Supplement 5. Probe sets for genes related to Alzheimer's and Parkinson's in serotonin neurons. All probe sets changed 2-fold or greater with E or E+P treatement.

Search	**Mean Signal Intensity**					
	Ovx	**E**	**E+P**	**Gene Identifie**	**Other ID**	**Gene Title**
Alzheimer's	54.5	4840.45	918.3	CO649101	AFFX-Mmu-gapdh-5_at	M. mulatta GEN=gapdh DB_XREF=gb:CO649101 DB_XREF=gi:50570595 DB_XREF=ILLUMIGEN_MCQ_42691 FEA=mRNA CLONE=IBIUW:22567 DEF=gapdh
	52.2	3976.65	893.05	N33009	MmugDNA.31898.1.S1_s_a	gDNA.Hs.169401.0.S1 FEA=U133PSR GEN=APOE DEF=Orthologous to 203381_s_at apolipoprotein E
	179.35	7001.75	2658.35	CB308652	Mmu.3902.1.S1_at	gb:CB308652 DB_XREF=gi:28831362 DB_XREF=AGENCOURT_11771965 CLONE=IMAGE:6882338 TID=Mmu.3902.1 CNT=4 FEA=EST TIER=ConsEnd STK=0
	244.25	6410.85	1160.8	CO649101	AFFX-Mmu-gapdh-M_x_at	M. mulatta GEN=gapdh DB_XREF=gb:CO649101 DB_XREF=gi:50570595 DB_XREF=ILLUMIGEN_MCQ_42691 FEA=mRNA CLONE=IBIUW:22567 DEF=gapdh
	134.65	3136.85	913	CX078587	Mmu.2238.1.S1_at	gb:CX078587 DB_XREF=gi:56592577 DB_XREF=ILLUMIGEN_MCQ_2018 CLONE=IBIUW:30225 TID=Mmu.2238.1 CNT=19 FEA=EST TIER=ConsEnd STK=0
	18.9	210.6	210.85	NM_004836	MmugDNA.30636.1.S1_at	gDNA.g4758891 FEA=U133PSR GEN=EIF2AK3 DEF=Orthologous to 218696_at eukaryotic translation initiation factor 2-alpha kinase 3
	300.9	5308.15	1231	NM_000041	MmugDNA.17966.1.S1_x_a	gDNA.g4557324 FEA=U133PSR GEN=APOE DEF=Orthologous to 203382_s_at apolipoprotein E
	177.45	2564.9	942.35	CX078600	Mmu.2126.1.S1_s_at	gb:CX078600 DB_XREF=gi:56592590 DB_XREF=ILLUMIGEN_MCQ_42100 CLONE=IBIUW:30247 TID=Mmu.2126.1 CNT=25 FEA=EST TIER=ConsEnd STK=0
	86.35	1024.8	512.35	CO580535	Mmu.7758.1.S1_at	gb:CO580535 DB_XREF=gi:50411701 DB_XREF=ILLUMIGEN_MCQ_48559 CLONE=IBIUW:19027 TID=Mmu.7758.1 CNT=9 FEA=EST TIER=ConsEnd STK=0
	125.5	1606.35	576.95	BC000649	MmugDNA.8653.1.S1_at	gDNA.g12653726 FEA=U133PSR GEN=UQCRFS1 DEF=Orthologous to 208909_at ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
	126.5	1711.95	475.25	CX078600	Mmu.2126.1.S1_at	gb:CX078600 DB_XREF=gi:56592590 DB_XREF=ILLUMIGEN_MCQ_42100 CLONE=IBIUW:30247 TID=Mmu.2126.1 CNT=25 FEA=EST TIER=ConsEnd STK=0
	46.65	639.2	150.1	U23850	MmugDNA.3681.1.S1_s_at	gDNA.Hs.198443.2.S1 FEA=U133PSR GEN=ITPR1 DEF=Orthologous to 216944_s_at inositol 1,4,5-triphosphate receptor, type 1
	22.9	257.25	84.15	NM_002496	MmugDNA.42544.1.S1_at	gDNA.g4505370 FEA=U133PSR GEN=NDUFS8 DEF=Orthologous to 203189_s_at NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
	9.55	96.7	42.65	AB050436	MmugDNA.38319.1.S1_at	gDNA.g13568406 FEA=U133PSR GEN=BACE1 DEF=Orthologous to 224335_s_at beta-site APP-cleaving enzyme 1 beta-site APP-cleaving enzyme 1
	435.85	4015.8	1669.65	NM_001861	MmugDNA.16704.1.S1_at	gDNA.g4502980 FEA=U133PSR GEN=COX4I1 DEF=Orthologous to 202698_x_at cytochrome c oxidase subunit IV isoform 1
	49.95	318.7	324.75	BC000251	MmugDNA.29314.1.S1_at	gDNA.g12652980 FEA=U133PSR GEN=GSK3B DEF=Orthologous to 209945_s_at glycogen synthase kinase 3 beta
	183.55	1617.6	599.2	NM_000933	MmugDNA.2360.1.S1_at	gDNA.g4505866 FEA=U133PSR GEN=PLCB4 DEF=Orthologous to 203896_s_at phospholipase C, beta 4
	54.7	284.5	273.2	NM_004346	MmugDNA.6342.1.S1_at	gDNA.g4757911 FEA=U133PSR GEN=CASP3 DEF=Orthologous to 202763_at caspase 3, apoptosis-related cysteine protease
	352.35	2232.9	1230.15	NM_003002	MmugDNA.27382.1.S1_at	gDNA.g4506864 FEA=U133PSR GEN=SDHD DEF=Orthologous to 202026_at succinate dehydrogenase complex, subunit D, integral membrane protein
	1280.1	8540.4	3545.3	AA854966	MmugDNA.39322.1.S1_s_a	gDNA.Hs.113205.2.S1 FEA=U133PSR GEN=COX4I1 DEF=Orthologous to 200086_s_at cytochrome c oxidase subunit IV isoform 1 cytochrome c oxidase subunit IV isoform 1
	67.3	378.4	253.35	AA834576	MmugDNA.32745.1.S1_at	gDNA.Hs.238272.0.A2 FEA=U133PSR GEN=ITPR2 DEF=Orthologous to 202660_at inositol 1,4,5-triphosphate receptor, type 2
	351.95	2097.8	1174.4	CO644739	Mmu.12382.1.S1_s_at	gb:CO644739 DB_XREF=gi:50566233 DB_XREF=ILLUMIGEN_MCQ_43431 CLONE=IBIUW:22477 TID=Mmu.12382.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
	251.5	1458	802.8	NM_003000	MmugDNA.9546.1.S1_s_at	gDNA.g9257241 FEA=U133PSR GEN=SDHB DEF=Orthologous to 202675_at succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
	667.7	3448.25	2326.75	CO581557	Mmu.5257.1.S1_at	gb:CO581557 DB_XREF=gi:50412949 DB_XREF=ILLUMIGEN_MCQ_47054 CLONE=IBIUW:18627 TID=Mmu.5257.1 CNT=3 FEA=EST TIER=ConsEnd STK=1
	108.55	716.95	215.15	CO580643	Mmu.1775.1.S1_at	gb:CO580643 DB_XREF=gi:50411831 DB_XREF=ILLUMIGEN_MCQ_48393 CLONE=IBIUW:18409 TID=Mmu.1775.1 CNT=3 FEA=mRNA TIER=ConsEnd STK=0
	262	1423.2	752.85	NM_004549	MmugDNA.29870.1.S1_at	gDNA.g4758783 FEA=U133PSR GEN=NDUFC2 DEF=Orthologous to 218101_s_at NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
