miRNA id (fold change in shell-repairing mantle)	Top 20 targets	Miranda Max score	Miranda Max energy	Top BLASTx hit against Swissprot	e-value	Query cover
lst-miR-4873 (-3.40X)	g58404.t1	185	-26.91	no hit	no hit	no hit
	g41826.t1	185	-28.49	no hit	no hit	no hit
	g25291.t1	184	-31.62	no hit	no hit	no hit
	g52447.t1	184	-26.43	no hit	no hit	no hit
	g114452.t7	183	-27.31	RecName: Full=Glucose transporter type 1; Flags: Precursor [Drosophila melanogaster]	5.00E-15	5%
	g114452.t6	183	-27.31	RecName: Full=Glucose transporter type 1; Flags: Precursor [Drosophila melanogaster]	2.00E-25	8%
	g2418.t1	183	-30.55	no hit	no hit	no hit
	g45713.t1	181	-26.59	no hit	no hit	no hit
	g94192.t1	181	-24.99	no hit	no hit	no hit
	g143281.t1	181	-29.91	RecName: Full=Dermatopontin; AltName: Full=Tyrosine-rich acidic matrix protein; Short=TRAMP [Biomphalaria glabrata]	1.00E-37	15%
	g14328.t2	181	-27.86	RecName: Full=Dermatopontin; AltName: Full=Tyrosine-rich acidic matrix protein; Short=TRAMP [Biomphalaria glabrata]	1.00E-37	13%
	g20244.t1	180	-25.75	no hit	no hit	no hit
	g6621.t1	180	-26.43	RecName: Full=Cubilin; AltName: Full=460 kDa receptor; AltName: Full=Glycoprotein 280; Short=gp280; AltName: Full=Intrinsic factor-cobalamin receptor; AltName: Full=Intrinsic factor-vitamin B12 receptor; Flags: Precursor [Rattus norvegicus]	5.00E-05	4%
	g62935.t1	180	-29.46	RecName: Full=Nostrin; AltName: Full=BAM247 homolog; AltName: Full=Nitric oxide synthase traffic inducer; AltName: Full=Nitric oxide synthase trafficker; AltName: Full=eNOS-trafficking inducer [Homo sapiens]	9.00E-16	27%
	g62936.t1	180	-29.46	RecName: Full=Guanine nucleotide exchange factor VAV3; Short=VAV-3 [Mus musculus]	1.00E-04	4%
	g57277.t1	180	-27.22	no hit	no hit	no hit
	g5510.t1	180	-27.09	no hit	no hit	no hit
	g20162.t1	180	-26.43	RecName: Full=Cubilin; AltName: Full=Intrinsic factor-cobalamin receptor; Flags: Precursor [Sus scrofa]	1.00E-09	19%
	g119139.t1	180	-30.39	no hit	no hit	no hit
	g45387.t7	179	-25.44	RecName: Full=Protein unc-79 homolog [Homo sapiens]	9.00E-33	16%
lst-miR-4881 (-2.62x)	g95900.t1	182	-25.22	RecName: Full=Prespore vesicle protein; Short=PSV; Flags: Precursor [Dictyostelium discoideum]	0.015	5%
	g102818.t1	182	-30.2	no hit	no hit	no hit
	g106566.t1	182	-30.75	no hit	no hit	no hit
	g110119.t1	178	-26.37	no hit	no hit	no hit
	g117811.t5	177	-29.04	no hit	no hit	no hit
	g123846.t1	177	-26.63	no hit	no hit	no hit
	g93758.t1	176	-28.06	no hit	no hit	no hit
	g3610.t1	174	-22.16	no hit	no hit	no hit
	g85468.t1	174	-23.72	RecName: Full=Sialate O-acetylesterase; AltName: Full=Sialic acid-specific 9-O-acetylesterase; Flags: Precursor [Pongo abelii]	4.00E-59	20%
	g85468.t2	174	-23.72	RecName: Full=Sialate O-acetylesterase; AltName: Full=Sialic acid-specific 9-O-acetylesterase; AltName: Full=Yolk sac protein 2; Contains: RecName: Full=Sialate O-acetylesterase small subunit; Contains: RecName: Full=Sialate O-acetylesterase large subunit; Flags: Precursor [Rattus norvegicus]	6.00E-45	22%
