## *Supplementary Figures*

### Figure S1

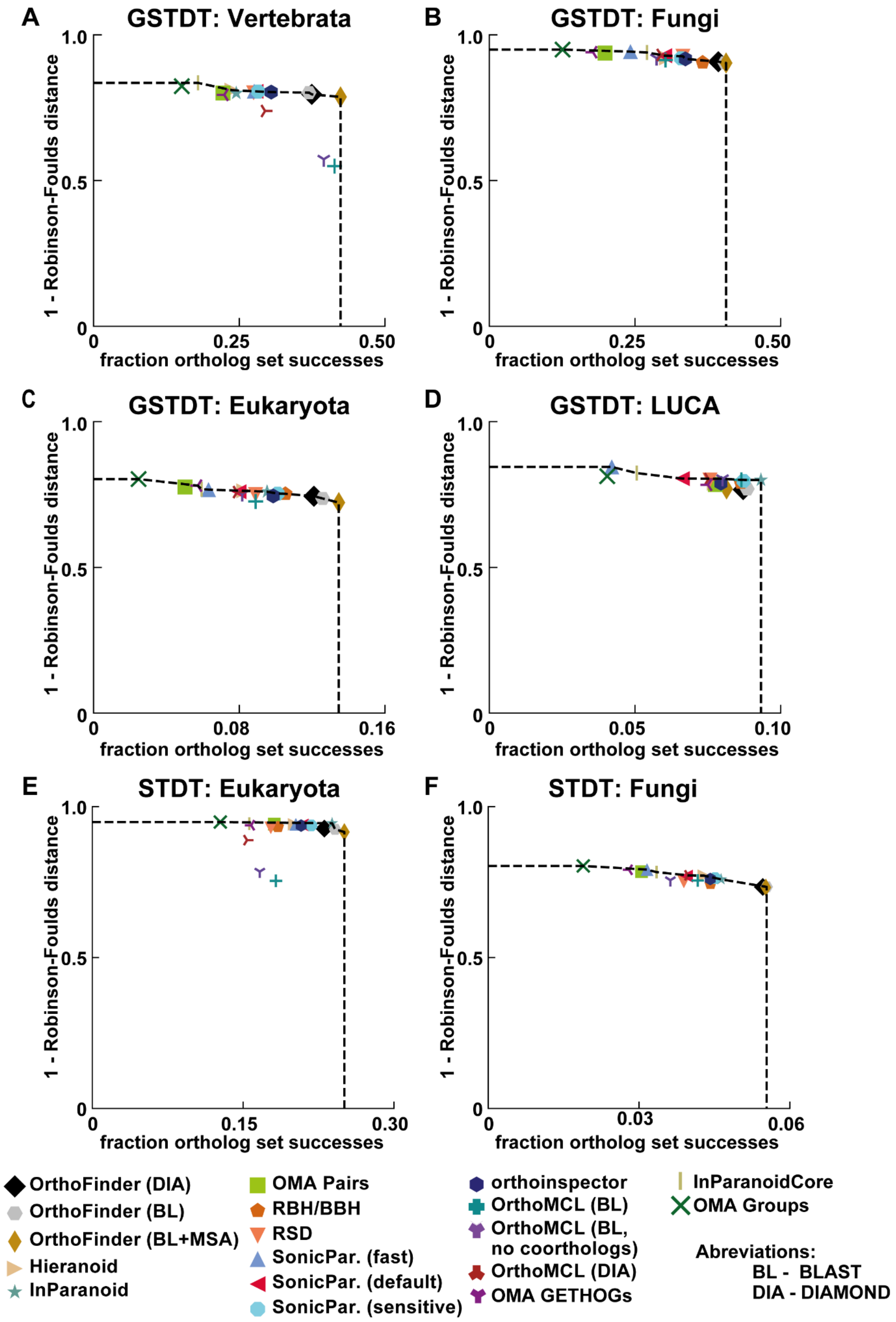


Figure S2

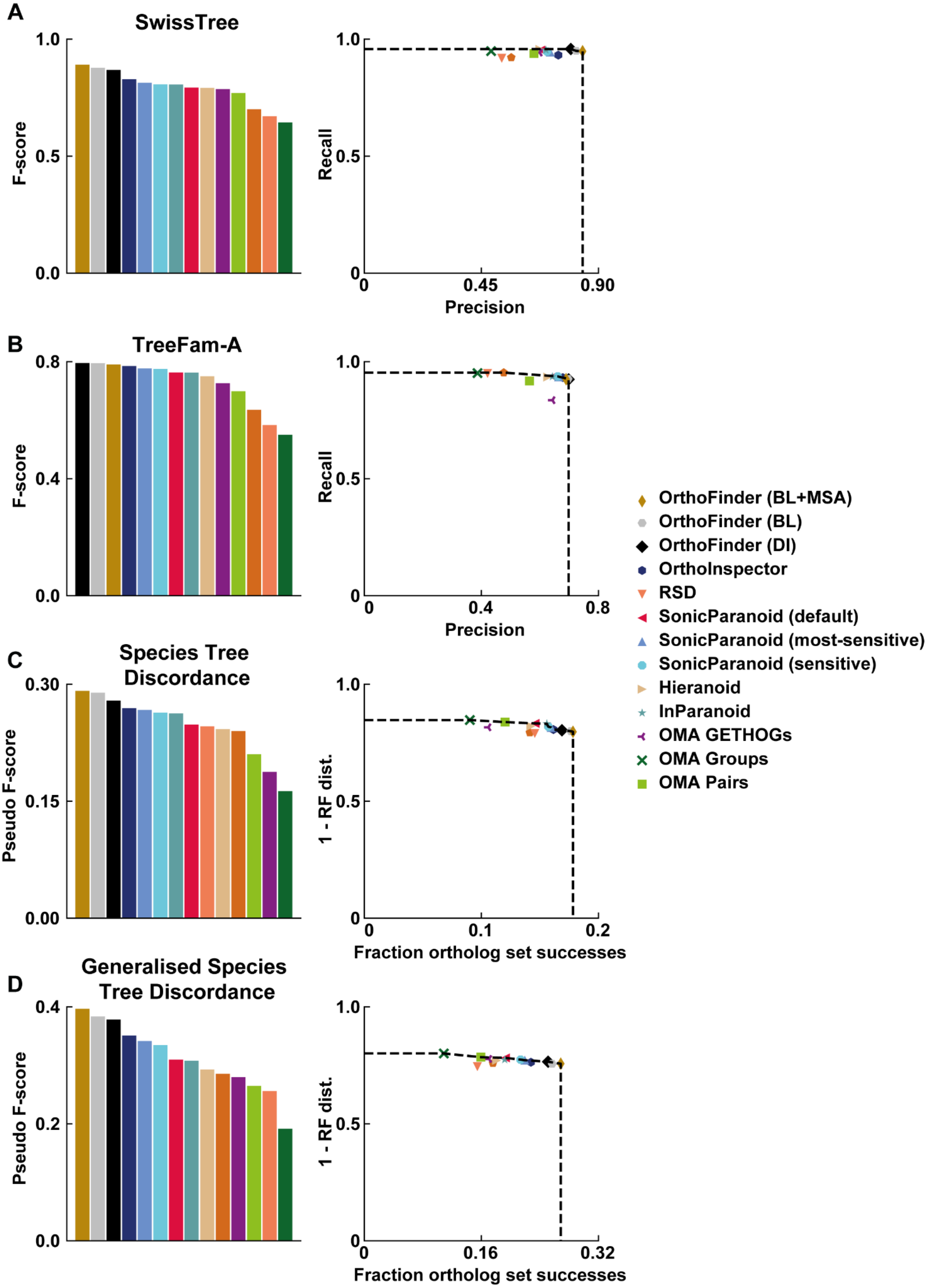

A
SwissTree
F-score
1.0
0.5
0.0
Recall
1.0
0.5
0
0
0.45
0.90
Precision
B
TreeFam-A
F-score
0.8
0.4
0.0
Recall
1.0
0.5
0
0
0.4
0.8
Precision
C
Species Tree Discordance
Pseudo F-score
0.30
0.15
0.00
1 - RF dist.
1.0
0.5
0
0
0.1
0.2
Fraction ortholog set successes
D
Generalised Species Tree Discordance
Pseudo F-score
0.4
0.2
0.0
1 - RF dist.
1.0
0.5
0
0
0.16
0.32
Fraction ortholog set successes
OrthoFinder (BL+MSA)
OrthoFinder (BL)
OrthoFinder (DI)
OrthoInspector
RSD
SonicParanoid (default)
SonicParanoid (most-sensitive)
SonicParanoid (sensitive)
Hieranoid
InParanoid
OMA GETHOGs
OMA Groups
OMA Pairs

