



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	M	M	exon	transmembrane protein, 19d (Tmem19d), transcript variant 1
52	UGAAGUCUAGUAGAGUUCUUGGCGUCU	51246455	51246480	+	non-candidate	26	M	M	exon	spanin1 (Spin1), 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	75503030	+	high confidence	26	M	N	exon	lTR
55	UGAAGUCUAGUAGAGUUCUUGGCGUCU	56830222	56830222	+	potential	26	M	N	exon	zinc finger protein, 280B (Zfp280b)
56	UGAAGUCUAGUAGAGUUCUUGGCGUCU	77210313	77210339	+	high confidence	27	Y	M	intron	RKEN cDNA, 2210015D19 gene (2210015D19R1), SINE
57	UGAAGUCUAGUAGAGUUCUUGGCGUCU	105919634	105919659	+	high confidence	26	Y	M	exon	haloacid dehalogenase-like hydrolase domain containing 2 (Hdhc2), transcript variant 1
58	UGAAGUCUAGUAGAGUUCUUGGCGUCU	156598617	156598643	-	non-candidate	27	M	M	exon	DBP1 and CUL4 associated factor 7 (Dbaf7)
60	UGAAGUCUAGUAGAGUUCUUGGCGUCU	31654657	31654684	+	non-candidate	28	M	Y	exon	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	66502266	66502292	-	potential	27	M	N	intron	zinc finger and BTB domain containing 44 (Zfpb44), transcript variant a
61	UGAAGUCUAGUAGAGUUCUUGGCGUCU	66558591	66558617	-	potential	27	M	N	intergenic	
62	UGAAGUCUAGUAGAGUUCUUGGCGUCU	174992474	174992474	-	potential	27	Y	N	intergenic	lTR
63	UGAAGUCUAGUAGAGUUCUUGGCGUCU	45409335	45409361	-	high confidence	26	M	N	exon	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	Y	Y	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	Y	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 (Tcfcpz1)
70	UGAAGUCUAGUAGAGUUCUUGGCGUCU	66109191	6610943	-	high confidence	25	Y	N	intergenic	
71	UGAAGUCUAGUAGAGUUCUUGGCGUCU	112363200	112363223	+	potential	24	Y	Y	intron	adaptor protein complex AP-1, gamma 1 subunit (Ap1a1)
72	UGAAGUCUAGUAGAGUUCUUGGCGUCU	31962155	31962183	+	high confidence	29	M	Y	exon	SUMO3entrom specific peptidase 5 (Semp5)
73	UGAAGUCUAGUAGAGUUCUUGGCGUCU	72935143	72935143	-	potential	25	M	Y	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	mRNA
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	17736121	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	AAUUCUUAGAGUAGAGUUCUUGGCGUCU	124798959	124798959	+	high confidence	26	Y	N	exon	transformed mouse 3T3 cell double minute 4 (Mdm4)
81	AAUUCUUAGAGUAGAGUUCUUGGCGUCU	134896038	134896033	-	potential	26	Y	N	intergenic	lTR
81	AAUUCUUAGAGUAGAGUUCUUGGCGUCU	20454819	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	85221705	85221732	+	non-candidate	28	N	N	intergenic	
84	UGAAGUCUAGUAGAGUUCUUGGCGUCU	10280978	10281005	+	high confidence	28	Y	M	exon	RKEN cDNA, 1810006K21 gene (1810006K21R1), transcript variant 1
85	UGAAGUCUAGUAGAGUUCUUGGCGUCU	134970329	134970353	-	non-candidate	25	Y	M	exon	regulator of calcium 3 (Rcan3)
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	GUAAAAGUCUAGUAGAGUUCUUGGCGUCU	186646345	186646367	-	non-candidate	23	Y	M	exon	MOCO sulphatase C-terminal domain containing 2 (Mosc2)
89	GUAAAAGUCUAGUAGAGUUCUUGGCGUCU			-	non-candidate	23				mmu-mR-1981
90	GCUUAGUAGUAGAGUUCUUGGCGUCU	16008	16033	-	potential	26	M	N	intergenic	
90	GCUUAGUAGUAGAGUUCUUGGCGUCU	98299971	98299966	-	potential	26	N	N	intergenic	
