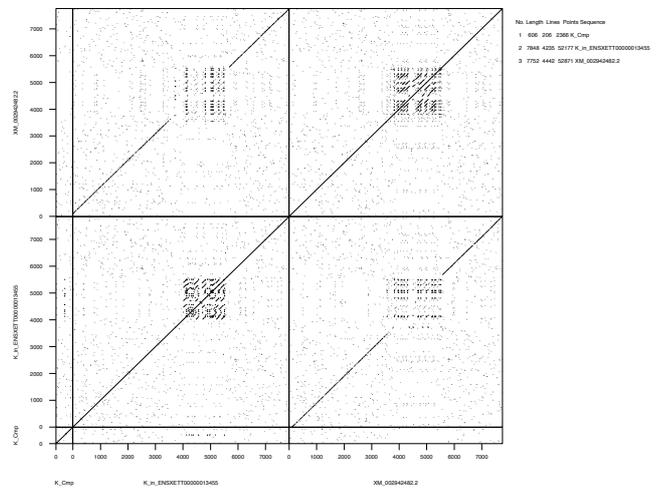
>NP\_001090704.1|N-acetylglucosamine-1-phosphotransferase subunits alpha/beta  
 MLLNSLLKLVQRQTYTCLSHRYGLYLFCFGLLLLLIVSALQFGEVVLWESRDQYH  
 VLFDTYRDNIAGKSFQNRCLPMPIDVVYTWVNGTDPDLVLQLOEYREQMEERQ  
 RAFREFLGRNKTEPTKRSKLELECLLTHCIKVPMLILDPLPANTTLKNLQASQ  
 PVFSSAVKIFNVAKPKNPSTNVTIVFEAIQEAENAQVNALFDNRKETIWRGYM  
 TTDKEAPGLVLIPLDLAFLSGFPETYKETDQLRAKLPETLSSKIKLLHLYSEASV  
 ALLQLNPKDFQELNIQAKKNMTIEGKELTSSAYLLWDLSSAVSLKQDEDISA  
 SRFEDNEELRYSLSRIEKHAPWVRHVIVTNGQIPSWLNLNPRVTIVTHQEIF  
 SNTSHLPTFSSPAIESHIHRIPGLSQKFIYMNDVDFGTSVWVDDFYSHSKGQK  
 VYLTWPVPCAEGCPSGWIKDGKACNNSACDWDGGDCLGNAAGRFPAPVPG  
 GLLNGQWQPGIGISGVSYCNOGCANSWLADKFCDAQCNVLSGCFDAGDCGQDH  
 FEEMYKINMYLNKTHYIVPKGEHLPYFSFDNMAKKVLDGVYSDNPVIRHASIAN  
 KWKTIHLIMYPGMNATLVHFNLTFLGLDDKEIKMQIVIAVDTGDEYKRNITATS  
 IKKGAMLTTPPEAEVLFEDIPEEKRFPRFRKYPVTDVRSVDTIPNINLSSLP  
 NKVQLALQNLQKLNKGDITLKGYNLSRFSLEPYRSLADPRDQSLDNKGNIQQ  
 SQRDNKTITQHKIGPKSSFTEVVNNKENAASKSISPIKRLTDLHREHPQTPKAN  
 IQKNAIEKENKAVVPGRMLQEQYQPNYEGFLPWEKMKYFQDLLDEEAALLSDLS  
 YITSSKQVGRKLQDTFADSLRHVNKLLNSKFGFASRKVPAHPHMDRIVMQEL  
 QDLYPEAFDKTSAHKVRHSEDMQFAPFSYFYLYMSAIQTLNISHVFEQVDTDSSG  
 VLSREIRTLATRIHQPLSLQDLTSLEQMLINCSKSIQHNSTDEGVVPPPTQES  
 YYDPNLPVSKVLVLSCKPVTDLIRKTYKDKNKYS**LQTAFRNYITHNALHCDVP**  
**FLIDITCAGNCWIRRMQAEGRLRIVNYCYIFFYFLSLKAVIQISRRTGSSA**