	g85468.t3	174	-23.72	RecName: Full=Sialate O-acetylesterase; AltName: Full=Sialic acid-specific 9-O-acetylesterase; AltName: Full=Yolk sac protein 2; Contains: RecName: Full=Sialate O-acetylesterase small subunit; Contains: RecName: Full=Sialate O-acetylesterase large subunit; Flags: Precursor [Rattus norvegicus]	6.00E-45	21%
	g85469.t1	174	-23.72	RecName: Full=Sialate O-acetylesterase; AltName: Full=Sialic acid-specific 9-O-acetylesterase; AltName: Full=Yolk sac protein 2; Contains: RecName: Full=Sialate O-acetylesterase small subunit; Contains: RecName: Full=Sialate O-acetylesterase large subunit; Flags: Precursor [Rattus norvegicus]	7.00E-49	12%
	g85469.t2	174	-23.72	RecName: Full=Sialate O-acetylesterase; AltName: Full=Sialic acid-specific 9-O-acetylesterase; AltName: Full=Yolk sac protein 2; Contains: RecName: Full=Sialate O-acetylesterase small subunit; Contains: RecName: Full=Sialate O-acetylesterase large subunit; Flags: Precursor [Mus musculus]	2.00E-105	19%
	g8360.t2	174	-23.47	RecName: Full=Tyrosine-protein kinase Dtl; AltName: Full=Protein derailed; Flags: Precursor [Drosophila melanogaster]	2.00E-10	6%
	g8360.t3	174	-23.47	RecName: Full=Tyrosine-protein kinase Dtl; AltName: Full=Protein derailed; Flags: Precursor [Drosophila melanogaster]	3.00E-06	3%
	g21948.t1	174	-29.86	RecName: Full=Nck-associated protein 5; Short=NAP-5; AltName: Full=Peripheral clock protein [Homo sapiens]	1.10E-02	2%
	g73735.t3	174	-21.42	no hit	no hit	no hit
	g73735.t5	174	-21.42	no hit	no hit	no hit
	g113352.t1	174	-22	no hit	no hit	no hit
	g113352.t2	174	-22	no hit	no hit	no hit
lst-miR-16924 (-1.67X)	g119619.t1	190	-43.84	no hit	no hit	no hit
	g51572.t1	177	-30.3	no hit	no hit	no hit
	g116818.t1	177	-30.27	RecName: Full=General transcription factor II-I repeat domain-containing protein 2A; Short=GTF2I repeat domain-containing protein 2A; AltName: Full=Transcription factor GTF2IRD2-alpha [Homo sapiens]	0.033	5%
	g117448.t1	177	-30.27	no hit	no hit	no hit
	g52356.t1	174	-28.13	no hit	no hit	no hit
	g34481.t1	174	-31.39	no hit	no hit	no hit
	g100794.t1	172	-28.03	RecName: Full=Uncharacterized 51.9 kDa protein in rps4-rps11 intergenic region; AltName: Full=ORF426 [Euglena longa]	1.00E-06	7%
	g31308.t1	172	-32.2	no hit	no hit	no hit
	g63790.t1	172	-32.21	no hit	no hit	no hit
	g116716.t2	172	-29.7	RecName: Full=Phospholipid-transporting ATPase IA; AltName: Full=ATPase class I type 8A member 1; AltName: Full=Chromaffin granule ATPase II; AltName: Full=P4-ATPase flippase complex alpha subunit ATP8A1 [Homo sapiens]	1.00E-40	7%
	g116716.t3	172	-29.7	RecName: Full=Phospholipid-transporting ATPase IA; AltName: Full=ATPase class I type 8A member 1; AltName: Full=Chromaffin granule ATPase II; AltName: Full=P4-ATPase flippase complex alpha subunit ATP8A1 [Homo sapiens]	4.00E-17	6%
