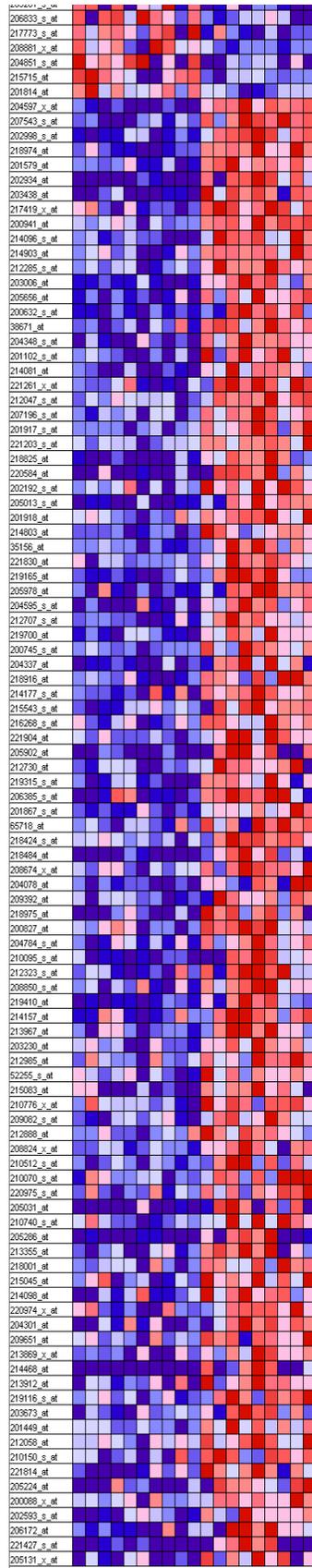


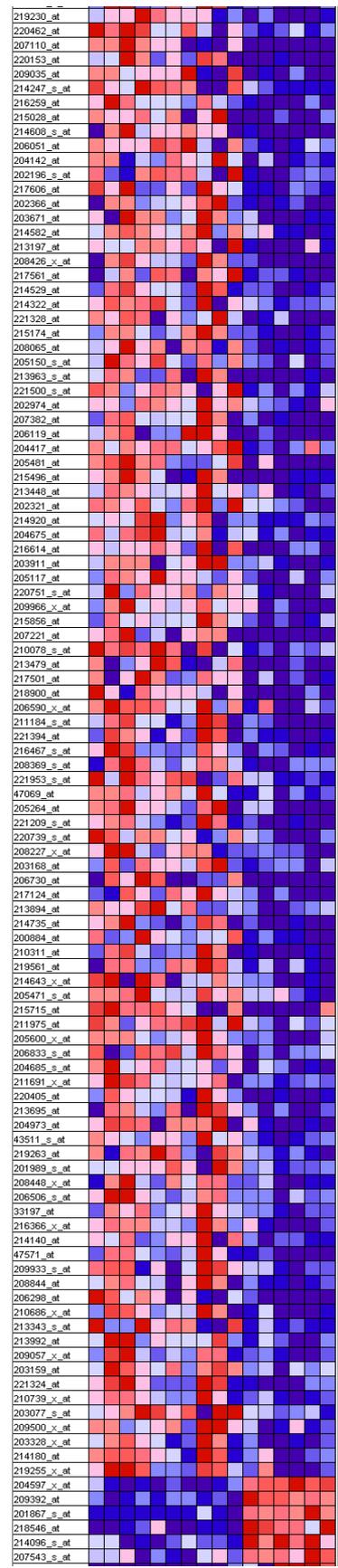


95 MEN2 0.75 206833\_s\_at acylphosphatase 2, muscle type  
96 MEN2 0.74 217773\_s\_at NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kD  
97 MEN2 0.74 208881\_x\_at isopentenyl-diphosphate delta isomeras  
98 MEN2 0.74 204851\_s\_at doublecortin; lissencephaly, X-linked (doublecortin  
99 MEN2 0.74 215715\_at solute carrier family 6 (neurotransmitter transporter, noradrenalin), member :  
100 MEN2 0.74 201814\_at TBC1 domain family, member 5  
101 VHL 2.05 204597\_x\_at stanniocalcin 1  
102 VHL 1.69 207543\_s\_at procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase  
103 VHL 1.61 202998\_s\_at lysyl oxidase-like 2  
104 VHL 1.54 218974\_at hypothetical protein FLJ10155  
105 VHL 1.46 201579\_at FAT tumor suppressor homolog 1 (Drosophila  
106 VHL 1.44 202934\_at hexokinase 2  
107 VHL 1.39 203438\_at stanniocalcin 2  
108 VHL 1.27 217419\_x\_at agrin  
109 VHL 1.26 200941\_at heat shock factor binding protein 1  
110 VHL 1.24 214096\_s\_at serine hydroxymethyltransferase 2 (mitochondrial  
111 VHL 1.24 214903\_at Homo sapiens clone 24527 mRNA sequenc  
112 VHL 1.22 212285\_s\_at agrin  
113 VHL 1.16 203006\_at inositol polyphosphate-5-phosphatase, 40kD:  
114 VHL 1.14 205656\_at protocadherin 17  
115 VHL 1.14 200632\_s\_at N-myc downstream regulated gene 1  
116 VHL 1.14 38671\_at KIAA0620 protein  
117 VHL 1.09 204348\_s\_at adenylate kinase 3  
118 VHL 1.09 201102\_s\_at phosphofructokinase, liver  
119 VHL 1.07 214081\_at tumor endothelial marker 7 precursor  
120 VHL 1.07 221261\_x\_at MAGE-E1 protein  
121 VHL 1.07 212047\_s\_at DKFZP566H073 protein  
122 VHL 1.05 207196\_s\_at Nef-associated factor 1  
123 VHL 1.04 201917\_s\_at hypothetical protein FLJ10616  
124 VHL 1.03 221203\_s\_at hypothetical protein FLJ10201  
125 VHL 1.03 218825\_at NEU1 protein  
126 VHL 1.02 220584\_at hypothetical protein FLJ22184  
127 VHL 1.02 202192\_s\_at growth arrest-specific 7  
128 VHL 1.02 205013\_s\_at adenosine A2a receptor  
129 VHL 1 201918\_at hypothetical protein FLJ10616  
130 VHL 1 214803\_at Homo sapiens mRNA; cDNA DKFZp564N1116 (from clone DKFZp564N1116  
131 VHL 1 35156\_at ESTs, Highly similar to T08701 hypothetical protein DKFZp564N123.1 - human  
132 VHL 1 221830\_at Homo sapiens cDNA FLJ37267 fis, clone BRAMY201129;  
133 VHL 0.99 219165\_at PDZ-LIM protein mystique  
134 VHL 0.98 205978\_at klotho  
135 VHL 0.98 204595\_s\_at stanniocalcin 1  
136 VHL 0.96 212707\_s\_at Ca2+-promoted Ras inactivator  
137 VHL 0.91 219700\_at tumor endothelial marker 7 precursor  
138 VHL 0.91 200745\_s\_at guanine nucleotide binding protein (G protein), beta polypeptide  
139 VHL 0.91 204337\_at regulator of G-protein signalling 4  
140 VHL 0.91 218916\_at hypothetical protein FLJ23436  
141 VHL 0.9 214177\_s\_at hematopoietic PBX-interacting protei  
142 VHL 0.9 215543\_s\_at like-glycosyltransferase  
143 VHL 0.89 216268\_s\_at jagged 1 (Alagille syndrome)  
144 VHL 0.89 221904\_at hypothetical protein MGC2168t  
145 VHL 0.89 205902\_at potassium intermediate/small conductance calcium-activated channel, subfamily  
146 VHL 0.88 212730\_at desmulin  
147 VHL 0.87 219315\_s\_at hypothetical protein FLJ2089t  
148 VHL 0.87 206385\_s\_at ankyrin 3, node of Ranvier (ankyrin G  