	21.35	55	117	AF486845	MmugDNA.424.1.S1_at	gDNA.Hs2.367945.4.S1 FEA=U133PSR GEN=CASP12P1 DEF=Orthologous to 1564736_a_at caspase 12 pseudogene 1
	544	2767.45	1483.5	AA129773	MmugDNA.1694.1.S1_at	gDNA.Hs.66151.0.S1 FEA=U133PSR DEF=Orthologous to 224621_at LOC440806
	122.55	550	404.6	BC005230	MmugDNA.13044.1.S1_at	gDNA.g13528857 FEA=U133PSR GEN=UQCRB DEF=Orthologous to 209065_at ubiquinol-cytochrome c reductase binding protein
	40.75	261.1	51.8	BF671883	MmugDNA.37191.1.S1_at	gDNA.Hs.158849.0.S1 FEA=U133PSR GEN=ATF6 DEF=Orthologous to 231927_at Activating transcription factor 6
	113.95	590.1	275.8	CO726069	Mmu.12831.2.S1_at	gb:CO726069 DB_XREF=gi:50707380 DB_XREF=ILLUMIGEN_MCQ_42734 CLONE=IBIUW:28236 TID=Mmu.12831.2 CNT=3 FEA=EST TIER=ConsEnd STK=0
	54.05	310.25	83.8	L38019	MmugDNA.20056.1.S1_at	gDNA.g1464750 FEA=U133PSR GEN=ITPR1 DEF=Orthologous to 211323_s_at inositol 1,4,5-triphosphate receptor, type 1
	618.85	2692.35	1722.4	BF222895	MmugDNA.26347.1.S1_at	gDNA.Hs.296261.0.S3 FEA=U133PSR GEN=GNAQ DEF=Orthologous to 202615_at guanine nucleotide binding protein (G protein), q polypeptide
	192.8	1008.15	364.2	T65537	MmugDNA.26473.1.S1_at	gDNA.Hs.6818.0.A1 FEA=U133PSR GEN=GRIN2A DEF=Orthologous to 231384_at Glutamate receptor, ionotropic, N-methyl D-aspartate 2A
	1169	5145.8	2985.5	NM_005006	MmugDNA.17856.1.S1_at	gDNA.g4826855 FEA=U133PSR GEN=NDUFS1 DEF=Orthologous to 203039_s_at NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
	603.1	2637.9	1547.2	AA911231	MmugDNA.41399.1.S1_s_a	gDNA.Hs.272458.0.S2 FEA=U133PSR GEN=PPP3CA DEF=Orthologous to 202457_s_at protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
	1207.15	5201.75	3000.4	NM_001685	MmugDNA.11379.1.S1_at	gDNA.g4502292 FEA=U133PSR GEN=ATP5J DEF=Orthologous to 202325_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
	107.95	414.2	314.35	BF672975	MmugDNA.10451.1.S1_at	gDNA.Hs.180878.0.A1 FEA=U133PSR GEN=LPL DEF=Orthologous to 203548_s_at lipoprotein lipase
	883.25	3354	2598.95	NM_002492	MmugDNA.42522.1.S1_at	gDNA.g4505362 FEA=U133PSR GEN=NDUFB5 DEF=Orthologous to 203621_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
	453.45	2121.4	932.95	NM_004551	MmugDNA.29873.1.S1_at	gDNA.g4758787 FEA=U133PSR GEN=NDUFS3 DEF=Orthologous to 201740_at NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
	1063.95	4505.7	2411.85	NM_005004	MmugDNA.17855.1.S1_at	gDNA.g4826853 FEA=U133PSR GEN=NDUFB8 DEF=Orthologous to 201226_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
	254.1	1105.9	508.25	NM_002493	MmugDNA.42525.1.S1_at	gDNA.g4505364 FEA=U133PSR GEN=NDUFB6 DEF=Orthologous to 203613_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
	1041.05	4327.75	2260.1	NM_001689	MmugDNA.11978.1.S1_at	gDNA.g4502300 FEA=U133PSR GEN=ATP5G3 DEF=Orthologous to 207508_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
	116.75	564.05	173.8	CN646982	Mmu.9989.1.S1_s_at	gb:CN646982 DB_XREF=gi:47160425 DB_XREF=ILLUMIGEN_MCQ_27514 CLONE=IBIUW:8046 TID=Mmu.9989.1 CNT=4 FEA=EST TIER=ConsEnd STK=0
	1227	4774.7	2778.45	AV711183	MmugDNA.356.1.S1_s_at	gDNA.Hs.155433.3.A1 FEA=U133PSR GEN=ATP5C1 DEF=Orthologous to 213366_x_at ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
	215.55	985.05	325	NM_002222	MmugDNA.18191.1.S1_at	gDNA.g10835022 FEA=U133PSR GEN=ITPR1 DEF=Orthologous to 203710_at inositol 1,4,5-triphosphate receptor, type 1
	528.5	2220.65	920.6	BG260394	MmugDNA.29351.1.S1_at	gDNA.Hs.76930.1.A1 FEA=U133PSR GEN=SNCA DEF=Orthologous to 204466_s_at synuclein, alpha (non A4 component of amyloid precursor)
	261.85	957.2	588.2	BE741920	MmugDNA.24918.1.S1_at	gDNA.Hs.1665.1.A1 FEA=U133PSR GEN=NDUFA11 DEF=Orthologous to 225304_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
	1468.85	4487.2	3958.6	NM_002494	MmugDNA.42530.1.S1_at	gDNA.g4505366 FEA=U133PSR GEN=NDUFC1 DEF=Orthologous to 203478_at NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
	802.2	2924.2	1641.05	NM_001916	MmugDNA.35607.1.S1_at	gDNA.g4503184 FEA=U133PSR GEN=CYC1 DEF=Orthologous to 201066_at cytochrome c-1
	1785.6	6266.9	3884.65	AF217092	MmugDNA.7413.1.S1_at	gDNA.g9651636 FEA=U133PSR GEN=DAP13 DEF=Orthologous to 223244_s_at 13kDa differentiation-associated protein
	1118.25	4664.65	1628.35	NM_001697	MmugDNA.11979.1.S1_at	gDNA.g4502302 FEA=U133PSR GEN=ATP5O DEF=Orthologous to 200818_at ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)
	695.3	2489.9	1415.7	BC003674	MmugDNA.23282.1.S1_s_a	gDNA.g13277539 FEA=U133PSR GEN=NDUFA2 DEF=Orthologous to 209224_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
	125.7	440.25	261.75	L36674	MmugDNA.8226.1.S1_s_at	gDNA.g556211 FEA=U133PSR GEN=SNCA DEF=Orthologous to 211546_x_at synuclein, alpha (non A4 component of amyloid precursor)
	189.6	685.4	366.45	CO648220	Mmu.9951.1.S1_at	gb:CO648220 DB_XREF=gi:50569714 DB_XREF=ILLUMIGEN_MCQ_41525 CLONE=IBIUW:25875 TID=Mmu.9951.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