	g59871.t1	171	-30.19	no hit	no hit	no hit
	g43709.t1	170	-23.34	no hit	no hit	no hit
	g30036.t1	170	-27.15	no hit	no hit	no hit
	g66302.t1	170	-29.18	RecName: Full=Seminal vesicle secretory protein 2; AltName: Full=Seminal vesicle secretory protein II; Short=SVS II; Flags: Precursor [Rattus norvegicus]	1.00E-05	15%
	g35808.t1	169	-26.7	no hit	no hit	no hit
	g35808.t3	169	-26.7	no hit	no hit	no hit
	g35808.t5	169	-26.7	RecName: Full=General transcription factor II-I repeat domain-containing protein 2B; Short=GTF2I repeat domain-containing protein 2B; AltName: Full=Transcription factor GTF2IRD2-beta [Homo sapiens]	3.00E-07	5%
	g35808.t2	169	-26.7	no hit	no hit	no hit
	g108322.t2	169	-24.33	RecName: Full=Heparan-alpha-glucosaminide N-acetyltransferase; AltName: Full=Transmembrane protein 76 [Homo sapiens]	5.00E-22	6%
lst-miR-33878 (-1.59X)	g101956.t1	184	-36.17	no hit	no hit	no hit
	g69594.t1	183	-26.53	RecName: Full=Low-density lipoprotein receptor-related protein 2; Short=LRP-2; AltName: Full=Glycoprotein 330; Short=gp330; AltName: Full=Megalin; Flags: Precursor [Sus scrofa]	3.00E-06	6%
	g108808.t1	182	-25.67	no hit	no hit	no hit
	g122744.t1	182	-29.46	RecName: Full=Ankyrin-3; Short=ANK-3; AltName: Full=Ankyrin-G [Mus musculus]	1.00E-20	59%
	g4536.10.t1	180	-23.6	RecName: Full=RNA-binding protein 12B; AltName: Full=RNA-binding motif protein 12B [Homo sapiens]	0.038	21%
	g108542.t1	179	-24.9	no hit	no hit	no hit
	g66682.t1	178	-26.46	no hit	no hit	no hit
	g112927.t3	176	-24.11	RecName: Full=CTTNBP2 N-terminal-like protein [Homo sapiens]	1.00E-55	17%
	g112927.t2	176	-24.11	RecName: Full=CTTNBP2 N-terminal-like protein [Homo sapiens]	1.00E-55	17%
	g97261.t1	176	-23.66	no hit	no hit	no hit
	g97261.t2	176	-23.66	RecName: Full=Sialin; AltName: Full=H(+)/nitrate cotransporter; AltName: Full=H(+)/sialic acid cotransporter; Short=AST; AltName: Full=Membrane glycoprotein HP59; AltName: Full=Solute carrier family 17 member 5; AltName: Full=Vesicular H(+)/Aspartate-glutamate cotransporter [Homo sapiens]	2.00E-33	15%
	g3413.t2	175	-29.91	RecName: Full=Centrosomal protein of 83 kDa; Short=Cep83; AltName: Full=Coiled-coil domain-containing protein 41 [Danio rerio]	6.00E-31	18%
	g3413.t1	175	-29.91	RecName: Full=Centrosomal protein of 83 kDa; Short=Cep83; AltName: Full=Coiled-coil domain-containing protein 41 [Danio rerio]	1.00E-22	16%
	g3441.t1	175	-23.74	no hit	no hit	no hit
	g25921.t4	175	-21.8	RecName: Full=Protocadherin Fat 4; AltName: Full=FAT tumor suppressor homolog 4; AltName: Full=Fat-like cadherin protein FAT-J; Flags: Precursor [Mus musculus]	8.00E-73	44%
	g25921.t5	175	-21.8	RecName: Full=Protocadherin Fat 4; AltName: Full=FAT tumor suppressor homolog 4; AltName: Full=Fat-like cadherin protein FAT-J; Flags: Precursor [Mus musculus]	2.00E-72	44%
	g94806.t1	175	-21.74	no hit	no hit	no hit
	g120222.t2	175	-30.16	no hit	no hit	no hit
