

Mature sequence	Chr	Start	Stop	Str	Class	length	R.n. SEED	H.s. SEED	Location	Type of RNA	Gene (Gene Symbol)
1 UGUAUCUUCUUGGAAAGGUAUAGGACUUCU	10	120849742	120849766	-	potential	27	Y	M	exon	mRNA	Ras association (Rai)GDS/AF-6 domain family member 3 (Rass3)
2 UAAUCAGUUGGCAUUAAGAUAUAGGAAAGU	8	106878673	106878698	+	high confidence	26	M	M	exon	mRNA	CKI-F-like MARYEL transmembrane domain containing 4 (Cmm4)
3 UAAUCAGUUGGCAUUAAGAUAUAGGAAAGU	17	36133244	36133248	+	non-scandiate	27	M	N	intron	ncRNA	RKEN-CDNA.A93001.5D033 (gene A93001.5D033Rk)
4 UGCAUUGUUCUUGGCAUUAAGAUAUAGGAAAGU	15	20850745	20850749	-	potential	27	N	N	intron	ncRNA	LINE
5 GAUUAUGUUGGCAUUAAGAUAUAGGAAAGU	8	72286149	72286175	-	potential	27	Y	N	intron	mRNA	RKEN-CDNA.D53003906R (gene D53003906Rk), LINE similarity
6 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	18	88248637	88248637	-	high confidence	25	Y	Y	intron	mRNA	nucleolin (Ncl)
7 UUCAUUGUUGGCAUUAAGAUAUAGGAAAGU	1	75529298	75529298	-	high confidence	26	M	M	exon	mRNA	predicted gene 672 (Gmf672)
8 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	12	72217431	72217431	-	high confidence	26	Y	M	exon	mRNA	smoothelin-like 2 (Smnl2)
9 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	84961975	84962001	-	high confidence	27	N	N	intron	ncRNA	transmembrane and coiled coil domains 1 (Tmc1)
10 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	3	116123772	116123772	+	high confidence	27	Y	Y	exon	mRNA	H2A histone family, member Z (H2afz)
11 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	137528111	137528137	+	high confidence	27	M	N	exon	mRNA	seminolethal kinase 4 (Slk4)
12 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	11	163980331	163980359	+	high confidence	29	M	M	exon	mRNA	DBP1 and CUL4 associated factor 7 (Dcaf7)
13 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	105918043	105918043	+	high confidence	27	M	M	exon	mRNA	
14 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	113783987	113783916	+	high confidence	30	Y	M	intron	ncRNA	
15 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	60895112	60895137	-	potential	26	Y	M	intron	ncRNA	
16 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	27476283	27476289	+	non-scandiate	27	Y	Y	intron	ncRNA	LTR
17 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	8	106877883	106877909	-	high confidence	27	Y	Y	intron	mRNA	predicted gene 4884 (Gmf4884)
18 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	48296789	48296794	+	high confidence	26	Y	N	intron	mRNA	predicted gene 5592 (Gmf5592)
19 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	48411584	48411584	-	high confidence	26	Y	N	exon	mRNA	predicted gene 5114 (Gmf5114)
20 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	46542183	46542188	-	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
21 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	46477894	46477894	-	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
22 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	46621028	46621053	+	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
23 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	46660511	46660511	+	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
24 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	39234704	39234729	+	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
25 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	3	39355242	39355267	+	high confidence	26	Y	N	intron	mRNA	predicted gene 5114 (Gmf5114)
26 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	3	19799839	19799866	+	high confidence	28	N	N	intron	mRNA	inhibitor of growth family, member 5 (Inp5)
27 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	1	95715748	95715773	+	non-scandiate	26	Y	M	exon	mRNA	
28 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	4	138451203	138451229	-	potential	27	M	M	intron	ncRNA	
29 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	108030821	108030821	-	high confidence	23	Y	Y	intron	mRNA	(Ahrgef17)
30 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	4	119300406	119300433	+	non-scandiate	28	Y	M	exon	mRNA	forkhead box J3 (Foxj3)
