# A single Hox locus in Drosophila produces functional microRNAs from opposite DNA strands

# **Supplementary Data**

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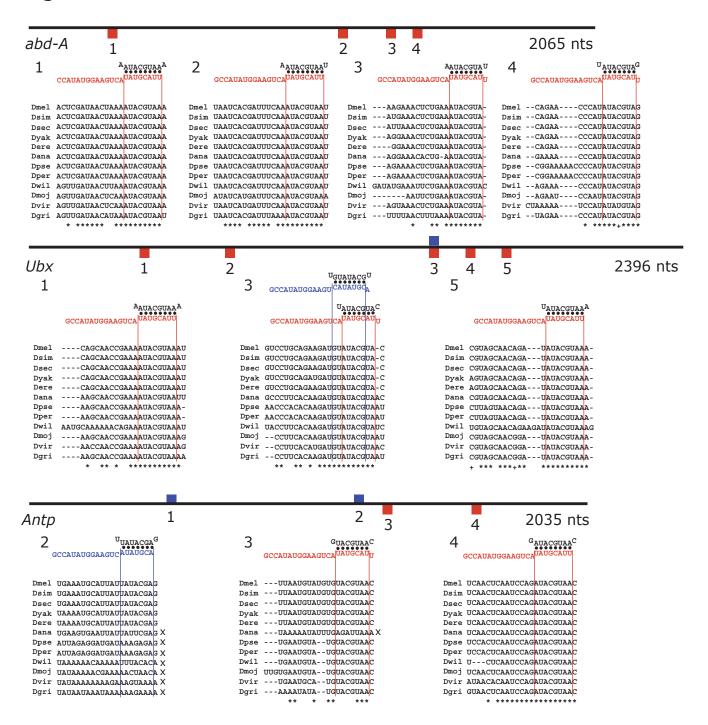
# Figure S1

pri-miR-iab-4 sense

emb	ryos	larv	ae	pup	ae	fema	les	mal	es
+ RT	- RT	+ RT	- RT	+ RT	- RT	+ RT	- RT	+ RT	- RT
-		_		-					
pri-miR-	iab-4 AS								
emb	oryos	lar	/ae	pur	oae	fema	ales	ma	les
+ RT	- RT	+ RT	- RT	+ RT	- RT	+ RT	- RT	+ RT	- RT
-	2000	-	100	-		-		-	

**Figure S1:** miR-iab-4 sense and anti-sense are expressed throughout fly development. Shown are strand-specific RT-PCR products (neg. control without RT) for the miR-iab-4 sense and anti-sense primary transcripts for different stages of fly development.

### Figure S2



**Figure S2**. miR-iab-4AS target sites the *Hox* genes *abd-A*, *Ubx*, and *Antp* miR-iab-4AS has 4 seed sites (nts 2-8 or A+2-7; Lewis et al., 2005; red) in *abd-A*, *5 in Ubx*, and 2 in *Antp* of which 4, 3, and 1 are fully conserved across 12 Drosophila species (*Drosophila melanogaster*, *simulans*, *sechellia*, *yakuba*, *erecta*, *ananassae*, *pseudoobscura*, *persimilis*, *willistoni*, *mojavensis*, *virilis*, *grimshawi*), respectively. 1 site in the 3'UTR of *Ubx* shows extended complementarity such that it also constitutes a seed site for miR-iab-4 (blue). *Antp* has 2 sites for miR-iab-4 that are distinct from the miR-iab-4AS sites, while *abd-A* has no such sites. \* denotes fully conserved sequence positions, and x denotes species where the site is not conserved.

# Table S1: Anti-sense transcripts near known miRNAs

# Drosophila miRNAs

miRNA	#transcripts	Transcript IDs
FlyBase Noncodin	g Genes	
dme-mir-281-1	1	CR33594
dme-mir-281-2	1	CR33596
ESTs		
dme-mir-277	2	EC255080,CO344262
dme-mir-2a-1	1	CO341270
dme-mir-284	1	CK135092
dme-mir-33	1	BI631776
dme-mir-2a-2	6	CO341270,EC253459,EC253459,CO341270,CO341 270,CO341270

#### Introns

dme-mir-289, dme-mir-31b, dme-mir-274

# Table S1: Anti-sense transcripts near known miRNAs (continued)

### **Human miRNAs**

miRNA	#transcripts	Transcript IDs
RefSeq Gene	.s	
hsa-mir-662	2	NM 001025190,NM 001025190
hsa-mir-328	4	NM_024712,NM_024712,NM_024712
hsa-mir-367	4	NM_015454,NM_016648,NM_015454,NM_016648
hsa-mir-191	1	NM_199074
UCSC Genes		
hsa-mir-662	2	uc002cjz,uc002cjz
hsa-mir-328	12	uc002esa,uc002esb,uc002esc,uc002esa,uc002esb,uc002 esc,uc002esa,uc002esb,uc002esc,uc002esa,uc002esb,uc002esc
hsa-mir-367	8	uc003iay,uc003iaz,uc003iba,uc003ibb,uc003iay,uc003iaz,uc003iba,uc003ibb
hsa-mir-99b	1	uc002pxg
hsa-let-7e	1	uc002pxg
hsa-mir-636	2	uc002jsz,uc002jta
hsa-mir-125a	1	uc002pxg
hsa-mir-191	1	uc003cvn
ESTs		
hsa-mir-639	11	DA578654,DB036923,BE163339,BX337999,BE173861,A W601441,AW601462,AW602622,AW602643,BE076002,B G978956
hsa-mir-26a-1	. 1	BG013974
hsa-mir-659	2	N64538,N64538
hsa-mir-632	4	CR982540,BF739929,BF986402,BG005263
hsa-mir-545	1	CF121922
hsa-mir-142	11	AA736584,AI214324,AA480329,AI803986,BM987623,AW 075941,BM994627,AA749202,AW075748,AA804593,AA8 04593
hsa-mir-1-2	2	AI220268,AI265999
hsa-mir-614	8	BG546987,AA494355,BE001688,BE001688,BE 001688,BE815242,BE825683
hsa-mir-34c	1	CB243753
hsa-mir-423	1	AW001018
hsa-mir-324	2	DB118628,AA428344
hsa-mir-609	5	BF946814,BF946811,BF946814,BF946814,BF946814
hsa-mir-143	3	AW750687,AW750687,BF328624
hsa-mir-612	13	BF371267,BF359112,BQ373809,BQ332593,BQ332596,B F808842,BF359123,BQ373809,BF877468,BG990102,AW 939381,BQ327427,BF894409
hsa-mir-124a-		BU738550
hsa-mir-570	1	BE162667
hsa-mir-631	10	CV569139,CN361157,BX644907,DA065297,BF827870,C R978078,BF922074,BF827870,BM709090,AA359490
hsa-mir-770	3	AI970289_dup1,AI636778_dup1,AI963928_dup1
hsa-mir-299	2	AW895894,AW895880

hsa-let-7i hsa-mir-503	1 10	CR992282 R79973,H01302,R79973,R79973,R79973,H01302,R7997
		3,R79973,R79973,R79973
hsa-mir-339	1	DB317795
hsa-mir-219-2	1	DA115674
hsa-mir-125b-	1	BG000222
hsa-mir-499	13	BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149,BE297149
hsa-mir-517a	1	BF994458
hsa-mir-141	4	AI695443,AA863389,AA863395,AI969882
hsa-mir-223	5	BQ012126,BQ010657,AW192334,AA845292,BQ011993
hsa-mir-371	2	DB508823,DB443882
hsa-mir-24-2	1	BF061990
hsa-mir-193a	1_	AI770050
hsa-mir-429	5	AI312008,AI312008,AI312008,AI312008
hsa-mir-568	18	CB054179,CA425784,AI383978,AI024792,CK902677,AA 489694,AW024848,AI912487,AA115749,BM668044,AA1 15749,BM668044,AA115749,BM668044,AA11 5749,AA115749,AA115749
hsa-mir-565	1	DC404319
hsa-mir-522	2	BI057935,BI057935
hsa-mir-24-1	1	CB852241
hsa-mir-516-3	2	BE466189,BF223893
hsa-mir-624	1	H66135
hsa-mir-224	1	BF367311
hsa-mir-328	20	BM792516,BE868797,BI092635,BI260928,BQ706797,CA 488307,CD243179,BM853445,BM789033,BX390378,BI0 92635,BX390378,BM792516,BQ706797,BE868797,BM85 3445,CA488307,CD243179,BI260928,BM789033
hsa-mir-7-1	1	AW367387
hsa-mir-663	1	BM893562
hsa-mir-643	1	BF356097
hsa-mir-320	1	AI041315
hsa-let-7a-1	1	BF372275
hsa-mir-214	11	AI961147,AI202700,BG055203,BQ012655,AI039268,CF 529290,BQ447950,AI658740,AI242334,AW296598,AI12 6848
hsa-mir-363	1	AA353588
hsa-let-7b	6	BX361219,BX349705,BU732454,AI382133,DB328200,A W028822
hsa-mir-296	1	BE044227
hsa-mir-590	2	AW812109,AW812109
hsa-mir-21	4	BX399365,AA837010,BE932516,CA414094
hsa-mir-186	3 1	AA258173,BQ271697,AW968323
hsa-mir-622 hsa-mir-495	3	BM542991 AA613245,AW593422,BE467211
hsa-mir-144	3 1	BX644926
1130 HIII - 144	1	DAQTTJZU

hsa-mir-205	60	BX454368,BU607326,BU687118,BU686798,BM976602,B F088470,BF088470,DB313515,AU158081,AU158081,R48 249,R73789,BG989285,AA627916,AI969511,AW275818, AW275825,AW662302,BU732467,CN478782,DB313077, W68529,H25944,AI800001,BM980083,BU676846,CB048 050,AW628474,R73789,AA631033,AI375939_dup1,CB40 9600,BQ378988,R48249,AA642987,BF088470,AI611676 ,R48249,R73789,BE717915,R48249,AW117862,CB40960 0,R48249,R73789,BE717919,BE717969,BE837877,BE71 7939,BE645803,R48249,BE717915,AW381579,AW38094 9,AA730105,R73789,R48249,BE717915,AI220853,AW11 7862
hsa-mir-125a	1	DB078945
hsa-mir-29b-1	1	BF447465
hsa-mir-641	1	BF805572
hsa-let-7d	8	AI360684,BF511039,BF511477,T85314,BE932147,BE70
		9888,BU736404,AA806216
hsa-mir-194-2	3	AI392832,AW294586,DB331974
hsa-mir-377	5	BF376962,BF376962,BF376962,BF376962
hsa-mir-23b hsa-mir-555	3 1	BG004545,BG004545,BG004545 BF842814
hsa-mir-655	2	BG000132,BG000132
hsa-mir-365-2	1	AA682513
hsa-mir-29a	2	AI261722,BF000417
hsa-mir-564	10	CF126629,BQ082498,BQ082492,BQ896914,BQ082492,B
		Q082498,AL532442,AL532442,AL532442
hsa-mir-675	83	AL571290,AL569789,BF997501,AL514065,AL571212,W7 2208,BQ366088,AW946259,AA864221,BF590747,AL571 290,AI738732,BG000974,BG012341,BQ367462,AL57129 0,AA928657,R93762,BM678988_dup1,AI146817,AI2473 86,BF985264,BX453708,AL564130,BG012341,AW19676 1,AW196780,BG009089,BG013206,BG000974,BG01173 8,BF985264,BG000974,BF985264,BF770659,BG012341,BX453708,BG000974,BX453708,BF770659,BI044667,BQ 367462,BG011738,BF770659,BG012341,AA928657,R93 762,BG013206,BG009089,BI044667,AA928657,BQ3674 62,BG000974,R93762,W72208,AA864221,AL564130,BG 012347,AA928657,BQ366088,BQ367462,BG011738,BQ3 67462,BF770659,BI044667,BQ367462,AI377593,BQ367 462,AI377593,AL564130,R93762,BQ367462,W72208,BG 012347,BQ367462,BI044667,BQ367462,W72208,AA864 221,R93762,AL569789,BQ367462,BG012347
hsa-mir-33b	1	DB361007
hsa-mir-103-2	5	AA477191,BE768941,BE768943,BE768941,BE768943
hsa-mir-130a	1	DA811291
hsa-mir-196b	2	BQ923616,BM549446
hsa-mir-647	7	AL708944,BF857645,DB066850,BI006021,BF857645,DB 066850,DB066850
hsa-mir-27a	4	AW797020,AW797020,AW797020
hsa-mir-611	4	AA602796,BQ130146,DV461029,AW104310
hsa-mir-190	1	DB288334
hsa-mir-421	1	H63707
hsa-mir-101-1	1	BU786820
hsa-mir-221	1 2	AW842797
hsa-mir-192	۷	AI672369,BG982441

hsa-mir-367	28	BG499366,BQ217140,H43466,BM796975,AA451825,BF7 90426,BG431297,BG898445,BM853135,BU854431,BX48 8044,CB146063,CB162796,CN346204,DT218636,W4983 9,W39691,CB135486,BQ920803,AA160180,AA372829,B F701214,CN419691,BU787911,BE748087,AV714955,BE7 48087,W39691
hsa-mir-567	1	AA054551
hsa-mir-122a	3	R91986,R91986,R91986
hsa-mir-30c-2	9	BQ022726,AI087792,AI474776,W93081,AW168091,BF4
	-	39917,BF439062,AI768381,BF594736
hsa-mir-133a-	4	AA211717,DB330925,AA211717,AA211717
hsa-mir-372	2	DB443882,AW833903
hsa-mir-630	10	BX454918,CB854863,BX412844,CF891283,BX412844,B X454918,CB854863,CF891283,BX454918,BX454918
hsa-mir-635	8	AA210899,BQ705942,BQ705942,BQ705942,BQ705942,B Q705942,BQ705942,AA210899
hsa-mir-198	11	AW364521,AW936518,AW936507,AA614015,BX395666, AA897679,BF733997,BF367500,AW364521,BM684744,B
		X395666
hsa-mir-202	1	AW340536
hsa-mir-106b	2	AA078024,AA078024
hsa-mir-508	1	AW665118
hsa-mir-98	1	BM956031
hsa-mir-130b	1	DV080646
hsa-mir-155	5	BG058661,BG058739,AI863758,AI863758,AI863758
hsa-mir-373	6	AI825624,AI656634,BE466114,AI825746,BE672151,BE0 46897
hsa-mir-516-2	1	BQ025835
hsa-mir-548a-	1	AW851470
hsa-mir-505	3	BF956603,BF956603,BF956603
hsa-mir-9-2	8	BM676994,DC425874,DB315227,BX412634,BM683678,B X412634,BX412634,BX412634
hsa-mir-135a-	1	BM918632
hsa-mir-636	24	AI890310,BX434220,BU608163,CA306910,AW316782,C B241746,CA420551,CA423953,AL581513,BI012130,BI0 84978,BU168060,BU628861,CA420567,CD367228,BX45 3763,BI010983,BU624553,BX434220,BX434220,CB2417 46,AI890310,BX434220,DB205468
hsa-mir-637	5	AI203861,AW974502,AA768246,AW974502,AW974502
hsa-mir-621	1	BF923438
hsa-mir-25	6	BE077684,BQ377098,BQ377098,BE077684,BE077684,B E077684
hsa-mir-411	2	AW895894,AW895880
hsa-mir-29c	43	AA832487,AA732327,AA814450,AA290626,AI949631,BF
		431339,AI796930,AI277016,AI139038,BF446797,BF196
		476,AW015122,AW055230,AI927692,BU686674,BQ0097
		86,BU607478,CA312488,CA312468,AI800208,AI582596,
		AI634533,BF592005,R48833,AI628443,AI935532,AI435
		146,BQ018823,BE043082,BE045365,DB302666,AW0585
		64,T59406,T59406,R48833,T59406,R48833,R48833,R48 833,T59406,T59406,R48833,R48833
hsa-mir-451	4	H90496,BX644926,H90496,H90496
hsa-mir-145	4	AI825923,AI678858,BF995019,AI659796
hsa-mir-133a-	8	BF508318,BF446240,AA063595,N80784,AI819052,DB32 7850,BX647033,AA063595
hsa-mir-548d-	2	BQ889295,BQ889295
hsa-mir-301	1	CV414363

hea mir 650 1 DUE05017	
hsa-mir-650 1 BU585017	
hsa-mir-616 11 BF839560,BF839556,BF839550,BF839561,BF839551,l 839555,BF839557,BF839558,BF839549,BF839554,BF8	
hsa-mir-30d 1 AA137041	
hsa-mir-15a 9 AA748510,BM272203,CK825000,BQ185483,AW97627	7,A
A867999,AI086232,AA748510,AW976277	
hsa-mir-29b-2 1 AA766259	_
hsa-mir-126 24 BX380871,BX397999,BX397999,BX380871,BX397999 X380439,BX340281,BX397999,BX397999,BX380439,B 381730,BX381730,BX380040,BX381730,BX380871,BX 81730,BX380782,BX459190,BX380439,BX380871,BX 0778,BX381730,BX397999,BX360778	3X (3
hsa-mir-191 8 BQ439253,BU594868,BQ645068,BQ652614,BQ646655 Q647682,DB059215,BQ439253	2,B
mRNAs	
hsa-mir-302c 1 AK000089	
hsa-mir-302b 1 AK000089	
hsa-mir-675 2 BC010054,BC004532	
hsa-mir-631 2 AK128372,AK026216	
hsa-mir-150 1 AK130324	
hsa-mir-647 1 AK128082	
hsa-mir-636 3 AF015188,AF015189,AF015190	
hsa-mir-661 1 AL834492	
hsa-mir-335 1 AK055108	
hsa-mir-328 12 AK023886,AK056923,BC015524,BC034410,DQ891332 Q894515,AK023886,AK056923,BC015524,BC034410,D 891332,DQ894515	
hsa-mir-589 1 AY927477	
hsa-mir-367 8 AK000089,AF068284,AK000274,AK225900,AL049996, 066945,BC107709,BX647100	ВС
hsa-mir-99b 1 AK125996	
hsa-mir-302a 1 AK000089	
hsa-let-7e 1 AK125996	
hsa-mir-126 1 BC114447 hsa-mir-499 1 AK098707	
hsa-mir-302d 1 AK00089	
hsa-mir-125a 1 AK000089	

Spliced ESTs		
hsa-mir-371	1	DB443882
hsa-mir-130b	1	DV080646
hsa-mir-639	11	DA578654,DB036923,BE163339,BX337999,BE173861,A
		W601441,AW601462,AW602622,AW602643,BE076002,B
		G978956
hsa-mir-155	1	BG058739
hsa-mir-632	3	BF739929,BF986402,BG005263
hsa-mir-365-2	1	AA682513
hsa-mir-423	1	AW001018
hsa-mir-324	1	AA428344
hsa-mir-565	1	DC404319
hsa-mir-564	4	AL532442,AL532442,AL532442
hsa-mir-124a-	1	BU738550
hsa-mir-675	7	AL571290,AL571212,AL571290,AL571290,AL564130,AL5
	_	64130,AL564130
hsa-mir-196b	2	BQ923616,BM549446
hsa-mir-24-1	1	CB852241
hsa-mir-637	5	AI203861,AW974502,AA768246,AW974502,AW974502
hsa-mir-636	24	AI890310,BX434220,BU608163,CA306910,AW316782,C
		B241746,CA420551,CA423953,AL581513,BI012130,BI0
		84978,BU168060,BU628861,CA420567,CD367228,BX45
		3763,BI010983,BU624553,BX434220,BX434220,CB2417
		46,AI890310,BX434220,DB205468
hsa-mir-611	4	AA602796,BQ130146,DV461029,AW104310
hsa-mir-25	6	BE077684,BQ377098,BQ377098,BE077684,BE077684,B
		E077684
hsa-mir-328	20	BM792516,BE868797,BI092635,BI260928,BQ706797,CA
		488307,CD243179,BM853445,BM789033,BX390378,BI0
		92635,BX390378,BM792516,BQ706797,BE868797,BM85
		3445,CA488307,CD243179,BI260928,BM789033
hsa-mir-367	28	BG499366,BQ217140,H43466,BM796975,AA451825,BF7
		90426,BG431297,BG898445,BM853135,BU854431,BX48
		8044,CB146063,CB162796,CN346204,DT218636,W4983
		9,W39691,CB135486,BQ920803,AA160180,AA372829,B
		F701214,CN419691,BU787911,BE748087,AV714955,BE7
		48087,W39691
hsa-mir-372	1	DB443882
hsa-mir-133a-	4	AA211717,DB330925,AA211717,AA211717
hsa-mir-15a	3	BM272203,AW976277,AW976277
hsa-mir-126	22	BX380871,BX397999,BX397999,BX380871,BX397999,B
		X380439,BX340281,BX397999,BX397999,BX380439,BX
		381730,BX381730,BX380040,BX381730,BX380871,BX3
		81730,BX380782,BX459190,BX380439,BX380871,BX38 1730,BX397999
hsa-mir-141	4	AI695443,AA863389,AA863395,AI969882
hsa-mir-205	15	BG989285,AA627916,AI969511,AW275818,AW275825,A
203	13	W662302,BU732467,CN478782,DB313077,W68529,H25
		944,AI800001,BM980083,BU676846,CB048050
		,,,,
hsa-mir-191	5	BU594868,BQ645068,BQ652614,BQ646652,BQ647682

#### Intronic miRNAs (anti-sense)

hsa-mir-662, hsa-mir-302c, hsa-mir-199a-1, hsa-mir-302b, hsa-mir-181a-2, hsa-mir-1-2, hsa-mir-324, hsa-mir-194-1, hsa-mir-16-2, hsa-mir-599, hsa-mir-486, hsa-mir-570, hsa-mir-631, hsa-mir-610, hsa-mir-328, hsa-mir-181b-2, hsa-mir-367, hsa-mir-133a-1, hsa-mir-215, hsa-mir-548d-2, hsa-mir-15b, hsa-mir-302a, hsa-mir-214, hsa-mir-199a-2, hsa-mir-199b, hsa-mir-302d, hsa-mir-549, hsa-mir-191

# Table S1: Anti-sense transcripts near known miRNAs (continued)

#### **Mouse miRNAs**

miRNA	#transcripts	Transcript IDs
RefSeq Genes mmu-mir-136 mmu-mir-127 mmu-mir-433 mmu-mir-434 mmu-mir-367 mmu-mir-762 mmu-mir-328 mmu-mir-135a-1 mmu-mir-431	3 2 2 2 2 2 3 4 2 2	NM_184109,NM_184109,NM_184109 NM_184109,NM_184109 NM_184109,NM_184109 NM_184109,NM_184109 NM_184109,NM_184109 NM_138593,NM_138593 NM_009746,NM_009746,NM_009746 NM_172760,NM_172760,NM_172760,NM_172760 NM_001039586,NM_174846 NM_184109,NM_184109
mmu-mir-760 mmu-mir-219-2 mmu-mir-684-1	1 1 13	BY724041 BQ174353 DV073242,BQ174174,AW537749,BE630457,CF578937,A U019690,AW912686_dup1,BF138984,BF138984,EH1065 32_dup1,EH106867_dup1,BB368041,BE630457
mmu-mir-320	2	AI317636,AU067584
mmu-let-7a-1 mmu-let-7b	2 6	CA895946,CA895946 BX634634,BE990520,BE691213,BP758973,AI481799,AI
IIIIIu-let-7b	0	551238
mmu-mir-410	9	BQ175773,C0039417,C0039417,C0039417,C0039417, C0039417,BQ175773,C0039417,CF586444
mmu-mir-703	69	AW475773,BM569675,BQ829508,AA408019,AW549861,BG061776,BM222193,AW323039,BM202365,CK619245,BM208748,BM209549,BM244993,BQ942052,BQ829508,AW549861,AW323039,BM569675,AA408019,AW475773,BG061776,BM222193,AI037476,BM202365,BM200056,BM235396,BI557490,BQ829508,AI037476,CK619245,AW549861,AI037476,BM202365,AW323039,BM569675,BQ829508,BM200056,BM209549,BM235396,BM244993,BM208748,BQ942052,AI894192,BM241195,BQ829508,BM202365,BM209549,BM235396,BM235396,BM202365,BM209549,BM241195,BQ829508,BM202365,BM209549,BM244993,BM569675,AW323039,BM222193,AI037476,BQ942052,CK619245,AA408019,AI894192,AW475773,BG061776,BM203696,BM208748,BM241195,BQ829508,BM293715,AW323039
mmu-mir-719 mmu-let-7c-2 mmu-mir-692-1 mmu-mir-762	3 1 1 48	BF319694,BF319694,BF319694 CX730031 EH109725_dup1 CB590046,BF123867,CB057904,AA219888,BI794412,AA 015463,CF583785,BP761456,CB522109,BG247738,BY01 1013,CB574482,CO806265,CA321672,BQ712754,BQ945 556,CB193807,CA464583,BE336140,BX516469,CB0574 30,BY311097,BY323578,CJ174327,CJ184526,BU935799, BY335256,BU936524,CF550740,CO800690,CO798695,B Q930905,CK792708,BE553370,CB182304,AV445615,BQ 928058,BB651583,CA977612,BF123867,AA015463,DV6 51350,BY022716,BF123867,AA015463,AA929912,BF123 867,AA929912

mmu-mir-124a-1 mmu-mir-133a-2 mmu-mir-484 mmu-mir-370 mmu-mir-127 mmu-mir-299 mmu-mir-195 mmu-mir-107 mmu-mir-205 mmu-mir-715	1 1 3 2 2 2 2 1 1 1 36	EL608186 CR517796 BI688308,BB628323,BI688308 BG870188,BG870188 AW060983,BF461489 CF578713,BI319615 BB469543 DT918023 BX636072 CN677041,CA540888,CA542066,CN675294,AV459680,B I441300,BI789633,CF899888,CD551120,CD553916,CD5 49707,BI441208,CD565318,CD553951,CA546775,CF902 843,CA546648,AV488839,AV458300,CA949213,BI65917 1,BI690957,BI659626,AV468375,AA538360,BI100293,A A538360,CA949213,BI100293,BG146738,W42347,AV45 9680,W42347,AV459680,AV459680,AV458300
mmu-mir-130b	2	BF318156,AI550467
mmu-mir-324	1	CK619771
mmu-mir-675	12	BG228779,CR757130,CR757163,CR757130,CR757163,B G228779,BG228779,CR757130,CR758026,CR756565,CR 757086,CR758028
mmu-mir-367	12	AA408246,CO795279,BU610513,BG802296,BF160578,C A857540,BM946683,BU525549,CF534412,CO814744,CV 561292,DV657845
mmu-mir-682	5	EH111758,BB646391,BF018818,BF018908,BQ033113_d up1
mmu-mir-153	1	BU921583
mmu-mir-101a	2	BX638239,BF318343
mmu-mir-296	1	BE990102
mmu-mir-700	1	AA028433
mmu-mir-129-2	1	CR519766
mmu-mir-704	4	BM519373,BM519462,BM519384,BM519373
mmu-mir-29b-2	2	AA184398,AI591965
	5	·
mmu-mir-411	5	CF578713,CF578713,CF578713,CF578713
mmu-mir-671	23	BG067525,BP766107,AW060945,BF020189,BP764469,C 86598,BP763209,AW744648,CD741762,AI551231,AI551 231,AW413604,AI551231,BF320330,BE993040,BM1977 93,BF458705,BE690893,AI551231,BF455885,C86598,B X638041,AW046089
mmu-mir-23b	2	AI848465,AW124037
mmu-mir-804	3	BY707319,BY707319,BX521364
mmu-mir-142	3	BE136127,AW909330,BE136127
mmu-mir-328	23	BY766110,CB950291,BF159242,BE569617,BF123539,BG 865727,BI691021,BF159242,BG865727,BF123539,BG86 5727,BE569617,BF159242,BI691021,BY766110,CB9502 91,AA266420,AI466854,BG865727,BG865727,BG86572 7,BG865727,BG865727
mmu-mir-135a-1	5	CB948426,BQ256452,BF780995,BF452753,BY105899
mmu-let-7d	3	BF662590,BQ031149,AI591449
mmu-mir-677	4	CK725393,BE859594,BG794909,EL605651
mmu-mir-713	1	BY019942
mmu-mir-29c	8	AA184398,AI591965,CO042247,BF465648,AW456678,B
	Č	E944441,EH094197,AW494050
mmu-mir-21	5	BP774280,EH103036,EH105192,DT931951,DT931951
mmu-mir-339	1	BX629854

mmu-mir-692-2	97	BG090122,AI876713,AI120525,C77615,BQ265350,BP77 1591,BM570058,AW212806,AW208734,C76709,EG5635 06,AU042028,BQ264923,C81314,C85950,AU041056,BM 198032,AU018935,AI042821,C85307,AW259615,AW742 780,AA066642,AU021287,BG090001,BF319101_dup1,B M199052,BF148348,C80431,BF148348,BF148348,AI503 783,AA066642,BP769370,AA066642,AI837703,AA06664 2,AA066642,BM199579,BM210661,AA086583,AI386321, AA086583,AW212806,CF583084,AA086583,AA086583,A A066642,AI839982,AA086583,BP769370,BM116361,AA0 86583,AA086583,BF148625,BM196958,BF146594,AA54 2429,AA561457,BM199549,BM199547,BQ264923,BM19 8032,BM198037,AA760480,BM199059,BM199182,BF319 100,BP774123,BM199052,BG146514,AA542429,AA5424 29,BM202444,AA542429,AA760480,AA561457,AA54242 9,AI837703,BM199579,BM210661,CD741947,AA086583, AA561457,AI386321,AA086583,EH109725,AA086583,BM 116361,AA086583,BP774123,AA086583
mmu-mir-689-1	5	AW211456,AW211456,AW211456,AW211456
mmu-mir-138-2 mmu-mir-685	1 9	AI854067 AA176001,AA177668,BE335968,BE335968,AA176001,A A177668,AA176001,AA177668,BE335968
mmu-mir-137 mmu-mir-678	3 30	AI852436,EL607439,BX638046 AI504737,AI851123,AI845257,BE954206,CD774044,AW 321042,AW541993,BM114883,BE993523,AI852462,CA8 89352,CA882196,BM227453,CA881388,BM021608,BM22 6267,C87892,CF582154,EH094417,EH101496,EH10223 5,EH106884,AA152773,AA152782,AA152773,AA152773, EH094419,AA152773,AA152773,AA152782
mmu-mir-763 mmu-mir-214	1 7	CF578614 BX631348,AI414009,CA774438,AI414009,BQ418332,AI 414009,CA947318
mmu-mir-705 mmu-mir-702	3 2	BX636473,AW046224,CF585469 AI647501,AI647501
mmu-mir-431	2	AA048217,BQ127396
mmu-mir-181b-2 mmu-mir-686	4 32	BI319432,CJ065621,CJ065471,BI319432 AW539968,AI848457,AW543310,AW557943,AW541849, BE200146,BM203159,AU045989,BF722037,AW492012,B Q126981,BQ268530,BE952271,BG228853,BG093897,AU 021597,AW539968,AU021597,AW541849,AU021597,AU 021597,AU045989,AU021597,AU045989,AU021597,BE9 52271,BE952271,BE952271,BE952271,BE952271,BG09 3897,BG093897
mRNAs		AVA001.202
mmu-mir-29c mmu-mir-207	1 1	AK081202 AK139286
mmu-mir-29b-2 mmu-mir-671	1 1	AK081202 AK158019
mmu-mir-715 mmu-mir-762	2	BC116307,BC131795 Y11905,BC058530,AK131935,BC005673,AK049064,Y11
mmu-mir-685	6	905 BC128280,BC128469,BC128470,BC128280,BC128469,B
mmu-mir-804	1	C128470 AK007228
mmu-mir-328	10	AK037067,AK157875,BC018516,BC026617,BC058752,A K037067,AK157875,BC018516,BC026617,BC058752

mmu-mir-135a-1	5	AK052709,BC025935,BC036136,BC033063,AK049425
mmu-mir-484 mmu-mir-181b-2	1 1	AK035704 AK082091
spliced ESTs		
mmu-mir-704	4	BM519373,BM519462,BM519384,BM519373
mmu-mir-320	2	AI317636,AU067584
mmu-mir-410	9	BQ175773,C0039417,C0039417,C0039417, C0039417,BQ175773,C0039417,CF586444
mmu-mir-719	3	BF319694,BF319694,BF319694
mmu-let-7c-2	1	CX730031
mmu-mir-762	46	CB590046,BF123867,CB057904,AA219888,BI794412,AA 015463,CF583785,BP761456,CB522109,BG247738,BY01 1013,CB574482,CO806265,CA321672,BQ712754,BQ945 556,CB193807,CA464583,BE336140,BX516469,CB0574 30,BY311097,BY323578,CJ174327,CJ184526,BU935799,BY335256,BU936524,CF550740,CO800690,CO798695,BQ30905,CK792708,BE553370,CB182304,AV445615,BQ928058,BB651583,CA977612,BF123867,AA015463,BF12 3867,AA015463,AA929912,BF123867,AA929912
mmu-mir-804 mmu-mir-328	3 23	BY707319,BY707319,BX521364 BY766110,CB950291,BF159242,BE569617,BF123539,BG 865727,BI691021,BF159242,BG865727,BF123539,BG86 5727,BE569617,BF159242,BI691021,BY766110,CB9502 91,AA266420,AI466854,BG865727,BG865727,BG86572 7,BG865727,BG865727
mmu-mir-484	3	BI688308,BB628323,BI688308
mmu-mir-677	4	CK725393,BE859594,BG794909,EL605651
mmu-mir-713	1	BY019942
mmu-mir-195	1	BB469543
mmu-mir-367	12	AA408246,CO795279,BU610513,BG802296,BF160578,C A857540,BM946683,BU525549,CF534412,CO814744,CV 561292,DV657845
mmu-mir-675	5	CR757130,CR757163,CR757130,CR757163,CR757130
mmu-mir-678	7	CD774044,CA881388,EH094417,EH101496,EH102235,E H106884,EH094419
mmu-mir-137	3	AI852436,EL607439,BX638046
mmu-mir-700	1	AA028433
mmu-mir-702	2	AI647501,AI647501
mmu-mir-686	26	AW539968,AI848457,AW543310,AW557943,AW541849, BE200146,BM203159,AU045989,BF722037,AW492012,B Q126981,BQ268530,BE952271,BG228853,BG093897,A W539968,AW541849,AU045989,AU045989,BE952271,B E952271,BE952271,BE952271,BE952271,BG093897,BG 093897

#### Intronic miRNAs (anti-sense)

mmu-mir-684-1, mmu-mir-199a-1, mmu-mir-133a-1, mmu-mir-486, mmu-mir-703, mmu-mir-1-2, mmu-mir-181a-2, mmu-mir-297-2, mmu-mir-215, mmu-mir-804, mmu-mir-328, mmu-mir-199a-2, mmu-mir-484, mmu-mir-194-1, mmu-mir-324, mmu-mir-199b, mmu-mir-689-2, mmu-mir-214, mmu-mir-695, mmu-mir-181b-2

Table S1: Anti-sense transcripts near known miRNAs. Shown are known miRNAs from human, mouse, and Drosophila (col. 1), the number of anti-sense transcripts near these miRNAs (within 50nts) and their sequence identifiers. The transcripts are separated into genes, ESTs, and spliced ESTs as indicated. The table also contains a list of known miRNAs that are located in introns of host genes, which are transcribed in the opposite direction.

