



Figure S3. *Nbr-CYP-22A1* groups with *Cel-DAF-9* by phylogenetic analysis.

N. brasiliensis transcripts predicted to encode polypeptides with a cytochrome P450 domain were translated; predicted protein sequences were aligned, along with *C. elegans* DAF-9A, using ClustalW. A neighbor-joining phylogenetic tree was constructed with 100 iterations of bootstrapping. *Nbr-CYP-22A1* grouped most closely with *Cel-DAF-9*. Scale bar represents number of substitutions per position.