	153.1	594.35	235.3	U23850	MmugDNA.3681.1.S1_at	gDNA.Hs.198443.2.S1 FEA=U133PSR GEN=ITPR1 DEF=Orthologous to 216944_s_at inositol 1,4,5-triphosphate receptor, type 1
	694.55	2074.75	1598.45	M23254	MmugDNA.34671.1.S1_at	gDNA.g511636 FEA=U133PSR GEN=CAPN2 DEF=Orthologous to 208683_at calpain 2, (m II) large subunit
	2989.55	10262.5	5317.05	AI653730	MmugDNA.27126.1.S1_at	gDNA.Hs.279009.6.A1 FEA=U133PSR GEN=CALM1 DEF=Orthologous to 211985_s_at calmodulin 1 (phosphorylase kinase, delta)

1949.15	6135.6	3990	NM_004547	MmugDNA.18635.1.S1_at	gDNA.g6041668 FEA=U133PSR GEN=NDUFB4 DEF=Orthologous to 218226_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
734.1	2760.4	974.15	NM_021132	MmugDNA.25461.1.S1_at	gDNA.g11036639 FEA=U133PSR GEN=PPP3CB DEF=Orthologous to 202432_at protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
1038.25	3615.45	1616.15	BC005960	MmugDNA.33303.1.S1_at	gDNA.g13543617 FEA=U133PSR GEN=ATP5F1 DEF=Orthologous to 211755_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
401.25	1450.15	533.65	AL353950	MmugDNA.13010.1.S1_at	gDNA.g7669991 FEA=U133PSR GEN=PPP3CA DEF=Orthologous to 202429_s_at protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha)
4597.25	9676.25	13037	BC000454	MmugDNA.5599.1.S1_s_a	gDNA.g12653368 FEA=U133PSR GEN=CALM1 DEF=Orthologous to 209563_x_at calmodulin 1 (phosphorylase kinase, delta)
802.35	2589.15	1349.05	AL080089	MmugDNA.38309.1.S1_s_a	gDNA.g5262506 FEA=U133PSR GEN=ATP5G1 DEF=Orthologous to 208972_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
1413.05	4999.65	1906.7	M27319	MmugDNA.1229.1.S1_s_a	gDNA.g179809 FEA=U133PSR GEN=CALM1 DEF=Orthologous to 200653_s_at calmodulin 1 (phosphorylase kinase, delta)
349.2	985.9	715.75	NM_005000	MmugDNA.13561.1.S1_at	gDNA.g13699821 FEA=U133PSR GEN=NDUFA5 DEF=Orthologous to 201304_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
346.2	970.2	691.75	AL567411	MmugDNA.19826.1.S1_s_a	gDNA.Hs.93597.0.S2 FEA=U133PSR GEN=CDK5R1 DEF=Orthologous to 204995_at cyclin-dependent kinase 5, regulatory subunit 1 (p35)
538.3	1908.5	655.5	NM_003365	MmugDNA.8160.1.S1_at	gDNA.g4507840 FEA=U133PSR GEN=UQCRC1 DEF=Orthologous to 201903_at ubiquinol-cytochrome c reductase core protein I
1069.45	3140.6	1864.85	NM_004542	MmugDNA.29850.1.S1_at	gDNA.g4758771 FEA=U133PSR GEN=NDUFA3 DEF=Orthologous to 218563_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
221.7	782.05	248.45	BQ807466	Mmu.3908.1.S1_s_at	gb:BQ807466 DB_XREF=gi:22031675 DB_XREF=NISC_kk04c11.y2 CLONE=IMAGE:5330325 TID=Mmu.3908.1 CNT=12 FEA=EST TIER=ConsEnd STK=0
1621	4740.55	2763.35	BC005299	MmugDNA.31771.1.S1_s_a	gDNA.g13529022 FEA=U133PSR GEN=CYCS DEF=Orthologous to 208905_at cytochrome c, somatic
445.25	1224.3	834.55	NM_021075	MmugDNA.30188.1.S1_at	gDNA.Hs.59745.0.S1 FEA=U133PSR GEN=NDUFV3 DEF=Orthologous to 226616_s_at NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
1380.9	3974.3	2381	NM_004552	MmugDNA.29879.1.S1_at	gDNA.g4758789 FEA=U133PSR GEN=NDUFS5 DEF=Orthologous to 201757_at NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
4121.7	10974.8	7867.1	AI587323	MmugDNA.23434.1.S1_at	gDNA.Hs.155101.3.A1 FEA=U133PSR GEN=ATP5A1 DEF=Orthologous to 213738_s_at ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
540.3	1558.75	902.35	NM_005001	MmugDNA.17832.1.S1_at	gDNA.g4826849 FEA=U133PSR GEN=NDUFA7 DEF=Orthologous to 202785_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
1014.95	2882.5	1691.65	NM_006830	MmugDNA.14855.1.S1_at	gDNA.g5803216 FEA=U133PSR GEN=UQCR DEF=Orthologous to 202090_s_at ubiquinol cytochrome c reductase, 6.4kDa subunit
261.8	536.95	619.1	BF969428	MmugDNA.30957.1.S1_at	gDNA.Hs.5437.3.A2 FEA=U133PSR GEN=GNAQ DEF=Orthologous to 224862_at Guanine nucleotide binding protein (G protein), q polypeptide
1822.15	4590.5	3391.4	NM_004374	MmugDNA.24731.1.S1_at	gDNA.g4758039 FEA=U133PSR GEN=COX6C DEF=Orthologous to 201754_at cytochrome c oxidase subunit VIc
133.65	367.8	213.7	AA576497	MmugDNA.24210.1.S1_at	gDNA.Hs.252497.0.A1 FEA=U133PSR GEN=ATF6 DEF=Orthologous to 217550_at Activating transcription factor 6
142.05	278.25	333.75	NM_016835	MmugDNA.27209.1.S1_at	gDNA.g8400712 FEA=U133PSR GEN=MAPT DEF=Orthologous to 203930_s_at microtubule-associated protein tau
311.1	868.05	434.95	AF092131	MmugDNA.23407.1.S1_at	gDNA.g5138911 FEA=U133PSR GEN=NDUFV1 DEF=Orthologous to 208714_at NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
1486.45	4239.9	1881.9	AF261090	MmugDNA.726.1.S1_at	gDNA.g9802311 FEA=U133PSR GEN=NDUFB9 DEF=Orthologous to 222992_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
240.95	526.8	462.35	AU135154	MmugDNA.7261.1.S1_at	gDNA.Hs.172028.1.A1 FEA=U133PSR GEN=ADAM10 DEF=Orthologous to 214895_s_at a disintegrin and metalloproteinase domain 10