91	ACCGGGAGUCUAGUAGAGUUCUUGGCGUCU	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	exon	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	UGAACAGCGUAAAGUAGGAAACACACCGCC	7	125258720	125258745	+	high confidence	26	Y	M	exon	ribosomal protein S15A (Rps15a)
101	UGACGACUUGUAGUACGUCGACGAGGAGUC	9	114416715	114416744	+	high confidence	30	M	M	Intergenic	
102	UGAGACUUGUAGUACGUCGACGAGGAGUC	6	70798481	70798508	-	high confidence	28	Y	N	exon	DEAH (Asp-Glu-Ala-His) box polypeptide 33 (Dhx33)
103	UGAGUUCUGUAGUACGUCGACGAGGAGUC	6	478211220	478211220	+	potential	26	M	N	Intergenic	SINE
104	UGUCUUGUAGUACGUCGACGAGGAGUC	6	128136274	128136274	+	high confidence	26	M	N	Intergenic	Tanpason
105	UGUCUUGUAGUACGUCGACGAGGAGUC	6	167254946	167254970	+	high confidence	25	Y	M	Intergenic	
106	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	59087405	59087430	-	potential	26	M	N	Intergenic	
107	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	164132500	164132525	+	high confidence	26	M	N	Intergenic	
108	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	120333227	120333252	+	high confidence	26	Y	M	exon	zinc finger protein, 106 (Zfp106)
109	UGGACCAUUGUAGGAGAAUUGGCGGAG	7	86049491	86049517	+	high confidence	27	M	N	Intergenic	apoptosis enhancing nuclease (Aen), transcript variant 1
110	UGGACCAUUGUAGGAGAAUUGGCGGAG	17	27474712	27474736	+	non-candidate	25	M	N	Intergenic	
111	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	72931610	72931635	-	potential	26	Y	M	Intergenic	
112	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	83186036	83186061	-	potential	26	Y	M	exon	RKEN_cDNA1770001L05 gene (1770001L05Rtk)
113	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	28239866	28239712	-	high confidence	27	N	N	Intergenic	cytochrome b5 domain containing 1 (Cytb5d1)
114	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	69208667	69208692	-	high confidence	27	Y	M	exon	
115	UGGACCAUUGUAGGAGAAUUGGCGGAG	14	24923943	24923968	+	high confidence	27	M	M	Intergenic	
116	UGGACCAUUGUAGGAGAAUUGGCGGAG	6	120837486	120837513	+	potential	28	M	M	exon	BC1-2 like 13 (apoptosis facilitator) (Bcl2l13), nuclear gene encoding mitochondrial protein
117	UGGACCAUUGUAGGAGAAUUGGCGGAG	12	99649011	99649037	-	high confidence	27	M	M	Intergenic	
118	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	167309426	167309453	-	high confidence	28	M	M	exon	spermatogenesis associated 2 (Spata2)
119	UGGACCAUUGUAGGAGAAUUGGCGGAG	17	23954443	23954468	+	high confidence	26	Y	M	exon	serine/arginine repetitive matrix 2 (Srm2)
120	UGGACCAUUGUAGGAGAAUUGGCGGAG	10	60226286	60226291	-	high confidence	26	Y	M	exon	unc-5 homolog B (C. elegans) (Unc5b)
121	UGGACCAUUGUAGGAGAAUUGGCGGAG	6	75303672	75303697	+	high confidence	26	M	M	Intergenic	
122	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	128398496	128398521	+	non-candidate	26	Y	N	Intergenic	predicted gene 10089 (Gm10089), transcript variant 2
123	UGGACCAUUGUAGGAGAAUUGGCGGAG	4	84781975	84781996	+	high confidence	22	Y	Y	Intergenic	RKEN_cDNA5031439507 gene (5031439507Rkn)
124	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	11580742	11580768	-	non-candidate	27	Y	M	Intergenic	
125	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	180759598	180759625	-	high confidence	28	Y	M	Intergenic	cholinergic receptor, nicotinic, alpha polypeptide 4 (Chrna4)