	g120222.t3	175	-30.16	no hit	no hit	no hit
	g10984.t1	175	-21.69	RecName: Full=Carboxypeptidase Y; Short=CPY; Flags: Precursor [Schizosaccharomyces pombe 972h-]	3.00E-07	4%
lst-miR-26499 (+1.44X)	g21839.t1	181	-30.17	RecName: Full=Postacrosomal sheath WW domain-binding protein; AltName: Full=WW domain-binding protein 2-like [Homo sapiens]	9.00E-06	5%
	g83213.t1	179	-32.52	RecName: Full=Sperm acrosomal protein FSA-ACR.1; Flags: Precursor [Vulpes vulpes]	6.00E-05	23%
	g72829.t1	179	-34.39	no hit	no hit	no hit
	g50484.t1	179	-29.76	no hit	no hit	no hit
	g53890.t1	176	-30.44	no hit	no hit	no hit
	g81916.t1	176	-30.02	no hit	no hit	no hit
	g19426.t1	176	-32.6	RecName: Full=Versican core protein; AltName: Full=Chondroitin sulfate proteoglycan core protein 2; Short=Chondroitin sulfate proteoglycan 2; AltName: Full=Large fibroblast proteoglycan; AltName: Full=PG-M; Flags: Precursor [Gallus gallus]	0.006	4%
	g85868.t1	175	-31.15	RecName: Full=PiggyBac transposable element-derived protein 1; AltName: Full=Cerebral protein 4 [Homo sapiens]	0.003	4%
	g11372.t1	175	-32.88	RecName: Full=Uncharacterized protein KD2A2.6 [Caenorhabditis elegans]	1.00E-50	33%
	g91102.t3	175	-29.61	no hit	no hit	no hit
	g91102.t5	175	-29.61	no hit	no hit	no hit
	g91102.t4	175	-29.61	no hit	no hit	no hit
	g124973.t1	173	-25.85	no hit	no hit	no hit
	g7272.t1	173	-31.71	RecName: Full=Guanine nucleotide exchange factor subunit RIC1; AltName: Full=Protein RIC1 homolog; AltName: Full=RAB6A-GEF complex partner 1 [Danio rerio]	0.003	12%
	g71517.t1	173	-26.16	RecName: Full=Protein TIC 214; AltName: Full=Translocon at the inner envelope membrane of chloroplasts 214; Short=atTIC214 [Pinus koraiensis]	0.01	9%
	g76587.t1	173	-31.63	no hit	no hit	no hit
	g65491.t1	173	-33.3	RecName: Full=Thioredoxin-like protein 1; AltName: Full=Thioredoxin-related protein [Rattus norvegicus]	3.00E-25	7%
	g65491.t3	173	-33.3	RecName: Full=Thioredoxin-like protein 1; AltName: Full=Thioredoxin-related protein [Rattus norvegicus]	3.00E-32	13%
	g44108.t1	172	-24.45	no hit	no hit	no hit
	g1372.t1	172	-24.54	RecName: Full=Baculoviral IAP repeat-containing protein 7-B; AltName: Full=E3 ubiquitin-protein ligase EIAP-B; AltName: Full=Embryonic/Egg IAP-B; Short=EIAP/XLX-B; AltName: Full=RING-type E3 ubiquitin transferase EIAP-B [Xenopus laevis]	4.00E-12	7%
lst-miR-28733 (+2.54X)	g79015.t1	200	-41.51	no hit	no hit	no hit
	g93983.t1	192	-36.56	no hit	no hit	no hit
	g52405.t1	192	-36.56	no hit	no hit	no hit
	g60588.t1	192	-36.56	RecName: Full=Elongation factor 1-beta; Short=EF-1-beta [Bos taurus]	2.00E-05	1%
	g84119.t1	192	-36.56	RecName: Full=Sodium/hydrogen exchanger 9B2; AltName: Full=Na(+)/H(+) exchanger NHA2; AltName: Full=Na(+)/H(+) exchanger-like domain-containing protein 2; Short=NHE domain-containing protein 2; AltName: Full=Sodium/hydrogen exchanger-like domain-containing protein 2; AltName: Full=Solute carrie	7.00E-46	12%