31 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	18	17002943	17002969	+	potential	27	N	N	intron	ncRNA	SINE
32 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	27257492	27257518	+	potential	27	N	N	intron	mRNA	van Z oncogene (Vaz2), LTR
33 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	16	33047780	33047780	+	potential	27	N	N	intron	mRNA	IQ motif containing G (Iqg), SINE
34 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	12871021	12871021	-	potential	27	Y	N	intron	ncRNA	SINE
35 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	12871095	12871095	-	potential	27	Y	N	intron	ncRNA	SINE
36 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	12874879	12874879	-	potential	27	Y	N	intron	ncRNA	SINE
37 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	41589351	41589351	-	high confidence	26	N	Y	intron	mRNA	low density lipoprotein-related protein 1B (deleted in tumors) (Lrp1b), LTR
38 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	40378419	40378419	-	potential	26	Y	Y	intron	mRNA	RKEN-CDNA.E330009.4J7 gene (E330009.4J7Rk)
39 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	8	87598919	87598946	-	potential	28	M	M	exon/intergenic	mRNA	deoxyxynuclease synthase (Dxps)
40 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	7	158850826	158850853	-	non-scandiate	28	Y	M	exon	mRNA	WD repeat domain containing 83 (Wdr83)
41 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	27	106653030	106653030	-	non-scandiate	26	Y	M	exon	mRNA	RALBP1 associated Fps domain containing protein 2 (Reps2)
42 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	5	140277933	140277958	+	potential	26	Y	N	intron	mRNA	fibronectin protein S3 (Rps3)
43 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	28	120578481	120578481	+	non-scandiate	26	N	N	intron	mRNA	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) (Mafk)
44 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	4	150054118	150054139	-	high confidence	22	N	N	intron	mRNA	transcription factor CP2-like 1 (Tcfcp2l1), snRNA
45 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	4	10535490	10535490	-	high confidence	22	N	N	intron	mRNA	SINE
46 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	14	53627361	53627382	+	high confidence	22	N	N	intron	mRNA	fragile histidine triad gene (Fhit), SINE
47 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	13	55341940	55341961	+	high confidence	22	N	N	intron	mRNA	SINE
48 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	15	81081200	81081221	+	high confidence	22	Y	N	intron	mRNA	nuclear receptor-binding SET-domain protein 1 (Nsd1), SINE
49 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	34870986	34870981	-	high confidence	26	Y	M	exon	mRNA	SINE
50 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	177507800	177507800	-	high confidence	28	N	N	intron	ncRNA	family with sequence similarity 168, member B (Fam168b), transcript variant 2
51 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	14	24906769	24906769	+	high confidence	28	M	N	intron	ncRNA	LTR
52 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	14	163978037	163978037	+	high confidence	28	M	N	intron	ncRNA	LTR
53 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	11	60389681	60389681	+	high confidence	26	M	M	intron	ncRNA	
54 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	16	163978037	163978037	+	high confidence	26	Y	M	exon	mRNA	serine/threonine kinase 4 (Slk4)
55 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	13462487	13462487	+	high confidence	27	N	N	intron	mRNA	neuroblastoma amplified sequence (Nbas)
56 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	12	40487043	40487043	+	high confidence	27	N	N	intron	ncRNA	
57 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	11	55501533	55501533	-	high confidence	27	N	N	intron	mRNA	phospholipase C-like 1 (Pc1l1)
58 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	34261983	34261983	-	high confidence	27	Y	Y	exon	mRNA	aldo-keto reductase family 1, member B3 (aldose reductase) (Akr1b3)
59 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	75503676	75503702	+	high confidence	27	M	N	exon	mRNA	zinc finger protein 280B (Zfp280b)
