

**Whole-genome resequencing reveals domestication and signatures of selection in Ujimqin, Sunit, and
Wu Ranke Mongolian sheep breeds**

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Table S1 GO terms between SNT and UJMQ

	<u>P-value</u>	<u>Term</u>	<u>Symbols</u>
<u>1</u>	<u>0.001324</u>	<u>gamma-aminobutyric acid catabolic process</u>	<u>ABAT</u>
<u>2</u>	<u>0.002647</u>	<u>gamma-aminobutyric acid metabolic process</u>	<u>ABAT</u>
<u>3</u>	<u>0.003968</u>	<u>estrogen biosynthetic process</u>	<u>HSD17B12</u>
<u>4</u>	<u>0.005288</u>	<u>estrogen metabolic process</u>	<u>HSD17B12</u>
<u>5</u>	<u>0.005288</u>	<u>behavioral response to cocaine</u>	<u>ABAT</u>
<u>6</u>	<u>0.006606</u>	<u>response to cocaine</u>	<u>ABAT</u>
<u>7</u>	<u>0.009239</u>	<u>neurotransmitter catabolic process</u>	<u>ABAT</u>
<u>8</u>	<u>0.009239</u>	<u>response to anesthetic</u>	<u>ABAT</u>
<u>9</u>	<u>0.010553</u>	<u>cellular response to increased oxygen levels</u>	<u>ATP6V1A</u>
<u>10</u>	<u>0.010553</u>	<u>response to increased oxygen levels</u>	<u>ATP6V1A</u>
<u>11</u>	<u>0.013467</u>	<u>monocarboxylic acid metabolic process</u>	<u>ABAT;HSD17B12</u>
<u>12</u>	<u>0.014486</u>	<u>response to alkaloid</u>	<u>ABAT</u>
<u>13</u>	<u>0.017101</u>	<u>cellular iron ion homeostasis</u>	<u>ATP6V1A</u>
<u>14</u>	<u>0.021013</u>	<u>hormone biosynthetic process</u>	<u>HSD17B12</u>
<u>15</u>	<u>0.024911</u>	<u>cellular transition metal ion homeostasis</u>	<u>ATP6V1A</u>
<u>16</u>	<u>0.026208</u>	<u>energy coupled proton transmembrane transport, against electrochemical gradient</u>	<u>ATP6V1A</u>
<u>17</u>	<u>0.026208</u>	<u>ATP hydrolysis coupled proton transport</u>	<u>ATP6V1A</u>
<u>18</u>	<u>0.026208</u>	<u>iron ion homeostasis</u>	<u>ATP6V1A</u>
<u>19</u>	<u>0.026208</u>	<u>response to ammonium ion</u>	<u>ABAT</u>
<u>20</u>	<u>0.026208</u>	<u>ATP hydrolysis coupled transmembrane transport</u>	<u>ATP6V1A</u>
<u>21</u>	<u>0.026208</u>	<u>ATP hydrolysis coupled ion transmembrane transport</u>	<u>ATP6V1A</u>
<u>22</u>	<u>0.027503</u>	<u>monocarboxylic acid catabolic process</u>	<u>ABAT</u>
<u>23</u>	<u>0.028439</u>	<u>small molecule metabolic process</u>	<u>ABAT;ATP6V1A;HSD17B12</u>
<u>24</u>	<u>0.035244</u>	<u>transition metal ion homeostasis</u>	<u>ATP6V1A</u>
<u>25</u>	<u>0.03653</u>	<u>cellular response to oxygen levels</u>	<u>ATP6V1A</u>
<u>26</u>	<u>0.039096</u>	<u>response to xenobiotic stimulus</u>	<u>ABAT</u>
<u>27</u>	<u>0.039096</u>	<u>cellular hormone metabolic process</u>	<u>HSD17B12</u>
<u>28</u>	<u>0.041656</u>	<u>adult behavior</u>	<u>ABAT</u>
<u>29</u>	<u>0.044211</u>	<u>ATP hydrolysis coupled cation transmembrane transport</u>	<u>ATP6V1A</u>
<u>30</u>	<u>0.04617</u>	<u>carboxylic acid metabolic process</u>	<u>ABAT;HSD17B12</u>
<u>31</u>	<u>0.04676</u>	<u>regulation of exocytosis</u>	<u>RPH3AL</u>
<u>32</u>	<u>0.04676</u>	<u>neurotransmitter metabolic process</u>	<u>ABAT</u>