Figure S3

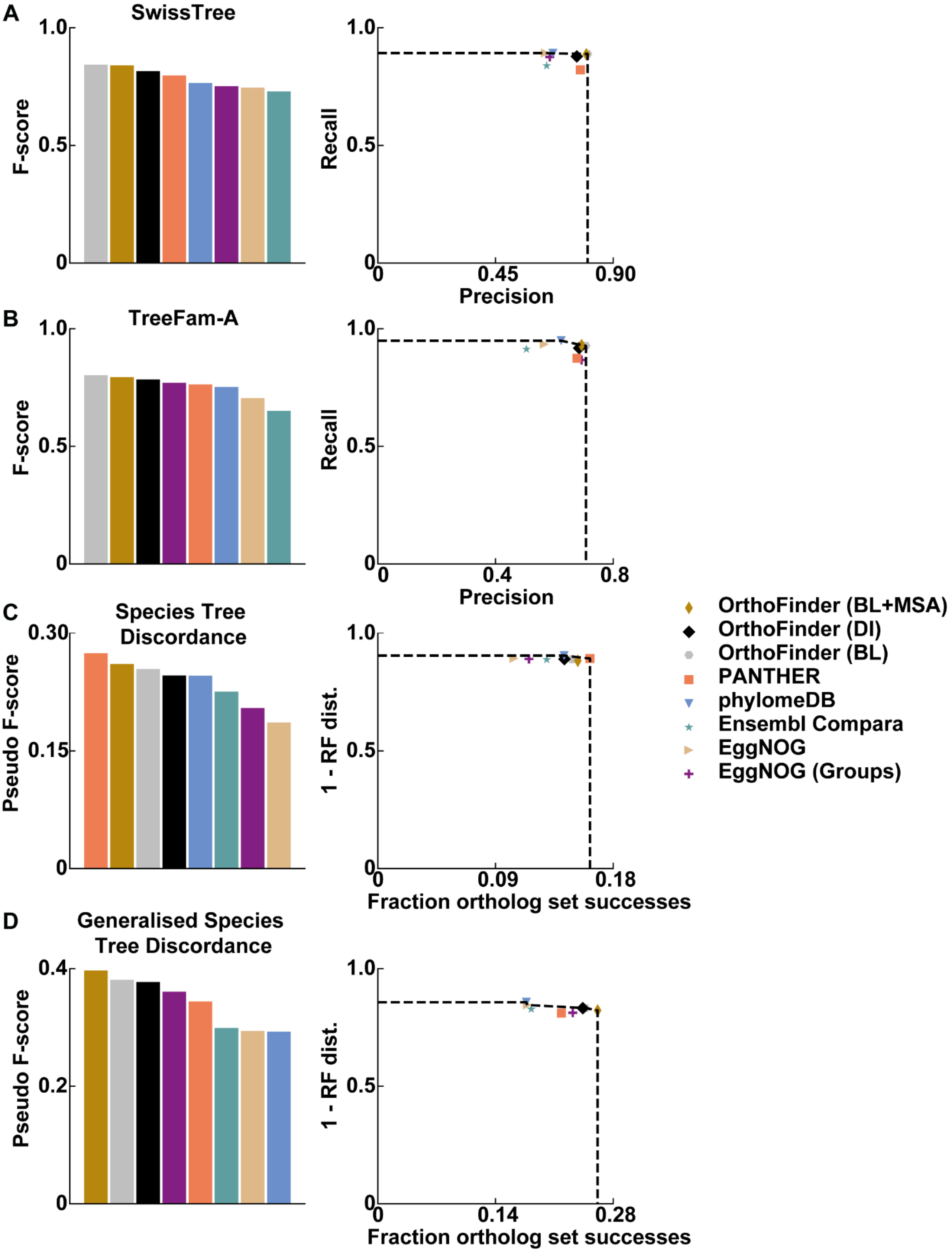

A
SwissTree
F-score
1.0
0.5
0
Recall
1.0
0.5
0
0
0.45
0.90
Precision
B
TreeFam-A
F-score
1.0
0.5
0
Recall
1.0
0.5
0
0
0.4
0.8
Precision
C
Species Tree Discordance
Pseudo F-score
0.30
0.15
0
1 - RF dist.
1.0
0.5
0
0
0.09
0.18
Fraction ortholog set successes
D
Generalised Species Tree Discordance
Pseudo F-score
0.4
0.2
0
1 - RF dist.
1.0
0.5
0
0
0.14
0.28
Fraction ortholog set successes
OrthoFinder (BL+MSA)
OrthoFinder (DI)
OrthoFinder (BL)
PANTHER
phylomeDB
Ensembl Compara
EggNOG
EggNOG (Groups)

**Figure S4**

**A.**

**B.**

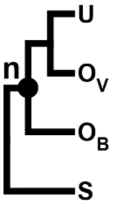
**Primary Overlap depth**

**Archetype**

**Sub-overlaps**

**Constraints**

**Case A**
**d=(1,0)**

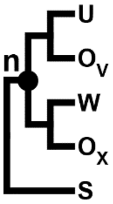


sub-cases

| | 1 | 2 | 3 | 4 |
|---|---|---|---|---|
| S&U | F | T | F | T |
| S &O | F | F | T | T |

¬U&O

**Case B**
**d=(1,1)**

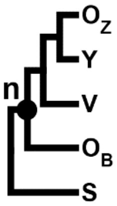


sub-cases

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---|---|---|---|---|---|---|---|---|
| S&O | F | F | F | F | T | T | T | T |
| S&U | F | T | F | T | F | T | F | T |
| S&W | F | F | T | T | F | F | T | T |

¬U&O
¬W&O
¬U &W

**Case C**
**d=(2,0)**



sub-cases

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S&V | F | F | F | F | F | F | F | F | T | T | T | T | T | T | T | T |
| S&Y | F | F | F | F | T | T | T | T | F | F | F | F | T | T | T | T |
| S&O | F | F | T | T | F | F | T | T | F | F | T | T | F | F | T | T |
| V&Y | F | T | F | T | F | T | F | T | F | T | F | T | F | T | F | T |

¬Y&O
¬V&O

**C.**

| Case | Input tree | DLC before | Reconciled tree | DLC after |
|---|---|---|---|---|
| - | (($O_A$, $O_B$), S) | 1D = 1 | (($O_A$, $O_B$), S) | 1D = 1 |
| A.1 | ((U, $O_V$), $O_B$), S) | D + L = 2 | ((($O_V$, $O_B$), U), S) | D + C = 1.5 |
| A.2 | ((U, $O_V$), $O_B$), S) | 2D + 2L = 4 | ((U, $O_V$), ($O_B$, S)) | D + C = 1.5 |
| A.3 | ((U, $O_V$), $O_B$), S) | 2D + 2L = 4 | ((($O_V$, $O_B$), U), S) | 2D + L + C = 3.5 |
| A.4 | ((U, $O_V$), $O_B$), S) | 2D + 2L = 4 | ((($O_V$, $O_B$), U), S) | 2D + L + C = 3.5 |
| B.1 | ((U, $O_V$), (W, $O_X$)), S) | D + 2L = 3 | ((W, (U($O_V$, $O_X$))), S) | D + 2C = 2 |
| B.2 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 5 | ((U, $O_V$), (S, $O_X$)), W) | D + 2C = 2 |
| B.3 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 5 | ((W, $O_X$), (S, $O_V$)), U) | D + 2C = 2 |
| B.4 | ((U, $O_V$), (W, $O_X$)), S) | 2D + L = 3 | ((U, $O_V$), ($O_X$, (W, S))) | D + 2C = 2 |