126	UGGACCAUUGUAGGAGAAUUGGCGGAG	1	158577746	158577771	+	high confidence	26	N	N	exon	v-ab1 Abelson murine leukemia viral oncogene homolog 2 (v-Ab1, Abelson-related gene) (Ab1p2), transcript variant 2
127	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	60591401	60591427	+	potential	27	Y	M	exon	Smihi-Magenis syndrome chromosome region, candidate 8 homolog (human) (Sme8b), transcript variant 1
128	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	66393624	66393649	-	high confidence	26	Y	M	exon	Smihi-Magenis syndrome chromosome region, candidate 8 homolog (human) (Sme8b), transcript variant 1
129	UGGACCAUUGUAGGAGAAUUGGCGGAG	18	33362063	33362088	-	non-candidate	25	M	N	exon	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 (S3gal1)
130	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	74478391	74478416	+	potential	26	Y	M	Intergenic	STAR-related lipid transfer (START) domain containing 4 (Stard4)
131	UGGACCAUUGUAGGAGAAUUGGCGGAG	8	119734788	119734825	+	non-candidate	28	M	N	Intergenic	
132	UGGACCAUUGUAGGAGAAUUGGCGGAG	9	44102003	44102029	+	high confidence	27	Y	M	Intergenic	
133	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	59091457	59091483	+	high confidence	27	M	M	Intergenic	
134	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	60379988	60371015	+	high confidence plus star	28	Y	M	exon	
135	UGGACCAUUGUAGGAGAAUUGGCGGAG	7	95823266	95823294	-	potential	29	Y	Y	exon	
136	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	123475940	123475965	-	high confidence	26	M	N	exon	alkB, alkylation repair homolog 5 (E. coli) (AlkBh5)
137	UGGACCAUUGUAGGAGAAUUGGCGGAG	8	122126151	122126176	-	high confidence	26	M	N	exon	insulin-like growth factor 2 mRNA binding protein 1 (Igf2bp1)
138	UGGACCAUUGUAGGAGAAUUGGCGGAG	7	95679059	95679084	-	high confidence	26	N	N	Intergenic	ribosomal protein S13 (Rps13)
139	UGGACCAUUGUAGGAGAAUUGGCGGAG	6	89571988	89571993	+	high confidence	26	N	N	Intergenic	TATA box binding protein (TBP) associated factor, RNA polymerase I, C (Taf1c)
140	UGGACCAUUGUAGGAGAAUUGGCGGAG	8	92137382	92137408	-	potential	27	M	N	Intergenic	
141	UGGACCAUUGUAGGAGAAUUGGCGGAG	17	37133722	37133747	-	high confidence	23	Y	M	Intergenic	zinc finger, FYVE domain containing 20 (Zfve20)
142	UGGACCAUUGUAGGAGAAUUGGCGGAG	5	38591872	38591897	-	potential	26	M	Y	exon	zinc finger and BTB domain containing 49 (Zfbd49)
143	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	78493609	78493634	-	high confidence	26	M	N	Intergenic	
144	UGGACCAUUGUAGGAGAAUUGGCGGAG	7	6594138	6594161	-	potential	24	N	N	Intergenic	
145	UGGACCAUUGUAGGAGAAUUGGCGGAG	4	133904334	133904355	+	high confidence	22	Y	M	Intergenic	solute carrier family 30 (zinc transporter), member 2 (Slc30a2)
146	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	59270213	59270239	+	high confidence	27	M	N	exon	limonin domain containing 4 (Limdc4)
147	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	39271345	39271370	-	high confidence	26	N	N	Intergenic	SINE
148	UGGACCAUUGUAGGAGAAUUGGCGGAG	12	37104097	37104122	-	high confidence	26	N	N	Intergenic	SINE
149	UGGACCAUUGUAGGAGAAUUGGCGGAG	3	92447656	92447681	+	high confidence	26	N	N	Intergenic	SINE