<u>33</u>	<u>0.049303</u>	<u>steroid biosynthetic process</u>	<u>HSD17B12</u>
<u>34</u>	<u>0.049642</u>	<u>oxoacid metabolic process</u>	<u>ABAT;HSD17B12</u>
<u>35</u>	<u>0.051578</u>	<u>organic acid metabolic process</u>	<u>ABAT;HSD17B12</u>
<u>36</u>	<u>0.053108</u>	<u>cellular amino acid catabolic process</u>	<u>ABAT</u>
<u>37</u>	<u>0.065698</u>	<u>fatty acid biosynthetic process</u>	<u>HSD17B12</u>
<u>38</u>	<u>0.065698</u>	<u>hormone metabolic process</u>	<u>HSD17B12</u>

39	0.066238	regulation of biological quality	ABAT:ATP6V1A:HSD17B12
40	0.069448	response to oxygen levels	ATP6V1A
41	0.081856	regulation of neurotransmitter levels	ABAT
42	0.083089	proton transmembrane transport	ATP6V1A
43	0.086781	organic acid catabolic process	ABAT
44	0.086781	carboxylic acid catabolic process	ABAT
45	0.089235	exocytosis	RPH3AL
46	0.09046	steroid metabolic process	HSD17B12
47	0.10626	ATP metabolic process	ATP6V1A
48	0.10626	regulation of vesicle-mediated transport	RPH3AL
49	0.107466	monocarboxylic acid biosynthetic process	HSD17B12
50	0.111075	fatty acid metabolic process	HSD17B12
51	0.114672	cellular metal ion homeostasis	ATP6V1A
52	0.114672	purine ribonucleoside triphosphate metabolic process	ATP6V1A
53	0.117064	purine nucleoside triphosphate metabolic process	ATP6V1A
54	0.117064	ribonucleoside triphosphate metabolic process	ATP6V1A
55	0.11945	cellular amino acid metabolic process	ABAT
56	0.123019	purine nucleoside monophosphate metabolic process	ATP6V1A
57	0.123019	purine ribonucleoside monophosphate metabolic process	ATP6V1A
58	0.123019	regulation of hormone levels	HSD17B12
59	0.124206	behavior	ABAT
60	0.124206	small molecule catabolic process	ABAT
61	0.126576	nucleoside triphosphate metabolic process	ATP6V1A
62	0.127759	ribonucleoside monophosphate metabolic process	ATP6V1A
63	0.1313	cellular cation homeostasis	ATP6V1A
64	0.132477	nucleoside monophosphate metabolic process	ATP6V1A
65	0.133654	metal ion homeostasis	ATP6V1A
66	0.136002	cellular ion homeostasis	ATP6V1A
67	0.148825	carboxylic acid biosynthetic process	HSD17B12
68	0.149983	organic acid biosynthetic process	HSD17B12
69	0.152295	cation homeostasis	ATP6V1A
70	0.154601	inorganic ion homeostasis	ATP6V1A
71	0.155752	regulation of secretion by cell	RPH3AL
72	0.158259	biological regulation	ABAT:ATP6V1A:ADGRE5;RPH3AL;HSD17B12
73	0.161489	cellular chemical homeostasis	ATP6V1A
74	0.162632	monovalent inorganic cation transport	ATP6V1A
75	0.163774	purine ribonucleotide metabolic process	ATP6V1A

76	0.16833	ribonucleotide metabolic process	ATP6V1A
77	0.169466	purine nucleotide metabolic process	ATP6V1A
78	0.169466	response to organic cyclic compound	ABAT
79	0.169466	ribose phosphate metabolic process	ATP6V1A
80	0.172865	regulation of secretion	RPH3AL
81	0.175124	ion homeostasis	ATP6V1A
82	0.187461	purine-containing compound metabolic process	ATP6V1A
83	0.191909	lipid biosynthetic process	HSD17B12
84	0.194125	intracellular protein transport	RPH3AL
