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|-----------|-----|------------------------------------|---|-----------|----------------------------|------------|
| MIN-58-25 | 499 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 483/485 (99%) | 1/485 (0%) |
| MIN-58-26 | 496 | g[11914850]gb U92454.1 JMU92454 | Mus musculus WW domain binding protein 5 mRNA, partial cds | 0 | 378/378 (100%) | - |
| MIN-58-27 | 422 | g[6651038]gb AF130357.1 AF130357 | Mus musculus domesticus X chromosome region similar to human DXS963E, complete sequence | 1.00E-136 | 253/256 (98%) | - |
| MIN-58-29 | 503 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/489 (99%) | 3/489 (0%) |
| MIN-58-30 | 432 | g[54095]emb X68837.1 JMSGIIA2 | M.musculus Sgll gene for secretogranin II, exon 2 | 0 | 363/363 (100%) | - |
| MIN-58-31 | 461 | g[2133878]gb AC000400.1 AC000400 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 1.00E-133 | 256/263 (97%), Positives = | - |
| MIN-58-32 | 499 | g[1336863]gb S81177.1 S81177 | TN2-retinoic acid-regulated gene/130 kDa leucine-rich protein homolog/LEU130 homolog [mice, P19 emb | 0 | 428/428 (100%) | - |
| MIN-58-33 | 501 | g[194066]gb M25389.1 JUSIAPP | Mouse islet amyloid polypeptide mRNA, complete cds | 0 | 430/430 (100%) | - |
| MIN-58-34 | 261 | g[7710045]gb NM_016705.1 | Mus musculus kinesin family member 21A (Kif21a), mRNA | 6.00E-90 | 176/177 (99%) | 1/177 (0%) |
| MIN-58-35 | 483 | g[6138992]gb AF051976.2 AF051976 | Homo sapiens unconventional myosin (MYO15) gene, partial sequence | 0.95 | 20/20 (100%) | - |
| MIN-58-36 | 499 | g[6680923]ref NM_007687.1 | Mus musculus cofilin 1, non-muscle (Cofil1), mRNA | 0 | 485/485 (100%) | - |
| MIN-58-37 | 431 | g[11329332]emb AL031681.16 HS862K6 | Human DNA sequence from clone RP5-862K6 on chromosome 20q12-13.13 Contains part of the gene for | 3.00E-53 | 173/190 (91%) | 6/190 (3%) |
| MIN-58-38 | 500 | g[1565212]db D87901.1 D87901 | Mouse mRNA for ARF4, complete cds | 0 | 494/494 (100%) | - |
| MIN-58-39 | 502 | g[4507842]ref NM_003966.1 | Homo sapiens ubiquinol-cytochrome c reductase core protein II (UQCRC2), mRNA | 6.00E-73 | 294/345 (85%) | - |
| MIN-58-40 | 501 | g[1134499]gb AC011495.6 AC011495 | Homo sapiens chromosome 19 clone CTB-33G10, complete sequence | 0.25 | 21/21 (100%) | - |
| MIN-58-41 | 499 | g[7740042]gb AC005703.2 AC005703 | Homo sapiens chromosome 17, clone hRPK_849_N_15, complete sequence | 7.00E-08 | 35/36 (97%) | - |
| MIN-58-42 | 498 | g[8393449]ref NM_017211.1 | Rattus norvegicus selectin, endothelial cell, ligand (C1g1), mRNA | 5.00E-55 | 183/203 (90%) | 3/203 (1%) |
| MIN-58-43 | 493 | g[10729537]gb AE002940.2 AE002940 | Drosophila melanogaster genomic scaffold 142000013385820, complete sequence | 0.062 | 22/22 (100%) | - |
| MIN-58-44 | 498 | g[4210518]gb AC002327.1 AC002327 | Mus musculus chromosome 7, clone 19K5, complete sequence | 0.004 | 24/24 (100%) | - |
| MIN-58-46 | 504 | g[667919]ref NM_008774.1 | Mus musculus poly A binding protein, cytoplasmic 1 (Pabpc1), mRNA | 0 | 448/450 (99%) | 2/450 (0%) |
| MIN-58-47 | 495 | g[10434010]db AK022554.1 AK022554 | Homo sapiens cDNA FLJ12492 fis, clone NT2RM2001632, weakly similar to KES1 PROTEIN | 1.00E-110 | 251/267 (94%) | - |
| MIN-58-48 | 501 | g[11121499]gb AJ251508.1 JMU251508 | Mus musculus mRNA for AWP1 protein (Awp1) gene | 0 | 473/482 (98%) | 4/482 (0%) |
| MIN-58-49 | 503 | g[199901]gb J64298.1 JUSMVP | Mouse vacuolar H(+)-ATPase (mvp) mRNA, complete cds | 0 | 487/489 (99%) | - |
| MIN-58-50 | 497 | g[7110730]ref NM_009438.1 | Mus musculus ribosomal protein L13a (Rp13a), mRNA | 0 | 490/491 (99%) | - |
| MIN-58-51 | 497 | g[4884902]emb AL050071.1 HSM800396 | Homo sapiens mRNA: cDNA DKFZp566B0846 (from clone DKFZp566B0846); partial cds | 8.00E-54 | 142/153 (92%) | - |
| MIN-58-52 | 499 | g[595667]gb U13176.1 JRN13176 | Rattus norvegicus clone ubc2e ubiquitin conjugating enzyme (E217k) mRNA, complete cds | 0 | 481/487 (98%) | 1/487 (0%) |
| MIN-58-53 | 440 | g[6680462]ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-58-55 | 504 | g[10438458]db AK025827.1 AK025827 | Homo sapiens cDNA: FLJ22174 fis, clone HRC00767 | 3.00E-04 | 71/86 (82%) | - |
| MIN-58-56 | 500 | g[3114215]gb AF022811.1 AF022811 | Mus musculus cornichon mRNA, complete cds | 0 | 486/488 (99%) | 1/488 (0%) |
| MIN-58-57 | 429 | g[11181860]gb AC023154.5 AC023154 | Homo sapiens clone RP11-752D24, complete sequence | 0.84 | 23/24 (95%) | - |
| MIN-58-58 | 497 | g[192186]gb M57734.1 JUSBGAL45 | Mouse beta-galactosidase (BGAL) gene, complete cds | 0 | 458/458 (100%) | - |
| MIN-58-59 | 500 | g[5441633]emb AL035890.10 HS202121 | Human DNA sequence from clone RP1-202121 on chromosome 6p21.1-21.2. Contains a novel gene, the GL | 3.00E-09 | 70/82 (85%), Positives = | - |
| MIN-58-60 | 495 | g[6678178]ref NM_009295.1 | Mus musculus syntaxin binding protein 1 (Stxbp1), mRNA | 0 | 481/481 (100%) | - |
| MIN-58-61 | 474 | g[667771]gb ref NM_009049.1 | Mus musculus regulated endocrine-specific protein 18 (Resp18), mRNA | 0 | 441/442 (99%) | - |
| MIN-58-62 | 501 | g[5803047]ref NM_006801.1 | Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 (KDEL1), mR | 3.00E-59 | 148/158 (93%) | - |
| MIN-58-63 | 499 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-58-65 | 501 | g[6679768]ref NM_007998.1 | Mus musculus ferroxidase (Fech), mRNA | 0 | 452/452 (100%) | - |
| MIN-58-66 | 503 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 490/490 (100%) | - |
| MIN-58-68 | 503 | g[8922156]ref NM_018457.1 | Homo sapiens DKFZp564J157 protein (DKFZP564J157), mRNA | 6.00E-33 | 277/345 (80%) | 6/345 (1%) |
| MIN-58-69 | 500 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-58-70 | 407 | g[6753363]ref NM_009861.1 | Mus musculus cell division cycle 42 homolog (S. cerevisiae) (Cdc42), mRNA | 1.00E-150 | 274/275 (99%) | - |
| MIN-58-71 | 500 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-58-72 | 495 | g[8923426]ref NM_017830.1 | Homo sapiens hypothetical protein FLJ20455 (FLJ20455), mRNA | 1.00E-83 | 291/335 (86%) | - |
| MIN-58-73 | 498 | g[3169207]gb AC002324.1 AC002324 | Mus musculus chromosome 11, clone 475_H_14, complete sequence | 1.00E-24 | 135/158 (85%) | 4/158 (2%) |
| MIN-58-75 | 493 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 478/479 (99%) | - |
| MIN-58-76 | 502 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 487/488 (99%) | - |
| MIN-58-78 | 503 | g[6048975]gb AF103804.1 AF103804 | Homo sapiens clone H63 unknown mRNA | 2.00E-42 | 120/129 (93%) | 2/129 (1%) |
| MIN-58-80 | 461 | g[9910407]ref NM_020007.1 | Mus musculus muscleblind (Drosophila)-like (Mbnl), mRNA | 0 | 453/455 (99%) | 2/455 (0%) |
| MIN-58-81 | 502 | g[50794]emb X61506.1 JMEEP | Mouse E46 mRNA for E46 protein | 0 | 405/407 (99%) | 2/407 (0%) |
| MIN-58-82 | 503 | g[515864]emb X78167.1 JNSDRPL15 | R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA | 0 | 464/489 (94%) | - |
| MIN-58-83 | 500 | g[3249127]gb AC004707.1 AC004707 | Homo sapiens chromosome 17, clone hRPC_117_B_12, complete sequence | 3.00E-10 | 51/56 (91%) | - |
| MIN-58-85 | 499 | g[5932000]gb AF131205.1 AF131205 | Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory p | 0 | 399/411 (97%) | 1/411 (0%) |
| MIN-58-86 | 404 | g[7019490]ref NM_013274.1 | Homo sapiens polymerase (DNA-directed), lambdaB (POLL), mRNA | 0.59 | 20/20 (100%) | - |
| MIN-58-87 | 401 | g[6680462]ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-135 | 248/249 (99%) | - |
| MIN-58-88 | 396 | g[11230779]ref NM_021884.1 | Mus musculus tumor susceptibility gene 101 (tsg101), mRNA | 0 | 338/338 (100%) | - |
| MIN-58-89 | 498 | g[8567405]ref NM_017472.1 | Mus musculus sorting nexin 3 (Snx3), mRNA | 2.00E-79 | 152/152 (100%) | - |
| MIN-58-90 | 499 | g[1813551]gb U72059.1 JMU72059 | Mus musculus chloride channel regulator Icln (Icln) pseudogene | 0 | 446/481 (92%) | 6/481 (1%) |
| MIN-58-91 | 500 | g[339543]gb M96868.1 HUMTGFABA | Human transforming growth factor-alpha (TGFa) gene, exon 1 and 5'end cds | 3.00E-04 | 26/26 (100%) | - |
| MIN-58-92 | 212 | g[6681154]ref NM_007839.1 | Mus musculus DEAD/H (Asp-Glu-Ala-Asp/H) box polypeptide 15 (RNA helicase A) (Ddx15), mRNA | 5.00E-90 | 169/169 (100%) | - |
| MIN-58-93 | 357 | g[510549]emb X80029.1 JRNHEM2 | R.norvegicus Hem-2 mRNA | 1.00E-152 | 326/342 (95%) | 1/342 (0%) |
| MIN-58-94 | 224 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-112 | 209/210 (99%) | - |
| MIN-58-95 | 451 | g[8546861]emb AJ278429.1 JMU278429 | Mus musculus partial Prkar1a gene for cAMP-dependent protein kinase regulatory subunit R1alpha, exons 8 | 1.00E-109 | 202/202 (100%) | - |
| MIN-58-96 | 170 | g[6755449]ref NM_011343.1 | Mus musculus SEC61, gamma subunit (S. cerevisiae) (Sec61g), mRNA | 2.00E-64 | 128/129 (99%) | - |
| MIN-60-24 | 75 | - | - | - | - | - |
| MIN-60-40 | 83 | g[4768839]gb AF117611.1 AF117611 | Dictyostelium discoideum Dosa protein (dosa) gene, complete cds | 0.008 | 25/26 (96%) | - |
| MIN-60-17 | 97 | g[10726480]gb AE003694.2 AE003694 | Drosophila melanogaster genomic scaffold 142000013386035 section 19 of 105, complete sequence | 0.041 | 24/25 (96%) | - |
| MIN-60-23 | 135 | g[7291950]gb AE003468.1 AE003468 | Drosophila melanogaster genomic scaffold 142000013386045 section 2 of 17, complete sequence | 0.06 | 21/21 (100%) | - |
| MIN-60-37 | 175 | g[10438215]db AK025636.1 AK025636 | Homo sapiens cDNA: FLJ21983 fis, clone HEP06219 | 2.00E-27 | 124/144 (86%) | - |
| MIN-60-78 | 131 | g[4929686]gb AF151867.1 AF151867 | Homo sapiens CGI-109 protein mRNA, complete cds | 2.00E-23 | 72/77 (93%) | - |
| MIN-60-52 | 204 | g[5348385]gb AC006111.2 AC006111 | Homo sapiens chromosome 16 clone RPC1-1_461A8, complete sequence | 1.00E-04 | 32/34 (94%) | - |
| MIN-60-75 | 177 | g[4582483]gb AC006312.8 AC006312 | Homo sapiens chromosome 9, clone hRPK401_g_18, complete sequence | 4.00E-16 | 64/69 (92%) | 1/69 (1%) |
| MIN-60-62 | 89 | g[4758393]ref NM_004475.1 | Homo sapiens flotillin 2 (FLOT2), mRNA | 2.2 | 18/18 (100%) | - |
| MIN-60-64 | 157 | g[7670575]db AP001621.1 AP001621 | Homo sapiens genomic DNA, chromosome 21, clone:KB1342D7, MX1-D21S171 region, complete sequence | 0.28 | 20/20 (100%) | - |
| MIN-60-72 | 113 | g[8923041]gb ref NM_017633.1 | Homo sapiens hypothetical protein FLJ20037 (FLJ20037), mRNA | 1.00E-27 | 88/96 (91%) | - |
| MIN-60-19 | 113 | g[6329914]db JAB032964.1 JAB032964 | Homo sapiens mRNA for KIAA1138 protein, partial cds | 6.00E-23 | 71/76 (93%) | - |
| MIN-60-07 | 151 | g[6330242]db JAB033007.1 JAB033007 | Homo sapiens mRNA for KIAA1181 protein, partial cds | 3.00E-38 | 125/138 (90%) | 1/138 (0%) |
| MIN-60-05 | 140 | g[7959310]db JAB040955.1 JAB040955 | Homo sapiens mRNA for KIAA1522 protein, partial cds | 7.00E-05 | 48/54 (88%) | 1/54 (1%) |
| MIN-60-93 | 192 | g[4210725]emb AJ132583.1 JSA132583 | Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial | 9.00E-05 | 38/42 (90%) | - |
| MIN-60-71 | 76 | g[6681763]ref NM_005002.1 | Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39kD) (NDUFA9), mRNA | 0.008 | 25/26 (96%) | - |
| MIN-60-28 | 148 | g[7705653]ref NM_015853.1 | Homo sapiens ORF (LOC51035), mRNA | 3.00E-13 | 103/124 (83%) | - |
| MIN-60-02 | 88 | g[5051939]gb AF143313.1 PTEN2 | Homo sapiens PTEN (PTEN) gene, exon 2 | 0.036 | 21/21 (100%) | - |
| MIN-60-47 | 128 | g[4885480]ref NM_005466.1 | Homo sapiens RNA polymerase II transcriptional regulation mediator (MED6, S. cerevisiae, homolog of) (ME | 9.00E-35 | 106/116 (91%) | - |
| MIN-60-18 | 168 | g[5902145]ref NM_007019.1 | Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA | 4.00E-16 | 124/149 (83%) | 1/149 (0%) |
| MIN-60-09 | 166 | g[500262]emb AL022329.9 HS407F11 | Human DNA sequence from clone CTA-407F11 on chromosome 22q12 Contains ADRBK2 gene for adrene | 0.3 | 23/24 (95%) | - |
| MIN-60-76 | 150 | g[11121089]emb AL445263.6 AL445263 | Human DNA sequence from clone RP11-227B14 on chromosome 1, complete sequence [Homo sapiens] | 0.27 | 20/20 (100%) | - |
| MIN-60-68 | 129 | g[11140022]emb AL109936.10 HSJ1057 | Human DNA sequence from clone RP5-1057J7 on chromosome 1, complete sequence [Homo sapiens] | 0.23 | 20/20 (100%) | - |
| MIN-60-84 | 136 | g[192089]gb LO1062.1 JUSATPSYX | Mouse ATP synthase alpha subunit, complete cds | 8.00E-57 | 113/113 (100%) | - |
| MIN-60-03 | 194 | g[193094]gb J03297.1 JUSERPX | Mouse Erp99 mRNA encoding an endoplasmic reticulum transmembrane protein | 7.00E-92 | 172/172 (100%) | - |
| MIN-60-06 | 71 | g[198393]gb M33934.1 JUSIMPDP | Mouse IMP dehydrogenase mRNA, complete cds | 9.00E-24 | 57/57 (100%) | - |
| MIN-60-16 | 189 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 3.00E-91 | 174/175 (99%) | - |
| MIN-60-25 | 300 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-155 | 282/283 (99%) | - |
| MIN-60-29 | 211 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-102 | 197/198 (99%) | 1/198 (0%) |
| MIN-60-38 | 334 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-175 | 319/320 (99%) | 1/320 (0%) |
| MIN-60-45 | 242 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-122 | 226/227 (99%) | - |
| MIN-60-51 | 174 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 2.00E-89 | 168/168 (100%) | - |
| MIN-60-87 | 260 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-135 | 245/245 (100%) | - |
| MIN-60-95 | 114 | g[342520]gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 5.00E-33 | 73/73 (100%) | - |
| MIN-60-56 | 246 | g[391760]db J16847.1 JUSSPCP1 | Mouse mRNA for stromal cell derived protein-1, complete cds | 1.00E-127 | 232/232 (100%) | - |
| MIN-60-67 | 168 | g[200396]gb M73329.1 JUSPLCA | Mouse phospholipase C-alpha (PLC-alpha) mRNA, complete cds | 7.00E-67 | 150/154 (97%) | 2/154 (1%) |
| MIN-60-15 | 146 | g[52714]emb X04724.1 JMINSIG | Mouse preproinsulin gene I | 5.00E-55 | 110/110 (100%) | - |
| MIN-60-36 | 164 | g[52714]emb X04724.1 JMINSIG | Mouse preproinsulin gene II | 2.00E-61 | 121/121 (100%) | - |

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| MIN-60-22 | 99 | gi 9055383 ref NM_018753.1 | Mus musculus 3 monoxygenase/tryptophan 5 monoxygenase activation protein, beta polypeptide (Ywhab), | 3.00E-40 | 85/85 (100%) | - |
| MIN-60-85 | 113 | gi 7188778 gb AF233282.1 AF233282 | Mus musculus calmodulin III (Calmd3) mRNA, 3' untranslated region | 1.00E-48 | 99/99 (100%) | - |
| MIN-60-43 | 114 | gi 7304968 ref NM_013493.1 | Mus musculus cellular nucleic acid binding protein (Cnbp), mRNA | 9.00E-47 | 96/96 (100%) | - |
| MIN-60-33 | 198 | gi 6671701 ref NM_007637.2 | Mus musculus chaperonin subunit 5 (epsilon) (Cct5), mRNA | 2.00E-95 | 185/186 (99%) | 1/186 (0%) |
| MIN-60-08 | 115 | gi 9558585 gb AC020967.2 AC020967 | Mus musculus chromosome 18 clone RP23-16108, complete sequence | 8.00E-38 | 96/101 (95%) | - |
| MIN-60-42 | 156 | gi 6753587 ref NM_010008.1 | Mus musculus cytochrome P450, 2j6 (Cyp2j6), mRNA | 1.00E-71 | 141/142 (99%) | - |
| MIN-60-27 | 149 | gi 4521187 dbj AB006360.1 AB006360 | Mus musculus DNA for MUSPUR, partial cds | 2.00E-67 | 134/135 (99%) | - |
| MIN-60-39 | 164 | gi 10946492 gb AF308696.1 AF308696 | Mus musculus ELAC2 mRNA, complete cds | 8.00E-79 | 150/150 (100%) | - |
| MIN-60-12 | 102 | gi 7799153 emb AL355706.1 JROEST075 | Mus musculus EST from clone 1969533, extrem' end | 4.00E-42 | 88/88 (100%) | - |
| MIN-60-35 | 236 | gi 6753707 ref NM_010097.1 | Mus musculus extracellular matrix protein 2 (Ecm2), mRNA | 1.00E-107 | 208/210 (99%) | 1/210 (0%) |
| MIN-60-49 | 112 | gi 6753913 ref NM_010240.1 | Mus musculus ferritin light chain 1 (Ft1), mRNA | 8.00E-44 | 98/99 (98%) | 1/99 (1%) |
| MIN-60-30 | 140 | gi 10946975 ref NM_021540.1 | Mus musculus g1-related zinc finger protein (G1rp), mRNA | 2.00E-39 | 84/84 (100%) | - |
| MIN-60-54 | 84 | gi 9910275 ref NM_019979.1 | Mus musculus heat shock protein 90 (Hsp90), mRNA | 3.00E-27 | 63/63 (100%) | - |
| MIN-60-11 | 164 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 1.00E-80 | 153/153 (100%) | - |
| MIN-60-44 | 144 | gi 4050090 gb AF110520.1 MMHC42501 | Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, | 6.00E-67 | 130/130 (100%) | - |
| MIN-60-01 | 240 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain C93A/He | 1.00E-124 | 226/226 (100%) | - |
| MIN-60-79 | 125 | gi 6723706 emb AJ237586.1 MM0237586 | Mus musculus mRNA for hypothetical protein expressed in thymocytes (clone MTA.D02.090), partial | 1.00E-55 | 111/111 (100%) | - |
| MIN-60-21 | 112 | gi 11037795 ref NM_021607.1 | Mus musculus nicastrin (Ncstn-pending), mRNA | 2.00E-22 | 58/59 (98%) | - |
| MIN-60-80 | 124 | gi 902578 gb U24173.1 MMU24173 | Mus musculus p21 (WAF1) mRNA, complete cds | 4.00E-46 | 104/107 (97%) | - |
| MIN-60-20 | 131 | gi 6754993 ref NM_011865.1 | Mus musculus poly(RC)-binding protein 1 (Pcbp1), mRNA | 3.00E-59 | 117/117 (100%) | - |
| MIN-60-88 | 174 | gi 9857943 gb AF273768.1 AF273768 | Mus musculus preproenkephalin Y (Npy) mRNA, complete cds | 9.00E-85 | 160/160 (100%) | - |
| MIN-60-74 | 205 | gi 6679496 ref NM_008944.1 | Mus musculus proteasome (brosome, macropain) subunit, alpha type 2 (Psm2), mRNA | 3.00E-97 | 187/189 (98%) | - |
| MIN-60-70 | 127 | gi 6677698 ref NM_009041.1 | Mus musculus radixin (Rdx), mRNA | 1.00E-52 | 112/114 (98%) | - |
| MIN-60-34 | 256 | gi 6677866 ref NM_009130.1 | Mus musculus secretogranin III (Scg3), mRNA | 1.00E-120 | 240/243 (98%) | 3/243 (1%) |
| MIN-60-91 | 100 | gi 6677986 ref NM_009193.1 | Mus musculus stem-loop binding protein (Slbp), mRNA | 7.00E-41 | 86/86 (100%) | - |
| MIN-60-77 | 218 | gi 6678146 ref NM_009280.1 | Mus musculus synovial sarcoma, translocated to X chromosome (Ssxt), mRNA | 1.00E-111 | 212/213 (99%) | 1/213 (0%) |
| MIN-60-86 | 145 | gi 9910591 ref NM_020012.1 | Mus musculus TRIAD2 type I (Triad2), mRNA | 1.00E-67 | 131/131 (100%) | - |
| MIN-60-31 | 242 | gi 3618221 emb X89968.1 RNSNAPGEN | Rattus norvegicus mRNA for alpha-soluble NSF attachment protein | 1.00E-105 | 216/222 (97%) | 1/222 (0%) |
| MIN-60-90 | 123 | gi 3551053 dbj AB011679.1 AB011679 | Rattus norvegicus mRNA for class I beta-tubulin, complete cds | 6.00E-14 | 65/73 (89%) | - |
| MIN-60-55 | 113 | gi 8392887 ref NM_017093.1 | Rattus norvegicus Murine thymoma viral (v-akt) oncogene homolog 2 (Akt2), mRNA | 3.00E-37 | 92/96 (95%) | - |
| MIN-60-58 | 258 | gi 6649520 gb U05334.1 RNU05334 | Rattus norvegicus rap7a mRNA, complete cds | 2.00E-90 | 215/230 (93%) | - |
| MIN-60-69 | 162 | gi 2088909 gb M11691.1 SYNNMUBGA | Synthetic beta-galactosidase/mouse ubiquitin fusion protein mRNA, clone arf3 | 3.00E-75 | 147/148 (99%) | - |
| MIN-60-48 | 83 | gi 10639147 emb AL445063.1 TACID1 | Thermoplasma acidophilum complete genome; segment 1/5 | 0.52 | 19/19 (100%) | - |
| MIN-60-82 | 182 | gi 4980648 gb AE001701.1 AE001701 | Thermotoga maritima section 13 of 136 of the complete genome | 0.085 | 21/21 (100%) | - |
| MIN-60-14 | 226 | gi 431749 gb L24101.1 YEPUREAH | Yersinia enterocolitica urease gamma, beta, and alpha subunits (ureA, ureB, ureC) genes, and accessory ge | 0.11 | 21/21 (100%) | - |
| MIN-60-59 | 400 | gi 10733353 gb AE003519.2 AE003519 | Drosophila melanogaster genomic scaffold 142000013386050 section 49 of 54, complete sequence | 0.05 | 22/22 (100%) | - |
| MIN-60-33 | 500 | gi 1072823 gb AE003493.2 AE003493 | Drosophila melanogaster genomic scaffold 142000013386053 section 10 of 30, complete sequence | 0.063 | 22/22 (100%) | - |
| MIN-60-41 | 501 | gi 606010 gb U18997.1 ECOUW67 | Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes | 1.00E-143 | 265/267 (99%) | - |
| MIN-60-16 | 504 | gi 10439393 dbj AK022510.1 AK022510 | Homo sapiens cDNA FL12448 fls, clone NT2RM100300 | 4.00E-28 | 138/162 (85%) | - |
| MIN-60-55 | 243 | gi 10438982 dbj AK026208.1 AK026208 | Homo sapiens cDNA: FLJ22555 fis, clone HSI01193 | 9.00E-15 | 83/95 (87%) | 1/95 (1%) |
| MIN-60-54 | 463 | gi 10765023 gb AC022014.3 AC022014 | Homo sapiens chromosome 11 clone RP11-91E22 map 11q, complete sequence | 0.91 | 20/20 (100%) | - |
| MIN-60-85 | 483 | gi 7960348 gb AC011088.8 AC011088 | Homo sapiens chromosome 11, clone RP11-292E14, complete sequence | 0.24 | 24/25 (96%) | - |
| MIN-60-35 | 501 | gi 6715703 gb AC007225.2 AC007225 | Homo sapiens chromosome 11, clone RP11-480G7, complete sequence | 3.00E-78 | 177/186 (95%) | - |
| MIN-60-44 | 501 | gi 9221189 gb AC008561.4 AC008561 | Homo sapiens chromosome 5 clone CTC-5354A, complete sequence | 3.00E-04 | 29/30 (96%) | - |
| MIN-60-93 | 459 | gi 3483880 gb AF086535.1 HJMZE07G05 | Homo sapiens full length insert cDNA clone ZEO7G05 | 3.00E-59 | 175/194 (90%) | - |
| MIN-60-43 | 498 | gi 7768713 dbj AP001708.1 AP001708 | Homo sapiens genomic DNA, chromosome 21q, section 52/105 | 0.25 | 21/21 (100%) | - |
| MIN-60-79 | 496 | gi 7661989 ref NM_014757.1 | Homo sapiens KIAA0200 gene product (KIAA0200), mRNA | 1.00E-100 | 399/470 (84%) | - |
| MIN-60-19 | 496 | gi 7662087 ref NM_015313.1 | Homo sapiens KIAA0382 protein: leukemia-associated rho guanine nucleotide exchange factor (GEF) (KIA | 4.00E-12 | 69/79 (87%) | - |
| MIN-60-46 | 310 | gi 6683706 dbj AB007924.2 AB007924 | Homo sapiens mRNA for KIAA0455 protein, partial cds | 9.00E-31 | 88/94 (93%) | - |
| MIN-60-72 | 503 | gi 7328165 emb AL162081.1 HSM802611 | Homo sapiens mRNA: cDNA DKFZ762K0911 (from clone DKFZ762K0911); complete cds | 1.00E-107 | 438/503 (87%) | 25/503 (4%) |
| MIN-60-86 | 500 | gi 5729723 ref NM_006621.1 | Homo sapiens S-adenosylhomocysteine hydrolase-like 1 (AHCYL1), mRNA | 1.00E-157 | 433/483 (89%) | - |
| MIN-60-95 | 480 | gi 4090213 emb AL031073.1 HS142F18 | Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to r | 0.24 | 21/21 (100%) | - |
| MIN-60-32 | 409 | gi 11121010 emb AL159161.1 AL159161 | Human DNA sequence from clone RP11-95N14 on chromosome 13, complete sequence [Homo sapiens] | 0.2 | 21/21 (100%) | - |
| MIN-60-01 | 500 | gi 8388653 emb AL121918.2 HJ342K1 | Human DNA sequence from clone RP3-342K12 on chromosome 20 Contains a pseudogene similar to Cytoc | 0.063 | 22/22 (100%) | - |
| MIN-60-47 | 499 | gi 9187334 emb AL034550.3 HS1184F4 | Human DNA sequence from clone RP5-1184F4 on chromosome 20q11.1-11.23. Contains the 3' end of gene | 1.00E-151 | 418/460 (90%) | 15/460 (3%) |
| MIN-60-14 | 429 | gi 9588477 emb AL136120.8 AL136120 | Human DNA sequence from clone RP5-975D15 on chromosome 1p31.3-32.2, complete sequence [Homo sa | 6.00E-08 | 32/32 (100%) | - |
| MIN-60-15 | 504 | gi 1524166 emb Y07688.1 MMNFIX1 | M.musculus mRNA for NfIX1-protein | 0.490 | 490/490 (100%) | - |
| MIN-60-25 | 500 | gi 50162 emb X15986.1 JMMBGLLEC | Mouse 3' mRNA for beta-galactoside specific lectin (14kDa) | 0.480 | 480/480 (100%) | - |
| MIN-60-17 | 312 | gi 193084 gb M92988.1 MUSERP60A | Mouse calregulin (ERP60) mRNA, complete cds | 1.00E-167 | 298/298 (100%) | - |
| MIN-60-60 | 503 | gi 193264 gb J03941.1 MUSFERH | Mouse ferritin heavy chain (MFH) mRNA, complete cds | 0.448 | 448/448 (100%) | - |
| MIN-60-11 | 502 | gi 193547 gb J04632.1 MUSGLUTA | Mouse glutathione S-transferase class mu (GST1-1) mRNA, complete cds | 0.488 | 488/488 (100%) | - |
| MIN-60-09 | 498 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.484 | 484/484 (100%) | - |
| MIN-60-12 | 498 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.484 | 485/485 (99%) | - |
| MIN-60-23 | 502 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.472 | 472/472 (100%) | - |
| MIN-60-31 | 501 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.487 | 487/487 (100%) | - |
| MIN-60-37 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.493 | 493/493 (100%) | - |
| MIN-60-38 | 263 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 1.00E-133 | 246/248 (99%) | - |
| MIN-60-51 | 123 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 6.00E-45 | 93/93 (100%) | - |
| MIN-60-52 | 502 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.488 | 488/488 (100%) | - |
| MIN-60-58 | 484 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.469 | 470/99 (%) | - |
| MIN-60-62 | 500 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.486 | 486/486 (100%) | - |
| MIN-60-68 | 501 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.487 | 487/487 (100%) | - |
| MIN-60-69 | 498 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.484 | 484/484 (100%) | - |
| MIN-60-74 | 495 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.481 | 481/481 (100%) | - |
| MIN-60-78 | 392 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.379 | 379/379 (100%) | - |
| MIN-60-82 | 503 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.497 | 497/497 (100%) | - |
| MIN-60-89 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.486 | 486/486 (100%) | - |
| MIN-60-91 | 494 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0.480 | 480/480 (100%) | - |
| MIN-60-94 | 246 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 5.00E-87 | 178/180 (98%) | 2/180 (1%) |
| MIN-60-03 | 414 | gi 54848 emb X57796.1 MMTNFRE5 | Mouse mRNA for 55-kDa tumor necrosis factor receptor | 0.400 | 400/401 (99%) | - |
| MIN-60-34 | 503 | gi 54848 emb X57796.1 MMTNFRE5 | Mouse mRNA for 55-kDa tumor necrosis factor receptor | 0.487 | 489/99 (%) | 1/489 (0%) |
| MIN-60-04 | 497 | gi 50620 emb X52803.1 MMCYCM | Mouse mRNA for cyclophilin (EC 5.2.1.8) | 0.483 | 483/483 (100%) | - |
| MIN-60-29 | 498 | gi 475011 dbj D29802.1 MUSGPBSL | Mouse mRNA for G protein beta subunit homologue, complete cds | 0.485 | 485/485 (100%) | - |
| MIN-60-56 | 495 | gi 666969 dbj D1252.1 MUSOSF3 | Mouse mRNA for OSF-3, complete cds | 0.481 | 481/481 (100%) | - |
| MIN-60-13 | 500 | gi 202158 gb M33385.1 MUSTRKB | Mouse tyrosine protein kinase B (trkB) mRNA, complete cds | 0.494 | 494/494 (100%) | - |
| MIN-60-42 | 503 | gi 902009 gb U27316.1 MMU27316 | Mus musculus adenine nucleotide translocase-2 (Ant2) mRNA, complete cds | 0.489 | 489/489 (100%) | - |
| MIN-60-70 | 499 | gi 902009 gb U27316.1 MMU27316 | Mus musculus adenine nucleotide translocase-2 (Ant2) mRNA, complete cds | 0.494 | 494/494 (100%) | - |
| MIN-60-90 | 472 | gi 7110193 gb AF192370.1 MMADAT4 | Mus musculus adenosine deaminase acting on tRNA 1 (mADAT1) gene, exon 5 | 1.00E-156 | 287/290 (98%) | - |
| MIN-60-05 | 500 | gi 6678765 ref NM_008537.1 | Mus musculus alpha-methylacyl-Coenzyme A racemase (Macr1), mRNA | 0.349 | 349/350 (99%) | 1/350 (0%) |
| MIN-60-22 | 323 | gi 6753207 ref NM_009770.1 | Mus musculus B-cell translocation gene 3 (Btg3), mRNA | 1.00E-141 | 306/318 (96%) | 4/318 (1%) |
| MIN-60-84 | 398 | gi 1399647 gb U53455.1 MMU53455 | Mus musculus chloride ion current inducer protein (CLCI) mRNA, partial cds | 1.00E-171 | 343/350 (98%) | 4/350 (1%) |
| MIN-60-53 | 358 | gi 11181790 gb AC068906.12 AC068906 | Mus musculus chromosome 1 clone rp23-240p23 strain C57BL/6J, complete sequence | 7.00E-04 | 31/33 (93%) | - |
| MIN-60-67 | 423 | gi 6862977 gb AC009287.17 AC009287 | Mus musculus chromosome 10 clone rp21-668b24 strain 129Sv/SvEvTac, complete sequence | 2.00E-04 | 26/26 (100%) | - |
| MIN-60-36 | 448 | gi 9837949 gb AC068903.1 AC068903 | Mus musculus chromosome 2 clone ct7-196d19 strain 129/SvEv ES cell line C.J7, complete sequence | 7.00E-17 | 84/95 (88%) | 1/95 (1%) |
| MIN-60-28 | 502 | gi 8927595 gb AC019026.12 AC019026 | Mus musculus chromosome 6 clone RP23-188E5 strain C57BL/6J, complete sequence | 1.00E-117 | 222/223 (99%) | 1/223 (0%) |
| MIN-60-77 | 499 | gi 6753489 ref NM_012001.1 | Mus musculus COP9 (constitutive photomorphogenic), subunit 4 (Arabidopsis) (Cops4), mRNA | 0.424 | 424/424 (100%) | - |
| MIN-60-20 | 497 | gi 7710013 ref NM_016716.1 | Mus musculus cullin 3 (Cul3), mRNA | 0.497 | 497/497 (100%) | - |
| MIN-60-80 | 340 | gi 7229405 gb AF185590.1 AF185590 | Mus musculus cyclin ania-6a gene, sequence | 3.00E-43 | 138/151 (91%) | 2/151 (1%) |
| MIN-60-45 | 502 | gi 6754029 ref NM_011937.1 | Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA | 0.25 | 21/21 (100%) | - |
| MIN-60-57 | 441 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0.333 | 333/333 (100%) | - |
| MIN-60-66 | 500 | gi 6754409 ref NM_011835.1 | Mus musculus katanin p60 (ATPase-containing) subunit A1 (Katn1), mRNA | 0.493 | 494/99 (%) | - |