145.4	442.2	154.05	NM_003001	MmugDNA.9551.1.S1_at	gDNA.g9257243 FEA=U133PSR GEN=SDHC DEF=Orthologous to 202004_x_at succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
142.75	385.2	198.35	NM_004935	MmugDNA.16390.1.S1_at	gDNA.g4826674 FEA=U133PSR GEN=CDK5 DEF=Orthologous to 204247_s_at cyclin-dependent kinase 5
474.75	1115.3	799.85	NM_002490	MmugDNA.42509.1.S1_at	gDNA.g4505358 FEA=U133PSR GEN=NDUFA6 DEF=Orthologous to 202001_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
156.5	460.35	167.95	NM_000345	MmugDNA.8691.1.S1_at	gDNA.g6806896 FEA=U133PSR GEN=SNCA DEF=Orthologous to 204467_s_at synuclein, alpha (non A4 component of amyloid precursor)
410.75	1123.95	519.35	NM_012104	MmugDNA.13727.1.S1_at	gDNA.g6912265 FEA=U133PSR GEN=BACE1 DEF=Orthologous to 217904_s_at beta-site APP-cleaving enzyme 1
690.4	1906.75	854.85	AA199717	MmugDNA.6394.1.S1_at	gDNA.Hs.101174.4.A1 FEA=U133PSR GEN=MAPT DEF=Orthologous to 225379_at microtubule-associated protein tau
594.95	1468.75	909.55	NM_004493	MmugDNA.28322.1.S1_at	gDNA.g4758503 FEA=U133PSR GEN=HADH2 DEF=Orthologous to 202282_at hydroxyacyl-Coenzyme A dehydrogenase, type II
1912.35	5351.5	2283.55	BC005299	MmugDNA.31771.1.S1_at	gDNA.g13529022 FEA=U133PSR GEN=CYCS DEF=Orthologous to 208905_at cytochrome c, somatic
290.65	780.6	357.9	CN646788	Mmu.8048.1.S1_at	gb:CN646788 DB_XREF=gi:47160231 DB_XREF=ILLUMIGEN_MCQ_27104 CLONE=IBIUW:8245 TID=Mmu.8048.1 CNT=3 FEA=EST TIER=ConsEnd STK=0
2596.15	5667.65	4387.65	NM_006886	MmugDNA.5716.1.S1_at	gDNA.g5901895 FEA=U133PSR GEN=ATP5E DEF=Orthologous to 217801_at ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
133.3	236	279.9	CN641932	Mmu.16123.2.S1_at	gb:CN641932 DB_XREF=gi:47152942 DB_XREF=ILLUMIGEN_MCQ_5624 CLONE=IBIUW:5394 TID=Mmu.16123.2 CNT=2 FEA=EST TIER=ConsEnd STK=0
1277.75	3027.05	1739.8	BC005270	MmugDNA.13810.1.S1_at	gDNA.g13528959 FEA=U133PSR GEN=NDUFS4 DEF=Orthologous to 209303_at NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
1009.95	2558.8	1198.95	NM_004550	MmugDNA.29871.1.S1_s_a	gDNA.g4758785 FEA=U133PSR GEN=NDUFS2 DEF=Orthologous to 201966_at NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
2895.45	6709.7	3833.35	BC006229	MmugDNA.8169.1.S1_s_a	gDNA.g13623258 FEA=U133PSR GEN=COX5B DEF=Orthologous to 211025_x_at cytochrome c oxidase subunit Vb cytochrome c oxidase subunit Vb
318.45	716.25	438.2	NM_002332	MmugDNA.29191.1.S1_at	gDNA.g4758685 FEA=U133PSR GEN=LRP1 DEF=Orthologous to 200785_s_at low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)
764.1	1759.65	958.85	NM_001864	MmugDNA.16709.1.S1_s_a	gDNA.g4502986 FEA=U133PSR GEN=COX7A1 DEF=Orthologous to 204570_at cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
2127.65	4441.15	2915.7	NM_006004	MmugDNA.38710.1.S1_at	gDNA.g5174744 FEA=U133PSR GEN=UQCRH DEF=Orthologous to 202233_s_at ubiquinol-cytochrome c reductase hinge protein
1269.85	2735.4	1646.3	M23114	MmugDNA.32704.1.S1_at	gDNA.g184100 FEA=U133PSR GEN=ATP2A2 DEF=Orthologous to 209186_at ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
781.3	1685.2	863.6	AI056359	MmugDNA.20201.1.S1_at	gDNA.Hs.101174.1.A3 FEA=U133PSR GEN=MAPT DEF=Orthologous to 203929_s_at microtubule-associated protein tau
846.8	2573.45	611	NM_015965	MmugDNA.37472.1.S1_at	gDNA.g7705733 FEA=U133PSR GEN=GRIM19 DEF=Orthologous to 220864_s_at cell death-regulatory protein GRIM19
367.9	863.9	366.5	NM_019056	MmugDNA.38548.1.S1_s_a	gDNA.g9506682 FEA=U133PSR GEN=NDUFB11 DEF=Orthologous to 218320_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa
460.05	929.35	442.45	NM_004146	MmugDNA.6319.1.S1_s_a	gDNA.g10764846 FEA=U133PSR GEN=NDUFB7 DEF=Orthologous to 202839_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
4825.45	9822.2	4378.65	CD768031	Mmu.7399.1.S1_at	gb:CD768031 DB_XREF=gi:32426533 DB_XREF=AGENCOURT_14718956 CLONE=IMAGE:6973306 TID=Mmu.7399.1 CNT=1 FEA=EST TIER=ConsEnd STK=1
536.45	256.8	577.1	AA993683	MmugDNA.5110.1.S1_at	gDNA.Hs.163867.1.A1 FEA=U133PSR GEN=PRO1580 DEF=Orthologous to 213550_s_at hypothetical protein PRO1580
268.6	120.4	270.55	BC000462	MmugDNA.5643.1.S1_at	gDNA.g12653384 FEA=U133PSR GEN=UQCR DEF=Orthologous to 223613_at ubiquinol cytochrome c reductase, 6.4kDa subunit
179.85	169.25	83.3	NM_003366	MmugDNA.8162.1.S1_at	gDNA.g4507842 FEA=U133PSR GEN=UQCRC2 DEF=Orthologous to 200883_at ubiquinol-cytochrome c reductase core protein II
227.95	171.4	108.6	NM_001196	MmugDNA.18041.1.S1_at	gDNA.g4557360 FEA=U133PSR GEN=BID DEF=Orthologous to 204493_at BH3 interacting domain death agonist
334.75	124.4	273.75	AL544951	MmugDNA.8199.1.S1_at	gDNA.Hs.278540.0.A2 FEA=U133PSR GEN=PPP3R1 DEF=Orthologous to 204506_at protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B1)
435.9	143.3	421.55	AF453834	MmugDNA.40691.1.S1_at	gDNA.Hs2.198271.3.S1 FEA=U133PSR GEN=NDUFA10 DEF=Orthologous to 1555548_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