150	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	156215243	156215268	-	high confidence	26	Y	N	Intergenic	SINE
151	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	33308031	33308056	-	potential	26	M	M	exon	RKEN_cDNA_2900097C17 gene (2900097C17Rkn)
152	UGGACCAUUGUAGGAGAAUUGGCGGAG	1	133924935	133924935	+	high confidence plus star	28	M	M	exon	zinc finger and BTB domain containing 43 (Zfbd43), transcript variant 2
153	UGGACCAUUGUAGGAGAAUUGGCGGAG	7	71033578	71033603	-	potential	26	Y	M	Intergenic	major facilitator superfamily domain containing 4 (Mfs44), transcript variant a
154	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	92433206	92433206	+	high confidence	27	M	M	exon	Kruppel-like factor 13 (Klf13)
155	UGGACCAUUGUAGGAGAAUUGGCGGAG	18	55030886	55030888	+	high confidence	19	N	N	Intergenic	
156	UGGACCAUUGUAGGAGAAUUGGCGGAG	15	40862391	40862411	+	non-candidate	23	N	N	No Match	
157	UGGACCAUUGUAGGAGAAUUGGCGGAG	4	58453985	58453917	+	high confidence	21	M	Y	Intergenic	zinc finger protein, multiple 2 (Zfpm2)
158	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	69204453	69204453	-	non-candidate	23	M	Y	Intergenic	lysophosphatidic acid receptor 1 (Lpar1), transcript variant 1
159	UGGACCAUUGUAGGAGAAUUGGCGGAG	4	28236526	28236526	-	non-candidate	29	M	N	Intergenic	LINE
160	UGGACCAUUGUAGGAGAAUUGGCGGAG	4	61881884	61881884	-	high confidence	27	M	N	Intergenic	
161	UGGACCAUUGUAGGAGAAUUGGCGGAG	17	27471454	27471481	+	high confidence	28	M	M	Intergenic	
162	UGGACCAUUGUAGGAGAAUUGGCGGAG	11	60598019	60598044	+	potential	26	M	M	exon	Smihi-Magenis syndrome chromosome region, candidate 8 homolog (human) (Sme8b), transcript variant 1
163	UGGACCAUUGUAGGAGAAUUGGCGGAG	1	157929636	157929660	+	potential	25	M	M	Intergenic	family with sequence similarity 163, member A (Fam163a)
164	UGGACCAUUGUAGGAGAAUUGGCGGAG	X	70271990	70272017	+	high confidence	28	M	N	Intergenic	zinc finger protein, 185 (Zfp185), transcript variant 2
165	UGGACCAUUGUAGGAGAAUUGGCGGAG	6	49186887	49186887	+	high confidence	28	N	N	Intergenic	
166	UGGACCAUUGUAGGAGAAUUGGCGGAG	9	123370959	123370986	+	high confidence	28	N	N	Intergenic	
167	UGGACCAUUGUAGGAGAAUUGGCGGAG	12	79451966	79451993	+	high confidence	28	N	N	exon	leucyl-tRNA synthetase, mitochondrial (Lars2), nuclear gene encoding mitochondrial protein
168	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	167121331	167121357	+	potential	20	M	N	Intergenic	gepivrin (Gepn), transcript variant 2
169	UGGACCAUUGUAGGAGAAUUGGCGGAG	1	177169056	177169085	-	potential	30	N	N	Intergenic	SET2 domain containing 2 (SET2d), SINE
170	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	177096391	177096391	-	potential	30	N	N	Intergenic	LTR
171	UGGACCAUUGUAGGAGAAUUGGCGGAG	2	176698905	176698934	-	potential	30	N	N	Intergenic	LTR

157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	175454561	175464890	-	potential	30	N	N	intergenic	LTR	
157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	177507922	177507951	+	potential	30	N	N	intergenic	LTR	
157	UUGUGAUGAUAACACACAGCAAGCAUUGAUAAGU	174789279	174789308	+	potential	30	N	N	intergenic	LTR	expressed sequence A1506816 (A1506816)
158	GGCCAAAGAAUUAUAACACACACACACACACAC	23219852	23219878	-	high confidence	27	Y	N	exon	ncRNA	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smc8), transcript variant 1