	g84120.t1	192	-36.56	RecName: Full=Sodium/hydrogen exchanger 9B2; AltName: Full=Na(+)/H(+) exchanger NHA2; AltName: Full=Na(+)/H(+) exchanger-like domain-containing protein 2; Short=NHE domain-containing protein 2; AltName: Full=Sodium/hydrogen exchanger-like domain-containing protein 2; AltName: Full=Solute carrie	2.00E-20	12%
	g84121.t1	192	-36.56	no hit	no hit	no hit
	g77804.t1	192	-36.56	no hit	no hit	no hit
	g53686.t1	192	-36.56	RecName: Full=Probable coatomer subunit beta'; AltName: Full=Beta'-coat protein; Short=Beta'-COP [Caenorhabditis elegans]	4.00E-16	2%
	g81079.t3	192	-36.19	RecName: Full=Serine/threonine-protein phosphatase PP1-beta catalytic subunit; Short=PP-1B [Xenopus tropicalis]	3.00E-73	12%
	g81079.t4	192	-36.19	RecName: Full=Serine/threonine-protein phosphatase PP1-beta catalytic subunit; Short=PP-1B [Sus scrofa]	0.00E+00	11%
	g81079.t1	192	-36.19	RecName: Full=Serine/threonine-protein phosphatase PP1-beta catalytic subunit; Short=PP-1B [Xenopus tropicalis]	3.00E-117	16%
	g112523.t1	188	-36.09	RecName: Full=RNA-directed DNA polymerase from mobile element jockey; AltName: Full=Reverse transcriptase [Drosophila melanogaster]	2.00E-17	17%
	g3574.t1	188	-32.54	no hit	no hit	no hit
	g63203.t2	188	-34.34	no hit	no hit	no hit
	g63203.t1	188	-34.34	no hit	no hit	no hit
	g50583.t1	188	-34.82	RecName: Full=Probable RNA-directed DNA polymerase from transposon BS; AltName: Full=Reverse transcriptase [Drosophila melanogaster]	0.004	18%
	g78741.t3	188	-34.34	RecName: Full=Importin-9; Short=Imp9; AltName: Full=Importin-9a; Short=Imp9a; AltName: Full=Importin-9b; Short=Imp9b; AltName: Full=Ran-binding protein 9; Short=RanBP9 [Mus musculus]	5.00E-46	6%
	g78741.t4	188	-34.34	RecName: Full=Importin-9; Short=Imp9; AltName: Full=Importin-9a; Short=Imp9a; AltName: Full=Importin-9b; Short=Imp9b; AltName: Full=Ran-binding protein 9; Short=RanBP9 [Mus musculus]	2.00E-22	6%
	g35031.t1	188	-36.09	RecName: Full=GA-binding protein alpha chain; Short=GABP subunit alpha [Mus musculus]	1.00E-110	21%
lst-miR-3847 (+2.76X)	g73090.t1	184	-31.07	no hit	no hit	no hit
	g6718.t1	179	-32.08	no hit	no hit	no hit
	g105919.t1	177	-30.42	no hit	no hit	no hit
	g5359.t3	176	-29.64	no hit	no hit	no hit
	g5359.t1	176	-29.64	no hit	no hit	no hit
	g5359.t2	176	-29.64	no hit	no hit	no hit
	g115331.t19	176	-31.69	RecName: Full=Protocadherin beta-13; Short=PCDH-beta-13; Flags: Precursor [Pan troglodytes]	4.00E-09	6%
	g115331.t11	176	-31.69	RecName: Full=Cadherin-related family member 2; Flags: Precursor [Mus musculus]	3.00E-52	30%
	g115331.t4	176	-31.69	RecName: Full=Cadherin-23; AltName: Full=Otocadherin; Flags: Precursor [Homo sapiens]	4.00E-73	32%
	g46276.t1	175	-27.89	RecName: Full=Fibrocystin-L; AltName: Full=Polycystic kidney and hepatic disease 1-like protein 1; Short=PKHD1-like protein 1; Flags: Precursor [Homo sapiens]	7.00E-18	18%