294.8	97.15	274.75	AW190316	MmugDNA.3420.1.S1_at	gDNA.Hs.2186.4.A1 FEA=U133PSR GEN=SHMT2 DEF=Orthologous to 214095_at serine hydroxymethyltransferase 2 (mitochondrial)
213.2	92.1	110.6	AI760495	MmugDNA.15069.1.S1_at	gDNA.Hs.205711.0.A1 FEA=U133PSR GEN=CYCS DEF=Orthologous to 244546_at cytochrome c, somatic
287.8	112.75	165.25	AA918442	MmugDNA.15670.1.S1_s_a	gDNA.Hs.326641.0.A1 FEA=U133PSR GEN=IDE DEF=Orthologous to 217496_s_at insulin-degrading enzyme
363.5	118.1	284.75	AB062482	MmugDNA.34532.1.S1_at	gDNA.Hs2.374685.1.S1 FEA=U133PSR GEN=NDUFS4 DEF=Orthologous to 1555057_at NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
91991.2	28858.2	54908.4	CO649101	AFFX-Mmu-gapdh-3_at	M. mulatta GEN=gapdh DB_XREF=gb:CO649101 DB_XREF=gi:50570595 DB_XREF=ILLUMIGEN_MCQ_42691 FEA=mRNA CLONE=IBIUW:22567 DEF=gapdh
15596.2	4570.5	8352.1	BC004369	MmugDNA.36988.1.S1_x_a	gDNA.g13325111 FEA=U133PSR GEN=APP DEF=Orthologous to 211277_x_at amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
402.65	99.1	314.3	NM_001867	MmugDNA.16732.1.S1_at	gDNA.g4502992 FEA=U133PSR GEN=COX7C DEF=Orthologous to 201134_x_at cytochrome c oxidase subunit VIIc
332	79.8	222.7	AF149794	MmugDNA.37633.1.S1_at	gDNA.g4929486 FEA=U133PSR GEN=APAF1 DEF=Orthologous to 211554_s_at apoptotic protease activating factor
166.65	59.4	55.3	AY004175	MmugDNA.4164.1.S1_at	gDNA.g9438228 FEA=U133PSR GEN=PLCB1 DEF=Orthologous to 211925_s_at phospholipase C, beta 1 (phosphoinositide-specific)

	248.65	69.25	104.15	NM_001036	MmugDNA.26610.1.S1_at	gDNA.g4506758 FEA=U133PSR GEN=RYR3 DEF=Orthologous to 206306_at ryanodine receptor 3
	539.35	140.7	242.2	AA382702	MmugDNA.43583.1.S1_x_a	gDNA.Hs.3462.1.S1 FEA=U133PSR GEN=COX7C DEF=Orthologous to 213846_at cytochrome c oxidase subunit VIIc
	75750	22910.4	26582	CO649101	AFFX-Mmu-gapdh-3_x_at	M. mulatta GEN=gapdh DB_XREF=gb:CO649101 DB_XREF=gi:50570595 DB_XREF=ILLUMIGEN_MCQ_42691 FEA=mRNA CLONE=IBIUW:22567 DEF=gapdh
	307.95	50.05	59.65	AK002110	MmugDNA.24532.1.S1_at	gDNA.Hs.90443.1.A1 FEA=U133PSR GEN=NDUFS8 DEF=Orthologous to 232169_x_at NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
Parkinson's						
	10.15	954.35	346.05	CO581006	Mmu.13573.1.S1_at	gb:CO581006 DB_XREF=gi:50412266 DB_XREF=ILLUMIGEN_MCQ_47894 CLONE=IBIUW:20870 TID=Mmu.13573.1 CNT=3 FEA=EST TIER=ConsEnd STK=0
	179.35	7001.75	2658.35	CB308652	Mmu.3902.1.S1_at	gb:CB308652 DB_XREF=gi:28831362 DB_XREF=AGENCOURT_11771965 CLONE=IMAGE:6882338 TID=Mmu.3902.1 CNT=4 FEA=EST TIER=ConsEnd STK=0
	134.65	3136.85	913	CX078587	Mmu.2238.1.S1_at	gb:CX078587 DB_XREF=gi:56592577 DB_XREF=ILLUMIGEN_MCQ_2018 CLONE=IBIUW:30225 TID=Mmu.2238.1 CNT=19 FEA=EST TIER=ConsEnd STK=0
	71.4	1264.65	325.3	CN648486	Mmu.6016.1.S1_at	gb:CN648486 DB_XREF=gi:47161929 DB_XREF=ILLUMIGEN_MCQ_30631 CLONE=IBIUW:6560 TID=Mmu.6016.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
	177.45	2564.9	942.35	CX078600	Mmu.2126.1.S1_s_at	gb:CX078600 DB_XREF=gi:56592590 DB_XREF=ILLUMIGEN_MCQ_42100 CLONE=IBIUW:30247 TID=Mmu.2126.1 CNT=25 FEA=EST TIER=ConsEnd STK=0
	86.35	1024.8	512.35	CO580535	Mmu.7758.1.S1_at	gb:CO580535 DB_XREF=gi:50411701 DB_XREF=ILLUMIGEN_MCQ_48559 CLONE=IBIUW:19027 TID=Mmu.7758.1 CNT=9 FEA=EST TIER=ConsEnd STK=0
	125.5	1606.35	576.95	BC000649	MmugDNA.8653.1.S1_at	gDNA.g12653726 FEA=U133PSR GEN=UQCRFS1 DEF=Orthologous to 208909_at ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
	126.5	1711.95	475.25	CX078600	Mmu.2126.1.S1_at	gb:CX078600 DB_XREF=gi:56592590 DB_XREF=ILLUMIGEN_MCQ_42100 CLONE=IBIUW:30247 TID=Mmu.2126.1 CNT=25 FEA=EST TIER=ConsEnd STK=0
	22.9	257.25	84.15	NM_002496	MmugDNA.42544.1.S1_at	gDNA.g4505370 FEA=U133PSR GEN=NDUFS8 DEF=Orthologous to 203189_s_at NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
	435.85	4015.8	1669.65	NM_001861	MmugDNA.16704.1.S1_at	gDNA.g4502980 FEA=U133PSR GEN=COX4I1 DEF=Orthologous to 202698_x_at cytochrome c oxidase subunit IV isoform 1
	206.45	1948	740.95	NM_004181	MmugDNA.7056.1.S1_at	gDNA.g4759283 FEA=U133PSR GEN=UCHL1 DEF=Orthologous to 201387_s_at ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
	48.4	383.6	173.9	AF184911	MmugDNA.35310.1.S1_s_a	gDNA.g10121319 FEA=U133PSR GEN=PRSS25 DEF=Orthologous to 211152_s_at protease, serine, 25
	54.7	284.5	273.2	NM_004346	MmugDNA.6342.1.S1_at	gDNA.g4757911 FEA=U133PSR GEN=CASP3 DEF=Orthologous to 202763_at caspase 3, apoptosis-related cysteine protease
	157.8	1130.65	440.4	CN645512	Mmu.4271.1.S1_at	gb:CN645512 DB_XREF=gi:47158955 DB_XREF=ILLUMIGEN_MCQ_24113 CLONE=IBIUW:10328 TID=Mmu.4271.1 CNT=4 FEA=EST TIER=ConsEnd STK=0
	352.35	2232.9	1230.15	NM_003002	MmugDNA.27382.1.S1_at	gDNA.g4506864 FEA=U133PSR GEN=SDHD DEF=Orthologous to 202026_at succinate dehydrogenase complex, subunit D, integral membrane protein
	100.9	611.65	369.75	NM_000360	MmugDNA.5125.1.S1_at	gDNA.g4507480 FEA=U133PSR GEN=TH DEF=Orthologous to 208291_s_at tyrosine hydroxylase