85	0.195231	response to organonitrogen compound	ABAT
86	0.19744	inorganic cation transmembrane transport	ATP6V1A
87	0.202939	nucleotide metabolic process	ATP6V1A
88	0.204035	response to drug	ABAT
89	0.206224	nucleoside phosphate metabolic process	ATP6V1A
90	0.209497	cellular homeostasis	ATP6V1A
91	0.218171	inorganic ion transmembrane transport	ATP6V1A
92	0.219249	secretion by cell	RPH3AL
93	0.219249	cation transmembrane transport	ATP6V1A
94	0.223552	response to nitrogen compound	ABAT
95	0.23634	nucleobase-containing small molecule metabolic process	ATP6V1A
96	0.239509	small molecule biosynthetic process	HSD17B12
97	0.248952	secretion	RPH3AL
98	0.251037	response to abiotic stimulus	ATP6V1A
99	0.251037	chemical homeostasis	ATP6V1A
100	0.259329	drug metabolic process	ATP6V1A
101	0.276695	ion transmembrane transport	ATP6V1A
102	0.279659	response to chemical	ABAT;ATP6V1A
103	0.279725	cell adhesion	ADGRE5
104	0.283747	translation	MRPL19
105	0.283747	cellular lipid metabolic process	HSD17B12
106	0.28475	biological adhesion	ADGRE5
107	0.288749	peptide biosynthetic process	MRPL19
108	0.297679	cation transport	ATP6V1A
109	0.308466	organophosphate metabolic process	ATP6V1A
110	0.310412	response to oxygen-containing compound	ABAT
111	0.315258	amide biosynthetic process	MRPL19
112	0.315258	organonitrogen compound catabolic process	ABAT
113	0.318152	peptide metabolic process	MRPL19
114	0.322953	carbohydrate derivative metabolic process	ATP6V1A
115	0.327725	intracellular transport	RPH3AL
116	0.343742	cellular protein localization	RPH3AL
117	0.345605	cellular macromolecule localization	RPH3AL

118	0.347196	cellular process	ABAT:ATP6V1A:ADGRE5:MRPL19:RPH3AL:HSD17B12
119	0.350244	vesicle-mediated transport	RPH3AL
120	0.363088	regulation of transport	RPH3AL
121	0.367623	cellular amide metabolic process	MRPL19
122	0.374823	transmembrane transport	ATP6V1A
123	0.376613	lipid metabolic process	HSD17B12
124	0.38814	homeostatic process	ATP6V1A
125	0.389898	establishment of localization in cell	RPH3AL
126	0.392061	organonitrogen compound metabolic process	ABAT:ATP6V1A:MRPL19
127	0.405528	ion transport	ATP6V1A
128	0.408955	protein transport	RPH3AL
129	0.416607	peptide transport	RPH3AL
130	0.423339	amide transport	RPH3AL
131	0.424176	establishment of protein localization	RPH3AL
132	0.425847	oxidation-reduction process	HSD17B12
133	0.427103	transport	ATP6V1A:RPH3AL
134	0.437426	primary metabolic process	ABAT:ATP6V1A:MRPL19:HSD17B12
135	0.440943	establishment of localization	ATP6V1A:RPH3AL
136	0.443962	cell surface receptor signaling pathway	ADGRE5
137	0.456671	cellular metabolic process	ABAT:ATP6V1A:MRPL19:HSD17B12
138	0.45916	response to stimulus	ABAT:ATP6V1A:ADGRE5
139	0.471019	cellular catabolic process	ABAT
140	0.476451	organic substance catabolic process	ABAT
141	0.491715	nitrogen compound transport	RPH3AL
142	0.498462	cellular localization	RPH3AL
143	0.499245	organic substance metabolic process	ABAT:ATP6V1A:MRPL19:HSD17B12