149 VHL 0.87 201867\_s\_at transducin (beta)-like 1X-linkc  
150 VHL 0.87 65718\_at tumor endothelial marker 5 precursor  
151 VHL 0.87 218424\_s\_at dudulin 2  
152 VHL 0.86 218484\_at NADH:ubiquinone oxidoreductase MLRQ subunit homolo  
153 VHL 0.86 208674\_x\_at dolichyl-diphosphooligosaccharide-protein glycosyltransferase  
154 VHL 0.86 204078\_at nucleolar autoantigen (55kD) similar to rat synaptonemal complex protei  
155 VHL 0.86 209392\_at ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin  
156 VHL 0.86 218975\_at collagen, type V, alpha 3  
157 VHL 0.86 200827\_at procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase  
158 VHL 0.86 204784\_s\_at myeloid leukemia factor 1  
159 VHL 0.84 210095\_s\_at insulin-like growth factor binding protein :  
160 VHL 0.84 212323\_s\_at KIAA0453 protein  
161 VHL 0.84 208850\_s\_at Thy-1 cell surface antigen  
162 VHL 0.84 219410\_at hypothetical protein FLJ10134  
163 VHL 0.84 214157\_at GNAS complex locus  
164 VHL 0.83 213967\_at Homo sapiens clone 24468 mRNA sequenc  
165 VHL 0.83 203230\_at dishevelled, dsh homolog 1 (Drosophila  
166 VHL 0.83 212985\_at Homo sapiens mRNA; cDNA DKFZp434E033 (from clone DKFZp434E033  
167 VHL 0.82 52255\_s\_at collagen, type V, alpha 3  
168 VHL 0.81 215083\_at Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133  
169 VHL 0.81 210776\_x\_at transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47  
170 VHL 0.81 209082\_s\_at collagen, type XVIII, alpha 1  
171 VHL 0.81 212888\_at Homo sapiens cDNA FLJ33775 fis, clone BRSSN200049t  
172 VHL 0.81 208824\_x\_at PCTAIRE protein kinase 1  
173 VHL 0.81 210512\_s\_at vascular endothelial growth factor  
174 VHL 0.81 210070\_s\_at carnitine palmitoyltransferase I, muscle  
175 VHL 0.8 220975\_s\_at C1q and tumor necrosis factor related protein 1  
176 VHL 0.8 205031\_at ephrin-B3  
177 VHL 0.8 210740\_s\_at inositol 1,3,4-triphosphate 5/6 kinase  
178 VHL 0.8 205286\_at transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)  
179 VHL 0.79 213355\_at alpha2,3-sialyltransferase  
180 VHL 0.79 218001\_at mitochondrial ribosomal protein S2  
181 VHL 0.79 215045\_at trinucleotide repeat containing 4  
182 VHL 0.79 214098\_at KIAA1107 protein  
183 VHL 0.79 220974\_x\_at similar to rat tricarboxylate carrier-like protein  
184 VHL 0.79 204301\_at KIAA0711 gene product  
185 VHL 0.78 209651\_at transforming growth factor beta 1 induced transcript :  
186 VHL 0.78 213869\_x\_at Thy-1 cell surface antigen  
187 VHL 0.78 214468\_at myosin, heavy polypeptide 6, cardiac muscle, alpha  
188 VHL 0.78 213912\_at KIAA0984 protein  
189 VHL 0.78 219116\_s\_at hypothetical protein FLJ10704  
190 VHL 0.78 203673\_at thyroglobulin  
191 VHL 0.77 201449\_at Homo sapiens cDNA FLJ36425 fis, clone THYMU201148;  
192 VHL 0.77 212058\_at KIAA0332 protein  
193 VHL 0.77 210150\_s\_at laminin, alpha 5  
194 VHL 0.76 221814\_at tumor endothelial marker 5 precursor  
195 VHL 0.76 205224\_at surfactin 2  
196 VHL 0.76 200088\_x\_at ribosomal protein L12  
197 VHL 0.76 202593\_s\_at membrane interacting protein of RGS1f  
198 VHL 0.76 206172\_at interleukin 13 receptor, alpha 2  
199 VHL 0.76 221427\_s\_at likely ortholog of mouse Paneth cell enhanced expressio  
200 VHL 0.76 205131\_x\_at stem cell growth factor; lymphocyte secreted C-type lectin