	g46277.t1	175	-27.89	RecName: Full=Fibrocystin-L; AltName: Full=Polycystic kidney and hepatic disease 1-like protein 1; Short=PKHD1-like protein 1; Flags: Precursor [Homo sapiens]	6.00E-18	23%
	g46278.t1	175	-27.89	RecName: Full=Fibrocystin-L; AltName: Full=Polycystic kidney and hepatic disease 1-like protein 1; Short=PKHD1-like protein 1; Flags: Precursor [Homo sapiens]	1.00E-18	21%
	g110919.t9	174	-28.84	no hit	no hit	no hit
	g110919.t10	174	-28.84	RecName: Full=Leucine-rich repeat serine/threonine-protein kinase 1 [Mus musculus]	2.00E-47	22%
	g104736.t1	174	-27.9	RecName: Full=Guanylate cyclase 32E; Flags: Precursor [Drosophila melanogaster]	2.00E-37	17%
	g104736.t2	174	-27.9	RecName: Full=Guanylate cyclase 32E; Flags: Precursor [Drosophila melanogaster]	2.00E-26	10%
	g104736.t3	174	-27.9	RecName: Full=Guanylate cyclase 32E; Flags: Precursor [Drosophila melanogaster]	3.00E-13	7%
	g104737.t2	174	-27.9	RecName: Full=Receptor-type guanylate cyclase Gyc76C; AltName: Full=DrGC-1; Flags: Precursor [Drosophila melanogaster]	8.00E-15	7%
	g1297.t1	174	-27.68	no hit	no hit	no hit
	g19007.t1	174	-31.61	RecName: Full=TWIK family of potassium channels protein 18 [Caenorhabditis elegans]	3.00E-15	10%
lst-miR-18140 (+7.83X)	g54280.t1	184	-30.31	RecName: Full=Variant surface antigen E; AltName: Full=VlpE prolipoprotein; Flags: Precursor [Mycoplasma hyorhinis]	1.00E-05	18%
	g50605.t1	184	-32.25	no hit	no hit	no hit
	g99428.t1	181	-31.52	RecName: Full=Laccase-2; AltName: Full=Benzenediol:oxygen oxidoreductase 2; AltName: Full=Diphenol oxidase 2; AltName: Full=Urishiol oxidase 2; Flags: Precursor [Botrytis cinerea]	4.00E-55	44%
	g26158.t1	180	-25.87	RecName: Full=Laccase-3; AltName: Full=Benzenediol:oxygen oxidoreductase 3; AltName: Full=Diphenol oxidase 3; AltName: Full=Urishiol oxidase 3; Flags: Precursor [Trametes villosa]	5.00E-13	6%
	g2946.t1	180	-32.37	no hit	no hit	no hit
	g116561.t1	180	-32.14	no hit	no hit	no hit
	g48920.t1	179	-31.33	RecName: Full=Metabotropic glutamate receptor-like protein N [Dictyostelium discoideum]	0.028	11%
	g47323.t1	178	-26.65	RecName: Full=Probable voltage-dependent N-type calcium channel subunit alpha-1B; AltName: Full=DOE-4; AltName: Full=Voltage-gated calcium channel subunit alpha Cav2.2 [Diplobatis ommata]	0.026	2%
	g3355.t2	177	-28.24	no hit	no hit	no hit
	g3356.t1	177	-29.75	RecName: Full=Shematrin-like protein 1; AltName: Full=Shematrin-3; Flags: Precursor [Pinctada margaritifera]	1.00E-24	15%
	g3357.t2	177	-28.24	RecName: Full=L-ascorbate oxidase; Short=AAO; Short=AO; Short=ASO; Short=Ascorbase; Flags: Precursor [Brassica rapa subsp. pekinensis]	9.00E-18	7%
	g3357.t3	177	-28.24	RecName: Full=L-ascorbate oxidase; Short=AAO; Short=AO; Short=ASO; Short=Ascorbase; Flags: Precursor [Brassica rapa subsp. pekinensis]	8.00E-10	8%
	g74245.t1	177	-24.83	RecName: Full=Deoxyribose-phosphate aldolase; Short=DERA; AltName: Full=2-deoxy-D-ribose 5-phosphate aldolase; AltName: Full=Phosphodeoxyriboaldolase; Short=Deoxyriboaldolase [Bos taurus]	3.00E-138	31%