144	0.502178	regulation of localization	RPH3AL
145	0.523996	protein localization	RPH3AL
146	0.528262	catabolic process	ABAT
147	0.52897	organonitrogen compound biosynthetic process	MRPL19
148	0.529883	cellular biosynthetic process	MRPL19:HSD17B12
149	0.534882	organic cyclic compound metabolic process	ATP6V1A:HSD17B12
150	0.535302	response to organic substance	ABAT
151	0.546296	organic substance biosynthetic process	MRPL19:HSD17B12
152	0.54912	organic substance transport	RPH3AL
153	0.553197	cellular response to chemical stimulus	ATP6V1A
154	0.559054	biosynthetic process	MRPL19:HSD17B12
155	0.571171	localization	ATP6V1A:RPH3AL
156	0.577024	macromolecule localization	RPH3AL
157	0.609752	metabolic process	ABAT:ATP6V1A:MRPL19:HSD17B12
158	0.611654	cellular response to stimulus	ATP6V1A:ADGRE5

<u>159</u>	<u>0.613031</u>	<u>cellular nitrogen compound metabolic process</u>	<u>ATP6V1A;MRPL19</u>
<u>160</u>	<u>0.643932</u>	<u>phosphate-containing compound metabolic process</u>	<u>ATP6V1A</u>
<u>161</u>	<u>0.64561</u>	<u>phosphorus metabolic process</u>	<u>ATP6V1A</u>
<u>162</u>	<u>0.672967</u>	<u>nitrogen compound metabolic process</u>	<u>ABAT;ATP6V1A;MRPL19</u>
<u>163</u>	<u>0.674183</u>	<u>organic cyclic compound biosynthetic process</u>	<u>HSD17B12</u>
<u>164</u>	<u>0.743578</u>	<u>cellular macromolecule biosynthetic process</u>	<u>MRPL19</u>
<u>165</u>	<u>0.764563</u>	<u>macromolecule biosynthetic process</u>	<u>MRPL19</u>
<u>166</u>	<u>0.766146</u>	<u>cellular nitrogen compound biosynthetic process</u>	<u>MRPL19</u>
<u>167</u>	<u>0.797056</u>	<u>gene expression</u>	<u>MRPL19</u>
<u>168</u>	<u>0.799151</u>	<u>signal transduction</u>	<u>ADGRE5</u>
<u>169</u>	<u>0.818175</u>	<u>signaling</u>	<u>ADGRE5</u>
<u>170</u>	<u>0.824483</u>	<u>cell communication</u>	<u>ADGRE5</u>
<u>171</u>	<u>0.825414</u>	<u>nucleobase-containing compound metabolic process</u>	<u>ATP6V1A</u>
<u>172</u>	<u>0.838883</u>	<u>heterocycle metabolic process</u>	<u>ATP6V1A</u>
<u>173</u>	<u>0.843458</u>	<u>cellular aromatic compound metabolic process</u>	<u>ATP6V1A</u>
<u>174</u>	<u>0.846262</u>	<u>cellular protein metabolic process</u>	<u>MRPL19</u>
<u>175</u>	<u>0.847017</u>	<u>regulation of cellular process</u>	<u>ADGRE5;RPH3AL</u>
<u>176</u>	<u>0.879982</u>	<u>multicellular organismal process</u>	<u>ABAT</u>
<u>177</u>	<u>0.88575</u>	<u>protein metabolic process</u>	<u>MRPL19</u>
<u>178</u>	<u>0.892937</u>	<u>regulation of biological process</u>	<u>ADGRE5;RPH3AL</u>
<u>179</u>	<u>0.947792</u>	<u>cellular macromolecule metabolic process</u>	<u>MRPL19</u>
<u>180</u>	<u>0.975561</u>	<u>macromolecule metabolic process</u>	<u>MRPL19</u>
<u>181</u>	<u>0.001538</u>	<u>4-aminobutyrate transaminase activity</u>	<u>ABAT</u>
<u>182</u>	<u>0.001538</u>	<u>4-aminobutyrate:2-oxoglutarate transaminase activity</u>	<u>ABAT</u>
<u>183</u>	<u>0.001538</u>	<u>(S)-3-amino-2-methylpropionate transaminase activity</u>	<u>ABAT</u>