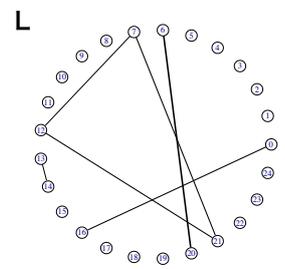
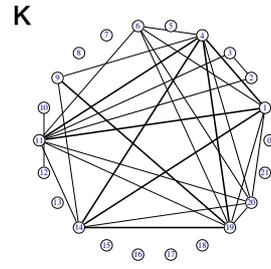
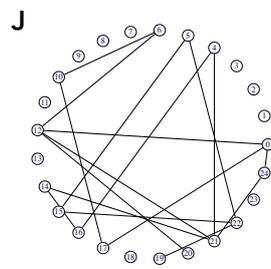
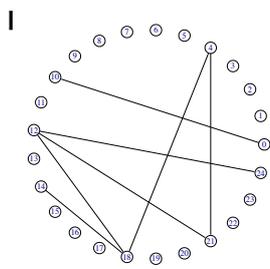
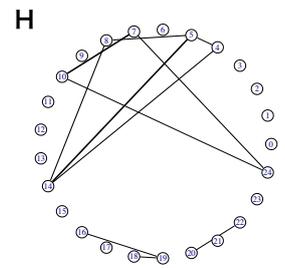
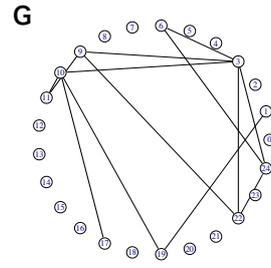
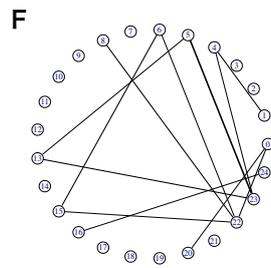
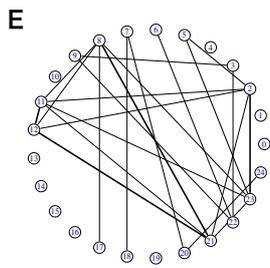
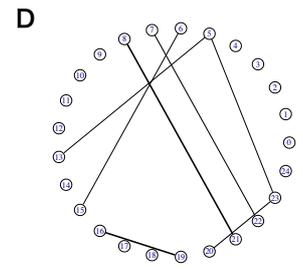
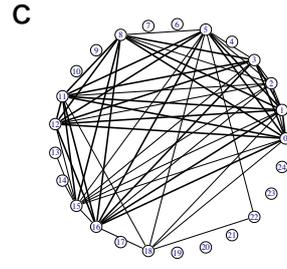
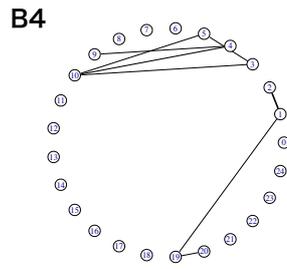
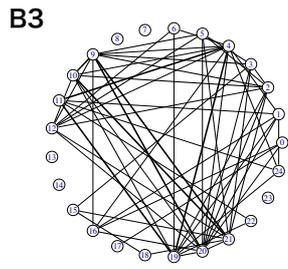
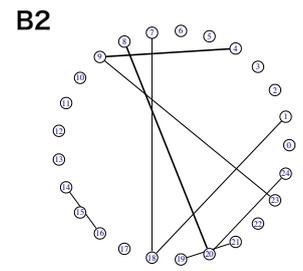
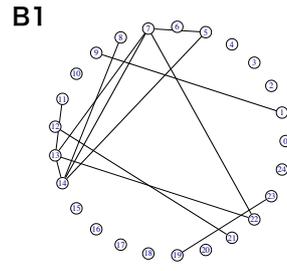
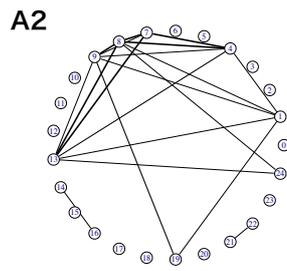
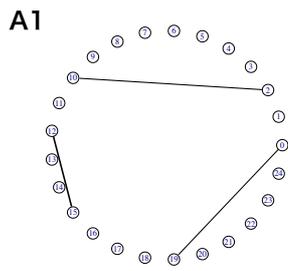
>gi|351721231|ref|NP\_001016255.2| uncharacterized  
 protein LOC549009  
 MATPFTETSQVHACFPKMSEDLKKRLEFPNSLIQTQAVTQLIASVLKENVSLGK  
 IKQSSNQTPALNILEWCKCSNNVVVTRACCEALVLLVEQDHADFDYVLNGILNL  
 IPSAGTVQGLLKCVWRLLYTQARNAEKDGEHKDLGIYKIW**VPQPCDLCSGELRS**  
**HFTAELQVGVTSPPSQQNNGGGAG**