| B.5 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 3 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 3 |
| B.6 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 5 | (($O_X$, $O_V$), (W, U)), S) | 2D + L + 2C = 4 |
| B.7 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 3L = 5 | (($O_X$, $O_V$), (W, U)), S) | 2D + L + 2C = 4 |
| B.8 | ((U, $O_V$), (W, $O_X$)), S) | 2D + 2L = 4 | (($O_X$, $O_V$), (W, U)), S) | 2D + 2C = 4 |
| C.1 | (((($O_Z$, Y), V), $O_B$), S) | D + 2L = 3 | (((($O_Z$, $O_B$), Y), V), S) | D + 2C = 2 |
| C.2 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 2L = 4 | ((($O_Z$, Y), (V, $O_B$)), S) | D + C = 1.5 |
| C.3 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 4L = 7 | (((($O_Z$, $O_B$), Y), V), S) | 2D + 2L + 2C = 5 |
| C.4 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 3L = 6 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + L + C = 3.5 |
| C.5 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 4L = 6 | ((($O_Z$, Y), V), ($O_B$, S)) | D + L + C = 2.5 |
| C.6 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 4L = 6 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + L + C = 3.5 |
| C.7 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 2L = 5 | ((($O_Z$, Y), V), ($O_B$, S)) | 3D + L + C = 4.5 |
| C.8 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 2L = 5 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + C = 2.5 |
| C.9 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 3L = 5 | ((($O_Z$, Y), V), ($O_B$, S)) | D + L + C = 2.5 |
| C.10 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 3L = 6 | ((($O_Z$, Y), V), ($O_B$, S)) | 2D + L + C = 3.5 |
| C.11 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 3L = 6 | ((($O_Z$, Y), V), ($O_B$, S)) | 3D + 2L + C = 5.5 |
| C.12 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 2L = 5 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + C = 2.5 |
| C.13 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 3L = 6 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + L + C = 3.5 |
| C.14 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 3L = 6 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + L + C = 3.5 |
| C.15 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 2L = 4 | (((($O_Z$, Y), V), $O_B$), S) | 2D + 2L = 4 |
| C.16 | (((($O_Z$, Y), V), $O_B$), S) | 3D + 2L = 5 | ((($O_Z$, Y), (V, $O_B$)), S) | 2D + C = 2.5 |