| | | | | | | |
|-----------|-----|-------------------------------------|---|-----------|----------------|-------------|
| MIN-63-27 | 381 | g[2944418]gb AF049850.1 MMHC438N1 | Mus musculus major histocompatibility locus class III region: complement C4 (C4) and cytochrome P450 hyc | 2.00E-90 | 179/182 (98%) | - |
| MIN-63-07 | 500 | g[3986751]gb AF109905.1 MMHC213L3 | Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds: smRNP, G7A, NG23, | 5.00E-55 | 140/147 (95%) | 2/147 (1%) |
| MIN-63-02 | 501 | g[3641670]dbj AB011678.1 AB011678 | Mus musculus mRNA for doublecortin, complete cds | 0 | 487/487 (100%) | - |
| MIN-63-48 | 360 | g[9623381]gb AF267747.1 AF267747 | Mus musculus p47-phox gene, complete cds | 2.00E-62 | 148/155 (95%) | 1/155 (0%) |
| MIN-63-71 | 500 | g[4107474]emb Y14119.1 MMY14119 | Mus musculus pkd2 exon 15 | 1.00E-137 | 252/253 (99%) | - |
| MIN-63-88 | 360 | g[6679502]ref NM_008948.1 | Mus musculus proteasome (prosome, macropain) 26S subunit, ATPase 3 (Psmc3), mRNA | 1.00E-160 | 293/295 (99%) | - |
| MIN-63-83 | 500 | g[6755193]ref NM_01184.1 | Mus musculus proteasome (prosome, macropain) subunit, alpha type 3 (Psm3a), mRNA | 0 | 486/486 (100%) | - |
| MIN-63-06 | 289 | g[6679464]ref NM_008925.1 | Mus musculus protein kinase C substate BOK-H (Pkrch), mRNA | 1.00E-154 | 276/276 (100%) | - |
| MIN-63-64 | 448 | g[6754071]ref NM_010347.1 | Mus musculus related to Drosophila groucho gene (Grg), mRNA | 0 | 351/351 (100%) | - |
| MIN-63-39 | 500 | g[6755353]ref NM_011290.1 | Mus musculus ribosomal protein L6 (Rpl6), mRNA | 0 | 460/462 (99%) | 1/462 (0%) |
| MIN-63-24 | 501 | g[6677866]ref NM_009130.1 | Mus musculus secretogranin II (Scg3), mRNA | 0 | 378/379 (99%) | 1/379 (0%) |
| MIN-63-61 | 499 | g[6863078]dbj AP001111.1 AP001111 | Oryza sativa genomic DNA, chromosome 5, clone:PO699E04 | 0.25 | 21/21 (100%) | - |
| MIN-63-75 | 433 | g[207463]gb M58040.1 RAATTRFR | Rat transferrin receptor mRNA, 3' end | 1.00E-125 | 282/296 (94%) | 5/298 (1%) |
| MIN-63-18 | 455 | g[7769682]gb AF253065.1 AF253065 | Rattus norvegicus chemokine-like factor 2 (CKLF2) mRNA, complete cds | 6.00E-85 | 329/331 (96%) | 3/331 (0%) |
| MIN-63-21 | 502 | g[1944357]dbj D84434.1 D84434 | Rattus norvegicus mRNA for 41-kDa phosphoribosylpyrophosphate synthetase-associated protein, comple | 0 | 459/474 (96%) | - |
| MIN-63-73 | 503 | g[1223843]gb U14937.1 RN14937 | Rattus norvegicus S-adenosyl-L-homocysteine hydrolase gene, complete cds | 7.00E-08 | 32/32 (100%) | - |
| MIN-63-08 | 499 | g[8547170]gb AF157026.1 AF157026 | Rattus norvegicus type IIb sodium-phosphate transporter mRNA, complete cds | 7.00E-05 | 30/31 (96%) | - |
| MIN-63-10 | 499 | g[4104320]gb AF034582.1 AF034582 | Rattus norvegicus vesicle associated protein (VAP1) mRNA, complete cds | 1.00E-149 | 431/484 (89%) | 1/484 (0%) |
| MIN-64-64 | 409 | g[10727462]gb AE003798.2 AE003798 | Drosophila melanogaster genomic scaffold 14200013386047 section 45 of 52, complete sequence | 0.8 | 20/20 (100%) | - |
| MIN-64-78 | 347 | g[10728536]gb AE003446.2 AE003446 | Drosophila melanogaster genomic scaffold 14200013386054 section 30 of 35, complete sequence | 0.011 | 23/23 (100%) | - |
| MIN-64-36 | 472 | g[2133878]gb AC000400.1 AC000400 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 1.00E-06 | 51/58 (87%) | - |
| MIN-64-66 | 404 | g[2133905]gb AC001230.1 AC001230 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 2.00E-29 | 86/92 (93%) | - |
| MIN-64-63 | 521 | g[2133878]gb AC000400.1 AC000400 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 0 | 400/400 (100%) | - |
| MIN-64-49 | 503 | g[49607]emb X03603.1 JMAAPRTG | Hamster aptt gene for adenine phosphoribosyl transferase | 0.004 | 36/40 (90%) | - |
| MIN-64-59 | 501 | g[1019071]ref NM_020675.1 | Homo sapiens AD024 protein (AD024), mRNA | 2.00E-54 | 257/306 (83%) | - |
| MIN-64-24 | 503 | g[8923831]ref NM_018685.1 | Homo sapiens anillin (LOC54443), mRNA | 1.00E-153 | 389/427 (91%) | - |
| MIN-64-72 | 503 | g[1043704]dbj AK024699.1 AK024699 | Homo sapiens cDNA: FLJ21046 fis, clone CAS00193 | 3.00E-22 | 137/164 (83%) | - |
| MIN-64-89 | 404 | g[10438545]dbj AK025891.1 AK025891 | Homo sapiens cDNA: FLJ22238 fis, clone HRC02173, highly similar to AF161377 Homo sapiens HSPC259 r | 5.00E-45 | 154/174 (88%) | - |
| MIN-64-85 | 362 | g[3858902]gb AC005884.1 AC005884 | Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence | 0.18 | 24/25 (96%) | - |
| MIN-64-92 | 286 | g[10048068]gb AC009499.4 AC009499 | Homo sapiens clone RP11-510D10, complete sequence | 0.035 | 22/22 (100%) | - |
| MIN-64-11 | 469 | g[4502616]gb ref NM_001759.1 | Homo sapiens cyclin D2 (CCND2), mRNA | 7.00E-11 | 100/119 (84%) | 4/119 (3%) |
| MIN-64-47 | 472 | g[11244779]gb AF279660.1 AF279660 | Homo sapiens DLEU1 gene, complete sequence, alternatively spliced | 0.015 | 26/27 (96%) | - |
| MIN-64-41 | 503 | g[4758311]ref NM_004453.1 | Homo sapiens electron-transferring-flavoprotein dehydrogenase (ETFDH), nuclear gene encoding mitocho | 1.00E-143 | 432/490 (88%) | - |
| MIN-64-21 | 500 | g[10092600]ref NM_003760.2 | Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA | 1.00E-30 | 172/206 (83%) | - |
| MIN-64-51 | 500 | g[7670576]dbj AP001622.1 AP001622 | Homo sapiens genomic DNA, chromosome 21, clone:KB1430A10, MX1-D21S171 region, complete sequence | 7.00E-08 | 35/36 (97%) | - |
| MIN-64-54 | 499 | g[8923484]ref NM_017858.1 | Homo sapiens hypothetical protein FLJ20516 (FLJ20516), mRNA | 1.00E-100 | 276/306 (90%) | - |
| MIN-64-45 | 381 | g[10047103]ref NM_016305.1 | Homo sapiens kIaa-iso protein (LOC51188), mRNA | 2.00E-56 | 146/157 (92%) | - |
| MIN-64-03 | 500 | g[7706231]ref NM_015904.1 | Homo sapiens KIAA0741 gene product (IF2), mRNA | 3.00E-84 | 312/363 (85%) | 3/363 (0%) |
| MIN-64-57 | 498 | g[3327133]dbj AB014560.1 AB014560 | Homo sapiens mRNA for KIAA0660 protein, complete cds | 2.00E-91 | 385/450 (85%) | 26/450 (5%) |
| MIN-64-91 | 481 | g[4499961]emb AL09229.1 HSM800014 | Homo sapiens mRNA: cDNA DKFZp564O1016 (from clone DKFZp564O1016) | 0.24 | 39/45 (86%) | - |
| MIN-64-04 | 494 | g[6013454]gb AF190631.1 AF190631 | Homo sapiens natriuretic peptide receptor A (NPR1) gene, complete cds | 0.97 | 23/24 (95%) | - |
| MIN-64-40 | 500 | g[11071534]emb AJ277662.1 HSA277662 | Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein | 1.00E-107 | 229/239 (95%) | - |
| MIN-64-01 | 499 | g[6005831]ref NM_007221.1 | Homo sapiens polyamine-modulated factor 1 (PMF1), mRNA | 5.00E-27 | 136/160 (85%) | - |
| MIN-64-67 | 377 | g[7705846]ref NM_016130.1 | Homo sapiens RNA helicase (LOC51139), mRNA | 1.00E-107 | 243/258 (94%) | - |
| MIN-64-70 | 499 | g[2224604]dbj AB002330.1 AB002330 | Human mRNA for KIAA0332 gene, partial cds | 1.00E-147 | 428/481 (88%) | 1/481 (0%) |
| MIN-64-05 | 490 | g[2022244]gb M28272.1 JMUSTUBMA2 | Mouse alpha-tubulin gene M-alpha-2, 3' end | 0 | 468/470 (99%) | 2/470 (0%) |
| MIN-64-82 | 497 | g[293320]gb L11318.1 JMUSCDC42M | Mouse CDC42Mm mRNA, 5' end | 0 | 419/420 (99%) | 1/420 (0%) |
| MIN-64-69 | 497 | g[198300]gb M20658.1 JMUSIL1TCR | Mouse interleukin-1 receptor mRNA, complete cds | 0 | 479/480 (99%) | 1/480 (0%) |
| MIN-64-07 | 457 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 449/449 (100%) | - |
| MIN-64-10 | 367 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 353/353 (100%) | - |
| MIN-64-13 | 501 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 487/487 (100%) | - |
| MIN-64-22 | 219 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 1.00E-112 | 206/206 (100%) | - |
| MIN-64-23 | 503 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 489/489 (100%) | - |
| MIN-64-27 | 500 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-64-29 | 503 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 489/489 (100%) | - |
| MIN-64-38 | 502 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/488 (99%) | 3/488 (0%) |
| MIN-64-44 | 502 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 488/488 (100%) | - |
| MIN-64-53 | 502 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 488/488 (100%) | - |
| MIN-64-61 | 501 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 1.00E-161 | 289/289 (100%) | - |
| MIN-64-66 | 501 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/487 (99%) | - |
| MIN-64-75 | 502 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 488/488 (100%) | - |
| MIN-64-77 | 501 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-64-80 | 491 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 478/479 (99%) | - |
| MIN-64-87 | 366 | g[342520]gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 360/360 (100%) | - |
| MIN-64-37 | 497 | g[55047]emb X04663.1 MMTUBBM5 | Mouse mRNA for beta-tubulin (isotype Mbeta.5) | 0 | 424/426 (99%) | - |
| MIN-64-55 | 500 | g[51141]emb X58069.1 MMH2AX | Mouse mRNA for Histone H2A.X | 0 | 489/494 (98%) | 2/494 (0%) |
| MIN-64-28 | 500 | g[6680715]ref NM_007476.1 | Mus musculus ADP-ribosylation factor 1 (Arf1), mRNA | 0 | 492/494 (99%) | - |
| MIN-64-71 | 304 | g[6753203]ref NM_011794.1 | Mus musculus bisphosphate 3'-nucleotidase 1 (Bpnt1), mRNA | 5.00E-163 | 266/267 (99%) | - |
| MIN-64-06 | 500 | g[7263202]gb AC012302.5 AC012302 | Mus musculus chromosome 10, clone RP21-247L16, complete sequence | 2.00E-95 | 106/114 (92%) | 1/114 (0%) |
| MIN-64-30 | 499 | g[4210518]gb AC002327.1 AC002327 | Mus musculus chromosome 7, clone 19K5, complete sequence | 4.00E-06 | 63/73 (86%) | 1/73 (1%) |
| MIN-64-35 | 499 | g[6753619]ref NM_010028.1 | Mus musculus DEAD (aspartate-glutamate-alanine-aspartate) box polypeptide 3 (Ddx3), mRNA | 0 | 488/488 (100%) | - |
| MIN-64-86 | 488 | g[1196653]gb L47235.1 JMUSXPDG1 | Mus musculus ERCC2 gene, genomic sequence | 3.00E-81 | 188/199 (94%) | - |
| MIN-64-25 | 499 | g[6680462]ref NM_003837.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-64-94 | 200 | g[6754271]ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 1.00E-100 | 186/186 (100%) | - |
| MIN-64-43 | 495 | g[6680571]ref NM_008448.1 | Mus musculus kinesin family member 5B (Kif5b), mRNA | 1.00E-77 | 155/157 (98%) | - |
| MIN-64-73 | 491 | g[2957156]gb AC004407.1 AC004407 | Mus musculus mbac6, complete sequence | 8.00E-57 | 144/154 (93%) | - |
| MIN-64-08 | 501 | g[9558449]dbj AB021969.1 AB021969 | Mus musculus mRNA for carboxypeptidase N, complete cds | 0 | 486/487 (99%) | 1/487 (0%) |
| MIN-64-17 | 500 | g[2289098]gb U82375.1 JMMU82375 | Mus musculus MSG2alpha, beta, gamma, delta and epsilon salivary protein (Vcs2) genes, complete cds | 3.00E-13 | 56/61 (91%) | - |
| MIN-64-84 | 317 | g[7684609]gb AF146793.2 AF146793 | Mus musculus Neurexin I precursor (Nrx1) gene, partial cds: PDCL2 (Pdc12) gene, partial cds; CLOCK (| 0.61 | 20/20 (100%) | - |
| MIN-64-31 | 362 | g[9622364]gb AF172642.1 AF172642 | Mus musculus ocular albinism type 1 protein (Oa1) gene, complete cds | 1.00E-121 | 277/294 (94%) | 1/294 (0%) |
| MIN-64-19 | 499 | g[6680689]ref NM_007452.1 | Mus musculus peroxiredoxin 3 (Prdx3), mRNA | 0 | 485/486 (99%) | 1/486 (0%) |
| MIN-64-81 | 500 | g[6679468]ref NM_008928.1 | Mus musculus protein kinase, interferon inducible double stranded RNA dependent inhibitor (Prki), mRNA | 0 | 441/448 (98%) | 3/448 (0%) |
| MIN-64-34 | 468 | g[9910531]ref NM_019958.1 | Mus musculus regulator of G-protein signaling 22 (Rgs22), mRNA | 1.00E-117 | 216/216 (100%) | - |
| MIN-64-65 | 495 | g[11140826]ref NM_021790.1 | Mus musculus SoxLZ/Sox6 leucine zipper binding protein in testis (Solzt-encoding), mRNA | 0 | 481/481 (100%) | - |
| MIN-64-93 | 442 | g[6756039]ref NM_011739.1 | Mus musculus tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypep | 0 | 413/413 (100%) | - |
| MIN-64-79 | 492 | g[9910599]ref NM_019912.1 | Mus musculus ubiquitin conjugating enzyme 2e (Ubc2e), mRNA | 1.00E-110 | 274/289 (94%) | 10/289 (3%) |
| MIN-64-74 | 452 | g[6678488]ref NM_009460.1 | Mus musculus ubiquitin-like 1 (Ubl1), mRNA | 0 | 438/438 (100%) | - |
| MIN-64-26 | 499 | g[9506496]ref NM_019299.1 | Rattus norvegicus clathrin, heavy polypeptide (Hc) (Cltc), mRNA | 2.00E-51 | 120/125 (96%) | - |
| MIN-64-33 | 500 | g[4335693]gb AF008554.2 AF008554 | Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds | 1.00E-89 | 181/185 (97%) | - |
| MIN-64-90 | 497 | g[6981447]ref NM_013080.1 | Rattus norvegicus Protein tyrosine phosphatase, receptor-type, zeta polypeptide (Ptpz1), mRNA | 0 | 442/476 (92%) | 6/476 (1%) |
| MIN-66-07 | 490 | - | - | - | - | - |
| MIN-66-92 | 278 | g[6598426]gb AC004561.2 AC004561 | Arabidopsis thaliana chromosome II section 166 of 255 of the complete sequence. Sequence from clones F1 | 0.53 | 20/20 (100%) | - |
| MIN-66-41 | 499 | g[1237028]emb X96768.1 BPACOPGEN | B.primigenius mRNA for alpha-cop coat protein | 0 | 446/487 (91%) | - |
| MIN-66-82 | 511 | g[9836509]dbj AB030902.1 AB030902 | Danio rerio mRNA for ERK1, complete cds | 3.00E-07 | 31/31 (100%) | - |
| MIN-66-38 | 359 | g[290091]gb M95495.1 DOGNACLTAA | Dog Na+/Cl--dependent taurine transporter mRNA, complete cds | 3.00E-37 | 115/125 (92%) | 1/125 (0%) |
| MIN-66-45 | 398 | g[290091]gb M95495.1 DOGNACLTAA | Dog Na+/Cl--dependent taurine transporter mRNA, complete cds | 2.00E-35 | 109/118 (92%) | 1/118 (0%) |
| MIN-66-25 | 431 | g[2133878]gb AC000400.1 AC000400 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 0 | 408/408 (100%) | - |
| MIN-66-60 | 499 | g[2133880]gb AC002121.1 AC002121 | Genomic sequence from Mouse 11, complete sequence [Mus musculus] | 3.00E-19 | 81/90 (90%) | 2/90 (2%) |
| MIN-66-66 | 499 | g[10190715]ref NM_020675.1 | Homo sapiens AD024 protein (AD024), mRNA | 3.00E-75 | 402/484 (83%) | 3/484 (0%) |
| MIN-66-72 | 494 | g[4503284]ref NM_001354.1 | Homo sapiens aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2: bile acid binding pro | 1.00E-27 | 218/269 (81%) | - |
| MIN-66-26 | 499 | g[10881056]gb AC069539.4 AC069539 | Homo sapiens chromosome 11 clone RP11-321E15, complete sequence | 1.00E-131 | 395/444 (88%) | 10/444 (2%) |