#### Table S2: Solexa reads matching sense/anti-sense miRNA pairs

#### Drosophila sense/anti-sense miRNAs

```
dme-mir-iab-4 chr3R 12681997 12682064 + TCGTAAACGTATACTGAATGTATCCTGAGTGTATCCTATCCGGTATACCTTCAGTATACGTAACACGA
TTACGTATACTGAAGGTATACCG 2 1
                                                                 TTACGTATACTGAAGGTATACC 4 1
                                                                TTACGTATACTGAAGGTATAC 2 1
                                                                 TTACGTATACTGAAGGTAT 8 1
                                     +++++++++++++++++++
                                                               CGGTATACCTTCAGTATACG 1 1
                                                                ACGTATACTGAATGTATCCTG 1 1
ACGTATACTGAATGTATCCTGA 5 1
dme-mir-312 chr2R 16471561 16471626 -
GATTTGGTTCGTCACAAGGGCAATTCTGCATTTTTTAACTAGTATTGCACTTGAGACGGCCTGATT
TTGCACTTGAGACGGCTGAT 1 1
TTGCACTTGAGACGGCCTGA 1 1
TTGCACTTGAGACGGCCTG 1 1
TGCACTTGAGACGGCCTGA 2 1
TGGTTCGTTGTGAGAACCAAAT 2 1
TGGTTCGTCACAAGGCAATTC 151
TGGTTCGTCACAAGGCAATTC 66 1
TGGTTCGTCACAAGGCAATT 90 1
TGGTTCTCTACAAGGGCAATT 44 1
TGGTTCGTCACAAGGGCAATT 44 1
                                          ++++++++++++++++++
                                                               TGGTTCGTCACAAGGGCAA 17 1
                                                               TGGTTCGTCACAAGGGCA 6 1
```

#### Mouse sense/anti-sense miRNAs

```
TCCTGTACTGAGCTGCCCCG 11 2
                                                            -----
                                                                                                      TCCTGTACTGAGCTGCCCCGA 66
                                                            ._____
                                                                                                      TCCTGTACTGAGCTGCCCCGAG 152 2
                                                                                                      TCCTGTACTGAGCTGCCCCGAGG 1 1 1
CGGGCAGCTCAGTACAGGA 1 2
CGGGGCAGCTCAGTACAGGA 1 2
                                                            +++++++++++++++++
                                                                                                      CGGGCAGCTCAGTACAGGA 1 2
CGGGCAGCTCAGTACAGGAT 46 1
CGGGCAGCTCAGTACAGGATG 56
TCCTGTACTGAGCTGCCCCGAGC 3
TCCTGTACTGAGCTGCCCCGAG 152
TCCTGTACTGAGCTGCCCCGA 66 2
                                                                                                      TCCTGTACTGAGCTGCCCCG 11 2 TCCTGTACTGAGCTGCCCC 1 2
                           +++++++++++++++
                                                                                                      TCCTGTACTGAGCTGCCC 2 2
TCCAGCATCAGTGATTTTGTT 25 1
                                                TCCAGCATCAGTGATTTTGT 12 1
TCCAGCATCAGTGATTTTG 1 1
                                                    ++++++++++++++++
                                                                              CATCAGTGATTTTGTTG 1 1
                                                                              TCAGCACCAGGATATTGTTG 1 1
TCAGCACCAGGATATTGTTGGGG 1 1
AACAATATCCTGGTGCTGAGT 11 1
CCAACAATATCCTGGTGCTGA 2 1
TGGAATGTAAAGAAGTATGTAT 45 2
                                                         TGGAATGTAAAGAAGTATGTA 2 2
                                    ++++++++++++++++++++
                                                         TGGAATGTAAAGAAGTATGT 1 2
                                                         TGGGTACATAAAGAAGTATGTGC 5 1
```