## *Supplementary Figure Legends*

### Figure S1

Results of the individual Generalised Species Tree Discordance tests (GSTDT) and Species Tree Discordance Tests (STDT) from the Quest for Orthologs benchmarks for four clades of species. A) GSTDT Vertebrata B) GSTDT Fungi C) GSTDT Eukaryota D) GSTDT LUCA (Last Universal Common Ancestor, a species set covering bacteria, archaea and eukaryotes) E) STDT Eukaryota F) STDT Fungi. See methods for description of Quest for Orthologs benchmarks.

### Figure S2

The 2018 Quest for Orthologs benchmark results for OrthoFinder versus software tools. A-B) F-score versus orthologs from gold standard trees C-D) Pseudo F-score on species tree discordance test E-F) Precision & Recall versus gold standard trees G-H) 1 minus normalised Robinson-Foulds (RF) distance & fraction of ortholog set successes on species tree discordance tests.

### Figure S3

The 2011 Quest for Orthologs benchmark results for OrthoFinder versus online databases. A-B) F-score versus orthologs from gold standard trees C-D) Pseudo F-score on species tree discordance test E-F) Precision & Recall versus gold standard trees G-H) 1 minus normalised Robinson-Foulds (RF) distance & fraction of ortholog set successes on species tree discordance tests.

### Figure S4

Deterministic tree reconciliation applied to nodes within a gene tree. If the sets of species below a node, n, overlap the node is analysed to find if there is a more parsimonious interpretation of the subtree under the duplication, loss, deep-coalescence (DLC) model. The analysis is done in the context of the sister clade, S, and the descendant clades, U, V, W, X, Y, Z and O. These clades may contain single or multiple genes. The overlapping clades under the two descendants of n are identified, down to a total combined depth of 2 (so that the problem remains tractable). Each case has a number of possible sub-cases according to whether the species sets in the clades overlap. The notation X&Y means that the species set for the genes in clade X overlap with the species sets in the clade Y. In order for a node to fit an archetype (the overlap in n’s descendants is in the clades ‘O’), constraints arise on some of the sub-overlaps. T=True, F=False.

**Table S1a: OrthoFinder & Software Methods Accuracy**

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave (psu.) F |
| OrthoFinder | 0.761 | 0.878 | 0.816 | 0.684 | 0.918 | 0.784 | 0.143 | 0.890 | 0.246 | 0.244 | 0.832 | 0.377 | 0.556 |
| OrthoFinder (BL) | 0.802 | 0.889 | 0.843 | 0.707 | 0.927 | 0.803 | 0.148 | 0.890 | 0.254 | 0.247 | 0.832 | 0.381 | 0.570 |
| OrthoFinder (BL+MSA) | 0.797 | 0.888 | 0.840 | 0.693 | 0.931 | 0.794 | 0.153 | 0.883 | 0.261 | 0.262 | 0.822 | 0.397 | 0.573 |
| Hieranoid | 0.691 | 0.883 | 0.775 | 0.604 | 0.926 | 0.731 | 0.122 | 0.912 | 0.215 | 0.175 | 0.850 | 0.291 | 0.503 |
| InParanoid | 0.688 | 0.883 | 0.774 | 0.632 | 0.929 | 0.752 | 0.142 | 0.915 | 0.246 | 0.191 | 0.848 | 0.311 | 0.521 |
| OMA Pairs | 0.652 | 0.883 | 0.751 | 0.578 | 0.903 | 0.705 | 0.106 | 0.920 | 0.190 | 0.137 | 0.845 | 0.236 | 0.470 |
| RBH/BBH | 0.621 | 0.884 | 0.730 | 0.493 | 0.948 | 0.648 | 0.114 | 0.896 | 0.203 | 0.209 | 0.840 | 0.335 | 0.479 |
| RSD | 0.572 | 0.884 | 0.695 | 0.452 | 0.949 | 0.612 | 0.108 | 0.898 | 0.193 | 0.193 | 0.849 | 0.314 | 0.453 |
| SonicParanoid (fast) | 0.656 | 0.888 | 0.754 | 0.591 | 0.927 | 0.722 | 0.117 | 0.921 | 0.208 | 0.156 | 0.858 | 0.264 | 0.487 |
| SonicParanoid (default) | 0.688 | 0.892 | 0.777 | 0.625 | 0.925 | 0.746 | 0.124 | 0.913 | 0.219 | 0.181 | 0.851 | 0.299 | 0.510 |
| SonicParanoid (sensitive) | 0.716 | 0.891 | 0.794 | 0.641 | 0.926 | 0.758 | 0.131 | 0.908 | 0.230 | 0.200 | 0.845 | 0.323 | 0.526 |
| orthoinspector | 0.701 | 0.877 | 0.779 | 0.655 | 0.927 | 0.768 | 0.126 | 0.907 | 0.221 | 0.205 | 0.842 | 0.330 | 0.524 |
| OrthoMCL (BL) | 0.652 | 0.834 | 0.732 | 0.594 | 0.846 | 0.698 | 0.112 | 0.755 | 0.195 | 0.223 | 0.715 | 0.340 | 0.491 |
| OrthoMCL (no coorths) | 0.611 | 0.829 | 0.703 | 0.505 | 0.854 | 0.635 | 0.101 | 0.780 | 0.180 | 0.211 | 0.730 | 0.327 | 0.461 |
| OrthoMCL (DI) | 0.591 | 0.884 | 0.708 | 0.519 | 0.924 | 0.664 | 0.097 | 0.865 | 0.174 | 0.186 | 0.824 | 0.303 | 0.462 |
| OMA Groups | 0.476 | 0.881 | 0.618 | 0.390 | 0.946 | 0.552 | 0.073 | 0.930 | 0.136 | 0.086 | 0.867 | 0.156 | 0.365 |
| InParanoidCore | 0.530 | 0.884 | 0.663 | 0.476 | 0.952 | 0.635 | 0.095 | 0.916 | 0.172 | 0.140 | 0.877 | 0.241 | 0.428 |
| OMA GETHOGs | 0.661 | 0.885 | 0.756 | 0.610 | 0.836 | 0.705 | 0.093 | 0.916 | 0.169 | 0.134 | 0.840 | 0.231 | 0.465 |