60 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	54869361	54869361	+	high confidence	27	M	N	exon	mRNA	
61 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	26762102	26762127	-	high confidence	26	Y	Y	intron	ncRNA	mediator complex, subunit 22 (Med22), transcript variant 1
62 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	2	26762102	26762127	-	high confidence	26	Y	Y	intron	ncRNA	mediator complex, subunit 22 (Med22), transcript variant 2
63 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	95709393	95709393	+	high confidence	25	Y	Y	exon	mRNA	inhibitor of growth family, member 5 (Inp5)
64 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	1	12813402	12813402	+	high confidence	27	N	N	intron	ncRNA	DNA segment, Chr 10, Wayne State University 102, expressed (D10Wsu102e)
65 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	10	82824844	82824871	+	high confidence	27	N	N	intron	ncRNA	LTR
66 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	6	71933932	71933932	+	potential	27	M	N	intron	ncRNA	G protein-coupled receptor 137B, pseudogene (Gpr137b-ps)
67 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	13	12709375	12709375	-	high confidence	27	M	N	intron	ncRNA	G protein-coupled receptor 137B (Gpr137b)
68 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	13	13452974	13452974	-	high confidence	27	M	N	intron	ncRNA	G protein-coupled receptor 137B (Gpr137b)
69 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	1	47806547	47806547	-	high confidence	29	Y	M	intron	ncRNA	
70 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	16	17260573	17260599	+	potential	27	Y	M	exon	mRNA	hypermethylated in cancer 2 (Hic2)
71 UAGAAGUUGGCAUUAAGAUAUAGGAAAGU	11	97255938	97255963	+	potential	26	M	M	exon	mRNA	suppressor of cytokine signaling 7 (Socs7)

47	UGAAGUCUAGUAGAGUUCUUGGCGUCU	45560552	45560578	+	non-candidate	27	N	N	intergenic	
47	UGAAGUCUAGUAGAGUUCUUGGCGUCU	20459885	20459885	-	non-candidate	27	N	N	intergenic	
48	UGAAGUCUAGUAGAGUUCUUGGCGUCU	79510938	79510938	+	non-candidate	27	M	M	intergenic	
49	UGAAGUCUAGUAGAGUUCUUGGCGUCU	72352994	72352924	+	non-candidate	26	N	M	exon	lysophosphatidic acid receptor 2 (Lpar2)
50	UGAAGUCUAGUAGAGUUCUUGGCGUCU	65811544	65811569	-	potential	26	N	N	intergenic	
51	UGAAGUCUAGUAGAGUUCUUGGCGUCU	127136204	127136204	+	high confidence	26	N	M	exon	transmembrane protein, 19d (Tmem19d), transcript variant 1
52	UGAAGUCUAGUAGAGUUCUUGGCGUCU	51246455	51246480	+	non-candidate	26	M	M	exon	spanin1 (Span1), transcript variant 1
52	UGAAGUCUAGUAGAGUUCUUGGCGUCU	82398583	82398583	-	non-candidate	26	M	N	intergenic	
53	UGAAGUCUAGUAGAGUUCUUGGCGUCU	27487398	27487424	+	potential	27	M	N	intergenic	
54	UGAAGUCUAGUAGAGUUCUUGGCGUCU	75503034	75503050	+	high confidence	26	M	N	exon	zinc finger protein, 280b (Zfp280b)
55	UGAAGUCUAGUAGAGUUCUUGGCGUCU	56830222	56830222	+	potential	27	M	N	intron	
56	UGAAGUCUAGUAGAGUUCUUGGCGUCU	77210313	77210339	+	high confidence	27	M	N	intron	RIKEN cDNA, 2210015D19 gene (2210015D19R1), SINE
57	UGAAGUCUAGUAGAGUUCUUGGCGUCU	105919634	105919659	+	high confidence	26	M	M	exon	haloacid dehalogenase-like hydrolase domain containing 2 (Hdhd2), transcript variant 1
58	UGAAGUCUAGUAGAGUUCUUGGCGUCU	15689843	15689843	-	non-candidate	27	M	M	exon	
59	UGAAGUCUAGUAGAGUUCUUGGCGUCU	31654657	31654684	+	non-candidate	28	M	Y	exon	DBP1 and CUL4 associated factor 7 (Dbaif7)
60	UGAAGUCUAGUAGAGUUCUUGGCGUCU	66502286	66502292	+	potential	27	M	N	intron	copine 1 (Copn1), transcript variant 2
61	UGAAGUCUAGUAGAGUUCUUGGCGUCU	30876816	30876843	+	high confidence	28	M	Y	exon	c-cad oncogene 1, receptor tyrosine kinase (Abl1), transcript variant 1
61	UGAAGUCUAGUAGAGUUCUUGGCGUCU	66558591	66558617	-	potential	27	M	N	intergenic	zinc finger and BTB domain containing 44 (Zfpb44), transcript variant a
62	UGAAGUCUAGUAGAGUUCUUGGCGUCU	174992474	174992474	-	potential	27	M	N	intergenic	LTR
63	UGAAGUCUAGUAGAGUUCUUGGCGUCU	45409335	45409361	-	high confidence	26	M	N	intergenic	mitochondrial carrier (triple repeat 1) (Mcart1), nuclear gene encoding mitochondrial protein
63	UGAAGUCUAGUAGAGUUCUUGGCGUCU	135302351	135302377	-	non-candidate	27	M	N	exon	
64	UGAAGUCUAGUAGAGUUCUUGGCGUCU	112254677	112254703	-	potential	27	M	N	intergenic	ataxin 1-like (Atxn1l)