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|-----------|-----|--------------------------------------|--|-----------|----------------|-------------|
| MIN-66-95 | 441 | gi 6806842 gb AC007216.2 AC007216 | Homo sapiens chromosome 16 clone RP11-166B2, complete sequence | 0.055 | 22/22 (100%) | - |
| MIN-66-88 | 406 | gi 5823550 gb AF179633.1 AF179633 | Homo sapiens chromosome 16 map 16q23.3-q24.1 sequence | 2.00E-35 | 199/239 (83%) | 4/239 (1%) |
| MIN-66-91 | 500 | gi 3264572 gb AC003041.1 AC003041 | Homo sapiens chromosome 17, clone HClT307A16, complete sequence | 4.00E-34 | 130/146 (89%) | 2/146 (1%) |
| MIN-66-37 | 500 | gi 3659494 gb AC005332.1 AC005332 | Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence | 0.016 | 23/23 (100%) | - |
| MIN-66-85 | 495 | gi 1181843 gb AC017028.1 AC017028 | Homo sapiens clone RP11-275G7, complete sequence | 0.98 | 23/24 (95%) | - |
| MIN-66-42 | 441 | gi 6325466 ref NM_006894.2 | Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA | 0.86 | 20/20 (100%) | - |
| MIN-66-35 | 499 | gi 6979002 dbj AB017654.1 AB017654 | Homo sapiens genomic DNA, chromosome 11q23.2, clone:KB4H11, complete sequence | 1.00E-49 | 131/138 (94%) | 2/138 (1%) |
| MIN-66-61 | 562 | gi 6841157 ref AF161372.1 AF161372 | Homo sapiens HSPC254 mRNA, partial cds | 1.00E-125 | 276/292 (94%) | - |
| MIN-66-89 | 543 | gi 8922588 ref NM_018178.1 | Homo sapiens hypothetical protein FLJ10687 (FLJ10687), mRNA | 3.00E-19 | 170/208 (81%) | 10/208 (4%) |
| MIN-66-79 | 500 | gi 8922749 ref NM_018263.1 | Homo sapiens hypothetical protein FLJ10398 (FLJ10398), mRNA | 2.00E-20 | 76/81 (93%) | 2/81 (2%) |
| MIN-66-21 | 499 | gi 8572054 gb AF216693.1 AF216693 | Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1) gene, complete cds | 0.25 | 21/21 (100%) | - |
| MIN-66-39 | 611 | gi 4504736 ref NM_002202.1 | Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA | 9.00E-88 | 206/220 (93%) | - |
| MIN-66-69 | 499 | gi 7661873 ref NM_015361.1 | Homo sapiens KIAA0029 protein (KIAA0029), mRNA | 1.00E-12 | 43/44 (97%) | - |
| MIN-66-57 | 499 | gi 7662437 ref NM_014950.1 | Homo sapiens KIAA0997 protein (KIAA0997), mRNA | 1.00E-127 | 425/488 (87%) | 6/488 (1%) |
| MIN-66-14 | 505 | gi 9844923 gb AF287270.1 AF287270 | Homo sapiens mucolin (MCOLN1) gene, complete cds | 0.25 | 21/21 (100%) | - |
| MIN-66-90 | 500 | gi 9966854 ref NM_020382.1 | Homo sapiens PR/SET domain containing protein 07 (SET07), mRNA | 1.00E-131 | 347/393 (88%) | - |
| MIN-66-34 | 498 | gi 5453951 ref NM_006244.1 | Homo sapiens protein phosphatase 2, regulatory subunit B (B56), beta isoform (PPP2R5B), mRNA | 1.00E-144 | 360/393 (91%) | - |
| MIN-66-55 | 499 | gi 11225261 ref NM_006275.1 | Homo sapiens splicing factor, arginine/serine-rich 6 (SFRS6), mRNA | 1.00E-126 | 424/488 (86%) | 3/488 (0%) |
| MIN-66-65 | 499 | gi 9994172 ref NM_020474.1 | Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (G | 6.00E-70 | 251/283 (88%) | 6/283 (2%) |
| MIN-66-04 | 499 | gi 3367610 emb AL022721.1 HS109F14 | Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced e | 0.98 | 20/20 (100%) | - |
| MIN-66-15 | 524 | gi 5791509 emb AL050341.1 HSJSDJ39G2 | Human DNA sequence from clone RP1-39G22 on chromosome 1p32.1-34.3. Contains the 3' part of the RL | 9.00E-29 | 88/95 (92%) | - |
| MIN-66-51 | 499 | gi 6018761 emb AL035663.1 HS611N7 | Human DNA sequence from clone RP4-611N7 on chromosome 20 Contains STSs and GSSs, complete seq | 0.25 | 21/21 (100%) | - |
| MIN-66-16 | 499 | gi 2058342 emb Y12634.1 MMVAT2 | M.musculus mRNA for vacuolar adenosine triphosphatase subunit B | 0 | 485/485 (100%) | - |
| MIN-66-23 | 499 | gi 410741 gb M93980.1 MUSADIPCT | Mouse 24.6 kda protein mRNA, complete cds | 0 | 484/485 (99%) | 1/485 (0%) |
| MIN-66-63 | 499 | gi 410741 gb M93980.1 MUSADIPCT | Mouse 24.6 kda protein mRNA, complete cds | 0 | 485/485 (100%) | - |
| MIN-66-53 | 500 | gi 293320 gb L11318.1 MUSCDC42M | Mouse CDC42Mm mRNA, 5' end | 0 | 421/422 (99%) | 1/422 (0%) |
| MIN-66-81 | 320 | gi 49865 emb X03672.1 MMACTBR | Mouse cytoskeletal mRNA for beta-actin | 1.00E-171 | 306/306 (100%) | - |
| MIN-66-71 | 499 | gi 193423 gb M32599.1 MUSGAPDH | Mouse glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds | 0 | 483/484 (99%) | - |
| MIN-66-02 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-66-10 | 496 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 479/482 (99%) | 3/482 (0%) |
| MIN-66-30 | 500 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-66-31 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-66-33 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/487 (99%) | - |
| MIN-66-64 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-66-68 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 483/486 (99%) | 1/486 (0%) |
| MIN-66-78 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 482/485 (99%) | - |
| MIN-66-96 | 170 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 7.00E-70 | 156/159 (98%) | 3/159 (1%) |
| MIN-66-40 | 499 | gi 53316 emb X16646.1 MMNAKATP | Mouse mRNA for Na,K-ATPase beta subunit | 0 | 366/367 (99%) | - |
| MIN-66-06 | 248 | gi 52712 emb X04725.1 MMINSIG | Mouse preproinsulin gene 1 | 1.00E-126 | 230/230 (100%) | - |
| MIN-66-05 | 499 | gi 1747303 dbj D50463.1 D50463 | Mouse SDR1 mRNA, complete cds | 0 | 484/485 (99%) | 1/485 (0%) |
| MIN-66-44 | 499 | gi 51127 emb Y00703.1 MMGTPAMU | Mouse uncoupled S49 cells mRNA for stimulatory GTP-binding protein alpha subunit | 0 | 482/485 (99%) | - |
| MIN-66-19 | 499 | gi 6753621 ref NM_011933.1 | Mus musculus 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal (Deacr2), mRNA | 1.00E-06 | 45/50 (90%) | - |
| MIN-66-32 | 497 | gi 8052319 emb AJ400878.1 MMU400878 | Mus musculus Asc3 gene, Cegp1 gene, D7H11orf14 gene, D7H11orf15 gene, D7H11orf16 gene and C11orf | 1.00E-61 | 226/259 (87%) | 4/259 (1%) |
| MIN-66-76 | 499 | gi 8052319 emb AJ400878.1 MMU400878 | Mus musculus Asc3 gene, Cegp1 gene, D7H11orf14 gene, D7H11orf15 gene, D7H11orf16 gene and C11orf | 1.00E-52 | 177/199 (88%) | 1/199 (0%) |
| MIN-66-73 | 500 | gi 7670507 dbj AB041655.1 AB041655 | Mus musculus brain cDNA, clone MNCB-2442, similar to Rattus norvegicus SERP1 mRNA | 0 | 485/486 (99%) | 1/486 (0%) |
| MIN-66-27 | 499 | gi 1666699 gb U58105.1 MMU58105 | Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kin | 7.00E-51 | 140/152 (92%) | - |
| MIN-66-08 | 496 | gi 6753243 ref NM_009790.1 | Mus musculus calmodulin (Calm), mRNA | 0 | 473/482 (98%) | 7/482 (1%) |
| MIN-66-24 | 499 | gi 6753243 ref NM_009790.1 | Mus musculus calmodulin (Calm), mRNA | 0 | 468/472 (99%) | 3/472 (0%) |
| MIN-66-01 | 499 | gi 6114859 gb AF109719.2 MMHC188A7 | Mus musculus casein kinase 2 beta subunit (gMCK2) gene, partial cds: BAT4, NG20 (NG20), BAT3, BAT2, A | 5.00E-18 | 75/81 (92%) | 2/81 (2%) |
| MIN-66-74 | 499 | gi 1181790 gb AC068906.12 AC068906 | Mus musculus chromosome 2 clone rp23-240p23 strain C57BL/6J, complete sequence | 2.00E-08 | 51/57 (89%) | - |
| MIN-66-87 | 499 | gi 3309171 gb AF071315.1 AF071315 | Mus musculus COP9 complex subunit 6 (COP56) mRNA, complete cds | 0 | 438/439 (99%) | 1/439 (0%) |
| MIN-66-83 | 499 | gi 10946643 ref NM_021331.1 | Mus musculus glucose-6-phosphatase, catalytic, related sequence (G6pc-rs), mRNA | 0 | 484/485 (99%) | - |
| MIN-66-77 | 497 | gi 9910275 ref NM_019979.1 | Mus musculus heat shock protein Q30 (HspQ30), mRNA | 0 | 484/484 (100%) | - |
| MIN-66-47 | 448 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-66-58 | 494 | gi 4050090 gb AF110520.1 MMHC42501 | Mus musculus major histocompatibility complex region NG27, NG28, RFS28, NADH oxidoreductase, NG29, | 2.00E-11 | 47/50 (94%) | - |
| MIN-66-49 | 499 | gi 4586404 dbj AB025010.1 AB025010 | Mus musculus mRNA for Trif, complete cds | 0 | 433/435 (99%) | 1/435 (0%) |
| MIN-66-62 | 505 | gi 6679268 ref NM_008814.1 | Mus musculus pancreatic and duodenal homeobox gene 1 (Pdx1), mRNA | 0 | 488/491 (99%) | 1/491 (0%) |
| MIN-66-70 | 487 | gi 6679268 ref NM_008814.1 | Mus musculus pancreatic and duodenal homeobox gene 1 (Pdx1), mRNA | 0 | 408/408 (100%) | - |
| MIN-66-46 | 466 | gi 7242180 ref NM_011116.1 | Mus musculus phospholipase D3 (Pld3), mRNA | 0 | 452/452 (100%) | - |
| MIN-66-18 | 499 | gi 6679298 ref NM_008831.1 | Mus musculus phosphoinositide 3-kinase (Pip3), mRNA | 1.00E-170 | 311/312 (99%) | 1/312 (0%) |
| MIN-66-08 | 499 | gi 10946733 ref NM_021391.1 | Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1A (Ppp1r1a), mRNA | 0 | 444/445 (99%) | 1/445 (0%) |
| MIN-66-29 | 500 | gi 6677778 ref NM_009081.1 | Mus musculus ribosomal protein L28 (Rpl28), mRNA | 0 | 487/488 (99%) | - |
| MIN-66-13 | 640 | gi 6677780 ref NM_009082.1 | Mus musculus ribosomal protein L29 (Rpl29), mRNA | 0 | 615/621 (99%) | 1/621 (0%) |
| MIN-66-56 | 499 | gi 4689089 gb AF047601.1 AF047601 | Mus musculus SMCD (Smcd) mRNA, complete cds | 0 | 485/486 (99%) | 1/486 (0%) |
| MIN-66-17 | 499 | gi 4868332 gb AF129888.1 AF129888 | Mus musculus Su1 homolog mRNA, complete cds | 0 | 481/485 (99%) | - |
| MIN-66-22 | 322 | gi 9845264 ref NM_019883.1 | Mus musculus ubiuitin/60S ribosomal fusion protein (LOC56512), mRNA | 1.00E-150 | 296/305 (97%) | 1/305 (0%) |
| MIN-66-59 | 499 | gi 1914850 gb U92454.1 MMU92454 | Mus musculus WW domain binding protein 5 mRNA, partial cds | 0 | 372/372 (100%) | - |
| MIN-66-75 | 500 | gi 1914850 gb U92454.1 MMU92454 | Mus musculus WW domain binding protein 5 mRNA, partial cds | 0 | 390/390 (100%) | - |
| MIN-66-86 | 472 | gi 6978612 ref NM_012829.1 | Rattus norvegicus Cholecystokinin (Cck), mRNA | 1.00E-168 | 406/440 (92%) | 1/440 (0%) |
| MIN-66-09 | 493 | gi 6729086 dbj AB019281.1 AB019281 | Rattus norvegicus CIZ mRNA for GAS-associated zinc finger protein, complete cds | 1.00E-172 | 435/470 (92%) | 11/470 (2%) |
| MIN-66-48 | 474 | gi 8100055 dbj AB031482.1 AB031482 | Rattus norvegicus mRNA for CTP-binding protein tc10, complete cds | 1.00E-108 | 376/430 (87%) | 11/430 (2%) |
| MIN-66-36 | 499 | gi 6474927 dbj AB006852.1 AB006852 | Rattus norvegicus mRNA for phosphoglycerin phosphatase, complete cds | 0 | 395/400 (98%) | - |
| MIN-66-43 | 499 | gi 3929925 dbj AB020504.1 AB020504 | Rattus norvegicus mRNA for PMF31, complete cds | 3.00E-53 | 187/212 (88%) | 6/212 (2%) |
| MIN-66-94 | 196 | gi 286201 dbj D13124.1 JRATATPSCP2 | Rattus norvegicus P2 mRNA for ATP synthase subunit c, complete cds | 1.00E-25 | 71/73 (97%) | 1/73 (1%) |
| MIN-66-84 | 474 | gi 1816428 dbj AB000717.1 AB000716S2 | Rattus rattus gene for non-hepatic-type S-adenosylmethionine synthetase, exon 2 and complete cds | 0 | 450/458 (98%) | 1/458 (0%) |
| MIN-66-11 | 500 | gi 256993 gb S45663.1 S45663 | SC2=synaptic glycoprotein [rats, brain, mRNA, 1178 nt] | 0 | 452/467 (96%) | - |
| MIN-66-93 | 487 | gi 160961 gb M86398.1 SCMEGFRC | Schistosoma mansoni epidermal growth factor receptor (SER, alternative splice class 4 product) mRNA, co | 0.24 | 21/21 (100%) | - |
| MIN-72-40 | 468 | - | - | - | - | - |
| MIN-72-59 | 501 | gi 7300931 gb AE003741.1 AE003741 | Drosophila melanogaster genomic scaffold 142000013386035 section 66 of 105, complete sequence | 1 | 20/20 (100%) | - |
| MIN-72-74 | 501 | gi 7298216 gb AE003647.1 AE003647 | Drosophila melanogaster genomic scaffold 142000013386055 section 40 of 63, complete sequence | 0.26 | 21/21 (100%) | - |
| MIN-72-45 | 468 | gi 7706580 ref NM_016567.1 | Homo sapiens cdk inhibitor p21 binding protein (TOK-1), mRNA | 1.00E-104 | 284/314 (90%) | - |
| MIN-72-26 | 507 | gi 10435249 dbj AK023351.1 AK023351 | Homo sapiens cDNA FLJ13289 fs, clone OVARC1001170 | 7.00E-45 | 250/302 (82%) | - |
| MIN-72-62 | 498 | gi 10437005 dbj AK024669.1 AK024669 | Homo sapiens cDNA: FLJ21016 fs, clone CAE05735 | 5.00E-95 | 201/206 (97%) | 2/206 (0%) |
| MIN-72-65 | 448 | gi 10438285 dbj AK025686.1 AK025686 | Homo sapiens cDNA: FLJ22093 fs, clone HEP0870, highly similar to HSUA3374 Human normal keratino | 4.00E-69 | 196/217 (90%) | - |
| MIN-72-19 | 509 | gi 4028941 gb AC006071.1 AC006071 | Homo sapiens chromosome 17, clone hClT.124_H_2, complete sequence | 0.26 | 24/25 (96%) | - |
| MIN-72-10 | 502 | gi 3808091 gb AC003665.1 AC003665 | Homo sapiens chromosome 17, clone hClT.211_P_7, complete sequence | 2.00E-35 | 120/134 (89%) | - |
| MIN-72-93 | 441 | gi 8844109 gb AC010389.7 AC010389 | Homo sapiens chromosome 5 clone CTD-207715, complete sequence | 0.22 | 27/29 (93%) | - |
| MIN-72-80 | 491 | gi 11177452 gb AF280107.1 AF280107 | Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds: cytochrome P450 polypeptide | 2.00E-05 | 40/44 (90%) | - |
| MIN-72-37 | 502 | gi 11425779 ref XM_005213.1 | Homo sapiens DKFZP434K171 protein (DKFZP434K171), mRNA | 1.00E-157 | 405/446 (90%) | - |
| MIN-72-02 | 267 | gi 4097992 gb U72845.1 HSAPEVPL3 | Homo sapiens epivlaklin (EVPL) gene, exons 2 through 9 | 2.1 | 19/19 (100%) | - |
| MIN-72-61 | 482 | gi 3483379 gb AF066034.1 HUMYW26F0 | Homo sapiens full length insert cDNA clone YW26F0 | 5.00E-61 | 280/333 (84%) | - |
| MIN-72-89 | 178 | gi 5174610 ref NM_005968.1 | Homo sapiens heterogeneous nuclear ribonucleoprotein M (HNRPM), mRNA | 3.00E-75 | 160/164 (97%) | 1/164 (0%) |
| MIN-72-04 | 498 | gi 8922080 ref NM_018489.1 | Homo sapiens hypothetical protein ASH1 (ASH1), mRNA | 3.00E-90 | 269/302 (89%) | - |
| MIN-72-63 | 501 | gi 5419886 emb AL096751.1 HSM800673 | Homo sapiens mRNA: cDNA DKFZP434J034 (from clone DKFZP434J034) | 2.00E-23 | 85/94 (90%) | - |
| MIN-72-55 | 505 | gi 5262468 emb AL080063.1 HSM800564 | Homo sapiens mRNA: cDNA DKFZP564I052 (from clone DKFZP564I052) | 7.00E-76 | 230/258 (89%) | - |
| MIN-72-84 | 415 | gi 11430598 ref XM_005775.1 | Homo sapiens similar to transmembrane phosphatase with tensin homology (H. sapiens) (LOC63290), mRN | 0.83 | 20/20 (100%) | - |
| MIN-72-39 | 506 | gi 11525650 ref XM_005748.1 | Homo sapiens ZW10 interactor (ZWINT), mRNA | 8.00E-17 | 146/178 (81%) | - |
| MIN-72-78 | 469 | gi 4490505 emb AL034408.2 HS710L4 | Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myo | 0.004 | 30/32 (93%) | - |
| MIN-72-05 | 467 | gi 10178428 emb AL139123.14 AL139123 | Human DNA sequence from clone RP11-500G10 on chromosome 10, complete sequence [Homo sapiens] | 2.00E-11 | 80/94 (85%) | - |
| MIN-72-48 | 502 | gi 54095 emb X68837.1 MMSGIIA2 | M.musculus SgII gene for secretogranin II, exon 2 | 0 | 494/494 (100%) | - |