	1280.1	8540.4	3545.3	AA854966	MmugDNA.39322.1.S1_s_a	gDNA.Hs.113205.2.S1 FEA=U133PSR GEN=COX4I1 DEF=Orthologous to 200086_s_at cytochrome c oxidase subunit IV isoform 1 cytochrome c oxidase subunit IV isoform 1
	351.95	2097.8	1174.4	CO644739	Mmu.12382.1.S1_s_at	gb:CO644739 DB_XREF=gi:50566233 DB_XREF=ILLUMIGEN_MCQ_43431 CLONE=IBIUW:22477 TID=Mmu.12382.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
	569.6	4181.6	1073.85	NM_001044	MmugDNA.2050.1.S1_at	gDNA.g4507040 FEA=U133PSR GEN=SLC6A3 DEF=Orthologous to 206836_at solute carrier family 6 (neurotransmitter transporter, dopamine), member 3
	251.5	1458	802.8	NM_003000	MmugDNA.9546.1.S1_s_a	gDNA.g9257241 FEA=U133PSR GEN=SDHB DEF=Orthologous to 202675_at succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
	191.85	1338.3	364.65	U90943	MmugDNA.21230.1.S1_at	gDNA.g2735306 FEA=U133PSR GEN=VDAC3 DEF=Orthologous to 208846_s_at voltage-dependent anion channel 3
	667.7	3448.25	2326.75	CO581557	Mmu.5257.1.S1_at	gb:CO581557 DB_XREF=gi:50412949 DB_XREF=ILLUMIGEN_MCQ_47054 CLONE=IBIUW:18627 TID=Mmu.5257.1 CNT=3 FEA=EST TIER=ConsEnd STK=1
	688.15	3861.55	2013.35	L08666	MmugDNA.6316.1.S1_at	gDNA.g190199 FEA=U133PSR GEN=VDAC2 DEF=Orthologous to 211662_s_at voltage-dependent anion channel 2 voltage-dependent anion channel 2
	262	1423.2	752.85	NM_004549	MmugDNA.29870.1.S1_at	gDNA.g4758783 FEA=U133PSR GEN=NDUFC2 DEF=Orthologous to 218101_s_at NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa
	122.55	550	404.6	BC005230	MmugDNA.13044.1.S1_at	gDNA.g13528857 FEA=U133PSR GEN=UQCRB DEF=Orthologous to 209065_at ubiquinol-cytochrome c reductase binding protein
	113.95	590.1	275.8	CO726069	Mmu.12831.2.S1_at	gb:CO726069 DB_XREF=gi:50707380 DB_XREF=ILLUMIGEN_MCQ_42734 CLONE=IBIUW:28236 TID=Mmu.12831.2 CNT=3 FEA=EST TIER=ConsEnd STK=0
	1169	5145.8	2985.5	NM_005006	MmugDNA.17856.1.S1_at	gDNA.g4826855 FEA=U133PSR GEN=NDUFS1 DEF=Orthologous to 203039_s_at NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
	1207.15	5201.75	3000.4	NM_001685	MmugDNA.11379.1.S1_at	gDNA.g4502292 FEA=U133PSR GEN=ATP5J DEF=Orthologous to 202325_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
	883.25	3354	2598.95	NM_002492	MmugDNA.42522.1.S1_at	gDNA.g4505362 FEA=U133PSR GEN=NDUFB5 DEF=Orthologous to 203621_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
	453.45	2121.4	932.95	NM_004551	MmugDNA.29873.1.S1_at	gDNA.g4758787 FEA=U133PSR GEN=NDUFS3 DEF=Orthologous to 201740_at NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
	1063.95	4505.7	2411.85	NM_005004	MmugDNA.17855.1.S1_at	gDNA.g4826853 FEA=U133PSR GEN=NDUFB8 DEF=Orthologous to 201226_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
	254.1	1105.9	508.25	NM_002493	MmugDNA.42525.1.S1_at	gDNA.g4505364 FEA=U133PSR GEN=NDUFB6 DEF=Orthologous to 203613_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa
	1041.05	4327.75	2260.1	NM_001689	MmugDNA.11978.1.S1_at	gDNA.g4502300 FEA=U133PSR GEN=ATP5G3 DEF=Orthologous to 207508_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
	1227	4774.7	2778.45	AV711183	MmugDNA.356.1.S1_s_at	gDNA.Hs.155433.3.A1 FEA=U133PSR GEN=ATP5C1 DEF=Orthologous to 213366_x_at ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
	528.5	2220.65	920.6	BG260394	MmugDNA.29351.1.S1_at	gDNA.Hs.76930.1.A1 FEA=U133PSR GEN=SNCA DEF=Orthologous to 204466_s_at synuclein, alpha (non A4 component of amyloid precursor)
	261.85	957.2	588.2	BE741920	MmugDNA.24918.1.S1_at	gDNA.Hs.1665.1.A1 FEA=U133PSR GEN=NDUFA11 DEF=Orthologous to 225304_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
	589.1	2743.75	705.3	CN805480	Mmu.1451.1.S1_at	gb:CN805480 DB_XREF=gi:47701456 DB_XREF=ILLUMIGEN_MCQ_36679 CLONE=IBIUW:11652 TID=Mmu.1451.1 CNT=17 FEA=EST TIER=ConsEnd STK=1
	1468.85	4487.2	3958.6	NM_002494	MmugDNA.42530.1.S1_at	gDNA.g4505366 FEA=U133PSR GEN=NDUFC1 DEF=Orthologous to 203478_at NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
	802.2	2924.2	1641.05	NM_001916	MmugDNA.35607.1.S1_at	gDNA.g4503184 FEA=U133PSR GEN=CYC1 DEF=Orthologous to 201066_at cytochrome c-1
	1785.6	6266.9	3884.65	AF217092	MmugDNA.7413.1.S1_at	gDNA.g9651636 FEA=U133PSR GEN=DAP13 DEF=Orthologous to 223244_s_at 13kDa differentiation-associated protein
	173.35	584.2	401.05	BC002775	MmugDNA.24283.1.S1_at	gDNA.g12803862 FEA=U133PSR GEN=UBE2G1 DEF=Orthologous to 209142_s_at ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)
	1118.25	4664.65	1628.35	NM_001697	MmugDNA.11979.1.S1_at	gDNA.g4502302 FEA=U133PSR GEN=ATP5O DEF=Orthologous to 200818_at ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring)
	695.3	2489.9	1415.7	BC003674	MmugDNA.23282.1.S1_s_a	gDNA.g13277539 FEA=U133PSR GEN=NDUFA2 DEF=Orthologous to 209224_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