<u>184</u>	<u>0.001538</u>	<u>3-oxo-arachidoyl-CoA reductase activity</u>	<u>HSD17B12</u>
<u>185</u>	<u>0.001538</u>	<u>3-oxo-behenoyl-CoA reductase activity</u>	<u>HSD17B12</u>
<u>186</u>	<u>0.001538</u>	<u>3-oxo-lignoceroyl-CoA reductase activity</u>	<u>HSD17B12</u>
<u>187</u>	<u>0.001538</u>	<u>3-oxo-cerotoyl-CoA reductase activity</u>	<u>HSD17B12</u>
<u>188</u>	<u>0.007671</u>	<u>estradiol 17-beta-dehydrogenase activity</u>	<u>HSD17B12</u>
<u>189</u>	<u>0.015292</u>	<u>steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor</u>	<u>HSD17B12</u>
<u>190</u>	<u>0.016811</u>	<u>transaminase activity</u>	<u>ABAT</u>
<u>191</u>	<u>0.016811</u>	<u>steroid dehydrogenase activity</u>	<u>HSD17B12</u>

<u>192</u>	<u>0.019842</u>	<u>transferase activity, transferring nitrogenous groups</u>	<u>ABAT</u>
<u>193</u>	<u>0.027385</u>	<u>Rab GTPase binding</u>	<u>RPH3AL</u>
<u>194</u>	<u>0.029576</u>	<u>calcium ion binding</u>	<u>ADGRE5;EFCAB3</u>
<u>195</u>	<u>0.043811</u>	<u>pyridoxal phosphate binding</u>	<u>ABAT</u>
<u>196</u>	<u>0.043811</u>	<u>vitamin B6 binding</u>	<u>ABAT</u>
<u>197</u>	<u>0.052672</u>	<u>iron-sulfur cluster binding</u>	<u>ABAT</u>
<u>198</u>	<u>0.052672</u>	<u>metal cluster binding</u>	<u>ABAT</u>
<u>199</u>	<u>0.052746</u>	<u>ion binding</u>	<u>ABAT:ATP6V1A:ADGRE5;EFCAB3;RPH3AL</u>
<u>200</u>	<u>0.056755</u>	<u>metal ion binding</u>	<u>ABAT:ADGRE5;EFCAB3;RPH3AL</u>
<u>201</u>	<u>0.058185</u>	<u>cation binding</u>	<u>ABAT:ADGRE5;EFCAB3;RPH3AL</u>
<u>202</u>	<u>0.067289</u>	<u>Ras GTPase binding</u>	<u>RPH3AL</u>
<u>203</u>	<u>0.067289</u>	<u>small GTPase binding</u>	<u>RPH3AL</u>
<u>204</u>	<u>0.073083</u>	<u>oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor</u>	<u>HSD17B12</u>
<u>205</u>	<u>0.081718</u>	<u>oxidoreductase activity, acting on CH-OH group of donors</u>	<u>HSD17B12</u>
<u>206</u>	<u>0.094544</u>	<u>vitamin binding</u>	<u>ABAT</u>
<u>207</u>	<u>0.104417</u>	<u>GTPase binding</u>	<u>RPH3AL</u>
<u>208</u>	<u>0.147209</u>	<u>drug binding</u>	<u>ABAT:ATP6V1A</u>
<u>209</u>	<u>0.160458</u>	<u>coenzyme binding</u>	<u>ABAT</u>
<u>210</u>	<u>0.257824</u>	<u>cofactor binding</u>	<u>ABAT</u>
<u>211</u>	<u>0.270931</u>	<u>protein homodimerization activity</u>	<u>ABAT</u>
<u>212</u>	<u>0.311136</u>	<u>small molecule binding</u>	<u>ABAT:ATP6V1A</u>
<u>213</u>	<u>0.32183</u>	<u>anion binding</u>	<u>ABAT:ATP6V1A</u>
<u>214</u>	<u>0.365863</u>	<u>oxidoreductase activity</u>	<u>HSD17B12</u>
<u>215</u>	<u>0.37632</u>	<u>protein dimerization activity</u>	<u>ABAT</u>
<u>216</u>	<u>0.430337</u>	<u>enzyme binding</u>	<u>RPH3AL</u>
<u>217</u>	<u>0.451197</u>	<u>identical protein binding</u>	<u>ABAT</u>
<u>218</u>	<u>0.462303</u>	<u>ATP binding</u>	<u>ATP6V1A</u>
<u>219</u>	<u>0.475923</u>	<u>adenyl ribonucleotide binding</u>	<u>ATP6V1A</u>
<u>220</u>	<u>0.476821</u>	<u>adenyl nucleotide binding</u>	<u>ATP6V1A</u>
<u>221</u>	<u>0.530029</u>	<u>transferase activity</u>	<u>ABAT</u>