99 MEN2 0.93 219230\_at hypothetical protein FLJ10970  
100 MEN2 0.93 220462\_at hypothetical protein FLJ11703  
101 MEN2 0.93 207110\_at potassium inwardly-rectifying channel, subfamily J, member 1  
102 MEN2 0.93 220153\_at lysosomal aprase-like protein 1  
103 MEN2 0.93 209035\_at midkine (neurite growth-promoting factor 2  
104 MEN2 0.93 214247\_s\_a dickkopf homolog 3 (Xenopus laevis  
105 MEN2 0.92 216259\_at Human clone IMAGE:35527 unknown protein mRNA, partial cd  
106 MEN2 0.92 215028\_at sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6  
107 MEN2 0.91 214608\_s\_a eyes absent homolog 1 (Drosophila)  
108 MEN2 0.91 206051\_at ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen C  
109 MEN2 0.91 204142\_at rTS beta protein  
110 MEN2 0.91 202196\_s\_a dickkopf homolog 3 (Xenopus laevis  
111 MEN2 0.91 217606\_at Homo sapiens mRNA; cDNA DKFZp686P24158 (from clone DKFZp686P24158  
112 MEN2 0.9 202366\_at acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain  
113 MEN2 0.9 203671\_at thiopurine S-methyltransferase  
114 MEN2 0.9 214582\_at phosphodiesterase 3B, cGMP-inhibitec  
115 MEN2 0.9 213197\_at astroctactin  
116 MEN2 0.9 208426\_x\_a killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, i  
117 MEN2 0.9 217561\_at ESTs, Highly similar to 1005250A calcitonin gene related peptide  
118 MEN2 0.9 214529\_at thyroid stimulating hormone, beta  
119 MEN2 0.9 214322\_at calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma  
120 MEN2 0.89 221328\_at claudin 17  
121 MEN2 0.89 215174\_at ESTs, Weakly similar to FMO3\_HUMAN Dimethylaniiline monooxygenase  
122 MEN2 0.89 208065\_at sialyltransferase 8C (alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase  
123 MEN2 0.88 205150\_s\_a KIAA0644 gene produc  
124 MEN2 0.88 213963\_s\_a sin3-associated polypeptide, 30kDa  
125 MEN2 0.88 221500\_s\_a ESTs, Moderately similar to hypothetical protein FLJ20489 [Homo sapiens  
126 MEN2 0.88 202974\_at membrane protein, palmitoylated 1, 55kDa  
127 MEN2 0.88 207382\_at tumor protein p63  
128 MEN2 0.88 206119\_at betaine-homocysteine methyltransferase  
129 MEN2 0.88 204417\_at galactosylceramidase (Krabbe disease)  
130 MEN2 0.88 205481\_at adenosine A1 receptor  
131 MEN2 0.88 215496\_at KIAA1053 protein  
132 MEN2 0.87 213448\_at Homo sapiens cDNA FLJ31688 fis, clone NT2RI200552I  
133 MEN2 0.87 202321\_at geranylgeranyl diphosphate synthase  
134 MEN2 0.87 214920\_at Homo sapiens cDNA FLJ11022 fis, clone PLACE100377  
135 MEN2 0.87 204675\_at steroid-5-alpha-reductase, alpha polypeptide 1  
136 MEN2 0.87 216614\_at Homo sapiens mRNA; cDNA DKFZp564F212 (from clone DKFZp564F212  
137 MEN2 0.87 203911\_at RAP1, GTPase activating protein 1  
138 MEN2 0.87 205117\_at fibroblast growth factor 1 (acidic)  
139 MEN2 0.87 220751\_s\_a chromosome 5 open reading frame 4  
140 MEN2 0.86 209966\_x\_a estrogen-related receptor gamma  
141 MEN2 0.86 215856\_at Homo sapiens cDNA FLJ38113 fis, clone D3OST200241;  
142 MEN2 0.86 207221\_at coagulation factor II (thrombin) receptor-like 1  
143 MEN2 0.86 210078\_s\_a potassium voltage-gated channel, shaker-related subfamily, beta member  
144 MEN2 0.86 213479\_at neuronal pentraxin I  
145 MEN2 0.86 217501\_at WD40 protein Ciao1  
146 MEN2 0.86 218900\_at cyclin M4  
147 MEN2 0.85 206590\_x\_a dopamine receptor D2  
148 MEN2 0.85 211184\_s\_a PDZ-73 protein  
149 MEN2 0.85 221394\_at G protein-coupled receptor 58  
150 MEN2 0.85 216467\_s\_a Homo sapiens mRNA; cDNA DKFZp564L102 (from clone DKFZp564L102  