65	UGAAGUCUAGUAGAGUUCUUGGCGUCU	129850258	129850283	+	high confidence	26	N	N	intergenic	
65	UGAAGUCUAGUAGAGUUCUUGGCGUCU	126433432	126433457	+	high confidence	26	N	Y	exon	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (Ctdsp2)
66	UGAAGUCUAGUAGAGUUCUUGGCGUCU	97255148	97255174	+	potential	27	M	M	exon	transcript variant a
67	UGAAGUCUAGUAGAGUUCUUGGCGUCU	92402706	92402733	+	high confidence	28	M	M	intergenic	suppressor of cytokine signaling 7 (Socs7)
68	UGAAGUCUAGUAGAGUUCUUGGCGUCU	67585842	67585870	+	high confidence	29	M	N	intergenic	
69	UGAAGUCUAGUAGAGUUCUUGGCGUCU	120578955	120578980	+	high confidence	26	N	N	exon	transcription factor CPZ-like 1 (Tcfcp2l1)
70	UGAAGUCUAGUAGAGUUCUUGGCGUCU	66109191	6610943	-	high confidence	25	Y	N	intergenic	
71	UGAAGUCUAGUAGAGUUCUUGGCGUCU	112363200	112363223	+	potential	24	Y	M	intron	adaptor protein complex AP-1, gamma 1 subunit (Ap1at)
72	UGAAGUCUAGUAGAGUUCUUGGCGUCU	31962155	31962183	+	high confidence	29	M	Y	exon	SUMO3entrom specific peptidase 5 (Semp5)
73	UGAAGUCUAGUAGAGUUCUUGGCGUCU	72935143	72935143	-	potential	25	M	M	exon	eukaryotic translation initiation factor 2C 2 (Eif2c2)
74	UGAAGUCUAGUAGAGUUCUUGGCGUCU	60040941	60040966	-	high confidence	26	M	M	exon	target of myx1-like 2 (Clnknt1), transcript variant 2
75	UGAAGUCUAGUAGAGUUCUUGGCGUCU	21505640	21505666	+	potential	27	Y	Y	exon	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (Smardc4), transcript variant 1
76	UGAAGUCUAGUAGAGUUCUUGGCGUCU	119734913	119734939	+	high confidence plus star	27	Y	Y	exon	
77	UGAAGUCUAGUAGAGUUCUUGGCGUCU	25195814	25195841	-	high confidence	28	N	M	intergenic	X-ray repair complementing defective repair in Chinese hamster cells 2 (Xcc2)
78	UGAAGUCUAGUAGAGUUCUUGGCGUCU	150595127	150595153	-	high confidence	27	M	N	intergenic	
79	UGAAGUCUAGUAGAGUUCUUGGCGUCU	141033165	141033190	-	high confidence	26	M	N	exon	SPEN homolog, transcriptional regulator (Drosophila) (Speen)
80	UGAAGUCUAGUAGAGUUCUUGGCGUCU	14691434	14691460	-	potential	27	N	N	intergenic	LINE
80	UGAAGUCUAGUAGAGUUCUUGGCGUCU	17736147	17736147	-	potential	27	N	N	intergenic	LINE
80	UGAAGUCUAGUAGAGUUCUUGGCGUCU	65383446	65383472	+	potential	27	N	N	intron	zinc finger protein, 369 (Zfp369), LINE
80	UGAAGUCUAGUAGAGUUCUUGGCGUCU	65400860	65400886	+	potential	27	N	N	intergenic	LINE
81	UGAAGUCUAGUAGAGUUCUUGGCGUCU	124798959	124798959	+	high confidence	26	Y	N	exon	transformed mouse 3T3 cell double minute 4 (Mdm4)
81	UGAAGUCUAGUAGAGUUCUUGGCGUCU	134896038	134896033	-	potential	26	Y	N	intergenic	LTR
82	UGAAGUCUAGUAGAGUUCUUGGCGUCU	20454849	20454844	-	potential	26	N	N	intergenic	LTR
82	UGAAGUCUAGUAGAGUUCUUGGCGUCU	56811628	56811653	+	potential	26	N	N	intergenic	LTR
82	UGAAGUCUAGUAGAGUUCUUGGCGUCU	12347932	12347932	+	potential	26	N	N	intergenic	LTR
82	UGAAGUCUAGUAGAGUUCUUGGCGUCU	51356873	51356898	+	potential	26	N	N	intergenic	LTR
83	UGAAGUCUAGUAGAGUUCUUGGCGUCU	85221735	85221732	+	non-candidate	28	N	N	intergenic	
84	UGAAGUCUAGUAGAGUUCUUGGCGUCU	10280978	10281005	+	high confidence	28	Y	M	exon	RIKEN cDNA, 1810006K21 gene (1810006K21R1), transcript variant 1
85	UGAAGUCUAGUAGAGUUCUUGGCGUCU	134970329	134970353	-	non-candidate	25	Y	M	exon	regulator of calcium 3 (Recan3)
86	UGAAGUCUAGUAGAGUUCUUGGCGUCU	7144899	7144925	+	non-candidate	27	Y	M	exon	leukemia inhibitor factor receptor (Lifr), transcript variant 1
87	UGAAGUCUAGUAGAGUUCUUGGCGUCU	119007293	119007293	-	non-candidate	26	Y	M	exon	TBC1 domain family, member 16 (Tbc1d16)
88	UGAAGUCUAGUAGAGUUCUUGGCGUCU	94716597	94716624	+	high confidence	28	M	M	intergenic	
89	UGAAGUCUAGUAGAGUUCUUGGCGUCU	186646345	186646367	-	non-candidate	23	Y	M	exon	MOCO sulphatase C-terminal domain containing 2 (Mosc2)
89	UGAAGUCUAGUAGAGUUCUUGGCGUCU			-	non-candidate	23				mmu-mir-1981
90	UGAAGUCUAGUAGAGUUCUUGGCGUCU	16008	16033	-	potential	26	M	N	intergenic	
90	UGAAGUCUAGUAGAGUUCUUGGCGUCU	98299971	98299966	-	potential	26	N	N	intergenic	
91	UGAAGUCUAGUAGAGUUCUUGGCGUCU	133723020	133723045	-	high confidence	22	Y	Y	intron	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeier-Vogt disease) (Cln3), transcript variant 1