	995.25	3629.65	1931.75	NM_001152	MmugDNA.9969.1.S1_at	gDNA.g4502098 FEA=U133PSR GEN=SLC25A5 DEF=Orthologous to 200657_at solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
	125.7	440.25	261.75	L36674	MmugDNA.8226.1.S1_s_a	gDNA.g556211 FEA=U133PSR GEN=SNCA DEF=Orthologous to 211546_x_at synuclein, alpha (non A4 component of amyloid precursor)
	189.6	685.4	366.45	CO648220	Mmu.9951.1.S1_at	gb:CO648220 DB_XREF=gi:50569714 DB_XREF=ILLUMIGEN_MCQ_41525 CLONE=IBIUW:25875 TID=Mmu.9951.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
	1949.15	6135.6	3990	NM_004547	MmugDNA.18635.1.S1_at	gDNA.g6041668 FEA=U133PSR GEN=NDUFB4 DEF=Orthologous to 218226_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
	83	204.35	221.85	AL562528	MmugDNA.16180.1.S1_at	gDNA.Hs.184325.0.A3 FEA=U133PSR GEN=UBE2J1 DEF=Orthologous to 217823_s_at ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
	697.6	2434.1	1112.9	BG531983	MmugDNA.35625.1.S1_s_a	gDNA.Hs.108104.0.S1 FEA=U133PSR GEN=UBE2L3 DEF=Orthologous to 200682_s_at ubiquitin-conjugating enzyme E2L 3
	1038.25	3615.45	1616.15	BC005960	MmugDNA.33303.1.S1_at	gDNA.g13543617 FEA=U133PSR GEN=ATP5F1 DEF=Orthologous to 211755_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1
	802.35	2589.15	1349.05	AL080089	MmugDNA.38309.1.S1_s_a	gDNA.g5262506 FEA=U133PSR GEN=ATP5G1 DEF=Orthologous to 208972_s_at ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1
	349.2	985.9	715.75	NM_005000	MmugDNA.13561.1.S1_at	gDNA.g13699821 FEA=U133PSR GEN=NDUFA5 DEF=Orthologous to 201304_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
	538.3	1908.5	655.5	NM_003365	MmugDNA.8160.1.S1_at	gDNA.g4507840 FEA=U133PSR GEN=UQCRC1 DEF=Orthologous to 201903_at ubiquinol-cytochrome c reductase core protein I
	1069.45	3140.6	1864.85	NM_004542	MmugDNA.29850.1.S1_at	gDNA.g4758771 FEA=U133PSR GEN=NDUFA3 DEF=Orthologous to 218563_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
	221.7	782.05	248.45	BQ807466	Mmu.3908.1.S1_s_at	gb:BQ807466 DB_XREF=gi:22031675 DB_XREF=NISC_kk04c11.y2 CLONE=IMAGE:5330325 TID=Mmu.3908.1 CNT=12 FEA=EST TIER=ConsEnd STK=0
	1621	4740.55	2763.35	BC005299	MmugDNA.31771.1.S1_s_a	gDNA.g13529022 FEA=U133PSR GEN=CYCS DEF=Orthologous to 208905_at cytochrome c, somatic
	445.25	1224.3	834.55	NM_021075	MmugDNA.30188.1.S1_at	gDNA.Hs.59745.0.S1 FEA=U133PSR GEN=NDUFV3 DEF=Orthologous to 226616_s_at NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa
	1380.9	3974.3	2381	NM_004552	MmugDNA.29879.1.S1_at	gDNA.g4758789 FEA=U133PSR GEN=NDUFS5 DEF=Orthologous to 201757_at NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)

4121.7	10974.8	7867.1	AI587323	MmugDNA.23434.1.S1_at	gDNA.Hs.155101.3.A1 FEA=U133PSR GEN=ATP5A1 DEF=Orthologous to 213738_s_at ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit1, cardiac muscle
540.3	1558.75	902.35	NM_005001	MmugDNA.17832.1.S1_at	gDNA.g4826849 FEA=U133PSR GEN=NDUFA7 DEF=Orthologous to 202785_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
1014.95	2882.5	1691.65	NM_006830	MmugDNA.14855.1.S1_at	gDNA.g5803216 FEA=U133PSR GEN=UQCR DEF=Orthologous to 202090_s_at ubiquinol cytochrome c reductase, 6.4kDa subunit
1822.15	4590.5	3391.4	NM_004374	MmugDNA.24731.1.S1_at	gDNA.g4758039 FEA=U133PSR GEN=COX6C DEF=Orthologous to 201754_at cytochrome c oxidase subunit VIc
622.8	1974.85	740.95	NM_003334	MmugDNA.7386.1.S1_at	gDNA.g4507762 FEA=U133PSR GEN=UBE1 DEF=Orthologous to 200964_at ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)
274.5	649.6	535.85	AW299555	MmugDNA.37118.1.S1_at	gDNA.Hs.78563.0.A3 FEA=U133PSR GEN=UBE2G1 DEF=Orthologous to 209141_at ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)
311.1	868.05	434.95	AF092131	MmugDNA.23407.1.S1_at	gDNA.g5138911 FEA=U133PSR GEN=NDUFV1 DEF=Orthologous to 208714_at NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
1486.45	4239.9	1881.9	AF261090	MmugDNA.726.1.S1_at	gDNA.g9802311 FEA=U133PSR GEN=NDUFB9 DEF=Orthologous to 222992_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
145.4	442.2	154.05	NM_003001	MmugDNA.9551.1.S1_at	gDNA.g9257243 FEA=U133PSR GEN=SDHC DEF=Orthologous to 202004_x_at succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa
474.75	1115.3	799.85	NM_002490	MmugDNA.42509.1.S1_at	gDNA.g4505358 FEA=U133PSR GEN=NDUFA6 DEF=Orthologous to 202001_s_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
156.5	460.35	167.95	NM_000345	MmugDNA.8691.1.S1_at	gDNA.g6806896 FEA=U133PSR GEN=SNCA DEF=Orthologous to 204467_s_at synuclein, alpha (non A4 component of amyloid precursor)
1912.35	5351.5	2283.55	BC005299	MmugDNA.31771.1.S1_at	gDNA.g13529022 FEA=U133PSR GEN=CYCS DEF=Orthologous to 208905_at cytochrome c, somatic
61.75	73.75	169.25	NM_016021	MmugDNA.15202.1.S1_at	gDNA.g7706311 FEA=U133PSR GEN=UBE2J1 DEF=Orthologous to 217826_s_at ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