151 MEN2 0.85 208369\_s\_a glutaryl-Coenzyme A dehydrogenase  
152 MEN2 0.85 221953\_s\_a matrix metalloproteinase 24 (membrane-inserted)  
153 MEN2 0.85 47069\_at Rho GTPase activating protein 1  
154 MEN2 0.85 205264\_at CD3-epsilon-associated protein; antisense to ERCC-1  
155 MEN2 0.85 221209\_s\_a otoraplin  
156 MEN2 0.85 220739\_s\_a cyclin M3  
157 MEN2 0.85 208227\_x\_a disintegrin and metalloproteinase domain 2  
158 MEN2 0.85 203168\_at cAMP responsive element binding protein-like 1  
159 MEN2 0.85 206730\_at glutamate receptor, ionotropic, AMPA 1  
160 MEN2 0.84 217124\_at hypothetical protein DKFZp434P121f  
161 MEN2 0.84 213894\_at KIAA0960 protein  
162 MEN2 0.84 214735\_at phosphoinositide-binding protein PIP3-1  
163 MEN2 0.84 200884\_at creatine kinase, brain  
164 MEN2 0.84 210311\_at fibroblast growth factor 5  
165 MEN2 0.84 219561\_at COP22 for nonclathrin coat protein zeta-COF  
166 MEN2 0.84 214643\_x\_a bridging integrator 1  
167 MEN2 0.83 205471\_s\_a dachshund homolog (Drosophila  
168 MEN2 0.83 215715\_at solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 1  
169 MEN2 0.83 211975\_at zinc finger protein 289, ID1 regulatec  
170 MEN2 0.83 205600\_x\_a homeo box B5  
171 MEN2 0.83 206833\_s\_a acylphosphatase 2, muscle type  
172 MEN2 0.83 204685\_s\_a ATPase, Ca++ transporting, plasma membrane 1  
173 MEN2 0.83 211691\_x\_a accession number AF293339.1  
174 MEN2 0.83 220405\_at syntrophin, gamma 1  
175 MEN2 0.83 213695\_at paraoxonase 3  
176 MEN2 0.83 204973\_at gap junction protein, beta 1, 32kDa (connexin 32  
177 MEN2 0.83 43511\_s\_at Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127  
178 MEN2 0.83 219263\_at hypothetical protein FLJ2351f  
179 MEN2 0.83 201989\_s\_a cAMP responsive element binding protein-like 1  
180 MEN2 0.82 208448\_x\_a interferon, alpha 16  
181 MEN2 0.82 206506\_s\_a suppressor of Ty 3 homolog (S. cerevisiae)  
182 MEN2 0.82 33197\_at myosin VIIA (Usher syndrome 1B (autosomal recessive, severe)  
183 MEN2 0.82 216366\_x\_a accession number AF047245.1  
184 MEN2 0.82 214140\_at hypothetical protein MGC39851  
185 MEN2 0.82 47571\_at zinc finger protein 236  
186 MEN2 0.82 209933\_s\_a leukocyte membrane antigen  
187 MEN2 0.82 208844\_at voltage-dependent anion channel 1  
188 MEN2 0.81 206298\_at hypothetical protein from clones 23549 and 2376;  
189 MEN2 0.81 210686\_x\_a solute carrier family 25 (mitochondrial carrier), member 1f  
190 MEN2 0.81 213343\_s\_a hypothetical protein PPI665  
191 MEN2 0.81 213992\_at collagen, type IV, alpha 1  
192 MEN2 0.81 209057\_x\_a CDC5 cell division cycle 5-like (S. pombe)  
193 MEN2 0.81 203159\_at glutaminase  
194 MEN2 0.81 221324\_at taste receptor, type 2, member 1  
195 MEN2 0.81 210739\_x\_a solute carrier family 4, sodium bicarbonate cotransporter, member 4  
196 MEN2 0.81 203077\_s\_a MAD, mothers against decapentaplegic homolog 2 (Drosophila  
197 MEN2 0.81 209500\_x\_a tumor necrosis factor (ligand) superfamily, member 1c  
198 MEN2 0.81 203328\_x\_a insulin-degrading enzyme  
199 MEN2 0.81 214180\_at Homo sapiens mRNA; cDNA DKFZp564H203 (from clone DKFZp564H203  
200 MEN2 0.8 219255\_x\_a interleukin 17B receptor  
201 SDH 2.57 204597\_x\_a stanniocalcin 1  
202 SDH 1.96 209392\_at ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin  
203 SDH 1.73 201867\_s\_a transducin (beta)-like 1X-linkec  
204 SDH 1.68 218546\_at hypothetical protein FLJ1414f  
205 SDH 1.47 214096\_s\_a serine hydroxymethyltransferase 2 (mitochondrial