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mmu-mir-34b chr9 50855792 50855875 - GTGCTCGGTTTGTAGGCAGTGTAATTAGCTGATTGTAGTGCGGTGCTGACAATCACTAACTCCACTGCCATCAAAACAAGGCAC
) (-34.50)
ATGGCAGTGGAGTTAGTGATTGT 1 1
TGGCAGTGGAGTTAGTGATTGT 5 1
ATCACTAACTCCACTGCATCAA 2 1
ATCACTAACTCCACTGCATCAA 51 1
AATCACTAACTCCACTGCCATCA 17
TCACTAACTCCACTGCCATC 1 1
ATCACTAACTCCACTGCCATC 2 4 1
                                                                     AATCACTAACTCCACTGCCATC 259 1
ATCACTAACTCCACTGCCAT 1 1
                                                                                                                   AATCACTAACTCCACTGCCAT 22 1
                                                                     ++++++++++++++++++
                                                                      ++++++++++++++++
                                                                                                                   ATCACTAACTCCACTGCCA 2 1
AATCACTAACTCCACTGCCA 28 1
                                                                     AATCACTAACTCCACTGCCA 28 1
CAATCACTAACTCCACTGCCA 1 1
CAATCACTAACTCCACTGCCC 1 1
GGCAGTGTAATTAGCTGATTGTA 1 1
TAGGCAGTGTAATTAGCTGATTGTA 2 1
GTAATTAGCTGATTGT 1 1
GTGTAATTAGCTGATTGT 3 1
ACCCCCALAGATCCCCACTTGT 3 1
                                                                    ++++++++++++++++++
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                        ++++++++++++++++++
                                                                                                                   AGTGTAATTAGCTGATTGT 6 1
AGGCAGTGTAATTAGCTGATTGT 638 1
                   TAGGCAGTGTAATTAGCTGATTGT 26 1
                       +++++++++++++++
                                                                                                                    AGTGTAATTAGCTGATTG 4 1
AGGCAGTGTAATTAGCTGATTG 23 1
                 TAGGCAGTGTAATTAGCTGATTG 117 1
TAGGCAGTGTAATTAGCTGATT 14 1
TAGGCAGTGTAATTAGCTGAT 1 1
TAGGCAGTGTAATTAGCTGAT 4 2
GTTGGCAAGTCTAGAACCACCG 2 1
                                          +++++++++++++++
                                                                                                       GTAAGGTAATGGGACCCG 43 1
                                                                                                       GTAAGGTAATGGGACCG 43 1
TTTGGCAATGGTAGAACTCACACCGG 8 1
TTTGGCAATGGTAGAACTCACACCG 95 1
AATGGTAGAACTCACACCG 40 1
GGCAATGGTAGAACTCACACCG 4 1
TGGCAATGGTAGAACTCACACCG 4 1
TTTGGCAATGGTAGAACTCACACCG 48 1
TTTGGCAATGGTAGAACTCACACCG 1377 1
TTTTGGCAATGGTAGAACTCACCCG 27 1
TGCCAATGGTAGAACTCACACCG 27 1
        TTTTGCAATGGTAGACTCACACCG 27 1
TGGCAATGGTAGACTCACACC 31
TTTGGCAATGGTAGAACTCACACC 1158 1
TTTGGCAATGGTAGAACTCACACC 11 1
TTTGGCAATGGTAGAACTCACAC 225 1
TTGGCAATGGTAGAACTCACA 4 1
TTTGGCAATGGTAGAACTCACA 1734 1
TTGGCAATGGTAGAACTCACA 1734 1
TTTGGCAATGGTAGAACTCAC 1 1
TTTGGCAATGGTAGAACTCAC 1024 1
TTTGGCAATGGTAGAACTCAC 250 1
           ++++++++++++++++++++
        +++++++++++++++++++++
        TTTGGCAATGGTAGAACTCA 250 1
TTTGGCAATGGTAGAACTC 113 1
                                                                                                       TTTGGCAATGGTAGAACT 20 1
        +++++++++++++++
                                                                                                       TTTGGCAATGGTAGAAC 4 2
GTGAAATGTTTAGGAC 1 3
GTGAAATGTTTAGGACCA 1 1
                                                                GTGAAATGTTTAGGACCA 1 1
GTGAAATGTTTAGGACCACT 16
GTGAAATGTTTAGGACCACT 16 1
GTGAAATGTTTAGGACCACTA 3 1
GTGAAATGTTTAGGACCACTAG 223 1
GTGAAATGTTTAGGACCACTAGA 11 1
TGAAATGTTTAGGACCACTAG 7 1
TGAAATGTTTAGGACCACTAG 13 0
TGAAATGTTTAGGACCACTAG 13 0
TGAAATGTTTAGGACCACTAGA 17 1
GAAATGTTTAGGACCACTAGG 17 1
                                                                 +++++++++++++++++
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                                                                GAAATGTTTAGGACCACTAG 1 1
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mmu-mir-27b chr13 63309934 63310006 + AGGTGCAGAGCTTAGCTGATAGCTGAACAGTGATTGGTTCCCCCTTTGTTCACAGTGGCTAAGTTCTGCACCT
 ) (-31.30)
TITCACCANTCAGCTAAGCTCTGC 1 1
CAGAGCTTAGCTGATTGGTGAACA 19 1
AGAGCTTAGCTGATTGGT 5 1
AGAGCTTAGCTGATTGGTGA 8 1
AGAGCTTAGCTGATTGGTGAA 65 1
AGAGCTTAGCTGATTGGTGAAC 87 1
AGAGCTTAGCTGATTGGTGAAC 87 7
AGAGCTTAGCTGATTGGT
           +++++++++++++++++++++
                                                                                                                                                                      AGAGCTTAGCTGATTGGTGAACAG 19
              AGAGCTTAGCTGATTGGTGAACAGT 1 1
                                                                                                                                                                     AGAGCTTAGCTGATCGTGAACAGT 1 1
GTTCACAGTGGCTAAGTT 2 2
GTTCACAGTGGCTAAGTTCT 64 1
GTTCACAGTGGCTAAGTTCTG 135 1
GTTCACAGTGGCTAAGTTCTG 188 1
TTCACAGTGGCTAAGTTCTGC 188 1
TTCACAGTGGCTAAGT 3 3
TTCACAGTGGCTAAGTT 109 3
TTCACAGTGGCTAAGTTC 1294 2
TTCACAGTGGCTAAGTTCT 1294 1
TTCACAGTGGCTAAGTTCT 1266 1
TTCACAGTGGCTAAGTTCT 1269 1
TTCACAGTGGCTAAGTTCT 1269 1
TTCACAGTGGCTAAGTTCT 1269 1
TTCACAGTGGCTAAGTTCTC 1269 1
TTCACAGTGGCTAAGTTCTCG 167 1
TTCACAGTGGCTAAGTTCTGC 3617 1
TTCACAGTGGCTAAGTTCTGC 3617 1
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                                                                                                           ++++++
                                                                                                             TTCACAGTGGCTAAGTTCTGCA 617 1
                                                                                                                                                                     TTCACAGTGGCTAAGTTCTGCA 617 1
TTCACAGTGGCTAAGTTCTGCAC 25 1
TCACAGTGGCTAAGTTCTG 54 1
TCACAGTGGCTAAGTTCTGC 16 1
TCACAGTGGCTAAGTTCTGC 16 1
TCACAGTGGCTAAGTTCTGC 2 1
CACAGTGGCTAAGTTCTGC 4 1
CACAGTGGCTAAGTTCTGC 1 1
ACAGTGGCTAAGTTCTGC 1 1
ACAGTGGCTAAGTTCTGC 1 1
ACAGTGGCTAAGTTCTGC 1 1
ACAGTGGCTAAGTTCTGC 7 7
                                                                                                              +++++++++++++++
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                                                                                                                                                                      ACAGTGGCTAAGTTCT 7 4
                                                                                                                                                                     ACAGTGGCTAAGTTCTG 25 3
ACAGTGGCTAAGTTCTGC 51 2
CAGTGGCTAAGTTCTGC 3 2
AGTGGCTAAGTTCTGC 3 9
AGTGGCTAAGTTCTGCA 9 2
                                                                                                                    +++++++++++++++
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mmu-mir-126 chr2 26413366 26413438 +
TGACAGCACATTATTACTTTTGGTACGCGCTGTGACACTTCAAACTCGTACCGTGAGTAATAATGCGCGGTCA
 CGCGTACCAAAAGTAATAATGT 1 1
                                                                                                                                                                     CGCGTACCAAAGGTAATAATGT 1 1
CATTATTACTTTTGGTAC 3 1
CATTATTACTTTTGGTACG 41 1
CATTATTACTTTTGGTACG 781 1
CATTATTACTTTTGGTACGC 786 1
CATTATTACTTTTGGTACGCG 786 1
CATTATTACTTTTGGTACGCGC 44 1
CATTATTACTTTTGGTACGCGCT 5 1
CATTATTACTTTTGGTACGCGCTGTGA 1 1
CATTATTACTTTTGGTACGCGCTGTGACA 1 1
CATTATTACTTTTGGTACGCGCCTGTACA 1 1
CATTATTACTTTTGGTACGCGCC 1 1
                  ++++++++++++++++++
                   ATTATTACTTTTGGTACGCGC 1 1
TTATTACTTTTGGTACGC 2 1
TATTACTTTTGGTACGCG 1 1
                          +++++++++++++++
                                                                                                                                                                     TATTACTTTTGGTAGGG 1 1
CTCGTACCGTAGTA 1 1
CTCGTACCGTAGATA 1 1
CTCGTACCGTAGATAATA 1 1
CTCGTACCGTAGATAATAATG 26 1
CTCGTACCGTAGATAATAATG 26 1
CTCGTACCGTGAGTAATAATGC 11 1
TCGTACCGTGAGTAATAATAATG 27
TCGTACCGTGAGTAATAAT 25 1
TCGTACCGTGAGTAATAATA 1 1
TCGTACCGTGAGTAATAATA 1 1
TCGTACCGTGAGTAATAATG 101 1
TCGTACCGTGAGTAATAATGC 1165 1
TCGTACCGTGAGTAATAATGC 1165 1
TCGTACCGTGAGTAATAATGC 116 1
TCGTACCGTGAGTAATAATGC 116 1
TCGTACCGTGAGTAATAATGC 116 1
TCGTACCGTGAGTAATAATG 1 1
                                                                                                     +++++++++++++++
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                                                                                                   TGGTACGGTGAGTAATAATGGG 2 1 CGTACCGTGAGTAATAATG 28 1 CGTACCGTGAGTAATAATG 28 1 CGTACCGTGAGTAATAATGG 240 1 CGTACCGTGAGTAATAATGG 561 2 CGTACCGTGAGTAATAATGGG 5 1 TACCGTGAGTAATAATGGG 1 1 TACCGTGAGTAATAATGGG 1 1 CGGTGAGTAATAATGGG 1 1 CGGTGAGTAATAATGGG 1 1 CGGTGAGTAATAATGGG 2 1 CGGTGAGTAATAATGGG 2 1
                                                                                                        +++++++++++++++++
                                                                                                        CCGTGAGTAATAATGCG 2 1
                                                                                                                                                                     GTGAGTAATAATGCG 1 1
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mmu-let-7b chr15 85535085 85535169 +
GCAGGGTGAGGTAGGTTGTGTGTGTGTTTCAGGGCAGTGATGTTGCCCCTCCGAAGATAACTATACAACCTACTGCCTTCCCTGA
. (-37.50)
TGAGGTAGTAGGTTG 6 10
TGAGGTAGTAGGTTGT 53 8
TGAGGTAGTAGGTTGTG 14 1
TGAGGTAGTAGGTTGTGT 94 1
TGAGGTAGTAGGTTGTGTG 1041 1
TGAGGTAGTAGGTTGTGTG 1351 1
TGAGGTAGTAGGTTGTGTGT 34985 1
         TGAGGTAGTAGGTTGTGTGTT 136624 1
TGAGGTAGTAGGTTGTGTGTTT 33456 1
          TGAGGTAGTAGGTTGTGTGTTTC 299 1
                                                                                                                                         TGAGGTAGTAGGTTGTGTGTTTC 299 1
TGAGGTAGTAGGTTGTGTGTTTCA 26 1
TGAGGTAGTAGGTTGTGTGTGTTTCAG 5 1
TGAGGTAGTAGGTTGTGTGTTTCAGGG 1
TGAGGTAGTAGGTTGTGTGTTTCAGGGCA
GAGGTAGTAGGTTGTGTGTT 104 1
GAGGTAGTAGGTTGTGTGTT 139 1
GAGGTAGTAGGTTGTGTGTTT 11 1
AGGTAGTAGGTTGTGTGTTT 1 1
AGGTAGTAGGTTGTGTGTTT 1 1
AGGTAGTAGGTTGTGTGTT 4 1
AGGTAGTAGGTTGTGTGTTGTT 4 1
          AGGTAGTAGGTTGTGTGGTT 44 1
AGGTAGTAGGTTGTGTGTGTTT 3 1
              +++++++++++++++++
                                                                                                                                          GGTAGTAGGTTGTGTGTT 4 1
                                                                                                                                         GGTAGTAGGTTGTTGTT 1 1
GTAGTAGGTTGTGGTT 1 1
GTAGTAGGTTGTGGGT 1 1
GTAGTAGGTTGTGTGGTT 22 1
GTAGTAGGTTGTGTGGTTT 1 1
TAGTAGGTTGTGTGTGTT 1 1
TAGTAGGTTGTGTGTGT 2 1
TAGTAGGTTGTGTGTGT 5 1
TAGTAGGTTGTGTGTGTT 4 1
              +++++++++++++++++
                ++++++++++++++
                AGTAGGTTGTGTGGTT 2 1
AGTAGGTTGTGTGGTTT 20 1
GTAGGTTGTGTGGTTT 2 3
                     +++++++++++++
                                                                                                                                         TAGGTTGTGTGTTCAGGGCAGTGA 1 1
TCAGGGCAGTGATGTTGCCCCTCCGAAGAT 1 1
AGATAACTATACAACCTACTGCCTTC 1 1
                       AGATACTATACAACCTACTGCCTTC
CTATACAACCTACTGCCTTC 15 1
CTATACAACCTACTGCCTTCC 43 1
CTATACAACCTACTGCCTTCCC 1 1
GTAGGTTGTATAGTTA 7 3
AGTAGGTTGTATAGTTA 4 1
                                                                                                                                         AGTAGGTTGTATAGTT 41 3
CAGTAGGTTGTATAGTT 1 1
AGTAGGTTGTATAGT 1 9
                                                                                              -----
                                                                                              -----
                                                                                               -----
ATACAACCTGCTAAGTG 1 5
TTAGCAGGTTGTATTATCATT 1 1
                                                                                  +++++++++++++++++++
                                                                                                                                                         CTTAGCAGGTTGTATTATCATT 114 1
                                                                                                                                                         CTTAGCAGGTTGTATTATCATT 114 1
ACTTAGCAGGTTGTATTATCATT 1 1
TTCTAGCACTTAGCAGGTTGTATTATCATT 1 1
CTTAGCAGGTTGTATTATCATT 1 1
ACTTAGCAGGTTGTATTATCAT 3 1
CTTAGCAGGTTGTATTAT 3 3
TAATACAACCTGCTAAGTGT 1 1
ATATATACAACCTGCTAAGTGT 1 1
ATATATACAACCTGCTAAGTGT 1 1
ATATAATACAACCTGCTAAGTGT 1 1
ATATATACAACCTGCTAAGTGT 1 5
                                                                     _____
                                                                                  +++++++++++++++
                                                                                                                                                          ATACAACCTGCTAAGTG 1 5
TAATACAACCTGCTAAGTG 1 2
                                       TAATACAACCTGCTAAGTG 1 2
TATAATACAACCTGCTAAGTG 1 2
TATAATACAACCTGCTAAGTG 3 1
ATATAATACAACCTGCTAAGTG 3 1
TATAATACAACCTGCTAAGTG 3 1
ATATAATACAACCTGCTAAGT 6 0 3 1
ATATAATACAACCTGCTAAGT 6 0 3 1
ATATAATACAACCTGCTAAGT 6 1
ATATAATACAACCTGCTAAG 2 8 1
ATATAATACAACCTGCTAA 5 1
                                    ++++++++++++++++++
```

# Table S3: Solexa reads matching sense/anti-sense miRNA pairs

### Drosophila miRNAs

Read Sequence	#cloned/sequenced	#matches to genome	miRNA matches	miRNA anti-sense matches
TTACGTATACTGAAGGTAT	8	1		dme-mir-iab-4
TGCACTTGAGACGGCCTGA	2	1	dme-mir-312	
TTACGTATACTGAAGGTATACCG	2	1		dme-mir-iab-4
TATTGCACTTGAGACGGCCTGA	3027	1	dme-mir-312	
TTGCACTTGAGACGGCCTGA	4	1	dme-mir-312	
TTGCACTTGAGACGGCCTGAT	1	1	dme-mir-312	
ACGTATACTGAATGTATCCTG	1	1	dme-mir-iab-4	
ATTGCCCTTGTGACGAACCAAAT	2	1		dme-mir-312
TATTGCACTTGAGACG	1	1	dme-mir-312	
TATTGCACTTGAGACGGCCTGATT	4	1	dme-mir-312	
TGGTTCGTCACAAGGGCAATTCT	151	1	dme-mir-312	
TTACGTATACTGAAGGTATAC	2	1		dme-mir-iab-4
TTGCACTTGAGACGGCCTG	1	1	dme-mir-312	
CGGTATACCTTCAGTATACG	1	1	dme-mir-iab-4	
TATTGCACTTGAGACGGCC	34	1	dme-mir-312	
TGGTTCGTCACAAGGGC	1	1	dme-mir-312	
TGGTTCGTCACAAGGGCAA	17	1	dme-mir-312	
TTACGTATACTGAAGGTATACC	4	1		dme-mir-iab-4
TGGTTCGTCACAAGGGCA	6	1	dme-mir-312	
TATTGCACTTGAGACGGCCTGAT	94	1	dme-mir-312	
TATTGCACTTGAGACGGC	27	1	dme-mir-312	
ACGTATACTGAATGTATCCTGA	5	1	dme-mir-iab-4	
TTACGTATACTGAAGGTATACCGG	1	1		dme-mir-iab-4
TGGTTCGTCACAAGGGCAATT	90	1	dme-mir-312	
TATTGCACTTGAGACGGCCT	225	1	dme-mir-312	
CACTTGAGACGGCCTGA	1	1	dme-mir-312	
TGGTTCGTCACAAGGGCAATTC	66	1	dme-mir-312	
TATTGCACTTGAGACGGCCTG	1165	1	dme-mir-312	
ATTGCACTTGAGACGGCCTG	3	1	dme-mir-312	
ATTGCACTTGAGACGGCCTGAT	6	1	dme-mir-312	
TGCACTTGAGACGGCCT	2	1	dme-mir-312	
TGGTTCGTCACAAGGGCAAT	44	1	dme-mir-312	
ATTGCACTTGAGACGGCCTGA	18	1	dme-mir-312	

#### Table S3: Solexa reads matching sense/anti-sense miRNA pairs

#### Mouse miRNAs

Read Sequence	#cloned/sequenced	#matches to genome	miRNA matches	miRNA anti-sense matches
GTAGGTTGTATGGTT	4	5	mmu-let-7c-2	
ACAGTGGCTAAGTTCT	7	4	mmu-mir-27b	
CAATCACTAACTCCACTGCC	1	1	mmu-mir-34b	
GCACCATTTGAAATCAGTGTT	39	2	mmu-mir-29b-2	
ACTTAGCAGGTTGTATTATCATT	1	1	mmu-mir-374	
GTAGTAGGTTGTATAGTT	21	2	mmu-let-7a-1	lab 7h
AGTAGGTTGTATAGTTA	4	1	lab 7a 1	mmu-let-7b
AGTAGGTTGTATAGTTT	1 561	2 1	mmu-let-7a-1	
CGTACCGTGAGTAATAATGCG AGTAGGTTGTATGGTT	8	3	mmu-mir-126 mmu-let-7c-2	
TGGAATGTAAAGAAGTATGTAT	45	2	mmu-mir-1-2	
TCGTACCGTGAGTAATAAT	25	1	mmu-mir-126	
CAGAGCTTAGCTGATTGGTGAACA	19	1	mmu-mir-27b	
TGAGGTAGTAGGTTGTATGGTT	198548	2	mmu-let-7c-2	
AGGTAGTAGGTTGTGGTT	44	1	mmu-let-7b	
TAGCACCATTTGAAATC	6	3	mmu-mir-29b-2	
CACCATTTGAAATCAGTG	4	3	mmu-mir-29b-2	
GTAGTAGGTTGTGGT	1	1	mmu-let-7b	
CGCGTACCAAAAGTAATATGT	1	1		mmu-mir-126
CTCGTACCGTGAGTAATAATGC	26	1	mmu-mir-126	
TGAGGTAGTAGAAGTGAGAGG	1041 4	1 1	mmu-let-7b	
GGCAATGGTAGAACTCACACCG GCTGGTTTCACATGGTGGCTTAGA	2	1	mmu-mir-182 mmu-mir-29b-2	
TGAGGTAGGTTGTATGG	1404	2	mmu-let-7c-2	
AGAGCTTAGCTGATTGGTGAACA	274	1	mmu-mir-27b	
TATACAATCTACTGTCTTTC	2	2	mmu-let-7a-1;mmu-let-7c-2	
TTTTGGCAATGGTAGAACTCACACCG	27	1	mmu-mir-182	
GTGAAATGTTTAGGACCACTA	3	1	mmu-mir-203	
TTTGGCAATGGTAGAACTCA	250	1	mmu-mir-182	
CTATACAATCTACTGTCTTT	218	2	mmu-let-7a-1;mmu-let-7c-2	
TGGCAGTGGAGTTAGTGATTGT	5	1		mmu-mir-34b
CACCATTTGAAATCAGTGTT	13	2	mmu-mir-29b-2	
TCGTACCGTGAGTAATAATG	101	1	mmu-mir-126	
CTCGTACCGTGAGTA	1	1	mmu-mir-126	
AGTAGGTTGTATGGTTT	2	2	mmu-let-7c-2	40C
TCCTGTACTGAGCTGCCCCG TAGCACCATTTGAAAT	11 6	2 6	mmu-mir-486 mmu-mir-29b-2	mmu-mir-486
CGGGGCAGCTCAGTACAGGAT	46	1	11111u-11111-230-2	mmu-mir-486
ATTTGAAATCAGTGTTT	1	4	mmu-mir-29b-2	1111114-11111-400
CTCGTACCGTGAGTAAT	1	1	mmu-mir-126	
ACAGTGGCTAAGTTCTG	25	3	mmu-mir-27b	
TGAGGTAGTAGGTTGTATAGTTTT	54	1	mmu-let-7a-1	
AGGCAGTGTAATTAGCTGATTG	23	1	mmu-mir-34b	
TGTGAAATGTTTAGGACCACTAG	29	1	mmu-mir-203	
GGTAGTAGGTTGTATAGT	5	2	mmu-let-7a-1	
GTAATTAGCTGATTGT	1	1	mmu-mir-34b	
GTGAAATGTTTAGGACCACTAGA	11	1	mmu-mir-203	
ACACGGACACCGCAGGG	6	1	mmu-let-7b	
TTTGGCAATGGTAGAACTCACACC	1358	1	mmu-mir-182	
TGAAATGTTTAGGACCACTA AATCACTAACTCCACTGCCAT	7 22	1 1	mmu-mir-203 mmu-mir-34b	
TTCACAGTGGCTAAGTTC	1294	2	mmu-mir-27b	
TTTGGCAATGGTAGAACTCAC	1024	1	mmu-mir-182	
ATGAGGTAGTAGGTTGTATAGTT	53	1	mmu-let-7a-1	
TTGGCAATGGTAGAACTCAC	1	1	mmu-mir-182	
ACCATTTGAAATCAGTGTT	24	2	mmu-mir-29b-2	
TGAGGTAGTAGGTTGTATGGT	30009	2	mmu-let-7c-2	
CGTACCGTGAGTAATAATGCGC	3	1	mmu-mir-126	
GTAGTAGGTTGTGGTT	22	1	mmu-let-7b	
GAGGTAGTAGGTTGTATGGT	65	2	mmu-let-7c-2	
TTTGGCAATGGTAGAAC	4	2	mmu-mir-182	
AGTAGGTTGTGTGGTTT	20	1	mmu-let-7b	
ATATAATACAACCTGCTAAGTGT	91	1	mmu-mir-374	mmu mir 220
TCAGCACCAGGATATTGTTGGGG TTAGGGTCACACCCACCACTGGG	1 1	1 1	mmu-let-7a-1	mmu-mir-338
TGAGGTAGTAGGTTGTGTGT	34985	1	mmu-let-7b	
GAGGTAGTAGGTTGTGTGT	104	1	mmu-let-7b	
CAGTGGCTAAGTTCTGC	3	2	mmu-mir-27b	
CTATACAATCTACTGTCTTTCCT	8	2	mmu-let-7a-1;mmu-let-7c-2	
CTAGCACCATTTGAAATCAGTGT	335	2	mmu-mir-29b-2	
CATCAGTGATTTTGTTG	1	1	mmu-mir-338	
AGAGCTTAGCTGATTGGTGAAC	87	1	mmu-mir-27b	
TGGAATGTAAAGAAGTATGT	1	2	mmu-mir-1-2	
GGTAGTAGGTTGTATAGTTT	2	2	mmu-let-7a-1	
ACAGTGGCTAAGTTC	2	13	mmu-mir-27b	
TGAGGTAGTAGGTTGTGTGTTTCAGGG	1	1	mmu-let-7b	
GTAAGGTAATGGGACCCG	43	1	mmu-mir-182	
TTCACAAAGCCCATACACTTT	35	1	mmu-mir-350	
CATTATTACTTTTGGTACGC TCACAGTGGCTAAGTTCTGCA	781 2	1 1	mmu-mir-126	
TAGTAGGTTGTATAG	1	4	mmu-mir-27b mmu-let-7a-1	
TCCAGCATCAGTGATTTTGTTG	15	1	mmu-mir-338	
	1.5	-	550	

		_		
CCATTTGAAATCAGTGTT TTGAACTGTCAAGAACCACT	15 1	2 1	mmu-mir-29b-2	mmu-mir-203
ATCTAGCACCATTTGAAATCAGTGTT	4	1	mmu-mir-29b-2	11111u-11111-203
CACAGTGGCTAAGTTCTGCA	1	1	mmu-mir-27b	
CTAGCACCATTTGAAATCAGTGTT	126	2	mmu-mir-29b-2	
TAGCACCATTTGAAATCAGTGTTTTA	5	1	mmu-mir-29b-2	
CACATGGAGTTGCTGTTACAC	3	1		mmu-mir-194-1
AATGGTAGAACTCACACCG	40	1	mmu-mir-182	
TGAAATGTTTAGGACCA	1	3	mmu-mir-203	
AGTAGGTTGTATAGT	1	9	mmu-let-7a-1	mmu-let-7b
TAGCACCATTTGAAATCAGTGTT	80418	2	mmu-mir-29b-2	
CCGTGAGTAATAATGC	1	1	mmu-mir-126	
GGTAGTAGGTTGTATGGTTT	1 20749	2 2	mmu-let-7c-2	
TAGCACCATTTGAAATCAGTGT ATCACTAACTCCACTGCCATCA	20749 51	1	mmu-mir-29b-2 mmu-mir-34b	
GCACCATTTGAAATCAGTGT	14	2	mmu-mir-29b-2	
GGCAGTGTAATTAGCTGATTGTA	1	1	mmu-mir-34b	
TTCACAAAGCCCATACACTTTCAC	145	1	mmu-mir-350	
TCCAGCATCAGTGATTTTG	1	1	mmu-mir-338	
TGAGGTAGTAGGTTGTATGGTTTTGGG	1	1	mmu-let-7c-2	
AAAGTGCATGCGCTTTGGG	8	1	mmu-mir-350	
TGAGGTAGTAGGTTG	6	10	mmu-let-7a-1;mmu-let-7c-2;mmu-let-7b	
GGTAGTAGGTTGTATAGTT	35	2	mmu-let-7a-1	
CTATACAACCTACTGCCTTC	15	1	mmu-let-7b	
TAGTAGGTTGTATAGTTT	6	2	mmu-let-7a-1	
TAATACAACCTGCTAAGTG	1	2	mmu-mir-374	mmu-mir-374
AAAGTGCATGCGCTTTGGGA	66 681	1	mmu-mir-350	
GAGGTAGTAGGTTGTATGGTT TTCACAGTGGCTAAGTT	109	2 3	mmu-let-7c-2 mmu-mir-27b	
AACACGGACACCGCAGGG	109	1	mmu-let-7b	
TTAGGGTCACACCCACCACTGGGAGATAA	28	1	mmu-let-7a-1	
GCTGGTTTCACATGGTGGCTTAGATTT	1	1	mmu-mir-29b-2	
TCAACAAAATCACTGATGCTGGAGT	11	1		mmu-mir-338
TGTAACAGCAACTCCATGTGGA	104	2	mmu-mir-194-1	
TATAATACAACCTGCTAAGT	4	1	mmu-mir-374	
ACCATTTGAAATCAGTG	1	5	mmu-mir-29b-2	
CTGGTTTCACATGGTGGCTTAG	4	1	mmu-mir-29b-2	
CGTACCGTGAGTAATAAT	3	1	mmu-mir-126	
AGAGCTTAGCTGATTGGTGAA	65	1	mmu-mir-27b	
TAGTAGGTTGTATAGTT	150	2	mmu-let-7a-1	
CATTATTACTTTTGGTACGCGCTGTGA	1	1	mmu-mir-126	
TGAGGTAGTAGGTTGTATAGTTTTAGG	1	1	mmu-let-7a-1	
GGTAGTAGGTTGTGTGTTT TGGCAATGGTAGAACTCACACCG	1 5	1 1	mmu-let-7b mmu-mir-182	
GTAGGTTGTAGAACTCACACCG	7	3	1111114-11111-102	mmu-let-7b
AGTTCCAGGACAGCCAGGGCTATACAGAGA	1	19184	mmu-mir-706	mind ice 75
TAGTAGGTTGTATGGTTT	2	2	mmu-let-7c-2	
CTAGCACCATTTGAAATCAGT	15	2	mmu-mir-29b-2	
TGAGGTAGTAGGTTGTATGGTTTTGG	1	1	mmu-let-7c-2	
TTCACCAATCAGCTAAGCTCTGC	1	1		mmu-mir-27b
TGGGTACATAAAGAAGTATGTGC	5	1		mmu-mir-1-2
AGGTAGTAGGTTGTATGGTT	25	2	mmu-let-7c-2	
TTCACAAAGCCCATACA	1	1	mmu-mir-350	
CAATCACTAACTCCACTGCCA	1	1	mmu-mir-34b	
ACAGTGGCTAAGTTCTGC	51	2	mmu-mir-27b	
TAGGTTGTGTGGTTTCAGGGCAGTGA	1	1	mmu-let-7b	
TTATTACTTTTGGTACGC	2 117	1 1	mmu-mir-126	
TAGGCAGTGTAATTAGCTGATTG CTTAGCAGGTTGTATTATCATT	117	1	mmu-mir-34b mmu-mir-374	
TTTGGCAATGGTAGAACTCACACCG	11377	1	mmu-mir-182	
TAGTAGGTTGTATGG	1	4	mmu-let-7c-2	
CACAGTGGCTAAGTTCTGC	4	1	mmu-mir-27b	
AGATAACTATACAACCTACTGCCTTC	1	1	mmu-let-7b	
CATTATTACTTTTGGTACGCGCTGTGACA	1	1	mmu-mir-126	
CTGGTTTCACATGGTGGCTTAGA	15	1	mmu-mir-29b-2	
ATACAACCTGCTAAGTG	1	5	mmu-mir-374	mmu-mir-374
CCATTTGAAATCAGTGT	6	2	mmu-mir-29b-2	
GGTAGTAGGTTGTGTGTT	4	1	mmu-let-7b	
TCGTACCGTGAGTAATAATGC	658	1	mmu-mir-126	
TCACAGTGGCTAAGTTCTG	54	1	mmu-mir-27b	
CATTATTACTTTTGGTACGCGCT	5 240	1 1	mmu-mir-126	
CGTACCGTGAGTAATAATGC TCTCTGTATAGCCCTGGCTGTC	1	25381	mmu-mir-126	mmu-mir-706
	1		mmu-mir-203	IIIIId-IIIII-700
	1	1		
GTGAAATGTTTAGGACCAC TAGTAGGTTGTGTGTTT	1 4	1 1	mmu-let-7h	
TAGTAGGTTGTGTGTTT  CAGTAGGTTGTATAGTT		1 1 1	mmu-let-7b	mmu-let-7b
TAGTAGGTTGTGGTTT	4	1	mmu-let-7b mmu-mir-126	mmu-let-7b
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT	4 1	1 1		mmu-let-7b
TAGTAGGTTGTGTGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC	4 1 2 6 1	1 1 1	mmu-mir-126	mmu-let-7b mmu-mir-486
TAGTAGGTTGTGTGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC	4 1 2 6 1 113	1 1 1 2 1	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTC	4 1 2 6 1 113	1 1 1 2 1	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTCACAC CTATACAATCTACTGTCTTTCC	4 1 2 6 1 113 11 102	1 1 1 2 1 1 2	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTCACAC CTATACAATCTACTGTCTTTCC TAGTAGGTTGTGTGTT	4 1 2 6 1 113 11 102 5	1 1 1 2 1 2 1 2	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAATAATGCGC AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAAACTCACAC CTATACAATCTACTGTTCC TAGTAGGTTGTGTGTGTT TAGTAGGTTGTATGGT	4 1 2 6 1 113 11 102 5	1 1 1 2 1 1 2 1 4	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b mmu-let-7c-2	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAGTAGTG AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTC CTATACAATCTACTGTCTTTCC TAGTAGGTTGTGTGGTT TAGTAGGTTGTAGGTT GAGGTTGTAGGT GAGGTTGTATGGT GAGGTTGTAGGTT GAGGGTTGTATGGTT GAGGGTTGTATGGTT GAGGGTTGTATGGTT	4 1 2 6 1 113 11 102 5 24 120	1 1 1 2 1 1 2 1 4 2	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b- mmu-let-7c-2 mmu-let-7c-2	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAGTAGTAGTG AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTCACAC CTATACAATCTACTGTCTTTCC TAGTAGGTTGTGTGGTT TAGTAGGTTGTATGGT GAGGTAGTAGGTTGTATGGTTT TCCTGTACTGACTGCCCCCGAGC	4 1 2 6 1 113 11 102 5 24 120 3	1 1 1 2 1 2 1 2 1 4 2	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b mmu-let-7c-2	mmu-mir-486
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAGTATAGTG AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTCACAC CTATACAATCTACTGTTTCC TAGTAGGTTGTATGGTT TAGTAGGTTGTATGGTT TAGTAGGTTGTATGGTT TCCTGTACTGAGCTGCCCCGAGC TCCTGTACTGAGCTGCCCCCGAGG	4 1 2 6 1 113 11 102 5 24 120 3 1	1 1 1 2 1 2 1 2 1 4 2 1	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b mmu-let-7c-2 mmu-let-7c-2 mmu-let-7c-2 mmu-let-7c-2 mmu-let-786	
TAGTAGGTTGTGTGGTTT CAGTAGGTTGTATAGTT TCGTACCGTGAGTAGTAGTAGTG AGTGTAATTAGCTGATTGT TCCTGTACTGAGCTGCCCC TTTGGCAATGGTAGAACTC TTGGCAATGGTAGAACTCACAC CTATACAATCTACTGTCTTTCC TAGTAGGTTGTGTGGTT TAGTAGGTTGTATGGT GAGGTAGTAGGTTGTATGGTTT TCCTGTACTGACTGCCCCCGAGC	4 1 2 6 1 113 11 102 5 24 120 3	1 1 1 2 1 2 1 2 1 4 2	mmu-mir-126 mmu-mir-34b mmu-mir-486 mmu-mir-182 mmu-let-7a-1;mmu-let-7c-2 mmu-let-7b- mmu-let-7c-2 mmu-let-7c-2	mmu-mir-486

CATTATTACTTTTGGTACGCGC	44	1	mmu-mir-126	
TGAAATGTTTAGGACCACTAGA	17	1	mmu-mir-203	
TGAGGTAGTAGGTTGTATA	95	2	mmu-let-7a-1	
TGAGGTAGTAGGTTGTATG	381	2	mmu-let-7c-2	
TGGTTTCACATGGTGGCTTAGA	2	1	mmu-mir-29b-2	
TTGGCAATGGTAGAACTCACACCG	48	1	mmu-mir-182	
CATTTGAAATCAGTGT	5	6	mmu-mir-29b-2	
GTACCGTGAGTAATAATGC	1	1	mmu-mir-126	
CTAGCACCATTTGAAATCAGTG	30	2	mmu-mir-29b-2	
CTAGCACCATTTGAAATCAG	2	2	mmu-mir-29b-2	
	64	1		
GTTCACAGTGGCTAAGTTCT			mmu-mir-27b	
TTTGGCAATGGTAGAACTCACACCGGT	8	1	mmu-mir-182	
AGGTAGTAGGTTGTATGGT	16	2	mmu-let-7c-2	
GGTAGTAGGTTGTATA	1	2	mmu-let-7a-1	
TAGCACCATTTGAAATCAGT	265	2	mmu-mir-29b-2	
TGAGGTAGTAGGTTGTGG	1351	1	mmu-let-7b	
TATTACTTTTGGTACGCG	1	1	mmu-mir-126	
AGTAGGTTGTATAGTT	41	3	mmu-let-7a-1	mmu-let-7b
ATGAGGTAGTAGGTTGTATAGT	5	1	mmu-let-7a-1	
TGAGGTAGTAGGTTGTATAGTT	66680	2	mmu-let-7a-1	
TAGTAGGTTGTGTGT	22	1	mmu-let-7b	
	41	1		
CATTATTACTTTTGGTACG			mmu-mir-126	
TGAGGTAGTAGGTTGT	53	8	mmu-let-7a-1;mmu-let-7c-2;mmu-let-7b	
ATCTATCTATCTATC	2	212505		mmu-mir-350
CATTTGAAATCAGTGTT	44	3	mmu-mir-29b-2	
AATCACTAACTCCACTGCCA	28	1	mmu-mir-34b	
CGGGGCAGCTCAGTACAGGATG	56	1		mmu-mir-486
AGTAGATTGTATAGTT	11	5		mmu-let-7a-1;mmu-let-7c-2
ATCACTAACTCCACTGCCATCAA	2	1	mmu-mir-34b	
TACCGTGAGTAATAATGCG	1	1	mmu-mir-126	
AAACCAGCTTCCAGAAG	1	3		mmu-mir-29b-2
AGGTAGTTGGTTGTTTT	7	2	mmu-let-7c-2	11111d 11111 250 2
	4			
AGTGTAATTAGCTGATTG	·	1	mmu-mir-34b	
TGGAATGTAAAGAAGTATGTA	2	2	mmu-mir-1-2	
GAGGTAGTAGGTTGTGGTTT	11	1	mmu-let-7b	
GTGTAATTAGCTGATTGT	3	1	mmu-mir-34b	
CGGGGCAGCTCAGTACAGGA	1	2	mmu-mir-486	mmu-mir-486
AGCACCATTTGAAATCAGTGT	3	2	mmu-mir-29b-2	
TAGCACCATTTGAAATCAG	45	2	mmu-mir-29b-2	
