**Table S4.** Phylogenetic signal of repeat cluster abundances obtained from the comparative  RE2 analysis of Loliinae genome skimming PE read samples assessed in (a) **a)** the Loliinae data set set (38 samples, 39 clusters) (b) the BL group (13 samples, 96 clusters); (c) the FL group (17 samples. 122 clusters), and (d) the Schedonorus group (17 samples,167 clusters)   using the *phylosig*option of the *phytools*R package. Values about cluster abundances (number of PE reads) are indicated in Supplementary Table S2. Blomberg’s K and Pagel’s lambda values close to one indicate phylogenetic signal, values close to zero phylogenetic independence, and values >1 more phylogenetic signal than expected. K, p-values based on 1000 randomizations; lambda, p-values based on the Likelihood Ratio test. Significant values are highlighted in bold.

|  |  |  |  |
| --- | --- | --- | --- |
| **N. Cluster** | **Cluster\_Name** | **Phylogenetic signal on combined tree** | |
| **K** | **p-value** |
| 35 | **LTR\_1** | 0.373703 | 0.2050 |
| 39 | **LTR\_2** | **0.583327** | **0.0060** |
| 86 | LTR\_3 | 0.267521 | 0.6150 |
| 6 | Angela\_1 | 0.441390 | 0.0960 |
| 7 | **Angela\_2** | **0.847919** | **0.0020** |
| 12 | Angela\_3 | 0.465467 | 0.0310 |
| 13 | Angela\_4 | 0.520696 | 0.0210 |
| 14 | Angela\_5 | 0.513860 | 0.0200 |
| 17 | Angela\_6 | 0.415452 | 0.1400 |
| 30 | Angela\_7 | 0.415190 | 0.1060 |
| 34 | Angela\_8 | 0.399333 | 0.1240 |
| 53 | **Angela\_9** | **0.649828** | **0.0030** |
| 71 | Angela\_10 | 0.448955 | 0.0910 |
| 94 | **Angela\_11** | **0.636886** | **0.0040** |
| 107 | **Angela\_12** | **0.743470** | **0.0010** |
| 3 | SIRE\_1 | 0.411074 | 0.1290 |
| 9 | SIRE\_2 | 0.313160 | 0.4690 |
| 22 | SIRE\_3 | 0.361960 | 0.2340 |
| 29 | SIRE\_4 | 0.380547 | 0.1730 |
| 58 | SIRE\_5 | 0.321802 | 0.4230 |
| 67 | SIRE\_6 | 0.329360 | 0.4050 |
| 84 | SIRE\_7 | 0.330350 | 0.3800 |
| 85 | SIRE\_8 | 0.355221 | 0.3070 |
| 103 | SIRE\_9 | 0.333838 | 0.4040 |
| 126 | **SIRE\_10** | **0.463612** | **0.0490** |
| 137 | SIRE\_11 | 0.339207 | 0.3850 |
| 50 | TAR\_1 | 0.358543 | 0.2190 |
| 139 | TAR\_2 | 0.279301 | 0.5300 |
| 28 | Athila\_1 | 0.386600 | 0.0910 |
| 41 | EnSpm\_CACTA\_1 | 0.375853 | 0.1800 |
| 59 | **EnSpm\_CACTA\_2** | **0.475749** | **0.0530** |
| 75 | EnSpm\_CACTA\_3 | 0.456950 | 0.1710 |
| 87 | **EnSpm\_CACTA\_4** | **0.555016** | **0.0520** |
| 108 | **EnSpm\_CACTA\_5** | **0.503111** | **0.0510** |
| 180 | EnSpm\_CACTA\_6 | 0.374766 | 0.1810 |
| 106 | .45S\_rDNA\_1 | 0.209001 | 0.8380 |
| 115 | 45S\_rDNA\_2 | 0.190001 | 0.8970 |
| 203 | 5S\_rDNA\_1 | 0.177649 | 0.9110 |

**Table 5.2.\_** Phylogenetic signal *Schedonorus* group obtained with Blomberg’s K and Pagel’s lambda tests. Significant values are highlighted in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **N. Cluster** | **Cluster**  **Name** | **Phylogenetic signal on combined tree** | | **N. Cluster** | **Cluster**  **Name** | **Phylogenetic signal on combined tree** | |
| **K** | **p-value** | **K** | **p-value** |
| 57 | LINE\_1 | 0.3705 | 0.3440 | 139 | SIRE\_10 | 0.1483 | 0.9960 |
| 157 | LINE\_2 | 0.2186 | 0.8270 | 67 | TAR | 0.1890 | 0.9090 |
| 2 | **LTR\_1** | **1.5842** | **0.0020** | 183 | Tork | 0.2287 | 0.8030 |
| 12 | LTR\_2 | 0.3209 | 0.5250 | 11 | Athila\_1 | 0.5269 | 0.1640 |
| 27 | **LTR\_3** | **1.5812** | **0.0010** | 26 | Athila\_2 | 0.4200 | 0.3390 |