206 SDH 1.32 207543\_s\_a procollagen-proline, 2-oxoglutarate 4-dioxygenase alpha polypeptide

207 SDH 1.31 204338\_s\_a regulator of G-protein signalling 4

208 SDH 1.29 221933\_at neuroigin

209 SDH 1.28 213400\_s\_a transducin (beta)-like 1X-linkec

210 SDH 1.25 212037\_at pinin, desmosome associated protein

211 SDH 1.23 217673\_x\_a accession number AA65055f

212 SDH 1.22 221261\_x\_a MAGE-E1 protein

213 SDH 1.21 202934\_at hexokinase 2

214 SDH 1.21 200094\_s\_a eukaryotic translation elongation factor 1

215 SDH 1.21 201868\_s\_a transducin (beta)-like 1X-linkec

216 SDH 1.2 204337\_at regulator of G-protein signalling 4

217 SDH 1.19 217868\_s\_a CGI-81 protein

218 SDH 1.18 201497\_x\_a myosin, heavy polypeptide 11, smooth muscl

219 SDH 1.17 212997\_s\_a tousled-like kinase 2

220 SDH 1.16 202499\_s\_a solute carrier family 2 (facilitated glucose transporter), member 2

221 SDH 1.16 208932\_at protein phosphatase 4 (formerly X), catalytic subunit

222 SDH 1.14 201594\_s\_a protein phosphatase 4, regulatory subunit 1

223 SDH 1.14 200941\_at heat shock factor binding protein 1

224 SDH 1.13 207961\_x\_a myosin, heavy polypeptide 11, smooth muscl

225 SDH 1.13 219602\_s\_a hypothetical protein FLJ23402

226 SDH 1.12 218317\_x\_a hypothetical protein MGC517f

227 SDH 1.09 212348\_s\_a KIAA0601 protein

228 SDH 1.08 203945\_at arginase, type II

229 SDH 1.08 200729\_s\_a ARP2 actin-related protein 2 homolog (yeast)

230 SDH 1.08 219791\_s\_a hypothetical protein FLJ1153f

231 SDH 1.07 203438\_at stanniocalcin 2

232 SDH 1.07 205603\_s\_a diaphanous homolog 2 (Drosophila)

233 SDH 1.07 206163\_at mab-21-like 1 (C. elegans)

234 SDH 1.07 205809\_s\_a Wiskott-Aldrich syndrome-like

235 SDH 1.07 200944\_s\_a high-mobility group nucleosome binding domain 1

236 SDH 1.05 823\_at chemokine (C-X3-C motif) ligand 1

237 SDH 1.04 204366\_s\_a general transcription factor IIC, polypeptide 2, beta 110kD;

238 SDH 1.04 218484\_at NADH:ubiquinone oxidoreductase MLRQ subunit homolog

239 SDH 1.04 214722\_at ESTs, Weakly similar to hypothetical protein FLJ2037f

240 SDH 1.03 204904\_at gap junction protein, alpha 4, 37kDa (connexin 37)

241 SDH 1.02 202133\_at transcriptional co-activator with PDZ-binding motif (TAZ)

242 SDH 1.02 213011\_s\_a triosephosphate isomerase 1

243 SDH 1.01 200790\_at ornithine decarboxylase 1

244 SDH 1.01 40560\_at T-box 2

245 SDH 1.01 213355\_at alpha2,3-sialyltransferase

246 SDH 1 204742\_s\_a androgen-induced prostate proliferative shutoff associated protein

247 SDH 1 201182\_s\_a chromodomain helicase DNA binding protein 4

248 SDH 0.98 205902\_at potassium intermediate/small conductance calcium-activated channel, subfamily

249 SDH 0.97 200012\_x\_a ribosomal protein L21

250 SDH 0.97 208797\_s\_a golgin-67

251 SDH 0.96 214803\_at Homo sapiens mRNA; cDNA DKFZp564N1116 (from clone DKFZp564N1116

252 SDH 0.96 209669\_s\_a PAI-1 mRNA-binding protein

253 SDH 0.96 219862\_s\_a nuclear prelamin A recognition factor

254 SDH 0.96 200745\_s\_a guanine nucleotide binding protein (G protein), beta polypeptide

255 SDH 0.96 203006\_at inositol polyphosphate-5-phosphatase, 40kD;

256 SDH 0.95 202332\_at casein kinase 1, epsilon

257 SDH 0.95 204396\_s\_a G protein-coupled receptor kinase 2