**Table S1b: OrthoFinder (default) v other software**

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | Ave (psu.) F |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | |
| OrthoFinder | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| OrthoFinder (BL) | -5.1% | -1.2% | -3.3% | -3.3% | -1.0% | -2.3% | -3.9% | 0.1% | -3.3% | -1.3% | -0.1% | -1.0% | -2.6% |
| OrthoFinder (BL+MSA) | -4.5% | -1.0% | -2.9% | -1.2% | -1.4% | -1.3% | -6.7% | 0.8% | -5.7% | -6.7% | 1.1% | -5.0% | -3.0% |
| Hieranoid | 9.2% | -0.5% | 4.9% | 11.8% | -0.8% | 6.8% | 14.6% | -2.3% | 12.6% | 28.1% | -2.2% | 22.9% | 9.5% |
| InParanoid | 9.6% | -0.5% | 5.1% | 7.7% | -1.2% | 4.1% | 0.2% | -2.7% | -0.2% | 21.8% | -1.9% | 17.4% | 6.3% |
| OMA Pairs | 14.3% | -0.6% | 8.0% | 15.5% | 1.6% | 10.1% | 25.9% | -3.2% | 22.9% | 43.8% | -1.6% | 37.4% | 15.4% |
| RBH/BBH | 18.4% | -0.7% | 10.5% | 28.0% | -3.2% | 17.3% | 19.8% | -0.7% | 17.5% | 14.2% | -0.9% | 11.2% | 13.8% |
| RSD | 24.9% | -0.7% | 14.8% | 34.0% | -3.3% | 22.0% | 24.1% | -0.8% | 21.5% | 20.9% | -2.0% | 16.7% | 18.4% |
| SonicParanoid (fast) | 13.8% | -1.1% | 7.5% | 13.7% | -1.0% | 7.9% | 18.0% | -3.4% | 15.6% | 36.1% | -3.0% | 30.1% | 12.4% |
| SonicParanoid (default) | 9.6% | -1.5% | 4.7% | 8.6% | -0.8% | 4.8% | 13.0% | -2.4% | 11.1% | 25.6% | -2.3% | 20.7% | 8.2% |
| SonicParanoid (sensitive) | 5.9% | -1.4% | 2.7% | 6.3% | -0.9% | 3.4% | 7.9% | -1.9% | 6.6% | 18.0% | -1.5% | 14.3% | 5.3% |
| orthoinspector | 8.0% | 0.2% | 4.5% | 4.3% | -1.0% | 2.1% | 11.8% | -1.8% | 10.1% | 16.0% | -1.2% | 12.6% | 5.7% |
| OrthoMCL (BL) | 14.4% | 5.1% | 10.3% | 13.2% | 7.8% | 11.0% | 21.4% | 15.3% | 20.6% | 8.6% | 14.0% | 9.9% | 11.6% |
| OrthoMCL (no coorths) | 19.8% | 5.6% | 13.7% | 26.1% | 7.0% | 19.0% | 28.9% | 12.4% | 27.0% | 13.5% | 12.2% | 13.2% | 17.0% |
| OrthoMCL (DI) | 22.4% | -0.6% | 13.2% | 24.2% | -0.6% | 15.3% | 32.1% | 2.8% | 29.2% | 23.9% | 1.0% | 19.7% | 16.8% |
| OMA Groups | 37.5% | -0.3% | 24.3% | 43.1% | -3.0% | 29.6% | 48.7% | -4.3% | 44.9% | 64.9% | -4.1% | 58.7% | 34.3% |
| InParanoidCore | 30.3% | -0.7% | 18.7% | 30.4% | -3.6% | 19.0% | 33.6% | -2.8% | 30.1% | 42.6% | -5.2% | 36.0% | 23.0% |
| OMA GETHOGs | 13.2% | -0.7% | 7.3% | 10.9% | 9.0% | 10.1% | 34.8% | -2.8% | 31.3% | 45.2% | -0.9% | 38.9% | 16.3% |
| OF v best non-OF | 5.9% | -1.5% | 2.7% | 4.3% | -3.6% | 2.1% | 0.2% | -4.3% | -0.2% | 8.6% | -5.2% | 9.9% | 5.3% |
| OF v worst non-OF | 37.5% | 5.6% | 24.3% | 43.1% | 9.0% | 29.6% | 48.7% | 15.3% | 44.9% | 64.9% | 14.0% | 58.7% | 34.3% |