92	UGAAGUCUAGUAGAGUUCUUGGCGUCU	167240541	167240541	-	high confidence	25	Y	M	exon	G protein-coupled receptor 161 (Gpr161)
93	UGAAGUCUAGUAGAGUUCUUGGCGUCU	129850068	129850092	+	potential	25	N	N	intergenic	
93	UGAAGUCUAGUAGAGUUCUUGGCGUCU	126433093	126433117	+	potential	25	N	Y	exon	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2 (Ctdsp2)
94	UGAAGUCUAGUAGAGUUCUUGGCGUCU	34870635	34870635	-	high confidence	26	Y	Y	exon	transcript variant a
95	UGAAGUCUAGUAGAGUUCUUGGCGUCU	28728199	28728226	-	potential	28	Y	Y	exon	family with sequence similarity 168, member B (Fam168b), transcript variant 2
96	UGAAGUCUAGUAGAGUUCUUGGCGUCU	191695054	191695080	+	high confidence	27	M	N	exon	serine/threonine-protein specific kinase 1 (Srk1)
97	UGAAGUCUAGUAGAGUUCUUGGCGUCU	69208832	69208857	-	high confidence	26	M	M	intergenic	protein tyrosine phosphatase, non-receptor type 14 (Ptpn14)
97	UGAAGUCUAGUAGAGUUCUUGGCGUCU	28239851	28239851	-	high confidence	26	M	M	intergenic	
98	UGAAGUCUAGUAGAGUUCUUGGCGUCU	27916186	27916193	+	non-candidate	28	M	M	exon	interleukin 17 receptor D (Il17rd)
99	UGAAGUCUAGUAGAGUUCUUGGCGUCU	152011383	152011408	-	high confidence	26	N	N	intergenic	
99	UGAAGUCUAGUAGAGUUCUUGGCGUCU	6073004	6073004	-	high confidence	26	N	N	intron	Nudc domain containing 3 (Nudc3)
99	UGAAGUCUAGUAGAGUUCUUGGCGUCU	63559873	63559898	-	high confidence	26	N	N	intergenic	
99	UGAAGUCUAGUAGAGUUCUUGGCGUCU	131563716	131563741	+	high confidence	26	N	N	intergenic	

99	UGAAGUUCUGCGGAGGAGUCUCUCUAAAG	5	137372523	137372548	+	high confidence	26	N	N	Intergenic	
100	UGAACAGCGUAAUUAAGGAACACACCGCC	7	125258720	125258745	+	high confidence	26	Y	M	exon	ribosomal protein S15A (Rps15a)
101	UGACGACUUGUAGUACGUCGACGAGGAGU	9	114416715	114416744	+	high confidence	30	M	M	Intergenic	
102	UGAGACUUGUAGUACGUCGACGAGGAGU	6	70798481	70798508	-	high confidence	28	Y	N	exon	DEAH (Asp-Glu-Ala-His) box polypeptide 33 (Dhx33)
103	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	478211220	478211220	+	potential	26	M	N	Intergenic	SINE
104	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	128136274	128136274	+	high confidence	26	M	N	Intergenic	Tanpason
105	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	167254946	167254970	+	high confidence	25	Y	M	Intergenic	
106	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	59087405	59087430	-	potential	26	M	N	Intergenic	
107	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	164132500	164132525	+	high confidence	26	M	N	Intergenic	
108	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	120333227	120333252	+	high confidence	26	Y	M	exon	zinc finger protein, 106 (Zfp106)
109	UGAGUUCUGUAGUACGUCGACGAGGAGU	7	86049491	86049517	+	high confidence	27	M	N	Intergenic	apoptosis enhancing nuclease (Aen), transcript variant 1
110	UGAGUUCUGUAGUACGUCGACGAGGAGU	17	27474712	27474736	+	non-candidate	25	M	N	Intergenic	
111	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	72931610	72931635	-	potential	26	Y	M	Intergenic	
112	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	83186036	83186061	-	potential	26	Y	M	exon	RKEN_cDNA_1700001L05 gene (1700001L05R1k)
113	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	28239866	28239712	-	high confidence	27	N	N	Intergenic	cytochrome b5 domain containing 1 (Cytb5d1)
114	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	69208667	69208692	-	high confidence	27	Y	M	exon	
115	UGAGUUCUGUAGUACGUCGACGAGGAGU	14	24923943	24923968	+	high confidence	27	M	M	Intergenic	mRNA
116	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	120837486	120837513	+	potential	28	M	M	exon	BC1-2 like 13 (apoptosis facilitator) (Bcl2l13), nuclear gene encoding mitochondrial protein
117	UGAGUUCUGUAGUACGUCGACGAGGAGU	12	99649011	99649037	-	high confidence	27	M	M	Intergenic	mRNA
118	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	167309426	167309453	-	high confidence	28	M	M	exon	spermatogenesis associated 2 (Spata2)
119	UGAGUUCUGUAGUACGUCGACGAGGAGU	17	23954443	23954468	+	high confidence	26	Y	M	exon	serine/arginine repetitive matrix 2 (Sirm2)
120	UGAGUUCUGUAGUACGUCGACGAGGAGU	10	60226286	60226291	-	high confidence	26	Y	M	exon	unc-5 homolog B (C. elegans) (Unc5b)
121	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	75303672	75303697	+	high confidence	26	M	M	Intergenic	mRNA