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|-----------|-----|-------------------------------------|---|--|-----------|----------------|------------|
| MIN-72-29 | 498 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 485/485 (100%) | - |
| MIN-72-43 | 500 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 486/486 (100%) | - |
| MIN-72-68 | 472 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 459/459 (100%) | - |
| MIN-72-70 | 500 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 486/486 (100%) | - |
| MIN-72-94 | 218 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 9.00E-98 | 199/205 (97%) | - |
| MIN-72-25 | 492 | gi 606073 gb AF065398.1 AF065398 | Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds | | 1.00E-150 | 297/305 (97%) | 3/305 (0%) |
| MIN-72-42 | 501 | gi 902007 gb U27315.1 JMU27315 | Mus musculus adenine nucleotide translocase-1 (Ant1) mRNA, complete cds | | 0 | 486/487 (99%) | 1/487 (0%) |
| MIN-72-01 | 500 | gi 6753085 ref NM_009687.1 | Mus musculus apurinic/apyrimidinic endonuclease (Apex), mRNA | | 0 | 478/479 (99%) | 1/479 (0%) |
| MIN-72-54 | 500 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | | 0 | 486/486 (100%) | - |
| MIN-72-69 | 465 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | | 0 | 415/416 (99%) | - |
| MIN-72-76 | 452 | gi 6806902 ref NM_009722.1 | Mus musculus ATPase, Ca++ transporting, cardiac muscle, slow twitching 2 (Atp2a2), mRNA | | 0 | 447/452 (98%) | 3/452 (0%) |
| MIN-72-21 | 511 | gi 7670507 cb AB041655.1 AB041655 | Mus musculus brain cDNA, clone MNCb-2442, similar to Rattus norvegicus SERP1 mRNA | | 0 | 497/497 (100%) | - |
| MIN-72-27 | 500 | gi 6680839 ref NM_007594.1 | Mus musculus calumenin (Calu), mRNA | | 1.00E-06 | 30/30 (100%) | - |
| MIN-72-47 | 504 | gi 6753447 ref NM_009906.1 | Mus musculus ceroid-lipofuscinosis, neuronal 2 (Cln2), mRNA | | 0 | 490/490 (100%) | - |
| MIN-72-71 | 498 | gi 11527409 gb AC084429.5 AC084429 | Mus Musculus Chromosome 2 Clone RP23-291P1, complete sequence [Mus musculus] | | 7.00E-82 | 163/164 (99%) | 1/164 (0%) |
| MIN-72-77 | 327 | gi 11527409 gb AC084429.5 AC084429 | Mus Musculus Chromosome 2 Clone RP23-291P1, complete sequence [Mus musculus] | | 5.00E-54 | 109/109 (100%) | - |
| MIN-72-34 | 462 | gi 6753493 ref NM_011778.1 | Mus musculus coronin, actin binding protein 1B (Coro1b), mRNA | | 0 | 448/448 (100%) | - |
| MIN-72-30 | 447 | gi 6753495 ref NM_011779.1 | Mus musculus coronin, actin binding protein 1C (Coro1c), mRNA | | 0 | 434/434 (100%) | - |
| MIN-72-46 | 507 | gi 6681152 ref NM_007838.1 | Mus musculus dolichyl-di-phosphooligosaccharide-protein glycotransferase (Ddost), mRNA | | 0 | 491/493 (99%) | - |
| MIN-72-38 | 369 | gi 5823354 gb AF176514.1 AF176514 | Mus musculus E2F1-inducible protein (Eig2) mRNA, partial cds | | 1.00E-131 | 246/247 (99%) | 1/247 (0%) |
| MIN-72-32 | 498 | gi 1196653 gb L47235.1 JUSXPDG1 | Mus musculus ERCC2 gene, genomic sequence | | 1.00E-15 | 93/106 (87%) | 6/106 (5%) |
| MIN-72-41 | 509 | gi 9256550 ref NM_018866.1 | Mus musculus galectin 8 (Lgals8), mRNA | | 1.00E-179 | 326/327 (99%) | 1/327 (0%) |
| MIN-72-82 | 492 | gi 9789960 ref NM_019749.1 | Mus musculus gamma-aminobutyric acid receptor associated protein (Gabaarap), mRNA | | 0 | 478/478 (100%) | - |
| MIN-72-50 | 503 | gi 6680159 ref NM_008210.1 | Mus musculus H3 histone, family 3A (H3f3a), mRNA | | 0 | 489/489 (100%) | - |
| MIN-72-73 | 448 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | | 0 | 333/333 (100%) | - |
| MIN-72-03 | 471 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 456/457 (99%) | 1/457 (0%) |
| MIN-72-09 | 500 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 486/486 (100%) | - |
| MIN-72-11 | 474 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 460/460 (100%) | - |
| MIN-72-14 | 499 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 485/485 (100%) | - |
| MIN-72-15 | 494 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 476/478 (99%) | - |
| MIN-72-58 | 474 | gi 10336604 gb AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | | 0 | 460/460 (100%) | - |
| MIN-72-75 | 497 | gi 3810875 gb AB012581.1 AB012581 | Mus musculus Munc18-1 gene, intron 1, partial sequence | | 2.00E-08 | 33/93 (35%) | - |
| MIN-72-83 | 499 | gi 6679268 ref NM_008814.1 | Mus musculus pancreatic and duodenal homeobox gene 1 (Pdx1), mRNA | | 0 | 484/488 (99%) | 1/485 (0%) |
| MIN-72-79 | 499 | gi 7242170 ref NM_011045.1 | Mus musculus proliferating cell nuclear antigen (Pcna), mRNA | | 0 | 493/493 (100%) | - |
| MIN-72-06 | 480 | gi 4140641 gb AF090314.1 AF090314 | Mus musculus proteasome beta-subunit C5 (Psmb1) mRNA, partial cds | | 2.00E-08 | 45/49 (91%) | - |
| MIN-72-90 | 428 | gi 9082185 gb AF263366.1 AF263366 | Mus musculus Rab3D (rab3d) gene, complete cds | | 0 | 424/424 (100%) | - |
| MIN-72-16 | 503 | gi 6679606 ref NM_009011.1 | Mus musculus RAD23b homolog (S. cerevisiae) (Rad23b), mRNA | | 1.00E-168 | 306/312 (98%) | - |
| MIN-72-88 | 348 | gi 6677746 ref NM_009065.1 | Mus musculus RAS-like protein expressed in neuron (Rin), mRNA | | 0 | 343/343 (100%) | - |
| MIN-72-92 | 314 | gi 6677772 ref NM_009078.1 | Mus musculus ribosomal protein L19 (Rpl19), mRNA | | 1.00E-164 | 298/300 (99%) | - |
| MIN-72-67 | 499 | gi 6677812 ref NM_009098.1 | Mus musculus ribosomal protein S8 (Rps8), mRNA | | 0 | 482/485 (99%) | - |
| MIN-72-33 | 505 | gi 11275386 gb AB043006.1 AB043006 | Mus musculus SDF2L1 mRNA for SDF2 like protein 1, complete cds | | 0 | 478/482 (99%) | 3/482 (0%) |
| MIN-72-36 | 499 | gi 1110716 ref NM_009155.1 | Mus musculus selenoprotein P, plasma, 1 (Sepp1), mRNA | | 0 | 485/485 (100%) | - |
| MIN-72-57 | 499 | gi 3779195 gb U96810.1 JMUJ96810 | Mus musculus Supt4h2 gene, complete cds | | 1.00E-06 | 42/46 (91%) | - |
| MIN-72-64 | 500 | gi 11140824 ref NM_021789.1 | Mus musculus syndecan binding protein 2 (Sdcbp2-pending), mRNA | | 0 | 489/491 (99%) | - |
| MIN-72-20 | 500 | gi 6755135 ref NM_011869.1 | Mus musculus thyroid hormone receptor-associated protein 100 kDa (Trap100-pending), mRNA | | 0 | 478/486 (98%) | - |
| MIN-72-23 | 499 | gi 6678436 ref NM_009429.1 | Mus musculus translationally regulated transcript (21 kDa) (Trt), mRNA | | 0 | 487/487 (100%) | - |
| MIN-72-08 | 501 | gi 9910599 ref NM_019912.1 | Mus musculus ubiquitin conjugating enzyme 2e (Ubc2e), mRNA | | 0 | 497/502 (99%) | 3/502 (0%) |
| MIN-72-53 | 471 | gi 1944613 emb X97772.1 RND3PGDEH | R.norvegicus mRNA for D-3-phosphoglycerate dehydrogenase | | 0 | 420/445 (94%) | 1/445 (0%) |
| MIN-72-66 | 507 | gi 2044398 gb M12672.1 JRAATGNPAI | Rat guanine nucleotide-binding protein G-i, alpha subunit mRNA, complete cds | | 0 | 474/497 (95%) | 4/497 (0%) |
| MIN-72-87 | 501 | gi 3494988 gb L12459.1 JRALTYSOZYM | Rat lysozyme gene exons 1-4, complete cds | | 5.00E-15 | 50/52 (96%) | - |
| MIN-72-49 | 505 | gi 1079552 gb U26033.1 RNU26033 | Rattus norvegicus carnitine octanoyltransferase mRNA, complete cds | | 1.00E-178 | 424/458 (92%) | 1/458 (0%) |
| MIN-72-51 | 508 | gi 6978612 ref NM_012829.1 | Rattus norvegicus Cholecystokinin (Cck), mRNA | | 1.00E-171 | 432/472 (91%) | 2/472 (0%) |
| MIN-72-52 | 499 | gi 457926 gb J00926.1 RNU00926 | Rattus norvegicus delta subunit of F1F0 ATPase gene, complete cds | | 1.00E-160 | 400/438 (91%) | - |
| MIN-72-85 | 495 | gi 3618221 emb X89968.1 RNSNAPGEN | Rattus norvegicus mRNA for alpha-soluble NSF attachment protein | | 0 | 472/481 (98%) | - |
| MIN-72-12 | 509 | gi 9507182 ref NM_019381.1 | Rattus norvegicus Testis enhanced gene transcript (Teg), mRNA | | 0 | 441/476 (92%) | 6/476 (1%) |
| MIN-72-60 | 497 | gi 9992911 gb S78114.1 S78114 | surfactant protein B [mouse, DBA/2J, liver, Genomic/mRNA, 11664 nt] | | 4.00E-09 | 40/42 (95%) | - |
| MIN-72-56 | 499 | gi 2828795 gb U53213.1 JTFU53213 | Tetraodon fluviatilis JAK1 tyrosine kinase (JAK1) gene, complete cds | | 0.25 | 24/25 (96%) | - |
| MIN-73-86 | 412 | gi 7270366 emb AL161585.2 ATCHRIVB1 | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81 | | 0.053 | 25/26 (96%) | - |
| MIN-73-39 | 502 | gi 1313935 emb X79864.1 CCMRP17 | C.cricetus Mmp17 mRNA | | 1.00E-148 | 426/478 (89%) | 3/478 (0%) |
| MIN-73-09 | 471 | gi 7291400 gb AE003457.1 AE003457 | Drosophila melanogaster genomic scaffold 142000013386038 section 6 of 15, complete sequence | | 0.95 | 20/20 (100%) | - |
| MIN-73-82 | 495 | gi 10727155 gb AE003602.2 AE003602 | Drosophila melanogaster genomic scaffold 142000013386043 section 6 of 8, complete sequence | | 3.9 | 19/19 (100%) | - |
| MIN-73-81 | 354 | gi 10728874 gb AE003663.2 AE003663 | Drosophila melanogaster genomic scaffold 142000013386055 section 56 of 63, complete sequence | | 0 | 26/28 (92%) | - |
| MIN-73-40 | 497 | gi 2133879 gb AC000399.1 AC000399 | Genomic sequence from Mouse 9, complete sequence [Mus musculus] | | 8.00E-17 | 50/51 (98%) | - |
| MIN-73-84 | 417 | gi 10432963 gb AK021723.1 AK021723 | Homo sapiens cDNA FLJ11661 fis, clone HEMBA1004617 | | 0.21 | 21/21 (100%) | - |
| MIN-73-52 | 505 | gi 10434048 gb AK022579.1 AK022579 | Homo sapiens cDNA FLJ12517 fis, clone NT2RM2001784 | | 2.00E-87 | 217/251 (86%) | - |
| MIN-73-46 | 500 | gi 11430732 ref XM_007862.1 | Homo sapiens CGI-128 protein (LOC51647), mRNA | | 5.00E-55 | 180/203 (88%) | - |
| MIN-73-77 | 505 | gi 2335202 gb AF015416.1 AF015416 | Homo sapiens chromosome 11 from 11p15.5 region, complete sequence | | 1.00E-27 | 179/217 (82%) | 3/217 (1%) |
| MIN-73-54 | 492 | gi 8698757 gb AC022308.1 AC022308 | Homo sapiens chromosome 15 clone RPT1-34L4, complete sequence | | 0.064 | 22/22 (100%) | - |
| MIN-73-48 | 488 | gi 1119449 gb AC010276.6 AC010276 | Homo sapiens chromosome 5 clone CTC-504A5, complete sequence | | 0.001 | 32/33 (96%) | 1/33 (3%) |
| MIN-73-43 | 434 | gi 3282162 gb AC005218.1 AC005218 | Homo sapiens chromosome 5, P1 clone 737H5 (LBNL H36), complete sequence | | 4.00E-43 | 169/195 (86%) | - |
| MIN-73-19 | 479 | gi 6841281 gb AF161434.1 AF161434 | Homo sapiens HSPC316 mRNA, partial cds | | 1.00E-111 | 366/416 (87%) | 5/416 (1%) |
| MIN-73-20 | 501 | gi 11545788 ref NM_022074.1 | Homo sapiens hypothetical protein FLJ22794 (FLJ22794), mRNA | | 3.00E-13 | 68/77 (88%) | - |
| MIN-73-23 | 501 | gi 11429024 ref XM_005496.1 | Homo sapiens isoleucine-tRNA synthetase (IARS), mRNA | | 9.00E-63 | 997/488 (81%) | - |
| MIN-73-33 | 505 | gi 7662283 ref NM_014632.1 | Homo sapiens KIAA0750 gene product (KIAA0750), mRNA | | 2.00E-54 | 251/298 (84%) | - |
| MIN-73-76 | 475 | gi 7662483 ref NM_014914.1 | Homo sapiens KIAA1099 protein (KIAA1099), mRNA | | 3.00E-78 | 253/285 (88%) | 8/285 (2%) |
| MIN-73-57 | 495 | gi 4210725 emb AJ132583.1 HSA132583 | Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial | | 9.00E-32 | 88/92 (95%) | 1/92 (1%) |
| MIN-73-30 | 342 | gi 11424064 ref XM_005098.1 | Homo sapiens poly(A)-binding protein, cytoplasmic 1 (PABPC1), mRNA | | 2.00E-72 | 177/188 (94%) | 1/188 (0%) |
| MIN-73-02 | 500 | gi 11525650 ref XM_005748.1 | Homo sapiens ZW10 interactor (ZWINT), mRNA | | 8.00E-17 | 146/179 (81%) | - |
| MIN-73-27 | 497 | gi 11544458 emb AL158824.1 AL158824 | Human DNA sequence from clone RP11-165N19 on chromosome 9, complete sequence [Homo sapiens] | | 3.00E-07 | 52/59 (88%) | - |
| MIN-73-55 | 418 | gi 10120085 emb AL359894.9 AL359894 | Human DNA sequence from clone RP11-379C1 on chromosome 1, complete sequence [Homo sapiens] | | 0.21 | 21/21 (100%) | - |
| MIN-73-89 | 457 | gi 1673440 emb X99946.1 JMMTSDNA | M.musculus 94kb genomic sequence encoding Tsx gene | | 3.00E-62 | 148/155 (95%) | 1/155 (0%) |
| MIN-73-36 | 499 | gi 619499 emb X83569.1 JMMN2 | M.musculus mRNA for neuronatin-2 | | 0 | 488/489 (99%) | 1/489 (0%) |
| MIN-73-08 | 508 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 493/494 (99%) | - |
| MIN-73-11 | 499 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 485/485 (100%) | - |
| MIN-73-12 | 487 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 487/487 (100%) | - |
| MIN-73-18 | 495 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 387/388 (99%) | - |
| MIN-73-34 | 504 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 491/491 (100%) | - |
| MIN-73-38 | 504 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 456/456 (100%) | - |
| MIN-73-47 | 480 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 374/374 (100%) | - |
| MIN-73-49 | 499 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 485/485 (100%) | - |
| MIN-73-69 | 500 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 363/363 (100%) | - |
| MIN-73-70 | 467 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | | 0 | 452/453 (99%) | - |
| MIN-73-22 | 242 | gi 52714 emb X04724.1 JMMINSIG | Mouse preproinsulin gene II | | 1.00E-106 | 201/203 (99%) | - |
| MIN-73-92 | 249 | gi 52714 emb X04724.1 JMMINSIG | Mouse preproinsulin gene II | | 1.00E-110 | 203/203 (100%) | - |
| MIN-73-16 | 495 | gi 9150274 gb L07095.1 JUSMTHYPA | Mus domesticus strain NZB/B1NJ mitochondrion genome, complete sequence | | 0 | 446/446 (100%) | - |
| MIN-73-79 | 506 | gi 9055383 ref NM_018753.1 | Mus musculus 3 monooxygenase/tryptophan 5 monooxygenase activation protein, beta polypeptide (Ywhab), | | 0 | 471/477 (98%) | 3/477 (0%) |
| MIN-73-65 | 489 | gi 7304888 ref NM_013471.1 | Mus musculus annexin A4 (Anxa4), mRNA | | 0 | 475/475 (100%) | - |
| MIN-73-94 | 332 | gi 6753185 ref NM_009750.1 | Mus musculus brain expressed X-linked 3 (Bex3), mRNA | | 1.00E-170 | 316/319 (99%) | 1/319 (0%) |
| MIN-73-26 | 414 | gi 6680933 ref NM_007694.1 | Mus musculus chromogranin B (Chgb), mRNA | | 0 | 400/400 (100%) | - |
| MIN-73-44 | 435 | gi 11527409 gb AC084429.5 AC084429 | Mus Musculus Chromosome 2 Clone RP23-291P1, complete sequence [Mus musculus] | | 0 | 421/421 (100%) | - |
| MIN-73-60 | 497 | gi 6753309 ref NM_009829.1 | Mus musculus cyclin D2 (Cnd2), mRNA | | 1.00E-170 | 304/304 (100%) | - |

| | | | | | | |
|-----------|-----|------------------------------------|--|-----------|----------------|-------------|
| MIN-73-29 | 496 | g 6753913 ref NM_012040.1 | Mus musculus ferritin light chain 1 (Ftl1), mRNA | 0 | 481/482 (99%) | - |
| MIN-73-90 | 396 | g 6753913 ref NM_012040.1 | Mus musculus ferritin light chain 1 (Ftl1), mRNA | 0 | 385/387 (99%) | 1/387 (0%) |
| MIN-73-85 | 500 | g 6679936 ref NM_008084.1 | Mus musculus glyceraldehyde-3-phosphate dehydrogenase (Gapd), mRNA | 0 | 485/486 (99%) | - |
| MIN-73-31 | 497 | g 6680158 ref NM_008210.1 | Mus musculus H3 histone, family 3A (H3f3a), mRNA | 0 | 483/483 (100%) | - |
| MIN-73-61 | 494 | g 8393533 ref NM_016957.1 | Mus musculus high mobility group protein 17 (Hmg17), mRNA | 0 | 478/480 (99%) | - |
| MIN-73-15 | 499 | g 7305130 ref NM_013916.1 | Mus musculus Hoxa1 regulated gene (Ha1r-pending), mRNA | 0 | 478/485 (98%) | 4/485 (0%) |
| MIN-73-42 | 459 | g 7949048 ref NM_016786.1 | Mus musculus huntingtin interacting protein 2 (Hip2), mRNA | 2.00E-26 | 63/63 (100%) | - |
| MIN-73-03 | 491 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-73-04 | 442 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-73-56 | 437 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-73-87 | 392 | g 3462454 gb U89915.1 MMU89915 | Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds | 0 | 371/375 (98%) | - |
| MIN-73-72 | 474 | g 2944418 gb AF049850.1 MMHC438N1 | Mus musculus major histocompatibility locus class III region: complement C4 (C4) and cytochrome P450 hcy | 0 | 443/459 (96%) | 5/459 (1%) |
| MIN-73-01 | 504 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 499/499 (100%) | - |
| MIN-73-21 | 503 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 489/489 (100%) | - |
| MIN-73-25 | 498 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 484/484 (100%) | - |
| MIN-73-74 | 487 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 479/481 (99%) | - |
| MIN-73-75 | 471 | g 6822202 emb AJ132657.1 MMU132657 | Mus musculus MOD1 gene, partial, 3' non-coding region | 1.00E-175 | 319/320 (99%) | 1/320 (0%) |
| MIN-73-14 | 498 | g 854738 gb U28068.1 MMU28068 | Mus musculus neurogenic differentiation factor (neuroD) mRNA, partial cds | 0 | 484/484 (100%) | - |
| MIN-73-13 | 479 | g 6679107 ref NM_008722.1 | Mus musculus nucleophosmin 1 (Npm1), mRNA | 0 | 465/465 (100%) | - |
| MIN-73-41 | 506 | g 9790136 ref NM_019716.1 | Mus musculus origin recognition complex subunit 6 (Orc6), mRNA | 5.00E-18 | 52/53 (98%) | - |
| MIN-73-45 | 501 | g 8546861 emb AJ278429.1 MMU278429 | Mus musculus partial Prkar1a gene for cAMP-dependent protein kinase regulatory subunit R1alpha, exons 6 | 0 | 480/482 (99%) | 2/482 (0%) |
| MIN-73-91 | 497 | g 7305362 ref NM_013625.1 | Mus musculus platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit (Pafah1b1), mRNA | 0 | 482/483 (99%) | 1/483 (0%) |
| MIN-73-17 | 495 | g 7242170 ref NM_011045.1 | Mus musculus proliferating cell nuclear antigen (Pcna), mRNA | 0 | 486/486 (100%) | - |
| MIN-73-95 | 503 | g 691713 gb U09419.1 MMU09419 | Mus musculus retinoid X receptor interacting protein (RIP15) mRNA, complete cds | 0 | 489/489 (100%) | - |
| MIN-73-73 | 502 | g 7110730 ref NM_009438.1 | Mus musculus ribosomal protein L13a (Rpl13a), mRNA | 0 | 488/489 (99%) | - |
| MIN-73-88 | 403 | g 6677916 ref NM_009156.1 | Mus musculus selenoprotein W, muscle 1 (Sepw1), mRNA | 0 | 387/389 (99%) | - |
| MIN-73-37 | 465 | g 950000 gb U20365.1 MMSMGAS2 | Mus musculus smooth muscle gamma-actin gene, complete cds | 6.00E-05 | 57/67 (85%) | - |
| MIN-73-58 | 482 | g 6755399 ref NM_011317.1 | Mus musculus scr associated in mitosis, 68 kDa (Sam68), mRNA | 0 | 468/468 (100%) | - |
| MIN-73-35 | 470 | g 9910591 ref NM_020012.1 | Mus musculus TRIAD2 type 1 (Triad2), mRNA | 0 | 456/456 (100%) | - |
| MIN-73-80 | 506 | g 8394459 ref NM_016963.1 | Mus musculus tropomodulin 3 (Tmod3), mRNA | 0 | 488/494 (98%) | 1/494 (0%) |
| MIN-73-07 | 500 | g 10946631 ref NM_012342.1 | Mus musculus tweety homolog 1 (Drosophila) (Ttyh1), mRNA | 0 | 414/414 (100%) | - |
| MIN-73-63 | 493 | g 6678482 ref NM_009457.1 | Mus musculus ubiquitin-activating enzyme E1, Chr X (Ube1x), mRNA | 0 | 479/479 (100%) | - |
| MIN-73-50 | 494 | g 7305646 ref NM_013844.1 | Mus musculus Zinc finger protein 68 (Zfp68), mRNA | 0 | 479/480 (99%) | 1/480 (0%) |
| MIN-73-59 | 335 | g 9947240 gb AE004560.1 AE004560 | Pseudomonas aeruginosa PA01, section 121 of 529 of the complete genome | 0.66 | 20/20 (100%) | - |
| MIN-73-67 | 516 | g 56709 emb X0091.1 JRNMSAR | Rat mRNA for multiplication stimulating activity (MSA) | 0 | 488/499 (97%) | 2/499 (0%) |
| MIN-73-64 | 478 | g 1292885 emb X59601.1 JRNPLECT | Rat mRNA for plectin | 0 | 437/469 (93%) | - |
| MIN-73-62 | 509 | g 7109703 gb AF000578.2 AF000578 | Rattus norvegicus Cdc5-like protein mRNA, complete cds | 0 | 465/508 (91%) | 4/508 (0%) |
| MIN-73-32 | 506 | g 6474927 dbj AB006852.1 AB006852 | Rattus norvegicus mRNA for phosphoarginine phosphatase, complete cds | 0 | 410/415 (98%) | - |
| MIN-73-53 | 501 | g 2384731 gb AF015911.1 AF015911 | Rattus norvegicus NAC-1 protein (NAC-1) mRNA, complete cds | 0.065 | 25/26 (96%) | - |
| MIN-73-28 | 492 | g 6981447 ref NM_013080.1 | Rattus norvegicus Protein tyrosine phosphatase, receptor-type, zeta polypeptide (Ptptr1), mRNA | 0 | 440/478 (92%) | 11/478 (2%) |
| MIN-77-87 | 109 | - | - | - | - | - |
| MIN-77-94 | 109 | g 1478356 gb S81393.1 S81393 | Aga-aspartylglucosaminidase [mouse, liver, brain, mRNA Partial, 1191 nt] | 1.00E-30 | 78/81 (96%) | - |
| MIN-77-10 | 376 | g 7670113 gb AC009890.12 AC009890 | Genomic Sequence For Homo sapiens Clone HJ_NH0262L04 From Chromosome 18, complete sequence | 0.19 | 21/21 (100%) | - |
| MIN-77-57 | 491 | g 10435241 dbj AK023347.1 AK023347 | Homo sapiens cDNA FLJ13285 fs, clone OVARC100129 | 3.00E-47 | 323/338 (95%) | - |
| MIN-77-53 | 78 | g 10801387 gb AC013357.19 AC013357 | Homo sapiens chromosome 10a25 clone 216j18, complete sequence | 1.9 | 18/18 (100%) | - |
| MIN-77-66 | 489 | g 3492893 gb AC005288.1 AC005288 | Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence | 7.00E-79 | 368/431 (85%) | 22/431 (5%) |
| MIN-77-04 | 376 | g 9954675 gb AC025447.4 AC025447 | Homo sapiens chromosome 5 clone CTD-2085H24, complete sequence | 1.00E-05 | 76/92 (82%) | - |
| MIN-77-55 | 499 | g 2852639 gb AF007157.3 AF007157 | Homo sapiens clone 23856 unknown mRNA, partial cds | 0 | 454/485 (93%) | - |
| MIN-77-24 | 457 | g 11181856 gb AC074191.3 AC074191 | Homo sapiens clone RP11-502G22, complete sequence | 0.23 | 21/21 (100%) | - |
| MIN-77-25 | 494 | g 11427169 ref XM_008553.1 | Homo sapiens DKFP564K1964 protein (DKFP564K1964), mRNA | 1.00E-123 | 334/370 (90%) | - |
| MIN-77-05 | 320 | g 5002511 emb Z98266.1 HSZ98266 | Homo sapiens gene encoding plakophilin (exons 1-13) | 0.04 | 22/22 (100%) | - |
| MIN-77-67 | 500 | g 11435161 ref XM_003204.1 | Homo sapiens leucine rich repeat (in FLII) interacting protein 2 (LRIFIP2), mRNA | 1.00E-100 | 286/319 (90%) | - |
| MIN-77-85 | 501 | g 11424211 ref XM_001802.1 | Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2), mRNA | 1.00E-113 | 314/348 (90%) | 1/348 (0%) |
| MIN-77-81 | 280 | g 7657547 ref NM_014563.1 | Homo sapiens spondyloepiphyseal dysplasia, late (SEDL), mRNA | 2.00E-56 | 143/153 (93%) | - |
| MIN-77-37 | 370 | g 11275668 gb AF225896.1 AF225896 | Homo sapiens tensin mRNA, complete cds | 0 | 344/348 (98%) | 1/348 (0%) |
| MIN-77-47 | 499 | g 11420568 ref XM_004830.1 | Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA | 1.00E-178 | 441/482 (91%) | - |
| MIN-77-01 | 503 | g 8745064 emb AL137007.9 AL137007 | Human DNA sequence from clone RP1-303F19 on chromosome 6q12 Contains fragments of a gene similar | 0.26 | 21/21 (100%) | - |
| MIN-77-15 | 287 | g 6503218 gb AF163772.2 AF163772 | Leishmania major chromosome 5 clone L7138 strain Friedlin, complete sequence | 0.56 | 23/24 (95%) | - |
| MIN-77-12 | 343 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 2.00E-84 | 160/160 (100%) | - |
| MIN-77-31 | 339 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 1.00E-175 | 321/325 (98%) | - |
| MIN-77-35 | 499 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/486 (100%) | - |
| MIN-77-38 | 493 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 479/479 (100%) | - |
| MIN-77-68 | 499 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-77-75 | 497 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 481/483 (99%) | - |
| MIN-77-96 | 125 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 4.00E-43 | 97/98 (98%) | 1/98 (1%) |
| MIN-77-28 | 450 | g 52712 emb X04725.1 JMINSIG | Mouse preproinsulin gene I | 0 | 408/409 (99%) | - |
| MIN-77-82 | 436 | g 6752953 ref NM_009609.1 | Mus musculus actin, gamma, cytoplasmic (Actg), mRNA | 0 | 422/425 (99%) | - |
| MIN-77-56 | 481 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 467/467 (100%) | - |
| MIN-77-72 | 274 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 1.00E-142 | 259/260 (99%) | - |
| MIN-77-73 | 501 | g 7304908 ref NM_013477.1 | Mus musculus ATPase, H+ transporting, lysosomal (vacuolar proton pump), 42 kDa (Atp6d), mRNA | 0 | 429/432 (99%) | - |
| MIN-77-77 | 499 | g 6753045 ref NM_011787.1 | Mus musculus autocrine motility factor receptor (Amfr), mRNA | 0 | 484/485 (99%) | - |
| MIN-77-08 | 487 | g 9624966 ref NM_019584.1 | Mus musculus beclin 1 (coiled-coil, myosin-like BCL2-interacting protein) (Becn1), mRNA | 0 | 378/379 (99%) | - |
| MIN-77-70 | 472 | g 6680887 ref NM_007653.1 | Mus musculus Cdc63 antigen (Cdc63), mRNA | 0 | 440/441 (99%) | - |
| MIN-77-90 | 364 | g 6680887 ref NM_007653.1 | Mus musculus Cdc63 antigen (Cdc63), mRNA | 0 | 350/350 (100%) | - |
| MIN-77-76 | 407 | g 6680919 ref NM_007681.1 | Mus musculus centromere autoantigen A (Cenpa), mRNA | 0 | 390/393 (99%) | 2/393 (0%) |
| MIN-77-29 | 496 | g 5305503 gb AF089815.1 AF089815 | Mus musculus chimeric 16S ribosomal RNA, complete sequence: mitochondrial gene for nuclear product | 1.00E-137 | 248/248 (100%) | - |
| MIN-77-84 | 259 | g 4731666 gb AC005818.6 AC005818 | Mus musculus chromosome 10 clone rp21-411d9 strain 129S6/SvEvTac, complete sequence | 3.00E-42 | 135/149 (90%) | 1/149 (0%) |
| MIN-77-45 | 499 | g 7263202 gb AC012302.5 AC012302 | Mus musculus chromosome 10, clone RP21-247L16, complete sequence | 3.00E-04 | 26/26 (100%) | - |
| MIN-77-33 | 424 | g 9929691 gb AC020972.3 AC020972 | Mus musculus chromosome 18 clone RP23-6P18, complete sequence | 0 | 410/410 (100%) | - |
| MIN-77-86 | 455 | g 4210518 gb AC002327.1 AC002327 | Mus musculus chromosome 7, clone 19K5, complete sequence | 0 | 442/442 (100%) | - |
| MIN-77-44 | 501 | g 8571379 gb AF231925.1 AF231925 | Mus musculus COPI coatomer complex, beta subunit (Cobp) mRNA, complete cds | 0 | 487/487 (100%) | - |
| MIN-77-02 | 375 | g 6681136 ref NM_007830.1 | Mus musculus diazepam binding inhibitor (Dbi), mRNA | 0 | 337/340 (99%) | - |
| MIN-77-52 | 500 | g 6753707 ref NM_010097.1 | Mus musculus extracellular matrix protein 2 (Ecm2), mRNA | 0 | 485/486 (99%) | - |
| MIN-77-16 | 395 | g 3420738 gb AF077860.1 MMUID2H1 | Mus musculus helix-loop-helix protein Id2 gene, complete cds | 0 | 380/382 (99%) | 1/382 (0%) |
| MIN-77-46 | 448 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-77-49 | 408 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-77-62 | 441 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-77-80 | 325 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-149 | 272/273 (99%) | - |
| MIN-77-09 | 499 | g 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 482/489 (98%) | 2/489 (0%) |
| MIN-77-54 | 500 | g 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 482/487 (98%) | 2/487 (0%) |
| MIN-77-58 | 417 | g 3228368 gb K02061.1 JMUSRPL4A | Mus musculus L32-4A pseudogene, complete sequence | 0 | 402/403 (99%) | 1/403 (0%) |
| MIN-77-48 | 495 | g 8866180 gb AF160982.1 AF160982 | Mus musculus mepirin 1 beta (Mep1b) gene, exons 3' and 1 and partial cds; alternatively spliced | 2.00E-05 | 31/32 (96%) | - |
| MIN-77-65 | 315 | g 7305288 ref NM_013827.1 | Mus musculus metal response element binding transcription factor 2 (Mtf2), mRNA | 1.00E-145 | 266/268 (99%) | - |
| MIN-77-39 | 501 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 497/498 (99%) | - |
| MIN-77-40 | 501 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 487/487 (100%) | - |
| MIN-77-59 | 502 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 496/496 (100%) | - |
| MIN-77-07 | 475 | g 8885512 dbj AB045313.1 AB045313 | Mus musculus mmCdc20 mRNA, complete cds | 0 | 454/456 (99%) | - |
| MIN-77-51 | 462 | g 6573296 dbj AB028857.1 AB028857 | Mus musculus mRNA for mDj7, complete cds | 0 | 437/437 (100%) | - |
| MIN-77-63 | 499 | g 8978233 dbj AB041263.1 AB041263 | Mus musculus mRNA for N-acetylneuraminic acid 9-phosphate synthetase, complete cds | 0 | 485/485 (100%) | - |
| MIN-77-20 | 502 | g 1205975 gb U14172.1 MMU14172 | Mus musculus p162 protein mRNA, complete cds | 0 | 488/488 (100%) | - |
| MIN-77-36 | 435 | g 6679316 ref NM_008389.1 | Mus musculus phosphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca), mRNA | 0 | 420/421 (99%) | - |