2596.15	5667.65	4387.65	NM_006886	MmugDNA.5716.1.S1_at	gDNA.g5901895 FEA=U133PSR GEN=ATP5E DEF=Orthologous to 217801_at ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
1277.75	3027.05	1739.8	BC005270	MmugDNA.13810.1.S1_at	gDNA.g13528959 FEA=U133PSR GEN=NDUFS4 DEF=Orthologous to 209303_at NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
1009.95	2558.8	1198.95	NM_004550	MmugDNA.29871.1.S1_s_a	gDNA.g4758785 FEA=U133PSR GEN=NDUFS2 DEF=Orthologous to 201966_at NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
2895.45	6709.7	3833.35	BC006229	MmugDNA.8169.1.S1_s_a	gDNA.g13623258 FEA=U133PSR GEN=COX5B DEF=Orthologous to 211025_x_at cytochrome c oxidase subunit Vb cytochrome c oxidase subunit Vb
148.3	354.8	181.75	BE964689	MmugDNA.35627.1.S1_at	gDNA.Hs.108104.0.S2 FEA=U133PSR GEN=UBE2L3 DEF=Orthologous to 200683_s_at ubiquitin-conjugating enzyme E2L 3
764.1	1759.65	958.85	NM_001864	MmugDNA.16709.1.S1_s_a	gDNA.g4502986 FEA=U133PSR GEN=COX7A1 DEF=Orthologous to 204570_at cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
2127.65	4441.15	2915.7	NM_006004	MmugDNA.38710.1.S1_at	gDNA.g5174744 FEA=U133PSR GEN=UQCRH DEF=Orthologous to 202233_s_at ubiquinol-cytochrome c reductase hinge protein
406.5	820.9	496.75	NM_001151	MmugDNA.9968.1.S1_s_a	gDNA.g4502096 FEA=U133PSR GEN=SLC25A4 DEF=Orthologous to 202825_at solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
269.45	569.35	283.75	NM_004223	MmugDNA.7052.1.S1_at	gDNA.g4759281 FEA=U133PSR GEN=UBE2L6 DEF=Orthologous to 201649_at ubiquitin-conjugating enzyme E2L 6
846.8	2573.45	611	NM_015965	MmugDNA.37472.1.S1_at	gDNA.g7705733 FEA=U133PSR GEN=GRIM19 DEF=Orthologous to 220864_s_at cell death-regulatory protein GRIM19
111.1	281.7	104.05	NM_013247	MmugDNA.43070.1.S1_at	gDNA.g7019476 FEA=U133PSR GEN=PRSS25 DEF=Orthologous to 203089_s_at protease, serine, 25
76.45	72.8	189	CO648050	Mmu.4246.1.S1_s_at	gb:CO648050 DB_XREF=gi:50569544 DB_XREF=ILLUMIGEN_MCQ_41314 CLONE=IBIUW:22812 TID=Mmu.4246.1 CNT=2 FEA=EST TIER=ConsEnd STK=0
367.9	863.9	366.5	NM_019056	MmugDNA.38548.1.S1_s_a	gDNA.g9506682 FEA=U133PSR GEN=NDUFB11 DEF=Orthologous to 218320_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa
460.05	929.35	442.45	NM_004146	MmugDNA.6319.1.S1_s_a	gDNA.g10764846 FEA=U133PSR GEN=NDUFB7 DEF=Orthologous to 202839_s_at NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
4825.45	9822.2	4378.65	CD768031	Mmu.7399.1.S1_at	gb:CD768031 DB_XREF=gi:32426533 DB_XREF=AGENCOURT_14718956 CLONE=IMAGE:6973306 TID=Mmu.7399.1 CNT=1 FEA=EST TIER=ConsEnd STK=1
536.45	256.8	577.1	AA993683	MmugDNA.5110.1.S1_at	gDNA.Hs.163867.1.A1 FEA=U133PSR GEN=PRO1580 DEF=Orthologous to 213550_s_at hypothetical protein PRO1580
268.6	120.4	270.55	BC000462	MmugDNA.5643.1.S1_at	gDNA.g12653384 FEA=U133PSR GEN=UQCR DEF=Orthologous to 223613_at ubiquinol cytochrome c reductase, 6.4kDa subunit
179.85	169.25	83.3	NM_003366	MmugDNA.8162.1.S1_at	gDNA.g4507842 FEA=U133PSR GEN=UQCRC2 DEF=Orthologous to 200883_at ubiquinol-cytochrome c reductase core protein II
147.1	89.25	73.3	AF184911	MmugDNA.35310.1.S1_at	gDNA.g10121319 FEA=U133PSR GEN=PRSS25 DEF=Orthologous to 211152_s_at protease, serine, 25
435.9	143.3	421.55	AF453834	MmugDNA.40691.1.S1_at	gDNA.Hs2.198271.3.S1 FEA=U133PSR GEN=NDUFA10 DEF=Orthologous to 1555548_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
294.8	97.15	274.75	AW190316	MmugDNA.3420.1.S1_at	gDNA.Hs.2186.4.A1 FEA=U133PSR GEN=SHMT2 DEF=Orthologous to 214095_at serine hydroxymethyltransferase 2 (mitochondrial)
213.2	92.1	110.6	AI760495	MmugDNA.15069.1.S1_at	gDNA.Hs.205711.0.A1 FEA=U133PSR GEN=CYCS DEF=Orthologous to 244546_at cytochrome c, somatic
363.5	118.1	284.75	AB062482	MmugDNA.34532.1.S1_at	gDNA.Hs2.374685.1.S1 FEA=U133PSR GEN=NDUFS4 DEF=Orthologous to 1555057_at NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
402.65	99.1	314.3	NM_001867	MmugDNA.16732.1.S1_at	gDNA.g4502992 FEA=U133PSR GEN=COX7C DEF=Orthologous to 201134_x_at cytochrome c oxidase subunit VIIc
332	79.8	222.7	AF149794	MmugDNA.37633.1.S1_at	gDNA.g4929486 FEA=U133PSR GEN=APAF1 DEF=Orthologous to 211554_s_at apoptotic protease activating factor
539.35	140.7	242.2	AA382702	MmugDNA.43583.1.S1_x_a	gDNA.Hs.3462.1.S1 FEA=U133PSR GEN=COX7C DEF=Orthologous to 213846_at cytochrome c oxidase subunit VIIc
358.15	209.95	68.9	AW500009	MmugDNA.16183.1.S1_at	gDNA.Hs.184325.0.A5 FEA=U133PSR GEN=UBE2J1 DEF=Orthologous to 217824_at ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
307.95	50.05	59.65	AK002110	MmugDNA.24532.1.S1_at	gDNA.Hs.90443.1.A1 FEA=U133PSR GEN=NDUFS8 DEF=Orthologous to 232169_x_at NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
251.95	15.05	236.55	AF258566	MmugDNA.21374.1.S1_at	gDNA.Hs2Affx.1.256.S1 FEA=U133PSR GEN=UBE1 DEF=Orthologous to 1555387_at ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)