122	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	128398496	128398521	+	non-candidate	26	M	N	Intergenic	predicted gene 10089 (Gm10089), transcript variant 2
123	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	84781975	84781996	+	high confidence	22	Y	Y	Intergenic	RKEN_cDNA_5031439507 gene (5031439507R1k)
124	UGAGUUCUGUAGUACGUCGACGAGGAGU	4	11580742	11580768	-	non-candidate	27	Y	M	Intergenic	
125	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	180759598	180759625	-	high confidence	28	Y	M	Intergenic	
126	UGAGUUCUGUAGUACGUCGACGAGGAGU	1	158577746	158577771	+	high confidence	26	N	N	exon	cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4)
127	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	60591401	60591427	+	potential	27	Y	M	exon	v-abl Abelson murine leukemia viral oncogene homolog 2 (Arg, Abelson-related gene) (Abl2), transcript variant 2
128	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	66393624	66393649	-	high confidence	26	Y	M	exon	Smi1-Magenis syndrome chromosome region, candidate 8 homolog (human) (Sme8b), transcript variant 1
129	UGAGUUCUGUAGUACGUCGACGAGGAGU	18	33362063	33362088	-	non-candidate	25	M	N	exon	variant 1
130	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	74478391	74478416	+	potential	26	Y	M	Intergenic	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 (S3gal1)
131	UGAGUUCUGUAGUACGUCGACGAGGAGU	8	119734788	119734825	+	non-candidate	28	M	N	Intergenic	STAR-related lipid transfer (START) domain containing 4 (Stard4)
132	UGAGUUCUGUAGUACGUCGACGAGGAGU	9	44102003	44102029	+	high confidence	27	Y	M	Intergenic	SINE
133	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	59091457	59091483	+	high confidence	27	M	M	Intergenic	LTR
134	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	60370988	60371015	+	high confidence plus star	29	Y	Y	exon	alB, alkylation repair homolog 5 (E. coli) (Alkhs5)
135	UGAGUUCUGUAGUACGUCGACGAGGAGU	7	95823266	95823294	-	potential	26	M	N	exon	insulin-like growth factor 2 mRNA binding protein 1 (Igf2bp1)
136	UGAGUUCUGUAGUACGUCGACGAGGAGU	8	123475940	123475965	-	high confidence	26	M	N	exon	ribosomal protein S13 (Rps13)
137	UGAGUUCUGUAGUACGUCGACGAGGAGU	8	122126151	122126176	-	high confidence	26	N	N	Intergenic	TATA box binding protein (TBP) associated factor, RNA polymerase I, C (Taf1c)
138	UGAGUUCUGUAGUACGUCGACGAGGAGU	7	95679034	95679059	-	high confidence	26	N	N	Intergenic	
139	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	89571988	89571993	+	high confidence	26	M	N	Intergenic	mRNA
140	UGAGUUCUGUAGUACGUCGACGAGGAGU	8	92137382	92137408	-	potential	27	M	N	Intergenic	zinc finger, FYVE domain containing 20 (Zfve20)
141	UGAGUUCUGUAGUACGUCGACGAGGAGU	17	37133722	37133747	-	high confidence	23	Y	M	exon	zinc finger and BTB domain containing 49 (Zfnd49)
142	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	38591872	38591897	-	potential	26	M	Y	exon	zinc finger and BTB domain containing 49 (Zfnd49)
143	UGAGUUCUGUAGUACGUCGACGAGGAGU	5	78493609	78493634	-	high confidence	26	M	N	Intergenic	SINE
144	UGAGUUCUGUAGUACGUCGACGAGGAGU	7	6594138	6594161	-	potential	24	N	N	Intergenic	
145	UGAGUUCUGUAGUACGUCGACGAGGAGU	4	133904334	133904355	+	high confidence	22	Y	M	Intergenic	solute carrier family 30 (zinc transporter), member 2 (Slc30a2)
146	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	59270213	59270239	+	high confidence	27	M	N	exon	limonin domain containing 4 (Lmdc4)
147	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	39271345	39271370	-	high confidence	26	N	N	Intergenic	SINE
148	UGAGUUCUGUAGUACGUCGACGAGGAGU	12	37104097	37104122	-	high confidence	26	N	N	Intergenic	SINE
149	UGAGUUCUGUAGUACGUCGACGAGGAGU	3	92447656	92447681	+	high confidence	26	N	N	Intergenic	SINE
150	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	156215243	156215268	-	high confidence	26	Y	N	exon	RKEN_cDNA_2900097C17 gene (2900097C17R1k)
151	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	33308031	33308056	-	potential	26	M	M	exon	zinc finger and BTB domain containing 43 (Zfndc43), transcript variant 2