TTCACAAAGCCCATACACTTTC	190	1	mmu-mir-350	
AGGTAGTAGGTTGTGTGT	6	1	mmu-let-7b	
GGTGAGGTAGGTTGTAT	1	1	mmu-let-7c-2	
GAGGTAGTAGGTTGTATGGTTTT	2	1	mmu-let-7c-2	
	66	2		mmu mir 196
TCCTGTACTGAGCTGCCCCGA			mmu-mir-486	mmu-mir-486
TAATACAACCTGCTAAGTGT	1	1	mmu-mir-374	
TGAGGTAGTAGGTTGTATAGT	7590	2	mmu-let-7a-1	
GAGGTAGTAGGTTGTATAGT	14	2	mmu-let-7a-1	
TTTGAAATCAGTGTT	1	21	mmu-mir-29b-2	
TTCACAAAGCCCATACACTT	4	1	mmu-mir-350	
GAACACGGACACCGCAGGG	2	1	mmu-let-7b	
CTGGTTTCACATGGTGGCTTAGATTTT	2	1	mmu-mir-29b-2	
TTGGGCTCTGCCCCGCTCTGCGGTAA	21	1	mmu-let-7c-2	
ATTTGAAATCAGTGTT	12	8	mmu-mir-29b-2	
TAGGCAGTGTAATTAGCTGATT	14	1	mmu-mir-34b	
ATATAATACAACCTGCTAAGT	603	1	mmu-mir-374	
GTGAGGTAGTAGGTTGTATGGTT				
	1	1	mmu-let-7c-2	
GGTAGTAGGTTGTATGGT	2	2	mmu-let-7c-2	
CATTATTACTTTTGGTACGCG	786	1	mmu-mir-126	
ATGGCAGTGGAGTTAGTGATTGT	1	1		mmu-mir-34b
TTTGGCAATGGTAGAACTCACA	1734	1	mmu-mir-182	
GTAGGTTGTGGTT	2	3	mmu-let-7b	
ACCATTTGAAATCAGTGT	9	2	mmu-mir-29b-2	
TGGCAATGGTAGAACTCACACC	3	1	mmu-mir-182	
CTCGTACCGTGAGTAATAATGCG	11	1	mmu-mir-126	
TTCACAGTGGCTAAG	2	20	mmu-mir-27b	
AGGTAGTAGGTTGTGGTTT	3	1	mmu-let-7b	
AGTGGCTAAGTTCTG	3	9	mmu-mir-27b	
GTAGTAGGTTGTATGGTTT	1			
		2	mmu-let-7c-2	
AGTAGGTTGTGTGGTT	2	1	mmu-let-7b	
AGAGCTTAGCTGATTGGTGAACAG	19	1	mmu-mir-27b	
TGAGGTAGTAGGTTGTGTGTT	136624	1	mmu-let-7b	
CACCATTTGAAATCAGTGT	14	2	mmu-mir-29b-2	
ATAGATAGATAGATA	4	210178	mmu-mir-350	
TAGGCAGTGTAATTAGCTGAT	1	1	mmu-mir-34b	
TGAGGTAGTAGGTTGTAT	327	4	mmu-let-7a-1;mmu-let-7c-2	
TCGTACCGTGAGTAATAA	1	1	mmu-mir-126	
GTTCACAGTGGCTAAGTTCTGC	188	1	mmu-mir-27b	
GTGAAATGTTTAGGACCACT	16	1	mmu-mir-203	
CCGTGAGTAATAATGCG	2	1	mmu-mir-126	
	8			
AGAGCTTAGCTGATTGGTGA		1	mmu-mir-27b	m= 400
TCCTGTACTGAGCTGCCC	2	2	mmu-mir-486	mmu-mir-486
AACAATATCCTGGTGCTGAGT	11	1	mmu-mir-338	
CTGGTTTCACATGGTGGCTTAGAT	7	1	mmu-mir-29b-2	
TTTGGCAATGGTAGAACTCACACCGG	95	1	mmu-mir-182	
GAGGTAGTAGGTTGTATGG	4	2	mmu-let-7c-2	
CTATACAACCTACTGCCTTCCC	1	1	mmu-let-7b	
TGAGGTAGTAGGTTGTA	34	4	mmu-let-7a-1;mmu-let-7c-2	
TGAGGTAGTAGGTTGTG	14	1	mmu-let-7b	
TGGTTTCACATGGTTGGTTAGAT	1	1	mmu-mir-29b-2	
	=	<del>-</del>	=== =	

TAGCACCATTTGAAATCAGTGTTTT				
	68	1	mmu-mir-29b-2	
ATATAATACAACCTGCTAAG	28	1	mmu-mir-374	
CATCTTTGCCGGTGACAGCA	7	1	mmu-mir-126	
GTTCACAGTGGCTAAGTTCTG	135	1	mmu-mir-27b	
TTGAACTGTCAAGAACCACTGG	1	1		mmu-mir-203
GTTGGCAAGTCTAGAACCACCG	2	1		mmu-mir-182
TTCACAAAGCCCATACACTTTCA	188	1	mmu-mir-350	
TGAGGTAGTAGGTTGTATAGTTTTAGGG	1	1	mmu-let-7a-1	
TCGTACCGTGAGTAATAATGCG	1165	1	mmu-mir-126	
TCCAGCATCAGTGATTTTGT	12	1	mmu-mir-338	
CGTACCGTGAGTAATAATG	28	1	mmu-mir-126	
AGTGGCTAAGTTCTGCA	9	2	mmu-mir-27b	
ATTTGAAATCAGTGT	1	29	mmu-mir-29b-2	
TGAGGTAGTAGGTTGTATGGTTTT	1395	1	mmu-let-7c-2	
AATCACTAACTCCACTGCCATC	259	1	mmu-mir-34b	
GAGGTAGTAGGTTGTATGGTTTTGG	2	1	mmu-let-7c-2	
ATCTATCTATC	1	246025	mind let /c 2	mmu-mir-350
	4		24h	11111111-11111-330
TAGGCAGTGTAATTAGCT	·	2	mmu-mir-34b	
ACTTAGCAGGTTGTATTATCAT	3	1	mmu-mir-374	
GTAGTAGTTGTGTGTTT	1	1	mmu-let-7b	
TGAGGTAGTAGGTTGTGTGTTTCA	26	1	mmu-let-7b	
GTGAGTTCCAGGACAGCCAGGGCTATACA	1	19153	mmu-mir-706	
TTCACAGTGGCTAAGTTCTGC	32597	1	mmu-mir-27b	
TAGCACCATTTGAAATCA	15	2	mmu-mir-29b-2	
TGAGGTAGTAGGTTGTATAGTTT	2680	2	mmu-let-7a-1	
TCACAGTGGCTAAGTTCTGC	16	1	mmu-mir-27b	
TTCACAGTGGCTAAGTTCTGCAC	25	1	mmu-mir-27b	
CACAGTGGCTAAGTTCTG	5	1	mmu-mir-27b	
AAAGTGCATGCGCTTTGGGACA	49	1	mmu-mir-350	
GTGAAATGTTTAGGACCACTAG	223	1	mmu-mir-203	
ATCTTTGCCGGTGACAGCA	4	1	mmu-mir-126	
TTCACAGTGGCTAAGTTCTG	12686	1	mmu-mir-27b	
TTTGGCAATGGTAGAACT	20	1	mmu-mir-182	
CTAGCACCATTTGAAATCA	1	2	mmu-mir-29b-2	
CCATTTGAAATCAGTGTTT	4	1	mmu-mir-29b-2	
GGTAGTAGGTTGTATGGTT	10	2	mmu-let-7c-2	
TGAGGTAGGTTGTATAGTTTTA	1	1	mmu-let-7c-2	
	24	1	mmu-mir-34b	
ATCACTAACTCCACTGCCATC	2295			
TTTGGCAATGGTAGAACTCACAC		1	mmu-mir-182	
AGTAGGTTGTATGGT	1	6	mmu-let-7c-2	
TTCTAGCACTTAGCAGGTTGTATTATCATT	1	1	mmu-mir-374	
TCAGGGCAGTGATGTTGCCCCTCCGAAGAT	1_	1	mmu-let-7b	
TGAGGTAGTAGGTTGTGGTTTCAGGGCA	7	1	mmu-let-7b	
CTTAGCAGGTTGTATTATCAT	5	1	mmu-mir-374	
GTGAAATGTTTAGGAC	1	3	mmu-mir-203	
TCCTGTACTGAGCTGCCCCGAG	152	2	mmu-mir-486	mmu-mir-486
TGAGGTAGTAGGTTGTATGGTTTTGGGCT	1	1	mmu-let-7c-2	
CTGGTTTCACATGGTGGCTTAGATT	7	1	mmu-mir-29b-2	
TTAGCAGGTTGTATTATCATT	1	1	mmu-mir-374	
TGAGGTAGTAGGTTGTATGGTTT	27795	2	mmu-let-7c-2	
CCAACAATATCCTGGTGCTGA	2	1	mmu-mir-338	
TCACAGTGGCTAAGTTC	1	4	mmu-mir-27b	
ATCACTAACTCCACTGCCAT	1	1	mmu-mir-34b	
AGAGCTTAGCTGATTGGT	5	1	mmu-mir-27b	
ACTATACAATCTACTGTCTTTC	4	2	mmu-let-7a-1;mmu-let-7c-2	
CTGGTTTCACATGGTGGCTTAGATTT	_			
	6	1	mmu-mir-29b-2	
GAGGTAGTAGGTTGTATAGTT	103	2	mmu-let-7a-1	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATGGTT	103 24	2 3	mmu-let-7a-1 mmu-let-7c-2	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATGGTT AGGCAGTGTAATTAGCTGATTGT	103 24 638	2 3 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG	103 24 638 316	2 3 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTGTGTGTAGTGTGAGGTAGTAGGTTGTGTGGGTTTCAG	103 24 638 316 5	2 3 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTGTGTGTGTGTGTGTGTG	103 24 638 316 5 1312	2 3 1 1 2	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTGTGGTTTCAG TGAGGTAGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG	103 24 638 316 5 1312	2 3 1 1 2 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTTGT	103 24 638 316 5 1312 130 94	2 3 1 1 1 2 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTAGGTTGTTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTTGTT GAAATGTTTAGGACCACTAG GAAATGTTTAGGACCACTAG	103 24 638 316 5 1312 130 94	2 3 1 1 1 2 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTGTGT	103 24 638 316 5 1312 130 94 1	2 3 1 1 1 2 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b	mmu mir 229
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTATTAGGTT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCATCA TTCAACAAAATCACTGCATGA	103 24 638 316 5 1312 130 94 1 17	2 3 1 1 1 2 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b	mmu-mir-338
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAAGTTGTTAGAGCACCACTAG TGAGGTAGTAGGACCACTAG TGAGATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGTGTGAG CTTAGCAGGTTGTATTA	103 24 638 316 5 1312 130 94 1 17 1	2 3 1 1 1 2 1 1 1 1 1 3	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b	mmu-mir-338 mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTAGGTTGTTGTATTAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTGTT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGGTTGTATTA	103 24 638 316 5 1312 130 94 1 17 1 1 3	2 3 1 1 1 2 1 1 1 1 1 3 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGAGGTGTATTAGGTT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTGATTGT TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTATTAGCTGATTGTA TAGCACCACTTTTGAAATCAGTGTTTT	103 24 638 316 5 1312 130 94 1 17 1 1 3 2	2 3 1 1 1 2 2 1 1 1 1 1 3 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-29b-2	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG AATCACTAACTCCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGGTTGTAATTAGCTGATTGTA TAGCCACTATTGTAATTAGCTGATTGTA TAGCACCATTTGAAATCAGTGTTTT TCCAGCATCAGTGATTTTTT TCCAGCATCAGTGATTTTTT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844	2 3 1 1 1 2 1 1 1 1 3 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-204 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTAGGTTGTATAGG TGAGGTAGTAGGTTGTATAGG TGAGATGTTAGGACCACTAG TGAGGTAGTAGGACCACTAG TGAGGTAGTTAGGACCACTAG AATGATTAGGACCACTAG AATGATTACCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGGTTGTATTAG TAGGACAGTTGTATTA TAGCACCATTTGAAATCAGTGTTT TCCAGCATCAGTTGTATTTT TCCAGCATCAGTTGAATTCAGTGTTT TGAGGTAGTAGGTTTTTT TGAGGTAGTAGGTTTTTT TGAGGTAGTAGGTTTTT	103 24 638 316 5 1312 130 94 1 1 7 1 3 2 844 25 4	2 3 1 1 1 2 1 1 1 1 3 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-29b-2	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGAGGTGTATTAGGTT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTGATTTCAG TGAGGTAGTAGGTTGATTAGG TGAGATGTTAGGTTGATAGG TGAAATGTTTAGGACCACTAG TGAGGTAGTAGGTTGTGTT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTATTAGCTGATTGTA TAGCACCATTCAGTAGTTGTT TCCAGCATCAGTGATTTTT TCCAGCATCAGTGATTTTTT TCAGCTAGTAGTGTAGT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4	2 3 1 1 1 2 2 1 1 1 1 1 3 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-38 mmu-mir-38 mmu-let-7c-2	
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGTAGGTTGATTAGGTT AGGAGGTGAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTAATTAGCTGATTGTA TAGCAGCATCAGTGATTTTTT TCCAGCATCAGTGATTTTTT TCCAGCATCAGTGATTTTTTT TCAGCATCAGTGATTTTTTT TGAGGTAGTTGTATTTTT TGAGCTAGTGTAGTTGTTTT TGAGCTAGTGTAGTTGTTTT TGAGCTAGTGTAGTTGTTTT TGAGCTTCGGCCCCCATGTCAGCAGATGC TCTTTGCCGGTGACAGCA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6	2 3 1 1 1 2 1 1 1 1 3 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-38b mmu-mir-29b-2 mmu-mir-38 mmu-let-7c-2 mmu-mir-126	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGATGTTAGGACCACTAG TGAGATGTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGGTTGTATTAGCTGATTGTA TAGCACCATTTGAAATCAGTGATTT TCCAGCATCATTTGAAATCAGTGTTT TCCAGCATCAGTGATTTTTT TGAGGTAGTAGGTTGTATTGAATTCAGTGTTT TGAGGTAGTAGGTTGTATTGAATTCAGTGTTT TGAGCTCAGTGAGTTTTGTT TGAGGTAGTAGGTTGTATTGGTTTTGCTGACTTCGGCCCCCATGTCAGCAGATGC TTTTGCCGGTGACACCCACCTGGGAGAT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6	2 3 1 1 1 2 1 1 1 1 3 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34c mmu-let-7a-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTTCAG TGAGGTAGTAGGTTGTGTAGGT TGAGATGTTTTAGGACCACTAG TGAGATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTAT TAGGCAGTGTATTATTAT TAGGCAGTGTAATTAGCTGATTGTA TAGCACCATCAGTGATTGTTT TCCAGCATCAGTGATTTGTT TCAGCTAGTAGTAGTTGTTTTT TCAGCTAGTAGTAGTTGTATGTA TGAGGTAGTAGTTGTATGTAGTAGTAGTAGTAGTAGTAGT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 241	2 3 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-38 mmu-let-7c-2 mmu-let-7c-2 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTAGAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG ATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGCAGCTGTAGTATTA TAGCACCATTTGAAATCAGTGTTT TCCAGCATCAGTGATTTTTT TCAGCAGTCAGTGATTTTTT TGAGGTAGTAGTAGTTTTTT TGAGGTAGTAGTAGTTTTTT TGAGGTAGTAGTAGTTTTTT TGAGGTAGTAGTAGTTTTTT TGAGGTAGTAGGTTGTATGGTTTT TGAGGTAGTAGGTTGTATGGTTTT TGAGGTAGCACCCCCATGTCAGCAGATGC TCTTTGCCGGTGACAGCA TTAGGGTCACACCCACCACCACTGGGAGAT CTATACAAATCTACTGTCTTTTC ATATAATACAACCTGCTAA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5	2 3 1 1 1 1 2 1 1 1 1 3 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-36 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAGT TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTTGTAATTAGCTGATTGTA TAGCACATTTAGAATCAGTGTTTT TCCAGCATCAGTGATGTTTTT TCCAGCATCAGTGATTTTTT TGAGCTAGTAGTTGTATTTT TGAGCTTGAGTTGTATTAGTTTTT TGAGCTTCGGCCCCCATGTCAGCAGATGC TCTTTGCCGGTGACAGCA TTAGCAGTCTACTGTCTTTC ATATACAATCTACTGTCTTTC ATATAATACAACCTGCTAA ATAATACAACCTGCTAA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5	2 3 1 1 1 1 2 1 1 1 3 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34c mmu-mir-34b mmu-mir-374 mmu-mir-374	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTTCAG TGAGGTAGTAGGTTGTGTAGG TGAAATGTTTAGGACCACTAG TGAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTTGTATTA TAGGCAGTTGTATTA TAGGCAGTCATTGAAATCAGTGTTTT TCCAGCATCAGTGATTGTTT TCCAGCATCAGTGTTATTGTT TGAGGTAGTAGTGTGTGTTTT TGAGGTTAGTAGTGTTTTGTT TGAGCTTCGGCCCCCATGTCAGCAGATGC TCTTTGCCGGTGACAGCA TTAGGAGTCACCCCCACCACTGGGAGAT CTATACAATCTACTGTCTTTC ATATAATACAACCTGCTAAGTGT TCCAGCATCAGTGATTTTGT TCCAGCATCAACTGTAGTGT TCCAGCATCAACTGTAAGTGT TCCAGCATCAACTGTAAGTGT TCCAGCATCAGTGATTTTTTT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 241 5 1 10	2 3 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-34b mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-let-7b mmu-mir-204 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-29b-2 mmu-mir-38 mmu-let-7c-2 mmu-let-7c-2 mmu-let-7c-2 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGTAGGTTGATTAGGTT AGGAGTGTATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGATTAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTTAGGTTGATAG TGAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTAT TAGGCAGTGTAATTAA TAGGCAGTGTAATTAA TAGCACATCAGTGATTGTTT TCCAGCATCAGTGATTGTTT TCCAGCATCAGTGATTTTTT TGAGGTAGATGAGTTGTATTGTT TGAGGTAGATGAGTGATTTTGTT TGAGGTAGATGAGTGATTTTGTT TGAGGTAGATGAGCACCCACCACTGGGAGATC TCTTTGCCGGTGACACCCACCACTGGGAGAT TTATACAATCTACTGTCTTTC ATATAATACAACCTGCTAA ATAATACAACCTGCTAAGTTTTGAA AGGTAGTAGGTTTTTTTG ATGGGTACACCCACTGCTAA ATAATACAACCTGCTAAGTGTT TCCAGCATCAGTGATTTTGTT TCCAGCATCAGGTGATTTTGTT TCCAGCATCAGTGATTTTGTTT TCAGGTTACAATCTACTGTCTTTTC ATATAATACAACCTGCTAAA ATAATACAACCTGCTAAGTGTT TCCAGCATCAGTGATTTTGTTGA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 241 5 1 10 20	2 3 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-34b mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-338 mmu-let-7a-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAGT TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTGTG GAAATGTTTAGGACCACTAG ATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGCATCA TTCAACAGATGTAGTATTA TAGCAGGTTGTATTA TAGCAGGTTGTATTA TAGCAGTTGTAATTAGCTGATTGTT TCCAGCATCAGTGATTGTTT TCCAGCATCAGTGATTTTTT TGAGTTAGTAGGTTGTATTGTT TGAGTTGTAGTTGTATTGTTTT TGAGTTAGTAGGTTGTATTGTTTT TGAGTTAGTAGGTTGTATGGTTTTT TGAGCTTCGGCCCCCATGTCAGCAGATGC TCTTTGCCGGTGACAGCA TTAGCATCTACTGTCTTTC ATATAATACAACCTGCTAA ATAATACAACCTGCTAAGTGT TCCAGCATCAGTGATTTTGTTG TCCAGCATCAGTGATTTTGTTG AGGTAGTAGTAGTTGTTTC TCAGCATCAGTGATTTTGTTG TCCAGCATCAGTGATTTTGTTG AGGTAGTAGGTTGTATAGTT TCCAGCATCAGTGATTTTGTTGA AGGTAGTAGGTTGTATAGTT TTCACAGTGGCTAAAGTTCT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140	2 3 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTTAGGTTGTATAGTTGTATATATA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140 1	2 3 1 1 1 1 2 1 1 1 3 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-375 mmu-let-7a-1 mmu-mir-27b mmu-mir-194-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGTAGGTTGATTAGGTT AGGAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTTCAG TGAGGTAGTAGGTTGTATAG TGAAATGTTTAGGACCACTAG TGAAGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTAATTAGCTGATTGTA TAGGCAGTGTAATTAGCTGATTGTT TCCAGCATCAGTGATTTTGTT TGAGGTAGATGAGTGTGTATTGTAT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 241 5 1 10 20 3140 1 3	2 3 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAAGTG TGAGGTAGTTAGGTTGTATAGTTGTATATATA	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140 1	2 3 1 1 1 1 2 1 1 1 3 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-375 mmu-let-7a-1 mmu-mir-27b mmu-mir-194-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAGTTGTATATATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTTGTAATTAGCTGATTGTA TAGCACATTTGAAATCAGTGTTTT TCCAGCATCAGTGATGTTTTTTTTCCAGCATCAGTGTAGTTTTTTTT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140 1 3 333456 1	2 3 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-374 mmu-mir-34b mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-126 mmu-mir-126 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-194-1 mmu-mir-374	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTGTT GAAATGTTTAGGACCACTAG ATCACTACACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTAATTAGCTGATTGTA TAGCACACATTTGAAATCAGTGTTT TCCAGCATCAGTGATTTTGTT TGAGGTAGTAGTAGTTAGTTTT TGAGGTAGTAGTAGTTAGT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140 1 3 3 33456	2 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-let-7c-2 mmu-mir-38 mmu-let-7c-2 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-374 mmu-let-7b	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAGTTGTATATATACAACCTGCTAAGTG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTTGTAATTAGCTGATTGTA TAGCACATTTGAAATCAGTGTTTT TCCAGCATCAGTGATGTTTTTTTTCCAGCATCAGTGTAGTTTTTTTT	103 24 638 316 5 1312 130 94 1 17 1 3 2 844 25 4 1 6 6 6 241 5 1 10 20 3140 1 3 333456 1	2 3 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-374 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-196 mmu-mir-126	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGTGTGTTCAG TGAGGTAGTAGGTTGTATAGG TGAAATGTTTAGGACCACTAG TGAAATGTTTAGGACCACTAG AATCACTAACTCCACTGCCATCA TTCAACAAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGGTTGTATTA TAGGCAGTGTAATTAGCTGATTGTA TAGACCATCAGTGATTTTTTTCCAGCATCATGATGTTTTTTCCAGCATCAGTGATTTTGTTT TCCAGCATCAGTGATTTTATTTT	103 24 638 316 5 1312 130 94 1 17 17 1 3 2 844 25 4 1 6 6 241 5 1 10 20 3140 1 3 33456 1 9	2 3 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7a-1 mmu-let-7b mmu-let-7b mmu-mir-203 mmu-let-7b mmu-mir-34b mmu-mir-34b mmu-mir-34b mmu-mir-38 mmu-let-7c-2 mmu-let-7c-2 mmu-let-7a-1 mmu-let-7a-1;mmu-let-7c-2 mmu-mir-374 mmu-mir-194-1 mmu-mir-374 mmu-mir-374 mmu-mir-126 mmu-let-7b mmu-mir-126 mmu-let-7a-1	mmu-mir-374
GAGGTAGTAGGTTGTATAGTT TAGTAGGTTGTATAGGTT TAGTAGGTTGATTAGGTT AGGCAGTGTAATTAGCTGATTGT ATATAATACAACCTGCTAAGTG TGAGGTAGTTAGGTTGATTAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTTAGGTTGATAG TGAGGTAGTAGGTTGTATAG TGAGGTAGTAGGTTGTAG TGAGGTAGTAGGTTGTGT GAAATGTTTAGGACCACTAG ATCACCACACTAG ATCACCACACTAG ATCACACAAATCACTGATGCTGGAG CTTAGCAGGTTGTATTA TAGGCAGTGTAATTAGCTGATTGTA TAGCACCATTTGAAATCAGTGTTT TCAGCAGTAGTATTAGTTTT TGAGGTAGTAGTAGTAGTTTTT TGAGGTAGTAGTAGTAGTTTTT TGAGGTAGTAGTAGTAGTTTTT TGAGGTCACACCCACCACTGGGAGAT CTCTTTGCCGGTGACACCACCACTGGGAGAT TTATACAACTCTACTGTTTTC ATATAATACAACCTGCTAA ATAATACAACCTGCTAAGTTTTTT TCACAGTAGTAGTTTTTTT TCACAGTAGTAGTTTTTTT TCACAGTAGGTAGTTTTTTT TCACAGTAGTAGTTTTTTT TCACAGTAGTAGTTTTTTT TTACACACCTGCTAAGTTTT TTCACAGTAGGTTAGTTTTTT TTCACAGTAGCTAAGTTCT TGTAACAACCTGCTAAGTTCT TGTAACAACCTGCTAAGTTCT TGTAACAACCTGCTAAGTTG TGAGGTAGTAGTTGTTTTTT TTTATACATTTTTTGTTAGGTT TTATATACTTTTTGGTACGCGC TGAGGTAGTAGGTTGTTTTATAGTTT ATTATTACTTTTTGGTACGCGC TGAGGTAGTAGGTTGTATAGTTT TTTATTACTTTTTGGTACGCGC TGAGGTAGTAGGTTGTATAGTTTTTAGGGT CTCGTACCGTGAGTAAATAATG	103 24 638 316 5 1312 130 94 1 17 17 1 3 2 844 25 4 1 6 6 241 5 1 10 20 3140 1 3 333456 1 9 4	2 3 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1	mmu-let-7a-1 mmu-let-7c-2 mmu-mir-34b mmu-mir-374 mmu-let-7b mmu-let-7b mmu-let-7a-1 mmu-mir-203 mmu-let-7b mmu-mir-203 mmu-mir-34b mmu-mir-34b mmu-mir-374 mmu-mir-38 mmu-let-7c-2 mmu-mir-126 mmu-let-7a-1 mmu-let-7a-1 mmu-let-7a-1 mmu-mir-338 mmu-let-7a-1 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-374 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-194-1 mmu-mir-126 mmu-let-7b mmu-mir-126 mmu-let-7a-1 mmu-mir-126 mmu-let-7a-1 mmu-mir-126	mmu-mir-374 mmu-mir-680-1;mmu-mir-680-2

TAGCACCATTTGAAATCAGTG	352	2	mmu-mir-29b-2
CATTTGAAATCAGTG	1	22	mmu-mir-29b-2
GTGAAATGTTTAGGACCA	1	1	mmu-mir-203
TTGGCAATGGTAGAACTCACA	4	1	mmu-mir-182
TAGTAGGTTGTATAGTTTTAGGG	2	1	mmu-let-7a-1
TTCACAGTGGCTAAGT	4	3	mmu-mir-27b
AGCACCATTTGAAATCAGTGTT	102	2	mmu-mir-29b-2
CGGTCAGCAGCCCAGCGCCA	1	1	mmu-mir-126
TTCACAGTGGCTAAGTTCTGCA	617	1	mmu-mir-27b
TAGTAGGTTGTATAGT	13	2	mmu-let-7a-1
CATTATTACTTTTGGTAC	3	1	mmu-mir-126
ATCACTAACTCCACTGCCA	2	1	mmu-mir-34b
AGAGCTTAGCTGATTGGTGAACAGT	1	1	mmu-mir-27b
GAGGTAGTAGGTTGTGTGTT	139	1	mmu-let-7b
AAAGTGCATGCGCTTTGGGAC	21	1	mmu-mir-350
TTAGGGTCACACCCACCACTGGGA	2	1	mmu-let-7a-1
GTAGTAGGTTGTATGGT	1	2	mmu-let-7c-2
CTATACAACCTACTGCCTTCC	43	1	mmu-let-7b
GTGAGTAATAATGCG	1	1	mmu-mir-126
GTTCACAGTGGCTAAGTT	2	2	mmu-mir-27b
TAGGCAGTGTAATTAGCTGATTGT	26	1	mmu-mir-34b
TTGGGCTCTGCCCCGCTCTGCGGT	2	1	mmu-let-7c-2
AGGTAGTAGGTTGTATAGT	4	2	mmu-let-7a-1
TGAGGTAGTAGGTTGTGTGTTTC	299	1	mmu-let-7b

Table S4: Solexa reads from wt and c-kit mutant ovaries matching mouse miRNAs

Part Commen				land services	*	la		do	#-1
Read Sequence TAGTAGTTTGTACAGT	#cloned	d Read Sequence AGTTGTGTGTGCATGTTCAT	#cloned	Read Sequence TCGAGGAGCTCACAGT	#cloned	Read Sequence TGTCTGGTAATGCCGT	#cloned	Read Sequence TCCCTGAGACCCTAACT	#cloned
GTTCACAGTGGCTAAGTTCCGC GCTGTCTCGGAGCCTGGGGCA	3 1	TATGGCTTTTCATTCCTATG TCAAGTAATCCAGGATAGG	1 6	TGAGAACTGAATTCCATGGGTT ATCACATTGCCAGGGATTTCCA	7 5799	CTATGCCAACATATTGCCATC CATCCCTTGCATGGTGGAGGG	1	TATTGGGAACATTTTGCATAAA AATCAGCAAGTATACTGCCCTA	1 4
TAAAGTGCTGACAGTGCA CCTGAACTAGGGGTCTGGAGA	4	CTTTCAGTCGGATGTTTGCAGC TAGTAGTTTGTGCTGTT	319 4	TTCAAGTAATCCAGGAT AATTCGTATCTAGGGGAAT	3	AACATTCATTGTTGTCGGTGGGTTGT TGTGCAAATCTATGCAAAACTG	27 140	GACCGATTTCTCCTGGTGTTCAGAGTC TCACAGCTCTGGTCCTTGGAGC	1 1
TCTACAGTGCACGTGTCT	2	CGGCTACTTCACAACACCAGGGC	1 4	GCAAAGCACAGGGCCTGCAGAGAGGTA	1 2	TAAAATGGGTTCCTAGGA	2	TGTAACGTTGTCTATATA	1 177
AGCTCGACTCATGGTTTGAACCATTACTTA AGCAGCATTGTACAGGGCTATGAAG ATAGTAGACCGTATAGCGTAC	12	AGGGGTGCTATCTGTGATTGAGGGACAT TTTCTTGGGACTCGGAAGC	1	CATCGGGAATGTCGTGT TGTAAACATCCCCGACTG AGTAATCCAGGATAGGC	1	CCGGTGCGGAGAGCCGTTCGTCTTGGGAA CTAGATTGTGAGCTGCTGGAG	2	AGCAGCATTGTACAGGGCTATGAAA CAGTGCAATGGTATTGTCAAAGC AACATTCAACCTGTCGGTGAGTTTG	10 12
ATAGTAGACCGTATAGCGTAC CTAGCACCATTTGAAATCGGTT CAATCACTAACTCCACTGCC	1	TGTCTGGTAATGCCG AGTAGTTTGTACAGTT AAGTGCTGTTCGTGCAGGTAGT	1	AGCACATCATGGTTT TATTGCACTTGTCCCGGCCTG	2 41	TGAAAGGTGCCATACTATGTATA CATTCAACGCTGTCGGTGAGTTT TGAGGTAGTAGTTTGTACAGTT	2 524	TAAGGTGCATCTAGTGCAGA CAAACCACACTGTGGTGTTAG	82 2
TTTCCTCATATCCATTCAGGAGT	i	GCACCATTTGAAATCAGTGTT	30	GCAGCGCCGAAGGAGCCTCGGTTGGCCCC	1	TAGGTAGTTTCATGTTGTTGG	179	TCTGCCTGTCTACACTTGCTGT	2
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AGTAGGTTGTATAGTTA	4	AGTAGGTTGTATAGTTT	1	CTCGTGTCTTGTGTTGCAG	5 1	CCCAGTGTTCAGACTACCTGTT	2 918	AGGGACTTTCAGGGGCAGCTGTGT	2
AAACATTCGCGGTGCACTTCTTTT AAGAGGTAGTAGGTTGCATAGT	1 28	TACGGTGAGCCTGTCATTATTC TGGTAGACTATGGAACGTAGG	1 16	TAATTGAATGGCGCCACTAGGGTTGTG TTGGCAGTGTCTTAGCTGGTTG	1	TATGTGCCTTTGGACTAC AGCAGCATTGTACAGGG	4	TTGCACTTGTCCCGGCCTGTT TGAGGTAGTAGATTGTATAGTTGT	2
CGTACCGTGAGTAATAATGCG TCGGTTATCATGGTACCGATG	552 1	ACATTCATTGTTGTCGGTGGGT CAAAGTGCTTACAGTGCAGGT	1 385	GGCAGTGTCTTAGCTGGTTGT TCCCTGAGACCCTAACTTGTG	1 3514	TTTTGCGATGTGTTCCTAATATGTGCTATA ACAGTCTACAGCCATGGTC	1 2	TTCAGCTCCTATATGATGCCTTT TTCAAGTAATTCAGG	1 2
AACATGAAGCGCTGCAACAC AGTAGGTTGTATGGTT	1 2	AACATTCATTGCTGTCGGTGGGT ATGGCACTGGTAGAATTCACT	193 1	GCTCGACTCATGGTTTGAAC TGAGATGAAGCACTGTAGC	3 53	GCTATTTCACGACACCAGGGT GCGCCGAAGGAGCCTCGGTTGGCCCCGGA	1 2	TCGGTTGGCCCCGGATAGCCG ACCCTGTAGAACCGAATTTGT	7
TGGAATGTAAAGAAGTATGTAT TGTGCAAATCTATGCAAAA	37 11	AACACTGTCTGGTAAAGATGGC TGTAAACATCCTACACTCTCA	6 546	TCGTACCGTGAGTAATAAT CAGCTTCTTTACAGTGTTGCCTTGT	23 16 2	GCACAGAAATATTGGC TTGTGCTTGATCTAACCATGTGCTT	2 7	ACCCTGTAGAACCGAATTTGT CCCTGAGACCCTAACTTGTG CAGTGCAATAGTATTGTCAAAGCA	60 15
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ACTGATTTCTTTTGGTGTTCAGAG TTCAAGTAATTCAGGATAGGTTG	10 87	TGAGGTAGTAGGTTGTATGGTT TAGCACCATTTGAAATC	35877 3	AGGTAGTAGGTTGTGTGTT ATACTGCCTGGTAATGATGAC	3 7	CCCCCAGGTGTGATTCTGATTT CGTTACCATTACTGAGTT	2	CTAACACTGTCTGGTAAAGAT TGTGAAAAGTAAGAAAGC	2
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AACATTCAACCTGTCGGTGAGT	179 3	TGTAAACATCCTACACTCAG CGAAGGAGCCTCGGTTGGCCCCGGATAG	50 1	CTATACAATCTATTGCCTTCCC TTGAGGTAGTAGGTTGTATGG TTATCAGAATCTCCAGGGGTA	1 5 18	AACATTCATTGCTGTCGGT CTTGGTACATCTTTGAGTGA CATGCCTTGAGTGTAGGACCGTT	3 28	ATGTATGTGTGCATGTGCATGT TAGCTTATCAGACTGAT	68
TGTAAACATCCTCGA AATCACATTGCCAGGGATTACCA AACCGTGGCTTTCGATTGTTA	3	TATACGACCTGCTGCCTTTCT CTCGTACCGTGAGTAATAATGC	1 26	GCCTGCTGGGGTGGAAC TAGCTTATCAGACTGATGTTGACTGTTG	1 6	CTTGCGAGGTATGAGAAAAA TATGCAAGGGCAAGCTCTCTT	1 9	GCACATTACACGGTCGACCTC AGTGCACGTGTCTCCAGT TGTGCAAATCCATGCAAAA	1 238
TGAGGTAGTAGGTTGTGTG	115	CACAGCTCCCATCTCAGAACA	5	ATCACTAACCACACAGCCAGG	1	GCTGGTTTCACATGGTGGCTTAGA	2	ACCGATTTCTCCTGGTGTTCAGA	12
CAGCTACATCTGGCTACTGGGTC TGAGGTAGTAGGTTGTATGG	818	TTGGTGTACTGTGTGGA TTCCTATGCATATACTTC	2	TGAGGTTGGTGTACTGTGTGTGAG AGAGCTTAGCTGATTGGTGAACA	6	CAACCCTAGGAGGGGGTGCCATTCACATAG TAATACTGCCTGGTAATGAT	513	CTGAAGCTCAGAGGGCTCTGATT CTAGACTGAGGCTCCTTG	1
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TCACATTGCCAGGGATTTCC TCCAGTTTTCCCAGGAATCC	8 4	GTAAGTGCCTGCATGTATATGCGT CACAGGGTAGAACCACGGA	2	TTTGGCAATGGTAGAACTCACACC TAACACTGTCTGGTAACGATG	2 963	ACTGCTGAGCTAGCACTTCCCG AGGTGCATCTAGTGCAGATAG	2	ACAGCAGGCACAGACAGGC TAACACTGTCTGGTAACGATGTT	2 7558
AATCACTAACTCCACTGCCAT AGCTACATCTGGCTACTGGG	12 6	CTAGCACCATCTGAAATCGGTTA TCCCCCAGGTGTGATTCTGATTTGTT	32 1	ATCGTAGAGGAAAATCCACGTT AGCTACATCTGGCTACTGGGTC	6 18	ATTGGGAACATTTTGCATGCAT GCCTGTCTACACTTGCTGT	27 1	CTAAAGGTACAGTACTGTGATAACTGAA TGAAGCTCAGAGGGCTCTGATT	1
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GCTGGTTTCATATGGTGGTTTAGATTT		1							
TACAGCAGGCACAGACA	2	AATACTGTCTGGTAATGCCG AAACCCGTAGATCCGATCTTGT	2	TCCTGACTCCAGGTCCTGTGTG GCACACGCAGGGCAACTCGATTGCTGT	3 2	TCAGTGCACTACAGAACTTTG CTCGTGTCTTGTGTTGCAGCCG	551 4	GCAGCAGCAATTCATGTTTTGG AAGTAATCCAGGATAGGC	1 5
CTCGGGGATCATCATGTCAC CAGTGCACTACAGAACTTTG	1 4	CAGTGCACTACAGAACTTTGT CTGTGAGGTGACTCTTGGTGT	1	ACATTCATTGCTGTCGGTGGGTTGA TGCACTGAGATGGGAGTGGTGTAA	1	TGCCATATCAACTCCTCTCTTCCCAAAAC CTAGCACCATTTGAAATCAGTGT	1 206	CTATACAATCTACTGTCTTTCCT AGGTAGGAGGTTGTATAGT	2
ACAAGTCAGGTTCTTGG	1	TTTGGTCCCCTTCAACCAGCT	6	GAAGTTGTTCGTGGTGGATT	1	TGAGGTAGTAGTTTGTACAG	14	TCTTTACAGTGTTGCCT	1
CAACGGAATCCCAAAAGCAGC TACTCAGTAAGGCATTGT	108 1	CATCAGTGATTTTGTTG ATCGGGAATGTCGTGTCCGCC	1	ACTCCATTTGTTTTGATGATG CTAGACTGAGGCTCCTTGA	4 6	AACCCGTAGATCCGAACTTG CTACAGTATAGATGATGTACT	4 5	TAATACTGCCTGGTAAT TGAGGTAGTAGTTTGTGC	4 7
AGTTCTTCAGTGGCAAGCTTTA CAGTGCACTACAGAACTTTGTC	314	TGCTGTGCGTGCGGAATCGACATCAAG TTAGCCGCTGAAATAGATGGA	1 20	TACAGTACTGTGATAGCTG AATCACATTGCCAGGGATTACCAC	1	AGAGCTTAGCTGATTGGTGAAC CTACTTCACAACACCAGGGC	2	CTACATTGTCTGCTGGGTTT CAGTGCAATAGTATTGT	2
TATGTAACATGGTCCACTAA	1	AATCCTTTGTCCCTGGGTGAAAATGCTATT	1	ACATTCAACGCTGTCGGTGAGT	13	CAAAGTGCTCATAGTGCAGGTAG	36	AAAACATGAAGCGCTGCAACA	7
AACAAATCACAGTCTGCCA TGGAATGTAAAGAAGTATGT	1	ACAAGCTTGTGTCTATAGGTA	1	CAAGAGGGCCTTTCTGG AGTATTACATGGCCAATCTC	1	TTGGTCCCCTTCAACCAGCT TACGTAGTATAGTGCTTTTCA	1	TCTACAGTGCACGTGTCTC	18 6
TCAACGCTGTCGGTGAGTT ATAGCTTATCAGACTGATGTT	1 2	CAGTTCAGCAGGAAC ACAAGCTTGTGTCTATAGGTA ACCAAGATAAATTCACACTCTAGTGCTT CAAAGTGCTGTTCGTGCAGG	1 49	AGGCAAGATGCTGGCATAGC TAAGGTGCATCTAGTGCAGATA	2 316	TGAGGTAGTAGTTTGTGCTGT CCTGAGACCCTAACTTGTGA	358 32	ACTGCAGTGAGGGCACTTGTAGC TCTACAGTGCACGTGTCTC TAACACTGTCTGGTAAGA TTCAGCTCCTATATGATGCCT	2
CCCAGTGTTTAGACTAC	1	GAGGGTTGGGTGGAGGCTCTCC	2	AACCCGTAGATCCGAACTTGT	54	GCACTGAGATGGGAGTGGTGT	404	CCCACTCAGTCGTGCCC	2