<u>222</u>	<u>0.559576</u>	<u>purine ribonucleoside triphosphate binding</u>	<u>ATP6V1A</u>
<u>223</u>	<u>0.576398</u>	<u>purine ribonucleotide binding</u>	<u>ATP6V1A</u>
<u>224</u>	<u>0.57715</u>	<u>purine nucleotide binding</u>	<u>ATP6V1A</u>
<u>225</u>	<u>0.5779</u>	<u>ribonucleotide binding</u>	<u>ATP6V1A</u>
<u>226</u>	<u>0.597024</u>	<u>binding</u>	<u>ABAT:ATP6V1A:ADGRE5;EFCAB3;RPH3AL</u>
<u>227</u>	<u>0.633129</u>	<u>carbohydrate derivative binding</u>	<u>ATP6V1A</u>
<u>228</u>	<u>0.635012</u>	<u>heterocyclic compound binding</u>	<u>ABAT:ATP6V1A</u>
<u>229</u>	<u>0.642373</u>	<u>nucleotide binding</u>	<u>ATP6V1A</u>
<u>230</u>	<u>0.642373</u>	<u>nucleoside phosphate binding</u>	<u>ATP6V1A</u>
<u>231</u>	<u>0.643237</u>	<u>organic cyclic compound binding</u>	<u>ABAT:ATP6V1A</u>

<u>232</u>	<u>0.70169</u>	<u>protein binding</u>	<u>ABAT:RPH3AL</u>
<u>233</u>	<u>0.712221</u>	<u>catalytic activity</u>	<u>ABAT:HSD17B12</u>
<u>234</u>	<u>0.001054</u>	<u>4-aminobutyrate transaminase complex</u>	<u>ABAT</u>
<u>235</u>	<u>0.006312</u>	<u>proton-transporting V-type ATPase, V1 domain</u>	<u>ATP6V1A</u>
<u>236</u>	<u>0.010502</u>	<u>proton-transporting two-sector ATPase complex, catalytic domain</u>	<u>ATP6V1A</u>
<u>237</u>	<u>0.01444</u>	<u>mitochondrial matrix</u>	<u>ABAT:MRPL19</u>
<u>238</u>	<u>0.01572</u>	<u>proton-transporting V-type ATPase complex</u>	<u>ATP6V1A</u>
<u>239</u>	<u>0.020915</u>	<u>microvillus</u>	<u>ATP6V1A</u>
<u>240</u>	<u>0.028364</u>	<u>cytoplasmic part</u>	<u>ABAT:ATP6V1A;MRPL19;RPH3AL:HSD17B12</u>
<u>241</u>	<u>0.040459</u>	<u>proton-transporting two-sector ATPase complex</u>	<u>ATP6V1A</u>
<u>242</u>	<u>0.044534</u>	<u>organellar large ribosomal subunit</u>	<u>MRPL19</u>
<u>243</u>	<u>0.044534</u>	<u>mitochondrial large ribosomal subunit</u>	<u>MRPL19</u>
<u>244</u>	<u>0.048595</u>	<u>large ribosomal subunit</u>	<u>MRPL19</u>
<u>245</u>	<u>0.048595</u>	<u>actin-based cell projection</u>	<u>ATP6V1A</u>
<u>246</u>	<u>0.05062</u>	<u>transport vesicle membrane</u>	<u>RPH3AL</u>
<u>247</u>	<u>0.066697</u>	<u>apical plasma membrane</u>	<u>ATP6V1A</u>
<u>248</u>	<u>0.075516</u>	<u>mitochondrial part</u>	<u>ABAT:MRPL19</u>
<u>249</u>	<u>0.075644</u>	<u>organellar ribosome</u>	<u>MRPL19</u>
<u>250</u>	<u>0.075644</u>	<u>mitochondrial ribosome</u>	<u>MRPL19</u>
<u>251</u>	<u>0.080585</u>	<u>apical part of cell</u>	<u>ATP6V1A</u>
<u>252</u>	<u>0.085505</u>	<u>transport vesicle</u>	<u>RPH3AL</u>
<u>253</u>	<u>0.088447</u>	<u>ribosomal subunit</u>	<u>MRPL19</u>
<u>254</u>	<u>0.101451</u>	<u>cytoplasm</u>	<u>ABAT:ATP6V1A;MRPL19;RPH3AL:HSD17B12</u>
<u>255</u>	<u>0.105939</u>	<u>ribosome</u>	<u>MRPL19</u>
<u>256</u>	<u>0.127433</u>	<u>protein-containing complex</u>	<u>ABAT:ATP6V1A;MRPL19</u>
<u>257</u>	<u>0.133614</u>	<u>mitochondrion</u>	<u>ABAT:MRPL19</u>
<u>258</u>	<u>0.140082</u>	<u>membrane</u>	<u>ATP6V1A;MRPL19;RPH3AL:HSD17B12</u>