(C) K : ENSXETT00000022421 : RefSeq(pdgfb)



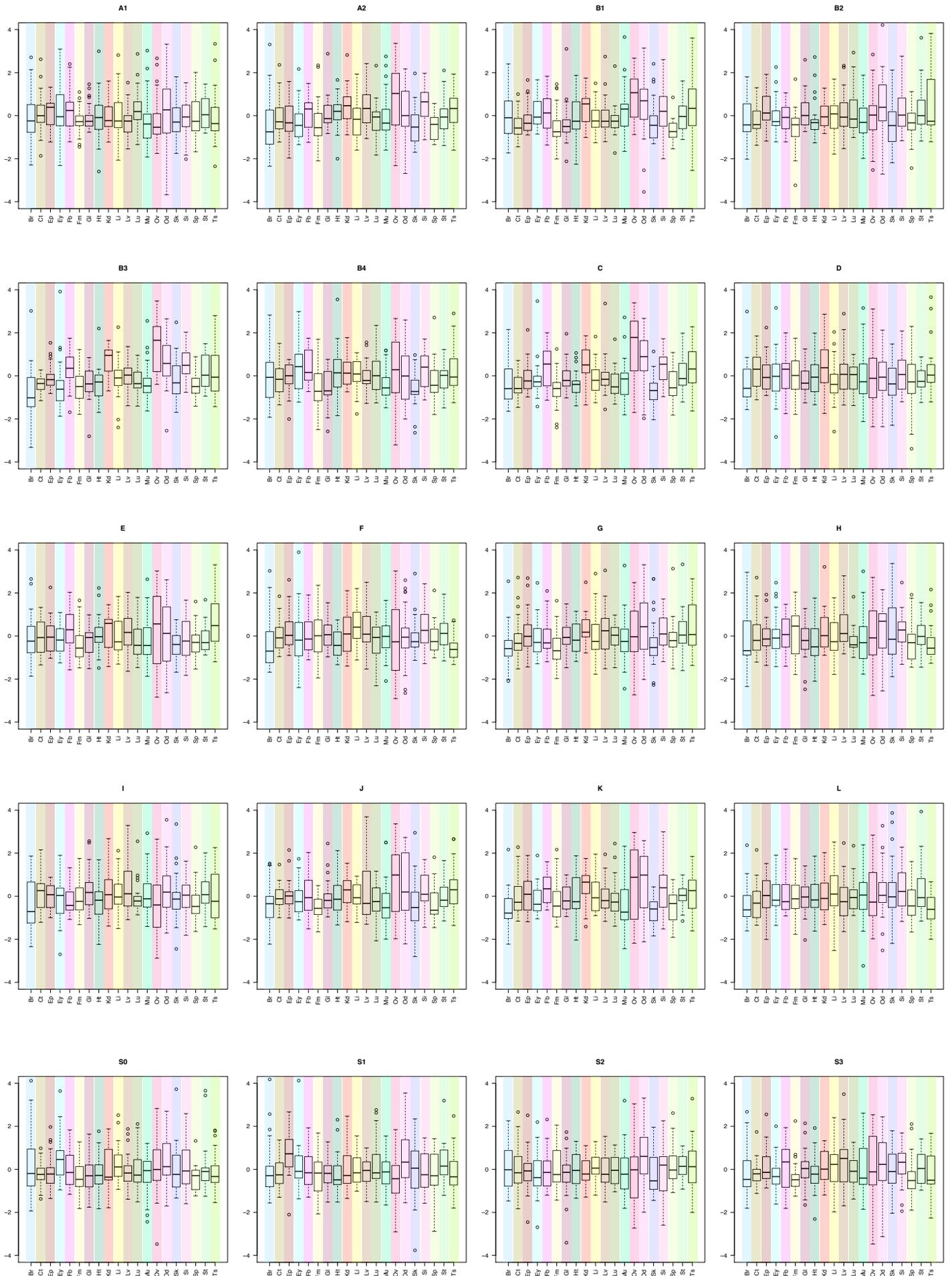
(D) K : ENSXETT00000013455 : RefSeq(mucin-2-like)

