

modules of size ℓ plotted in different colors. We show the identified modules corresponding to *C12*-neural system and *C13*-eye system (full structure is in Fig. 2c and SI-Fig. 6), which first appear at $\ell = 15$ and $\ell = 11$, respectively. At other scales the box-covering algorithm detects new functional relations between cell types expressed in the obtained sub and super-modules. For instance, at $\ell = 11$ the neural lineage is further divided into two sub-modules, while at $\ell = 19$ the two functions merge into a super-module. **c**, The network of modules at different ℓ values, as detected through the box-covering algorithm. Every node corresponds to one of the three following types, in terms of increasing scale: (i) Sub-modules (small grey dots), which are fractions of a fully functional module, (ii) Known functional biological modules (colored circles), whose color corresponds to the functions *C1-C19*, and (iii) Super-modules (pie-charts), which represent the union of more than one known functional module, described by the colors of the pie-chart. The links that stem from known functional modules and super-modules are shown in red, and they progressively span the entire network as we increase ℓ .

Fig. 3. Modular properties of the NHCD. **a**, Degree of modularity of the network, $\mathcal{M}(\ell)$ at different times T_a (indicated in the figure) as a function of the scale of observation, ℓ . **b**, Number of boxes/modules, N_B , versus the size of the modules ℓ identified by the box-covering algorithm for different networks at time T_a .

Fig. 4. Growth properties of the NHCD. **a**, Number of cell types in the network, $N(t)$, as a function of time. We find precise information about the appearance time T_a for 782 among the 873 cell types. Those cells with missing appearance time have not been taken into account in this plot. Also shown are the time evolution of the number of surviving and non-surviving cells. **b**, Number of nodes whose degree increases at time t (red histogram) and number of new links appearing in the network (blue histogram) as a function of time. If all nodes were giving just one child then the two histograms would coincide. Inset: The average number of new links per node at a given time can be found by dividing the two histograms in the main plot. This plot shows how intense is the activity at that particular time. Despite the variation in activity, the new connections average around 1, which gives a critical branching ratio of $\langle k \rangle \simeq 2$. **c**, Number of cell types versus the chemical distance to the first node, ℓ_{N1} . This distance is only determined by the connections between the cell types, and is not influenced by the appearance time, so that we include all 873 cell types. **d**, Average degree $\langle k \rangle$ of the network as a function of time showing that the network achieves