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|-----------|-----|-------------------------------------|--|-----------|------------------|------------|
| MIN-77-69 | 502 | g 8778119 gb AF274044.1 AF274044 | Mus musculus PKC delta gene, complete cds | 3.00E-13 | 80/93 (86%) | - |
| MIN-77-42 | 503 | g 8132350 gb AF154337.1 AF154337 | Mus musculus putative seven pass transmembrane protein (Tm7sf1) mRNA, complete cds | 1.00E-175 | 323/325 (99%) | 1/325 (0%) |
| MIN-77-17 | 228 | g 108080347 emb AJ297131.1 JMMAJ297 | Mus musculus SIL, MAP_7, CYP_a, SCL & CYP_b genes | 1.00E-104 | 217/223 (97%) | 3/223 (1%) |
| MIN-77-27 | 502 | g 6755615 ref NM_012031.1 | Mus musculus sperm associated antigen 1 (Spag1), mRNA | - | 0/487/488 (99%) | - |
| MIN-77-71 | 319 | g 4868332 gb AF129888.1 AF129888 | Mus musculus Sui1 homolog mRNA, complete cds | 1.00E-168 | 304/305 (99%) | - |
| MIN-77-26 | 496 | g 6755437 ref NM_011519.1 | Mus musculus syndecan 1 (Sdc1), mRNA | - | 0/482/482 (100%) | - |
| MIN-77-92 | 187 | g 6678264 ref NM_009342.1 | Mus musculus t-complex testis expressed 1 (Tctex1), mRNA | 2.00E-89 | 171/172 (99%) | - |
| MIN-77-79 | 365 | g 6678444 ref NM_009433.1 | Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA | - | 0/359/359 (100%) | - |
| MIN-77-06 | 475 | g 6678435 ref NM_009429.1 | Mus musculus translationally regulated transcript (21 kDa) (Trt), mRNA | - | 0/441/443 (99%) | - |
| MIN-77-41 | 498 | g 6677980 ref NM_009190.1 | Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA | - | 0/484/485 (99%) | 1/485 (0%) |
| MIN-77-43 | 498 | g 9858802 gb AF282919.1 AF282919 | Mus musculus Zfp228 (Znf228) mRNA, complete cds | - | 0/473/480 (98%) | 2/480 (0%) |
| MIN-77-23 | 502 | g 6594243 emb AL031746.9 PFMAL1P3 | Plasmodium falciparum MAL1P3, complete sequence | 0.001 | 25/25 (100%) | - |
| MIN-77-13 | 286 | g 9255756 gb AF209196.1 AF209196 | Rattus norvegicus calcium transporter CaT2 (CaT2) mRNA, complete cds | 1.00E-114 | 251/261 (96%) | 3/261 (1%) |
| MIN-77-83 | 360 | g 4102603 gb AF013498.1 AF013498 | Rattus norvegicus clone 2 alpha-2u globulin gene, partial cds | 1.00E-08 | 33/33 (100%) | - |
| MIN-77-03 | 501 | g 6978464 ref NM_012776.1 | Rattus norvegicus G-protein-linked receptor kinase (beta adrenergic receptor kinase 1) (Adrbk1), mRNA | - | 0/476/488 (97%) | - |
| MIN-77-19 | 472 | g 2352085 gb U96490.1 JRNJ96490 | Rattus norvegicus liver mRNA, complete cds | 1.00E-169 | 369/427 (92%) | 7/427 (1%) |
| MIN-77-74 | 498 | g 7110604 ref NM_012728.1 | Rattus norvegicus Pancreatic beta cell receptor for the gluco-incretin hormone glucagon-like peptide 1 (GLP-1) (GLP1R), mRNA | 4.00E-31 | 132/150 (88%) | 3/150 (2%) |
| MIN-77-32 | 504 | g 7677175 gb AF200359.1 AF200359 | Rattus norvegicus UDP-glucose glycoprotein:glucosyltransferase precursor (Uggt) mRNA, complete cds | 1.00E-155 | 333/351 (94%) | - |
| MIN-77-50 | 503 | g 9957833 gb AF279619.1 AF279619 | Salmonella enterica isolate M1952 dTDP-D-glucose-4,6-dehydratase (mlbB), dTDP-6-deoxy-L-mannose-6-phosphate synthase (mlbC) [Mus musculus] | - | 1/20/20 (100%) | - |
| MIN-78-14 | 500 | g 2347182 gb AC002109.1 AC002109 | Genomic sequence from Mouse 9, complete sequence [Mus musculus] | 0.016 | 23/23 (100%) | - |
| MIN-78-20 | 497 | g 11418136 ref XM_009995.1 | Homo sapiens chromobox homolog 6 (CBX6), mRNA | 5.00E-12 | 72/83 (86%) | - |
| MIN-78-75 | 502 | g 3287444 gb AC005212.1 AC005212 | Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence | 0.016 | 23/23 (100%) | - |
| MIN-78-57 | 497 | g 9653120 gb AC027121.5 AC027121 | Homo sapiens chromosome 3 clone RP11-25C11 map 3p, complete sequence | 0.003 | 24/24 (100%) | - |
| MIN-78-33 | 499 | g 4753221 gb AC005088.2 AC005088 | Homo sapiens clone RG313A17, complete sequence | 0.054 | 22/22 (100%) | - |
| MIN-78-24 | 498 | g 11419885 ref XM_010152.1 | Homo sapiens GDP dissociation inhibitor 1 (GDI1), mRNA | 1.00E-112 | 122/146 (83%) | 5/146 (3%) |
| MIN-78-90 | 257 | g 11435317 ref XM_006814.1 | Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1), mRNA | 0.032 | 22/22 (100%) | - |
| MIN-78-48 | 500 | g 8923597 ref NM_017916.1 | Homo sapiens hypothetical protein FLJ20643 (FLJ20643), mRNA | 8.00E-91 | 291/331 (87%) | - |
| MIN-78-78 | 502 | g 11429356 ref XM_002403.1 | Homo sapiens KIAA1099 protein (KIAA1099), mRNA | 7.00E-08 | 65/76 (85%) | - |
| MIN-78-80 | 492 | g 10047340 dbj AB046852.1 AB046852 | Homo sapiens mRNA for KIAA1632 protein, partial cds | 7.00E-11 | 85/101 (84%) | - |
| MIN-78-52 | 503 | g 6807712 emb AL137648.1 HSM80191 | Homo sapiens mRNA; cDNA DKFZp434J1813 (from clone DKFZp434J1813); partial cds | 1.00E-142 | 431/489 (88%) | - |
| MIN-78-26 | 498 | g 11421250 ref XM_004899.1 | Homo sapiens oxoglutarate dehydrogenase (lipamide) (OGDH), mRNA | 5.00E-89 | 264/296 (89%) | - |
| MIN-78-54 | 501 | g 11420630 ref XM_009488.1 | Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA | 1.00E-122 | 401/460 (87%) | - |
| MIN-78-76 | 484 | g 6911646 emb AL109865.3 HSG120K | Human DNA sequence from clone GS1-120K12 on chromosome 1q25.3-31.2. Contains the gene for ring finger protein 120 (RNF120) [Homo sapiens] | 1.00E-40 | 201/239 (84%) | - |
| MIN-78-25 | 201 | g 1044341 dbj AL35193.7 AL35193 | Human DNA sequence from clone RP11-137F15 on chromosome 20. Contains ESTs, STSs, GSSs and CpG islands [Homo sapiens] | 1.00E-10 | 63/72 (87%) | - |
| MIN-78-02 | 498 | g 11120979 emb AL136314.12 AL136314 | Human DNA sequence from clone RP4-579A14 on chromosome 6, complete sequence [Homo sapiens] | 0.016 | 23/23 (100%) | - |
| MIN-78-88 | 342 | g 4376000 emb AL034377.1 HS751H9 | Human DNA sequence from clone RP4-751H9 on chromosome 6q13. Contains the 3' end of a novel gene, E | 0.17 | 24/25 (96%) | - |
| MIN-78-40 | 503 | g 8218095 emb AL109824.2 HJ1181N | Human DNA sequence from clone RP5-1181N3 on chromosome 20 Contains the gene for KIAA0181 protein [Homo sapiens] | 2.00E-32 | 125/142 (88%) | 4/142 (2%) |
| MIN-78-21 | 497 | g 407465 emb X75312.1 MNRNAQM | M.musculus (C57BL/6) QM mRNA | - | 0/484/484 (100%) | - |
| MIN-78-66 | 500 | g 57965 emb Z19599.1 JMMZ1433IS | M.musculus epsilon 14-3-3 isoform mRNA | - | 0/460/460 (100%) | - |
| MIN-78-16 | 414 | g 194034 gb J19141.1 JMSHSPCA | Mouse heat shock protein 70 cognate mRNA, complete cds | - | 0/399/400 (99%) | - |
| MIN-78-01 | 501 | g 198849 gb J03302.1 JMSLPL | Mouse lipoprotein lipase mRNA, 3' end | - | 0/486/488 (99%) | - |
| MIN-78-07 | 503 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/490/490 (100%) | - |
| MIN-78-22 | 132 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 3.00E-50 | 102/102 (100%) | - |
| MIN-78-27 | 356 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 1.00E-169 | 302/302 (100%) | - |
| MIN-78-42 | 502 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/489/489 (100%) | - |
| MIN-78-73 | 355 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/340/342 (99%) | - |
| MIN-78-86 | 500 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/488/488 (100%) | - |
| MIN-78-87 | 502 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/396/396 (100%) | - |
| MIN-78-89 | 497 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | - | 0/484/484 (100%) | - |
| MIN-78-68 | 479 | g 6880505 gb J3812.1 J3812 | Msx-1/Hox-7.7.1=Msx-1 [Gen, Genomic, 5421 nt] | - | 0/465/466 (99%) | 1/466 (0%) |
| MIN-78-71 | 498 | g 6753073 ref NM_009679.1 | Mus musculus adaptor protein complex AP-2, mu1 (Ap2m1), mRNA | - | 0/483/484 (99%) | - |
| MIN-78-15 | 500 | g 6671580 ref NM_007495.1 | Mus musculus astrotactin (Astrn), mRNA | - | 0/475/479 (99%) | 3/479 (0%) |
| MIN-78-82 | 495 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, complete cds | - | 0/481/481 (100%) | - |
| MIN-78-62 | 377 | g 861212 gb U27129.1 JMMU27129 | Mus musculus breast heat shock 73 protein (hsc73) mRNA, complete cds | - | 0/354/358 (98%) | 3/358 (0%) |
| MIN-78-38 | 493 | g 6753243 ref NM_009790.1 | Mus musculus calmodulin (Calm), mRNA | - | 0/475/479 (99%) | 3/479 (0%) |
| MIN-78-93 | 217 | g 6753243 ref NM_009790.1 | Mus musculus calmodulin (Calm), mRNA | 2.00E-98 | 200/203 (98%) | 2/203 (0%) |
| MIN-78-41 | 501 | g 6671671 ref NM_007604.1 | Mus musculus capping protein alpha 2 (Cappa2), mRNA | - | 0/494/495 (99%) | - |
| MIN-78-13 | 501 | g 4731666 gb AC005818.6 AC005818 | Mus musculus chromosome 10 clone rp21-411d9 strain 129S6/SvEvTac, complete sequence | 3.00E-10 | 80/94 (85%) | 3/94 (3%) |
| MIN-78-65 | 494 | g 6553965 gb AC011013.1 AC011013 | Mus musculus chromosome 11, clone RP23-218N2, complete sequence | 3.00E-13 | 56/60 (93%) | 1/60 (1%) |
| MIN-78-36 | 504 | g 11465071 gb AC012526.30 AC012526 | Mus musculus chromosome 16 clone rp21-67111 strain 129S6/SvEvTac, complete sequence | 1.00E-06 | 39/42 (92%) | - |
| MIN-78-77 | 200 | g 4096089 gb AC006289.1 AC006289 | Mus musculus chromosome 17, clone 29_N_7, complete sequence | 2.00E-36 | 82/83 (98%) | - |
| MIN-78-72 | 392 | g 6753597 ref NM_010015.1 | Mus musculus defender against cell death 1 (Dad1), mRNA | - | 0/376/386 (97%) | 3/386 (0%) |
| MIN-78-67 | 501 | g 7305018 ref NM_013506.1 | Mus musculus eukaryotic translation initiation factor 4E2 (Eif4a2), mRNA | - | 0/443/444 (99%) | 1/444 (0%) |
| MIN-78-28 | 498 | g 6679820 ref NM_008033.1 | Mus musculus farnesyltransferase, CAAX box, alpha (Fnta), mRNA | - | 0/484/484 (100%) | - |
| MIN-78-69 | 488 | g 9507186 ref NM_019502.1 | Mus musculus fractured callus expressed transcript 1 (Fxc1), mRNA | 1.00E-143 | 259/259 (100%) | - |
| MIN-78-05 | 501 | g 6680070 ref NM_008157.1 | Mus musculus G protein-coupled receptor 19 (Gpr19), mRNA | - | 0/487/487 (100%) | - |
| MIN-78-31 | 436 | g 1018121 ref NM_020588.1 | Mus musculus hypothetical protein MNCB-2755 (LOC57439), mRNA | - | 0/406/406 (100%) | - |
| MIN-78-55 | 459 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | - | 0/333/333 (100%) | - |
| MIN-78-11 | 500 | g 6754409 ref NM_011835.1 | Mus musculus katanin p60 (ATPase-containing) subunit A1 (Katna1), mRNA | - | 0/485/486 (99%) | - |
| MIN-78-34 | 317 | g 10181181 ref NM_020626.1 | Mus musculus kidney-specific membrane protein (Nkx17-pending), mRNA | 1.00E-164 | 301/302 (99%) | 1/302 (0%) |
| MIN-78-60 | 499 | g 6754621 ref NM_010764.1 | Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA | - | 0/485/485 (100%) | - |
| MIN-78-18 | 423 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | - | 0/408/409 (99%) | - |
| MIN-78-30 | 499 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | - | 0/483/485 (99%) | 2/485 (0%) |
| MIN-78-59 | 498 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | - | 0/485/485 (100%) | - |
| MIN-78-79 | 504 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | - | 0/498/498 (100%) | - |
| MIN-78-92 | 281 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 1.00E-139 | 270/275 (98%) | 1/275 (0%) |
| MIN-78-46 | 502 | g 3928492 emb AJ130961.1 JMMU13096 | Mus musculus mRNA for ubiquitin-conjugating enzyme | - | 0/471/471 (100%) | - |
| MIN-78-06 | 500 | g 6679175 ref NM_008765.1 | Mus musculus origin recognition complex, subunit 2 homolog (S. cerevisiae) (Orc2), mRNA | - | 0/485/487 (99%) | 1/487 (0%) |
| MIN-78-49 | 503 | g 6679439 ref NM_008907.1 | Mus musculus peptidylprolyl isomerase A (Ppia), mRNA | - | 0/489/489 (100%) | - |
| MIN-78-91 | 501 | g 7242190 ref NM_011179.1 | Mus musculus prosaposin (Psap), mRNA | - | 0/485/487 (99%) | - |
| MIN-78-64 | 504 | g 6755225 ref NM_011200.1 | Mus musculus protein tyrosine phosphatase 44 (Ptp4a1), mRNA | - | 0/483/484 (99%) | - |
| MIN-78-35 | 412 | g 11850077 gb U47333.1 JMMU47333 | Mus musculus Rb-related p130 mRNA, complete cds | - | 0/405/406 (99%) | - |
| MIN-78-70 | 498 | g 6677822 ref NM_009103.1 | Mus musculus ribonucleotide reductase M1 (Rrm1), mRNA | - | 0/484/484 (100%) | - |
| MIN-78-39 | 388 | g 6677778 ref NM_009081.1 | Mus musculus ribosomal protein L28 (Rpl28), mRNA | - | 0/368/369 (99%) | - |
| MIN-78-10 | 228 | g 11275386 dbj AB043006.1 AB043006 | Mus musculus SDF2L1 mRNA for SDF2 like protein 1, complete cds | 3.00E-85 | 189/193 (97%) | 4/193 (2%) |
| MIN-78-44 | 499 | g 9256639 ref NM_018875.1 | Mus musculus SDP8 protein (SDP8), mRNA | - | 0/482/486 (99%) | 4/486 (0%) |
| MIN-78-53 | 406 | g 6677864 ref NM_009129.1 | Mus musculus secretogranin II (Scg2), mRNA | - | 0/376/377 (99%) | 1/377 (0%) |
| MIN-78-23 | 499 | g 6677866 ref NM_009130.1 | Mus musculus secretogranin III (Scg3), mRNA | - | 0/485/486 (99%) | 1/486 (0%) |
| MIN-78-17 | 275 | g 4868332 gb AF129888.1 AF129888 | Mus musculus Sui1 homolog mRNA, complete cds | 1.00E-133 | 260/264 (98%) | 4/264 (1%) |
| MIN-78-61 | 499 | g 9625044 ref NM_019571.1 | Mus musculus tetraspanin Tspan-5 (Tspan5), mRNA | - | 0/367/367 (100%) | - |
| MIN-78-47 | 496 | g 9790030 ref NM_019801.1 | Mus musculus thymic dendritic cell-derived factor 1 (LOC56374), mRNA | - | 0/476/482 (98%) | - |
| MIN-78-03 | 494 | g 6678468 ref NM_009448.1 | Mus musculus tubulin alpha 6 (Tuba6), mRNA | - | 0/482/482 (100%) | - |
| MIN-78-43 | 495 | g 10946631 ref NM_021324.1 | Mus musculus tweety homolog 1 (Drosophila) (Ttyh1), mRNA | - | 0/421/422 (99%) | 1/422 (0%) |
| MIN-78-84 | 409 | g 1153233 emb AJ000938.1 OLJ000938 | Oryzias latipes, Pax6 gene | 0.21 | 21/21 (100%) | - |
| MIN-78-83 | 456 | g 1838934 dbj D63411.1 JRATMPR | Rat mRNA for mitochondrial precursor receptor, complete cds | - | 0/429/452 (94%) | 5/452 (1%) |
| MIN-78-51 | 486 | g 202969 gb M86705.1 JRATARFPOLY | Rattus norvegicus ADP-ribosylation factor mRNA, 3' untranslated region including alternate poly-A signals | 1.00E-176 | 398/424 (93%) | 9/424 (2%) |
| MIN-78-94 | 330 | g 6978612 ref NM_012829.1 | Rattus norvegicus Cholecystokinin (Cck), mRNA | 1.00E-107 | 272/295 (92%) | 1/295 (0%) |
| MIN-78-37 | 497 | g 10637995 emb AJ43266.1 RNO24326 | Rattus norvegicus mRNA for mitochondrial aconitase (nuclear aco2 gene) | - | 0/469/482 (97%) | - |
| MIN-78-96 | 179 | g 2317755 gb AF013967.1 AF013967 | Rattus norvegicus Zis mRNA, complete cds | 2.00E-67 | 152/158 (96%) | 1/158 (0%) |
| MIN-79-04 | 431 | g 267 emb X15112.1 BTCCOVB | Bovine mRNA for cytochrome c oxidase subunit VIb (AED) | 2.00E-78 | 240/270 (88%) | - |
| MIN-79-94 | 418 | g 10727496 gb AE003804.2 AE003804 | Drosophila melanogaster genomic scaffold 142000013386047 section 39 of 52, complete sequence | 0.21 | 21/21 (100%) | - |

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|-----------|-----|-------------------------------------|---|-----------|----------------|-------------|
| MIN-79-13 | 498 | g 233766 gb S50213.1 S50213 | HMG1-related DNA-binding protein [Mice, mRNA, 2569 nt] | 1.00E-167 | 316/319 (99%) | 2/319 (0%) |
| MIN-79-28 | 502 | g 7023426 dbj AK001883.1 AK001883 | Homo sapiens cDNA FLJ11021 fis, clone PLACE1003704, weakly similar to SPLICING FACTOR, ARGININE | 1.00E-168 | 441/488 (90%) | - |
| MIN-79-64 | 499 | g 10434024 dbj AK022563.1 AK022563 | Homo sapiens cDNA FLJ12501 fis, clone NT2RM2001681 | 9.00E-29 | 307/387 (79%) | - |
| MIN-79-10 | 92 | g 10439427 dbj AK026546.1 AK026546 | Homo sapiens cDNA: FLJ22893 fis, clone KAT04792 | 2.00E-07 | 49/55 (89%) | 4/55 (7%) |
| MIN-79-39 | 493 | g 7706334 ref NM_016056.1 | Homo sapiens CGI-119 protein (LOC51643), mRNA | 1.00E-37 | 228/278 (82%) | - |
| MIN-79-26 | 503 | g 7670171 gb AC005517.6 AC005517 | Homo sapiens chromosome 17, clone RP11-726O12, complete sequence | 0.065 | 22/22 (100%) | - |
| MIN-79-25 | 501 | g 2895558 gb AF088554.1 AF088554 | Homo sapiens density regulated protein drp1 mRNA, partial cds | 1.00E-107 | 258/278 (92%) | - |
| MIN-79-65 | 501 | g 5523989 gb AF108138.1 AF108138 | Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds | 3.00E-22 | 83/92 (90%) | - |
| MIN-79-80 | 501 | g 11545858 ref NM_022130.1 | Homo sapiens Golgi protein (GPP34), mRNA | 3.00E-38 | 175/203 (86%) | 12/203 (5%) |
| MIN-79-66 | 498 | g 11434738 ref XM_007387.1 | Homo sapiens hypothetical protein FLJ11090 (FLJ11090), mRNA | 0.004 | 30/32 (93%) | - |
| MIN-79-22 | 293 | g 11432322 ref XM_007634.1 | Homo sapiens MORF-related gene 15 (MRG15), mRNA | 5.00E-60 | 184/201 (91%) | 5/201 (2%) |
| MIN-79-03 | 499 | g 11242765 ref XM_008495.1 | Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide p101 (P101-P13K), mRNA | 1.00E-95 | 260/287 (90%) | - |
| MIN-79-16 | 497 | g 11434070 ref XM_002646.1 | Homo sapiens putative 28 kDa protein (LOC56902), mRNA | 1.00E-120 | 367/415 (88%) | 1/415 (0%) |
| MIN-79-20 | 502 | g 10442024 gb AF261758.1 AF261758 | Homo sapiens seladin-1 mRNA, complete cds | 0.26 | 39/45 (86%) | - |
| MIN-79-74 | 495 | g 8923925 ref NM_018462.1 | Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS027 (MDS027), mRNA | 1.00E-118 | 342/378 (90%) | 8/378 (2%) |
| MIN-79-24 | 499 | g 5679448 emb AL049610.9 H1055C14 | Human DNA sequence from clone 1055C14 on chromosome Xq22.1-22.3 Contains genes for TCEAL1 (tran | 1.00E-122 | 338/375 (90%) | 1/375 (0%) |
| MIN-79-96 | 222 | g 10045359 emb AL161725.13 AL161725 | Human DNA sequence from clone RP11-165F24 on chromosome 9, complete sequence [Homo sapiens] | 0.43 | 20/20 (100%) | - |
| MIN-79-15 | 499 | g 1112100 emb AL449165.1 AL449165 | Human DNA sequence from clone RP11-53E16 on chromosome 6, complete sequence [Homo sapiens] | 0.004 | 24/24 (100%) | - |
| MIN-79-68 | 502 | g 579655 emb Z19599.1 JMME1433IS | M.musculus epsilon 14-3-3 isoform mRNA | 0 | 488/488 (100%) | - |
| MIN-79-72 | 499 | g 579655 emb Z19599.1 JMME1433IS | M.musculus epsilon 14-3-3 isoform mRNA | 0 | 461/462 (99%) | - |
| MIN-79-92 | 474 | g 993005 emb Z37988.1 JMLLARMRN | M.musculus LAR mRNA encoding protein tyrosine phosphatase | 0 | 460/460 (100%) | - |
| MIN-79-40 | 504 | g 540955 emb X68837.1 JMMSGIIA2 | M.musculus Sgll gene for secretogranin II, exon 2 | 0 | 361/361 (100%) | - |
| MIN-79-47 | 417 | g 540955 emb X68837.1 JMMSGIIA2 | M.musculus Sgll gene for secretogranin II, exon 2 | 0 | 363/363 (100%) | - |
| MIN-79-55 | 500 | g 194026 gb M36829.1 JMUSHSP84B | Mouse heat-shock protein hsp84 mRNA | 0 | 486/486 (100%) | - |
| MIN-79-01 | 500 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-79-09 | 501 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 486/487 (99%) | - |
| MIN-79-30 | 500 | g 342520 gb J01420.1 JMUSMTCG | Mouse mitochondrion, complete genome | 0 | 494/494 (100%) | - |
| MIN-79-60 | 501 | g 49842 emb X59379.1 JMMABP | Mouse mRNA for amyloid beta precursor (protease nexin II) | 0 | 487/487 (100%) | - |
| MIN-79-82 | 456 | g 1255629 dbj D50418.1 JMUSAREC3C | Mouse mRNA for AREC3, partial cds | 1.00E-120 | 237/242 (97%) | 1/242 (0%) |
| MIN-79-57 | 502 | g 662844 gb L39795.1 JMUSALRE | Mus musculus (clone MAR1) aldose reductase mRNA, complete cds | 0 | 489/489 (100%) | - |
| MIN-79-76 | 503 | g 6671568 ref NM_007475.1 | Mus musculus acidic ribosomal phosphoprotein PO (Arpb), mRNA | 0 | 487/489 (99%) | 1/489 (0%) |
| MIN-79-06 | 502 | g 7288504 gb AF214656.1 AF214656 | Mus musculus alpha(1,2)-fucosyltransferase FUT2 (Fut2) gene, complete cds | 0.016 | 35/39 (89%) | - |
| MIN-79-19 | 503 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 489/489 (100%) | - |
| MIN-79-27 | 482 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 467/468 (99%) | 1/468 (0%) |
| MIN-79-90 | 500 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 486/486 (100%) | - |
| MIN-79-23 | 498 | g 9506418 ref NM_019517.1 | Mus musculus beta-site APP-cleaving enzyme 2 (Bace2), mRNA | 1.00E-157 | 289/291 (99%) | - |
| MIN-79-37 | 501 | g 439606 gb L24755.1 JMUSBMP1A | Mus musculus bone morphogenetic protein (Bmp-1) mRNA, complete cds | 0 | 488/488 (100%) | - |
| MIN-79-69 | 391 | g 6680835 ref NM_007591.1 | Mus musculus calreticulin (Calr), mRNA | 0 | 373/373 (100%) | - |
| MIN-79-73 | 495 | g 6753557 ref NM_009844.1 | Mus musculus cathepsin L (CtSL), mRNA | 0 | 476/481 (98%) | - |
| MIN-79-81 | 501 | g 3986408 gb AF033350.1 AF033350 | Mus musculus CDCREL-1 homolog (Cdcrel-1) mRNA, partial cds | 0 | 488/495 (98%) | 2/495 (0%) |
| MIN-79-51 | 495 | g 10835914 gb AF204176.2 AF204176 | Mus musculus chromosome 10 popeye protein 3 (Pop3), complete cds | 0 | 481/481 (100%) | - |
| MIN-79-49 | 499 | g 5069486 gb AC007049.8 AC007049 | Mus musculus chromosome 1q21-23 clone unknown strain 129X1/SvJ ES cell line RW4, complete sequence | 0.004 | 58/68 (85%) | 1/68 (1%) |
| MIN-79-17 | 500 | g 9790062 ref NM_019649.1 | Mus musculus cleft lip and palate associated transmembrane protein 1 (Clpmt1), mRNA | 0 | 486/486 (100%) | - |
| MIN-79-62 | 500 | g 6753309 ref NM_009829.1 | Mus musculus cyclin D2 (Cncd2), mRNA | 1.00E-149 | 269/269 (100%) | - |
| MIN-79-86 | 475 | g 1150723 gb U41341.1 JMMU41341 | Mus musculus endothelial monocyte-activating polypeptide I mRNA, complete cds | 0 | 330/331 (99%) | 1/331 (0%) |
| MIN-79-52 | 503 | g 7799153 emb AL355706.1 JROEST075 | Mus musculus EST from clone 1969533, extrem' end | 0 | 488/489 (99%) | - |
| MIN-79-84 | 432 | g 7949044 ref NM_016750.1 | Mus musculus H2A histone family, member Z (H2afz), mRNA | 0 | 409/413 (99%) | 1/413 (0%) |
| MIN-79-59 | 447 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-175 | 329/334 (98%) | 1/334 (0%) |
| MIN-79-63 | 457 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-79-78 | 452 | g 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-79-54 | 503 | g 6754339 ref NM_010561.1 | Mus musculus interleukin enhancer binding factor 3 (Ilf3), mRNA | 0 | 491/492 (99%) | - |
| MIN-79-45 | 360 | g 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 346/347 (99%) | 1/347 (0%) |
| MIN-79-87 | 503 | g 4050107 gb AF111102.1 JMMHC21401 | Mus musculus major histocompatibility complex class I region | 0 | 477/492 (96%) | 3/492 (0%) |
| MIN-79-70 | 500 | g 3986763 gb AF109906.1 JMMHC310M6 | Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, a | 3.00E-47 | 144/158 (91%) | 1/158 (0%) |
| MIN-79-43 | 500 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 487/487 (100%) | - |
| MIN-79-56 | 500 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 486/486 (100%) | - |
| MIN-79-75 | 501 | g 9506932 ref NM_019435.1 | Mus musculus neuronal protein 15.6 (NP15.6), mRNA | 0 | 488/488 (100%) | - |
| MIN-79-11 | 502 | g 6679157 ref NM_008749.1 | Mus musculus nucleobindin (Nucb), mRNA | 0 | 463/463 (100%) | - |
| MIN-79-08 | 498 | g 6679438 ref NM_008907.1 | Mus musculus peptidylprolyl isomerase A (Ppia), mRNA | 0 | 486/486 (100%) | - |
| MIN-79-33 | 501 | g 6680689 ref NM_007452.1 | Mus musculus peroxiredoxin 3 (Prdx3), mRNA | 0 | 494/495 (99%) | 1/495 (0%) |
| MIN-79-41 | 500 | g 9790150 ref NM_019840.1 | Mus musculus phosphodiesterase 4B, cAMP specific (Pde4b), mRNA | 1.00E-122 | 223/223 (100%) | - |
| MIN-79-95 | 499 | g 9857943 gb AF273768.1 AF273768 | Mus musculus preproenkephalin Y (Npy) mRNA, complete cds | 0 | 389/393 (98%) | 4/393 (1%) |
| MIN-79-53 | 500 | g 2463667 gb AF007560.1 AF007560 | Mus musculus prenesilin-1 gene, alternatively spliced transcripts, complete cds | 3.00E-07 | 40/43 (93%) | - |
| MIN-79-58 | 499 | g 6679500 ref NM_008947.1 | Mus musculus protease (prosome, macropain) 26S subunit, ATPase 1 (Psmc1), mRNA | 0 | 466/470 (99%) | 1/470 (0%) |
| MIN-79-21 | 470 | g 9256518 ref NM_018853.1 | Mus musculus ribosomal protein, large, P1 (Rplp1), mRNA | 0 | 455/457 (99%) | - |
| MIN-79-18 | 365 | g 7453621 gb AF234171.1 AF234171 | Mus musculus STAT5B (Stat5b) gene, partial cds | 5.00E-05 | 27/27 (100%) | - |
| MIN-79-85 | 498 | g 6680673 ref NM_007434.1 | Mus musculus thymoma viral proto-oncogene 2 (Akt2), mRNA | 0 | 479/484 (98%) | - |
| MIN-79-02 | 502 | g 7305598 ref NM_013697.1 | Mus musculus transthyretin (Ttr), mRNA | 0 | 488/488 (100%) | - |
| MIN-79-83 | 499 | g 7305598 ref NM_013697.1 | Mus musculus transthyretin (Ttr), mRNA | 0 | 481/485 (99%) | - |
| MIN-79-31 | 504 | g 9910591 ref NM_020012.1 | Mus musculus TRIAD2 type I (Triad2), mRNA | 0 | 503/504 (99%) | 1/504 (0%) |
| MIN-79-14 | 500 | g 10946631 ref NM_021324.1 | Mus musculus tweety homolog 1 (Drosophila) (Ttyh1), mRNA | 0 | 484/486 (99%) | 1/486 (0%) |
| MIN-79-91 | 499 | g 1914850 gb U92454.1 JMMU92454 | Mus musculus WW domain binding protein 5 mRNA, partial cds | 0 | 393/393 (100%) | - |
| MIN-79-44 | 500 | g 57670 emb X62528.1 JRRRI | R.rattus mRNA for ribonucleas inhibitor | 1.00E-174 | 379/402 (94%) | - |
| MIN-79-79 | 495 | g 416553 emb X14181.1 JRRRPL18A | Rat mRNA for ribosomal protein L18a | 0 | 462/481 (96%) | - |
| MIN-79-50 | 496 | g 206696 gb J03867.1 JRATCYB5R | Rat NADH-cytochrome b-5 reductase mRNA, complete cds | 0 | 442/468 (94%) | - |
| MIN-79-89 | 501 | g 208077 gb J04943.1 JRATB23A | Rat nucleolar protein B23.2 mRNA, complete cds, clone JH2 | 1.00E-158 | 319/331 (96%) | - |
| MIN-79-46 | 334 | g 206680 gb M24542.1 JRATRIP | Rat Rieske iron-sulfur protein mRNA, complete cds | 2.00E-72 | 210/232 (90%) | 1/232 (0%) |
| MIN-79-34 | 500 | g 6978612 ref NM_012829.1 | Rattus norvegicus Cholecystokinin (Cck), mRNA | 1.00E-165 | 440/487 (90%) | 7/487 (1%) |
| MIN-79-71 | 392 | g 11415013 gb AF239045.1 AF239045 | Rattus norvegicus KIDINS220 (Kidins220) mRNA, complete cds | 3.00E-77 | 195/211 (92%) | - |
| MIN-79-67 | 497 | g 7671717 gb AF200359.1 AF200359 | Rattus norvegicus UDP-glucose glycoylprotein:glucosyltransferase precursor (Ugg2) mRNA, complete cds | 9.00E-66 | 170/181 (93%) | 2/181 (1%) |
| MIN-79-48 | 497 | g 6321173 ref NC_001139.1 | Saccharomyces cerevisiae chromosome VII, complete chromosome sequence | 4 | 19/19 (100%) | - |
| MIN-80-10 | 363 | g 4376750 gb AE001631.1 AE001631 | Chlamydia pneumoniae section 47 of 103 of the complete genome | 0.18 | 21/21 (100%) | - |
| MIN-80-07 | 501 | g 537406 emb X60785.1 JCGTUBB2 | Cricetus griseus (chinese hamster) mRNA for beta tubulin (clone B3T) | 0 | 443/463 (95%) | 3/463 (0%) |
| MIN-80-22 | 156 | g 3201661 gb AF042191.1 AF042191 | Danio rerio paraxial protocadherin mRNA, complete cds | 0.001 | 30/32 (93%) | - |
| MIN-80-87 | 491 | g 546520 gb S71213.1 S71213 | G protein Gi2 alpha [Mice, CBA/J, cochlea, mRNA Partial, 1548 nt] | 0 | 478/478 (100%) | - |
| MIN-80-92 | 331 | g 1032991 emb Z60887.1 JH38A9F | Hsapiens CpG island DNA genomic MseI fragment, clone 38a9, forward read cpg38a9.ft.1a | 0.042 | 22/22 (100%) | - |
| MIN-80-81 | 499 | g 11423446 ref XM_001663.1 | Homo sapiens cDNA CLL/lymphoma 9 (BCL9), mRNA | 1.00E-154 | 436/488 (89%) | 3/488 (0%) |
| MIN-80-47 | 501 | g 10435249 dbj AK023351.1 AK023351 | Homo sapiens cDNA FLJ13289 fis, clone OVARC1001170 | 7.00E-42 | 280/343 (81%) | 1/343 (0%) |
| MIN-80-78 | 500 | g 10438394 dbj AK025776.1 AK025776 | Homo sapiens cDNA: FLJ21223 fis, clone HEP19337, highly similar to AB032251 Homo sapiens BPTF mRNA | 1.00E-158 | 428/476 (89%) | - |
| MIN-80-94 | 248 | g 3108034 gb AC004562.1 AC004562 | Homo sapiens chromosome 17, clone hRPC_34_M_24, complete sequence | 0.081 | 22/22 (100%) | - |
| MIN-80-46 | 502 | g 11024827 gb AC008818.6 AC008818 | Homo sapiens chromosome 5 clone CTD-2124H11, complete sequence | 0.065 | 22/22 (100%) | - |
| MIN-80-70 | 490 | g 9755100 gb AF270558.1 AF270558 | Homo sapiens clone 18ptel_778a_c22t7_b92c23sp5 sequence | 0.016 | 32/35 (91%) | - |
| MIN-80-61 | 412 | g 471244 emb Z29574.1 JHSEBCEMA | Homo sapiens gene for BCMA peptide | 9.00E-04 | 25/25 (100%) | - |
| MIN-80-11 | 484 | g 4454709 gb AF070664.1 AF070664 | Homo sapiens HSPC008 mRNA, complete cds | 0 | 442/470 (94%) | - |
| MIN-80-02 | 502 | g 7106867 gb AF151073.1 AF151073 | Homo sapiens HSPC239 mRNA, complete cds | 3.00E-53 | 276/332 (83%) | - |
| MIN-80-73 | 399 | g 11422526 ref XM_001443.1 | Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITG3BP), mRNA | 1.00E-111 | 59/66 (89%) | - |
| MIN-80-03 | 499 | g 9963838 gb AF225418.1 AF225418 | Homo sapiens lipase mRNA, complete cds | 3.00E-78 | 254/286 (88%) | 2/286 (0%) |
| MIN-80-90 | 501 | g 11424747 ref XM_001832.1 | Homo sapiens quiescin Q6 (QSCN6), mRNA | 6.00E-30 | 105/117 (89%) | - |
| MIN-80-54 | 295 | g 11421885 ref XM_009649.1 | Homo sapiens sodium calcium exchanger (NCKX3), mRNA | 5.00E-20 | 67/72 (93%) | - |
| MIN-80-66 | 500 | g 7657372 ref NM_014399.1 | Homo sapiens tetraspan NET-6 protein (NET-6), mRNA | 8.00E-97 | 286/321 (89%) | - |
| MIN-80-82 | 501 | g 6572184 emb Z83838.2 HS127B20 | Human DNA sequence from clone RP1-127B20 on chromosome 22 Contains the 3' end of the ARHGAP8 g | 2.00E-63 | 209/237 (88%) | - |