	g52514.t1	176	-28.27	no hit	no hit	no hit
	g14760.t7	176	-28.12	RecName: Full=Selenocysteine insertion sequence-binding protein 2; Short=SECIS-binding protein 2 [Homo sapiens]	1.00E-07	1%
	g14760.t1	176	-28.12	RecName: Full=Selenocysteine insertion sequence-binding protein 2; Short=SECIS-binding protein 2 [Rattus norvegicus]	1.00E-15	12%
	g14760.t3	176	-28.12	RecName: Full=Selenocysteine insertion sequence-binding protein 2; Short=SECIS-binding protein 2 [Rattus norvegicus]	1.00E-15	10%
	g14760.t4	176	-28.12	RecName: Full=Selenocysteine insertion sequence-binding protein 2; Short=SECIS-binding protein 2 [Homo sapiens]	4.00E-08	4%
	g14760.t10	176	-28.12	RecName: Full=Selenocysteine insertion sequence-binding protein 2-like; Short=SECIS-binding protein 2-like [Mus musculus]	2.00E-78	27%
	g121892.t1	176	-27.5	RecName: Full=Uncharacterized protein RP688 [Rickettsia prowazekii str. Madrid E]	3.00E-05	14%
lst-miR-8292 (+9.41X)	g81173.t1	200	-36.52	no hit	no hit	no hit
	g86115.t1	192	-33.48	no hit	no hit	no hit
	g24619.t1	188	-27.39	no hit	no hit	no hit
	g2840.t3	184	-24.01	no hit	no hit	no hit
	g123193.t1	184	-23.13	no hit	no hit	no hit
	g42674.t1	184	-21.49	RecName: Full=Histone-lysine N-methyltransferase EHMT1; AltName: Full=Euchromatic histone-lysine N-methyltransferase 1; Short=Eu-HMTase1; AltName: Full=G9a-like protein 1; Short=GLP; Short=GLP1; AltName: Full=Lysine N-methyltransferase 1D [Mus musculus]	6.00E-11	11%
	g73881.t1	182	-24.79	no hit	no hit	no hit
	g126076.t1	182	-23.75	no hit	no hit	no hit
	g46139.t2	180	-22.34	no hit	no hit	no hit
	g46139.t1	180	-22.34	no hit	no hit	no hit
	g103495.t2	180	-20.43	no hit	no hit	no hit
	g129832.t1	180	-20.84	no hit	no hit	no hit
	g82053.t1	180	-25.39	RecName: Full=Mitogen-activated protein kinase 11; Short=MAP kinase 11; Short=MAPK 11; AltName: Full=Mitogen-activated protein kinase p38 beta; Short=MAP kinase p38 beta; Short=p38b; AltName: Full=Stress-activated protein kinase 2b; Short=SAPK2b; AltName: Full=p38-2 [Homo sapiens]	1.00E-122	6%
	g82052.t1	180	-25.39	RecName: Full=Mitogen-activated protein kinase 14; Short=MAP kinase 14; Short=MAPK 14; AltName: Full=Mitogen-activated protein kinase 2; Short=MAP kinase 2; Short=MPK2 [Xenopus laevis]	7.00E-12	6%
	g14517.t2	180	-22.84	RecName: Full=Pre-mRNA-processing factor 19; AltName: Full=PRP19/PSO4 homolog; AltName: Full=RING-type E3 ubiquitin transferase PRP19 [Bos taurus]	0	31%
	g14517.t1	180	-22.84	RecName: Full=Pre-mRNA-processing factor 19; AltName: Full=PRP19/PSO4 homolog; AltName: Full=RING-type E3 ubiquitin transferase PRP19 [Bos taurus]	0	32%
	g89330.t1	180	-20.1	no hit	no hit	no hit
	g55742.t1	180	-24.69	RecName: Full=Uncharacterized protein KD2A2.6 [Caenorhabditis elegans]	4.00E-11	10%
	g114275.t1	180	-21.8	no hit	no hit	no hit