TCCCCCAGGTGTGATTCTGATTTGTTT TACTGCCGGGTAATGATG	1	TTTCAGTCGGATGTTTAC CAAAGTGCTGTTCGTGCAG	6	TTTCCTCATATCCATTCAGGAG CAGTGGTTTTACCCTATGGTAGG	2 2	CCGCACTGTGGGTACTTGCTGCT GGTAGTAGGTTGCATAGTT	7	AGCTTCTTTACAGTGTTGC GAATGTTGCTCGGTGAACCCC	1
TAGCAGCACAGAAATATTGG	3	CAAGTAATCCAGGATAGGC	7	CAGCGGGAACAGTACTGCAG	3 2615	TACAGTAGTCTGCACATTGGTT	1267	AGCAGCATTGTACAGGGCTATGAAAG	1
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CGCATCCCCTAGGGCATTGGTGTAA	2 7	ACACTGTCTGGTAAAGATGG	2	CTGTGCGTGTGACAGC	2	GCACCATCTGAAATCGGTT	43 2	IGGGGTTCCTGGGGATGGGA	25 1
TGTAGGGATGGAAGCCATGAAA TTAGGGTCATACCCCATCTTGGAGATAA	5 2	TGGAGAGAAAGGCAGTTCCTG GTAAACATCCTTGACTGGAAGC	6	CATTATTACTTTTGGTACGC TCAGTTATCACAGTGCTGATG	781 59	ATACTGCATCAGGAACTGACTGG CATTGCCAGGGATTTCCA	2	CTGAGGTAGTAGTTTGTACAGT AGGAGGTTGTATAGTTG	9
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CTTTCAGTCAGATGTTTGCTG GGTTTTGTTTGGGTTTGTT TCCGTCTCAGTTACTTTATAG	8	TCCAGCATCAGTGATTTTGTTG GTGTAGTTAGCTGATTGC TAGCTTATCAGACTGATGTTGACTGT TTCACAGTGGCTAAGTTCCG	15 2	GTACAGTACTGTGATAGCTGA TGTCTTGCAGGCCGTCATG AGGTTGGTGTACTGTGTGA ACCATCTGAAATCGGTT	4	TTTTCCCAGGAATCCC TTTTGCGATGTGTTCCTAATAT CAGTTATCACAGTGCTGATG TGTGTGTGTACATGTACAT	3 1592	CCATTTGAAATCAGTGTT TAACAGTCTACAGCCATGGTCG CCGTCTCAGTTACTTTATAGC	12 82
TCCGTCTCAGTTACTTTATAG CCGTCCTGAGGTTGTTGAGCTGT	2 38	TAGCTTATCAGACTGATGTTGACTGT	8	AGGTTGGTGTACTGTGTGA	1	CAGTTATCACAGTGCTGATG	10	CCGTCTCAGTTACTTTATAGC ATATACAAGGGCAAGCTCTCTGT	2
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AAAACATGAAGCGCTGCAACAC	3	CTGGCCCTCTCTGCCCTTCCG	5	GGTCAAGAGGCGCCTGGGA	3	GGTAGTTTCCTGTTGTTG	3 20	CTGGACTTGGAGTCAGAAGGCC	2
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CTTTCAGTCGGATGTTTAC TTTCATTGATCTTGGTGTCCTCAAATTGA	21 1	CTGACCTATGAATTGACAGCCA CCAATATTGGCTGTGCTCCCA	57 1	AATCCTTTGTCCCTGGGTG TCCCTGAGGAGCCCTTTGAGC	1 801	TATGGCTTTTTATTCCTATGT CGCATCCCCTAGGGCATTGGTGT	51 439	AACATCCTACACTCTCAG GACCGATTTCTCCTGGTGTTCAGAGT	1
AAGCTGCCAGTTGAAGAAC CCCAGTGTTTAGACTACCTG	52 3	CAGCATTGTACAGGGCTATGA TGAAATGTTTAGGACCA	47	TGGAGAGAAAGGCAGTTCCTGAT TATTGCACATTACTAAGTTGCAT	3	GTAGAACCGAATTTGT CAAAGTGCTTACAGTGCAG	2 22	AGGTTGCCCTTGGTGAATTCGCTTTATTGA TTAATGCTAATTGTGATAGG	1
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GGCTTCTTTACAGTGCTGCCT TATTGCACTTGTCCCGG TTCAAGTAATCCAGGATAGGCT	1 31185	CACGCAGGGCAACTCGATTGCTG GTATGTGCCTTTGGACTACATCGT TTTGAACCATCACTCGACTCC	1	TCTGGCTCCGTGTCTTCAC CTATGCATATACTTCTT TCAGTTATCACAGTGCTGA	1	AGGCAAGATGCTGGCATAGCTGT TAGCACCATTTGAAATCAGTGTT CTCGGTTGGCCCCGGATAGCCGGGTCCCCG	21723	GCAGTCCACGGGCATATACACTT AAACATGAAGCGCTGCAA AGTAATTCAGGATAGGT	2
AGTGTTTCCTACTTTATGGAT	116	TATTGCACATTACTAAGTTGCA	16 13	AAAAGCTGGGTTGAGAGGGCGAA	30	TAAAGTGCTGACAGTGCAGATAGT	14 9	TTTCCTATGCATATACTTCTTT	203
CAAAGTGCTTACAGTGCAGGTA GAATGGCGCCACTAGGGTTGT	134 1	GTTCAGACTACCTGTT GGTAGTAGGTTGCATAGT	1 4	CAACAGCAGTCGATGGGCTGT TAGTAGGTTGCATAGTT	1 12	CATAAAGTAGAAAGCACTACTA TAGCAGCACAGAAATATTG	6 3	AATGGCGCCACTAGGGTTGTG CCGTGAGTAATAATGC	610 1
CAGCAATTCATGTTTTGGA TTTGCAGTATGTTCCTGAATAC	4	GTTCTTCAGTGGCAAGCTTTA TGAGGTAGGAGGTTGTATAGTTGA	2	TATTGCACTTGTCCCGGCCTGTT	63	AGGGTAGAACCACGGAC	1	TTTTGCGATGTGTTCCTAAT	133
CATTGCACTTGTCTCGGTC	18	GACCTTAGTCATGGGGGCTC	16 1	GGTAGTAGGTTGTATGGTTT CCCAGTGTTCAGACTACCT	14	AAGAGGTAGTAGGTTGCATAGTT GCTGGTTTCATATGGTGGTTTAGAT	22 3	CATTCAACGCTGTCGGTGAGT ACCGTGGCTTTCGATTGTT	1 2
TAATACTGCCTGGTAATG TACAGTATAGATGATGTACTA TCAAGAGCAATAACGAAAAATG	10 2	CAGCAGCAATTCATGTTTTGG TAATCTCAGCTGGCAACTGTG ATTGGGAACATTTTGCATAAA	355 1	TAGCACCATTTGAAATCAGTGT TGTAAACATCCTACACTCAGCTGTCATAC CTAGCACCATCTGAAATCGGTTAT	13176 1	TAAGTGCCTGCATGTATATGCG TGAGGTAGTAGGTTGTATGGTTTAG TGTAAACATCCCCGACTGGAA CAAGCTCGTTTCTATTGGGTCT	527 20	ATCACTAACTCCACTGCCATCA TAATACTGCCTGGTAATGATGACG GCACCATTTGAAATCAGTGT	26 13
TCAAGAGCAATAACGAAAAATG CTGTCTGGTAAAGATG	16 10	ATTGGGAACATTTTGCATAAA TGTAAACATCCTCGACTGGAAGCT	1	CTAGCACCATCTGAAATCGGTTAT CACGGGTTAGGCTCTTGGGA	4	TGTAAACATCCCCGACTGGAA	24	GCACCATTTGAAATCAGTGT CTATGCCAACATATTGCCAT	14
GGCAGTGTAATTAGCTGATTGTA	10	GCTGGTGTTGTGAATCAGG	362 2	TCCCTGAGGAGCCCTTTGAGCCTGGAG	2	CTTTCAGTCGGATGTTTGCAGCT	4	ACTGATTTCTTTTGGTGTTCA	12
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CTGAGACCCTAACTTGTGA	23	TGTAAACATCCTCGACTGGAAGC	1208	TTTCCCTGAGGAGCCCTTTGAGC	1	CTCCCACATGCAGGGTTTGC	3	TCGAGGAGCTCACAGTCTAG	39
TAATACTGCCTGGTAATGATGAC TGAGGTAGTAGTTTGTGCTG ATCCTTGGAACCTAGGTGTGA	2602 31	CCTCCCACACCCAAGGCTTGCA ACAGTAGTCTGCACATTGGTTAG CACTGACATGGGAGTGGTGT ACAGCAGGCACAGACAGG	20 18	TCCCTGTCCTCCAGGAGCTCAC AGCTGGTGTTGTGAATCAGGCCG AGCGAGGTTGCCCTTTGTATAT ACTGGACTTGGAGTCAGAAG	2 2005	AGTTCTTCAGTGGCAAGCT TCAGCTCCTATATGATGCC AATCCTTTGTCCCTGGGTGA CTCCCAACCCTTGTACCAGT	4	TCCAGCATCAGTGATTTTG TTTGGTCCCCTTCAACCAGCTGTA	1
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GCTTACAGTGCAGGTAG	1	AAGCTGGGTTGAGAGGGCGA	3	CAGCACGTAAATATTGGC	1	ATTGCACTTGTCCCGGCCTGT	13	AGTAGTCTGCACATTGGTT	11
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CCTTGGATGCTAAGATGGGGAT TACAGTACTGTGATAGCTGA ATAGCTTATCAGACTGATGTTG	5	AGCTCGACTCATGGTTTGA CATTGCACTTGTCTCGGT	54	ATTCCTAGAAATTGTTCACAAT TGGCAGTGTCTTAGCTGGTTG TAGCACCATTTGAAATCGGTTAT	227	TTGAGGTAGTAGGTTGTATAGT	5	TATGGCTTTTTATTCCTATG CCACTGCCCCAGGTGCTGCTG TACTCAGTAAGGCATTGTTCT	5
AATCCCAAAAGCAGCTG	130 1	TGAGGAGCCCTTTGAGCCT TTTGGTCCCCTTCAACCAG	4	TAGCAGCGGGAACAGT	13 2	TACTGCCTGGTAATGATGA	3	CTATACAACCTACTGCCTTC	6 13
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TGCTGACCCCTAGTCCAGTG GCTGGTGTTGTGAATCAGGC TTGTGCAAATCTATGCAAAACTG	2	TTCACAGTGGCTAAGTT ATACATACACGCACACATAAGA AATGGCGCCACTAGGGTTGTGC	44 2	GCTTATCAGACTGATGTTGACT AACACGGACACCGCAGGG TCAGTGCATGACAGACTTGG TTAGGGTCACCACCCACCACTGGGAGATAA	3 1	ACAGTAGTCTGCACATT CTAACACTGTCTGGTAAAG CATTGTACAGGGCTATG	2	TGTAAACATCCTACACTCAGCTG GAGACCTCTAGCATGGTGTTGTGGGAC CAAGTAATCCAGGATAGG	17 1
TTGTGCAAATCTATGCAAAACTG	15	AATGGCGCCACTAGGGTTGTGC	43 14	TCAGTGCATGACAGAACTTGG	955	CATTGTACAGGGCTATG	7	CAAGTAATCCAGGATAGG	1
TAATACTGCCTGGTAATGATG TTAATGCTAATTGTGATAGGG	3241 7	ATCATGATGGGCTCCTCGGTGT AAGGGATTCTGATGTTGGTCACA	14 8	CGGTGCGGAGAGCCG	28 1	TAGGTTATCCGTGTTGCCTTC ACAAACATGGTGCACTTCTTTT	28 1	TACCCTGTAGATCCGAATTTGT TTTTGCGATGTGTTCCTAATATG	152 11
ACCATCGACCGTTGATTGTAC GCTGGTTTCACATGGTGGCTTAGATTT	2	ATGGCTTTTTATTCCTATGTGA CTGTAGAACCGAATTTGTGT	2	TCCCTGAGACCCTTTAACCTGT TCCATCTTCCAGTGCAGTG	102	TGGCAGTGTATTGTTAGCTGGT ACACGAGACTTTGCCTAG	37	CCCTGAGACCCTTTAACCTGTGA TAAAGTGCTTATAGTGCAGGTAGTGTGTAG	3
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AGGTTGTCTGTGATGAGTTCG ATATACATACACACACCTACAC	2 6	TCCAGTTTTCCCAGGAATC TCAGTTATCACAGTGCTGATGC	2 173	TGTAAACATCCTCGACTGGAAGCTGT AATGCACCCGGGCAAGGATTTGG	2	CACTGCCCCAGGTGCTGCTGG AGCTACATCTGGCTACTGGGTCTCTG	2	ATGTGCCTTTGGACTACATCGT CCCCAGGTGTGATTCTGATTTG	1
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ACCACAGGGTAGAACCACGGA TITGGCAGTGTCTTAGCTGGTTG	4	TGAGGGGCAGAGAGCGAGACTTTT	10 4	AACATGAAGCGCTGCAACA	1	AGCGCCGAAGGAGCCTCGGTTGGCCCCG CACAGCTCCCATCTCAGAACAA	3	TAGCTTATCAGACTG TGTAAACATCCTACACTCAGCT	2 1817
	4 224 2	TGAGGGCAGAGAGCGAGACTTTT CCATCTGAAATCGGTTA	4	AACATGAAGCGCTGCAACA GCAGCACAGAAATATTGGCAT	1 1 1	CACAGCTCCCATCTCAGAACAA AATGGCGCCACTAGGGTTGT	3 9 200 1	TGTAAACATCCTACACTCAGCT AGTTTTGTGTGCATGTGCAT	2
GGTGCAGTGCTGCATCTCTGGTCAGTTGGG	2 7	TGAGGGGCAGAGAGCGAGACTTTT CCATCTGAAATCGGTTA AGAGGTAGTAGGTTGCATA AACATTCATTGCTGTCGGTGGGTTG	4	AACATGAAGCGCTGCAACA GCAGCACAGAAATATTGGCAT ACCATTTGAAATCAGTG AACATTCATTGCTGTCGGTGGGTTT	1 1 1 453	CACAGCTCCCATCTCAGAACAA AATGGCGCCACTAGGGTTGT CGGTGCGGAGAGCCGTTCGTCTTGGGAA TTCTTCAGTGGCAAGCTTTA	1	TGTAAACATCCTACACTCAGCT AGTTTTGTGTGCATGTGCAT AACATTCGCGGTGCACTTCTTTT CTGGTTTCACATGGTGGCTTAG	2
TITGGCAGTGTCTTAGCTGGTTG GGTGCAGTGCTGCATCTCTGGTCAGTTGGG CCCCTAAAGTAGAAAGCACTA TGTAAACATCCTTGACTGGAAGCTGT		TGAGGGCAGAGACCAGACTTTT CCATCTGAAATCAGTTTA AGAGGTAGTAGGTTGCATA AACATTCATTGCTGTCGGTGGGTTG CAGTCGGATGTTTACAGC CCAATATTGGCTGTGCTCCTC	4 1 27 3 1 2	AACATGAAGCGCTGCAACA GCAGCACAGAAATATTGGCAT ACCATTTGAAATCAGTG AACATTCATTGCTGTCGGTGGGTTT AATCACATTGCCAGGGATTTCC CTGCGCAAGCTACTGCCTTGCT	1 1 1 453 4	CACAGCTCCCATCTCAGAACAA AATGGCGCCACCTAGGGTTGT CGGTGCGGAGAGCCGTTCGTCTTGGGAA TTCTTCAGTGGCAAGCTTTA TTTCAGTCGGAAGCTTTACAGC CGTACCGTGAGTATTAAT	1 1 17 1	TGTAAACATCCTACACTCAGCT AGTTTTGTGTGCATGTGCAT AACATTCGCGGTGCACTTCTTTT CTGGTTTCACATGGTGGCTTAG CTGTGCAAATCCATGCAAAACTG CCGGTGCGGAAACCGCGTCGTGTCTTGGG	2
TGTAAACATCCTTGACTGGAAGCTGT CTATACGACCTGCTGC CACTGGCTCAGTTCAGCAGGAACAG	2 7 6 7 1	TGAGGGCAGAGACCGAGACTITTI CCATCTGAAATCGGTTA AGAGGTAGTAGGTTGCATA AACATICATTIGCTGTCGGTGGGTTG CAGTCGGATGTTTACAGC CCAATATTGGCTGTGGTTGCTC TAACACTGTCTGGTAAAGATGGC TAATACTGCCGGGGTATGA	4 1 27 3 1 2 3961 59	AACATGAAGCGCTGCAACA GCAGCACAGAAATATTGGCAT ACCATTTGAAATCAGTG AACATCATTGCTGCGGTGGGTTT AATCACATTGCCAGGGATTTCC CTGCGCAAGGTACTGCCTTTGCT CGGTTATCATGGTACCGATGGCTG ATGACCTTGTATCATGGTACCGATGCGT ATGACCTTATGATTGACAGACC	4 17 1	CACAGCTECCATCTCAGAACAA AATGGCGCACACTAGGGTTGT CGGTGCGGAAGACCCGTTCGTCTTGGGAA TICTTCAGTGGCAAGCTTTA TITCAGTCGGATGTTTACAGC CGTACCGTGAGTAATAAT CTATACGGCCTCCTAGCTTTCC CACTGAGTGATGATTAC	1	TGTAAACATCCTACACTCAGCT AGTITTGTGTGCATGTGCAT AACATTCGCGGTGCACACTTCTTTT CTGGTTTCACATGGTGGCTTAG CTGTGCAAATCCATGCAAAACTG CCGGTGCGAAGACCGTTCGTCTTGG TGTCTCTCTCTCTGTGTCCTGC TGCGCGGGGGCCTCCA	2 1817 2 1 3 1 1 1 7
TGTAAACATCCTTGACTGGAAGCTGT CTATACGACCTGCTGC CACTGGCTCAGTTCAGCAGGAACAG TAGCAGCACATAATGGTTTGTGG	2 7 6 7 1 1 3	TGAGGGGAGAGACCAGAGATTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTCCATA AACATTCATTGCTGTCGGTGGGTTG CAGTGGAGTGTTTACAGC CCAATATTGGCTGTCGTCGTC TAACACTGTCTGGTAAAGATGGC TAATACTGCCGGGTAATGA GTAAGTGCTGCATGTATGGC TGAAGTGGCTGATGATGGC TGAAGTGCTGCATGTATGGC	4 1 27 3 1 2 3961 59 16	AACATGAAGCGCTGCAACA GCAGCACCAAAATATTGGCAT ACCATTTGAAATCAGTG AACATTCATTGCTGCTGCTGTGGTGTTT AATCACATTGCCAGGGATTTCC CTGCGCAAGCTACTGCCTTGCT CGGTTATCATGGTACCGAGCCT ATGACCTATCATTGACAGACC CATGCCTTACAGACCC	4 17 1 1 246	CACAGCTCCCATCTAGAACAA AATGGGCCACTAGGGTTGT CGGTGCGGAAGACCGTTCGTCTTGGGAA TTCTTCATGGCAAGCTTTACAGC CGTACCGTAGCTATAAT CTTACAGCGGAGTTTACAGC CGTACCGTAGCTATAAT CTTATACGGCCTCCTAGCTTTCC CACTGAGATGGGAGTGGTGTA AATACTGCTGGTAATGCC	1 1 17 1	TGTAAACATCCTACACT AGTITTIGTGECATGTGCAT AACATTCGCGGTGCACTTCTTT CTGGTTTCACATGGTGGCTTAG CTGTCAAATCCATGCAAACCTG CCGGTGCGGAGAGCCGTTCGTCTTGGG TGTCTCTACTGTGTCCTCG CTCGCTGGGGCCCCCA TAGATGCTATTATTT	2 1817 2 1 3 1 1 1 7
TGTAAACATCCTTGACTGGAAGCTGT CTATACGACCTGCTGC CACTGGCTCAGTTCAGCAGGAACAG TAGCAGCACATAATGGTTTGTGG TCCCTGAGGAGCCCTTTGAGCCTGG CAAGGAGCTCACAGTTTTG	2 7 6 7 1	TRAGGGGCAGAGCCAGACTTT CCACTICGAACTCGGTTA AGAGGTAGTAGGTGCTGCAGTG CAGCCGGAGTTTACAGC CAGCCGGAGTTTACAGC CAGCCGGAGTTTACAGC TACACTCGTGCGGTGGGTTG CAGCCGGGTGTTACAGC TACACTCGCTGGTAAGAGTGC TAACACTCTCTGTAAGAGTGC TAAGTCGCTGGTAAGGTAC	4 1 27 3 1 2 3961 59 16 12 1	AACATGAAGGGCTGCAACA GCAGCACAGAGATTTGGAT ACCATTTGAAATCAGTG AACCATTTGAAATCAGTG AACATTGCCAGGGATTTCCT AGTGCAATTGCCAGGGATTTCCT CGGTTATCATGGACACATGCTG ATGACCATTGCAAGACC CATGCATTGAACAGACC CATGCATTGAACAGACC GCATGCATTGAACAGACC GCAATGTTAAAAGGCCAT ACTGATTTAAAAGGCCAT ACTGATTTAAAAGGCCAT ACTGATTTAAAAGGCCAT ACTGATTTTAAAAGGCCAT ACTGATTTAAAATGGTTCAG	4 17 1	CACAGCTECCATTCAGAACA ANTAGGGCCACTAGGGTTG CGGTGCGGAGAGCCGTTGGGAA TTTCAGTGGAGCTTAGAGC TTTCAGTGGAGCTTAGAGC CTATAGAGCTCAGCTTGGGAA TTCAGTGGAGTGTTAGAGC CTATAGAGCTCAGGTTTC CACTAGAGTGGAGTG	1 17 1 26 7 1 2	TGTAMACATCCHACATCAGCT AGTTHICTGTGCATGCAT AACATTCGCGGTGCATTCCTTT CTGGTTTCAATGGTGGCTTTAG CTGGTTCAATCAGTGGTGCATTAG CTGTGCAATCCATCAGTGGTGCTTTGG CTGTGCAATCCATCAGTGCAATCCTTGGG CTGCTGCTGGTGCTGCTGCCTCGCTGGGGGCCTCCA TAGTAGGTGTATAGTT AGTACATCTGGCTCGGCCCACTACC TTGAGGTGATGAGTGTATGGTT TTGAGGTGATGAGTGTTATGTT	2 1817 2 1 3 1 1 1 7
TGTAAACATCCTTGACTGGAAGCTGT CTATACGACCTGCTGC CACTGGCTCAGTTCAGCAGGAACAG TAGCAGCACATAATGGTTTGTGG TCCCTGAGGAGCCCTTTGAGCCTGG CAAGGAGCTCACATCTATTG AACATTCATTGTTGTCGGTGGGTTG CATITATTGTTGTCGGTGGGTTG CATTATTACTTTTTGTGTCGCGTGTGA	2 7 6 7 1 1 3 10 1 1	TRAGGGGCAGAGCCAGACTTT CCATCTGAATCGGTTA AGAGGTAGTAGTGGTGCTGGGTTG AGAGGTAGTAGTGGTGGTGGGTTG CAGTCGGATGTTTACAGC CAGTCGGATGTTTACAGC TAGACTGTGTGGTAGAGTGC TAGACTGTGTGGTAGAGTGC TAGACTGTGTGTAGAAGTGC TAGACTGTGTGTAGAAGTGC AGCTACATTGTGTGTAGAGTGC AGCTACATTGTGTGGGGTT TAGATGTGCTGTGTAGAGTGC AGCTACATTGTGTGGGGT TAGATGTGCTGTGC	4 1 27 3 1 2 3961 59 16 12 1 52 5	AACATGAAGCGTGCAACA GCAGCACAGAGATTTGGAAT ACCATTTGAAATCAGTG AACATTTGAAATCAGTG AACATTGCAAGGGATTTCC TGGGCAAGCTAGCTTCCTGGGTGTT CGGCAAGCTAGCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	4 17 1 1 246 1	CACAGCTECCATCAGACACA ANTAGGGCCACTAGGGTTG CGGTCCGGCAGACCCGTTCGGGAA TITCAGTGCAGACCTTA TITCAGTGCAGACCTTA TITCAGTGCAGACCTTA CTARCAGCCGTAGATATA CTARCAGCCCCTACAGCTGTGA ANTACCTGCTGGTAGATAGAC TGCAGTTGTAAATACC TGCAGTTGTAAATACC TGCAGTTGTAAATACC TGCAGTTGTAAATACC TACCTGAGAACCGAATTGTGT TAACACTGCTGGTAACGAT CACCTGTGAGACCGATTGTGTAACAGT CACGTACAGACCGTATGTGTAACGAT CACGTACAGACGCTACTGGTACCGAT CACGTACAGCTCCTGTGACCGAT CACGTACAGCTCCTCTGTACCGAT CACGTACAGCTCCTCTGTACCGTCT	1 17 1 26 7 1	TGTAMACATCCTACATCTAGCT AGTTTTGTATCCCGGTGCATTCCAT AACATTCCGGGTGCATTCCTTTT CTGGTTTCACATGTGGCTTTGG CTGGTTCACATGTGGTGCCTTGG TGTCTCTCTGTTCCTCTGG TGTCTCTCTGTTTCTGG TGTCTCTTGTTTCTGG TGTCTTTGGTTTGGT TGTCTTTGTTTG	2 1817 2 1 3 1 1 7 37 1 25 3 19
TGTAMACATCCTIGATGGAAGCTGT CTATACGACCTGGTCGCTGCTGCTGCTGCTGCTGGTTCAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2 7 6 7 1 1 3 10 1	TRAGGGGCARAGCCARACTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTCGATT AGAGGTAGTAGGTTCGATT AGAGGTAGTAGGTTCGATT CCAATTGGCTGCGTGGGTTG CCAATTGGCTGCTGCTCT TAAACATCTGCTGGTAAAGATGGC TAATACTGCCGGGTAATGA GGTAAGTGCTGCATGTATTGC AGGTAACTTGCTGCTGGTTT AGGTAGTGCTGCATGTATTGC AGGTAAGTTGCTGCTGGTGTTATTGC AGGTAGTGATGTAGTGATGATGATGATGATGATGATGATG	4 1 27 3 1 2 3961 59 16 12 1	AACATGAAGCGTGCAACA GCAGCACAGAGATTTGGAT ACCATTTGAAATCAGTG ACCATTTGAAATCAGTG ACCATTTGAAATCAGTG CTGACGAAGCTACTTGCT CTGACGCAAGCTACTTGCT CTGACGCAAGCTACTTGCT ATGACCTATGATTTGACAGACC ACTACCTATGATTTGACAGACC GCAATCATTGAATTGA	4 17 1 1 246 1 27 8	CACAGCTECCATTCAGAACA ANTAGGSCCACTAGGGTTCT CGGTCCGGAACACCGTTCGTCTTGGGAA TTTCAGTCGGATGTTTACAGC CGTACCGTGAGTAATAAT CTTTACAGTCGGATGTTACAGC CGTACCGTGAGTGATAATAT CTTTACAGTCGGATGTAGTCC CACTGAGAGTGGAGTG	1 17 17 1 26 7 1 2 11 132	TGTAMACATCCTACATCTAGCT AGTTTIGTATCCACTGTAGCT AACATTCCCCGTGCACTTCTTT CTGGTTTCACATGTGGCTTTAGCTGTGCTCTGTGGCTGTGCTGTGGGGACTCCTTTGGG CCGGTGCGGACAACCCGTTCGTCTGGG CCGGTGCGGACAACCCGTTCGTCTGGG CTGCTGCTGGGGGCTCCA AGTACACTCGGGTCGGCCCACTACC TTGAGCTGATGAGGTTGTAGGTT TTGAGCTAGTAGGTTGTAGGTT TTTCCAGGAATTCATTGG TTTCCAGGAATTCCTT	2 1817 2 1 3 1 1 7 37 1 25 3
TGTAMACATCCTTGACTGGAAGCTGT CTATACGACCTGGTGCT CACTGGGTCAGTCAGCAGGAACAG TAGCAGGACAGTAATGGTTTGTGG TCCCTGAGGAGGCCCTTTGAGCCTGG AAGGAGGATTGTGTGGTGGTGGTGGACAGGAGGTGTGGGTTGGCATTTTATACTTTTTGTACCGCCTGTGA CAACGGAGTCCCAAAGCAGGTG TATGTATGTGTGCATTGCAT	2 7 6 7 1 1 3 10 1 1 1 572 1 7	TRAGGGGCAGAGCCAGACTTT CCACTIGAGATCAGGTTA AGAGGTAGAGGTTGCAGGTTG AGAGGTAGGTGGTGGTTG AGAGTTGCTGCTGCTGGTTG CCACATATTGGCTGTGCTGCTC CAAAATTGGCTGTGCTGCT TAAACACTGCTGGTAAGAGGC TAATACTGCCGGGTAATGA GCTAAGTGCTGCAGTGTAAGAGC AGCTACATTGCTGCGGGTT AAGTGCTGCAGTGTAAGAGC AGCTACATTGCTGCGGGTT CATCCACTAGTTGCTGCGTGCTTCATATTGC AGCTACATTGCTGCTGGCTTCATATTGCTGCTGGTTAGTGCTGCTGCTGCTGACACC TACACTCACTGCTGCTGCACTCATTTTCACTGCTGGTTAGTGTTGCTGGTGAGCGTTGAAGACC TAACACTCAGTGCTGCACACC TAACACTGCTGCTGCACACC TAACACTGCTGCTGGTAACG	4 1 27 3 1 2 3961 59 16 12 1 52 5 4	AACATGAGCGTGCAACA GCACCACGAAGTTGGATT ACATTTGAATCAGTG AACATTTGAATCAGTG ACATTTGAATCAGTG ACATTTGAATCAGTG ACATTTGATTGATTGATTGATTGATTGATTGATTGATTGA	4 17 1 1 246 1 27 8 3 1 1 1 88	CACAGCTECCATTCAGAACA ANTAGGGCCACTAGGGTTG CGGTGCGGAAGACCGTTCAGGGAA TICTTCAGTGGCAAGCTTA CGTACCGGAAGCTGTA CGTACCGGGAAGACCGTCAGCTGCGGAA CGTACAGCGGAAGCTGAAGCGCGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGGAAGCGGGAAGCGGGAAGCGGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGGAAGCGAAGCGAAGCGAAGCGAAGCGAAGACGAAGACGAAGACGAAGACGAAGAGCGAAGCGAAGCGAAGCGAAGCGAAGCGAAGCGAAGAGCGAAGCGAAGAGCGAAGAGCGAAGAGCGAAGCGAAGAGCGAAGCGAAGCGAAGAGCGAAGAGGAAGCGAAGAGGAAGCGAAGCGAAGAGCGAAGCGAAGAGCGAAGAA	1 17 17 1 26 7 1 2 11 132 1	TGTAMACATCCHACATCAGCT AGTTHIGTAGCATGCAT AACATTCCGCGTGCATGCAT ACATTCCGCGTGCATCATCATC CCGGTTCAACATGCTGCTCTTT CCGGTTCAACATGCTGCTCTGCT	2 1817 2 1 3 1 1 7 37 1 25 3 19 1
TGTAMACATCCTTGACTGGAAGCTGT CTATAGGACCTGGTGCT CACTGGGTCAGTCAGGTAGGACAG TAGCAGGACAGTTAGACCTGG TCCCTGAGGAGCCCTTTGAGCCTGG CACGGAGCTCAGACGTCATGTGG CACGGAGCTCTTGAGCCTGTGA CACGGAGTCTGAGCCGTGTGA CACGGAGTCCCAGAGCAGCTGTGA CAACGGAGTCCCAAAGCAGCTGT TATGTATGTGTGCATGCATGTGATGTG	2 7 6 7 1 1 3 10 1 1 572 1 7 2	TRAGGGGCAGAGCCAGACTTT CCACTICGAACTCGGTTA AGAGGTAGTAGTGCTGCTGGGTGG CAGTCGGATGTTTACAGC CAGTCGGATGTTTACAGC CAGTCGGATGTTTACAGC TAGACTGCTGGTAGAGGTGG TAACAGCTGTGGTAGAGGTGG TAACAGCTGTGTGGTAGAGGTGGTT AACAGTGCTGGATGTATACC AGCTACATTGCTGGGGTT TAAGTGCATGTGTGCAGGCCTCAT CATCCACTGATGTATACC GTAAGTGCATGTGTACAGCGTGATGTATACC GTAAGTGCATGTGTACAGCGTGAGCG GTAATGCAGGTGAGGGGT TAACAGGTGTGCTGCAGCAGC GTAATCAGGGTAGGGGTGTAGAGGGGGGGGGG	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 14 1 1	AACATGAGCGTGCAACA GCAGCACAGGAGCATGGATA ACCATTIGAAATCAGTG ACCATTIGAAATCAGTG ACCATTIGAAATCAGTG ACCATTIGAAATCAGTG CTGAGCAAGCTACTTGCT CTGAGCAAGCTACTTGCT CTGAGCAAGCTACTTGCT CTGATCAATCAGTACCATTGCT ATGACCTATGATTTGACAGACC ACTACCTCTTGATTGACAGACC GCAATCTTAAAAGGGCAT ACCATTCTTTAAAAGGGCAT CTCCACAGGTGTAAAATGGTTACAGTTTACAGTTACATGATTTTAGCAGCACAATCAGTTTAAATGTTACAGTTACATTTAGAGACCAACAGCAATGGTTAAAAATCAATTGTTACAGTTACAATTGTTACAGTAACAACAAGCAATGGTTAAAATCAATGATTGAATGAA	4 17 1 246 1 27 8 3 1 1 1 88 10 4	CACAGCTECCATCTCAGAACA ANTAGGGCCACTAGGGTAG CGGTAGCGGAAGACCATTAGGGTAG TICTTLAGTGGCAAGCTTA TICTTLAGTGGCAAGCTTA TICTTLAGTGGCAAGCTTA TICTTLAGTGGCCATGAGCTTAG TICTTLACGGCCTCAGCTTTCC CACTAGAATGGGAATAGT CTATAGCGGCCTCAGCTTTCC CACTAGAATGGGAATGGTATAA ATACTGTCTGGTAAGTCC TGTCAGTTGTAAATACC TGTCAGTTGTCAAATACC TGTCAGTTGTCAGATTGTGT TAACACTGCTGTGTGAACGTAT ATCCCTTGAGATGTGTAGCTAGACTGAA ACCCTGAACTGTGTAGCGTAACCGTAACCTGAAGCGCTATTGTGTAACGTATTGTGTAACGTACTGAAGCGGAACCCGTTTCCAGTGTGTAGTGGTGAACCTGAAGCGGGTCCGGTGCAGTGGGGCGGGGGCGGGTCGGTGCAGGCGGTTCCATGGCGGAACCCGTTTCCCTAGCGAAACCCGGTTCCCATGCGGGAACCCGTTTCCCTAGCGAAACCCGTTTCCCTAGCGAAACCCGTTTCCCTAGCGAAACCCGTTTCCCTAGCGAAACTCTCTTTGTGTGTG	1 17 17 1 26 7 1 2 11 132 1 1 45 4 2 3	TGTAMACATCCHACATCAGCT AGTTHIGTAGCATGCAT AACATTCCGCGTGCATTCCTTT CTGGTTTCAATGGTGCATTAGC CTGGTTCAATGGTGCATTAGC CTGGTGCAATCAGTCAGC CTGGTGCAATCAGTCAGC CTGGTGCATTCAGTCAGC CTGCGTGGGGCCTCCA TGTGTCTCTGTGTGTCTGG CTGCGTGGGGCCTCCA TAGTAGGTTATAGAT AGTACATCGGCTCGGC	2 1817 2 1 3 1 1 1 7 37 1 25 3 19 1 2 5
TGTAMACATCTTGACTGGAAGCTGT CTATAGACCTGCTGCTGC CACTGGGTCAGTTCAGCTAGGACAG TAGCAGCACATATATGGTTTGTGG TCCCTGAGGAGCCCTTTGAGCCTGG CAGGAGCCCTTTGAGCCTGG CAGGAGCCCTTTGAGCCTGG CATGATTCATTTTTGGTACCGCCTGTGA CATGATTCATTTTTGGTACCGCCTGTGA CANGAGCTTATAGCTATACG AGAGCTATAGCCTATAGCTACC AGAGCGTATAGCCTATAGCTACC AGAGCGTATAGCCTATCG AGAGCTATAGCCTATCG AGGACTTTTGGGGCAGATGT AGGGCACTTTTGGGGCAGATTT CAGCAGCTTTTGGGGCAGATTT CAGCACTTTTGGGGCAGATTT CAGCACTTTTGGGGCAGATTT CAGCACTTTTGGGGCAGATTT	2 7 6 7 1 1 3 10 1 1 1 572 1 7 2 1250 2	TRAGGGGCAGAGACCTAT  CCATCIGAANTCAGGTA  AGAGGTAGTAGGTGCTGCTGGTGG  CAGTCGGATGTTTACAGC  CAGTCGGATGTTTACAGC  CAGTCGGATGTTTACAGC  CAGTCGGATGTTTACAGC  CAGTCGGATGTTTACAGC  TAATAGTCCCGGGTAATGA  GGATAGTCACTGCAGTGTAGATGC  TAATAGTCCCGGGTAATGA  CAGTCACATGTATATCC  AGCTACATTGCTGGGGTT  CATCCCACTGATGTATATCC  AGCTACATTGCATGCGTGCCC  TAATACTCCATGGATGCAGC  GTAATCCAGCATGATGTATCC  GTAATCCAGCTGAGCACC  GTAATCCAGCTGAGCACC  GTAATCCAGGTAGGC  GTAATCCAGGTAGGC  GTAATCCAGGTAGGC  GTAACTGCTGCAGCAGC  GTAATCCAGGTAGGC  GTACTCCAGGTAGGC  GTACTCCAGGTAGGC  GTGCTGTTCCTGCAGGTAG  GGGTCCCGGGAGAGCCGTTCCTTT  GGGTCTTCAGGTGGGGGAGAGCCGTTCCTTT  GGGTCTTTTACAGGTGTGCTGTTT	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 14 11	ARACIAGAGGGTGCARCA GCAGCAGGAGGAGTGCAGCA ACCATTIGAAGTCAGTG ACCATTIGAAGTCAGTG ACCATTIGAAGTCAGTG ACCATTIGAAGTCAGTG CTGCGCAAGCTACTTGCTTGCT CGGGCAAGCTACTGCCTTGCT AGACCTATGAGTTGACCAGTGCTG ATGACCTATGATTTGACAGACC ACTGCATTTGATTTG	4 17 1 1 246 1 27 8 3 1 1 1 88	CACAGCTECCATTCAGAACA ANTIGGGCCACTAGGGTAT COGTICGGAACACCATTCAGGAA TITCAGTCGGATGTTAGGAA TITCAGTCGGATGTTAGAGC CGTACCGTGAGTAATAAT CTATAGGGCGTCAGTTAGCC CACTAGAGTGGGAATGAGTGTA ANTACTGTCTGTAAGTAGCCTTAGTTGTCAATACT TGTAAGTGGCTGATATGTC TGTCAGTTGTCAAATACTTGTGT TAACACTGTCTGTAACACGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT CAGCTGAACAGT TCCCTGAGTGAACTGT AGCTGATGTGAACAGT TCCTGAAGTGTGCATAGAACTGT TCCTTAGGAACTGTCATAGAACTGTT TCCTTAGGAACTGTTCATAGAACTGTT TCCTTAGGAATACTTCTTTGGAACAGT TTCCTTAGGAACTGTT TCCTTAGGAACTGTT	1 17 17 1 26 7 1 2 11 132 1	TGTAMACATCCHACATCAGCT AGTTHIGTGTGCATGCATT ACATTCCCGGTGCATCTCTTT ACATTCCCGGTGCATCTCTTTT CCTGTCAMACCATCCATGCAMACTG CCGGTGCAMACTGCATGCAMACTG CCGGTGCAMACTGCATGCAMACTG CCGGTGGGGGCCTCCA TAGTCAGCTTGCATCAGCAMACTG AGTCAGCTTGGGTCAGCATCAGCATCAGCATCAGCATCAGCATCAGCAGCATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	2 1817 2 1 3 1 1 1 7 37 1 1 25 3 19 1 2
TGTAMACATCCTIGACTIGGAAGCTGT CTATACGACCTGCTGCTGC CACTGGGTCAGTTCAGT	2 7 6 7 1 1 3 10 1 1 1 572 1 7 2 2 2 2 5 9	TRAGGGGCARAGCCARACTTT CCATCTGAANTCGGTAT AAGAGTAGTAGTGCAGTGGTGGTG AAGAGTAGTAGGTGCAGTGGGTGGAGTGGA	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 14 1 1 1 1 1	AACATGAAGCGCTGCAACA GCAGCACAGAGATTGGGAT ACCATTGAAATCAGTG ACCATTGAAATCAGTG ACCATTGAAATCAGTG CTGCGCAAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	4 17 1 246 1 27 8 3 1 1 88 10 4 6	CACAGCTECCATTCAGAACA ANTIGGGCCACTAGGGTA CGGTCCGGAGAACCGTTCTTGGGAA ANTIGGAGCCACTAGGTTAGGAA TITCAGTCGGATGTTAGAGC CGTACCGTGAGTAATAAT CTTTACAGTCGGATGATGTAGCC CACTGAGATGGGATGATAAT CTTTACAGCCGATGATGTAGCC TGTCAGGTTGTAGCCC TGTCAGTTTGTCAAGTACC TGTCAGTTGTCAGTTGT CACCTGACTGACTGTGT CACCTGACTGACTGTGT CACCTGACTGACTGTGT CACCTGACTGACTGTGT CACCTGACTGACTGTGT CACCTGACTGACTGTCTGTCATCCTGGTCT TCCCTGAGTGATGTCGGTCAACCTGAAAGCTGCCAGTGTGTAGAGAACTGTG CAGCTGCCAGTGTGCATGTGTGTACCCTGATGTGTCATTGCCAGTGTTGCATGTGTGAAGAACTGTT CGGGACCCGGGTCCGTTCCAGTGCTGTTCCTTGCATCGATGAGAACTGTT CGGGACCCGGGGTCCGGTCC	1 1 17 1 26 7 1 1 2 11 132 1 45 4 2 2 3 1 1 26 1 1 2 1 1 2 1 2 1 2 1 2 1 2 1 2	TGTAMACATCCTACATCTAGCT AGTTTIGTATCCACTGTAGCT AACATTCCCGGTGCATTCTTT CTGGTTTCACATGTGGCTTTAGCT CCGGTGCACTTCTTTGGG CCGGTGCGGACACTCCTTGGG CCGGTGCGGACACCCTTGGG CCGGTGCGGGACACCCTTGGGG CTGCTGCTGCTGCTGCGGCCCACTACC TTGAGCTGATCAGTTAGGT AGTACACTCGGGTCGGCCCACTACC TTGAGCTGATGAGGTGTAGGGTT TTGCCAGGATTAGGT AATCCAGGATTAGGT TTCCAGGATTAGGTT TAAGGGTCCTTCCTGTGCTT TAAGGGTCCTTCCTGTGCTT TAAGGGTCCTTCCTGTGCTT TAAGGGTCCTTCCTGTGCTT TAAGGGTCCTTCCTGTGCTT TAAGGGCTCTTGTGTGCAGCT TTCCAGTGCAGTTTGCAGCT TTCCAGTGCAGTTTGCAGCT TTCCAGTGCAGTTTTGCAGCGCT TTCCAGTGCAGTTTTGCAGCGCATTAGCTTTCCAGTGCATTTTCCAGTGCAGTTTTGCAGTGCAGCTTTGCAGGCATAGCGCT ACCAGTTGCTGTGCTTGCAGGCAT ACCAGTCCAGT	2 1817 2 1 3 1 1 7 7 37 1 25 3 19 1 2 5 1 7 7
TGTAMACATCCTIGAGGAGCTGT CTATAGGACCTGGTGCT CATTGGCTCAGTTAGGAGGAAGG TAGCAGCAGATAGGTTTGGG CAGGGAGCTCACAGTTATG CAGGGAGCTCACAGTCTATTG ACATTCATTGTGTGGTGGTGGACAGTGTGTGACAGGAGCTCACAGTCTATTG ACATTCATTTGTGTGGTGGGTTG CATTATACTTTTGTACAGCGCTGTGA CAGGGAGTCCCAGAGGAGCTGTAATTAGTAGACCGCATTTTCATTTTCATTTTCCTTGCATCCAGGTTTTTCATTTCCTTCC	2 7 6 7 1 1 3 10 1 1 1 572 1 7 2 1250 2	TRAGGGGCAGAGCCTAGACTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTCATA AGAGGTAGTAGGTTCATA AGAGGTAGTAGGTTCATA AGAGGTAGTAGGTTCATA AGAGGTAGTAGGTTCATC CAAAATTGGCTGCTGCTC CAAAATTGGCTGTGCTCCTC TAAACACTGCTGGTAGAGAGGC TAATACTGCCGGGTAATGA AGCTAGTAGTAGTAGC AGCTACATTGATTGCCGGGTT AAGACTGCCAGTGATATAGC AGCTACATTGTTGCCGGGTT AAGTGCAGTGAGTGCCCCC TAAACTGCAGTAGTGCCCCC TAAACTGCAGTAGGCGTGCCCCC TAAACTGCAGTAGGCGTGCCCCC TAAACTGCAGTAGGCGCCCCCCC CAACTGCTGCTGCTGCCCCC CAACTGCTGCTGCCCCCCCCCC	4 1 27 3 1 2 3961 59 16 12 1 55 4 14 1 1 1 1 2	AACATGAAGCGTGCAACA GCAGCAGCAGGAGTT ACCATTIGAAATCAGTG AACATTIGAAATCAGTG AACATTIGAAATCAGTG AACATTIGAAATCAGTG ACCATTIGAAATCAGTG ACCATTIGAATCAGTGCTGCTTCCC CGGGCAAGCTACTGCCTTGCT CGGTTACAATGACCATACGTG ATGACCTATGATTTGACAGACC ACTACCTATGATTTGACAGACC GCAATGTTAAAAGGGCAT TCCCCCAGGGTTGAACTTAGACTTACAGTACTACAGTACTAGATTCAGTACTACAGTACTACAGTACTACAGTACTACAGTACTACAGTACTACAGTACTACAGTACTACAGTACTACAGTACATACA	4 17 1 1 246 1 1 27 8 3 1 1 1 88 10 4 6 6 3 2 1 5	CACAGCTECCATCTCAGAACA ANTIGGGCCACTAGGGTTA CGGTCCGGAACACCGTTAGGAA TITTCAGTGGCAACCTTA CGGTCCGGAACACCGTTAG CGGACCGGAACCGTTAG CGGACCGGAACCGTTAG CGGACCGGAGACTGAACCGTAG CGGACCGGAGACGGAGCGGTA ANTACTGCTCGGTAACCGC TGTCAGTTGTCAAATACC TGTCAGTTGTCAAATACC TGTCAGTTGTCAAATACC TGTCAGTTGTCAGAACCGAGTTGT TAACACTGTCGGGAACCGGGTT TACCCTGAGTGTGTGTAGCACCGAGTTGTCAGAACCGAGTTGTCAGAACCGGGGTCAGTTCCAGGAGACCGGGTCCAGTTCCAGGAGACCGGGTCCAGTTCCAGAGAACTGTCGAGAACCTGAAGAGCTGCAGGAGCCGTTTCCTAGCAAACTGTCAGAACCGGGGTCCGTTCCAGCGGGAGCCGTTTCCTAGCAAACTGTGGGAACCGGGGTCCGGTCCGGTCCGGTCGGGGGAGCCGTTCCCTAGCAACTGTTGAGAACTGTGGTAACCGGGGTCGGTTGAGGGTGTTAGAGAACTGTTGGGAACCGGGGTTCAGGGTGTGGGGTGAGGGTGTGAGGGTGTGAGGGGTGTGAGGGGTGTGAGGGGTGTGAGGGGTGTTAGAGAACTGTGGGTGAGGGGTGTTAGAGGACCTGTTGAGGGGTGTTGAGGGGTGTTGAGGGGGTGTTGAGGGGGTGTTGAGGGGGTTTTACAGCTGCAGAGACCTTTTCAGCGCAACAGACTTTGT	1 1 17 1 26 7 1 1 2 2 11 1 32 1 45 4 2 3 1 26 18978 35 55	TGTAMACATCCHACATCAGCT AGTTHICTAGCATGTAGCT AACATTCCCGGTGCATTCCTTTT CTGGTTTCAATCGTGGTCATTCTCTTGG CCGGTGCGGAACACCCTTCGTCTGGC CCGGTGCGGAACACCCTTCGTCTGGG TGTCTCTCTGTGTGCTGCT CCGGTGGGGCACACCCTTGGCT TGTCTCTCTCTGTGCTGCT AGTACACTCGGCTCGG	2 1817 2 1 3 1 1 1 7 7 37 1 25 3 19 1 2 5 1 7 7 7 7 7 7 7 7 7 1 2 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
TGTAMACATCCTTGACTGGAAGCTGT CTATACCACCTGTGCTGC CTATCTGTGCTGCTGCTGCTGTGTGTGTGTGTGTGTGTGT	2 7 6 7 1 1 3 10 1 1 572 1 7 2 2 1250 2 2 5 5 5 9 5 9 5 9	TRAGGGGCAGAGACCTAT  CACATIGAATCAGGTA  AGAGTAGTAGGTTCAGGTT  AGAGTAGTAGGTTCAGGTT  AGAGTAGTAGGTTCAGGTT  AGAGTAGTAGTTCAGGTT  AGAGTAGTAGTTCAGGTT  CACATIGGAGTTTCAGGTT  TACACTGTGTGTAGAGGTT  TACACTGTGTGTAGAGGTT  TACACTGTGTGTAGAGGTT  TACACTGTGTGTAGAGGTT  TACACTGTGTAGTAGGTT  TACACTGTGTGTAGGTAGGTT  TACACTGTGTGTAGGTGTGT  TACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4 1 27 3 1 2 3961 59 16 12 1 55 4 14 1 1 1 1 2	ARACHAGGEGTECANCA GCACCACGAMATTIGGAT ACCHTTIGAMICAGTG ACCHTTIGAMICAGTG ACCHTTIGAMICAGTG ACCHTTIGAMICAGTG ACCHTTIGAMICAGTG CTGCGCAMGCTACTGCCTTGCT CGGGCAMGCTACTGCCTTGCT ATGACTATGATTTGACAGACC ATGACTATGATTTGACAGACC ATGACTATGATTTGACAGACC ACTGATTCATTTGATTGACAGCC ACTGATTCATTTGATTGACAGCC ACTGATTCATTTGATTGATAGACC ACTGATTCATTTGATTGATAGACC ACTGATTCATTTGATTGATAGACC ACTGATTCATTTGATTTAGATACTACAG ACTGATTCATTGATTTAGATTTAGA ATGATGACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	4 17 1 1 246 1 27 8 3 1 1 1 88 10 4 6 3	CACAGCTECCATTCAGAACA ANTAGGGCCACTAGGGTAT CGGTAGCGGAAGCCGTTCAGGGAA TICTTCAGTGGCAAGCTTA CGTAGCGGAAGCCGTTCGGGAA TICTTCAGTGGCAAGCTTA CGTACCGTGAGGTAATAGT CGTACCGTGAGGTAATAGT CGTACCGTGAGGTAATAGT CGTACCGTGAGGTAATAGT CGTACAGCTGAGTTGC ANTACGGCCTGAGGTTGC ANTACGGCCTGAGGTAGCC TGTCAGTTGTCAAATACC ACCTGTAGAGCACGGAATTGTGT TAACAGCTGCTGGTGAACAGT TAACAGCTGCTGGTGAACAGT AAGCTGCCAGTTGGAACAGT AGCTGCCAGTTGAGAACTGTG AGCGTACATTGGTCATAG AGCTGCCAGTTGAGAACTGTT CGGGAACCGGGGTCCAGTGCGACGGAACCCGT TCCTAGCAGTAACTTGTTCAGAGAACTGTT GGGAATAGTTGTGAGTTT CCTAGCCAATAGTTCATTGAGGAACCGGTTTCCTAGCGAATACTTGTTGGGTTT CCTATCCAATACTTCTTTGTGGTTT CACTCCAATAGTACTTCTTTGGA TACCTTCCATGCCAGTTGGAGTTT CACTCCAAGTGCACTGTTGGAGTTT CACTCCAAGTGCACTGTTGGATTGGGTTT CACTCCAAGTGCACTGTTGGATTGGGTTT TCCTTGCGAATACTCATTTTGGATTGCGGTTT TCCTTGCGACTGCTGCTGTTTGGGTTT TCCTTGGGCCTGTCTCTTGGGTTT TCCTTGGGCCTGTCTTTGGGTTT TCCTTGGGCCTGTGTCTTAGG	1 17 17 1 26 7 1 1 2 2 11 1 32 1 45 4 2 3 3 1 26 1 8 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9	TGTAMACATCCTACATCTAGCT AGTTTIGTGTGCATGTCATT ACATTCCCGGTGCATTCTTTT ACATTCCCGGTGCATTCTTTTT CCTGCCAMTCCATGCAAACTG CCGGTGCAATCCTTTTGCTCTTCGCTGCATGCAAACTG CCGGTGCGAATCCATGCAAACTG CCGGTGCAATCCTATGCAACTGCACACCATGCAACCATTCATCATCCCACACCAACCA	2 1817 2 1 3 1 1 7 37 1 25 3 19 1 2 5 1 7 7
