55 (n=27, var=0.08)
56 (n=30, var=0.44)
57 (n=113, var=0.23)
58 (n=39, var=0.12)
59 (n=32, var=0.12)
60 (n=63, var=0.09)
61 (n=47, var=0.09)
62 (n=35, var=0.19)
63 (n=32, var=0.09)
64 (n=132, var=0.24)
65 (n=21, var=0.50)
66 (n=24, var=0.12)
67 (n=27, var=0.41)
68 (n=69, var=0.12)
69 (n=24, var=0.02)
70 (n=33, var=0.03)
71 (n=35, var=0.13)
72 (n=154, var=0.18)

163 (n=69, var=0.20)
164 (n=34, var=0.05)
165 (n=28, var=0.10)
166 (n=25, var=0.08)
167 (n=25, var=0.13)
168 (n=20, var=0.16)
169 (n=24, var=0.10)
170 (n=37, var=0.31)
171 (n=17, var=0.12)
172 (n=10, var=1.25)
173 (n=35, var=0.15)
174 (n=39, var=0.07)
175 (n=17, var=0.10)
176 (n=33, var=0.17)
177 (n=12, var=0.08)
178 (n=45, var=0.12)
179 (n=19, var=0.40)
180 (n=21, var=0.19)

Two hundred and seven co-expression modules for genes with similar mRNA abundance patterns across the different developmental stages. Each line represents a gene, with genes of particular interest labeled with different colors and/or line patterns. The CPM (counts per million) represents the proportion of reads mapped to each Leishmania gene multiplied by one million.