**Table S1c: OrthoFinder (BLAST) v other software**

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave (psu.) F |
| OrthoFinder | 5.1% | 1.2% | 3.3% | 3.3% | 1.0% | 2.3% | 3.9% | -0.1% | 3.3% | 1.3% | 0.1% | 1.0% | 2.6% |
| OrthoFinder (BL) | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| OrthoFinder (BL+MSA) | 0.6% | 0.1% | 0.4% | 2.1% | -0.3% | 1.0% | -3.0% | 0.7% | -2.4% | -5.5% | 1.2% | -4.0% | -0.5% |
| Hieranoid | 13.8% | 0.7% | 8.1% | 14.7% | 0.2% | 9.0% | 17.9% | -2.4% | 15.5% | 29.1% | -2.1% | 23.7% | 11.8% |
| InParanoid | 14.2% | 0.7% | 8.3% | 10.7% | -0.1% | 6.3% | 4.1% | -2.8% | 3.1% | 22.8% | -1.9% | 18.3% | 8.7% |
| OMA Pairs | 18.7% | 0.6% | 11.0% | 18.3% | 2.6% | 12.2% | 28.8% | -3.3% | 25.4% | 44.5% | -1.6% | 38.1% | 17.5% |
| RBH/BBH | 22.5% | 0.5% | 13.5% | 30.4% | -2.2% | 19.2% | 22.9% | -0.8% | 20.2% | 15.3% | -0.9% | 12.1% | 16.0% |
| RSD | 28.7% | 0.5% | 17.6% | 36.2% | -2.3% | 23.8% | 27.1% | -0.9% | 24.1% | 21.9% | -2.0% | 17.5% | 20.5% |
| SonicParanoid (fast) | 18.3% | 0.1% | 10.5% | 16.5% | 0.0% | 10.1% | 21.2% | -3.5% | 18.4% | 37.0% | -3.0% | 30.8% | 14.6% |
| SonicParanoid (default) | 14.2% | -0.3% | 7.9% | 11.6% | 0.3% | 7.0% | 16.3% | -2.5% | 14.1% | 26.5% | -2.3% | 21.5% | 10.5% |
| SonicParanoid (sensitive) | 10.8% | -0.2% | 5.9% | 9.4% | 0.2% | 5.6% | 11.4% | -2.0% | 9.7% | 19.1% | -1.5% | 15.1% | 7.8% |
| orthoinspector | 12.7% | 1.4% | 7.7% | 7.4% | 0.1% | 4.4% | 15.2% | -1.9% | 13.1% | 17.1% | -1.1% | 13.5% | 8.1% |
| OrthoMCL (BL) | 18.8% | 6.2% | 13.3% | 16.0% | 8.8% | 13.0% | 24.4% | 15.2% | 23.2% | 9.8% | 14.1% | 10.8% | 13.9% |
| OrthoMCL (no coorths) | 23.9% | 6.7% | 16.6% | 28.6% | 7.9% | 20.9% | 31.7% | 12.3% | 29.4% | 14.6% | 12.3% | 14.1% | 19.1% |
| OrthoMCL (DI) | 26.3% | 0.6% | 16.0% | 26.7% | 0.4% | 17.2% | 34.8% | 2.7% | 31.5% | 24.8% | 1.1% | 20.5% | 18.9% |
| OMA Groups | 40.7% | 0.9% | 26.8% | 44.9% | -2.0% | 31.2% | 50.7% | -4.4% | 46.7% | 65.4% | -4.0% | 59.1% | 36.0% |
| InParanoidCore | 33.9% | 0.5% | 21.4% | 32.7% | -2.6% | 20.9% | 36.1% | -2.9% | 32.5% | 43.4% | -5.1% | 36.7% | 25.0% |
| OMA GETHOGs | 17.7% | 0.5% | 10.3% | 13.8% | 9.9% | 12.2% | 37.3% | -2.9% | 33.6% | 45.9% | -0.9% | 39.5% | 18.4% |
| OF v best non-OF | 10.8% | -0.3% | 5.9% | 7.4% | -2.6% | 4.4% | 4.1% | -4.4% | 3.1% | 9.8% | -5.1% | 10.8% | 7.8% |
| OF v worst non-OF | 40.7% | 6.7% | 26.8% | 44.9% | 9.9% | 31.2% | 50.7% | 15.2% | 46.7% | 65.4% | 14.1% | 59.1% | 36.0% |

**Table S1d: OrthoFinder (BLAST+MSA) v other software**

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave (psu.) F |
| OrthoFinder | 4.5% | 1.0% | 2.9% | 1.2% | 1.4% | 1.3% | 6.7% | -0.8% | 5.7% | 6.7% | -1.1% | 5.0% | 3.0% |
| OrthoFinder (BL) | -0.6% | -0.1% | -0.4% | -2.1% | 0.3% | -1.0% | 3.0% | -0.7% | 2.4% | 5.5% | -1.2% | 4.0% | 0.5% |
| OrthoFinder (BL+MSA) | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| Hieranoid | 13.3% | 0.5% | 7.7% | 12.9% | 0.5% | 8.0% | 20.4% | -3.1% | 17.6% | 33.0% | -3.3% | 26.8% | 12.2% |
| InParanoid | 13.7% | 0.5% | 7.9% | 8.8% | 0.2% | 5.3% | 6.9% | -3.5% | 5.5% | 27.1% | -3.0% | 21.5% | 9.1% |
| OMA Pairs | 18.2% | 0.5% | 10.7% | 16.6% | 3.0% | 11.3% | 30.9% | -4.0% | 27.2% | 47.6% | -2.7% | 40.5% | 17.9% |
| RBH/BBH | 22.1% | 0.4% | 13.1% | 28.9% | -1.8% | 18.4% | 25.2% | -1.5% | 22.2% | 20.0% | -2.0% | 15.6% | 16.4% |
| RSD | 28.3% | 0.4% | 17.3% | 34.8% | -1.9% | 23.0% | 29.2% | -1.7% | 25.9% | 26.3% | -3.1% | 20.8% | 20.9% |
| SonicParanoid (fast) | 17.8% | 0.0% | 10.2% | 14.7% | 0.3% | 9.1% | 23.5% | -4.2% | 20.3% | 40.4% | -4.1% | 33.6% | 15.0% |
| SonicParanoid (default) | 13.7% | -0.4% | 7.5% | 9.7% | 0.6% | 6.1% | 18.8% | -3.3% | 16.2% | 30.6% | -3.4% | 24.6% | 11.0% |
| SonicParanoid (sensitive) | 10.2% | -0.4% | 5.5% | 7.5% | 0.5% | 4.6% | 14.0% | -2.8% | 11.9% | 23.6% | -2.7% | 18.5% | 8.2% |
| orthoinspector | 12.1% | 1.2% | 7.3% | 5.4% | 0.4% | 3.4% | 17.7% | -2.6% | 15.2% | 21.7% | -2.3% | 17.0% | 8.5% |
| OrthoMCL (BL) | 18.3% | 6.0% | 12.9% | 14.3% | 9.1% | 12.1% | 26.7% | 14.5% | 25.1% | 14.8% | 13.1% | 14.4% | 14.3% |
| OrthoMCL (no coorths) | 23.4% | 6.6% | 16.3% | 27.0% | 8.2% | 20.1% | 33.7% | 11.7% | 31.2% | 19.4% | 11.2% | 17.5% | 19.5% |
| OrthoMCL (DI) | 25.9% | 0.5% | 15.7% | 25.1% | 0.7% | 16.4% | 36.7% | 2.0% | 33.2% | 29.0% | -0.1% | 23.6% | 19.3% |
| OMA Groups | 40.4% | 0.8% | 26.5% | 43.8% | -1.6% | 30.5% | 52.2% | -5.1% | 48.0% | 67.3% | -5.1% | 60.7% | 36.3% |
| InParanoidCore | 33.5% | 0.4% | 21.1% | 31.2% | -2.3% | 20.0% | 38.0% | -3.6% | 34.1% | 46.5% | -6.3% | 39.2% | 25.3% |
| OMA GETHOGs | 17.1% | 0.3% | 10.0% | 12.0% | 10.2% | 11.3% | 39.2% | -3.6% | 35.2% | 48.9% | -2.1% | 41.9% | 18.8% |
| OF v best non-OF | 10.2% | -0.4% | 5.5% | 5.4% | -2.3% | 3.4% | 6.9% | -5.1% | 5.5% | 14.8% | -6.3% | 14.4% | 8.2% |
| OF v worst non-OF | 40.4% | 6.6% | 26.5% | 43.8% | 10.2% | 30.5% | 52.2% | 14.5% | 48.0% | 67.3% | 13.1% | 60.7% | 36.3% |