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| MIN-80-17 | 490 | gi 10443458 emb AL390068.1 AL390068 | Human DNA sequence from clone RP13-185D13 on chromosome X, complete sequence [Homo sapiens] | 0.001 | 28/29 (96%) | - |
| MIN-80-04 | 212 | gi 7406515 emb AL078605.3 HSJ894D1 | Human DNA sequence from clone RP5-894D12 on chromosome 6q26-27. Contains part of the gene for a r | 0.1 | 21/21 (100%) | - |
| MIN-80-36 | 502 | gi 57965 emb Z19599.1 MME1433IS | M.musculus epsilon 14-3-3 isoform mRNA | 0 | 488/488 (100%) | - |
| MIN-80-69 | 502 | gi 57965 emb Z19599.1 MME1433IS | M.musculus epsilon 14-3-3 isoform mRNA | 0 | 487/487 (100%) | - |
| MIN-80-15 | 499 | gi 468354 gb J01420.1 MUSMTCG | Mouse kinesin heavy chain (Khc) mRNA, 5' end | 0 | 481/485 (99%) | - |
| MIN-80-67 | 501 | gi 4050108 gb AF111103.1 MMHC322F1 | Mouse major histocompatibility complex region containing the Q region of class I | 0 | 435/459 (94%) | 7/459 (1%) |
| MIN-80-06 | 502 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 488/488 (100%) | - |
| MIN-80-32 | 500 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 489/489 (100%) | - |
| MIN-80-38 | 502 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 489/489 (100%) | - |
| MIN-80-41 | 452 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 433/436 (99%) | - |
| MIN-80-42 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-80-63 | 385 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 365/371 (98%) | 1/371 (0%) |
| MIN-80-85 | 500 | gi 2982191 gb U95030.1 MMU95030 | Mus musculus activated leukocyte cell adhesion molecule CD166 (ALCAM) mRNA, complete cds | 0 | 486/487 (99%) | - |
| MIN-80-25 | 498 | gi 6680715 ref NM_007476.1 | Mus musculus ADP-ribosylation factor 1 (Arf1), mRNA | 0 | 484/484 (100%) | - |
| MIN-80-27 | 353 | gi 7949002 ref NM_016774.1 | Mus musculus ATP synthase, H+ transporting mitochondrial F1 complex, alpha subunit (Atp5b), mRNA | 0 | 337/339 (99%) | - |
| MIN-80-34 | 502 | gi 6680749 ref NM_007506.1 | Mus musculus ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1 (A | 0 | 465/467 (99%) | - |
| MIN-80-26 | 500 | gi 9790004 ref NM_019634.1 | Mus musculus cell (LOC56308), mRNA | 0 | 486/486 (100%) | - |
| MIN-80-60 | 353 | gi 6671701 ref NM_007637.1 | Mus musculus chaperonin subunit 5 (epsilon) (Cct5), mRNA | 0 | 338/339 (99%) | - |
| MIN-80-48 | 503 | gi 6680931 ref NM_007693.1 | Mus musculus chromogranin A (Chga), mRNA | 0 | 409/409 (100%) | - |
| MIN-80-89 | 500 | gi 4731666 gb AC005818.6 AC005818 | Mus musculus chromosome 10 clone rp21-411 dr strain 129S6/SvEvTac, complete sequence | 1.00E-09 | 45/47 (95%) | 1/47 (2%) |
| MIN-80-20 | 503 | gi 11527409 gb AC084429.5 AC084429 | Mus Musculus Chromosome 2 Clone RP23-291P1, complete sequence [Mus musculus] | 7.00E-82 | 156/156 (100%) | - |
| MIN-80-75 | 497 | gi 11245588 gb AC006404.2 AC006404 | Mus musculus chromosome 6 clone ct7-141k23 strain 129/Sv ES cell line Cj7, complete sequence | 0.016 | 23/23 (100%) | - |
| MIN-80-52 | 462 | gi 4092493 gb AF067824.1 AF067824 | Mus musculus clone SMT3B-g1/mSMT3 SMT3B pseudogene, complete sequence | 0 | 446/448 (99%) | - |
| MIN-80-18 | 463 | gi 6753485 ref NM_009939.1 | Mus musculus COP9 (constitutive photomorphogenic, subunit 2 (Arabidopsis) (Cops2), mRNA | 0 | 449/449 (100%) | - |
| MIN-80-64 | 288 | gi 9055197 ref NM_018737.1 | Mus musculus CTP synthetase homolog (CTPsh), mRNA | 1.00E-152 | 274/274 (100%) | - |
| MIN-80-40 | 367 | gi 6681152 ref NM_007838.1 | Mus musculus dolichyl-dl-phosphooligosaccharide-protein glycotransferase (Dost), mRNA | 0 | 354/355 (99%) | 1/355 (0%) |
| MIN-80-68 | 501 | gi 9790156 ref NM_019682.1 | Mus musculus dynein, cytoplasmic, light chain 1 (Dncl1), mRNA | 0 | 488/488 (100%) | - |
| MIN-80-79 | 501 | gi 6679686 ref NM_007952.1 | Mus musculus endoplasmic reticulum protein (Erp), mRNA | 0 | 482/487 (98%) | 3/487 (0%) |
| MIN-80-24 | 485 | gi 6857780 ref NM_010121.1 | Mus musculus eukaryotic translation initiation factor 2 alpha kinase 3 (Eif2ak3), mRNA | 0 | 470/471 (99%) | - |
| MIN-80-08 | 499 | gi 10181215 ref NM_020593.1 | Mus musculus F-box protein FBA (Fba), mRNA | 0 | 468/468 (100%) | - |
| MIN-80-56 | 496 | gi 8895494 gb AF216290.1 AF216290 | Mus musculus heterochromatin protein 1 alpha mRNA, complete cds | 0 | 476/482 (98%) | 5/482 (1%) |
| MIN-80-49 | 501 | gi 5833935 gb AF171080.1 AF171080 | Mus musculus histone macroH2A1.2 variant mRNA, complete cds | 0 | 486/487 (99%) | 1/487 (0%) |
| MIN-80-13 | 445 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-80-14 | 443 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-80-31 | 443 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-80-76 | 454 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-80-12 | 502 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 487/492 (98%) | 2/492 (0%) |
| MIN-80-96 | 200 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 5.00E-99 | 190/192 (98%) | - |
| MIN-80-21 | 498 | gi 6678829 ref NM_008566.1 | Mus musculus mini chromosome maintenance deficient 5 (S. cerevisiae) (Mcmd5), mRNA | 0 | 484/485 (99%) | - |
| MIN-80-23 | 500 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 495/495 (100%) | - |
| MIN-80-57 | 503 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 488/490 (99%) | - |
| MIN-80-95 | 502 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 484/488 (99%) | - |
| MIN-80-53 | 501 | gi 6678985 ref NM_008659.1 | Mus musculus myosin Ic (Myo1c), mRNA | 0 | 486/487 (99%) | - |
| MIN-80-39 | 502 | gi 6679139 ref NM_008740.1 | Mus musculus N-ethylmaleimide sensitive fusion protein (Nsf), mRNA | 0 | 387/394 (98%) | 3/394 (0%) |
| MIN-80-19 | 501 | gi 9506932 ref NM_019435.1 | Mus musculus neuronal protein 15.6 (NP15.6), mRNA | 0 | 494/495 (99%) | 1/495 (0%) |
| MIN-80-05 | 452 | gi 6679149 ref NM_008745.1 | Mus musculus neurotrophic tyrosine kinase, receptor, type 2 (Ntrk2), mRNA | 0 | 393/393 (100%) | - |
| MIN-80-55 | 502 | gi 6679228 ref NM_008792.1 | Mus musculus proprotein convertase subtilisin/kexin type 2 (Pcsk2), mRNA | 0 | 488/488 (100%) | - |
| MIN-80-86 | 424 | gi 7110700 ref NM_011874.1 | Mus musculus proteasome (prosome, macropain) 26S subunit, ATPase, 4 (Psmc4), mRNA | 0 | 405/410 (98%) | - |
| MIN-80-30 | 248 | gi 9790060 ref NM_019698.1 | Mus musculus pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase) (Pycs), m | 2.00E-99 | 185/185 (100%) | - |
| MIN-80-62 | 442 | gi 1938405 gb U93864.1 MMU93864 | Mus musculus ribosomal protein S11 mRNA, complete cds | 0 | 428/428 (100%) | - |
| MIN-80-91 | 502 | gi 6755681 ref NM_011499.1 | Mus musculus serine/threonine kinase receptor associated protein (Strap), mRNA | 0 | 486/491 (98%) | 4/491 (0%) |
| MIN-80-09 | 501 | gi 7108527 gb AF127669.1 AF127669 | Mus musculus small GTPase (Rab11a) gene, complete cds | 4.00E-06 | 41/45 (91%) | - |
| MIN-80-83 | 472 | gi 6755697 ref NM_011512.1 | Mus musculus surfactant protein 4 (Surf4), mRNA | 0 | 458/458 (100%) | - |
| MIN-80-72 | 499 | gi 6677890 ref NM_008304.1 | Mus musculus syndecan 2 (Sdc2), mRNA | 0 | 494/494 (100%) | - |
| MIN-80-29 | 500 | gi 2358069 gb AE000663.1 MAE000663 | Mus musculus TCR beta locus from bases 1 to 250611 (section 1 of 3) of the complete sequence | 4.00E-68 | 184/200 (92%) | 2/200 (1%) |
| MIN-80-59 | 437 | gi 6678436 gb ref NM_009429.1 | Mus musculus translationally regulated transcript (21 kDa) (Trt), mRNA | 0 | 422/423 (99%) | - |
| MIN-80-44 | 496 | gi 7305598 ref NM_013697.1 | Mus musculus transthyretin (Tr), mRNA | 0 | 490/490 (100%) | - |
| MIN-80-58 | 502 | gi 9910591 ref NM_020012.1 | Mus musculus TRIAD2 type I (Triad2), mRNA | 0 | 430/435 (98%) | 1/435 (0%) |
| MIN-80-84 | 264 | gi 6755862 ref NM_011631.1 | Mus musculus tumor rejection antigen gp96 (Tra1), mRNA | 1.00E-136 | 249/250 (99%) | - |
| MIN-80-37 | 496 | gi 2088622 gb U96635.1 MMU96635 | Mus musculus ubiquitin protein ligase Nedd4-4 mRNA, complete cds | 0 | 475/482 (98%) | 3/482 (0%) |
| MIN-80-50 | 316 | gi 1066007 dbj D63665.1 JRA1TNGPCP2R | Rat mRNA for novel G protein-coupled P2 receptor, complete cds | 1.00E-36 | 104/112 (92%) | - |
| MIN-80-74 | 442 | gi 57701 emb X51705.1 RRRPL35 | Rat mRNA for ribosomal protein L35 | 1.00E-166 | 372/397 (93%) | - |
| MIN-80-45 | 501 | gi 4104320 gb AF034582.1 AF034582 | Rattus norvegicus vesicle associated protein (VAP1) mRNA, complete cds | 0 | 452/487 (92%) | - |
| MIN-98-01 | 460 | gi 391760 dbj D16847.1 MUSSCP1 | Mouse mRNA for stromal cell derived protein-1, complete cds | 0 | 442/446 (99%) | - |
| MIN-98-02 | 498 | gi 8052319 emb J400878.1 MMU400878 | Mus musculus Asc3 gene, Cegp1 gene, D7H11orf14 gene, D7H11orf15 gene, D7H11orf16 gene and C11or | 2.00E-17 | 54/56 (96%) | - |
| MIN-98-03 | 576 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 556/558 (99%) | - |
| MIN-98-04 | 495 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 363/368 (98%) | - |
| MIN-98-05 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 484/485 (99%) | - |
| MIN-98-06 | 263 | gi 8393279 ref NM_016843.1 | Mus musculus spinocerebellar ataxia 10 homolog (human) (Sca10), mRNA | 8.00E-74 | 155/159 (97%) | 1/159 (0%) |
| MIN-98-07 | 499 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 485/485 (100%) | - |
| MIN-98-08 | 290 | gi 9790282 ref NM_019806.1 | Mus musculus VAMP-associated protein 33b (Vamp33b), mRNA | 1.00E-143 | 274/277 (98%) | 2/277 (0%) |
| MIN-98-09 | 498 | gi 9789912 ref NM_019817.1 | Mus musculus nonclathrin coat protein zeta1-COP (Cops1), mRNA | 0 | 484/484 (100%) | - |
| MIN-98-10 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 392/393 (99%) | - |
| MIN-98-11 | 499 | gi 6486650 emb X71972.2 MMMRPS24 | Mus musculus MRP S24 gene | 0 | 453/455 (99%) | - |
| MIN-98-12 | 269 | gi 243439 gb S76673.1 S76673 | Mus sp. transcriptional factor E3 mRNA, partial cds | 2.00E-96 | 238/256 (92%) | 2/256 (0%) |
| MIN-98-13 | 433 | gi 407465 emb X75312.1 MMRNAQM | M.musculus (C57BL/6) QM mRNA | 0 | 419/419 (100%) | - |
| MIN-98-14 | 475 | gi 508525 gb L31642.1 MUSCAMC | Mus musculus calmodulin (CamC) mRNA, 5' end | 0 | 439/446 (98%) | 2/446 (0%) |
| MIN-98-15 | 388 | gi 7106276 ref NM_008975.1 | Mus musculus casein kinase II, beta subunit (Csk2b), mRNA | 0 | 372/375 (99%) | - |
| MIN-98-16 | 498 | gi 6677866 ref NM_009130.1 | Mus musculus secretogranin III (Scg3), mRNA | 0 | 486/486 (100%) | - |
| MIN-98-17 | 169 | gi 6650998 gb AF125313.1 AF125313 | Mus musculus X chromosome: Cg1/Xap80 gene, complete sequence | 8.00E-005 | 29/30 (96%) | - |
| MIN-98-18 | 463 | gi 7188778 gb AF233282.1 AF233282 | Mus musculus calmodulin III (Calm3) mRNA, 3' untranslated region | 0 | 442/449 (98%) | - |
| MIN-98-19 | 497 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 481/483 (99%) | - |
| MIN-98-20 | 354 | gi 1030073 gb M69293.1 MUSID2A | Mouse Id2 protein (Id-2) mRNA, 3' end | 1.00E-162 | 303/306 (99%) | 1/306 (0%) |
| MIN-98-21 | 142 | gi 430732 gb L26349.1 MUSTNFX | Mus musculus Tumor Necrosis Factor Receptor 55 KD (TNF 55) mRNA, complete cds | 6.00E-64 | 128/129 (99%) | - |
| MIN-98-22 | 231 | gi 1197524 gb U44437.1 MXU44437 | Myxococcus xanthus photolyase (phrA) gene, complete cds | 1.7 | 22/23 (95%) | - |
| MIN-98-23 | 500 | gi 6679458 ref NM_008921.1 | Mus musculus DNA primase, p49 subunit (Prim1), mRNA | 3.00E-44 | 93/93 (100%) | - |
| MIN-98-24 | 507 | gi 193445 gb M55413.1 MUSGCG | Mus musculus vitamin D-binding protein (GC) mRNA, partial cds | 0 | 462/463 (99%) | 1/463 (0%) |
| MIN-98-25 | 492 | gi 11140823 ref NM_021790.1 | Mus musculus SoxL/Sox6 leucine zipper binding protein in testis (Soltz-pending), mRNA | 1.00E-52 | 107/107 (100%) | - |
| MIN-98-26 | 502 | gi 10834957 gb AC021063.15 AC021063 | Mus musculus chromosome 18 clone RP23-179K16 strain C57BL6/J, complete sequence | 1.00E-113 | 263/281 (93%) | - |
| MIN-98-27 | 499 | gi 7949102 ref NM_016739.1 | Mus musculus GPI-anchored membrane protein 1 (Gpia-pending), mRNA | 0 | 486/486 (100%) | - |
| MIN-98-28 | 471 | gi 6679986 ref NM_008112.1 | Mus musculus guanosine diphosphate (GDP) dissociation inhibitor 3 (Gdi3), mRNA | 0 | 360/362 (99%) | - |
| MIN-98-29 | 502 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 488/488 (100%) | - |
| MIN-98-30 | 513 | gi 6679582 ref NM_008997.1 | Mus musculus RAB11b, member RAS oncogene family (Rab11b), mRNA | 0 | 505/509 (99%) | 1/509 (0%) |
| MIN-98-31 | 470 | gi 7619720 emb AL021127.2 MMCMX137 | Mus musculus chromosome X contigA: putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase a | 0.061 | 22/22 (100%) | - |
| MIN-98-32 | 420 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 379/386 (98%) | - |
| MIN-98-33 | 390 | gi 4050108 gb AF111103.1 MMHC322F1 | Mouse major histocompatibility complex region containing the Q region of class I | 2.00E-13 | 50/53 (94%) | - |
| MIN-98-34 | 369 | gi 6753641 ref NM_010052.1 | Mus musculus delta-like homolog (Drosophila) (Dlk1), mRNA | 1.00E-155 | 284/287 (99%) | - |
| MIN-99-01 | 497 | gi 1122421 emb X90875.1 MMFXR1PRT | M.musculus mRNA for FXR1 protein | 0 | 483/483 (100%) | - |
| MIN-99-02 | 476 | gi 1403377 emb Z47784.1 MMBTC3X58 | M.musculus mRNA expressed in islet cells (clone 58) | 4.00E-09 | 43/47 (91%) | - |
| MIN-99-03 | 499 | gi 6756038 ref NM_011739.1 | Mus musculus tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein, theta polypep | 0 | 486/486 (100%) | - |
| MIN-99-04 | 492 | gi 7305598 ref NM_013697.1 | Mus musculus transthyretin (Tr), mRNA | 0 | 466/478 (97%) | - |