152	UGAGUUCUGUAGUACGUCGACGAGGAGU	1	133924935	133924935	+	high confidence plus star	28	M	M	Intergenic	major facilitator superfamily domain containing 4 (Mfsd4), transcript variant a
153	UGAGUUCUGUAGUACGUCGACGAGGAGU	7	71033578	71033603	-	potential	26	Y	M	exon	Kruppel-like factor 13 (Klf13)
154	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	92433206	92433206	+	high confidence	27	M	M	Intergenic	SINE
155	UGAGUUCUGUAGUACGUCGACGAGGAGU	18	55030886	55030888	+	non-candidate	19	N	N	Intergenic	No Match
156	UGAGUUCUGUAGUACGUCGACGAGGAGU	15	40862231	40862411	+	high confidence	21	M	Y	Intergenic	zinc finger protein, multiple 2 (Zfpn2)
157	UGAGUUCUGUAGUACGUCGACGAGGAGU	4	58453895	58453917	+	high confidence	23	M	Y	Intergenic	lysophosphatidic acid receptor 1 (Lpar1), transcript variant 1
158	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	69204453	69204453	-	non-candidate	29	M	N	Intergenic	LINE
159	UGAGUUCUGUAGUACGUCGACGAGGAGU	4	28236526	28236526	-	non-candidate	29	N	N	Intergenic	LINE
160	UGAGUUCUGUAGUACGUCGACGAGGAGU	4	61881864	61881864	-	high confidence	27	M	M	Intergenic	
161	UGAGUUCUGUAGUACGUCGACGAGGAGU	17	27471454	27471481	+	high confidence	28	M	M	Intergenic	
162	UGAGUUCUGUAGUACGUCGACGAGGAGU	11	60598019	60598044	+	potential	26	M	M	exon	Smi1-Magenis syndrome chromosome region, candidate 8 homolog (human) (Sme8b), transcript variant 1
163	UGAGUUCUGUAGUACGUCGACGAGGAGU	1	157292636	157292660	+	potential	25	M	N	Intergenic	variant 1
164	UGAGUUCUGUAGUACGUCGACGAGGAGU	X	70271990	70272017	+	high confidence	28	M	N	Intergenic	family with sequence similarity 163, member A (Fam163a)
165	UGAGUUCUGUAGUACGUCGACGAGGAGU	6	49186887	49186887	-	high confidence	28	N	N	Intergenic	zinc finger protein, 185 (Zfp185), transcript variant 2
166	UGAGUUCUGUAGUACGUCGACGAGGAGU	9	123370959	123370986	+	high confidence	28	N	N	Intergenic	mRNA
167	UGAGUUCUGUAGUACGUCGACGAGGAGU	12	79451966	79451993	+	high confidence	28	N	N	Intergenic	leucyl-tRNA synthetase, mitochondrial (L-arS2), nuclear gene encoding mitochondrial protein
168	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	167121331	167121357	+	potential	20	M	N	Intergenic	gepbyrin (Gepn), transcript variant 2
169	UGAGUUCUGUAGUACGUCGACGAGGAGU	1	177169056	177169056	-	potential	30	N	N	Intergenic	SET2 domain containing 2 (SET2c), SINE
170	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	177096391	177096391	-	potential	30	N	N	Intergenic	LTR
171	UGAGUUCUGUAGUACGUCGACGAGGAGU	2	176698905	176698934	-	potential	30	N	N	Intergenic	LTR

157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	175454561	-	potential	30	N	N	intergenic	LTR	
157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	177507922	+	potential	30	N	N	intergenic	LTR	
157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	174789279	+	potential	30	N	N	intergenic	LTR	expressed sequence A1506816 (A1506816)
158	GGCCAAAGAAUUAAGAAACUUAACACUUAAC	23219852	-	high confidence	27	Y	N	exon	ncRNA	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smc8), transcript variant 1
159	UGGAAACAAAGACACUUGGGAUUGUAGUAC	60601516	+	high confidence	27	M	M	exon	mRNA	zinc finger protein, 532 (Zfp532)
160	UGGUAAGUUCUUGUGAAGAAAGAAAGGAC	65792365	+	high confidence	26	Y	M	intron	mRNA	huntingtin interacting protein 1 (Htp1)
161	UAGAAACACUUAAGCAUUAAGACUUGGAC	135907570	-	high confidence	26	Y	M	exon	mRNA	No Match
162	UGGUCUUAACAGAGUUAUCUACAGAAACA	36796588	-	potential	23	M	N	intergenic		SINE
163	UGGAAACACAGGAGCAAGUUAUAU	86354831	-	potential	23	M	N	intergenic		SINE
164	UGAGACACAGGAAACACUUCACAGACUUC	25702331	-	potential	27	M	M	exon	mRNA	spermatogenesis and oogenesis specific basic helix-loop-helix 1 (Sohlh1)
166	UUCACUUAACAGUUAAGAAAGAAAGGAC	32098489	+	high confidence	27	Y	M	exon	mRNA	HLA-B associated transcript 2-like (Bat2l), transcript variant 2
167	UUCUUAACAGUUAAGAAAGAAAGGAC	1011376643	+	high confidence	25	Y	M	exon	mRNA	adenylate kinase 3-like 1 (AK3l1), nuclear gene encoding mitochondrial protein
168	GUAGAAAGAGGUGUAUAUUGAAGAAAC	126017024	-	non-candidate	27	Y	M	intron	mRNA	cyclin-dependent kinase 16 (Cdk16)
170	UGGUCUUAUAUCUGGGAAGAAAGAA	20273594	+	high confidence	26	M	M	exon	mRNA	golgi coiled coil 1 (Gcc1)