159	UGGAAACAAAGACACACACACACACACACACAC	60601516	60601542	+	high confidence	27	M	M	exon	mRNA	zinc finger protein, 532 (Zfp532)
160	UGGAAACAAAGACACACACACACACACACACAC	65792365	65792390	+	high confidence	26	Y	M	intron	mRNA	huntingtin interacting protein 1 (Htt1)
161	UGGAAACAAAGACACACACACACACACACACAC	135907570	135907595	-	non-candidate	26	Y	M	exon	mRNA	No Match
162	UGGAAACAAAGACACACACACACACACACACAC	36796588	36796620	-	potential	23	M	N	intergenic	SINE	SINE
163	UGGAAACAAAGACACACACACACACACACACAC	86354839	86354831	-	potential	23	M	N	intergenic	SINE	SINE
164	UGGAAACAAAGACACACACACACACACACACAC	25702331	25702357	-	potential	27	M	M	exon	mRNA	spermatogenesis and oogenesis specific basic helix-loop-helix 1 (Sohlh1)
166	UUCGAAACAAAGACACACACACACACACACAC	32098489	32098515	+	high confidence	27	Y	M	exon	mRNA	HLA-B associated transcript 2-like (Bat2l), transcript variant 2
167	UUCGAAACAAAGACACACACACACACACACAC	101137663	101137643	+	high confidence	25	Y	M	exon	mRNA	adenylyl kinase 3-like 1 (AK3l1), nuclear gene encoding mitochondrial protein
168	UGGAAACAAAGACACACACACACACACACACAC	126016998	126017024	-	non-candidate	27	Y	M	intergenic	mRNA	cyclin-dependent kinase 16 (Cdk16)
170	UGGAAACAAAGACACACACACACACACACACAC	20273594	20273619	+	high confidence	26	M	M	exon	mRNA	golgi coiled coil 1 (Gcc1)
171	UGGAAACAAAGACACACACACACACACACACAC	28371357	28371357	-	potential	26	M	M	exon	mRNA	
171	UGGAAACAAAGACACACACACACACACACACAC	75390798	75390824	-	non-candidate	27	Y	M	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	103087934	103087962	-	potential	29	N	N	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	94413229	94413257	-	potential	29	N	N	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	72185919	72185947	-	potential	29	N	N	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	72616258	72616286	-	potential	29	N	N	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	93157323	93157351	+	potential	29	N	N	intergenic	LTR	LTR
171	UGGAAACAAAGACACACACACACACACACACAC	11255396	11255424	+	potential	29	N	N	intergenic	LTR	LTR
172	UCCGAAACAAAGACACACACACACACACACAC	6240651	6240671	+	high confidence	22	Y	M	intergenic	SINE	SINE
173	UAGGAAACAAAGACACACACACACACACACAC	136654781	136654807	-	high confidence	27	M	M	intergenic	mRNA	protein phosphatase 1, regulatory (inhibitor) subunit 12B (Ppp1r12b)
174	UAGGAAACAAAGACACACACACACACACACAC	80896036	80896062	-	high confidence	27	M	M	exon	mRNA	eukaryotic translation initiation factor 4E binding protein 2 (EIF4ebp2)
175	UGGAAACAAAGACACACACACACACACACACAC	80264650	80264675	+	high confidence	26	M	N	intergenic	SINE	SINE
176	UUCGAAACAAAGACACACACACACACACACAC	65776415	6577641	+	high confidence	27	N	N	intergenic	LINE	LINE
176	UUCGAAACAAAGACACACACACACACACACAC	108191759	108191785	-	high confidence	27	N	N	intergenic	LINE	LINE
177	UCCGAAACAAAGACACACACACACACACACAC	24914742	24914742	+	high confidence	25	M	N	intergenic	LINE	LINE
178	UCCGAAACAAAGACACACACACACACACACAC	92132716	92132737	-	potential	22	N	N	intergenic	SINE	SINE
178	UCCGAAACAAAGACACACACACACACACACAC	71873925	71873946	-	potential	22	N	N	intergenic	mRNA	NDC90 homolog, kinetochore complex component (S. cerevisiae) (Ndc90) SINE