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|------------|-----|--------------------------------------|--|-----------|----------------------------|------------|
| MIN-99-05 | 501 | gi 57965 emb Z19599.1 JMM14331S | M.musculus epsilon 14-3-3 isoform mRNA | 0 | 473/473 (100%) | - |
| MIN-99-06 | 497 | gi 6755762 ref NM_011568.1 | Mus musculus Tora enhancer-binding factor interacting protein 1 (Tebip-pending), mRNA | 0 | 473/483 (97%) | 1/483 (0%) |
| MIN-99-07 | 499 | gi 6753971 ref NM_010276.1 | Mus musculus GTP binding protein (gene overexpressed in skeletal muscle) (Gem), mRNA | 0 | 482/486 (99%) | 4/486 (0%) |
| MIN-99-08 | 498 | gi 6679686 ref NM_007952.1 | Mus musculus endoplasmic reticulum protein (Erp), mRNA | 0 | 479/484 (98%) | 3/484 (0%) |
| MIN-99-09 | 500 | gi 9885845 gb AF296832.1 T1M15 | Arabidopsis thaliana BAC T1M15 | 0.9 | 23/24 (95%) | - |
| MIN-99-10 | 389 | gi 6598745 gb AC007268.4 AC007268 | Arabidopsis thaliana chromosome II section 67 of 255 of the complete sequence. Sequence from clones T2 | 0.18 | 21/21 (100%) | - |
| MIN-99-11 | 502 | gi 6553965 gb AC011013.1 AC011013 | Mus musculus chromosome 11, clone RP23-218N2, complete sequence | 2.00E-07 | 31/31 (100%) | - |
| MIN-99-12 | 499 | gi 6679614 ref NM_009015.1 | Mus musculus RAD54 like (S. cerevisiae) (Rad54), mRNA | 0 | 392/397 (98%) | 2/397 (0%) |
| MIN-99-13 | 499 | gi 6677806 ref NM_009095.1 | Mus musculus ribosomal protein S5 (Rps5), mRNA | 0 | 484/485 (99%) | 1/485 (0%) |
| MIN-99-14 | 505 | gi 9506418 ref NM_019517.1 | Mus musculus beta-site APP-cleaving enzyme 2 (Bace2), mRNA | 0 | 487/493 (98%) | - |
| MIN-99-15 | 220 | gi 6653208 gb AF181560.1 AF181560 | Mus musculus proSAA gene, complete cds | 4.00E-84 | 193/204 (94%) | 1/204 (0%) |
| MIN-99-16 | 379 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 346/349 (99%) | - |
| MIN-99-17 | 424 | gi 3860028 gb AF090334.1 AF090334 | Mus musculus FK506 binding protein (Fkbp63) mRNA, complete cds | 0 | 407/410 (99%) | - |
| MIN-99-18 | 513 | gi 4322418 gb AF084548.1 AF084548 | Mus musculus vasodilator-stimulated phosphoprotein (Vasp) mRNA, complete cds | 0 | 499/499 (100%) | - |
| MIN-99-19 | 540 | gi 9790056 ref NM_019793.1 | Mus musculus tetraspanin TM4-A homolog (LOC56434), mRNA | 0 | 420/421 (99%) | - |
| MIN-99-20 | 260 | gi 2944418 gb AF09850.1 JMMH438N1 | Mus musculus major histocompatibility locus class III region: complement C4 (C4) and cytochrome P450 hvg | 2.00E-61 | 140/147 (95%) | 1/147 (0%) |
| MIN-99-21 | 484 | gi 3551181 dbj AB012265.1 AB012265 | Mus musculus mRNA for wizL, complete cds | 0 | 468/470 (99%) | - |
| MIN-99-22 | 513 | gi 9937096 gb AF127033.1 AF127033 | Mus musculus fatty acid synthase mRNA, complete cds | 0 | 499/499 (100%) | - |
| MIN-99-23 | 209 | gi 8347621 gb AF250927.1 AF250927 | Mus musculus PNGase mRNA, complete cds | 1.00E-62 | 164/178 (92%) | - |
| MIN-99-24 | 387 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 363/373 (97%) | 1/373 (0%) |
| MIN-99-25 | 496 | gi 6755353 ref NM_011290.1 | Mus musculus ribosomal protein L6 (Rpl6), mRNA | 0 | 469/471 (99%) | - |
| MIN-99-26 | 284 | gi 6755353 ref NM_011290.1 | Mus musculus ribosomal protein L6 (Rpl6), mRNA | 5.00E-163 | 270/271 (99%) | 1/271 (0%) |
| MIN-99-27 | 476 | gi 6681152 ref NM_007838.1 | Mus musculus dolichyl-di-phosphooligosaccharide-protein glycotransferase (Ddost), mRNA | 1.00E-138 | 260/262 (99%) | 1/262 (0%) |
| MIN-99-28 | 430 | gi 4322418 gb AF084548.1 AF084548 | Mus musculus vasodilator-stimulated phosphoprotein (Vasp) mRNA, complete cds | 0 | 412/416 (99%) | - |
| MIN-99-29 | 451 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 433/437 (99%) | 1/437 (0%) |
| MIN-99-30 | 502 | gi 10946731 ref NM_021388.1 | Mus musculus exotoxins (multiple)-like 2 (Ext2), mRNA | 0 | 488/488 (100%) | - |
| MIN-99-31 | 473 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 456/459 (99%) | 2/459 (0%) |
| MIN-99-32 | 240 | gi 3252661 gb AF141294.1 AF141294 | Mus musculus bamacan (Bam) mRNA, complete cds | 1.00E-132 | 239/239 (100%) | - |
| MIN-99-33 | 315 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-142 | 256/256 (100%) | - |
| MIN-99-34 | 510 | gi 6753447 ref NM_009096.1 | Mus musculus ceroid-lipofuscinosis, neuronal 2 (Cln2), mRNA | 0 | 496/496 (100%) | - |
| MIN-99-35 | 84 | gi 2811283 gb AF043285.1 AF043285 | Mus musculus ribosomal protein S7 (rpS7) gene, complete cds | 2.00E-31 | 70/70 (100%) | - |
| MIN-99-36 | 490 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 472/478 (98%) | 3/478 (0%) |
| MIN-99-37 | 373 | gi 7670449 dbj AB041593.1 AB041593 | Mus musculus brain cDNA, clone MNCb-2778, similar to Homo sapiens anaphase-promoting complex subu | 0 | 353/355 (99%) | 1/355 (0%) |
| MIN-99-38 | 424 | gi 6753361 ref NM_009806.1 | Mus musculus cell division cycle 25 homolog C (S. cerevisiae) (Cdc25c), mRNA | 1.00E-141 | 256/256 (100%) | - |
| MIN-99-39 | 490 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 416/416 (100%) | - |
| MIN-99-40 | 220 | gi 4038734 dbj AB021289.1 AB021289 | Mus musculus mRNA for epididymal secretory protein, complete cds | 1.00E-111 | 205/205 (100%) | - |
| MIN-99-41 | 409 | gi 8393783 ref NM_017380.1 | Mus musculus MLL septin-like fusion (Msf), mRNA | 1.00E-164 | 306/309 (99%) | 1/309 (0%) |
| MIN-99-42 | 86 | gi 9910175 ref NM_020027.1 | Mus musculus DNA segment, Chr 17, human D6S51E (D17H6S51E), mRNA | 1.00E-26 | 65/66 (98%) | - |
| MIN-99-43 | 259 | gi 9055261 ref NM_018811.1 | Mus musculus alpha/beta hydrolase fold phosphoprotein (LOC56408), mRNA | 1.00E-129 | 234/234 (100%) | - |
| MIN-99-44 | 156 | gi 8546861 emb AJ278429.1 JMMU278429 | Mus musculus partial Prkar1a gene for cAMP-dependent protein kinase regulatory subunit R1alpha, exons 5 | 4.00E-74 | 142/142 (100%) | - |
| MIN-99-45 | 484 | gi 4588501 gb AF108835.1 AF108835 | Lama glama von Willebrand factor (vWF) gene, exon 28 and partial cds | 0.001 | 25/25 (100%) | - |
| MIN-99-46 | 500 | gi 9910125 ref NM_019982.1 | Mus musculus acupuncture induced gene 1 (AIG1), mRNA | 0 | 428/428 (100%) | - |
| MIN-99-47 | 282 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-127 | 232/232 (100%) | - |
| MIN-99-48 | 497 | gi 8052319 emb AJ403878.1 JMMU403878 | Mus musculus Ascl3 gene, Ccgp1 gene, D7H11orf14 gene, D7H11orf15 gene, D7H11orf16 gene and C11orf | 0.004 | 36/40 (90%) | - |
| MIN-99-49 | 472 | gi 8546861 emb AJ278429.1 JMMU278429 | Mus musculus partial Prkar1a gene for cAMP-dependent protein kinase regulatory subunit R1alpha, exons 5 | 0 | 455/458 (99%) | 1/458 (0%) |
| MIN-99-50 | 427 | gi 6679936 ref NM_008084.1 | Mus musculus glyceraldehyde-3-phosphate dehydrogenase (Gapd), mRNA | 0 | 415/415 (100%) | - |
| MIN-99-51 | 444 | gi 9790062 ref NM_019649.1 | Mus musculus thymic epithelial cell surface antigen (LOC56457), mRNA | 0 | 431/431 (100%) | - |
| MIN-99-52 | 328 | gi 6677866 ref NM_009130.1 | Mus musculus secretogranin III (Scg3), mRNA | 1.00E-176 | 314/314 (100%) | - |
| MIN-99-53 | 183 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 1.00E-93 | 182/183 (99%) | 1/183 (0%) |
| MIN-99-54 | 178 | gi 10181131 ref NM_020569.1 | Mus musculus DJ-1 protein (DJ-1), mRNA | 2.00E-82 | 163/164 (99%) | 1/164 (0%) |
| MIN-99-55 | 284 | gi 6862977 gb AC009287.1 AC009287 | Mus musculus chromosome 10 clone rp21-668b24 strain 12956/SvEvTac, complete sequence | 6.00E-44 | 101/104 (97%) | - |
| MIN-99-56 | 527 | gi 1546824 gb U68542.1 JMMU68542 | Mus musculus mCASP (cux) mRNA, complete cds | 0 | 490/490 (100%) | - |
| MIN-99-57 | 275 | gi 9256518 ref NM_018853.1 | Mus musculus acidic ribosomal phosphoprotein P1 (Arpp1), mRNA | 1.00E-145 | 261/261 (100%) | - |
| MIN-99-58 | 298 | gi 6708456 gb AF213396.1 AF213396 | Ovis aries fibroblast growth factor 10 (FGF-10) mRNA, complete cds | 0.54 | 20/20 (100%) | - |
| MIN-99-59 | 322 | gi 9957624 gb AF182068.1 AF182068 | Mus musculus secretory protein BV8 (Bv8) gene, exons 3 and 4 and complete cds | 0.15 | 21/21 (100%) | - |
| MIN-99-60 | 253 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-132 | 240/240 (100%) | - |
| MIN-99-61 | 87 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 1.00E-41 | 87/87 (100%) | - |
| MIN-99-62 | 335 | gi 8574073 emb AJ251835.1 JMMU251835 | Mus musculus Kcng1, Ltrpc5, Mash2, Tapa-1, Tssc4 and Tssc6 genes, alternative transcripts | 0.01 | 32/35 (91%) | - |
| MIN-99-63 | 205 | gi 7106386 ref NM_011967.1 | Mus musculus proteasome (prosome, macropain) subunit, alpha type 5 (Pasma5), mRNA | 1.00E-101 | 190/191 (99%) | - |
| MIN-99-64 | 507 | gi 6680931 ref NM_007693.1 | Mus musculus chromogranin A (Chga), mRNA | 0 | 400/400 (100%) | - |
| MIN-99-65 | 481 | gi 8394026 ref NM_016891.1 | Mus musculus serine/threonine protein phosphatase A subunit type 2A (Ppp2r1a), mRNA | 0 | 466/467 (99%) | 1/467 (0%) |
| MIN-99-66 | 494 | gi 1914850 gb U92454.1 JMMU92454 | Mus musculus WW domain binding protein 5 (Wwbp), partial cds | 0 | 333/333 (100%) | - |
| MIN-99-67 | 505 | gi 1378121 gb U58361.1 JMSU58361 | Manduca sexta serpin 1 gene, exons 1-10, including alternative exons 9A-Z, complete cds | 0.06 | 22/22 (100%) | - |
| MIN-99-68 | 315 | gi 6503218 gb AF163772.2 AF163772 | Leishmania major chromosome 5 clone LT138 strain Friedlin, complete sequence | 0.57 | 23/24 (95%) | - |
| MIN-99-69 | 362 | gi 7242176 ref NM_011109.1 | Mus musculus phospholipase A2, group IID (Pla2g2d), mRNA | 1.00E-171 | 305/305 (100%) | - |
| MIN-99-70 | 157 | gi 6754309 ref NM_010514.1 | Mus musculus insulin-like growth factor 2 (Igf2), mRNA | 6.00E-70 | 142/143 (99%) | 1/143 (0%) |
| MIN-99-71 | 157 | gi 255999 gb S45812.1 S45812 | monoamine oxidase A [rats, liver, mRNA Partial, 2104 nt] | 5.00E-58 | 129/134 (96%) | - |
| MIN-99-72 | 166 | gi 6755353 ref NM_011290.1 | Mus musculus ribosomal protein L6 (Rpl6), mRNA | 1.00E-71 | 147/151 (97%) | - |
| MIN-99-73 | 390 | gi 6755135 ref NM_011889.1 | Mus musculus thyroid hormone receptor-associated protein 100 kDa (Trap100-pending), mRNA | 0 | 372/376 (98%) | - |
| MIN-99-74 | 396 | gi 6671671 ref NM_007604.1 | Mus musculus capping protein alpha 2 (Cappa2), mRNA | 0 | 380/382 (99%) | - |
| MIN-99-75 | 325 | gi 342520 gb J01420.1 JUSMTCG | Mouse mitochondrion, complete genome | 0 | 323/323 (100%) | - |
| MIN-99-76 | 294 | gi 6755962 ref NM_011694.1 | Mus musculus voltage-dependent anion channel 1 (Vdac1), mRNA | 1.00E-152 | 281/282 (99%) | 1/282 (0%) |
| MIN-99-77 | 506 | gi 6755900 ref NM_011653.1 | Mus musculus tubulin alpha 1 (Tuba1), mRNA | 0 | 478/482 (99%) | - |
| MIN-99-78 | 345 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 1.00E-159 | 286/286 (100%) | - |
| MIN-99-79 | 363 | gi 9256518 ref NM_018853.1 | Mus musculus acidic ribosomal phosphoprotein P1 (Arpp1), mRNA | 0 | 349/349 (100%) | - |
| MIN-99-80 | 142 | gi 6753913 ref NM_010240.1 | Mus musculus ferritin light chain 1 (Fh1), mRNA | 3.00E-68 | 141/143 (98%) | 1/143 (0%) |
| MIN-99-81 | 142 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 3.00E-44 | 95/96 (98%) | - |
| MIN-99-82 | 502 | gi 6679706 ref NM_007964.1 | Mus musculus ecotropic viral integration site 5 (Evis5), mRNA | 1.00E-09 | 71/83 (85%) | - |
| MIN-99-83 | 208 | gi 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 3.00E-94 | 189/194 (97%) | - |
| MIN-99-84 | 157 | gi 6754309 ref NM_010514.1 | Mus musculus insulin-like growth factor 2 (Igf2), mRNA | 4.00E-68 | 141/143 (98%) | 1/143 (0%) |
| MIN-99-85 | 444 | gi 9910457 ref NM_020003.1 | Mus musculus kidney predominant protein NCU-G1 (NCU-G1), mRNA | 0 | 429/430 (99%) | - |
| MIN-99-86 | 388 | gi 7299062 gb AE003680.1 AE003680 | Drosophila melanogaster genomic scaffold 142000013386035 section 5 of 105, complete sequence | 0.046 | 22/22 (100%) | - |
| MIN-99-87 | 170 | gi 6753379 ref NM_009870.1 | Mus musculus cyclin-dependent kinase 4 (Cdk4), mRNA | 1.00E-80 | 155/156 (99%) | - |
| MIN-99-88 | 288 | gi 9502281 gb AF287271.1 AF287271 | Mus musculus ribosomal protein L23 (Rpl23) mRNA, complete cds | 1.00E-153 | 275/275 (100%) | - |
| MIN-99-89 | 401 | gi 7948998 ref NM_016764.1 | Mus musculus peroxiredoxin 4 (Prdx4), mRNA | 4.00E-153 | 275/275 (100%) | - |
| MIN-99-90 | 256 | gi 8809807 gb AF242377.1 AF242377 | Mus musculus KRAB zinc finger protein (Mzf22) mRNA, complete cds | 5.00E-75 | 159/164 (96%) | - |
| MIN-99-91 | 429 | gi 7949044 ref NM_016750.1 | Mus musculus H2A histone family, member Z (H2afz), mRNA | 0 | 415/415 (100%) | - |
| MIN-99-92 | 98 | gi 4521187 dbj AB006360.1 JMSU6360 | Mus musculus DNA for MUSPUR, partial cds | 4.00E-33 | 81/84 (96%) | - |
| MIN-99-93 | 182 | gi 52714 emb X04724.1 JMMINSIG | Mouse preproinsulin gene I | 3.00E-72 | 139/139 (100%) | - |
| MIN-99-94 | 132 | gi 9790280 ref NM_019729.1 | Mus musculus putative deubiquitinating enzyme (Ubp), mRNA | 7.00E-54 | 117/120 (97%) | - |
| MIN-99-95 | 84 | gi 6754501 ref NM_010685.1 | Mus musculus lysosomal membrane glycoprotein 2 (Lamp2), mRNA | 2.00E-25 | 67/70 (95%) | - |
| MIN-100-01 | 499 | gi 7012905 gb AF224669.1 AF224669 | Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (U | 0.77 | 20/20 (100%), Positives = | - |
| MIN-100-02 | 498 | gi 193540 gb M76437.1 JUSGLUR5A | Mouse glutamate-gated ion channel gene, exon Tm2 | 0 | 421/431 (97%), Positives = | 1/431 (0%) |
| MIN-100-04 | 502 | gi 55756 emb X06942.1 JRNARAF | Rat A-raf mRNA | 0 | 396/410 (96%), Positives = | - |
| MIN-100-05 | 502 | gi 6677866 | Mus musculus secretogranin III (Scg3), mRNA | 0 | 488/488 (100%), Positive = | - |
| MIN-100-06 | 498 | gi 6694224 gb AF184245.1 AF184245 | Danio rerio ribonucleoprotein (hug) mRNA, complete cds | 0.049 | 28/30 (93%), Positives = | - |
| MIN-100-07 | 497 | gi 6006528 emb AL049713.19 HSDJ247C | Human DNA sequence from clone 247C2 on chromosome 11p13, complete sequence [Homo sapiens] | 1.00E-48 | 148/164 (90%), Positives = | - |
| MIN-100-08 | 502 | gi 1495998 emb X99807.1 JMSSELP | M.musculus mRNA for selenosprotein P | 0 | 445/445 (100%), Positive = | - |
| MIN-100-09 | 498 | gi 7630118 emb AL049866.2 MM437P9 | Mus musculus chromosome X contigB: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc | 1.00E-129 | 236/236 (100%), Positive = | - |
| MIN-100-10 | 462 | gi 6680462 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%), Positive = | - |
| MIN-100-12 | 440 | gi 6680462 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%), Positive = | - |