258 SDH 0.95 219165\_at PDZ-LIM protein mystique

259 SDH 0.95 205031\_at ephrin-B3

260 SDH 0.94 201215\_at plastin 3 (T isoform)

261 SDH 0.94 212876\_at UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4

262 SDH 0.94 208923\_at cytoplasmic FMR1 interacting protein 1

263 SDH 0.94 202112\_at von Willebrand factor

264 SDH 0.94 215111\_s\_a transforming growth factor beta-stimulated protein TSC-2;

265 SDH 0.94 212285\_s\_a agrin

266 SDH 0.94 200934\_at DEK oncogene (DNA binding)

267 SDH 0.93 208693\_s\_a glycyl-tRNA synthetase

268 SDH 0.93 202548\_s\_a Rho guanine nucleotide exchange factor (GEF)

269 SDH 0.93 212273\_x\_a GNAS complex locus

270 SDH 0.93 211700\_s\_a trophinin

271 SDH 0.93 219024\_at pleckstrin homology domain containing, family A member 1

272 SDH 0.92 204115\_at guanine nucleotide binding protein 1

273 SDH 0.91 210776\_x\_a transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E4)

274 SDH 0.91 221878\_at Homo sapiens cDNA FLJ35653 fis, clone SPLEN201369f

275 SDH 0.91 210512\_s\_a vascular endothelial growth factor

276 SDH 0.9 203708\_at phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog)

277 SDH 0.9 221923\_s\_a nucleophosmin (nucleolar phosphoprotein B23, numatrin)

278 SDH 0.9 201054\_at heterogeneous nuclear ribonucleoprotein A1

279 SDH 0.9 214743\_at cut-like 1, CCAAT displacement protein (Drosophila)

280 SDH 0.9 211651\_s\_a accession number M20206.1

281 SDH 0.89 204622\_x\_a nuclear receptor subfamily 4, group A, member 2

282 SDH 0.89 209024\_s\_a NS1-associated protein 1

283 SDH 0.89 202233\_s\_a ubiquinol-cytochrome c reductase hinge protein

284 SDH 0.88 200888\_s\_a ribosomal protein L23

285 SDH 0.88 221726\_at ribosomal protein L22

286 SDH 0.88 206385\_s\_a ankyrin 3, node of Ranvier (ankyrin G)

287 SDH 0.88 201917\_s\_a hypothetical protein FLJ1061f

288 SDH 0.88 218834\_s\_a hypothetical protein FLJ2053f

289 SDH 0.87 205407\_at reversion-inducing-cysteine-rich protein with kazal motif

290 SDH 0.87 201970\_s\_a nuclear autoantigenic sperm protein (histone-binding)

291 SDH 0.87 203098\_at chromodomain protein, Y chromosome-like

292 SDH 0.86 209137\_s\_a ubiquitin specific protease 1C

293 SDH 0.86 217419\_x\_a agrin

294 SDH 0.85 218378\_s\_a hypothetical protein FLJ1390f

295 SDH 0.85 209162\_s\_a PRP4 pre-mRNA processing factor 4 homolog (yeast)

296 SDH 0.85 209087\_x\_a melanoma cell adhesion molecule

297 SDH 0.85 214039\_s\_a putative integral membrane transporter

298 SDH 0.85 200679\_x\_a high-mobility group box 1

299 SDH 0.85 201296\_s\_a SOCS box-containing WD protein SWIP-1

300 SDH 0.85 217057\_s\_a accession number AF10784f

301 SDH 0.85 221766\_s\_a chromosome 6 open reading frame 37

302 SDH 0.85 206481\_s\_a LIM domain binding 2

303 SDH 0.84 200981\_x\_a GNAS complex locus

304 SDH 0.84 201887\_at interleukin 13 receptor, alpha 1

305 SDH 0.84 207030\_s\_a cysteine and glycine-rich protein 2

306 SDH 0.84 212865\_s\_a collagen, type XIV, alpha 1 (undulin)

307 SDH 0.84 205304\_s\_a potassium inwardly-rectifying channel, subfamily J, member 1

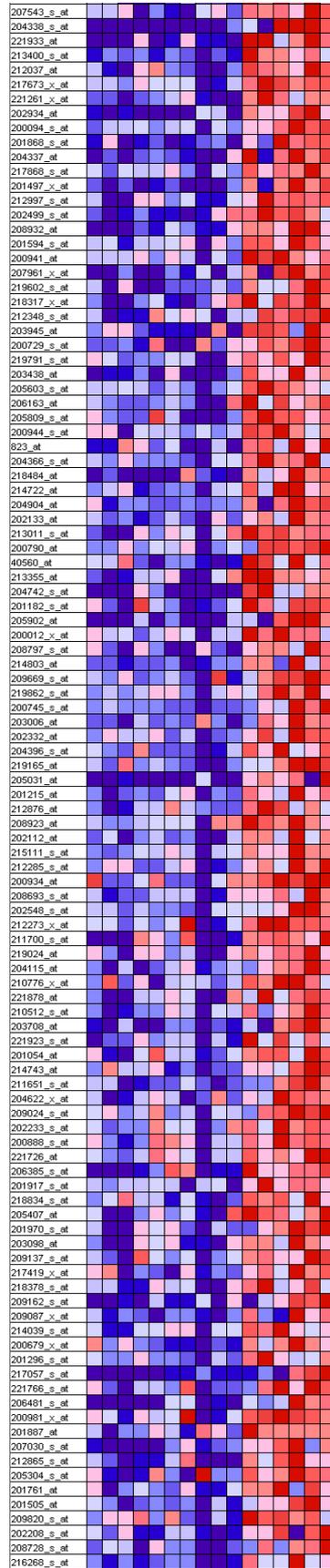
308 SDH 0.84 201761\_at methylene tetrahydrofolate dehydrogenase (NAD+ dependent)