TGTAMACATCCTIGATGGAAGCTGT CTATACGACCTGCTGCTGC CACTGGCTGCTGTGCTG	2 7 7 6 7 1 1 1 3 3 10 1 1 1 1 5722 1 2 2 2 599 529 1 1 9 9 2	TRAGGGGCARAGCCARACTTT CCATCTGAAATCGGTTA AGAGGTAGTAGGTTGCATG AGAGGTAGTAGGTTGCATGAGGTTGAGAGGTTGAGAGGTTGAGAGGTTGAGAGGTTGAGAGGTTGAGAGTGGATTGAGAGGTTGAGAGTGGGTTAGAGGGTAGAGGTGGT	4 1 27 3 1 2 3961 59 16 12 1 1 55 4 4 1 1 1 1 2 2 8 1 1 2 8 8	AACATGAGGCGTGCAACA GCAGCACAGGAATTGGGAT ACCATTRGAATCAGTG ACCATTRGAATCAGTG ACCATTRGAATCAGTG CTGCGCAAGCATCAGGATTCC CTGCGCAAGCATCTGCTTGCT CGGTTACATTGACTAGGACC ATGACTATGATTTGACAGACC CATGCTTTACATTGACAGACC CATGCTTTACATTGACAGACC CATGCTTTACATTGACAGACC CATGCTTTACATTGACAGC CATGCTTTACATTGACAGC CACATGCTTTACATTGACAGC TACACCACACACTAGGTTTACATTACA	4 17 1 1 246 1 1 27 8 3 1 1 1 88 10 4 6 6 3 2 1 5	CACAGCTECCATCTCAGAACA ANTIGGGCCACTAGGGTTA CGGTGCGGAAGACCGTTCTCTGGGAA ATGGGGCCACTAGGTTAGGAC CGTACCGTGAGTAGTAGCC CGTACCGTGAGTAGTAGCC CGTACCGTGAGTAGTAGC CGTACCGTGAGTTGCC CACTGAGTGGCAGTAGTAGC TGTACGGCCTCGTGTTC CACTGAGTGGCAGTAGTAGC TGTACGGCCTCGTGTTGTCAAGTAGCTGTGT TACACCTGCTGTGTAAGCCG TGCAGTTGTCAAGTAGCTGTGT TACACCTGCTGTGTAGCGGTCT TACACCTGCTGTGTAACCGAT AGCTGCCACTGTGCTAGCTGGTCT TCCTTAGTGGTGTAGCAGT CACTGTGTGTAGAGACTGTT CACTGTGTGTGTGATGTGGTGAACCGAT TCCTTAGTGTGTGCATGCGGTGT TCCTTAGTGTGTGCATGCGGTGT TCCTTAGTGTGTGTGATGTGTGTGAGACCTGTGTGTGTGT	1 17 17 1 26 7 1 1 2 1 1 1 4 5 4 2 3 3 1 26 1 1 26 1 1 2 3 3 3 5 4 6 8 1 8 1 2 8 3 8 3 1 8 3 8 3 8 3 8 3 8 8 8 8 8 8 8	TGTAMACATCCHACATCAGCT AGTTHIGTGTGCATGCATT AACATTCCGCGTGCATTCATT AACATTCCCCGTGCATCATTCATT CCTGCAMATCCATTGCATCATCATCATCATCATCATCATCATCATCATCATCATC	2 1817 2 1 3 1 1 7 37 1 25 3 19 1 2 5 1 7 7 3 1 1 2 5 1 1 2 2 5 1 1 1 2 2 2 2 2 2 2 2
TGTAMACAICCTIGACTIGGAAGCTGT CITATICGACCTGCTGCT CACTIGGTCAGTTCAGTTGTGG CACTIGGGTCAGTTCAGTTGTGG TCCTGCAGGAGCCTTTGAGG CACTIGGTCAGTTGTTGTGG CAGGAGCCTTGAGAGCCTTGTGAG CAGGAGCTCACAGTCTATTG AACATTCATTTGTTGCGGTGGGTTG CATTATTACTTTTGTGAGCGCGTGTGA CAACGGAATTCCCAAAAGCAGCTG TAACTATGCTGCAAGAACTGT AACATCACTTGAAGAACTGT AAGGACTTTTGGGGCAGAGTTG CAATCATGTGAGAACTGT CAATCATGTGTAGTGCAAGTTT CAGGACTTTTTGGGGCAGAGTTG CAATCATGTGTAGTGCAGGTTTTTTGTGTGCAGGTTTTTTTT	2 7 7 6 7 1 1 1 3 3 100 1 1 1 1 5722 1 250 2 2 2 59 529 1 1 9 9 2 8 8 7	TRAGGGGCAGAGACCTAT TCACCTGGTA AGAGGTAGTAGGTTCAGTAG AGAGGTAGTAGGTTCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 14 1 1 1 2 8 1 1 2 8 8 1	AACATGAAGGGTGCAACA GCACCACAGAATTGCAT AAAATTATTCCTATGGGTGGGTT AACATTCATTCCTATGGGTGGGTT AACAATTCATTCCTATGGGTGGGTT ATCACCTATGATGATGATGATCC CTGGGCAAGCTACTGCCTTGCT GGTTACATGATGACGATCCTG ATGACCTATGATTTGACAGACC ATGACTATGATTTGACAGACC ACAATGTTAAAGGGCAT ACTGATTCTTTGGTGTTCAG TACCCCAGAGTGTATCATTTTAGG ACCACACACACACAGCAG ACAGTTCACACACACACACACACACACACACACACACACA	4 17 1 1 246 1 27 8 3 1 1 888 10 4 6 3 2 1 5 40 1 1 5 40 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA ANTIGGGCCACTAGGGTAT COGTICGGAACACCATTCAGGAACA ANTIGGACCACTAGGTTAGGAA TITCAGTCGGATGATGTAGACC CGTACCGTGAGTAATAAT CTTTACAGTCGGATGATGACC CACCTGAGATGAGCACCACCACCACCACCACCACCACCACCACCACCACC	1 1 17 1 26 7 1 2 11 132 1 45 4 2 2 3 3 1 26 18978 35 56 8 19 14 46488	TGTAMACATCCHACATCHAGCT AGTTHIGTAGTCAATGTCAATTCAATTCAATTCAATCTAATTCAATCCAATCTAATCAATCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCCAATCAATCAATCAAATCCAATCAATCAATCAAATCCAATCAATCAATCAAATCCAATCAATCAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAAATCAA	2 1817 2 1 3 1 1 7 37 1 25 3 19 1 2 5 1 7 7 3 1 2 2 5 1 1 1 2 2 5 1 1 1 2 5 1 1 1 2 2 2 2
TGTAMACATCCTIGACTIGGAAGCTGT CTATACGACCTGCTGCTGC CACTGGGTCAGTTCAGT	2 7 7 6 7 7 1 1 1 3 3 10 0 1 1 1 1 5772 1 7 2 2 2 59 529 1 1 1 9 2 8	TRAGGGGCARAGCCARACTTT CCATCTGAATCAGGTA AGAGGTAGTAGGTGCATA AGAGGTAGTAGGTGCATG AGAGTAGTAGGTGCATG AGAGTAGTAGGTGCATG AGAGTAGTAGGTGCATG AGATTGGCTGCTGCTC CAAAATTGGCTGCTGCTC TAAACACTGCTGGTAGAGAGGC TAATACTGCCGGGTATGA AGCTAGTAGTAGCATGATATGC AGCTACATTGCTGGGTT AAGTGCATGATGATGC AGCTACATGTGTGCCCC TAATCACTGCAGGTAGTAGAGC TAAGTGCATGATGTGCCCC TAATCAGGTAGGAGGC TAAGTGCTGCTGGTGTGCCCC TAACTGCAGTAGGC TAACTGCTGGTGGTGCCCC TAACTGCTGGTGCCCC TAACTGCTGGTGCCCC TAACTGCTGGTGCCCC TAACTGCTGGTGCTGGTGGCTGCTGTGTGCGGTGTGCGTGTGGTG	4 1 1 27 3 1 2 3961 59 16 12 1 1 55 4 14 1 1 1 2 8 8 68 8	AACATGAAGCGTGCAACA GCAGCAGCAGGAGTTGCAACA GCAGCACAGGAGTTTGGATTTGAATTCAGTG ACATTTGAATTCAGTG ACCATTTGAATTCAGTG ACCATTTGAATTCAGTG ACCATTGAATTCAGTGCTGCTTTCC CGGGCAAGCTACTGCCTTGCT CGGTTACATTGACTAGCACTGCTTGCT GCATACTTTGACTTAGACCCTG GCATACTTTGACTTAGACCCTG GCATACTTTGACTTAGACCCTG GCATACTTTGACTTAGACTCAGT TACACTGACTTGATTTACATACTACAG TCAGGTTGATAGTTTGATTTACATACTACAG TCAGGTTGATAGTTTGATTTACATACTACAG TCAGGTTGATAGTTGATTTACATACTACAG ACTAGTTTCACAGACTACTGTTAA AATCACTTACACAACTGCTAA AATCACTTGCACACTTGGTTA AATCACTTACCACACTGCTTA AATCACTTGCACACTGCTAGAT AATCACTTGCACACTGCTAGAT AATCACTTGCACAGTTGCAGAT AATCACTTGCACAGTGCAGAT TGTAGACTCCAGGACATGCAGAT AATCACTTGCACACTGCAGAT AATCACTTGCACACTGCAGAT AATCACTTGCACACTGCAGAT TGTAGACTCCAGGACCCTT TGTAGATCCCAGGACATGCAGAT AATCACTTGCACACTGCAGAT TGTAGATCCCAGGACATGCAGAT TGTAGATCCCAGGACATGCAGAT TGTAGATCCAGGACATGCAGAT TGTAGATCCAGTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	4 17 1 1 246 1 27 8 8 3 1 1 1 88 10 4 6 3 2 1 5 40 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA ANTAGGGCCACTAGGGTAT CGGTACCGAACTTA CGGTACCGAACTTA CGGTACCGAACTTA CGGTACCGAACTTA CGGTACCGGAACTTA CGGTACCGGAACTTA CGGTACCGGAACTTA CGGTACCGGAACTTA CGGTACCGGGAACTTA CGGTACGGGGTAATAAT CTATAGGGCCTCGTAGTTCC CACTGAGATGGGAACTGGTA ANTACTGTCTGGTAACCAC TGTACAGTTGTCAAATACC CACCTGTAGAGACTGGAACTGGT TAACAGTTGTCGGTAACCAC TGTACAGTTGTCAGGAACTGGT TAACAGTTGTCGGGAACCAGT TAACAGTTGTCGGGAACCAGT CACCTGAGGAACTGTT CACCTGAGGTGTGTCATAG AGGTGACCGGGTCCGGTCC	1 17 17 1 26 7 1 1 2 1 1 1 1 3 4 5 4 2 3 1 1 26 1 1 1 26 1 1 1 25 1 1 26 1 2 1 2 1 2 2 3 3 5 3 5 5 6 8 8 8 8 8 8 9 8 8 8 8 8 8 8 8 8 8 8 8	TGTAMACATCCHACATCAGCT AGTTHICTAGGATGTAGT AACATTCCGCGTGCATTCCTTTT CTGGTTTCAATCGTGGTCATTCTTT CTGGTTTCAATCGTGGTCATTCTCTTGG CCGGTGCGGAACACCCTTCGTCTGGCTGTCTGTGTGGTGTGTGT	2 1817 2 1 1 1 1 1 1 2 5 1 1 1 2 5 1 1 1 2 5 1 1 1 1
TGTAMACATCCTTGACTGGAAGCTGT CTATACCACCTGTGCTGGAAGCTGT CTATACCACCTGTGTGCTGCTGGAACAG TAGCAGCACATAATGGTTGTTGG TCCCTGCAGGAGCCCTTTGAGTTGTGG CCCTGAGGAGCCCTTTGAGCCTGGTGG CAAGGAGCTCACAGTCTATTG AACATCATTTGTTGCGGTGGGTTG CATTATACTTTTGGTGGTGGGTTG CATTATACTTTTGGTGACACCGCTGTGA CAAGGGATTCCCAAAACCAGCAGTG TAGTATGTGTGGTGAAGAACTGT AAGAGGTTAGATGAGCAATGTGCAATATTGGGGAAGAAGAAGAGTGCCAATGTAAGAACTGTAAGGAACTGTAAGGAACTGTAAGGAAGTTGGAGAGAAGAAGAGAGTGTAAGTAGTAG	2 7 7 6 7 7 1 1 1 3 3 100 1 1 1 1 5772 1 2 2 2 2 59 9 529 1 1 9 2 8 7 7 4 7 1 1	TRAGGGGCAGAGACTTT CCATCGAATCGGTA AGAGGTAGTAGGTGCAGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGTGCAGTGGCGGTAGTGAGGCGGTAGTGCAGTGCGGCCAATCGCAGTGGCGCCAATCGCAGTGGCGCCAATCGCAGTGGCGCCAAACATGGCGGCGCAGTGGTGCGGCCCAAACATGGGCGGAGGGGGGGG	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 4 11 1 1 2 8 8 8 8 8 8 8 8 1 1 3	AACATGAGGCGTGCAACA GCAGCAGGAGGATTGGATT ACCATTIGAAGTCAGGGTT ACCATTIGAAGTCAGGGTT ACCATTIGAAGTCAGGGTT ACCATTIGAAGTCAGGGTTT CTGGGCAAGCTACTGCCTTGCT CGGGCAAGCTACTGCCTTGCT CGGTTACATTGACTAGGACC CANGTTTAAAAGGCAT AGACCTATGATTTGACAGAC CCATGGTTTAAAAGGCAT TAGCCCAGAGGTTAGACTAGAC	4 17 1 1 246 1 27 8 8 3 1 1 1 8 8 8 10 4 6 3 2 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1	CACAGCTECCATCTAGAACA ANTAGCSCCACATAGGGTTCT COGTICCOGAGAACCATTCAGGAA TITCAGTCGGATAGTTCTCGGAA TITCAGTCGGATAGTTCAGCAC CGTACCGTGAGTAGTAGT CACAGTGAGTAGTAGT CACAGTGAGTAGTAGT AAACATCTCTGGTAAGCC ACCAGTAGTAGTAGCC CACAGTGAGTAGCAC ACCAGTAGAACCGAATTTGTGT AACACTCTGCTGGTAACCAGT CACCTGAGTAGTAGCAC ACCAGTAGAACCGAATTTGTGT AACACTCTGCTGGTAACCAGTACCAGT CACCTGAGTAGTAGTCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	1 1 17 1 26 7 1 1 2 11 132 1 45 4 2 3 1 26 6 7 1 1 2 1 1 2 1 1 2 1 1 2 5 5 6 6 8 8 1 1 2 8 8 8 9 8 9 8 8 9 8 8 9 8 8 9 8 8 9 8 8 8 9 8 8 8 9 8 8 8 9 8 8 8 8 8 8 9 8	TGTAMACATCCHACATCAGCT AGTTHIGTGGCATGCATT AACATTCCGCGTGCATTCTTT AACATTCCGCGTGCATCTCTTTT CTGTCAMATCCATGCAGAACTG CCGGTGCAGATCCATGCAAACTG CCGGTGCAAATCCATGCAAACTG CCGGTGCAAATCCATGCAAACTG ATGTCAACTCTAGCAAACTG ATGTCAACTCTAGCAAACTG ATGTCAACTCATGCAAACTG ATGTCAACTCATGCAAACTG ATCCAAGGAAAACTG ATCCAAGGAAAACTG AATCCAAGGAAAACTG AATCCAAGGAAAACTG TTGCAAAATCATGCTGCTTT TTAAGGCTCACTCTGCTTT TTAAGGCTCACTCTGCTTT TTAAGGCTCACTCTGCTTT TTTCAATCTATGCTGAAAAACTG ACAATTCGTATCTAGCGAAAA ACAATTCGTATCTGCTGAAAAACTAAACAAATCGTATCTAGCGAAAAAAAA	2 1817 2 1 1 1 1 1 7 7 7 7 7 7 7 7 7 7 7 7 7
TGTAMACAICCTIGACTIGGAAGCTGT CTATACGACCTGTCTGCTGC CACTGGCTCAGTTCAGT	2 7 6 7 1 1 1 3 3 100 1 1 1 1 572 2 1250 2 2 2 59 9 529 1 1 9 9 2 8 7 7 1 2889 1 1	TRAGGGGCAGAGACTATT CCATCIGAATCAGTATA AGAGGTAGTAGAGTTGCATA AGAGGTAGTAGAGTTGCATA AGAGGTAGTAGAGTTGCATA AGAGGTAGTAGAGTTGCATA AGAGGTAGTAGAGTTGCATA AGATTGCATTTACAGC CCAATATTGCTGCTGCTTC TAACACTGCTGCATGTAACAGTGC TAATACTCCGGGGTAATGA AGCTACATTGCTGCTGCTGCTC AGACTAGTCTGCTGCATGTATAC AGCTACATTGCTTGCTGCGTCC AGACTAGTAGTGCCC AGACTAGTAGTAGAGC TAATCACTGCTGCAGTGCTCAAT CATCCACTGAGTAGAGC TAATCACAGGAGAGCCGTCACACC GTAATCCAGGTAGTGGCC AGACTGCAGTAGAGCCGTGCACACG TAACCACTGCAGTAGGC TAACCAGGTCCAGGTAGGCG TAACCAGGTCCAGGTAGGGC TAACCAGGTCCAGGTAGGGGAGCCGTTGCTGTT GGCTTCTTTGCAGGCAGGCTGCTGCTGTT GGCTTCTTTACAGGCAGGCTGCAGGAGCCGTTACAGGAGAGCCTGTAGCAGGAGCCTGCAGGTTGCGGGAGGCGTTACAGGGAGCCGTTACAGGAGAGCCTGTTACAGGCAGG	4 1 27 3 1 2 3961 59 16 12 1 52 5 4 4 11 1 1 2 8 8 1 1 1 2 8 8 8 8 8 8 8 8 8	AACATGAGCGTGCAACA GCACCACGAAGTTTGGAT ACCATTRGAATCAGTG ACCATTRGAATCAGTG ACCATTRGAATCAGTG ACCATTRGAATCAGTG CTGCGCAAGCTACTGCTTGCT CTGCGCAAGCTACTTGCTTGCT CTGCTACATTGATTTGACAGACC CATACTTTGAATTGACAGACC CATACTTTGAATTGACAGACC CATACTTTGAATTGACAGACC CATACTTTGAATTGACAGACC CATACTTTGAATTGACAGACC CATACTTTGAATTGACAGACC CACATTGATTAAAAGGCAT TAGCCACAGTGATTTAAAAGGCATTTGAATCAGATTGAACAACACCACCACACCACCACCACCACCACCACCACCA	4 17 1 1 246 1 27 8 8 3 1 1 1 88 10 4 6 3 2 1 5 40 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACA ANTIGGGCCACTAGGGTTA COGTICGGAACACCATTCAGGAACA ANTIGGGCCACTAGGTTAGGAA TITCAGTCGGATGTTAGGAC CITACGGCCTAGCTTCC CACTAGATGGCAGTAGTAGCC CACTAGATGCAGTAGTAGCC TGTAGGGCCTCAGCTTCC CACTAGATGGCAGTAGTAGCC TGTAGGGCCTGAGTTGTCAATACC TGTAGGGCCTGAGTAGCC TGTAGGTGTGTAGACCAT CAGCTAGCTGAGTAGCCAT CAGCTAGCTGAGAACACTAGCAGT CAGCTAGCTGAGAACACTAGCAGCAGCAGCCGGT CAGCTAGCAGCAGTCGTGTGAGAACCTGAACAGCTGCAGCAGTCGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGTGAGAACCTGAGTGAG	1 1 17 1 26 7 1 2 11 132 1 1 45 2 3 1 26 18978 35 56 8 8 19 1 444488 3 2 1 1 445488 3 2 1 1 445488 3 2 1 1 445488 3 1 1 4454888 4 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1	TGTAMACATCCHACATCAGCT AGTTHICATGCATGCATTCACT AACATTCCCGGTGCACTTCATTT CTCGTTTCACATCAGCT ACCTTCCCACCTCAGCT CCGGTTCACATCAGCT CCGGTGCACTCCTCTTT CCGGTTCACATCAGCT CCGGTGCACATCAGCT CCGGTGCACATCAGCT AGTACACTCAGCTCAG	2 1817 2 1 1 1 1 1 1 2 5 1 1 1 2 5 1 1 1 2 5 1 1 1 1
TGTAMACANCCTIGACTIGGAAGCTGT CTATACGACCTGCTGCTGC CACTGGGTCAGTTCAGT	2 7 7 6 7 1 1 3 3 100 1 1 1 1 1 5722 1 2 2 2 599 1 1 1 9 9 2 8 8 7 4 7 1 2899 1 1 1 2 2 3 3 9 1 1 1 2 2 3 3 9 1 1 1 2 3 3 1 1 1 2 3 3 1 1 1 1 2 3 3 1 1 1 1	TRAGGGGCAGAGACTAT  CACATICAMATCAGTATA  AGAGGTAGTAGAGTTCCATA  AGAGGTAGTAGAGTTCCATA  AGAGGTAGTAGAGTTCCATA  AGAGGTAGTAGAGTTCCATA  AGAGGTAGTAGAGTTCCATA  AGAGGTAGTAGAGTTCCATA  AGACTAGTCAGTAGAGAGAGTAGAGAGAGAGAGAGAGAGA	4 1 27 3 3961 1 599 16 12 1 1 55 4 4 4 1 1 1 2 8 8 1 1 2 8 8 8 8 8 8 8 8 8 1 1 1 2 1 1 2 1 1 2 1 1 1 1	AACATGAGCGTGCAACA GCAGCAGGAGGAGTTGGATT ACCATTIGAATICAGTG GCAGCAGGAAGTATTGGGATT ACCATTIGAATICAGTG CTGGCGAAGCTACTGCTTGGT CTGGCGAAGCTACTGCTTGGT CTGGCGAAGCTACTGCTTGGT CTGGTTACATGTGACCATGCTG ATGACTTAGAATTGACAGACC ATGACTTAGAATTGACAGACC CATGATTTAAAAGGCAT CACCATGATTTAAAAGGCAT TAGCCACAGTGTTACATTTTAT TAGCAGCACATGATTACATTTTAGCAGCACATGATTAGATTTAGCAGCACATGATTACATTTTAGCAGCACATGATTACATACA	4 17 1 1 246 1 27 8 3 1 1 1 88 10 4 6 3 2 1 1 5 4 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACA ANTIGGGCCACATAGGGTTA CGGTCCGGAACACCATTCAGGAACA ANTIGGACCACATAGGTTAGGAA TITCAGTCGGATGATAGACT CACAGTGAGTAGAACACTAGCATGATGACACACACACACA	1 1 1 17 1 26 7 1 1 1 1 1 1 1 2 1 1 2 1 2 3 3 1 2 6 8 1 8 9 7 8 1 2 3 5 6 8 8 8 9 7 8 8 9 8 8 9 8 8 8 9 8 8 8 8 9 8 9	TGTAMACATCCHACATCAGCT AGTTHICATIONAGT ACATTCCCGGTGCATTCCTTT CTGGTTTCAMACGTGGCTTAGC TGGTTCAMACGTGGCTTAGC TGGTTCAMACGTGGGCTTAGC CCGGTGGGGAACCCGTTCGTCTGGG TGCTCCTGTGGGGGGAACCCGTTCGTCTGGG TGCTCTCTGTGGGGGGAACCCGTTCGTCTTGGG TGCTCTCTGTGGGGGGCTCCA AGTCAGCTCGGGCCCACACC TTGAGCTAGTAGGTTTAGGTT AGTGACTCAGGAGTTGGGTT TTCAGCTGAGTAGGTTGTAGGTT TTCAGCTGAGTAGCAAAACTG AATCCAAGGATAGGCT TAAGGGCTCTCCTGCTGTTT TAAGGGTCCTTCCTGTGCTT TTCAGCTGAATCATGAGAAACTG AACAATTCGTATCTAGGGGAAT ACAATTCGTATCTAGGGGAAT ACAATTCGTATCTAGGGGAAT ACAATTCGTATCTAGGGGAAT TAGTGAATTCTATCTTTGGAAGAAC CAGCAGCATTCATGTTTTGGAAGAC CAGCAGCATTCATGTTTTGGAAGACC CAGCAGCATTCATGTTTTGGAAGACC TGTGAGAGGGGTCCCCGCGTGTGAAGCTTGAACATCTGTTTTGGAAGAACC TGTAAAATTCGTATCTGGGGAAAGC TTATACAACTCTACTGTTTTGGAAGAAC CTATACAACTCTACTGTTTTTGGAAGAAC TGTAAAAATTCGTATCTGGGGAAAGC TTATACAACTCTACTGTTTTTGGAAGAAC TTATACAACTCTACTGTTTTCAGGGGAAA TGTTAAACAATCTACTTTTCC TGTAAACAACCTCCCACTGGAAG CTTATACAACTCTACTTTTCC TTTTTAAATTCTCCTCGAAGA CTATACAACTCTACTCT	2 1817 2 1 1 1 1 1 2 5 1 1 1 2 5 1 1 1 2 5 1 1 1 1
TGTAMACATCCTIGACTIGGAAGCTGT CTATAGGACCTGTGTGTG CTATAGGACCTGTGTGTG TAGCAGCACAATAATGGTTGTTGG TCCCTGAGGAGCCCTTGAGGACCGG CAGGAGCACTAATAGGTTGTTGG TCCCTGAGGAGCCCTTGAGACCTGG CAAGGAGCTCACAGTCTATTG ACACTTATTACTTTTGGTGTGTGGGTTG CATTATTACTTTTGGTACCGCTGTGA ACACTTATACCTATCGAAGCTGTA ACAGTCATTAGCCATCGGAAGAAGAAGAGTGTAAGACCGTATAGCCAAGTGTAAGACCGTATAGCCAAGTGTAAGACGTTCAAGTCAAGTGTAAGACCTTCAAGTCAAGTGTAACTGACAGTTTAATAGACCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCTTTAACTCCC CAAAGTGCATTAGCTGTTAACTCCC CAAAGTGCAAGAGAGTTGTAACTCCCAAGCAGTTTAACTCCCTAACTCCTTAACTCCCTAACTCCAAGCAGGTTTAACTCAAGCAAAGCAAGTTGTAACTCAAGCAAAGCAAGTTGTAACTCAAGCAAAGCAATTGTAACTCAAGTAAGAAGAAATTTAACTCAAAGCAAAAGCAAATTTTAACTCCTAAGTAAAGCAATTGTTAACTAAAGCAATTTTAACGTAAATTTTTAGCGC CCCTGAGACCCTTAACTTTTAACGCT TCACAGTGAAAACCGCTTCTTTTAACGT TCACAGTGAAAACCGCTTCTTTTAACTTTTTAACGTCAAGTTTAACCGCTTTTTAACTTAAAGCAATTTTAACGTAAATTTTAGCGC CCCTGAGACCCTTAACTTTTTAACGCT TCACAGTGAAAACCGGTCTCTTTTAACGT TCACAGTGAAAACCGGTCTCTTTTAACGT TCACAGTGAAAACCGGTCTCTTTTTAACGT TCACAGTCAAAACCGGTCTCTTTTTAACGT TCACAGTCAAAACCGGTCTCTTTTTAACGT TCACAGTCAAAACCGGTCTCTTTTTAACTCCTTTCTAACTTAACTAAACTAAACTAACTAATTTTTAACCGCTTTTTAACTCTTAACTAATTTTTAACTCTTAAACTAATTTTTAAACCAATTTTAACACTAAATTTTTAAACCAATTTTAAACCAATTCTTAAACTAAACTAATTTTAAAACAATAAT	2 7 7 6 7 7 1 1 3 3 100 10 1 1 1 1 1 572 572 572 579 529 529 529 529 1 1 1 9 9 2 8 8 7 7 4 7 7 1 289 1 1 2 2 3 3 10	TRAGGGGCAGAGCCTAGACTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTCATA AGAGGTAGTAGTGCATGAGTGGTTG AGAGTAGTAGTGCATGAGTGGTTG AGAGTAGTAGTGCATGAGTGGTTG AGAGTAGTGCAGTGGTTGCTC CAAAATTGGCTGGCTGCTCCTC TAAACACTGCTGGTAGTAGAGGC TAATACTGCCGGGTATGAG AGCTAGTTGTTGCTGGTTGATTAGC AGCTACATTGCTGGTTGATTAGC AGCTACATTGCTGCTGGTT AAACTGCATGATGTAGCCCC TAATCAGCAGTAGAGC TAAGTGCTGCTGGTTGCCCC TAACTGCAGTAGTGCTGCCCC TAACTGCAGTAGGC TAACTGCTGGTGGTGCCCCC TAACTGCTGGTGGTGCCCCC TAACTGCTGCTGTGTGGCGCTGCTGTGTGCCGTGCTGTGTGGTG	4 1 27 3 3961 59 16 12 1 52 5 4 4 1 1 1 2 8 8 1 1 2 8 8 8 3 1 1 3 1 1 2 8 8 8 1 1 1 1 1 2 8 8 8 8 8 8 8 8	ARACHAGGETIGCARCA GCACCACGAMATITIGGAT ACCHTTIGAMTCAGTG GCACCACGAMATITIGGAT ACCHTTIGAMTCAGTG GCACCACGAMACTACTGC GCGCAMACTACTGCTGCT GCGCAMACTACTGCCTTGCT GCGCAMACTACTGCCTTGCT GCGTTACATCTGCATTGCATTGCACTGCT ATGACTATGATTTGCACGACCT ATGACTATGATTTGCACGACCT ACCACTATGATTTCACACTCCT ACCACGACTACTACTACTACTACTACTACTACTACTACTACTACTA	4 17 1 1 1 246 1 1 27 8 3 1 1 1 88 8 10 4 6 6 3 2 1 1 5 40 1 1 16 8 2 2 47 1 1 16 8 2 2 47 1 1 8 8 4 4 2534 4 22 2	CACAGCTECCATTCAGAACA ANTAGCSCCCACTAGGATA ANTAGGATCATTCAGTAGATA CAGTAGATAGATAGATAGATAGATAGATAGATAGATAGAT	1 1 1 17 1 26 7 1 1 2 1 1 1 1 45 4 4 2 3 3 1 1 26 6 7 1 1 2 1 1 1 2 3 5 6 6 7 7 8 9 9 9 9 9 1 9 1 9 1 9 1 9 1 9 1 9 1 9	TGTAMACATCCHACATCAGCT AGTTITICTICAGCATTCAGCT AACATTCCCGGTGCACTTCTTT AACATTCCCGGTGCACTTCTTTT CTGTCAMATCCATGCAAACTG CCGGTGCAACTCCTTTTGCCTCTCTCTGGGTGCTCTCTCT	2 1817 2 1 1 1 1 7 7 7 3 7 1 1 5 5 6 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACANCETTGACTIGGAAGCTGT CTATACAGCTCTGCTGC CTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2 7 7 6 7 7 1 1 3 3 10 1 1 1 1 5772 2 1250 2 2 599 529 1 1 1 9 2 8 7 7 7 4 4 7 7 7 2 1 2 8 9 1 2 2 3 3 10 1 1 1 1	TRAGGGGCARAGCCARACTTT CCATCTGAANTCAGGTA AGAGGTAGTAGGTTCAGT AGAGGTAGTAGGTTCAGTAGGTTGAGTAGAGTA	4 1 1 27 3 1 1 2 2 39611 559 166 12 1 1 5 5 2 5 4 4 14 1 1 1 2 2 8 8 1 1 1 2 2 8 8 8 3 3 1 1 1 3 3 668 573 17 4 4 1 1 193 3 3 3 3 3	ARACIAGAGGCITGCARCA GCAGCAGGAGGATTIGGAT ACCATTIGAAGTCAGTG GCAGCAGGAAGTAGTGGGTT ACCATTIGAAGTCAGGGTT ACCATTIGAAGTCAGGGTTT CTGGGCAAGCTACTGCTTGCT CGGGCAAGCTACTTGCTTGCT GCGTTACATTIGACAGCC GCAGTGTTACATTIGACAGCC GCAGTGTACATTIGACAGCC GCAGTGTACATTIGACAGCC GCAGTGTATTAGACGGACC GCAGTGTACATTIGACAGCC GCAGTGTACAGCGAGTTGCAGTTTAGATT TAGCAGCACATCAGTGTTTACATTAGCAG TAGCGGTAGACCAGCAGTGTTAGAGTTTAGG ACTAGTGTCAGCAGTGTTAGAGTTTAGG ACTAGGTGTTAGAGTTTAGAGTTAGAG ACCAGTGAGCCAGCAGTGTTG ACCAGTGAGCCAGCAGTGTTG ACTCAGCCAGCAGCAGTGTTG ACTCAGCCAGCAGCAGTGTTG ACTCAGCCGAGCAGCAGTGTTG ACTCAGCCGAGCAGTGTTG ACTCAGCCGAGCAGCAGTGTGTG ACTCAGCCGAGCAGCAGTGTGTG ACTCAGCCGAGCAGCAGTGTTG CGGTGCTGAGCAGGAGCAGTGTGTG CGGTGCTGAGCAGCAGTGTGTG CGGTGCTGAGCAGCAGCAGTGTTG CGGTGCTGAGCAGCAGTGTGTG CGGTGCTGAGCAGGGGAGCAGTGGGGGAGCAGTGGGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	47 11 1246 11 27 8 3 1 1 1 88 810 4 6 3 2 1 1 5 40 1 1 2 7 1 1 1 6 8 3 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACA ANTIGGGCCACTAGGGTTA COGTICGGAACACCATTCAGGAACCA ANTIGGACCACTAGGTTAGGAA TITCAGTCGGATGTTAGAGC CGTACCGTGAGTAGAACCATTCAGCACCACCACCACCACCACCACCACCACCACCACCACC	1 1 1 17 1 26 7 1 1 1 1 1 1 1 2 1 1 2 1 2 3 3 1 2 6 8 1 8 9 7 8 1 2 3 5 6 8 8 8 9 7 8 8 9 8 8 9 8 8 8 9 8 8 8 8 9 8 9	TGTAMACATCCHACATCAGCT AGTTHIGTGGCATGCATT AACATTCCGCGTGCATTCTTT AACATTCCGCGTGCATCTCTTTT CTGTCAMATCCATGCAGAACTG CCGGTGCAGATCCTTTGGCTGCTGCTGCGGGGGCTCCTCTGGGGGGGG	2 1817 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACANCCTIGACTIGGAMACTGT CITATICAGCCTGCTGCTGC CACCAGAMACTGCTTGTGG TCCCTGCAGGAGACCAGT TCCCTGCAGGAGCCCTTGAGCACCTGG CAAGGAGCCTTCAGCAGCCTGG CAAGGAGCCTTCAGCAGCCTGGG CAAGGAGCCTCAAGCCCTGGGTGG CATTATACTTTTGGTGGTGGGTTG CATTATACTTTTGTGCTGGTGGTTG TATTATGTTGTGTGGTGCATGT AAGAGGTATCCCAAAACCAGCAGAAA AAGAGGTATAGCCAATGGAAAAA AAGAGGTATAGCCAATGGAAAAA AAGAGGTATAGCCAATGGAAAAA AAGAGGTATTGAGCCAATGGAAAAA AAGAGGTATTGAGCCAATGTCCAATAT TCTGGCTCCTGTTTGGGGCCAATAT CCAAGTGCTATTGAGTGCCATGT CAAGCACAATTGAAAATCAGT ACTGTCCGTTGTAGCTGGTTGTT CTAGCACCATTTGAAATCAGT ACATGCACGTGTAGCAGGCCTGAAAAAAAAAA	2 7 6 7 1 1 3 3 10 1 1 1 1 5772 2 1250 2 2 59 529 1 1 1 289 1 1 2 2 3 3 10 0 1 1 1 1 7 9	TRAGGGGCARAGCCARACTTT CCATCTGAANTCGGTAT AGAGGTAGTAGGTGGTGGTG AGAGGTAGTAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	4 1 27 3 3 1 1 2 39611 59 16 6 12 12 15 52 5 5 4 14 11 12 2 8 8 11 2 8 8 8 8 8 8 8 8 8 8 8	ARACIAGAGGCITGCARCA GCAGCAGGAGGATAITTIGGAT ACCATTIGAATICAGTG GCAGCAGGAAGTATTIGGATT ACCATTIGAATICAGTG CTGGCGAAGCTACTIGCTTGCT CTGGCGAAGCTACTTGCTTGCT CTGGTTACATTIGAAGTACGATTTGCT ATGACTATGATTTGAAGAGC CATATTTGAATTAGAAGC CATATTTGAATTTGACAGACC CATATTTGAATTTGACAGACC CATATTGATTTGACAGACC CATATTGATTTGACAGACC CATATTGATTTGACAGACC CATATTGATTTGACAGACC CACATTGATTAGATTTTAGCAGACCAGCACCAGCACCAGCACCAGCAGCAGCAGCAG	4 17 1 1 1 246 1 1 1 27 8 3 3 1 1 1 88 100 4 6 6 3 2 2 1 5 5 40 1 1 2 2 1 1 16 8 8 2 47 1 8 4 4 2534 222 8	CACAGCTECCATCTCAGAACA ANTIGGGCCACTAGGGTAT COGTICGGAACACCATTCAGGAACA ANTIGGGCCACTAGGTTAGGAA TITCAGTCGGATGTTAGGAC CITACGGCCCTAGCTTCC CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGCAGTAGTAGT CACTAGGATGGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	1 1 1 1 1 26 7 1 1 2 1 1 1 1 1 3 4 5 4 4 2 2 3 3 1 1 2 2 8 1 9 7 1 1 2 1 2 3 3 5 6 8 8 8 9 9 8 8 1 9 1 9 1 1 1 1 1 1 1 1 1	TGTAMACATCCHACATCAGCT AGTTHIGTGTGCATGCATT ACATTCCGCGTGCACTCTCTTT CTGGTTTACACCTCGCGTGCACTCTCTTT CTGGTTCACCACCTCGCGCGCCCCCGCGCGCGCCCCGCGCGCG	2 1 3 3 1 1 1 7 7 3 7 7 3 7 7 3 7 7 3 7 7 3 7 7 3 7 7 3 7 7 3 7
TGTAMACANCCTIGACTIGGAMACTIGT CTATACAGACCTGACTIGCT CTATACGACCTCTGCTC TAGCAGCACATAATIGGTTTGTGG TCCCTGAGGAGCCCTTGAGCACCTGG CAGGAGCACTAATIGGTTTGTGG TCCCTGAGGAGCCCTTGAGCACCTGG CAGGGAGCTCACAGTCTATTG ACATTCATTTTGTTCGGTGGGTTG CATTATACTTTTGTTACCGCCTGTGA CAMCGGATTCCCAMACCAGCTG ATAGTAGACCGTATACCGACAG AGGGGTTTACCCATACCAGAGAAGA AAGGGTGCCAGTTGAAGACTGT ATAGTAGACCGTTGAGCAGAAGA AAGGGTCACATTGAGCAGATGT CAMCTACTGTTGTGTGCAATAT CAGGGACTTTTGAGCAGTGT TTTTCATTATTGCTCCTGAC GCCAGTGACTTGAGCAGTGT TCTACCACCATTTGAGATCAGT ACTGTCGTGTAGACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGACACCGGTGAT ACTGTCGTGTGAACCGGTGAT ACTGTCGTGTGAACCGGTGAT ACTGCCGTGTGTGAATTCCGT ACTGCAGTGAGGGCACTTGTA ACTGTAAGTTTTGCGT TCACAGTGAAGGCCATTTTT TTCACAAGGCCATTTGAGGT ACTGCAGTGAAGGCCATTTTT TTCACAAAGCCCTTACT TTTTCACAAGCCCGTTGTT TTTCACAAGTGAACCGGTCTTTT TTCACAAAGCCCTTTGTTGAGGT TCTGCACTGAACCCGTTGTTTTTTTTTT	2 7 6 7 1 1 3 3 100 1 1 1 1 572 2 1250 2 2 2 599 529 1 1 1 9 9 2 8 7 4 7 1 289 1 2 3 3 100 1 1 1 7 17 17 9 30	TRAGGGGCAGAGACTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTCCATGGGTTA AGAGGTAGTAGGTTGCATGAGGTTG AGAGGTAGTAGGTTGCAGGTTG AGAGGTAGTAGGTTGCAGGTTG AGAGGTAGTAGGTTGCAGGTTGCAGTAGGTTGCAGGTTGAGAGTTGCAGGTTGAGAGTAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTTGAGGTGAGGTTGAGGTGAGGTGAGGTGAGAGGTGAGAGGGTTAGAGGGTAGGAGG	4 1 1 27 3 1 1 2 2 39611 559 166 12 1 1 5 5 2 5 4 4 14 1 1 1 2 2 8 8 1 1 1 2 2 8 8 8 3 3 1 1 1 3 3 668 573 17 4 4 1 1 193 3 3 3 3 3	ARACHAGGEGTECANCA GCACCAGGAMATITIGGAT ACCHTTIGAMICAGT GCACCAGGAMATITIGGAT ACCHTTIGAMICAGT GCACCAGGAMATICAGT CTGCGCAMACTACTTICATT CTGCGCAMACTACTTICATTICAGT ATCACTTTICATTICAGT ATCACTTTICATTICAGT ACTACTTICATTICAGT ACTACTTICATTICAGT ACTACTTICATTICAGT TAGAGTACTAGTATTICAGT TAGAGTACTAGTATTICATTICAG ANTITICATTICAGTAGTAGACC CAGTITICATTICAGT TAGAGTAGTAGTAGTATTICAGT TAGAGTAGTAGTAGTATTICAGT TAGAGTAGTAGTAGTATTICAGT TAGAGTAGTAGTAGTATTICAGT TAGAGTAGTAGTAGTAGTAGTAGTAGT ANTITICAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	4 17 1 1 246 1 1 27 8 3 1 1 1 8 8 3 10 4 6 3 2 1 5 4 0 1 1 2 7 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA ANTAGCSCCCACTAGGATA COGTICCOGAGACCCCTTCCTTGGGAA ATTCCACCTAGGATAGTTTTCCACCGGATAGTTTTCCACCGGATAGTTTTCCACCGGATAGTTTTCCACCGGATAGTTTTCCACCGGATAGTTTCCACCTAGTTTCC CACTGAGATGGATAGTATAT TITCAGTCGGATGATAGTCC CACTGAGATCGTAGACCCTAGTTTCC CACTGAGATCGGATAGTCCC ACCCTGAGATGTAGACCC ACCCTGAGATGTAGACCT CACCTGAGTGTAGACCT CACCTGAGTGTAGACCT CACCTGAGTGTAGACCTTTTCCATGCATACTGTCACATCTGCATCTGGTCATCTGGATACACTTCCTGAGTAGTAGTGTTTTGAGATACTTCTTTGTAGAGACCTTTTCCATGCATATACTTCTTTGTAGATACTTCTTTGTAGATACTTCTTTGTAGATACTTCTTTGTAGATACTTCTTTGTAGATACTTCTTTGAGATACTTCTTTGAGATACTTCTTTGAGATACTTCTTTGAGATACTACTTGTTTGAGTATAGATAG	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCTACACTCAGCT AGTTITICTGTCACTCTAGCT AACATTCCCGGTGCACTTCTTT AACATTCCCGGTGCACTTCTTTT CCTGCCAATCCCATGCAAACTG CCGGTGCACTCTTTTGCTCTCTCTCTGGGT TGTCCTACTCTGTCATGCAAACTG CCGGTGGGGCCTCCA TGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTATACGCCCACTACC TTGAAGGTTGTACGCAAAACTG AATCCAAGGAAAACTG AATCCAAGGAAAACTG TTGCAAATCCTACTCTGCTTG TTTCAAGGTTGTACACAAACTG AATCCAAGGAAAACTG AATCCAAGGAATACGTTTTTCAAGGTTTTTTAAGGTTCTTTTAAGGTTCTTTTTAAGGTTCTTTTAAGGTTTTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAA ACAAATTCGTACTTAAGAAAAAAAAAA	2 1817 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACATCCTIGACTIGGAMACTET CITATICGACCTICTETC CITATICGACCTCTICTCT CITATICGACCTCTICTCTC TAGGAGCACAATAATIGGTTTGTGG TCCCTGAGGAGCACTTTGTGACCCTGG CAAGGAGCTCACAGTCTATTG AACATCAATTTGTTCGGTGGGTTG CATATTACTTTTGTTCGGTGGGTTG CATATTACTTTTGTTCGGTGGGTTG CATATTACTTTTGTCCCCCTGTGA CAAGGAGCTCCCAATATCACAAGAACAAGAAGAAGAAGAAGAACAAGACAAAACAAGAACAAAAAA	2 7 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACTTT CCATCTGAATCGGTTA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGGTTGCATA AGAGGTAGTAGTAGGTTAGAGGTTAGAGGTTAGAGGTAGTA	4 1 1 27 3 1 1 2 2 3864 1 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 8 8 1 1 1 1	ARACTAGAGGGTGCARCA GCACCACGAGATTTGGATT ACCHTTGAATCAGTG GCACCACGAGATTGGGGTT ACCATTTGAATCAGTG GCACCACGAGGGTTTCC CTGCGCAAGCTACTTGCTTGGTTGGTTTGATTTGA	4 17 1 1 1 246 1 27 88 3 1 1 1 1 88 8 10 4 6 6 3 2 2 1 1 1 1 6 6 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA  ANTIGGEGCCATCAGGATA  COGTICGGAAGACCTTCTCTGTGGAA  ANTIGGGCCATCAGGATA  TITCAGTCGGATAGACCTTGTTTGGGAA  TITCAGTCGGATAGTATAAT  CTATAGGGCCTCAGTTTCC  CACTGAGTGGAGATAGTAT  TITCAGTCGGATAGTAGCC  CACTGAGTGGAGATGGTGTA  ANTICTCTGTGTAGAACCGATTGTTGTGT  ACCCTGTAGGAACCGATTGTGTT  CACTGACTGATAGACCTAGTAGACCTA  ACCTGATGGAACCGATTGTGTGTAACCATCCTGAGTAGACCTGAACATCTGTGAACATCTGTGAACATCTGTGTAGACATCTGTTGAGACATCTGTTGAGACATCTGTTGTGTGTG	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACHTCAGCT AGTTITICTGTCAGTCTGTCATT AACATTCCGCGTGCATTCTTTT AACATTCCGCGTGCATTCTTTTT CATGCAATCCATGCAAACTG CCGGTGCACTCTTTTGCCTCTCTCTGCGT TGTCCAATCCTGTGCAAACTG CCGGTGCGGACCCTCCATGCAACTG TGTCATCCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	2 1817 2 1 1 1 1 1 1 1 1 7 7 37 7 3 1 1 1 2 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACATCCTIGACTIGGAAGCTGT CTATACAGCCTGTGTC CTATACGACCTCTGTCTGC CAGGAACACATATTGGTTGTGT TCCCTGAAGGACCATTATGA ACATTCATTTGTTGGTTGGTTGTGT CCCTGAAGGACCCTTTGAACACCTGG CAAGGACTCACAGTCTATTG ACATTCATTTGTTGTGTGTGTGTGTGT ACATTCATTTGTTGTGTGTGTGTGTGTGTATTATATTTTTTGTGTGAAGCTGTGAACACGTGTATATATA	2 7 