**Additional file 4 — The performance of NHMC and other methods in predicting FUN annotations of yeast genes**

The $AU\overline{PRC}$ of models learned by HMC-GA, HMC-LMLP, hmAnt-Miner and NHMC (using $\alpha = 0.5$ and the DIP PPI network), for 7 FUN annotated yeast datasets, as used in Cerri at al. [33].

| Dataset/Method | HMC-GA | HMC-LMLP | hmAnt-Miner | NHMC ($\alpha = 0.5$) |
|---|---|---|---|---|
| pheno | 0.148 | 0.085 | 0.162 | 0.241 |
| cellcycle | 0.150 | 0.144 | 0.154 | 0.173 |
| church | 0.149 | 0.140 | 0.168 | 0.152 |
| derisi | 0.152 | 0.138 | 0.161 | 0.172 |
| eisen | 0.165 | 0.173 | 0.180 | 0.196 |
| gasch2 | 0.151 | 0.132 | 0.163 | 0.186 |
| spo | 0.151 | 0.139 | 0.174 | 0.181 |