178	UCCGAAACAAAGACACACACACACACACACAC	90875686	90875707	+	potential	22	N	N	intergenic	SINE	SINE
178	UCCGAAACAAAGACACACACACACACACACAC	132325485	132325506	+	potential	22	N	N	intergenic	SINE	SINE
178	UCCGAAACAAAGACACACACACACACACACAC	77823831	77823852	+	potential	22	N	N	intergenic	SINE	SINE
178	UCCGAAACAAAGACACACACACACACACACAC	44298061	44298082	+	potential	22	N	N	intergenic	SINE	SINE
178	UCCGAAACAAAGACACACACACACACACACAC	121847510	121847531	-	potential	22	Y	N	intron	mRNA	ATP-binding cassette, sub-family A (ABC1), member 4 (Abca4) SINE
178	UCCGAAACAAAGACACACACACACACACACAC	43465813	43465834	-	potential	22	Y	N	intergenic	SINE	SINE
179	UAGUAAAGAAAGAAUUGAAGAAAGU	67543485	67543485	-	potential	26	Y	N	intergenic	mRNA	ERR3 homolog B (S. cerevisiae) (Err3b)
180	UACGAAACAAAGACACACACACACACACACAC	39768923	39768949	-	non-candidate	27	M	M	exon	mRNA	lysophosphatidic acid receptor 2 (Lpar2)
181	UCCGAAACAAAGACACACACACACACACACAC	72353146	72353171	-	potential	26	M	N	exon	mRNA	vasohibin 1 (Vasb1)
182	UUAAGAAAGAAAGAAUUAUCUAGAAAC	88033485	88033512	-	potential	28	M	M	exon	mRNA	cholinergic receptor, nicotinic, alpha polyanionic 4 (Chrna4)
183	UUCGAAACAAAGACACACACACACACACACAC	18078865	18078865	-	high confidence	27	Y	Y	exon	mRNA	ubiquitin-associated protein 2 (Uba2)
184	UUAUUAUUGAAGAAAGAAUUAUCUAGAAAC	41151099	41150127	-	non-candidate	29	Y	N	intron	mRNA	ubiquitin specific peptidase 29 (Ubp29)
185	UAGGAAACAAAGACACACACACACACACACAC	6756349	6756349	+	high confidence	22	Y	N	intron	mRNA	
186	CUUAAGAAAGAAAGAAUUGAAGAAAGU	37542855	37542855	+	potential	19	Y	N	intergenic	mRNA	MAD homolog 3 (Drosophila) (Smad3)
187	UCCGAAACAAAGACACACACACACACACACAC	63496817	63496842	-	high confidence	26	M	M	exon	mRNA	
188	UAGUAAAGAAAGAAUUGAAGAAAGU	87725937	87725962	+	high confidence	26	Y	Y	exon	mRNA	mitochondrial ribosomal protein L24 (Mpl24), nuclear gene encoding mitochondrial protein
189	UCCGAAACAAAGACACACACACACACACACAC	82847050	82847078	+	high confidence	29	N	N	intergenic	LTR	LTR
190	UGGAAACAAAGACACACACACACACACACACAC	117863593	117863614	+	high confidence	22	M	N	intron	mRNA	phosphatidylcholine:orthophosphate synthase 1 (Pgst1)
191	UACGAAACAAAGACACACACACACACACACAC	119735479	119735504	-	high confidence	26	M	N	intergenic	mRNA	
192	UAGGAAACAAAGACACACACACACACACACAC	37103490	37103490	-	high confidence	26	N	N	intergenic	mRNA	
192	UAGGAAACAAAGACACACACACACACACACAC	156214636	156214661	-	non-candidate	26	Y	M	exon	ncRNA	RIKEN cDNA 2900097C17 clone (2900097C17R1k)
193	UCCGAAACAAAGACACACACACACACACACAC	119349075	119349075	+	high confidence	25	M	N	intergenic	mRNA	
194	UAGCAUAGCUGAAGACACACACACACACACAC	3156891	31568916	+	high confidence	26	Y	N	intergenic	mRNA	
194	UAGCAUAGCUGAAGACACACACACACACACAC	128132947	128132947	-	high confidence	26	Y	N	intergenic	mRNA	
195	UAGGAAACAAAGACACACACACACACACACAC	66209684	66209710	+	potential	22	Y	M	exon	mRNA	SM domain containing 1 (Lsmg1)
196	UAGGAAACAAAGACACACACACACACACACAC	4623929	4623929	+	high confidence	27	Y	M	intron	mRNA	RCE1 homolog, prenyl protein peptidase (S. cerevisiae) (Rce1)
197	UAGGAAACAAAGACACACACACACACACACAC	10204485	10204485	+	non-candidate	25	Y	Y	exon	mRNA	zinc finger protein 740 (Zfp740)
198	UGGAAACAAAGACACACACACACACACACACAC	43952722	43952729	-	high confidence	28	M	M	intergenic	mRNA	