<u>259</u>	<u>0.140117</u>	<u>cytoplasmic vesicle membrane</u>	<u>RPH3AL</u>
<u>260</u>	<u>0.141985</u>	<u>vesicle membrane</u>	<u>RPH3AL</u>
<u>261</u>	<u>0.14679</u>	<u>intracellular organelle part</u>	<u>ABAT:MRPL19;RPH3AL:HSD17B12</u>
<u>262</u>	<u>0.164428</u>	<u>organelle part</u>	<u>ABAT:MRPL19;RPH3AL:HSD17B12</u>
<u>263</u>	<u>0.165058</u>	<u>mitochondrial protein complex</u>	<u>MRPL19</u>
<u>264</u>	<u>0.167793</u>	<u>transferase complex</u>	<u>ABAT</u>
<u>265</u>	<u>0.227437</u>	<u>organelle membrane</u>	<u>MRPL19;RPH3AL</u>
<u>266</u>	<u>0.227893</u>	<u>cytoplasmic vesicle part</u>	<u>RPH3AL</u>
<u>267</u>	<u>0.246575</u>	<u>plasma membrane region</u>	<u>ATP6V1A</u>
<u>268</u>	<u>0.248255</u>	<u>ribonucleoprotein complex</u>	<u>MRPL19</u>
<u>269</u>	<u>0.254233</u>	<u>membrane-enclosed lumen</u>	<u>ABAT:MRPL19</u>
<u>270</u>	<u>0.254233</u>	<u>organelle lumen</u>	<u>ABAT:MRPL19</u>
<u>271</u>	<u>0.254233</u>	<u>intracellular organelle lumen</u>	<u>ABAT:MRPL19</u>
<u>272</u>	<u>0.258273</u>	<u>endoplasmic reticulum membrane</u>	<u>HSD17B12</u>

273	0.259104	endoplasmic reticulum subcompartment	HSD17B12
274	0.263243	mitochondrial inner membrane	MRPL19
275	0.264068	nuclear outer membrane-endoplasmic reticulum membrane network	HSD17B12
276	0.275549	organelle inner membrane	MRPL19
277	0.286886	endoplasmic reticulum part	HSD17B12
278	0.29027	endomembrane system	RPH3AL;HSD17B12
279	0.297017	intracellular	ABAT;ATP6V1A;MRPL19;RPH3AL;HSD17B12
280	0.297017	intracellular part	ABAT;ATP6V1A;MRPL19;RPH3AL;HSD17B12
281	0.302835	membrane protein complex	ATP6V1A
282	0.320822	mitochondrial membrane	MRPL19
283	0.331588	mitochondrial envelope	MRPL19
284	0.331588	catalytic complex	ABAT
285	0.33616	whole membrane	RPH3AL
286	0.347203	membrane-bounded organelle	ABAT;MRPL19;RPH3AL;HSD17B12
287	0.363069	organelle subcompartment	HSD17B12
288	0.369658	plasma membrane bounded cell projection	ATP6V1A
289	0.381955	plasma membrane part	ATP6V1A
290	0.386962	cell projection	ATP6V1A
291	0.389098	endoplasmic reticulum	HSD17B12
292	0.40109	organelle envelope	MRPL19
293	0.40109	envelope	MRPL19
294	0.416329	bounding membrane of organelle	RPH3AL
295	0.417698	cytoplasmic vesicle	RPH3AL
296	0.417698	intracellular vesicle	RPH3AL
297	0.435273	vesicle	RPH3AL
298	0.473813	intracellular organelle	ABAT;MRPL19;RPH3AL;HSD17B12
299	0.484874	cell part	ABAT;ATP6V1A;MRPL19;RPH3AL;HSD17B12
300	0.495606	cell	ABAT;ATP6V1A;MRPL19;RPH3AL;HSD17B12
301	0.502257	organelle	ABAT;MRPL19;RPH3AL;HSD17B12
302	0.5326	cytosol	ATP6V1A
303	0.552015	membrane part	ATP6V1A;HSD17B12
304	0.604898	intracellular membrane-bounded organelle	ABAT;MRPL19;HSD17B12
305	0.633825	plasma membrane	ATP6V1A
306	0.645476	cell periphery	ATP6V1A
307	0.72242	non-membrane-bounded organelle	MRPL19
308	0.72242	intracellular non-membrane-bounded organelle	MRPL19
309	0.761944	integral component of membrane	HSD17B12
310	0.774067	intrinsic component of membrane	HSD17B12