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	75390798	-	potential	27	Y	M	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	103087934	-	potential	29	N	N	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	94413229	-	potential	29	N	N	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	72185919	-	potential	29	N	N	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	72616258	-	potential	29	N	N	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	93157323	+	potential	29	N	N	intergenic		LTR
171	UGGUGAUAACACACAGCAAGUUAUGAAGGUA	11255396	-	potential	29	N	N	intergenic		LTR
172	UGGUCUUAACACACAGCAAGUUAU	6240651	-	high confidence	22	Y	M	intergenic		SINE
173	UAGGACUUCUUAAGCAGUAGAAAGGU	136654781	-	high confidence	27	M	M	intergenic		SINE
174	UGGACUUCUGGAGCAUUGACACAGAC	80896036	-	high confidence	27	M	M	exon	mRNA	protein phosphatase 1, regulatory (inhibitor) subunit 12B (Ppp1r12b)
175	UGGAAACUACAGUUCUAUAUAUAUAUA	80264650	-	high confidence	26	M	M	intergenic		SINE
176	UUCGAGGAAAGGUGCAAGAAAGUUCG	6577641	+	high confidence	27	N	N	intergenic		SINE
176	UUCGAGGAAAGGUGCAAGAAAGUUCG	108191759	-	high confidence	27	N	N	intergenic		LINE
177	UCCUUAUCUUGAAGGAAACGCAAGAA	24914742	+	high confidence	25	M	N	intergenic		LINE
178	UUCACUUAUGAAGGAAAGGACG	92132716	-	potential	22	N	N	intergenic		SINE
178	UUCACUUAUGAAGGAAAGGACG	71873925	-	potential	22	N	N	intron	mRNA	NDC90 homolog, kinetochore complex component (S. cerevisiae) (Nkc80) SINE
178	UUCACUUAUGAAGGAAAGGACG	90875686	-	potential	22	N	N	intergenic		SINE
178	UUCACUUAUGAAGGAAAGGACG	132325485	+	potential	22	N	N	intergenic		SINE
178	UUCACUUAUGAAGGAAAGGACG	77823831	+	potential	22	N	N	intergenic		SINE
178	UUCACUUAUGAAGGAAAGGACG	44298061	-	potential	22	N	N	intergenic		SINE
178	UUCACUUAUGAAGGAAAGGACG	121847510	-	potential	22	Y	N	intron	mRNA	ATP-binding cassette, sub-family A (ABC1), member 4 (Abca4) SINE
178	UUCACUUAUGAAGGAAAGGACG	43465813	-	potential	22	Y	N	intergenic		SINE
179	UAGUAAAGAAAGAAUUGAAGAAAGU	67543485	-	potential	26	Y	N	intergenic		SINE
180	UACUAGGACUUAAGGAAAGGAAAGAAC	39768923	-	non-candidate	27	M	M	exon	mRNA	ERR3 homolog B (S. cerevisiae) (Err3b)
181	UCCAAAGGCAAGAAUUAUCUAGGAC	72353146	-	potential	26	M	M	exon	mRNA	lysophosphatidic acid receptor 2 (Lpar2)
182	UUAAGAAAGGAAAGGAAAGGAAAGAAU	89033485	-	potential	28	M	M	exon	mRNA	vasohibin 1 (Vasb1)
183	UUCGAAUCUUAUCGGAAGGACUAGCAUUC	18076865	-	high confidence	27	Y	Y	exon	mRNA	cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4)
184	UUAUUAUGGGAUUGGUAUUAUUCUGAAGU	41150127	-	non-candidate	29	Y	N	intron	mRNA	ubiquitin-associated protein 2 (Uba2)
185	UAGGCUAAGGAAAGGUGUGGGAA	6756349	+	high confidence	22	Y	N	intron	mRNA	ubiquitin specific peptidase 29 (Ubp29)
186	CUUAAGUUCAGUUGUUCU	37542855	-	potential	19	Y	N	intergenic		SINE
187	UCGAAAGGACAAACACAUUGGACU	63496817	-	high confidence	26	M	M	exon	mRNA	MAD homolog 3 (Drosophila) (Smad3)
188	UGAUAAGACUUGGCAACUUAUUCUGU	87725937	+	high confidence	26	Y	Y	exon	mRNA	mitochondrial ribosomal protein L24 (Mpl24), nuclear gene encoding mitochondrial protein
189	UCGACAGAAUUUUAAGCCUUUUCACAA	82847050	+	high confidence	29	N	N	intergenic	LTR	
190	UGGCGCAUCUUAAGAACUCCUU	117863593	+	high confidence	22	M	M	intron	mRNA	phosphatidylcholine:orthophosphate synthase 1 (Pgst1)
191	UACUUCUUUCUUUCUCCAGAGCUUC	119735479	-	high confidence	26	M	N	intergenic		SINE
192	UAGGAGUUGUUCAGUGAAGAAAGUUG	37103490	-	non-candidate	26	N	N	intergenic		ncRNA
192	UAGGAGUUGUUCAGUGAAGAAAGUUG	156214636	-	non-candidate	26	Y	M	exon	ncRNA	RIKEN cDNA 2900097C17 clone (2900097C17R1)
193	UCCGCGACUUGUUGGGAACUGUU	119349075	+	high confidence	25	M	N	intergenic		SINE
194	UGACUAGCUGAAGCAUCUCAAAGAUUG	3156891	+	high confidence	26	Y	N	intergenic		SINE
194	UGACUAGCUGAAGCAUCUCAAAGAUUG	128132947	-	high confidence	26	Y	N	intergenic		SINE
195	UGAUGGGAAGAAAGGAAAGCAUCCGCGGC	69209684	+	potential	22	Y	M	exon	mRNA	SM domain containing 1 (Lsmg1)
196	AGGGAAAGGAAAGGAAAGCAAAACCA	4623929	-	high confidence	27	Y	M	intron	mRNA	RCE1 homolog, prenyl protein peptidase (S. cerevisiae) (Rce1)
197	UGAAGAAAGGAAAGGAAAGCAUUCGAAUUG	10204485	+	non-candidate	25	Y	Y	exon	mRNA	zinc finger protein 740 (Zfp740)
198	UGGAAAGGAAAGGAAAGCAUUCGAAUUG	43952272	-	high confidence	28	M	M	intergenic		SINE