## Table S1e: OrthoFinder & Ortholog Database Accuracy

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave (psu.) F |
| OrthoFinder | 0.761 | 0.878 | 0.816 | 0.684 | 0.918 | 0.784 | 0.143 | 0.890 | 0.246 | 0.244 | 0.832 | 0.377 | 0.556 |
| OrthoFinder (BL) | 0.802 | 0.889 | 0.843 | 0.707 | 0.927 | 0.803 | 0.148 | 0.890 | 0.254 | 0.247 | 0.832 | 0.381 | 0.570 |
| OrthoFinder (BL+MSA) | 0.797 | 0.888 | 0.840 | 0.693 | 0.931 | 0.794 | 0.153 | 0.883 | 0.261 | 0.262 | 0.822 | 0.397 | 0.573 |
| EggNOG | 0.641 | 0.893 | 0.746 | 0.566 | 0.934 | 0.705 | 0.104 | 0.893 | 0.186 | 0.178 | 0.845 | 0.294 | 0.483 |
| Ensembl Compara | 0.646 | 0.839 | 0.730 | 0.505 | 0.913 | 0.651 | 0.129 | 0.888 | 0.226 | 0.183 | 0.828 | 0.299 | 0.476 |
| PANTHER 8.0 (all) | 0.775 | 0.821 | 0.797 | 0.677 | 0.874 | 0.763 | 0.162 | 0.893 | 0.275 | 0.218 | 0.811 | 0.344 | 0.545 |
| phylomeDB | 0.670 | 0.892 | 0.765 | 0.623 | 0.949 | 0.752 | 0.142 | 0.905 | 0.246 | 0.177 | 0.857 | 0.293 | 0.514 |

## Table S1f: OrthoFinder (default) v other

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave (psu.) F |
| OrthoFinder | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| OrthoFinder (BL) | -5.1% | -1.2% | -3.3% | -3.3% | -1.0% | -2.3% | -3.9% | 0.1% | -3.3% | -1.3% | -0.1% | -1.0% | -2.6% |
| OrthoFinder (BL+MSA) | -4.5% | -1.0% | -2.9% | -1.2% | -1.4% | -1.3% | -6.7% | 0.8% | -5.7% | -6.7% | 1.1% | -5.0% | -3.0% |
| EggNOG | 15.8% | -1.6% | 8.5% | 17.3% | -1.8% | 10.1% | 27.1% | -0.3% | 24.2% | 27.1% | -1.6% | 22.1% | 13.1% |
| Ensembl Compara | 15.2% | 4.5% | 10.5% | 26.2% | 0.5% | 17.0% | 9.5% | 0.3% | 8.3% | 25.2% | 0.5% | 20.7% | 14.3% |
| PANTHER 8.0 (all) | -1.7% | 6.5% | 2.2% | 1.1% | 4.7% | 2.7% | -12.0% | -0.3% | -10.4% | 10.4% | 2.5% | 8.7% | 2.0% |
| phylomeDB | 12.0% | -1.5% | 6.2% | 8.9% | -3.3% | 4.0% | 0.2% | -1.6% | -0.1% | 27.6% | -3.0% | 22.3% | 7.5% |
| **OF v best non-OF** | -1.7% | -1.6% | 2.2% | 1.1% | -3.3% | 2.7% | -12.0% | -1.6% | -10.4% | 10.4% | -3.0% | 8.7% | 2.0% |
| **OF v worst non-OF** | 15.8% | 6.5% | 10.5% | 26.2% | 4.7% | 17.0% | 27.1% | 0.3% | 24.2% | 27.6% | 2.5% | 22.3% | 14.3% |

