This is an outline of steps required to get MEGAN to tell you your taxonomic path based on raw blast results.

1. Generate blast results
   1. See commands in blast\_commands.txt
2. Import file into MEGAN
   1. Select File -> Import from BLAST
   2. Use the GUI to find your blast outputs. Select the format to match your blast results. XML format from BLAST seems to work great.
3. Export taxonomies from MEGAN
   1. Click Rank within the MEGAN window and select Species (if you want to look at Species)
   2. Click Select (next to File at the very top of your screen) -> All Nodes
   3. Select File -> Export -> Export CSV
   4. On the top dropdown menu, select readName\_to\_taxonPath.
   5. On the second dropdown, select assigned
   6. The third just controls your export format. Probably keep comma selected.
   7. Click OK. You’ll be prompted to save your file. Do so, and those will be your taxonomies.