6 7 7 1 1 1 3 3 10 0 1 1 1 1 2 2 5 9 9 1 1 1 2 8 9 9 3 10 1 1 1 1 1 7 7 7 7 7 1 1 2 8 9 9 1 1 1 1 7 7 9 9 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACCTAT  CACATIGAANTICAGGTTA  AAGAGTAGTAGTTACAGG  CCANATTGAATTTACAGC  CCANATTGAATTTACAGC  CCANATTGAATTTACAGC  CCANATTGAGATTTACAGC  CCANATTGAGATTTACAGC  CANATTGAGATTTACAGC  TARACTCGTCGTAGTAGAGTG  TARACTCGTCGTAGTAGAGTG  TARACTCGTCGTAGTAGAGTG  TARACTCGTCGTAGTAGAGTG  TARACTCGTCGTAGTAGTG  ACCTACATTGCTGCGGCGC  CANACTGAGAGCGGAGAGCCGTCTCAT  CATTCCAGCTAGTAGGC  TARACTGCTGTGTGCCC  AAACTGAGGCGGAGAGCCGTGTTGTT  CATTCCAGCTAGTAGGC  TARACTGCTGTAGTGGTGC  TARACTGTTTTAGAGGTGGTGTGTGTGTGTGTGTGTGTGTGTG	4 1 1 27 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AACATGAGCICACACA GCOCACACAGAMATITIGGAT ACCATTIGAAMICAGTI GCOCACACAGAMATITIGGAT ACCATTIGAAMICAGTI CITICAGAMICAGTI CITICAGAMICAGACACACAGAMICACACACACACACACACACACACACACACACACACAC	4 17 1 1 1 246 1 1 1 1 1 1 88 8 10 0 4 6 6 3 3 2 1 1 1 1 2 2 2 4 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACA  ANTIGGGCCACTAGGGTTA  COGTICGGAAGACCATTCAGGAACA  ANTIGGGCCACTAGGGTTA  COGTICGGAAGACCGTTCGTCTTGGGAA  TITCAGTCGGATGTTTACAGC  CGTACCGTGAGTATAAT  CTTTACGGCCGATGTTTCC  CACTGAGTGGGAAGACGGTTGTA  ANTICTGTCGATAGTCCC  ANTICTGTCAGATAGCC  TOTACGGCCTCGTAGTTCC  CACTGAGTGGGAAGACGTGTA  ANTICTGTCAGTAGCCAT  CACTGATGTAGACCAT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  CACTGATGTGAACAGT  TCCCTAGTGTGAACAGT  TCCTAGAGTAGTTGATGTGAACACTGAA  AGCTTACCAATACTTCTTTGGGAACAGCTGT  TCCTAGCATATACTTCTTTGGAACAGCTGT  TCCTAGCAATACTTCTTTGGAACAGCTGAACAGCTGAACAGCTGAACAGCTGTGAACAGCTGTGAACAGCTGAACAGCTGAACAGCTGTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCTGAACAGCAGCAACAGCAGCATGAACAGCTGAACAGCAACAGCAGCATGAACAGCTGAACAGCAACAGCAGCAGCTTGAACAGCAACAGCAGCAACAGCAGCAGCAGCAGCAGCAGC	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACHTCAGCT AGTTHIGTGTGCATGCATT AACATTCCGCGTGCATTCTTTT AACATTCCGCGTGCATTCTTTTT CTGTCAMATCCATGCAGAACTG CCGGTGCAGATCCTTTTGCGTGCTGCTGCTGCGGGGGGGG	2 1817 2 1 1 3 3 1 1 1 1 7 7 3 7 3 7 3 1 1 1 1 5 5 6 6 9 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACANCCTIGACTIGGAMACTGT CTATACAGCCTGCTGCTGC CACTGGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2 7 7 6 7 7 1 1 1 3 3 10 0 1 1 1 1 1 1 1 572 2 1 2 579 9 529 9 529 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACCTAT TCACCTAGATA AGAGGTAGTAGATT AGAGGTAGTAGATT AGAGGTAGTAGATT AGAGGTAGTAGATT AGAGGTAGTAGATT AGAGGTAGTAGATT CACATTGAGTAGATT AGACTAGTAGTAGATT AGACTAGTAGTAGATT AGACTAGTAGTAGATT AGACTAGTAGTAGATT AGACTAGTAGTAGATT AGACTAGTAGTAGTAGATT AGACTAGTAGTAGTAGATT AGACTAGTAGTAGTAGATT AGACTAGTAGTAGTAGATT AGACTAGTAGTAGTAGTAGATT AGACTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT	4 1 1 27 3 1 1 2 2 39661 1 1 1 2 2 1 1 1 2 2 1 1 1 2 2 8 8 1 1 1 1	ARACHAGGEGTIGCARCA GCAGCAGGAGGATATTIGGAT ACCATTIGAAGTCAGTG GCAGCAGGAAGTATTIGGATT ACCATTIGAAGTCAGTG GCAGCAGGAAGTCACTGCT CTGGGCAAGCTACTTGCT CTGGGCAAGCTACTTGCT CTGGCAAGCTACTTGCT CTGGTTACATTGAAGACC ACTATGATTTGACAGACC CATATGATTTGACAGACC CATATGATTTGACAGACC CATATGATTTGACAGACC CATATGATTTGACAGACC CATATGATTTGACAGACC CATATGATTACAATTTT TAGCAGCACACTAGTTTTACATTATT TAGCAGCACACTAGTTTTACATTTTAGCAGCACACTAGGTTTACATTTTAGCAGCACACTAGCTTTACATTTTAGCAGCACACTAGCTTACACTACCACTAGCTTACACTACCACTAGCTTACACTACCACTAGCTTACACTACCACTAGCTTACACTACCACTACCACTAGCTTGTACACTACCACTACTAGCTACACTACCACTACTAGCACCACTACTAGCACTACTACTACCACTACCACTACTAGCACCACTACTACACCCACTACTAGCACCACCACTACTAGCACCACACTACTACACCCCACTACTAGCACCACCACTACTACACCCCACTACTACACCCCACTACTA	4 17 1 1 1 246 1 1 1 1 1 1 1 88 8 3 3 1 1 1 1 1 1 2 2 1 3 3 2 1 1 1 1 1 1	CACAGCTECCATCAGAACA ANGGGGCCACATAGGGTTA COGTICGGAACACCATTAGGAA TITCAGTCGGATAGTAGTAGT CACAGTGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACATCAGCT AGTTHICATIONAGT AACATTCCCGGTGCATTCCTTT TCGGTTTCANTGGGGCTTTAC TCGGTTTCANTGGGGCTTTAC TCGGTTTCANTGGGGCTTTAC TCGGTTTCANTGGGGCTTTAC TCGGTTCANTGGGGCTTAC TCGGTGGGGAAACCCGTTCGTCGTCGG TCGCTGGGGGGAAACCCGTTCGTCTTGGG TGTCTCTCTGTGGTTGTAGT TGTCACTCTGGGGGGCTCCA TGTCAGCTAGTAGGTTTAGGT TTCAGCTAGTAGTTAGGTT TTCAGCTAGTAGTAGGTT TTCAGCTAGTAGTAGGTT TTAGGGTAGTAGTAGGTT TAGGGTCCTTCCTGTGCTT TAGGGTCCTTCCTGTGCTT TAGGGTCCTTCTGTGTTT TAGGGTCCTTCTGTGTTT TGGGATCTTGTGTGAGAAACT AACATCTATCTTTTTGGAAACACTAGGAAACACAATCATGTTTTGGAAAACACAATCATGTTTTGGAAAACACAATCATGTTTTGGAAAACACAATCATGTTTTGGAAAACTAGAATCAATC	2 1817 2 1 1 3 3 1 1 1 1 1 7 7 3 3 1 3 1 4 1 1 1 1 1 1 1 1 1 1 3 3 1 1 4 1 1 1 1
TGTAMACAICCTIGACTIGGAMACTIGT CITATICGACCTIGTETC CITATICGACCTIGTETC CITATICGACCTIGTETC TAGGAGCACAATAATIGGTTTGTGG TCCCTGAGGAGCCCTTGAGACCTIGTG CAGGAGCACTAATAGTTGTTGGT CCCTGAGGAGCCCTTTGAGCCTGGGTGG CAAGGAGTTCCAAAACCAGCTGGTGA CAAGGAGTTCCCAAAACCAGCTGGTGA CAAGGAGTTCCCAAAACCAGCTGGAAAAAAAAAA	2 7 7 6 7 7 1 1 1 3 3 100 1 1 1 1 1 1 1 1 2 2 2 9 9 2 2 8 8 7 4 4 4 4 1 2 2 1 2 2 9 9 3 3 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACTTT CCATCIGAATCAGGTA AGAGTAGTAGGTTCAGTA AGAGTAGTAGTAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTAGTCAGTAGTCAGAGTAGTCAGAGTAGTCAGAGTAGTCAGAGTAGTCAGAGTAGTCAGAGTAGTCAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGAGTAGAGAGTAG	4 1 1 27 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ARACATRAGEGETIGCARCA GCACCACAGAMATITAGGAT ACCATTRIGAMICAGT GCACCACAGAMATITAGGAT ACCATTRIGAMICAGT CTGCGCAMAGCATCTGCTTGCT CTGCGCAMAGCATCTGCTTGCT CTGCGCAMAGCATCTGCTTGCT CTGCTATGATTTGAATCAGCTGT ATGACCTATGATTTGACAGCCGT ATGACCTATGATTTGACAGCCGT ATGACCTATGATTTGACAGCCGT ACCACTATGATTTGACAGCCGT ACCACTATGATTTCATAGTTCAGA ACTGATTCTTTTGGTGTTCAG ACTGATTCATTTTTTGGTGTTCAG ACTGATTCATTTTTTGGTGTTCAGA ACTGATTCCTAGGTGTTCATAGTTTAGG ANTICTTCCCAGGGATCCCTTTA AATCACTACACCACAGCCAG CAGTTTTCCCAGGGATCCCTTT ACCAGGATCCCTTTA ACTCACACTACCAGCCAGC CAGTTTTCCCAGGGATCCCTTT CCTGGTAGCCCAGCTCTTGTGTGCCC CTGTGAGCCCAGCTCTTGTGTGCCC CTGTGAGCTCCAGTCTGTGTGCCC CTGTGAGCTCCAGCTCTTTCAGTTCCAGCTCTTCTGTGTGCCC CTGTGAGCTCCAGCTCTTTCAGTTCCAGCTCTTCTGTGTGCCCCTTTAGAGTCCAGCTCTTGTGTGCCC CTGTGAGCTCCAGCTCTTGTGTGCCC CTGTGAGCTCCAGCTCTTGTGTGCCC CTGTGAGCTCCAGCTCTTTCTTTTTTGAGTTTTCCATTGTGTTTCCAGTGTGACCACTCTTTTTTTT	4 17 1 1 1 246 1 1 27 8 8 8 3 3 1 1 1 8 8 8 1 1 1 2 1 1 1 1 1 6 6 3 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA  ANTAGCSCCCACTAGGATA  COGTICCOGAGACCCCTTCCTCTTGGGAA  ATTACTAGCTCAGATATTACAGC  CITACCGTGAGTATTACAGC  CITACCGTGAGTATTACAGC  CACTAGATAGTAGACC  CACTAGATAGTAGACC  CACTAGATAGACCCAGATTAGACC  CACTAGATAGACCCAGATTAGACC  CACTAGAACCCAGATTAGACC  CACTAGAACCCAGATTAGTC  CACTAGATAGACCCAGATTAGTC  CACTAGATAGACCCAGATTAGTC  CACTAGATAGACCCAGATTAGTC  CACTAGATAGACCTAGACCAGT  CACTAGATAGACCTAGACCAGT  CACTAGATAGACCTAGTAGACCTT  CACTAGACTAG	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACATCAGCT AGTTITICTICAGCATTCAGCT AACATTCCCGGTGCACTTCTTTT AACATTCCCGGTGCACTTCTTTT CTGTCAMATCCATGCAGAACTG CCGGTGCAGATCCTTTTGCTCTTGCGT TGTCCATCTCTGTCATGCAAACTG CCGGTGGGGCCTCCA TGAGGTGTATAGCTCCACACC TGAGGTGTATAGCTCCACACC TGAGGTGTATAGCTCCACACC TGAGGTTGTAGCTCCTCTTGCTGT TTCCAGGATACTCATTCCTTGCTG TTCCAGGATACTCATTCCTTGCTG TTCCAGGATACTCATTCCTTGCTG TTCCAGGATACTCGTTGTTGTTGCAGATCACCACACACAC	2 1817 2 1 1 3 3 1 1 1 1 7 7 37 73 73 73 1 1 1 2 2 2 2 2 2 2 131 1 1 1 1 1 1 1
TGTAMACANCCTIGACTIGGAMACTIGT CTAMACANCCTIGATIC CITATICGACCTICTICT CITATICGACCTICTICT CTAMACANCCTICTICTICT TAGGAGCACAATAATIGGTTTGTGG TCCCTGAGGAGCCCTTTGACACCCTGG CAAGGAGCTCACAGTCTATTG AACATTCATTTGTTGCGGTGGGTTG CATTATACTTTTGTTGTGTGGTGGTTG CATTATACTTTTGTCACCCCTGTGA CAAGGAGTTCCCAAAGCCGTACACACCTG AAGAGGTATAGCCAAAACCGTAAAACCGTAAAACACCGTATAACACCGTATAACACCGTATAACACCGTATATACTCCTACCACCAATATTCTTCATTATTCATTC	2 7 7 6 7 1 1 1 3 3 100 1 1 1 1 1 1 1 5 7 2 2 5 9 9 5 2 9 9 5 2 9 9 2 8 8 7 7 1 1 2 8 9 9 1 1 1 1 1 2 3 3 1 1 1 1 1 1 1 3 2 3 1 1 1 1	TRAGGGGCAGAGACCTAT  CACATIGAATCAGGTA  AGAGGTAGTAGGTTCAGTA  AGAGGTAGTAGGTTCAGTAGGTTCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	4 1 1 27 3 3 1 1 59 16 6 12 1 1 1 1 1 2 2 8 8 1 1 1 1 1 2 2 8 8 8 6 8 8 8 8 8 8 8 8 1 1 1 1 1 1 1 1	ARACIAGAGGCITCANACA GCACACAGGAMATITAGGAT ACAUTIGAMATICAGT GCACACAGGAMATITAGGAT ACAUTIGAMATICAGT CITICAGAGCAGGAMTICC CITICAGCAMACTACTICAGT ATRICATTICATAGACC ATTACATTICATAGACC ACTACATTICATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICAGACC ACTACATTICACATICAGACC ACTACATTICACATICAGACC ACTACATTICACATICAGACC ACTACATTICACATICAGACC ACTACATTICACATICACATICAGACC ACTACATTICACATICACATICAGACC ACTACATTICACATICACATICAGACC ACTACATTICACATICACATICACATICAGACC ACTACATTICACATI	4 17 1 1 2466 1 17 27 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACAA ANTIGGGCCACTAGGGTTAT COGTICGGGAAGACCGTTCATCAGGAA TITCAGTCGGATATTAGAT CATAGGATGCATTAGATCATCAGGAA TITCAGTCGGATATTAGAT CATAGGATGCAGATGATAGAT CACAGTAGATGCAGATGATAGAT CACAGTAGATGCAGATGATAGAT CACAGTAGAACCGAATTAGATCACTAGAACCAGATTAGACCACTAGAACCAGATTTAGACCATCAGATGCAGATGAGACCATTAGACCATCAGATGAGACCAGATTTAGACCAGATGAGAACCAGATTTAGACATCATCAGATGAGACCATTAGACATCATCAGATGAGACCATTAGACATCATCAGATGAGACCATTAGACATCATCAGATGAGACCATTAGACATCATCAGATGAGACCATTAGCATTAGAACATCATCAGATGAGAACCTTTAGACATCATCAGATGAGAACCATTAGACATCATCAGATGAGAACCATTAGACATCATCAGATGAGAACCATTAGCATTAGACATCATCAGATGATGAGATGATGAGAGATGAGAGATGA	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACHTCAGCT AGTTHIGTGTGCATGCATT ACATTCCGCGTGCATTCTTTT ACATTCCGCGTGCATTCTTTTT CTGTCAMTCCGTGTGCATTCTTTTGCTTGGT TGTCAMTCTGTGCATGCATGCATGCATGCATGCATGCATGCATGCA	2 1817 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACANCCTIGACTIGGAAGCTGT CTATACAGCCTGTGTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTGTCTC CTATCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2 7 7 6 7 1 1 1 3 3 100 1 1 1 1 1 1 1 2 572 2 1 2 5 9 9 529 9 529 9 529 9 30 0 1 1 1 1 1 1 1 1 2 3 1 1 1 1 1 1 1 3 2 3 1 1 1 1	TRAGGGGCAGAGACCTAT TCACCATCHANATCAGGTA AGAGGTAGTAGAGTTACAGGAGAGTTACAGAGAGAGTTACAGAGAGAG	4 1 1 27 3961 59 16 11 21 1 5 5 1 1 7 101 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ARACIAGAGGCITGCARCA GCAGCACAGAGATITIGGAT ACCATTIGAATICAGT ACCATTIGAATICAGT ACCATTIGAATICAGT ACCATTIGAATICAGT CITICAGAGCAGGATTCC CITICAGCAGAGCACACAGGATTCC CITICAGCAGAGCACACACACACACACACACACACACACACAC	4 17 1 1 1 2246 1 2246 1 2 2 2 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2	CACAGCTECCATTCAGAACA ANTIGGGCCACTAGGGTTA COGTICGGAAGACCATTCAGGAACCA ANTIGGGCCACTAGGGTTA CAGTAGGATGAGACCATTCAGGAA TITCAGTCGGATGATGTTAGAGC CITACGGCCTCAGCTTCC CACTAGATGGGAAGACGGTTGTA ANTICTGTCAGGATGGATAGACCT TOTAGGGCCTCAGTTTCC CACTAGATGGGAAGACGAT CAGTAGACGATGGATAGACCT TOTAGATGCCTCAGTTTGTAGACCT TAGACATCTGCTGAACGAT CAGCTAGATGGAACGAT CAGCTAGATGGAACGAT CAGCTAGATGGAACGAT CAGCTAGATGAACGAT CAGCTAGATGAGAACTGT CAGCTAGATGAGACTGT CAGCTAGATGATGTGGAACCTGAA AAGCTTCCCTAGTGTGAACCTGAA CAGCTAGATGAGACGAT TTCCTAGCATATACTTCTTTGGAAGACCTGT TTCCTAGCATATACTTCTTTGGAAGACCTGAAGACGAT TTCCTAGCATATACTTCTTTGGAAGACCTGAAGACGATGTGAAGACGATGACGATGAAGACCTGAAGACACCTGAAGACCTGAAGACACCTGAAGACACCTGAAGACACCTGAAGACACCTGAAGACACCTGAAGACACCAACCTGACGATGTTGGAACCTGAACCAACC	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACATCAGCT AGTHTIGTGTGCATGCATTCAGT AACATTCCGCGTGCATTCTTTT CTGTCAMATCCATGCAGTAGTAGTAGT CCGGTGCAGTCCATTGCAGTAGTAGTAGT CCGGTGCAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	2 1817 2 1 1 3 1 1 1 1 1 1 7 3 7 7 3 1 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACAICCTIGACTIGGAMACTIGT CTAMACAICCTIGTACT CTAMACAICCTIGTACT CTAMACAICCTIGTACT TAGCAGCACAATAATIGGTTTGTGG TCCCTGAGGAGCACTTGTGAGCCTGG CAGGAGCACTAATAGTTGTTGGT TCCCTGAGGAGCCCTTTGAGCCTGGGTGG CAGGAGCTCTACAGTCTATTG ACACTATTGTTTTGTT	2 7 7 6 7 7 1 1 1 3 100 1 1 1 1 5722 2 8 8 7 7 7 1 1 1 1 1 1 1 1 7 9 1 1 1 1 1 1 1	TRAGEGGCARAGCCARACTTT CCCTATGRAATGCATTACACCTGGTA AGAGGTAGTAGTAGTTACACC CCATAGTAGTAGTACACCTGCATACACCCACCACCACCACCACCACCACCACCACCACCA	4 1 27 3961 59 61 59 61 59 61 50 61	ARACHAGGEGTECANCA GCACCACGAMATITAGGAT ACCHTTRAMICAGTG GCACCACGAMATITAGGAT ACCHTTRAMICAGTG GCACCACGAMACTACTGC GCGCAMACTACTGCTGCT GCGCAMACTACTGCTGCT GCGCAMACTACTGCTGCT ATGACTATGATTTGATTGATACACC ATGACTATTGATTTGAT	4 17 1 1 2466 1 17 27 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECATCAGAACA ANTAGCSCCCACTGAGGTTGCTTGGGAA ATTACAGCTGATTGCAGGATGTTTACAGC CGTACCGTGAGTGTTTACAGC CGTACCGTGAGTGTTTACAGC CGTACCGTGAGTGTTTACAGC CGTACCGTGAGTGTTTACAGC CGTACCGTGAGTGTTACAGC CACCGTGAGTGTTACAGC CACCGTGAGTAGTAGCC CACCGTGAGTAGTAGCC ACCCGTGAGTAGACCC ACCCGTGAGTAGACCC ACCCGTGAGTAGACCC CACCGTGAGAACCGTTTGCAGCAGCT CACCGTGAGAACCGTACGTGAGACCGT CACCGTGAGAACCGTTTGCAGCAGCAGCCGT CCCGTGAGGACGTGTGGAGACCGT CACCGTGAGAACCGTGTGGAGACCGT CACCGTGAGAACCGTGTGAGACGTGT CACCGTGAGAGACGTGTGGAGACGCTGTGCAGCAGCGTGGAGAGCGTGTGAGAGGTGTGGGTT CCATGCAGTGAGACGTGTGGAGACGCTGTGCAGCAGCAGCGGGAGAGACCGT TCCATGCAGTGAGACGTGTGGAGAGCCGT CACCGTGAGAGACGTGTGGAGAGACCGT TCCATGCAGTGAGAGACTGTT CACGGACCGTGGAGAGACCGT TCCATGCAGTGAGAGACTGTT CACGGACCAGGAGACCGT TCCATGCAGTGTGGGTTGAGATGGAGTGGGTGTGAGAGGTGGAGAGAGCGTGAGAGAGCGTGAGAGAGA	1 1 17 1 26 7 1 1 1 132 1 1 45 4 2 3 3 1 26 18978 35 56 8 8 19 9 1 1 46488 3 2 1 1 46448 3 2 1 1 4 2 2 1 1 4 2 2 1 1 4 4 4 4 4 4 4	TGTAMACATCCHACATCAGCT AGTTITICTICAGCATTCAGCT AACATTCCCGGGGCATTCTTTT AACATTCCCGGGGCATTCTTTTT CTGTCAMATCCATGCAGAACTG CCGGGGAGACTCGTTTTGCTCTTCGGG TGTCTCTCTCTGTGCTGCTGCGCGCGGCGGCGGCGCCCCCATTGCAGCAGCCGTTTGAGAGGTGTTAGAGCTCCTTTGCTGTGTTTGAGTGCTCACCAGGAGATCCCT TGAGGGTGTAGTAGCTCCACACC TTGAGGTGTAGTAGCTCCACACC TTGAGGTAGTAGGTTGTTGCTGCTG TTCCAGGAATCCTTGCTGGTT TAAGGCTCTCTTGCTGGTT TAAGGCTCTCTTGCTGGTTTTAGAGCTCAGAACACAGAAACTGAATCCGTGTTTTGAGAACACAGAAACACAACACACAC	2 1817 2 1 1 3 1 1 1 1 1 1 7 3 7 7 3 1 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACAICCTIGACTIGGAMACTIGT CTATACAGCCTGTCTC CTATACGACCTCTGTCTC CTATACGACCTCTGTCTC TAGGAGCACAATAATIGGTTTGTGG TCCCTGAGGAGCCCTTTGACCCCTGG CAAGGAGCTCACAGTCTATTG AACATTCATTTGTTGCGTGTGGTTG CATATTACTTTTGGTGTGTGGTTG CATATTACTTTTGTGTGTGTGTGGTTG CATATTACTTTTGTCACCCCTGTGA CAAGGAGTCCCAAAACCCACCTGTA ATAGTAGACCGTATACCCAAACCCAAACA AAGAGGTTAATAGCCATACCGAAAAC AAGAGGTTAATAGCCATACCAATAT CAAGTCCCAATTTGAAGCCAATAT CAAGTCCCATTTGAAGCCAATAT CAAGTCCTTTAGCTGTTCTGCAAGAG TCTTTCATTTCA	2 7 7 6 7 1 1 1 3 3 100 1 1 1 1 1 1 1 25 2 2 2 2 2 2 2 2 8 7 7 1 1 2 2 9 9 5 2 3 9 9 2 2 8 8 7 7 1 1 2 2 3 3 100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACCTAT  CACATIGAATCAGGTA  AGAGTAGTAGGTTCAGTA  AGAGTAGTAGGTTCAGGTTA  AGAGTAGTAGTAGTTCAGGTTA  AGAGTAGTAGTAGTTAGAGT  CANTIGGAGTTAGAGT  CANTIGGAGTTAGAGT  AGACTAGTAGTAGTAGAGT  AGACTAGTAGTAGTAGAGT  AGACTAGTAGTAGTAGTAGAGT  AGACTAGTAGTAGTAGTAGT  AGACTAGTAGTAGTAGTAGT  AGACTAGTAGTAGTAGTAGT  AGACTAGTAGTAGTAGTAGT  AGACTAGTAGTAGTAGTAGT  TAAACAGTAGTAGTAGTAGTAGT  TAAACAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	4 1 1 27 3 3961 59 16 11 12 5 5 5 4 4 14 14 11 1 1 2 2 8 8 8 8 8 8 8 1 1 1 2 8 8 8 8	ARACIAGAGGCITCANACA GCACACAGGAMATITAGGAT ACAUTTGAMATICAGT GCACACAGGAMATITAGGAT ACAUTTGAMATICAGT CTGCGCAMAGCATCAGGATTCC CTGCGCAMAGCATCAGGATTCC CTGCGCAMAGCATCAGGATTCC CTGCGCAMAGCATCAGGATTCC ATGACTATGATTTGACAGACC ATGACTATGATTTGACAGACC ACTGATTCATTTGATTGAGACC CTGCCCAGGGTGTATCAGATTTAGA ACTGATTCATTTGGTGTTAGA ACTGATTCATTTGGTGTTAGA ACTGATTCATTTGGTGTTAGA ACTGATTCATTGATTTAGG ANTICTTCCCAGGGATGCATTTA ACTCAGCACACACAGCAGA ACTGATTCCAGGATCCAGTTA ACTGATCACACAGCAGA ACTGATTCCAGGATCCAGTTAGA ACTGATCACACAGCAGACAGCAGA CAGGTTTCCAGGATCCAGTTAGACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	4 17 1 1 246 6 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATCTCAGAACA  ANTIGGEGCCATCAGGATAGT  COGTICGGAAGACCCTTCCTCTTGGGAA  TITCAGTCGGATAGTTTTACAGC  GTACCGTGAGTTTTACAGC  GTACCGTGAGTTTTACAGC  CITACCGGCTCCTAGCTTTCC  CACTGAGATGGGATATTAAT  CTATAGGGGCTCCTAGCTTTCC  CACTGAGATGGGATGG	1 1 1 1 2 2 5 1 1 1 1 1 2 2 5 2 2 2 2 1 1 1 2 2 1 1 1 1	TGTAMACATCCHACATCAGCT AGTTITICTGTCAGTCATTCAGCT AACATTCCCGGTGCACTTCTTTT AACATTCCCGGTGCACTTCTTTTT CTGTCAATCCCAGTGCAAACTG CCGGTGCAGATCCTTTTGCGTCTGCTGCGGCGCCTCCTGTGCGGGCCTCCATGCGGGGCCTCCATGCGGGGGCTCCATGCGGGGCGCTCCATGCGGGGCTCCATGCGGGGCTCCATGCGGGGGCTCCATGCGGGGGCTCCATGCGGGGGCTCCATGCGGGGGCTCCATGCAGCGGGGGGCGGGGGGGG	2 1817 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
TGTAMACANCCTIGACTIGGAMACTIGT CTAMACANCTIGTETIC CITATICGACCTICTICT CITATICGACCTICTICT CITATICGACCTICTICTICT CAGGAGCACAATANTGGTTTGTGG TCCCTGAGGAGCCCTTTGACACCTIGG CAGGAGCCCTTTGACACCCTIGT CAGGAGTCCCAATATTGTTTGTGGTGTGGTTG CATATTACTTTTGGTGGTGGGTTG CATATTACTTTTGTGTGGTGGGTTG CATATTACTTTTGTGCTGTGTGGTTG ATGAGGACCTGCAAAACCCGAAAA AGGCTGCCAGTTGAAGACCTTG AGGAGGTTTTGGGGAAGAA AGGCTGCCAGTTGAAGACCTTT AGGGACTTTTGGGGGCAAGATTG CAGTCACTTTGAAGCCCAATAT CTTGTGCTGTGTGTTCTCCAAC GCGAGTGTCTTGACTGCGGTTGT TCTTGCCTGTTGACACCGGCTGTT CAGACCATTTGAAATCAGT ACTGCACTGTTGACAGCGGCTGT CAGACCAATTGAAATCAGT ACTGCACTGTGAAAACCGGTCTTGTACACCGGCTGTTACACACCAATTGAAATCAGT ACTGCACTGTACAACCTGCTTTTTTTCACACCACATTTGAAATCAGT ACTGCACTGTACAACCTGCTTTTTTTCACAAGCACACTTGTATTCCAACTGTAAATTTTGCACTTTTTTTCAAAAGTACCACATTGAAATTTTTCAAAAGTACCACAACTGCTACTTTTTTTCACAAGCACACTTGTTTTTTCACAAGCACACTGTTTTTTTCACAAAGCACACTGTTTTTTTCACAAGCACACTGTTTTTTTCACAAGCACACTGTTTTTTTCACAAAGCACACTGTTTTTTTCACAAGCACACTGTTTTTTTCACAAGCACACTGTTTTTTTCACAAAGCACACTGGCTTTTTTTT	2 7 7 6 7 7 1 1 1 3 100 1 1 1 1 1 1 1 1 5722 2 2 1 1 50 2 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACCTAT  CACATICAAATCAGTATA AGAGTAGTAGTAGTAGAGTAGTAGAGAGTAGTAGTAGTAG	4 1 1 27 3961 59 16 11 1 1 1 1 1 1 2 2 8 8 1 1 1 1 1 1 1 2 2 8 8 1 1 1 1	ARACIAGAGGCITGCARCA GCACCACAGAGATITGGCAT ACCATTIGAATICAGT ACCATTIGAATICAGT ACCATTIGAATICAGT ACCATTIGAATICAGT CITICAGAGCAGGATTCC CITICAGCAACCACTAGGATTCC CITICAGCAGCAACCACTAGGATTCC CITICAGCAGCATTCCCTTGC CACATTIGATTTAAAAGGCC CACATTIGATTTAAAAGGCC CACATTIGATTTAAAAGGCC CACATTIGATTTAAAAGGCC CACATTIGATTTAAAAGGCC CACATTIGATTAAAAGGCC CACATTIGATTACATACTAG ACCACACACACTAGGTTTACATTACA	4 17 1 1 246 6 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECCATTCAGAACA  ANTIGGGCCACTAGGGTTGT  COGTICGGAAGACCATTCAGGAACA  ANTIGGGCCACTAGGGTTGT  COGTICGGAAGACCGTTCGTCTTGGGAA  TITCAGTCGGATGTTTACAGC  CITACCGCTCCTAGCTTTCC  CACTGAGTGGAAGACTGTTCC  CACTGAGTGGAAGACTGTTGAGCC  TOTACGGCCTCCTAGCTTTCC  CACTGAGTGGGAAGACTGTTGAGCCT  TOTACGGCCTCTGAGTAGCCC  TOTACGGCCTCTGTAGACCAT  CACTGCTCTGTAACACCTTTGTGT  TACACCTTCTGTGTAACCAGT  CACTGCTAGTAGCAGTTTGGGTACCAT  AGCTTACTCTGAGTACCTGTT  TCCTTAGTGTACTAGCTGTTGGAACACTGT  TCCTTAGTGCTATTGGGAACCAGT  TCCTTAGTGCTATTGGAACCAGTTTGGATAGCAGTTTGCATTAGCATTTTGGAACTGTTTGGAACACTGTTGGAACACTGTTGGAACACTGTTGAGAACACTGTTGGAACACTGTTGGATTGGATTGCATTGCATTGCATTTGGAACACTGTTGGAACACTGTTGCAT	1 1 1 1 1 2 1 2 1 1 1 1 1 2 2 1 1 1 1 1	TGTAMACATCCHACATCAGCT AGTTITGTGTGCATTGCATT AACATTCCGCGTGCATTCTTTT AACATTCCGCGTGCATTCTTTTT CTGTCAMATCCATGCAGAACTG CCGGTGCAGATCCATTGCATTCAGCTGCAGAACTG CCGGTGCGAACTCCTTTGCGTGTGTGTGTGTGTGTGTGTG	2 1817 2 1 1 1 1 1 1 1 1 1 1 2 2 2 2 1 1 1 1
TGTAMACANCCTIGACTIGGAMACTIGT CTATAGGACCTIGTETC CTATAGGACCTCTGTCTC CTATAGGACCTCTGTCTC TAGGAGCACAATAATGGTTTGTGG TCCCTGAGGAGCCCTTGTGAGCCCTGG CAAGGAGCTCACAGTCTATTG ACAATTACTTTTGTGTGTGTGGTGTG	2 7 7 6 7 1 1 1 3 3 100 1 1 1 1 1 1 1 25 2 2 2 2 2 2 2 2 8 7 7 1 1 2 2 9 9 5 2 3 9 9 2 2 8 8 7 7 1 1 2 2 3 3 100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TRAGGGGCAGAGACCTAT TCACCTAGTAA AAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTA	4 1 1 27 3961 59 16 112 1 1 1 1 1 1 1 2 2 8 8 3 1 1 1 2 2 8 8 3 1 1 1 2 2 8 8 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ARACTAGAGGETICANACA GCACCACAGAGATITICGCAT AMATTACTACTACTAGGETICATACA AMATTACTACTAGGETICAGGETIT AMACTACTACTAGGETICAGGETIT AMACTACTACTAGGETICAGGETIT AMACTACTAGGETICAGGETIT AGCACCAAGGATITCC CTGGGCAAGCTACTAGGATTACACTAGGATTACACTAGGATTACACTAGATTACACTAGACTAGATTACACTAGACTAGATTACACTAGACACACAC	4 17 1 1 1 246 1 17 27 28 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACAGCTECATTCAGAACA  ANTAGCSCCCACTAGGATA  ANTAGCSCCACAGACAC  ANTAGGATAGATAGATAGATAGATAGATAGATAGATAGAT	1 1 1 1 1 1 2 6 6 7 7 1 2 6 1 1 1 1 1 1 1 2 6 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TGTAMACATCCHACATCAGCT AGTTHICATION CONTROL TO THE C	2 1817 2 1 1 3 3 1 1 1 1 2 2 5 5 5 6 9 9 1 1 1 1 1 7 9 9 1 1 1 1 1 1 1 1 1 1

TGCCATCAGAAGACTGAAGGAACTGAAAGA	1 242	CAGTAGTCTGCACATTGGTTA	135 10	AAACAAACATGGTGCACTTCTT	16	AGCATTGTACAGGGCTATGA	3	CATTGCACTTGTCTCGGTCTGAC	2
CTAGCACCATCTGAAATCGGTT GGCTCAGTTCAGCAGGAACAG AATAATACATGGTTGATCTT	1	AATATAACACAGATGGCCTGT TTTGGTCCCCTTCAACCAGCTG CCCGGAGTCGGGAAAAGCTGGGTTGAGAG	29 1	TGAGGTAGTAGATTGTATAGTTTT TGAGGTAGTAGATTGTATAGTTGTGGGGTA CCCTGAGACCCTAACTTGT	1 1 2	AGCTGCCAGTTGAAGAACTGT ACAAGAGGGCCTTTCTGG AATGACACGATCACTCCCGTTGAGTGGG	8	CGGTGCTGGTGGAGCAGTGAGCACG CAAATTCGTATCTAGGGGAAT GCTGGGGTGGAACCTGGTTTGT	3 41 2
AATAATACATGGTTGATCTT CTGCCTGGTAATGATGA TGCGGGGCTAGGGCTAACAGC	3 5	TAGTAGGTTGTATGG TAAGTGCCTGCATGTATATGC	1 159	TCCCTGAGACCCTTTAACCTGTG ATGGTTGACCATAGAACATGC	607 1	ACAAGAGGGCCTTTCTGG AATGACACGATCACTCCCGTTGAGTGGG TAGCAGCGGGAACAGTACTGCAG CACAGTGGCTAAGTTCTGC	197 1	CAAATTCGTATCTAGGGGAAT GCTGGGGTGGAACCTGGTTTGT TGTACTGCCCTGCTGATGGAT AGATAACTATACAACCTACTGCCTTC	2
CTTTGTCCCTGGGTGAAAATGC CATTATTACTTTTGGTACGCGCTGTGACA	1	AAGGGATTCTGATGTTGGTCACACT CCGAAGGAGCCTCGGTTGGCCC	211 1	CCTGCCGCGCCCCCGGGC CTGGTTTCACATGGTGGCTTAGA	1 12	TAAGGTGCATCTAGTGCAGATAGTGA TCCATCTTCCAGTGCAGTG	2	AACGGAATCCCAAAAGCAGCTG TGATATGTTTGATATATTAGGT	4 78
CATTGCACTTGTCTCG CCATTTGAAATCAGTGT	1 5	CAAAGTGCTTACAGTGCA	3 1	GTACAGTACTGTGATAGCTGAA AAGGAGCCTCGGTTGGCCCCGGATAGCC	2	ATACAACCTGCTAAGTG GTAAGTGCCTGCATGTATATG	1 2	AAGTGCCTGCATGTATATGC GGTAGTAGGTTGTGTGGTT	1 2
TGGCAGTGTCTTAGCTGGTTGTTG TATGTAACATGGTCCACTAACT	8	ATAGGTTATCCGTGTTGCCTTCG TGGCCATGCACCCGTGTCTCGGTGC GTAGGTTGCATAGTT TGAGGTAGTAGATTGTATAGTTG	1	ACATTCATTGCTGTCGGTGGGT TCCCTGTCCTCCAGGAGCT TGGAAGACTAGTGATTTTGTTG TGAGGTAGTAGATTTTATTGTTT	7	CAAAGTGCTTACAGTGCAGGTAGTG TTCCCTTTGTCATCCTATGC GTACTGCCCTGCTGATGGAT AGGGGTGCTATCTGTGATTGAGGG	1 88	ATACTGCCGGGTAATGATGGA TATTGCACTTGTCCCGGCCTGTTGA TCGTACCGTGAGTAATAGC TCTTTGGTTATCTAGCTGAT	10 1
ATTCAACGCTGTCGGTGAGT TACAGTAGTCTGCACATTGGTTAG	1	GTAGGTTGCATAGTT TGAGGTAGTAGATTGTATAGTTG	1 26	TGGAAGACTAGTGATTTTGTTG TGAGGTAGTAGATTGTATAGTTT	104	GTACTGCCCTGCTGATGGAT AGGGGTGCTATCTGTGATTGAGGG	2 17	TCGTACCGTGAGTAATAATGC TCTTTGGTTATCTAGCTGTAT	656 5
AACTGGCCTACAAAGTC GTAGTGTTTCCTACTTTATGGATG	2	CTCGGGGATCATCATGTCACGA TTCAAGTAATTCAGGATAG	237 42	TAATCCTTGCTATCTGGGTGCTTAGTG AATAATACATGGTTGATCTTTTT	3	TGGCTCCGTGTCTTCACTCCC TTTGTTCGTTCGGCTCGCGTGA	1 117 366	GCGCCGAAGGAGCCTCGGTTGGCCCCGG GGGTGCTATCTGTGATTGAGGGACA	1 1 42
CTTTCAGTCGGATGTTTGC ATCACATTGCCAGGGATTTCCAAC	21 3 5	CTACACTGCCGGCCTCTGGG AGCTTCTTTACAGTGTTGCCT	2 7 6	CAACAAATCACAGTCTGCCATAT TGTGACAGATTGATAACTGAAAG	16 235	AACATTCAACGCTGTCGGTGA AACACCCCAGCTAACCTTT	1	TCCGTCTCAGTTACTTTATAGCC TAACACTGTCTGGTAACGATGT TAGGTAGTTTCCTGTTGTTGG	3654 189
ATCACATTGCCAGGGATTTCCAAC CATTATTACTTTTGGTACGCGCT TGTGCGTGTGACAGCGGCTGA ATCGTACAGGGTCATCCACTT TGCCTGTCTACACTTGCTGT	1	TGTGCAAATCCATGCAAAACTGATT TGAGGTAGTAGATTGTATAG GTTGAGGTTAGTAGGTTGTATTGGT GTAGAACCGAATTTGTG	188 3	CGTACCGTGAGTAATAATGC ACACTGTCTGGTAACCATGT TGCAAATCCATGCAAACTGA AGTAGGTTGCATAGTTT	1	TAAAGTGCTGACAGTGC CTAGACTGAGGCTCCTTGAGGA GTTTTGTGTGCATGTGCATG TAGCACCATCTGAAATCGG	15 1	TAGGTAGTTTCCTGTTGTTGG GAGGTAGTAGGTTGCATA ATGAAGCGCTGCAAC TATGTGGGACGGTAAACCGCT	1 1
TGCCTGTCTACACTTGCTGT TGAGAACTGAATTCCATAGGC	10 2	GTAGAACCGAATTTGTG ATCACATTGCCAGGGATTACCA	1 2852	AGTAGGTTGCATAGTTT GTTGAAAAGGTGCAGGCCATACTGTGCTG	3	TAGCACCATCTGAAATCGG GTGAAATGTTTAGGACCAC	6	TATGTGGGACGGTAAACCGCT TCCATCTTCCAGTGCAGTG	1 36
TTCAAGTAATCCAGGATAG TATGGCACTGGTAGAATTCACTG	507 1	TAGTAGGTTGTGTGGTTT ATTGCACTTGTCCCGGC	1	AACACTGTCTGGTAAAGATGGCC AATCATTCACGGACAACACTTT	3 4	GTAAGTCTGGGTCTTCCACATGGGCA TAAAGTGCTGACAGTGCAGA	1 71	GTCCAGTTTTCCCAGGAAT AGGTTGCCCATGGTGTTCATTTTATTTA	73 1
CTATACAATCTATTGCCTTC ACCGTGGCTTTCGATTGTTACT	7 58	GTCCGGTGCGGAGAGCCGTTCGTCTTGGGA	5 8	TAAGGCACGCGGTGAATGC GTATGTGCCTTTGGACTACATCG	1 10	CCGCACTGTGGGTACTTGCTGC	44 1	TCAAGTAATCCAGGATAGGCTG AGAGGTAGTAGGTTGCATAGTTT	1 568
CGTGTCTTGTGTTGCAGCCGGA TCGTACCGTGAGTAATAATAGCGC CTGTAACCATGTTGTAGTGTG TAGCAGCGGGAACAGTACTGCAGTGAGT	3 2	CCGTCTCAGTTACTTTATAGCCA TGACCGATTTCTCCTGGTGTTC ACTGCAGTGCCAGCACTTCTT TATGCAAGGGCAAGCTCTCT	1 3	CTGTGCTGACGTTTGATTCTTGAGCAG GTTGGCCCCGGATAGCCGGGTCCCCGTCCG TGTGACAGATTGATAACTGAAA TAAACATCCCCGACTGGAAGC	3 1	TGAGCGCCTCGGCGACA TAGGAGGTTGTATAGTT CACTGAGATGGGAGTGGTGTAA ATACTGCCGGGTAATGA	2	AGAGGTAGTAGGTTGCATAGTTT TAGCAGCGGGAACAGTACTGCAGTG TGAGGTTTGGTGTACTGTGTGTG TCCCTGAGGAGCCCTTTGAG	1 129
CTGTAACCATGTTGTAGTGTG TAGCAGCGGGAACAGTACTGCAGTGAGT	1	ACTGCAGTGCCAGCACTTCTT TATGCAAGGGCAAGCTCTCT	2	TGTGACAGATTGATAACTGAAA TAAACATCCCCGACTGGAAGC	7	CACTGAGATGGGAGTGGTGAA ATACTGCCGGGTAATGA	5 1	I CGCCGAAGGAGCCTCGGTTGGCCCCGGATA	397 7
CAGTGTCTTAGCTGGTTGT CTAATACTGCCGGGTAATGAT	10	GGGGGTCCCCGGTGCTCGGATCT TTGTCTCCAGAGCATTCCA	1	GCAGTCCACGGGCATATACAC CCGTCCTGAGGTTGTTG	1	TGTAAACATCCTCGACTGG TCTCCCAACCCTTGTACCAG	57 3	TTAAGACTTGCAGTGATGTT AGGAGCTTACAATCTAGCTGG	1
TGAGCGCCTCGGCGACAGAG TCACAGTGAACCGGTCTCTT	2 5	TACCCTGTAGAACCGAATTT TCCTGTACTGAGCTGCCCC	1	TGCTATGCCAACATATTG AGGTAGTAGATTGTATAGTTGTGGGGTAGT	1 48	TAGCACCATCTGAAATC TCCCTGAGACCCTTTAACCTGTGA	4 418	TGGGTCTTTGCGGGCAAGATG CACATCTGCACATGCTTGGGG	1
TTCCTATGCATATACTT ATCACATTGCCAGGGATTACCACG CTGGCCCTCTCTGCCCTTCCGT	7 11 22	GTACAGTACTGTGATAACT AAACATCCCCGACTGGAAGC GTGCTTATAGTGCAGGTAG	1	AACATTCATTGCTGTCGGTGG AAACAAACATGGTGCACTTC TTTCCTCATATCCATTCAGGA	1	AAGGAGCTTACAATCTAGCTGGGG TGCCGGGTAATGATGG TATGCAAGGGCAAGCTCTCTTC	2 1 24	AATTCAGGATAGGTT CAGTCCACGGGCATATACACT TAAAGTGCTTATAGTGCAG	3 22
TAGGTAGTTTCCTGTTGTTG TCCCCCAGGTGTGATTCTGATTTG	22 74 4	GTGCTTATAGTGCAGGTAG CTCTACAACCTTAGGACTTGCA ATCACACAAAGGCAACTTTTGT	1 4	CATCTTCCAGTGCAGTGTTGGAT CTATACAATCTACTGTCTTTCC	1	AAGTAATTCAGGATAGGT TTGCACTTGTCCCGGCCT	24 2 1	GAGGTAGTAGTTGTGCTGTT CCCCCAGGTGTGATTCTGATTTGTTT	2
TGAACAGTGCCTTTCTGTGTAGG TGCCTGTCTACACTTGCTGTGC	4 2 412	AGATCAGAAGGTGACTGTGGCT TCACATTGCCAGGGATTAC	3 22	GCTGTTCGTGCAGGTAGT AACAAACATGGTGCACTTCTT	17 2 4	CAGTTATCACAGTGCTGATGCT CTTATCAGACTGATGTTG	25 2	TAGTAGGTTGTGTGGTT ATGTATGTGTGCATGTGCATGTG	4
CTGTACAACCTTCTAGCTTTCC	5 1	CTTTCAGTCGGATGTTTACAG	118	LCCTCCCACACCCAAGGCTTGC	47 7	ATACCCTGTAGAACCGAATTTGTG	1 370	LCTCGGGGATCATCATGTCACG	31 1
TAGTTAGCTGATTGC GCAGCACGTAAATATTGGCGT ACCCTGTAGAACCGAATTTGTG	4 50	AGAGTTGTCATGTGTCT TAGTAGGTTGTATGGT GCTCAGTTCAGCAGGAACAG TGAGGTAGTAGATTGT	2 2 1	ACAGGTGAGGTTCTTGGGAGC AATGGCGCCACTAGGGT CACTCTTTCCCTGTTGCACTAC TCCCTGTCCTCAGGAGCTC	1	TAAAGTGCTTATAGTGCAGGT ACCAATATTATTGTGCTGCTT AGAATCTCCAGGGGTAC GAAGTTGCCCATGTTATTTTTCGCTT	1	AAGCCCTTACCCCAAAAAGTA TGAGGTTGGTGTACTGTGTGTGA TGTAGTGTTTCTACTTTATGG GTAGTGTTTCCTACTTTATGGA	1505 880
CCCCCAGGTGTGATTCTGATTTGTT GAGGTAGTAGGTTGTATGGTTT	4	CATTCATTGCTGTCGGTGGGT	1	CTGACCTATGAATTGACAGC	5 50	GCTCAGTTCAGCAGGAAC	1	AGCTACATTGTCTGCT	661 1