## Table S1g: OrthoFinder (BLAST) v other

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave. (psu.) F |
| OrthoFinder | 5.1% | 1.2% | 3.3% | 3.3% | 1.0% | 2.3% | 3.9% | -0.1% | 3.3% | 1.3% | 0.1% | 1.0% | 2.6% |
| OrthoFinder (BL) | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| OrthoFinder (BL+MSA) | 0.6% | 0.1% | 0.4% | 2.1% | -0.3% | 1.0% | -3.0% | 0.7% | -2.4% | -5.5% | 1.2% | -4.0% | -0.5% |
| EggNOG | 20.1% | -0.4% | 11.5% | 20.0% | -0.7% | 12.2% | 29.9% | -0.4% | 26.8% | 28.0% | -1.6% | 22.9% | 15.4% |
| Ensembl Compara | 19.5% | 5.6% | 13.5% | 28.6% | 1.5% | 18.9% | 13.0% | 0.1% | 11.3% | 26.1% | 0.5% | 21.5% | 16.5% |
| PANTHER 8.0 (all) | 3.4% | 7.6% | 5.5% | 4.4% | 5.7% | 5.0% | -8.5% | -0.4% | -7.4% | 11.6% | 2.6% | 9.7% | 4.5% |
| phylomeDB | 16.5% | -0.3% | 9.3% | 11.9% | -2.3% | 6.3% | 4.0% | -1.7% | 3.2% | 28.5% | -2.9% | 23.1% | 9.9% |
| **OF v best non-OF** | 3.4% | -0.4% | 5.5% | 4.4% | -2.3% | 5.0% | -8.5% | -1.7% | -7.4% | 11.6% | -2.9% | 9.7% | 4.5% |
| **OF v worst non-OF** | 20.1% | 7.6% | 13.5% | 28.6% | 5.7% | 18.9% | 29.9% | 0.1% | 26.8% | 28.5% | 2.6% | 23.1% | 16.5% |

## Table S1h: OrthoFinder (BLAST + MSA) v other

| | SwissTree | | | TreeFam-A | | | STDT | | | GSTDT | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | R | P | F | R | P | F | Olog. recov | 1-RF | Psu. F | Olog. recov | 1-RF | Psu. F | Ave. (psu.) F |
| OrthoFinder | 4.5% | 1.0% | 2.9% | 1.2% | 1.4% | 1.3% | 6.7% | -0.8% | 5.7% | 6.7% | -1.1% | 5.0% | 3.0% |
| OrthoFinder (BL) | -0.6% | -0.1% | -0.4% | -2.1% | 0.3% | -1.0% | 3.0% | -0.7% | 2.4% | 5.5% | -1.2% | 4.0% | 0.5% |
| OrthoFinder (BL+MSA) | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% | 0.0% |
| EggNOG | 19.7% | -0.6% | 11.2% | 18.3% | -0.4% | 11.3% | 32.0% | -1.1% | 28.5% | 32.0% | -2.7% | 25.9% | 15.7% |
| Ensembl Compara | 19.0% | 5.5% | 13.1% | 27.1% | 1.9% | 18.1% | 15.5% | -0.6% | 13.5% | 30.2% | -0.7% | 24.6% | 16.9% |
| PANTHER 8.0 (all) | 2.9% | 7.5% | 5.1% | 2.4% | 6.0% | 4.0% | -5.7% | -1.1% | -5.0% | 16.5% | 1.4% | 13.3% | 4.9% |
| phylomeDB | 16.0% | -0.5% | 9.0% | 10.0% | -2.0% | 5.3% | 6.9% | -2.4% | 5.6% | 32.4% | -4.1% | 26.2% | 10.3% |
| **OF v best non-OF** | 2.9% | -0.6% | 5.1% | 2.4% | -2.0% | 4.0% | -5.7% | -2.4% | -5.0% | 16.5% | -4.1% | 13.3% | 4.9% |
| **OF v worst non-OF** | 19.7% | 7.5% | 13.1% | 27.1% | 6.0% | 18.1% | 32.0% | -0.6% | 28.5% | 32.4% | 1.4% | 26.2% | 16.9% |

## Table S2a: Precision, recall and F-score for gene duplication event identification

| | Flies | | | Primates | | | Metazoa | | | Overall | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **Precision** | **Recall** | **F-score** | **Precision** | **Recall** | **F-score** | **Precision** | **Recall** | **F-score** | **Precision** | **Recall** | **F-score** |
| **OrthoFinder tree resolution** | 74.3% | 77.3% | 75.8% | 91.7% | 91.5% | 91.6% | 60.4% | 83.9% | 70.3% | 79.5% | 85.2% | 82.2% |
| **Overlap (no resolve)** | 58.8% | 65.4% | 61.9% | 87.7% | 89.7% | 88.7% | 58.2% | 83.3% | 68.5% | 71.6% | 79.9% | 75.5% |
| **DLCPpar*** | 91.6% | 90.3% | 91.0% | 92.6% | 92.0% | 92.3% | 92.5% | 92.5% | 92.5% | 92.2% | 91.5% | 91.8% |
| **DLCpar_search*** | 41.8% | 69.7% | 52.3% | 77.8% | 87.5% | 82.3% | 64.1% | 91.0% | 75.2% | 59.7% | 81.5% | 68.9% |
| **Forester*** | 19.8% | 65.4% | 30.4% | 59.8% | 89.7% | 71.8% | 51.7% | 93.3% | 66.5% | 37.0% | 81.4% | 50.8% |

## Table S2b: True positives, false positives and false negatives for gene duplication event identification

| | Flies | | | Primates | | | Metazoa | | | Overall | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **TP** | **FP** | **FN** | **TP** | **FP** | **FN** | **TP** | **FP** | **FN** | **TP** | **FP** | **FN** |
| **OrthoFinder tree resolution** | 9304 | 3221 | 2728 | 14707 | 1330 | 1359 | 4168 | 2729 | 799 | 28179 | 7280 | 4886 |
| **Overlap (no resolve)** | 7868 | 5502 | 4164 | 14406 | 2023 | 1660 | 4138 | 2975 | 829 | 26412 | 10500 | 6653 |
| **DLCPpar*** | 10869 | 997 | 1163 | 14776 | 1173 | 1290 | 4593 | 375 | 374 | 30238 | 2545 | 2827 |
| **DLCpar_search*** | 8388 | 11674 | 3644 | 14053 | 4013 | 2013 | 4518 | 2526 | 449 | 26959 | 18213 | 6106 |
| **Forester*** | 7869 | 31905 | 4163 | 14416 | 9695 | 1650 | 4632 | 4328 | 335 | 26917 | 45928 | 6148 |