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|------------|-----|-------------------------------------|---|-----------|----------------------------|-------------|
| MIN-100-13 | 501 | gi 4996920 gb AC007461.8 AC007461 | Homo sapiens chromosome 17, clone 84_E_24, complete sequence | 0.2 | 21/21 (100%), Positives = | - |
| MIN-100-14 | 500 | gi 1699358 gb S82464.1 S82464 | vacuolar H(+)-ATPase subunit=13.7 kDa F-ATPases subunit b homolog [cattle, adrenal medulla, chromaffin cells] | 1.00E-135 | 329/357 (92%), Positives = | - |
| MIN-100-15 | 502 | gi 2555188 gb AF027865.1 MMMMH461 | Mus musculus Major Histocompatibility Locus class II region | 0.003 | 27/28 (96%), Positives = | - |
| MIN-100-16 | 489 | gi 160555 emb AJ223293.1 MJMAJ3293 | Mus musculus mRNA for kinesin-related mitotic motor protein | 0 | 474/475 (99%), Positives = | - |
| MIN-100-17 | 500 | gi 6754271 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 483/488 (98%), Positives = | 2/488 (0%) |
| MIN-100-18 | 501 | gi 3483727 gb AF086382.1 HUMZD7000 | Homo sapiens full length insert cDNA clone ZD7000 | 0.2 | 21/21 (100%), Positives = | - |
| MIN-100-19 | 499 | gi 10440658 gb AC022173.7 AC022173 | Homo sapiens chromosome 7 clone RP11-299B3, complete sequence | 2.00E-17 | 72/80 (90%) | - |
| MIN-100-20 | 502 | gi 9690323 gb AC020974.4 AC020974 | Mus musculus chromosome 18 clone RP23-92D17, complete sequence | 0.004 | 24/24 (100%) | - |
| MIN-100-21 | 502 | gi 563737 gb U11812.1 MMU11812 | Mus musculus putative protein tyrosin phosphatase mRNA, complete cds | 0 | 488/488 (100%) | - |
| MIN-100-22 | 368 | gi 6680992 ref NM_007750.1 | Mus musculus cytochrome c oxidase, subunit VIII (Cox8a), mRNA | 1.00E-171 | 312/313 (99%) | 1/313 (0%) |
| MIN-100-23 | 499 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 444/445 (99%) | 1/445 (0%) |
| MIN-100-24 | 431 | gi 10946651 ref NM_021338.1 | Mus musculus ribosomal protein L35a (Rpl35), mRNA | 0 | 395/406 (97%) | 1/406 (0%) |
| MIN-100-25 | 500 | gi 164055 gb M35520.1 DOGRAB5A | C.familiaris GTP-binding protein (rab5) mRNA, complete cds | 1.00E-113 | 250/264 (94%) | - |
| MIN-100-26 | 496 | gi 6680909 ref NM_007671.1 | Mus musculus cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (Cdkn2c), mRNA | 0 | 448/450 (99%) | 2/450 (0%) |
| MIN-100-27 | 493 | gi 6679438 ref NM_008907.1 | Mus musculus peptidylprolyl isomerase A (Ppia), mRNA | 0 | 479/479 (100%) | - |
| MIN-100-28 | 502 | gi 4884333 emb AL050125.1 HSM800425 | Homo sapiens mRNA: cDNA DKFZ588F071 (from clone DKFZp588F071) | 1.00E-18 | 70/76 (92%) | 3/76 (3%) |
| MIN-100-29 | 448 | gi 52852 emb X06406.1 MML40KD | Mouse mRNA for translational controlled 40 kDa polypeptide p40 | 0 | 423/432 (97%), Positives = | - |
| MIN-100-30 | 496 | gi 7804453 dbj AB042523.1 AB042523 | Mus musculus mitochondrial DNA, complete genome, strain:SAMR1 | 0 | 476/483 (98%), Positives = | - |
| MIN-100-31 | 501 | gi 7684609 dbj AF146793.2 AF146793 | Mus musculus neurexin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, partial cds | 0 | 478/487 (98%), Positives = | - |
| MIN-100-32 | 499 | gi 11119454 gb AC011475.6 AC011475 | Homo sapiens chromosome 19 clone CTC-539A10, complete sequence | 3.00E-44 | 111/117 (94%) | - |
| MIN-100-33 | 500 | gi 49911 emb X03351.1 MMLALBR | Mouse mRNA for prealbumin | 0 | 486/486 (100%), Positive = | - |
| MIN-100-34 | 500 | gi 6754271 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 482/487 (98%), Positives = | 2/487 (0%) |
| MIN-100-35 | 500 | gi 1526544 dbj D87663.1 D87663 | Mus musculus mRNA for 14-3-3 epsilon, complete cds | 0 | 368/371 (99%), Positives = | - |
| MIN-100-36 | 499 | gi 6678436 | Mus musculus translationally regulated transcript (21 kDa) (Trt), mRNA | 0 | 485/485 (100%), Positive = | - |
| MIN-100-37 | 442 | gi 6680462 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%), Positive = | - |
| MIN-100-38 | 501 | gi 201905 gb M94080.1 MUSTCRVAD | Mouse T-cell receptor (TCR V-alpha 16.1) gene exons 1-2, (TCR V-delta 3/V-alpha 6) gene exons 1-2, alpha chain | 8.00E-07 | 45/50 (90%), Positives = | - |
| MIN-100-39 | 499 | gi 6677680 ref NM_009030.1 | Mus musculus retinoblastoma binding protein 4 (Rbpb4), mRNA | 0 | 485/485 (100%) | - |
| MIN-100-40 | 501 | gi 6680571 | Mus musculus kinesin family member 5B (Kif5b), mRNA | 0 | 487/487 (100%), Positive = | - |
| MIN-100-41 | 499 | gi 559716 dbj D38555.1 HUMORF008 | Human mRNA for KIAA0079 gene, complete cds | 2.00E-53 | 174/194 (89%), Positives = | 4/194 (2%) |
| MIN-100-42 | 499 | gi 685220 dbj D26483.1 MUSTALLA | Mouse mRNA for PEB3/TALLA, complete cds | 0 | 485/485 (100%), Positive = | - |
| MIN-100-43 | 500 | gi 6272684 gb AF181897.1 HSWRNG2 | Homo sapiens WRN (WRN) gene, complete cds | 0.2 | 24/25 (96%), Positives = | - |
| MIN-100-45 | 501 | gi 7804453 dbj AB042523.1 AB042523 | Mus musculus mitochondrial DNA, complete genome, strain:SAMR1 | 0 | 481/488 (98%), Positives = | - |
| MIN-100-46 | 501 | gi 1098540 gb U23921.1 MMU23921 | Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds | 1.00E-24 | 60/60 (100%), Positives = | - |
| MIN-100-47 | 500 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 482/485 (99%) | - |
| MIN-100-48 | 501 | gi 11428081 ref NM_002138.1 | Homo sapiens membrane protein CH1 (CH1), mRNA | 0.004 | 42/48 (87%) | - |
| MIN-100-50 | 433 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-100-51 | 499 | gi 2133879 gb AC00399.1 AC00399 | Genomic sequence from Mouse 9, complete sequence [Mus musculus] | 0 | 484/486 (99%) | 1/486 (0%) |
| MIN-100-52 | 494 | gi 6754271 ref NM_010491.1 | Mus musculus islet amyloid polypeptide (Iapp), mRNA | 0 | 437/437 (100%) | - |
| MIN-100-53 | 497 | gi 5306305 gb AC005006.2 AC005006 | Homo sapiens clone RP1-56J10, complete sequence | 0.065 | 22/22 (100%) | - |
| MIN-100-54 | 502 | gi 4868392 gb AF129888.1 AF129888 | Mus musculus Su11 homolog mRNA, complete cds | 0 | 486/490 (99%) | - |
| MIN-100-55 | 501 | gi 99558089 gb AC009192.7 AC009192 | Mus musculus chromosome 6 clone ct7-555d9 strain 129/SV ES cell line CJ7, complete sequence | 1.00E-37 | 118/130 (90%) | - |
| MIN-100-56 | 498 | gi 10179918 gb AF283103.1 AF283103 | Pineapple mealybug wilt associated virus-2 polyprotein (ORF1a) and RNA-dependent RNA polymerase genes | 0.26 | 21/21 (100%) | - |
| MIN-100-57 | 499 | gi 4468857 emb AJ023913.5 HS1068F16 | Human DNA sequence from clone 1068F16 on chromosome 2Qp12 Contains gene for SNAP-25(SYNAPTOBREVIN 2) | 3.00E-56 | 129/133 (96%) | 1/133 (0%) |
| MIN-100-58 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%) | - |
| MIN-100-59 | 390 | gi 10437538 dbj AK025092.1 AK025092 | Homo sapiens cDNA: FLJ21439 fis, clone COL04352 | 8.00E-78 | 251/285 (88%) | - |
| MIN-100-60 | 498 | gi 11417258 ref NM_004008.1 | Homo sapiens KIAA0171 gene product (KIAA0171), mRNA | 1.00E-156 | 433/484 (89%) | - |
| MIN-100-61 | 499 | gi 7595832 gb AF240003.1 AF240003 | Mus musculus adenine nucleotide translocase 2 (ANT2) gene, complete cds; nuclear gene for mitochondrial DNA | 2.00E-05 | 31/32 (96%) | - |
| MIN-100-62 | 499 | gi 9256631 ref NM_018878.1 | Mus musculus Pax transcription activation domain interacting protein (PTIP), mRNA | 0 | 474/479 (98%) | - |
| MIN-100-63 | 400 | gi 3947813 emb Z98747.1 HS37J18 | Human DNA sequence from clone 37J18 on chromosome 1p36.2-36.3. Contains a putative novel gene, EST | 8.00E-04 | 25/25 (100%) | - |
| MIN-100-64 | 501 | gi 8393928 ref NM_017229.1 | Rattus norvegicus phosphodiesterase 3B, cGMP-inhibited (Pde3b), mRNA | 3.00E-38 | 132/146 (90%) | 2/146 (1%) |
| MIN-100-66 | 499 | gi 6755848 ref NM_011623.1 | Mus musculus topoisomerase (DNA) II alpha (Top2a), mRNA | 0 | 484/484 (100%) | - |
| MIN-100-67 | 499 | gi 11527409 gb AC084429.5 AC084429 | Mus Musculus Chromosome 2 Clone RP23-291 P1, complete sequence [Mus musculus] | 5.00E-86 | 163/163 (100%) | - |
| MIN-100-69 | 466 | gi 7268064 emb AL161537.2 ATCHRIV37 | Arabidopsis thaliana DNA chromosome 4, contig fragment No. 37 | 0.06 | 22/22 (100%) | - |
| MIN-100-72 | 500 | gi 7020824 dbj AK000613.1 AK000613 | Homo sapiens cDNA FLJ20606 fis, clone KAT06232, highly similar to AF132943 Homo sapiens CGI-09 protein | 5.00E-95 | 340/394 (86%) | - |
| MIN-100-73 | 502 | gi 6681208 ref NM_007872.1 | Mus musculus DNA methyltransferase 3A (Dnmt3a), mRNA | 0 | 488/488 (100%) | - |
| MIN-100-74 | 499 | gi 3355875 emb AL023284.1 HS406A7 | Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to the human DNA sequence from clone RP1-159G19 on chromosome 6q14.1-14.3 Contains an STS and GSSs, c | 0.065 | 25/26 (96%) | - |
| MIN-100-75 | 500 | gi 6002338 emb AL078462.9 HSJ159G19 | Human DNA sequence from clone RP1-159G19 on chromosome 6q14.1-14.3 Contains an STS and GSSs, c | 7.00E-08 | 93/112 (83%) | 1/112 (0%) |
| MIN-100-76 | 498 | gi 11450289 ref NM_003295.1 | Homo sapiens translation factor su11 homolog (GC220), mRNA | 3.00E-56 | 258/302 (85%) | 7/302 (2%) |
| MIN-100-77 | 494 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 480/480 (100%) | - |
| MIN-100-78 | 500 | gi 274634 gb AF037205.1 AF037205 | Mus musculus RING zinc finger protein (Rzf) mRNA, complete cds | 0 | 485/486 (99%) | 1/486 (0%) |
| MIN-100-79 | 497 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 483/483 (100%) | - |
| MIN-100-80 | 502 | gi 7292275 gb AE003476.1 AE003476 | Drosophila melanogaster genomic scaffold 1420000133866045 section 10 of 17, complete sequence | 0.065 | 22/22 (100%) | - |
| MIN-100-83 | 502 | gi 7242172 ref NM_011049.1 | Mus musculus PCTAIRE-motif protein kinase 1 (Pctk1), mRNA | 0 | 488/488 (100%) | - |
| MIN-100-84 | 502 | gi 11417463 ref NM_004092.1 | Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA | 0.065 | 22/22 (100%) | - |
| MIN-100-86 | 501 | gi 6678364 ref NM_009391.1 | Mus musculus RAN, member RAS oncogene family (Ran), mRNA | 0 | 486/487 (99%) | 1/487 (0%) |
| MIN-100-87 | 500 | gi 5668902 gb AF076605.1 AF076605 | Homo sapiens heparan N-deacetylase/N-sulfotransferase 3 (HSST3) mRNA, complete cds | 2.00E-60 | 348/424 (82%), Positives = | - |
| MIN-100-88 | 499 | gi 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/485 (100%), Positive = | - |
| MIN-100-89 | 499 | gi 192364 emb M27844.1 MUSCAM | Mus musculus calmodulin synthesis (CaM) cDNA, complete cds | 0 | 445/447 (99%), Positives = | 1/447 (0%) |
| MIN-100-90 | 500 | gi 560492 emb X78443.1 JRNRLP24 | R.norvegicus (Sprague Dawley) mRNA for ribosomal protein L24 | 0 | 462/486 (95%), Positives = | - |
| MIN-100-91 | 502 | gi 4165334 gb AC006421.1 AC006421 | Drosophila melanogaster, chromosome 2R, region 44C1-44C5, P1 clones DS08614 and DS00667, complete cds | 0.2 | 21/21 (100%), Positives = | - |
| MIN-100-92 | 473 | gi 51336 emb X12944.1 MMHMG17 | Mouse mRNA for HMG-17 chromosomal protein | 0 | 390/391 (99%), Positives = | - |
| MIN-100-94 | 446 | gi 7023397 dbj AK001865.1 AK001865 | Homo sapiens cDNA FLJ11003 fis, clone PLACE1002851 | 5.00E-08 | 55/62 (88%), Positives = | 3/62 (4%) |
| MIN-100-95 | 497 | gi 4506062 | Homo sapiens protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (Pif1), mRNA | 0.049 | 28/30 (93%), Positives = | - |
| MIN-143-01 | 496 | gi 6166315 gb AF107563.1 MUSPEX1 | Mus musculus Cast (Cast) and peroxisomal membrane anchor protein (Pex14) genes, partial sequence | 0.004 | 24/24 (100%) | - |
| MIN-143-02 | 502 | gi 9910199 ref NM_020236.1 | Homo sapiens BMO22 protein (BMO22), mRNA | 5.00E-33 | 243/296 (82%) | 5/296 (1%) |
| MIN-143-03 | 437 | gi 52714 emb X04724.1 MMINSIG | Mouse preproinsulin gene I | 1.00E-118 | 216/216 (100%) | - |
| MIN-143-04 | 496 | gi 687208 gb AF005742.1 AC005742 | Mus musculus chromosome 11, BAC clone 111-181 (LBNL M01), complete sequence | 2.00E-07 | 34/35 (97%) | - |
| MIN-143-05 | 499 | gi 202209 gb M13446.1 MUSTUBA2M | Mouse alpha-tubulin isotype M-alpha-2 mRNA, complete cds | 0 | 481/482 (99%) | - |
| MIN-143-06 | 499 | gi 6806902 ref NM_009722.1 | Mus musculus ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Atp2a2), mRNA | 0 | 485/485 (100%) | - |
| MIN-143-07 | 497 | gi 1914850 gb U49254.1 MMU92454 | Mus musculus WU domain binding protein 5 mRNA, partial cds | 0 | 400/400 (100%) | - |
| MIN-143-08 | 500 | gi 1911760 gb S83456.1 S83456 | GTP-binding protein [mice, C3H/HeJ spleens, LDS responder, mRNA, 1166 nt] | 0 | 487/487 (100%) | - |
| MIN-143-09 | 500 | gi 6679228 ref NM_008792.1 | Mus musculus proprotein convertase subtilisin/kexin type 2 (Pcsk2), mRNA | 0 | 487/487 (100%) | - |
| MIN-143-10 | 461 | gi 6678488 ref NM_009460.1 | Mus musculus ubiquitin-like 1 (Ubl1), mRNA | 0 | 444/447 (99%) | - |
| MIN-143-11 | 495 | gi 3319943 emb AL021397.1 HS69E11 | Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase 1 gene | 2.00E-20 | 79/85 (92%) | 2/85 (2%) |
| MIN-143-12 | 422 | gi 52712 emb X04725.1 MMINSIG | Mouse preproinsulin gene I | 0 | 404/404 (100%) | - |
| MIN-143-13 | 463 | gi 6753363 ref NM_009861.1 | Mus musculus cell division cycle 42 homolog (S. cerevisiae) (Cdc42), mRNA | 0 | 434/450 (96%) | 1/450 (0%) |
| MIN-143-14 | 499 | gi 192439 gb M11739.1 MUSCCKRA | Mouse cholecystokinin (CCK) mRNA, 3' end | 0 | 353/357 (98%) | 3/357 (0%) |
| MIN-143-15 | 502 | gi 1184664 gb U13842.1 MMU13842 | Mus musculus vacuolar adenosine triphosphatase subunit c gene, complete cds | 0 | 486/489 (99%) | - |
| MIN-143-16 | 434 | gi 6680747 ref NM_007505.1 | Mus musculus ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1 (Atp5a1), mRNA | 0 | 416/420 (99%) | - |
| MIN-143-17 | 500 | gi 3142425 gb AF058764.1 AF058764 | Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds | 0.9 | 20/20 (100%) | - |
| MIN-143-18 | 501 | gi 463133 gb L29769.1 MUSHNRNPK | Mouse hnRNP K homologue mRNA | 0 | 483/487 (99%) | - |
| MIN-143-19 | 500 | gi 6679438 ref NM_008907.1 | Mus musculus peptidylprolyl isomerase A (Ppia), mRNA | 0 | 486/486 (100%) | - |
| MIN-143-20 | 497 | gi 8096291 dbj AB042809.1 AB042809 | Mus musculus mitochondrial DNA, complete genome, strain:SAMP8 | 0 | 484/484 (100%) | - |
| MIN-143-21 | 321 | gi 9910601 ref NM_019949.1 | Mus musculus E2 ubiquitin conjugating enzyme (UbcM8), mRNA | 1.00E-156 | 291/295 (98%) | - |
| MIN-143-22 | 526 | gi 9506864 ref NM_018854.1 | Mus musculus uterine protein (LOC55978), mRNA | 0 | 511/512 (99%) | - |
| MIN-143-23 | 471 | gi 6680462 ref NM_008387.1 | Mus musculus insulin II (Ins2), mRNA | 0 | 333/333 (100%) | - |
| MIN-143-24 | 530 | gi 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 488/490 (99%) | - |
| MIN-143-25 | 538 | gi 8926740 emb AJ250394.1 MMU250394 | Mus musculus mRNA for hypothetical protein (human Hc11orf5 gene ortholog) | 0 | 510/510 (100%) | - |
| MIN-143-26 | 526 | gi 1237028 emb X96768.1 BPACOPGEN | B.primigenius mRNA for alpha-cop coat protein | 1.00E-124 | 296/319 (92%) | - |
| MIN-143-27 | 344 | gi 6997238 ref NM_011042.1 | Mus musculus poly(rC) binding protein 2 (Pcbp2), mRNA | 1.00E-166 | 336/348 (96%) | 12/348 (3%) |
| MIN-143-28 | 389 | gi 8809805 gb AF242376.1 AF242376 | Mus musculus KRAB zinc finger protein (Mzf13) mRNA, complete cds | 2.00E-41 | 93/95 (97%) | - |

| | | | | | | |
|------------|-----|------------------------------------|---|-----------|----------------|------------|
| MIN-143-29 | 502 | g 6224681 gb AF144093.1 AF144093 | Mus musculus unconventional myosin-15 gene, complete sequence | 4.00E-15 | 65/72 (90%) | - |
| MIN-143-30 | 446 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 0 | 432/432 (100%) | - |
| MIN-143-31 | 437 | g 52712 emb X04725.1 JMINSIG | Mouse preproinsulin gene I | 0 | 404/404 (100%) | - |
| MIN-143-32 | 507 | g 2582527 gb AF026537.1 AF026537 | Mus musculus prodynorphin mRNA, complete cds | 0 | 501/501 (100%) | - |
| MIN-143-33 | 488 | g 1335846 gb U39077.1 MMU39077 | Mus musculus thymopoietin gamma mRNA, complete cds | 1.00E-104 | 201/202 (99%) | 1/202 (0%) |
| MIN-143-34 | 488 | g 1518873 gb U31241.1 CGU31241 | Cricetulus griseus integral membrane protein CII-3 mRNA, nuclear gene encoding mitochondrial protein, co | 1.00E-145 | 422/474 (89%) | 1/474 (0%) |
| MIN-143-35 | 499 | g 6755551 ref NM_011288.1 | Mus musculus ribosomal protein L23 (Rpl23), mRNA | 0 | 494/494 (100%) | - |
| MIN-143-36 | 489 | g 6753485 ref NM_009939.1 | Mus musculus COP9 (constitutive photomorphogenic, subunit 2 (Arabidopsis) (Cops2), mRNA | 0 | 480/480 (100%) | - |
| MIN-143-37 | 461 | g 1854947 gb U77330.1 MMU77330 | Mus musculus extracellular matrix protein precursor SC1 mRNA, complete cds | 0 | 445/447 (99%) | - |
| MIN-143-38 | 501 | g 6678823 ref NM_008562.1 | Mus musculus myeloid cell leukemia sequence 1 (Mcl1), mRNA | 0 | 485/488 (99%) | 2/488 (0%) |
| MIN-143-39 | 499 | g 6755261 ref NM_011229.1 | Mus musculus RAB5B, member RAS oncogene family (Rab5b), mRNA | 0 | 338/338 (100%) | - |
| MIN-143-40 | 485 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 462/473 (97%) | - |
| MIN-143-41 | 481 | g 3719448 gb AF093677.1 AF093677 | Mus musculus ATPase subunit 6 (Atpase6) mRNA, mitochondrial gene encoding mitochondrial protein, com | 0 | 455/464 (98%) | - |
| MIN-143-42 | 183 | g 10336604 dbj AB049357.1 AB049357 | Mus musculus mitochondrial DNA, complete genome, strain:C3H/He | 2.00E-67 | 160/170 (94%) | 1/170 (0%) |
| MIN-143-43 | 488 | g 8452897 gb AF187066.1 AF187066 | Mus musculus p75NTR-associated cell death executor (Nade) mRNA, complete cds | 1.00E-136 | 247/247 (100%) | - |
| MIN-143-44 | 498 | g 8096291 dbj AB042809.1 AB042809 | Mus musculus mitochondrial DNA, complete genome, strain:SAMP8 | 0 | 444/463 (95%) | 1/463 (0%) |
| MIN-143-45 | 399 | g 2801800 gb AF042730.1 AF042730 | Mus musculus lithium-sensitive myo-inositol monophosphatase A1 (IMPA1) mRNA, complete cds | 0 | 372/380 (97%) | 2/380 (0%) |
| MIN-143-46 | 300 | g 6671568 ref NM_007475.1 | Mus musculus acidic ribosomal phosphoprotein PO (Arp), mRNA | 1.00E-159 | 286/286 (100%) | - |
| MIN-143-47 | 322 | g 9955722 emb AJ297390.1 MMU297390 | Mus musculus mRNA for twisted gastrulation protein (tsg gene) | 1.00E-168 | 307/308 (99%) | 1/308 (0%) |
| MIN-143-48 | 423 | g 49911 emb X03351.1 MMALBR | Mouse mRNA for prealbumin | 0 | 396/410 (96%) | 1/410 (0%) |
| MIN-143-49 | 499 | g 6681134 ref NM_007829.1 | Mus musculus Fas death domain-associated protein (Daxx), mRNA | 0 | 467/467 (100%) | - |
| MIN-143-50 | 484 | g 6806902 ref NM_009722.1 | Mus musculus ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (Atp2a2), mRNA | 0 | 468/473 (99%) | - |
| MIN-143-51 | 485 | g 52848 emb X06407.1 JMLL21KD1 | Mouse mRNA for 21 kd polypeptide under translational control | 0 | 472/473 (99%) | - |
| MIN-143-52 | 429 | g 50300 emb X53337.1 JMMCATHD | Mouse mRNA for cathepsin D (EC 3.4.23.5) | 0 | 410/414 (99%) | - |
| MIN-143-53 | 475 | g 7949046 ref NM_016763.1 | Mus musculus hydroxyacyl-Coenzyme A dehydrogenase, type II (Hadh2), mRNA | 0 | 444/463 (95%) | - |
| MIN-143-54 | 499 | g 9800521 gb AF289666.1 AF289666 | Mus musculus GTF2I and GTF2IRD1 genes, partial cds | 0.25 | 24/25 (96%) | - |
| MIN-143-55 | 501 | g 52714 emb X04724.1 JMINSIG | Mouse preproinsulin gene II | 1.00E-160 | 287/287 (100%) | - |
| MIN-143-56 | 499 | g 841327 gb U23184.1 MMU23184 | Mus musculus carboxypeptidase E (Cpe) mRNA, complete cds | 0 | 484/485 (99%) | 1/485 (0%) |
| MIN-143-57 | 477 | g 1518873 gb U31241.1 CGU31241 | Cricetulus griseus integral membrane protein CII-3 mRNA, nuclear gene encoding mitochondrial protein, co | 1.00E-138 | 403/454 (88%) | - |
| MIN-143-58 | 292 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 1.00E-151 | 276/278 (99%) | - |
| MIN-143-59 | 499 | g 393424 emb X171922.1 MMIGF1IE6 | M.musculus gene for IGF-II, exon 6 | 0 | 485/487 (99%) | 2/487 (0%) |
| MIN-143-60 | 494 | g 3549610 gb AF085348.1 AF085348 | Mus musculus proline-rich protein (Bppr) mRNA, complete cds | 0 | 416/417 (99%) | - |
| MIN-143-61 | 499 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 484/485 (99%) | - |
| MIN-143-62 | 499 | g 2944418 gb AF049850.1 JMMH438N1 | Mus musculus major histocompatibility locus class III region: complement C4 (C4) and cytochrome P450 hyc | 0 | 468/485 (96%) | 5/485 (1%) |
| MIN-143-63 | 588 | g 52714 emb X04724.1 JMINSIG | Mouse preproinsulin gene II | 0 | 354/354 (100%) | - |
| MIN-143-64 | 272 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 1.00E-134 | 255/258 (98%) | 1/258 (0%) |
| MIN-143-65 | 499 | g 893392 dbj D55720.1 JMSNPPTCC | Mouse mRNA for nuclear pore-targeting complex, complete cds | 0 | 485/485 (100%) | - |
| MIN-143-66 | 595 | g 49911 emb X03351.1 MMALBR | Mouse mRNA for prealbumin | 0 | 581/581 (100%) | - |
| MIN-143-67 | 537 | g 194066 gb J25389.1 JMSIAPP | Mouse islet amyloid polypeptide mRNA, complete cds | 0 | 464/464 (100%) | - |
| MIN-143-68 | 297 | g 6598551 gb AC006284.3 AC006284 | Arabidopsis thaliana chromosome II section 14 of 255 of the complete sequence. Sequence from clones T18 | 0.15 | 24/25 (96%) | - |
| MIN-143-69 | 499 | g 54854 emb X53333.1 JMMTP11R | Mouse mRNA for triosephosphate isomerase (EC 5.3.1.1) | 0 | 483/485 (99%) | - |
| MIN-143-70 | 500 | g 49911 emb X03351.1 MMALBR | Mouse mRNA for prealbumin | 0 | 486/486 (100%) | - |
| MIN-143-71 | 499 | g 6680162 ref NM_008212.1 | Mus musculus hydroxyacyl-Coenzyme A dehydrogenase (Hadh), mRNA | 0 | 485/487 (99%) | 1/487 (0%) |
| MIN-143-72 | 498 | g 49644 emb X62678.1 MAP5PROMR | M.auratus mRNA for P5 protein | 3.00E-84 | 212/228 (92%) | 1/228 (0%) |
| MIN-143-73 | 497 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 483/483 (100%) | - |
| MIN-143-74 | 499 | g 7106430 ref NM_011543.1 | Mus musculus transcription elongation factor B (SIII), polypeptide 1 (15 kDa),-like (Tceb10), mRNA | 0 | 487/488 (99%) | 1/488 (0%) |
| MIN-143-75 | 494 | g 1184660 gb U13838.1 MMU13838 | Mus musculus vacuolar adenosine triphosphatase subunit B gene, complete cds | 0 | 471/479 (98%) | 2/479 (0%) |
| MIN-143-76 | 502 | g 3641670 dbj AB011678.1 AB011678 | Mus musculus mRNA for doublecortin, complete cds | 0 | 487/488 (99%) | - |
| MIN-143-77 | 498 | g 8885512 dbj AB045313.1 AB045313 | Mus musculus mmCdc20 mRNA, complete cds | 0 | 484/484 (100%) | - |
| MIN-143-78 | 460 | g 1001938 gb U13152.1 JMAU13152 | Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds | 2.00E-35 | 87/90 (96%) | - |
| MIN-143-79 | 292 | g 6679274 ref NM_008817.1 | Mus musculus paternally expressed gene 3 (Peg3), mRNA | 1.00E-133 | 256/261 (98%) | - |
| MIN-143-80 | 257 | g 6679686 ref NM_007952.1 | Mus musculus endoplasmic reticulum protein (Erp), mRNA | 1.00E-106 | 230/243 (94%) | - |
| MIN-143-81 | 498 | g 4868332 gb AF129888.1 AF129888 | Mus musculus Su11 homolog mRNA, complete cds | 0 | 480/484 (99%) | - |
| MIN-143-82 | 498 | g 755006 gb L35575.1 CHKGABAARA | Gallus domesticus gamma-aminobutyric acid A receptor gene, promoter region, exon 1 | 0 | 20/20 (100%) | - |
| MIN-143-83 | 387 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 361/373 (96%) | - |
| MIN-143-84 | 498 | g 8546861 emb AJ278429.1 MMU278429 | Mus musculus partial Prkar1a gene for cAMP-dependent protein kinase regulatory subunit R1alpha, exons 6 | 0 | 462/464 (99%) | - |
| MIN-143-85 | 500 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 0 | 485/486 (99%) | - |
| MIN-143-86 | 299 | g 52712 emb X04725.1 JMINSIG | Mouse preproinsulin gene I | 1.00E-152 | 277/279 (99%) | - |
| MIN-143-87 | 199 | g 9623381 gb AF267747.1 AF267747 | Mus musculus p47-phox gene, complete cds | 0.006 | 26/27 (96%) | - |
| MIN-143-88 | 159 | g 342520 gb J01420.1 MUSMTCG | Mouse mitochondrion, complete genome | 7.00E-70 | 144/146 (98%) | 1/146 (0%) |
| MIN-143-89 | 490 | g 9082148 gb AF242431.1 AF242431S1 | Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2- | 2.00E-14 | 90/103 (87%) | 2/103 (1%) |
| MIN-143-90 | 499 | g 951219 gb L43843.1 MUSUGA | Mus musculus (cell line L1021) small-nuclear RNA (snRNA) gene | 5.00E-61 | 128/129 (99%) | 1/129 (0%) |
| MIN-143-91 | 499 | g 6755559 ref NM_011899.1 | Mus musculus signal recognition particle 54 kDa (Srp54), mRNA | 0 | 485/485 (100%) | - |
| MIN-143-92 | 499 | g 11466673 ref NC_001319.1 | Marchantia polymorpha chloroplast, complete genome | 0.064 | 22/22 (100%) | - |
| MIN-143-93 | 499 | g 9838361 ref NC_002511.1 | Beta vulgaris mitochondrion, complete genome | 0.064 | 22/22 (100%) | - |
| MIN-143-94 | 499 | g 6671745 ref NM_007688.1 | Mus musculus cofilin 2, muscle (Cfl2), mRNA | 0 | 479/485 (98%) | 2/485 (0%) |
| MIN-143-95 | 499 | g 556300 gb J22342.1 MUSEFTU | Mus musculus protein synthesis elongation factor Tu (eEF-Tu, eEF-1-alpha) mRNA, complete cds | 0 | 484/485 (99%) | - |
| MIN-143-96 | 499 | g 6680158 ref NM_008210.1 | Mus musculus H3 histone, family 3A (H3f3a), mRNA | 0 | 487/487 (100%) | - |

マウス胎児膵組織移植モデルを用いた解析

分担研究者 安波 洋一 福岡大学医学部第一外科助教授

研究要旨

胎児膵組織移植では移植後30日の間にグラフト内の膵島β細胞の分化増殖が発現し膵島が形成されることが明らかとなった。

A. 研究目的

幹細胞からの膵β細胞分化誘導を明らかにする為には適切な実験モデルの開発が必須である。本研究ではマウス胎児膵組織をストレプトゾトシン糖尿病マウスに移植する実験系を用いて移植後の胎児膵グラフトにおける膵内分泌細胞の分化誘導、幹細胞の同定およびその動態解析を試みた。

B. 研究方法

C57BL/6 マウスをドナー、レシピエントに用いた。胎生18日目の膵臓を実体顕微鏡下に摘出しストレプトゾトシン(STZ)糖尿病マウスの腎皮膜下に移植した。移植後週3回血糖値(非空腹時)および体重を測定した。移植後経時的にグラフトを免疫組織学的に解析した。

(倫理面への配慮)

本研究は福岡大学アニマルセンター倫理委員会の承認を受けている。

C. 研究結果

実験モデル: 本実験系では2匹分の胎児膵組織をドナーとした場合、移植

後レシピエントの血糖値は正常化せず高血糖で推移した。更に4匹分の胎児膵組織移植でレシピエントは移植後30日前後で正常血糖となり、この条件下では高血糖を是正できる十分量の膵島β細胞が移植後グラフト内に分化増殖したと考えられた。本モデルでは移植後にグラフト内の膵島細胞と膵管のみが残存し、外分泌細胞は移植後14日までに全て消失、脂肪変性していた。小膵管の増殖像も認められた。移植後経時的(14, 30, 90日目)にグラフトを含む腎臓を摘出し、胎児膵グラフトを免疫組織学的に解析した。レシピエントはグラフト摘出直後(24時間以内)より再度高血糖状態となり、レシピエントの移植後の正常血糖がグラフトによるものであることが確認できた。

免疫組織染色: 移植前グラフトの免疫組織染色でインスリン陽性細胞は通常の膵島としてではなく、ほとんどが小集積(クラスター)として膵内に散在していた。移植後の時間の経過と

ともにいわゆる膵島を形成していた。サイトケラチンとインスリンの二重染色によりグラフトの一部の膵管上皮にインスリン陽性細胞が出現した。PPは膵島のみではなく、膵管上皮に陽性細胞を認めた。REG 蛋白は移植後14日に一部の膵管上皮細胞が陽性であった。インスリン陽性 PCNA 陽性細胞は移植後14日目をピークとして出現し、正常血糖となった90日ではほとんど認められなかった。

D. 考察

胎児膵組織移植では移植後30日の間にグラフト内の膵島β細胞の分化増殖が発現し膵島が形成されることが明らかとなった。この分化増殖過程に幹細胞の関与が想定される。今回の研究でPP陽性細胞、膵管上皮細胞の一部がβ細胞に分化する幹細胞である可能性が示唆された。REG 蛋白は膵β細胞の再生増殖に重要な役割を担っていると考えられるが、今回の実験では幹細胞との関連性は明らかにできなかった。ネスチン陽性細胞が幹細胞である可能性が高いがネスチンについては現在検討中である。

E. 結論

胎児膵組織移植では移植後30日の間にグラフト内の膵島β細胞の分化増殖が発現し膵島が形成されることが明らかとなった。この分化増殖過程に幹細胞の関与が想定され、今回の研究でPP陽性細胞、膵管上皮細胞の一部がβ細胞に分化する幹細胞である可能性が示唆された。

F. 健康危険情報

とくになし。

G. 研究発表

1. 論文発表

なし

2. 学会発表

なし

H. 知的財産権の出願・登録状況

1. 特許取得

なし

2. 実用新案登録

なし

3. その他

なし

【Ⅲ】研究成果の刊行に関する一覧表

研究成果の刊行に関する一覧表

雑誌

| 発表者氏名 | 論文タイトル名 | 発表誌名 | 巻号 | ページ | 出版年 |
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【Ⅳ】研究成果の刊行物・別刷

200100469A

以降は 雑誌/図書等に掲載された論文となりますので P.74-75 の
「研究成果の刊行に関する一覧表」をご参照ください。