CAGCAGCACACTGTGGTTTGTA TGCTGACCCCTAGTCCAGTGCTT	43 7	TAGGTTATCCGTGTTGCCTT CAGTGCAATGTTAAAAGGG	5 95	AATGACACGATCACTCCCGTTGA ACTGCCCCAGGTGCTGCTGG	17 30	GCAGCACATCATGGTTTACA AGGGGTGCTATCTGTGATTGAGGGA	3 48	TAGGTAGTTTCCTGTTGT TACCCTGTAGAACCGAATTTGTGT	1 33
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CACAGCTCCCATCTCAGAAC	72 7	TGTGACTGGTTGACCAGAGG GCCCTAAGGTGAATTTTTTGGGA	1	GACCGATTTCTCCTGGTGT TAATGCCCCTAAAAATCCTTATT	109	TTGGTCCCCTTCAACCAGCTGT	2 131	AGCGCCGAAGGAGCCTCGGTTGGCCCCGG TCTCTGGGCCTGTGTCTTAG	4
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CACGCGGGAACCGAGTCCAC	1 10	TCACAAGTCAGGTTCTTGGGAC	22	TGTAAACATCCTACACTCTCAGCT	1331 54	TCCCTGAGACCCTAA TAGGTAGTTTCCTGTTGTT AGCACATAATGGTTTGT	4	TGGCAGTGTATTGTTAGCTGGTT	3 8
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ATAGCTTATCAGACTGATGTTGACT CAGTTATCACAGTGCTGATGCTGTCCATT	5	AGGTTACCCGAGCAACTTTGCAT ATACCCTGTAGATCCGAATTTG	3	GTCTTACCCAGCAGTGTTTGG TATGCAAGGGCAAGCTCT	1	TGGAATGTAAAGAAGTATGTA ATGCAGTCCACGGGCATATACA	2	TATTGGCTGGCTCTGGGTC GTGTAATTAGCTGATTGT	1
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TGCACTGAGATGGGAGTGGTGTA TGTCAGTTTGTCAAATACCCC	2	TGAGGTAGTAGATTGTAT AAAGCTGGGTTGAGAGGGCGA	10 8	ACATTGCCAGGGATTTCCAA	3 1	CCCACGTGCGGTGCTTGAAGA CAACTAGACTGTGAGCTTCTAGA	1	CTGAGGAGCCCTTTGAGCCTG TCAGCTCCTATATGATGCCTT	1 3
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TAGGTTATCCGTGTTGCCTTCGCTT TATGGCTTTTCATTCCTATGTG	1 2 4	TAATACAACCTGCTAAGTGT TAATACTGTCTGGTAATG	1 6 1	GCAGCACGTAAATATTGGC ATAGCTTATCAGACTGATGTTGAC	6 22	TTGTGCTTGATCTAACC TGAGGTTGGTGTACTGTGTGAGTAT	1 3 5	TCAAAGTGCTTACAGTGCAGGTA CCCCTTCAACCAGCTGT	8
CAAAGTGCTGTTCGTGCAGGTAGTG  AAAGCTGGGTTGAGAGGGCGAAAA  AACATTCATTGTTGTCGGTGGGT	2 89	GTTGTGTGCATGTTCATGT TGAGGTAGTAGGTTGTATAGT AACATTCATTGCTGTCGGTGGGTTTGA	3054	AATATAACACAGATGGCCT TGTAAACATCCTCGACTGGAA TTGTGCAAATCTATGCAAA	1 117 1	CAGTTATCACAGTGCTGATGCTG TAACACTGTCTGGTAAAGATGGCC TCACAAGTCAGGTTCTTGGGA	145 13	GCCTGTCTACACTTGCTGTGCA TCAAAGTGCTTACAGTGCAG TAGCAGCACAGAAATATTGGCAT	29 7 40
GAGGGTTGGGTGGAGGCTCTC TGTATGCCCTAACCGCTCAGT	1	ACCTTGGCTCTAGACTGCTTA GAGGTAGGTTGTTATAGT	2	TGTGTGCATGTGCATGTGT TCGTGTCTTGTGTTGCAGCCG	1 13	GAACGGCTACTTCACAACACCAGGGC CCATCTGAAATCGGTT	1 2	TTTTGCAGTATGTTCCTGAATAC GGGGTGCTATCTGTGATTGAGGGACAT	11 6
AGTGCATGACAGAACTTGGG ATAGTTGTGTGTGGATGTGTATTT	1 5	CCACAGGGTAGAACCACGG TAGTAGATTGTATAGT	2	TCCGTCTCAGTTACTTTATAGCCA TGTTGTGAATCAGGC	3	CAACCCTAGGAGGGGGTGCCATTC TTTGAAATCAGTGTT	5	TCGGTCGATCGGTCGGTCGGT GCAGCAGCAATTCATGTTTT	1 2
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TGAGCGCCTCGGCGACAGAGCC TTCACAAAGCCCATACACTT	3 4	TTGTGCAAATCTATGCAAAACTGAT CAACAAGTCCCAGTCTGCCACA	2 5	ACTGCCGGGTAATGATGG	1	AGCTGGTGTTGTGAATCAGGC AAAAGCTGGGTTGAGAGGGGCGAAAAAG	228 1	CACAAGTCAGGTTCTTGGGA ACCACCGACCGTTGACTGTAC	1
AAGGGATTCTGATGTTGGT TTCCCTTTGTCATCCTATGCCT	1 1357	GTTACCATTACTGAGTTT ACTGTCTGGTAAAGATGG	1 2	TGCCTGTCTACACTTG CAGCGCCGAAGGAGCCTCGGTTGGCCCCGG AAGTGCTGACAGTGCAG	21 1	AACAGTCTACAGCCATGGTC TAACAGTCTCCAGTCACGGCCA	1 3	AGGTGCAGTGCTGCATCTCTGGTC AGAGGTTTTCTGGGTCTCTGTTTC	1
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ACTGCAGTGAGGGCACTTGTAG ACCCTGTAGATCCGAATTTGT GCTCTGACTAGGTTGCACTAC	2 11	ACAGTAGTCTGCACATTGG AGCTACATTGTCTGCTGGGTTTCA	16 7	TCCGGTTCTCAGGGCTCCACCT TAGCAGCACATCATGGTTTA CCCTGAGACCCTTTAACCTGT	1 211	TCCCTGTCCTCCAGGAGCTCACGTAT TCAAGAGCAATAACGAAAAAT TGCGGGGCTAGGGCTAA	3 10	CCCCTTCAACCAGCTG CCTGTCTACACTTGCTGTGCAG	1
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ATTTGAAATCAGGTAGTT TATTGCACATTACTAAGTTGC	10 264	TCTCGCTGGCTGTTCCTTT CTCCTGACTCCAGGTCCTGTG	1 18	ACTGTGCGTGTGACAGCGGCTGA GTAAACATCCTACACTCAGCT	9	AGAGGTAGTAGTGCAGAT AGAGGTAGTAGGTTGCATAGTTTT ACCACCGACCGTTGACTGTACC	58 2	CCCAGTGTTTAGACTACCTGTTCAGGAC CAGTTATCACAGTGCTGATGC	1 25
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Manuscript	AGAGGTATAGCGCATGGGA	2	TGAAGAGAGGTTATCCTTTGTGTGT	9 7	CAGTGCAATAGTATTGTCAA	1 29	TTCAAGTAATTCAGGATAGG		ACCATTTGAAATCAGTGT	17 9
Second content	TGAGGTAGGAGGTTGTATAGTT	593	GCAAAGCACAGGGCCTGCAGAGAGGT	55	CAAAGTGCTTACAGTGCAGGTAG		CTTTCAGTCAGATGTTTGCTGCT	2	CTGTTGCCACTAACCTCAAC	1
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Section   1	AGGGTTGGGTGGAGGCTCTC	1	CTTTCAGTCGGATGTTTGCA	46	ACATTCAACGCTGTCGGTGAGTTT	8	TAGCAGCACGTAAATATTG	6	TCAAAGTGCTTACAGTGCAGG	8
Control of the Cont	AGCAGCATTGTACAGGGCTATCAAA CAAAGTGCTTACAGTGCAGG		TGAGGTAGTAGGTTGTAT GAAAGGTGCCATACTATGTATA	121	TCGTACCGTGAGTAATAA TTGTGGTGGCTACTGGGC	1	TCCCTGTCCTCCAGGAGCTCA	8	ACAAGTCAGGTTCTTGGGA GAAGTTGTTCGTGGTGGATTCG	15
Control of the Cont	AGCTGGTGTTGTGAATCAGGCCGA TTCCTCATATCCATTCAGGAGT	184 1	AGCTGGTGTTGTGAATCAGGCCGT GGTCAAGAGGCGCCTGGGAAC	667 50	CTGCAGTGAGGGCACTTGTAG AATCCTTGGAACCTAGGTGTG	1 42	CTGTGCAAATCCATGCAAAACTGA TGTGTGCATGTGCATGTGTGT	1	TAAACATCCTACACTCTCAGC TGTAGGGATGGAAGCCATGA	2
April	GTTCACAGTGGCTAAGTTCTGC AGAGCTTAGCTGATTGGTGA	2	TAATGCCCCTAAAAATCCTTA TCAAGCAGCATTGTACAGGGCTATGA	1	GTGAAATGTTTAGGACCACT ACTCTTTCCCTGTTGCACTACT	6	CCGTGAGTAATAATGCG CAGTGTTTAGACTACCTGTTCAGGACTC	2 1	CTTGGATGCTAAGATGGGG CAAGTAATTCAGGATAGGTT	2 4
March   Marc	ATAGTTGTGTGTGGATGTGTGT	29	CTAATACTGCCGGGTAATGATGGA	18	TACAGTAGTCTGCACATTGGTTA	9	LCCCTGAGGAGCCCTTTGAGCCT	2	AACCCGTAGATCCGATC	1 1 2
March   Marc	CTGACCTATGAATTGACAGCCAGTACTCT TAAGTCACTAGTGGTTCCGTTTAGT	1 18	AAAGCTGGGTTGAGAGGGCGAA TCCTGTACTGAGCTGCCC	2 2	TAATACTGTCTGGTAATGCC TGTGCAAATCCATGCAAAACTGAC		AATGCCCCTAAAAATCCTTA TGTGCAAATCCATGCAAAACTGAT	1 63	CAGCCCATCCCACTCAGTCGTGCCC CAAAGTGCTTACAGTGCAGGTAGTGA	1 3
Telephone	AACAATATCCTGGTGCTGAGT	1 11	CAATGTTAAAAGGGCAT ACTGCCCTAAGTGCTCCTTCT	1 2	CAAGCTCGTTTCTATGGGTCTG	4	GAATGTTGCTCGGTGAAC	95	GTACTGTGATAGCTGAA	1
Committee   1	TAAACATCCTACACTCAGCT	1	CTGTGGGCCACCTAGTCACCA	42 1	TGTGCAAATCCATGCAAAACTGA	1 4075	TGGCAGTGTCTTAGCTGGTTGTT	7 875	AGGTGCAGTGCTGCATCTCTG	3
Temporal processor	GCAGTGTCTTAGCTGGTTG GCAGTGTCTTAGCTGGTTG		TGTTGACCCCTAGTCCAGTGCT TGTTGAAAAGGTGCAGGCCATACTGTG	3	CATTGCCAGGGATTACCA	15 2	AGAGGTAGTAGGTTGCATAGTT GGTAGTAGTTTGTGCTGTTG	1	AACATTCATTGCTGTCGGTGGGTTTG	6
Temporal processor	AATCCTTGCTATCTGGGTGCTTAGTG TTGTGCTTGATCTAACCATGTGG	13	TTCCTACTTTATGGATG	1	CGTGTATTTGACAAGCTGAGTTGGAC AAAATGGGTTCCTAGGA	2	CTCCTGACTCCAGGTCCTG CAGGTCGTCTTGCAGGGCTTC		TTGTGCTTGATCTAACCATGTGC AACATTCAACGCTGTCGG	16
Committed	GTGCTTATAGTGCAGGTAGT TTTTTGCGGTCTGGGCTTGCTGT	1	TAGCAGCACATCATGGTTTACATACTAC CTGTGCGTGTGACAGCGGCTGAT	5	TGTGCAAATCTATGCAAAACTGAT TTAATGCTAATTGTGATAGGGGTTTT	12	ACAACTGGCCTGAGGAGC TTAATGCTAATTGTGATAGGGG	1 9	AGTTCTTCAGTGGCAAGCTTTAT TGATATGTTTGATATATTAGG	8 14
STATE   STAT	TAATACTGCCGGGTAATGATGGA	4379	ATGGTTTACCGTCCCACATACA CTGGACTTGGAGTCAGAAG	1	CTCGGTGCTGGTGGAGCAGTGAGCACG	3 1	AACATTCAACGCTGTCGGTGAGTT	1 220	GACCGATTTCTCCTGGTGTTCAG	1 1144
STATE   Content   Conten	TATTGCACTTGTCCCGGCCT AATGACACGATCACTCCCGTTGAGTGGGCA	1	ACCITGGCTCTAGACTGCTTAC TTCCCTTTGTCATCCTATGCCTG	160	AGGGACTTTCAGGGGCAGCTGTG TGAGGTAGTAGGTTGTA	17	TAGTTGTGTGTGCATGTTCATGTCT TGAGGTAGTAGGTTGTG	9	AATACTGCCTGGTAATGAT CCTGTAGAACCGAATTTGTG	1
STATE   STAT	TAGCACCATTTGAAATCAGTGTTTT GGATTCCTGGAAATACTGTTCT	27 7	TAGCAGCACATAATGGTTTGTGGA	4	ATATAATACAACCTGCTAAG GCTGGTGTTGTGAATCAGGCCG	1	CAGTAGTCTGCACATTGGTTAG  AGTTTTGCAGGTTTGCATCCAGCTGT		ACTGTGCGTGTGACAGCGGCT	1
TREATMEND   1   SOLVENDE CONTROL   1   TOURN ADDRESS   1   TOURN	CATCTTTGCCGGTGACAGCA TATACATACACGCACACATAAG	, 7 2	AATGGCGCCACTAGGGTTG	24	CAAAGAATTCTCCTTTTGGGC	3	TCTCCCAACCCTTGTACCAGTGC	54 1	TTGGTCCCCTTCAACCAGCTG	5
Model   Mode	TACTGTCTGGTAATGCCG TTCACAAAGCCCATACACTTTCA		GGACTTGGAGTCAGAAGGC GCTACTTCACAACACCAGGG	1	TGAGATGAAGCACTGTAGCTCA ACCAGGAGGCTGAGGTCCCTTA	145 1	ATAGTTGTGTGGGATGTGTGTATT TGTGACTGGTTGACCAGAGGGG	15 23	AAAGTGCTTACAGTGCAGGTAG CAAGCTCGTGTCTGTGGGT	2 9
Security	ATCATACACGGTTGACCTATT CTATACAGTCTACTGTCTTT		TGAGGTAGTAGGTTGTATAGTTTTAGGG ATCACATTGCCAGGGATTTCCAA		GGTCAAGAGGCGCCTGGGAACT AGTTTTCCCAGGAATCCCT	42 34	AAACCGTTACCATTACTGAGTTTAGT TACGTAGATTGGTACCTATCATG	40 1	TGTAAACATCCTTGA GTTTCATGTTGTTGGGA	1
TRACEMENT   1   SEGUIDACIONAMENTE   2   CONTINUENCE   3   CONTINUENCE   1   CONTINUENCE	CGTATGTGCCTTTGGACTGCAAGCT	5	TCCAGCATCAGTGATTTTGT	12	TGGCAGTGTCTTAGCTGGTTGT	2253	TACCCTGTAGAACCGAATTTGT TACCCTGTAGATCCGAATTTGTGTA	348	TGTAGTGTTTCCTACTTTATGGAT	15
TRANSPERSON   1   TRANSPERSON   2   TRANSPERSON   2   TRANSPERSON   2   TRANSPERSON   2   TRANSPERSON   3   TRANSPERSO	TACAGTACTGTGATAACTG	1 7	TAGCAGCACATAATGGTTT	2	CGTACCGTGAGTAATAATG	28 2	TATGGCACTGGTAGAATTCACT	7	CAGTAGTCTGCACATTGG	1 2
MACHIGUE   SALE   MACHIGUE	ACGGAATCCCAAAAGCAGCTGT	1 3	AGCAGCATTGTACAGGGCT		CCTCTGGGCCCTTCCTCCAGT	60 2	ATTTGAAATCAGTGT	1 233	TTATCAGACTGATGTTGA	3 1
MACHIGUE   SALE   MACHIGUE	CGAATCATTATTTGCTGCT ACAGTAGTCTGCACATTG	2 7	TACTGCCTGGTAATGATGAC TAAAGTGCTTATAGTGCAGGTAGTG	2	ACTGCATTACGAGCACTTAAAG ACCTGGCATACAATGTAGATTTCTGT	3	TTTCAGTCGGATGTTTGCA ATGAGGTAGATGATGTATAG		AACATTCAACCTGTCGGTGAGTTT ATACTGCATCAGGAACTGACTGGAT	1
## AMACHTINICHEMENT    1	TCAGGCTCAGTCCCCTCCCGATA	19	ATCACATTGCCAGGGATTT	356 4	CCATCCCACTCAGTCGTGCC	1 1	ATACTGCCTGGTAATGATG	7	CAAAACATGAAGCGCTGCA	5 1
CAMITECTRICRETERIOR   3	ACAAGCTTGTGTCTATAGGT	1	GCAGCATTGTACAGGGCTATC	1 7	AGTTTTGTGTGCATGTGCATGTGTGT	1 8	AGAGGTTTTCTGGGTCTCTGTT	1 3	GTCAAGAGGCGCCTGGGAAC	8 2
TRECHEMENT   1   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATICA   3   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATI	CCAATATTGGCTGTGCTGCT	2	TCAGTTATCACAGTGCTGATGCTG	1	TCAGGCTCAGTCCCCTCCCG	1	CCAATATTGGCTGTGCTGCTCC		TGTCTTGCAGGCCGTCA	1 4
TRECHEMENT   1   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATICA   3   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATICA   3   CACAGERIAMATICA   CACAGERIAMATI	AGGTTACCCGAGCAACTTTGCA AAATCACATTGCCAGGGATTACCAC	1	TAGCACCATTTGAAATCGGTTA TAGTCTGCACATTGGTT	143 2	TTCAAGTAATCCAGGATAGGCTGT GTCTGCACATTGGTTA	20	GGCAGCGCCGAAGGAGCCTCGGTTGGCC AAGTAATTCAGGATAGGTT	1	ACCGTGGCTTTCGATTGTTA GGCAGAGGAGGGCTGTTCTTCCCTT	1
GTMARM   1	TGTAGAACCGAATTTGTG	1	TAGTAGGTTGCATAGTTT	2	AGCGCCGAAGGAGCCTCGGTTGGCC	1	TAGCAGCACGTAAATATTGGCGT	1 378	TCAGTGCATGACAGAA	1 2
International Continues	GTTTGATATATTAGGTT	1	GACCGATTTCTCCTGGTGTTC TCAGGCTCAGTCCCCTCCCGAT	2 193	GAGGTTGGTGTACTGTGTG TCTCACACAGAAATCGCACCCGTCA	2 7	TGAGGTAGTAGGTTGTGTGTTTCA	12	GTGAGTTCCAGGACAGCCAGGGCTATACA TGAAGCACTGTAGCTC	1 5
TRIGHT   T	TATTGCACTTGTCCCGGC AAGAGGCGCCTGGGAAC	1	TTCAGTGATGATTAGCTTCTGACTTT AAGAGGTATAGCGCATGGGAAG	1 9	CAGTTTTCCCAGGAATCC AACATTCATTGTTGTCGGTG	4 2	CITATCAGACTGATGTTGA TTCACAGTGGCTAAGTTCTGC	6	GAGGTAGTAGGTTGCATAGTT ATGCAGTCCACGGGCATATACAC	18 1
Trigle-Gride   Committed   C	TGAGGTAGTAAGTTGTATTGTT TAGCACCATTTGAAATCA	80 2	TAGCACCATTTGAAATCG	1	AGCTGCCAGTTGAAGAA	75 1	AGCTGGTGTTGTGAATCAGGCC	133	TTTCAGTCAGATGTTTGCT TGAGGTAGTAGGTTGTATAGTTT	
TRACECTATICACEPTICT   1   TIGARAGA/CAPTITENTITIES   1   MACACATTICACTURE   MACACATTICACTURE   1   MACACATTICACTURE   1   MACACATTICACTURE   MACACATTICAC	TGTGACTGGTTGACCAGAGGG	9	GCTGGTTTCATATGGTGGTTTAGATTTAAA	1	CAGTTGCTAGCTGCACTACCCT	1 2741	CTTTTTGCGGTCTGGGCTTG	3	GCAGTGCAATGATGAAAGGGC	12
ACCIDENTIAGAMACTERT   1   GRAMATTERGACCAMEN   3   TRECTORGATACTER   1   TRECALCATE CONTROL   1	TGACCCCTAGTCCAGTGCTTGT	1 4	TGGAAGACTAGTGATTTTGTTGTTG	1 5	TAGCACCATTTGAAATCGG	2	CTGAGATGAAGCACTGTAGCT		CATCGGGAATGTCGTGTCCGC	
ACCIDENTIAGAMACTERT   1   GRAMATTERGACCAMEN   3   TRECTORGATACTER   1   TRECALCATE CONTROL   1	CACAGTGGCTAAGTTCTG AGGGCCCCCCCTCAATCCTGT	1	AACATTCATTGCTGTCGGTG TCCCTGAGGAGCCCTTT	14 1	TCACAAGTCAGGTTCTTGGG TTTTTCATTATTGCTCCTGACC	2 5	TCCCTGAGACCCTAACTTGTGA CTGTAGAACCGAATTTGTG	8378 1	TGGTTTACCGTCCCACATACAT GCCTGTCTACACTTGCTGTGC	7
TRACKERTEMANTCO	CAACGACATCAAACCACCTGAT AGCTGCCAGTTGAAGAACTGTT	1	GTGAAATGTTTAGGACCACTAG	1 95	ATCTTTGCCGGTGACAGCA	4	TATTGGGAACATTTTGCATA TTGGATGTTGGCCTAGTTCTGTG	1	TGGAAGACTAGTGATTTTGTTGTT	7
THISGEARGEMACT   1	TAGCACCATCTGAAATCG		ATTGTGTCAATATGCGATGATGT	2	TGACCTATGAATTGACAGCCAGT		CTGTGCGTGTGACAGCGGCTG	27	AGCAGCATTGTACAGGGCTATGAA	227
AAACGTTGCATTAGATTAGATTAGATTAGATTAGATTAG	TTTGGCAATGGTAGAACT	1	CCAGGAGGCTGAGGTCCCTTA	1 28	CCAGTTTTCCCAGGAATCC	4	AGGGGTGCTATCTGTGATTGAG	9	ACATGGTGCACTTCTTT CCGTCCTGAGGTTGTTGAG	1
AGTHICTIGRECATION 1 7 TIGGACTITIAGGICACTOR 1 1 TIGGACAGTITAGGICTAGA 1 1 COLORICOGO CITTORIGAGT 1 1 TIGGACAGTITAGTACAC 4 8 1 COLORICOGO CITTORIGAGT 1 1 TIGGACAGTITAGTACAC 4 8 1 COLORICOGO CITTORIGAGT 1 1 TIGCACAGGICAGACACACAGGAC 4 8 1 COLORICOGO CITTORIGAGT 1 1 TIGCACAGGICAGACACACAGGAC 4 8 1 COLORICOGO CITTORIGAGT 1 1 TIGCACAGGICAGACACACAGACACACAGACACACAGACACAGACACACAGACACAGACACACAGACACACAGACACACAGACACACAGAC	AAGAGCAATAACGAAAAATGTT		AAACCGTTACCATTACTGAGTTTAGTAAT	1 2	AAACATTCGCGGTGCACTTCTTT	17	ACTGCATTACGAGCACTTAAA	4	TTCAAGTAATCCAGGATAGGCTG	
CAMTRIGATICITICISCITICS   266   CAMTRIGAMICATICITY   2   GATTCCTGGAMARCTITTY   1   ACASTICACAGG   4   ACASTICACAGG   3   ACTIONICISCIC   3   GATCAGTICACAGG   1   ACASTICACAGG   1   ACASTICACAGG   1   ACASTICACAGG   1   ACTIONICISCIC   1   ACASTICACAGG   1   ACTIONICISCIC   1   ACASTICACAGG   1   ACTIONICISCIC   1   ACTIONICISCIC   1   ACASTICACAGG   1   ACTIONICISCIC   1   ACASTICACAGG   1   ACTIONICISCIC   1   ACASTICACAGG   ACASTICACAGG   1	TTTTTATTCCTATGTGA AGTTTTGTGTGCATGTGCATGT	17	ATTGGGAACATTTTGCATAAAT TTGGACTGTGAGGTGACTCTTGGT	4	TCAAAGTGCTTACAGTGCAGGTAG	51	ATCCCTGAGTGTATGTG		AATGGCGCCACTAGGG TTGTGACAGATTGATAACTGAAA	1
AGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	CTAGCACCATTTGAAATCA	1	CCATTTGAAATCAGTGTTT	2	GATTCCTGGAAATACTGTTCT	4	GGTAGTAGGTTGTATGGTT	6 48	ATCACATTGCCAGGG	4
CAMAGICACRAGRACTICACAGAGA   CAMAGIGETCHARGIGAGAGAGAT   CAMAGIGETCHARGIGAGAGAGAT   CAMAGIGATCHARGIGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	CACAGGGTAGAACCACGGAC TGGCAGTGTATTGTTAGC	1	AGTIGTGTGTGCATGTTCATGTCT TAGTGTTTCCTACTTTATG	29	GATAGAAGTCAGTGCACTACAGAACTTTGT	1	CCCATCCCACTCAGTCGTGCCC CCTGTAGAACCGAATTTGT	1	GGAGTATTGTTTCCACTGCCTGG	1
CCCTAGGGGATTHTTGGGA   1   AGGTTGGATTGCTCCATTCC   3   AACCCTGTAGATTGTTTGGT   28   TCCGTCTCATTACTTTAT   2   AAAGCTGGGTTAGAGGGCGAAA   107   TATATGCTATAGTGGATGGGGTT   18   TTAATGCTATAGTGGAGGGGTT   18   TTAATGCTATAGTGGAGGGCTTGGGAA   2   CTATAGTGCTAGTGGG   18   TATATGCTATAGTGATAGGGGATAC   1   TATATGCTATAGTGGAGGGCTTGGGTAGACGGCCTTGGGAAA   2   CTATAGTGCTAGTGGGGAGGCGCTGGGAAA   2   CTATAGTGCTAGTGGGGAGGGGGAGACGCGCTGGGAAA   2   CTATAGTGCTAGAGGGCTAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	TGAGGTAGTAGGTTGTATAGTTTTA	7 1	ATCACTAACTCCACTGCCATC		TGGTGTCCTCAAATTGAAAGCCAAGG	1	CCCAACCCTTGTACCAGTGC		TAGCACCATCTGAAATCGGT TITTCCCTGAGGAGCCCTTTGAGCCTG	
TATGECCTTIGGACTICATICGT	CCCTAAGGTGAATTTTTTGGGAA	1	AGGTTGGGATTTGTCGCAATGC	3	ACCCTGTAGATCCGAATTTGTGT	28	TCCGTCTCAGTTACTTTAT	2	AAAAGCTGGGTTGAGAGGGCGAAA	107
TRACATTICCAGGGATACCGG   TRACATCGGGAACCGGAACCGGAACCGGAACGGAACCGGAACGGAACGGAACGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACGAACG	TATGTGCCTTTGGACTACATCGTG		ACTGCTGAGCTAGCACTTCCC		TATTGCTTAAGAATACGCGTAG	1	GTCAAGAGGCGCCTGGGAACT	3	TCGATCGGTCGGTCAGT	18 5
GGARGAGCTCGGTTGGCCCCGAGA   CACATTGCCAGGGATTTCCACT   1   CGGATCCGTCTGAGCTTGGCT   1   CAGTGCACGTTGTTCCACT   2   ACCCCCTCGAGGACAGAGCCGG   1   TCGTGACATTGCTTCCTCCT   1   TCGTGACATTGCTGCTCCT   1   TCGTGACATTGCTGCTCCTCAGAGT   1   TCGTGACATTGCTGCTCCTCAGGAC   1   TCGTGACGTTGTTGCCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCTCCGAGAT   1   TCGTGACGTTGTTGCCTCCTCGTGGCC   1   TCGTGACGTTGTTGCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCCTCGAGAT   1   TCGTGACGTTGTTGCCCCTCCGAGAT   1   TCGTGACGTTGTTGCCCCGGCGACTTG   1   TCGTGACGTTGTTGCCCCGGGCATTGCC   1   TCGTGACGTTGCACTCCCCGGGCATTGCC   1   TCGTGACGTGCTGCCCCCCTCGAGAT   1   TCGTGACGTGCACCCACCTTG   1   TCGTGACGTGCACCCACCTTGCACCCACCACCACCACCACCACCACCACCACCACCACCA	TCACATTGCCAGGGATTACCACG TGAAACATACACGGGAAACCTC	2	TCCCTGTCCTCCAGGAGCTCACG AATCCTTTGTCCCTGGGTGAAAATGCT	7 9	AACATTCAACGCTGTCGGTGAG CAGCATTGTACAGGGCTATC	287	TAGCAGCACAGAAATATTGGCA CAGCATTGTACAGGGCTATG	459	GCAGCACATCATGGTTTAC	
STCCAGTTTTCCCAGGANTCCCT   15921   ANTCCATTGTTGGGGGTGTT   1   GGTCTTTTACAGTGCTTGCCTTGTTGC   1   CACCGTGAAACCGACCTGC   1474	TTCTAGCACTTAGCAGGTTGTATTATCATT		TCACATTGCCAGGGATTTCCAACT TCAGTTATCACAGTGCTGATGCT	1 43	CAGGCCATACTGTGCTGCCTCA	1 24	CAGTGCACGTGTCTCCA TCAGGGCAGTGATGTTGCCCCTCCGAAGAT	1	GCAGTCCACGGGCATATA	1
CAMAGACAGGGCTECAGAGA 1 2 TCCAGGGAGCTCAAGTC 1 TCCTCTTACAGCTGCCCGAG 3 5 TTACAGTGCAGGTGCCCC 3 1 ACCTCTATAGCTTTC 3 1 ACCTCTTACAGCGATTTC 3 1 ACCTCTTACAGCGATTC 3 1 ACCTCTTACAGCGCATTTC 3 1 ACCTCCTTACAGCGCATTTC 3 1 ACCTCCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTC 4 1 ACCTCTTACAGCGCATTTC 4 1 ACCTCTTACAGCGCATTC 4 1 ACC	GTCCAGTTTTCCCAGGAATCCCT	1 15921	AATCCTTGCTATCTGGGTGCTT	8	GGCTTCTTTACAGTGCTGCCTTGTTGC	7	CACCCGTAGAACCGACCTTG	19	GTCCAGTTTTCCCAGGAATCCC	3 1474
Traceatriccarges   Traceatricc	CAAAGCACAGGGCCTGCAGAGA		TCGAGGAGCTCACAGTC		TCCTGTACTGAGCTGCCCCGAG		CTTACAGTGCAGGTAG	1	ACATTCATTGCTGTCGGTGGGTTT	
TAGACAAAAATATTGGATGGAGAAA   TAGACAAATATTGGTT   206   TGTGCAATCCATGCA   2   TGTATATTTTGATTATTAGGTT   206   TGTGCAATCCATCCA   2   TGATATTTTGATTATTAGGTT   3   TATCCTGGTAATCATTCAGGC   2   TGATATCTTTTCAAGTTT   1   ACAGGTATTAGGCAGAGA   2   TGATATCTTTCAAGTTT   1   ACAGGTATTAGCGCATGGGAGA   2   TGATATCTTTCAAGTTT   1   ACAGGTATTAGCGCATGGGAGAG   2   TGATATCTTTCAAGTTT   1   ACAGGTATTAGCGCATGGGAGAG   2   TGATATCTTTCAAGTTT   1   ACAGGTATTAGCCATTGGGAGAGAGTCC   1   TGATATCTTCAAGTTT   1   ACAGGTATTAGCGCATGGGAGAGTC   1   ACCTATTAGAGTTCAAGTTT   1   ACAGGTATTAGCCATTGGAGAGAGTCC   1   ACCTATTAGAGTTCAA	CTGGTTTCACATGGTGGCTTAGATT	7	ATCACATTGCCAGGGA	6	TGAGGTAGTAGATTG	1	CATCGGGAATGTCGTGTCCGCC	11	TTAGCAGGTTGTATTATCATT	1 4
TATGECCTTIGGACTACATCGTGAAGCCA  1 ACCCCTATATGATGCCTTCT  1 CAGGGCAAGTGCATTC  1 CAGGGCAAGTGCATTC  1 CAGGGCAAGTGCATTC  1 CAGGGCAAGTGCATTC  1 CAGGGCAAGTGCATTC  1 CAGGGCAAGTGCATCATC  1 CAGGGCAAGTGCATCATC  1 CAGGGCAAGTGCATCAGCAT  1 CAGGGCAAGTGCATCAGCAT  1 TAACAGTTACCAGCATGCCC  2 GGGTCCGGGGAGAGCCGTGCTGCC  1 ATCCCTGGACCAGTGC  1 ATCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCCTGGACCAGTGCC  1 ATCCCTGGACCAGTGCC  1 ATCCCCTGGACCAGTGCC  1 ATCCCCTGGACCAGTGCC  1 ATCCCCTGGACCAGCCC  1 ATCCCCTGGACCAGTGCC  1 ATCCCCTTGACCAGTGCC  1 AGGCCCGCAGGACCACCAGTGCC  1 AGGCCCTGGACCACCTGCC  1 AGGCCCTGGACCACCTGCC  1 AGGCCCTGGACCACCTGCC  1 AGGCCCCTGGACCACCCCC  1 AGGCCCTGCACAGTCCC  1 AGGCCCTGCACAGTCCC  1 AGGCCCTGCACAGTCCC  1 AGGCCCTGCACAGTCCC  1 AGGCCCTGCACAGTCCC  1 AGGCCCTGCACAGTCCCC  1 AGGCCCTGCACAGTCCCCC  1 AGGCCCTGCACAGTCCCCCC  1 AGGCCCTCCTCCCCCCCCCCC  2 ACCCATAGCACCCCCTTC  1 AGGCCCTCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TAGCAGCACAGAAATATTGGCATGGGGAAG TGAGGTAGGAGGTTGTATAGT	1 309	CCAACAATATCCTGGTGCTGA ATACTGCCTGGTAATGAT	2	GCTGGTGTTGTGAATCAGGCC ATTCCTGGAAATACTGTTC	2	TGATATGTTTGATATATTAGGTT GTAGTAGTTTGTACAGTTT	206 1	TGTGCAAATCCATGCA AGAGGTATAGCGCATGGGAAG	2
ATCACTRACTCCACTIGCAT 1 CAGGAGAGAGAGTGCTTCAAAGCC 699 ATTATGCTGAAACTCCCTCGGTGGGA 1 TATAACGTCTACACGCCATGGTGC 4 TGTAAACACTCCTACACTC 3 GCGCCGAAGGAGCCTCGTTGGGA 1 ATCCTGGGAACCTGCTCCCC 1 CAGGAGGAGCCCTTCTGGTGGAACCTTCTTGGATTGAAGTT 6 TTACAGTATCACGCCATGGATC 1 ATCCTGGGAACCTGCTTGGATTGAAGTT 6 TTACAGTATCACGCATGGATC 1 ATCCTGGAACCTGCTGTGCATCACCACC 1 ACTCCAGTGATTCACGAGACCACCTGTGATT 6 TTACAGTATCACGAAGAGCC 2 CAGGATCACTGTGCTGT 2 CAGGATCACTGTGCTGTGACCACCACCACC 1 ACTCCACTGTAACGAGCCACCTGTGCACCACCACCACC 1 ACTCCACTGTAACGAGCCACCTGTGCACCACCACCACCACCACCACCACCACCACCACCACCAC	GAGGGACTITCAGGGGCAGCTGTGT TATGTGCCTTTGGACTACATCGTGAACGCA	3 1	TAGCACCATCTGAAATCGGTT AGCTCCTATATGATGCCTTTCT	1	TGAGGTAGTAGGTTGTATGGTTTAGAGTT AGGTAGTAGGTTGCATAGTT	2 5	CAAAACATGAAGCGCTGCAACA TCACAGTGGCTAAGTTC	30 1	TCTAGGTATGGTCCCAGGGATCC ACCGATTTCTCCTGGTGTTC	1 1
TAGISTITICCIAGNICATIC  AGAINTICCACTOR  CARTIFICATION  CARTIFICACITIATICATIC  ACTIVITICACAGAGATICCT  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGATICCT  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCC  ACTIVITICACAGAGAGCCC  ACTIVITICACAGAGAGCCC  ACTIVITICACAGAGAGCCCC  ACTIVITICACAGAGCCCCC  ACTIVITICACAGAGCCCCCC  ACTIVITICACAGAGCCCCCCCC  ACTIVITICACAGAGCCCCCCCCC  ACTIVITICACAGAGCCCCCCCCCCCCC  ACTIVITICACAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TGAGGTAGGAGGTTGTATAG	61	CATCGGGAATGTCGTGTCCGCCC	2	GGGTCCGGTGCGGAGAGCCGTTCGTCTTGG		CTGGTTTCACATGGTGGCTTAGATTT	6	TGTCACTCGGCTCGGCCCACTACC	1
TRANGFICCHTMATGEAGGEAGTGT  18 CTATACTECCTGGTAATCATGA  2 TITTGGCCTCTTCAACCAG  6 CAGGGTAGTAGGTTGATATGTT  6 TITGGCTTAACTAGCTGTG  1261  75  TITTGCGATGTTACTATAGTT  2 TOCAGTGCATGTAGTGGC  2 TOCAGTGCATGTTCCTAATTGTGC  2 TOCAGTGCATGTTCCTAATTGTGC  1 TOCAGTGCATGTTCCTAATTGTGC  1 TOCAGTGCATGTTCCTAATTGTGC  1 TOCAGTGCTTAGGTTTAGGTTT  1 ACACTGCCCGCGTGTGGCTCT  1 TOCAGTGCTTGGGTGCATTCT  1 TOCAGTGCTTGGGTGATGGGTGGCTTT  1 TOCAGTATTCAGGATAGGGTGGATGGGGGGGGGGGGGGGG	TAGTGTTTCCTACTTTATGGATG	2	ACTGTCTGGTAACGATGT		TGCTATGCCAACATATTGCCATCT		TATGTGTGTACATGTACAT	1	TGTAAACATCCTACACTCAGCTGT	4
TITTIGCASTICTICTATATGTGCT 2 TCCAGTGCTCGATCTCTGG 3 AACAACTGGTGCACTTCT 1 TCCTGGAAATACTGTTCTT 1 ACACTGCCGGCCTTGGG 3 TTTIGCAGTATGTGCTCTATGTCTT 1 TTTIGCAGTATGTGCAGTCTCTT 1 TTTIGCAGTATGTGCAGTCTGGAGTCAGAAGGCC 1 TAGGTAGTGAGTGGTGAGTGCAGTCT 9 ACTCAGTTATTTTAGAGTGCTGGGAGTCAGAAGGCC 1 TAGGTAGATGAGGGCGCTTT 1 TCCAGTAGATCAGGGAGCAGGAGGCCTGGGGAGGCCTGGGGAGGCCTGGGGAGGCCTGGGAGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	TAAAGTGCTTATAGTGCAGGTAGTGT CAGTGCAATGATGAAAGGGC	18 2	CTAATACTGCCTGGTAATGATGA ACCCGTAGATCCGAACTTGTGC	2 2	TTTGGTCCCCTTCAACCAGC AGAACGGCTACTTCACAACACCAGGGC	6	GAGGTAGTAGGTTGTATAGTT AGAGGCTGGCCGTGATGAAT		TTGTGCTTGATCTAACCATGTG TTTGGTCCCCTTCAACCAGCTGT	1261 75
TGTTHAGACTACCTGTTC 1 GAATGTIGCTCGGTGAACCCCTTT 2 TGTAGACTCGAATTIGTGT 1 AACGGCCTACAAAGTCCCA 36 AGGCAGTGTAATTAGACT 37 AGGCAGTGTAATTAGACT 37 AGGCAGTGTAATTAGACT 37 AGGCAGTGTAATTAGACT 38 AGAGCGTGGAGAACCCTGTAGATTGCAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGCAGAGACCCTGCAGTAGACTGCCAT 1 ACGACTAGAGAGCCTCGAACAATTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGAGACCAGGAACTATTAGAGTGTAGAGTGTAGAGTGTAGAGTGTAGAGAGACCAGGAACTATTAGAGTGTAGAGTGTAGAGTGTAGAGAGACCAGGAACTATTAGAGTTAGAGTGTAGAGTGTAGAGTGTAGAGAGACCAGGAAGCATTGAGAGAGCACTGAGAGAGCACTGTAGAGAGACCATGAGAGAGCACTGAGAGAGCACTGAGAGAGCACTGAGAGAGCACTGAGAGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAGAGACCACTGAAAAGACCACTGAAGAGGACCACTGAAAAGACCACTGAAAAGACCACTGAAAGAACACACTGAAAAGACCACTGAAGAGGACACTGAAAAAACACCACTGAAGAGACACTGAAAAAACACCTGCAAGAGGACACTGAAAAAAACACCTGAAAAGAACACTGACAAGAAAAACACCTGCTAAGAGGAACACTGAAAAAAAA	TTTTGCGATGTGTTCCTAATATGTGCT TTTTGCAGTATGTTCCTGAAT	2 12	TGCAGTGCTGCATCTCTGG TTGAGGTAGTAGGTTGTATG	3 1	AACAAACATGGTGCACTTCT ACTCCATTTGTTTTGATGATGG		TTCCTGGAAATACTGTTCTT ACTGGACTTGGAGTCAGAAGGCC		ACACTGCCGGCCTCTGGG TAGTAGGTTGTATGGTT	3 9
ATCACTITECCAGGGAT 8 AGAGGCTGGCCGTGATAATTCG 3 GGGACCAGGAAGTAITGATGTTT 6 GCCCAAGGAGCCTCGGTTGGCCCCGGAT 1 ACGACTAGGAGGCCTCT 1 TGTAGGGATGGAAGCCATCGAAACCTCTCAAGTG 237 TCTAACCTGTCAGTGT 1 TATATATAACACTCCTCAAGTG 237 TCTAACCTGTCAGTGT 1	TGTTTAGACTACCTGTTC	1	GAATGTTGCTCGGTGAACCCCTTTT	2	TGTAGATCCGAATTTGTGT	1	AACTGGCCTACAAAGTCCCA	36	AGGCAGTGTAATTAGCTGATTGT	36
TGAGGTAGGTAGGTTGTGGTTTCAG 5 TGACCGATTTCTCCTGGTGT 2 TTGAGGTAGTAGGTTGTATGGT 28 ACCCTGTAGATCCGAATTTGTG 98 TCACATTGCCAGGGATTA 1	ATCACATTGCCAGGGAT		AGAGGCTGGCCGTGATGAATTCG	2 3 1	GGGAGCCAGGAAGTATTGATGTTT		GCCGAAGGAGCCTCGGTTGGCCCCGGAT ATATAATACAACCTGCTAAGTG	1	ACGACTAGGAGGCCTCT TTCAACGCTGTCGGTGAGT	1 1
	TGAGGTAGTAGGTTGTGTGTTCAG	5	TGACCGATTTCTCCTGGTGT	2	TTGAGGTAGTAGGTTGTATGGT	28	ACCCTGTAGATCCGAATTTGTG		TCACATTGCCAGGGATTA	1

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CCTAAGGTGAATTTTTTGGGAA	5 3	TAGCACCATTTGAAATCAGTGTTC	15	TAGGCAGTGTAATTAGCTGATTGTA TAGCACCATTTGAAATCAGTGTTT	272	TACAGTACTGTGATAACTGAA	10	GCTGGTTTCATATGGTGGTTTGT	202 5
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CAATTTAGTGTGTGTGATATT TGAGGGTCTATGATACCACCCGGTACAGGA	7 13	ACAAGTCAGGTTCTTGCCACC	20	AACATTCAACCTGTCGGTCACTT					
CAATITAGTGTGTGTGATATT TGAGGGTCTATGATACCACCCGGTACAGGA TGCCTACTGAGCTGATATCAGT		ACAAGTCAGGTTCTTGGGACC	38	AACATTCAACCTGTCGGTGAGTT	85	ATGGCGCCACTAGGGTTGTG	7	CCCAGTGTTCAGACTACCTGTTCAGGAC	106
CAATTTAGTGTGTGTGATATT TGAGGGTCTATGATACCACCCGGTACAGGA TGCCTACTGAGCTGATATCAGT TGGCAGTGTCTTAGCTGGT	2 7	ACAAGTCAGGTTCTTGGGACC GCATTGTACAGGGCTATG	4	AACATTCAACCTGTCGGTGAGTT CGAAGGAGCCTCGGTTGGCCCCGGATAGC	2	TAGGCAGTGTAATTAGCTGATTGT	7	TTTTGCGATGTGTTCCTAATA	106
CAATTIAGTGTGTGGTATATT TGAGGGTCTATGATACCACCCGGTACAGGA TGCCTACTGAGCTGGTATCAGT TGGCACTGTCTTIAGCTGGT TGAATGGCGCCACTAGGGTTGT	2 7 3	ACAAGTCAGGTTCTTGGGACC GCATTGTACAGGGCTATG CTGACCTATGAATTGACAGCC	38 4 115 5	AACATTCAACCTGTCGGTGAGTT CGAAGGAGCCTCGGTTGGCCCCGGATAGC AATCACTAACCACACAGCCAGG	2 25 27	TAGGCAGTGTAATTAGCTGATTGT TATGGCTTTTCATTCCTATGT	7 1	TTTTGCGATGTGTTCCTAATA TGGCAGTGTCTTAGCT	
CAATTHACTGTGTGTGATATT TGAGGGTCTATGATACACCCGGTACAGGA TGCCTACTGAGCTGATATCAGT TGGCAGTGTCTTAGCTGGT TGAATGGCGCCCACTAGGGTTGT CAAAGTGCTCATAGTGCAGGT TTTGCAGTGTGTTCTAATA	2 7	ACAAGTCAGGTTCTTGGGACC GCATTGTACAGGGCTATG CTGACCTATGAATTGACAGCC GTAGTCTGCACATTGGTTA AGGTAGTAGAGTTGTATAGT	4	AACATTCAACCTGTCGGTGAGTT CGAAGGAGCCTCGGTTGGCCCCGGATAGC AATCACTAACCACAACAGCCAGG TCCGAGCCTGGGTCTCCCTCT TGAGGTAGGAGGTTTATTAGTTG	2 25 27 109	TAGGCAGTGTAATTAGCTGATTGT TATGGCTTTTCATTCCTATGT GCAGTGCAATAGTATTGTCAAAG TAAACATCCTCGACTGGAA	7 1 1	TITTGCGATGTGTTCCTAATA TGGCAGTGTCTTTAGCT GCTGACCCCTAGTCCAGTG AGTATCCAGGATAGG	106
CAATITAGTGTGTGTATATT TGAGGGTCTATGAATATA TGCCTACTGAGCTGATATCAGT TGCCAGTGTCTTAGCTGT TGGAATGCCAGCTAGGGTTGT TGAATGCCCCACTAGGGTTGT CAAAGTGCTCATAGTGCAGGTA TTTGCGATGTGTTCATAGTCAGGTA TTTGCGATGTGTTCCTAATATCCAGGTA TTTGTGTGTGCA	2 7 3	ACAAGTCAGGTTCTTGGGACC GCATTGTACAGGGCTATG CTGACCTATGAATTGACAGCC GTAGTCTGCACATTGGTTA AGGTAGTAGGTGTATAAGT CCCTAAGGTGAATTTTTTGGG	4	AACATTCAACCTGTCGGTGAGTT CGAAGGAGCCTCGGTTGGCCCCGGATAGC AATCACTAACCACACACGCAGG TCCGAGCCTGGGTCTCCCTCT TGAGGTTAGCAGGTTGTATAGTTG CAACAAATCACAGTCTGCCATA	2 25 27	TAGGCAGTGTAATTAGCTGATTGT TATGGCTITTCATTCCTATGT GCAGTGCAATAGTATTGTCAAAG TAAACATCCTCGACTGGAA CTGGTGTTGTGAATCAGG	7 1 1 1	TTTTGCGATGTGTTCCTAATA TGGCAGTGTCTTAGCT GCTGACCCCTAGTCCAGTG AGTAATCCAGGATAGG AGTAATCCAGGATAGG	106
CAATTHACTGTGTGTGATATT TGAGGGTCTATGATACACCCGGTACAGGA TGCCTACTGAGCTGATATCAGT TGGCAGTGTCTTAGCTGGT TGAATGGCGCCCACTAGGGTTGT CAAAGTGCTCATAGTGCAGGT TTTGCAGTGTGTTCTAATA	2 7 3	ACAAGTCAGGTTCTTGGGACC GCATTGTACAGGGCTATG CTGACCTATGAATTGACAGCC GTAGTCTGCACATTGGTTA AGGTAGTAGAGTTGTATAGT	4	AACATTCAACCTGTCGGTGAGTT CGAAGGAGCCTCGGTTGGCCCCGGATAGC AATCACTAACCACAACAGCCAGG TCCGAGCCTGGGTCTCCCTCT TGAGGTAGGAGGTTTATTAGTTG	2 25 27 109	TAGGCAGTGTAATTAGCTGATTGT TATGGCTTTTCATTCCTATGT GCAGTGCAATAGTATTGTCAAAG TAAACATCCTCGACTGGAA	7 1 1 1 1 23	TITTGCGATGTGTTCCTAATA TGGCAGTGTCTTTAGCT GCTGACCCCTAGTCCAGTG AGTATCCAGGATAGG	106