	g17956.t1	180	-21.34	RecName: Full=UPF0303 protein Arad_3071 [Agrobacterium radiobacter K84]	0.047	2%
lst-miR-3861 (+11.26X)	g11857.t2	180	-29.34	RecName: Full=Multidrug resistance-associated protein 1; AltName: Full=ATP-binding cassette sub-family C member 1; AltName: Full=Glutathione-S-conjugate-translocating ATPase ABCC1; AltName: Full=Leukotriene C(4) transporter; Short=LTC4 transporter [Homo sapiens]	5.00E-80	9%
	g25869.t1	180	-23.69	no hit	no hit	no hit
	g106087.t1	180	-24.15	RecName: Full=Translation initiation factor IF-2 [Borreliella bavariensis PBi]	9.00E-07	15%
	g21035.t1	180	-24.89	RecName: Full=Battenin; AltName: Full=Protein CLN3; Flags: Precursor [Canis lupus familiaris]	2.00E-103	30%
	g113055.t1	180	-23.99	no hit	no hit	no hit
	g37920.t1	179	-23.61	no hit	no hit	no hit
	g14866.t5	178	-23.53	RecName: Full=52 kDa repressor of the inhibitor of the protein kinase; Short=p52rIPK; AltName: Full=58 kDa interferon-induced protein kinase-interacting protein; Short=p58IPK-interacting protein; AltName: Full=Death-associated protein 4; AltName: Full=THAP domain-containing protein 0; AltName: Full=THAP d	1.00E-05	19%
	g77854.t1	178	-21.95	no hit	no hit	no hit
	g106709.t1	178	-28.91	no hit	no hit	no hit
	g46636.t4	176	-22.27	RecName: Full=E3 ubiquitin-protein ligase NEDD4; AltName: Full=Cell proliferation-inducing gene 53 protein; AltName: Full=HECT-type E3 ubiquitin transferase NEDD4; AltName: Full=Neural precursor cell expressed developmentally down-regulated protein 4; Short=NEDD-4 [Homo sapiens]	5.00E-18	14%
	g124065.t1	176	-27.07	RecName: Full=Pesticidal crystal protein Cry11Bb; AltName: Full=84 kDa crystal protein; AltName: Full=Crystaline entomocidal protoxin; AltName: Full=Insecticidal delta-endotoxin CryIIB(b) [Bacillus thuringiensis serovar medellin]	2.00E-04	8%
	g75266.t1	176	-20.13	no hit	no hit	no hit
	g123025.t1	176	-22.78	no hit	no hit	no hit
	g7901.t2	176	-20.67	RecName: Full=Lysosomal alpha-glucosidase; AltName: Full=Acid maltase; Flags: Precursor [Mus musculus]	1.00E-158	36%
	g118657.t5	176	-23.21	RecName: Full=Poly [ADP-ribose] polymerase tankyrase-1; AltName: Full=ADP-ribosyltransferase diphtheria toxin-like 5; Short=ARTD5; AltName: Full=Poly [ADP-ribose] polymerase 5A; AltName: Full=Protein poly-ADP-ribosyltransferase tankyrase-1; AltName: Full=TNKS-1; AltName: Full=TRF1-interacting ankyrin-	8.00E-10	8%
	g118657.t4	176	-23.21	RecName: Full=Beta-hexosaminidase; AltName: Full=Beta-GlcNAcase; AltName: Full=Beta-N-acetylhexosaminidase; AltName: Full=N-acetyl-beta-glucosaminidase; Flags: Precursor [Candida albicans]	5.00E-04	11%
	g22669.t1	176	-25.12	RecName: Full=Titin homolog [Caenorhabditis elegans]	1.00E-15	17%
	g56858.t1	176	-23.19	no hit	no hit	no hit
	g32266.t1	175	-21.19	RecName: Full=DNA-binding protein HEXBP; AltName: Full=Hexamer-binding protein [Leishmania major]	1.00E-12	10%
	g91300.t1	175	-21.05	no hit	no hit	no hit