Figure 2: A neighbor-joining (NJ) phylogenetic tree showing relationships between all known HRV serotypes created on the basis of full genome sequences. The HEV-C sequences (poliovirus 1M, coxsackievirus a13, and coxsackievirus a21) were used as outgroups. Branch lengths are proportional to similarity (p-distance). Key nodes on this tree are annotated with NJ bootstrap values (percentage of 2000 sampled trees). Asterisks in the strain names identify sequences obtained from published data (table S1). All other taxa are from this study. Letters in the outer rings designate whether that virus uses the major (M) ICAM-1 receptor or the minor (m) LDLR receptor (7) and whether its relative reactivity was more like group “1” or group “2” (if known) toward a panel of small-molecule antiviral compounds.