309 SDH 0.84 201505\_at laminin, beta 1

310 SDH 0.84 209820\_s\_a transducin (beta)-like 3

311 SDH 0.83 202208\_s\_a ADP-ribosylation factor-like 7

312 SDH 0.83 208728\_s\_a cell division cycle 42 (GTP binding protein, 25kDa)



313 SDH 0.83 216268\_s\_a\_jagged 1 (Alagille syndrome)

314 SDH 0.83 221502\_at karyopherin alpha 3 (importin alpha 4)

315 SDH 0.82 210999\_s\_a growth factor receptor-bound protein 1f

316 SDH 0.82 221427\_s\_a likely ortholog of mouse Paneth cell enhanced expression

317 SDH 0.82 213401\_s\_a transducin (beta)-like 1X-linker

318 SDH 0.82 216331\_at integrin, alpha 7

319 SDH 0.82 213230\_at paraneoplastic antigen

320 SDH 0.82 203946\_s\_a arginase, type II

321 SDH 0.82 208981\_at platelet/endothelial cell adhesion molecule (CD31 antigen)

322 SDH 0.82 205224\_at surfeit 2

323 SDH 0.82 204472\_at GTP binding protein overexpressed in skeletal muscle

324 SDH 0.81 218258\_at RNA polymerase I 16 kDa subunit

325 SDH 0.81 209210\_s\_a mitogen inducible 2

326 SDH 0.81 208798\_x\_a golgin-67

327 SDH 0.81 209161\_at PRP4 pre-mRNA processing factor 4 homolog (yeast)

328 SDH 0.81 200878\_at Homo sapiens clone 23698 mRNA sequence

329 SDH 0.81 207966\_s\_a golgi apparatus protein 1

330 SDH 0.81 52255\_s\_at collagen, type V, alpha 3

331 SDH 0.81 213301\_x\_a transcriptional intermediary factor 1

332 SDH 0.8 213268\_at accession number Z98884

333 SDH 0.8 208803\_s\_a signal recognition particle 72kDa

334 SDH 0.8 206397\_x\_a growth differentiation factor 1

335 SDH 0.8 218137\_s\_a stromal membrane-associated protein

336 SDH 0.8 202146\_at interferon-related developmental regulator 1

337 SDH 0.8 211503\_s\_a RAB14, member RAS oncogene family

338 SDH 0.8 213491\_x\_a ribophorin II

339 SDH 0.8 213940\_s\_a formin-binding protein 17

340 SDH 0.8 209655\_s\_a brain cell membrane protein 1

341 SDH 0.8 205463\_s\_a platelet-derived growth factor alpha polypeptide

342 SDH 0.8 201209\_at histone deacetylase 1

343 SDH 0.8 201551\_s\_a lysosomal-associated membrane protein 1

344 SDH 0.8 201216\_at chromosome 12 open reading frame 8

345 SDH 0.8 221830\_at Homo sapiens cDNA FLJ37267 fis, clone BRAMY201129

346 SDH 0.79 201540\_at four and a half LIM domains 1

347 SDH 0.79 219532\_at elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like

348 SDH 0.79 202672\_s\_a activating transcription factor 2

349 SDH 0.79 218974\_at hypothetical protein FLJ10155

350 SDH 0.79 204078\_at nucleolar autoantigen (55KD) similar to rat synaptonemal complex protein

351 SDH 0.79 202458\_at protease, serine, 23

352 SDH 0.79 200746\_s\_a guanine nucleotide binding protein (G protein), beta polypeptide

353 SDH 0.78 200598\_s\_a tumor rejection antigen (gp96) 1

354 SDH 0.78 200606\_at desmoplakin (DPI, DPL)

355 SDH 0.78 204937\_s\_a zinc finger protein 274

356 SDH 0.78 201496\_x\_a myosin, heavy polypeptide 11, smooth muscle

357 SDH 0.78 205656\_at protocadherin 17

358 SDH 0.78 219249\_s\_a FK506 binding protein 10, 65 kDa

359 SDH 0.77 208661\_s\_a tetratricopeptide repeat domain 3

360 SDH 0.77 220584\_at hypothetical protein FLJ22184

361 SDH 0.77 221560\_at MAP/microtubule affinity-regulating kinase 4

362 SDH 0.77 40472\_at Homo sapiens clone 23763 unknown mRNA, partial cd

363 SDH 0.77 209337\_at PC4 and SFRS1 interacting protein 2

364 SDH 0.77 208775\_at exportin 1 (CRM1 homolog, yeast)

365 SDH 0.77 210095\_s\_a insulin-like growth factor binding protein 3

366 SDH 0.77 201190\_s\_a phosphatidylinositol transfer protein

367 SDH 0.77 218669\_at hypothetical protein similar to small G proteins, especially RAP-2f

368 SDH 0.77 204339\_s\_a regulator of G-protein signalling 4

369 SDH 0.76 210407\_at protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform

370 SDH 0.76 200999\_s\_a cytoskeleton-associated protein 4

371 SDH 0.76 209281\_s\_a ATPase, Ca++ transporting, plasma membrane 1

372 SDH 0.76 220694\_at HSPC054 protein

373 SDH 0.76 212979\_s\_a KIAA0738 gene product

374 SDH 0.76 212967\_x\_a nucleosome assembly protein 1-like 1

375 SDH 0.76 212730\_at desmuslin

376 SDH 0.75 212643\_at likely ortholog of mouse MAPK-interacting and spindle-stabilizing protein

377 SDH 0.75 209099\_x\_a jagged 1 (Alagille syndrome)

378 SDH 0.75 211564\_s\_a LIM domain protein

379 SDH 0.75 213901\_x\_a RNA binding motif protein 5

380 SDH 0.75 200632\_s\_a N-myc downstream regulated gene 1

381 SDH 0.75 201125\_s\_a integrin, beta 5

382 SDH 0.75 200755\_s\_a calumenin

383 SDH 0.74 204099\_at SWI/SNF related, matrix associated, regulator of chromatin, subfamily d, member 1

384 SDH 0.74 204464\_s\_a endothelin receptor type A

385 SDH 0.74 208985\_s\_a eukaryotic translation initiation factor 3, subunit 1 alpha, 35kD

386 SDH 0.74 203749\_s\_a retinoic acid receptor, alpha

387 SDH 0.74 204621\_s\_a nuclear receptor subfamily 4, group A, member 2

388 SDH 0.74 205303\_at potassium inwardly-rectifying channel, subfamily J, member 1

389 SDH 0.74 200713\_s\_a microtubule-associated protein, RP/EB family, member 1

390 SDH 0.74 218181\_s\_a hypothetical protein FLJ20373

391 SDH 0.74 214093\_s\_a Homo sapiens mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122)

392 SDH 0.74 201892\_s\_a IMP (inosine monophosphate) dehydrogenase 1

393 SDH 0.74 221846\_s\_a cask-interacting protein 2

394 SDH 0.73 208900\_s\_a topoisomerase (DNA) I

395 SDH 0.73 200650\_s\_a lactate dehydrogenase A

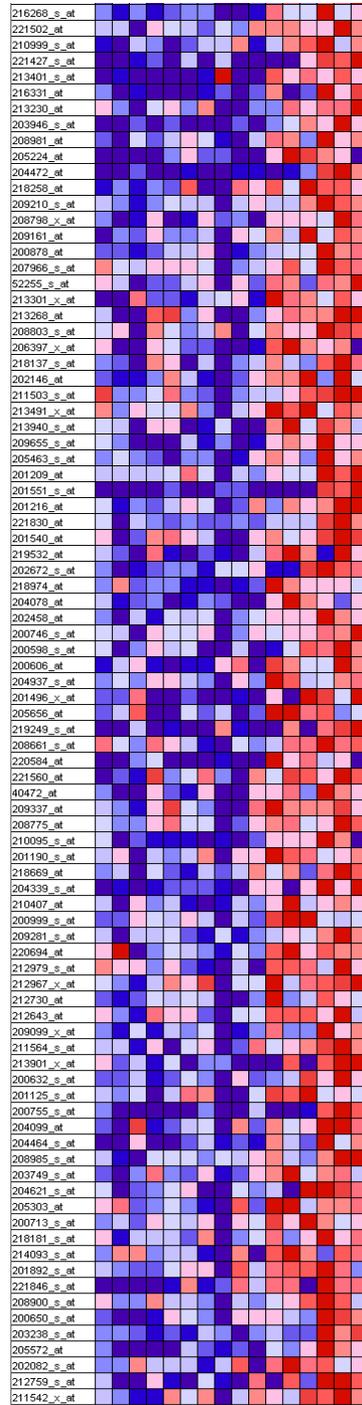
396 SDH 0.73 203238\_s\_a Notch homolog 3 (Drosophila)

397 SDH 0.73 205572\_at angiotensin II

398 SDH 0.73 202082\_s\_a SEC14-like 1 (S. cerevisiae)

399 SDH 0.73 212759\_s\_a transcription factor 7-like 2 (T-cell specific, HMG-box)

400 SDH 0.73 211542\_x\_a ribosomal protein S10



Application of the two-class prediction models to a test set made up of the entire dataset