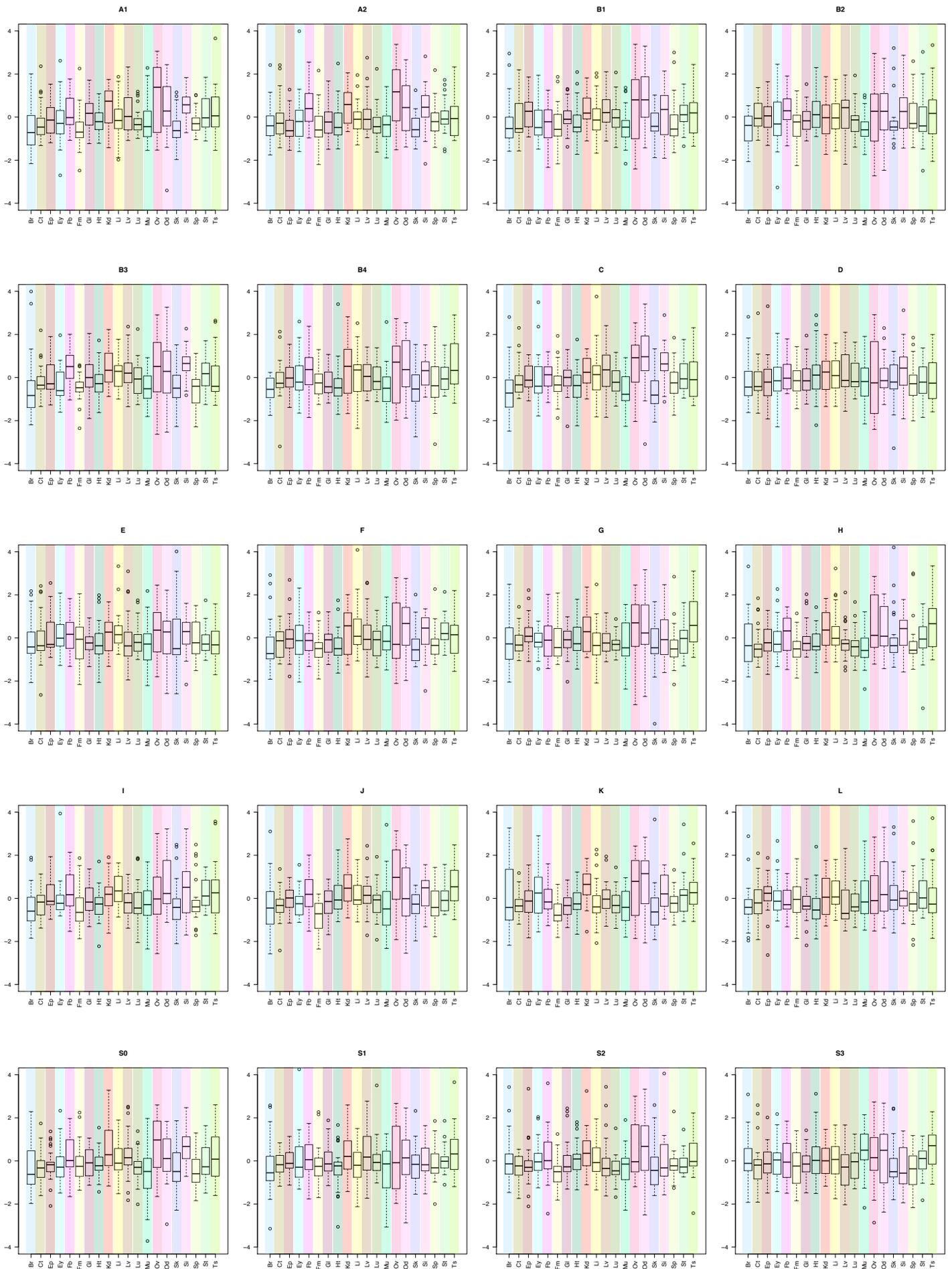




— correlation  $\geq 0.6$   
— correlation  $\geq 0.7$   
— correlation  $\geq 0.8$

(A) upstream





Supplementary Data S7 (continued)