MEN2 vs. VHL model		MEN2 vs. SDH model		FPT vs. VHL model		FPT vs. SDH model		Observed	Cluster men
Sample	Predicted	Sample	Predicted	Sample	Predicted	Sample	Predicted		
P101	VHL	P101	SDH	P101	VHL	P101	SDH	B_SDHB	1
P103	MEN2	P103	MEN2	P103	FPT	P103	FPT	MEN2A	2
P105	MEN2	P105	MEN2	P105	FPT	P105	FPT	SPOR	2
P106	MEN2	P106	MEN2	P106	FPT	P106	FPT	MEN2A	2
P107	VHL	P107	SDH	P107	VHL	P107	SDH	B_SDHB	1
P108	MEN2	P108	MEN2	P108	FPT	P108	FPT	SPOR	2
P111	MEN2	P111	MEN2	P111	FPT	P111	FPT	SPOR	2
P112	VHL	P112	MEN2	P112	FPT	P112	FPT	SPOR	2
P115	MEN2	P115	MEN2	P115	FPT	P115	FPT	MEN2A	2
P120	VHL	P120	SDH	P120	VHL	P120	SDH	SPOR	1
P122	MEN2	P122	MEN2	P122	FPT	P122	FPT	SPOR	2
P128	VHL	P128	MEN2	P128	VHL	P128	SDH	SPOR	1
P136	VHL	P136	SDH	P136	VHL	P136	SDH	B_SDHB	1
P140	VHL	P140	SDH	P140	VHL	P140	SDH	D_SDHD	1
P142	VHL	P142	SDH	P142	VHL	P142	SDH	VHL	1
P143	MEN2	P143	MEN2	P143	FPT	P143	FPT	NF1	2
P144	VHL	P144	SDH	P144	VHL	P144	FPT	SPOR	2
P145	MEN2	P145	MEN2	P145	FPT	P145	FPT	FP2	2
P146	MEN2	P146	MEN2	P146	FPT	P146	FPT	SPOR	2
P148	MEN2	P148	MEN2	P148	FPT	P148	FPT	SPOR	2
P149	MEN2	P149	MEN2	P149	FPT	P149	FPT	FP2	2
P150	MEN2	P150	MEN2	P150	FPT	P150	FPT	SPOR	2
P152	VHL	P152	SDH	P152	VHL	P152	SDH	FP3	1
P153	VHL	P153	SDH	P153	VHL	P153	SDH	VHL	1
P154	VHL	P154	SDH	P154	VHL	P154	SDH	VHL	1
P155	VHL	P155	MEN2	P155	VHL	P155	SDH	VHL	1
P156	VHL	P156	SDH	P156	VHL	P156	SDH	VHL	1
P157	MEN2	P157	MEN2	P157	VHL	P157	FPT	SPOR	2
P158	VHL	P158	SDH	P158	VHL	P158	SDH	SPOR	1
P16	VHL	P16	SDH	P16	VHL	P16	SDH	SPOR	1
P166	MEN2	P166	MEN2	P166	FPT	P166	FPT	SPOR	2
P167	MEN2	P167	MEN2	P167	FPT	P167	FPT	NF1	2
P171	MEN2	P171	MEN2	P171	FPT	P171	FPT	FP1	2
P172	MEN2	P172	MEN2	P172	FPT	P172	FPT	SPOR	2
P173	MEN2	P173	MEN2	P173	FPT	P173	FPT	SPOR	2
P174	MEN2	P174	MEN2	P174	FPT	P174	FPT	SPOR	2
P175	MEN2	P175	MEN2	P175	VHL	P175	FPT	SPOR	2
P176	MEN2	P176	MEN2	P176	FPT	P176	FPT	SPOR	2
P177	MEN2	P177	MEN2	P177	FPT	P177	FPT	SPOR	2
P178	MEN2	P178	MEN2	P178	FPT	P178	FPT	SPOR	2
P181	MEN2	P181	MEN2	P181	FPT	P181	FPT	SPOR	2
P182	MEN2	P182	MEN2	P182	FPT	P182	FPT	MEN2A	2
P188	MEN2	P188	MEN2	P188	FPT	P188	FPT	SPOR	2
P192	VHL	P192	MEN2	P192	VHL	P192	SDH	VHL	1
P195	MEN2	P195	MEN2	P195	FPT	P195	FPT	FP2	2
P196	MEN2	P196	MEN2	P196	FPT	P196	FPT	FP4	2
P197	MEN2	P197	MEN2	P197	FPT	P197	FPT	FP4	2
P198	MEN2	P198	MEN2	P198	FPT	P198	FPT	MEN2A	2
P203	VHL	P203	SDH	P203	VHL	P203	FPT	SPOR	1
P204	MEN2	P204	MEN2	P204	FPT	P204	FPT	SPOR	2
P205	MEN2	P205	MEN2	P205	FPT	P205	FPT	MEN2A	2
P207	MEN2	P207	MEN2	P207	FPT	P207	FPT	MEN2A	2
P208	VHL	P208	SDH	P208	VHL	P208	SDH	SPOR	2
P209	VHL	P209	SDH	P209	VHL	P209	SDH	SPOR	2
P210	MEN2	P210	MEN2	P210	FPT	P210	FPT	MEN2A	2
P215	MEN2	P215	MEN2	P215	FPT	P215	FPT	FP5	2
P216	MEN2	P216	SDH	P216	FPT	P216	SDH	SPOR	1
P218	MEN2	P218	MEN2	P218	FPT	P218	FPT	SPOR	2
P219	VHL	P219	SDH	P219	VHL	P219	SDH	SPOR	1
P220	VHL	P220	SDH	P220	VHL	P220	SDH	FP7	1
P26	MEN2	P26	MEN2	P26	FPT	P26	FPT	FP1	2
P27	MEN2	P27	MEN2	P27	FPT	P27	FPT	FP1	2
P29	VHL	P29	MEN2	P29	FPT	P29	FPT	FP1	2
P37	VHL	P37	SDH	P37	VHL	P37	SDH	SPOR	1
P54	MEN2	P54	MEN2	P54	FPT	P54	FPT	SPOR	2
P55	MEN2	P55	MEN2	P55	FPT	P55	FPT	SPOR	2
P56	MEN2	P56	MEN2	P56	FPT	P56	FPT	SPOR	2
P58	VHL	P58	SDH	P58	VHL	P58	SDH	B_SDHB	1
P61	MEN2	P61	MEN2	P61	FPT	P61	FPT	MEN2A	2
P76	VHL	P76	MEN2	P76	FPT	P76	FPT	FP6	2
P85	VHL	P85	SDH	P85	VHL	P85	SDH	SPOR	1
P87	MEN2	P87	MEN2	P87	FPT	P87	FPT	SPOR	2
P89	VHL	P89	SDH	P89	VHL	P89	SDH	B_SDHB	1
P91	MEN2	P91	MEN2	P91	FPT	P91	FPT	MEN2A	2
P92	VHL	P92	SDH	P92	VHL	P92	SDH	FP3	1
P93	VHL	P93	SDH	P93	VHL	P93	SDH	FP3	1
% correct		92%		93%		93%		95%	

Yellow highlight=incorrect predictions