| 56 | **LTR\_4** | **1.4556** | **0.0010** | 29 | Athila\_3 | 0.3408 | 0.5330 |
| 64 | **LTR\_5** | **0.8215** | **0.0210** | 31 | Athila\_4 | 0.2637 | 0.7040 |
| 71 | **LTR\_6** | **1.2780** | **0.0010** | 33 | Athila\_5 | 0.4679 | 0.2820 |
| 79 | **LTR\_7** | **1.6481** | **0.0010** | 42 | Athila\_6 | 0.6943 | 0.0380 |
| 113 | **LTR\_8** | **1.5144** | **0.0010** | 44 | Athila\_7 | 0.3594 | 0.4870 |
| 149 | **LTR\_9** | **1.3891** | **0.0020** | 45 | Athila\_8 | 0.1765 | 0.9040 |
| 158 | **LTR\_10** | **1.4747** | **0.0020** | 47 | Athila\_9 | 1.5761 | 0.0010 |
| 187 | LTR\_11 | 0.2718 | 0.6820 | 48 | Athila\_10 | 0.2335 | 0.7880 |
| 82 | 45S\_rDNAS1 | 0.6840 | 0.0570 | 54 | Athila\_11 | 0.3823 | 0.4270 |
| 93 | 45S\_rDNA\_2 | 0.5688 | 0.1450 | 59 | **Athila\_12** | **1.5937** | **0.0010** |
| 127 | 5S\_rDNA | 0.3046 | 0.5960 | 60 | Athila\_13 | 0.2908 | 0.6600 |
| 83 | **Repeat\_1** | **0.8499** | **0.0050** | 65 | Athila\_14 | 0.7097 | 0.0500 |
| 99 | Repeat\_2 | 0.5225 | 0.1030 | 76 | Athila\_15 | 0.1966 | 0.8560 |
| 105 | **Repeat\_3** | **1.1762** | **0.0010** | 78 | Athila\_16 | 0.2506 | 0.7410 |
| 116 | Repeat\_4 | 0.4963 | 0.2720 | 80 | Athila\_17 | 0.2559 | 0.7610 |
| 130 | **Repeat\_5** | **1.1488** | **0.0010** | 124 | Athila\_18 | 0.5208 | 0.1130 |
| 1 | Satellite\_1 | 0.7178 | 0.0290 | 190 | Athila\_19 | 0.2890 | 0.6350 |
| 9 | Satellite\_2 | 0.3350 | 0.5370 | 7 | CRM\_1 | 0.4637 | 0.1690 |
| 37 | Satellite\_3 | 0.5394 | 0.1320 | 30 | CRM\_2 | 0.2489 | 0.7650 |
| 39 | Satellite\_4 | 0.3527 | 0.4060 | 41 | CRM\_3 | 0.2486 | 0.7790 |
| 46 | Satellite\_5 | 0.4842 | 0.1040 | 61 | CRM\_4 | 0.4670 | 0.1910 |
| 97 | Satellite\_6 | 0.3450 | 0.5240 | 69 | CRM\_5 | 0.2767 | 0.6630 |
| 106 | Satellite\_7 | 0.3020 | 0.6540 | 123 | CRM\_6 | 0.2620 | 0.7110 |
| 109 | Satellite\_8 | 0.6066 | 0.0950 | 150 | CRM\_7 | 0.2515 | 0.7470 |
| 111 | Satellite\_9 | 0.5399 | 0.2640 | 154 | **CRM\_8** | **0.8502** | **0.0050** |
| 126 | Satellite\_10 | 0.6675 | 0.0420 | 175 | CRM\_9 | 0.5515 | 0.0930 |
| 133 | Satellite\_11 | 0.4684 | 0.2770 | 4 | Retand\_1 | 0.2663 | 0.7290 |
| 171 | Satellite\_12 | 0.4450 | 0.2800 | 8 | Retand\_2 | 0.3144 | 0.5930 |
| 179 | Satellite\_13 | 0.3971 | 0.4150 | 10 | Retand\_3 | 0.3599 | 0.4780 |
| 185 | Satellite\_14 | 0.6319 | 0.0940 | 17 | Retand\_4 | 0.3321 | 0.5640 |
| 186 | Satellite\_15 | 0.5587 | 0.0530 | 18 | Retand\_5 | 0.2748 | 0.6990 |
| 22 | EnSpm\_CACTA\_1 | 0.1688 | 0.9490 | 19 | Retand\_6 | 0.2932 | 0.6330 |
| 32 | EnSpm\_CACTA\_2 | 0.2353 | 0.8030 | 21 | Retand\_7 | 0.3357 | 0.5110 |
| 87 | EnSpm\_CACTA\_3 | 0.4075 | 0.2460 | 24 | Retand\_8 | 0.2946 | 0.6320 |
| 135 | EnSpm\_CACTA\_4 | 0.3635 | 0.3550 | 38 | Retand\_9 | 0.2642 | 0.7020 |
| 136 | EnSpm\_CACTA\_5 | 0.4831 | 0.1960 | 49 | Retand\_10 | 0.3449 | 0.5200 |
| 137 | EnSpm\_CACTA\_6 | 0.1642 | 0.9480 | 53 | Retand\_11 | 0.2818 | 0.6370 |
| 203 | EnSpm\_CACTA\_7 | 0.2418 | 0.7860 | 58 | Retand\_12 | 0.3672 | 0.4280 |
| 148 | MuDR\_Mutator\_1 | 0.3375 | 0.4670 | 72 | Retand\_13 | 0.3412 | 0.5230 |
| 169 | **MuDR\_Mutator\_2** | **0.8000** | **0.0050** | 74 | Retand\_14 | 0.2868 | 0.6490 |
| 194 | **MuDR\_Mutator\_3** | **1.7396** | **0.0010** | 77 | Retand\_15 | 0.3579 | 0.3890 |
| 20 | PIF\_Harbinger\_1 | 0.7504 | 0.0140 | 84 | Retand\_16 | 0.3713 | 0.3760 |
| 141 | PIF\_Harbinger\_2 | 0.6238 | 0.0500 | 89 | Retand\_17 | 0.2949 | 0.6100 |
| 3 | Angela\_1 | 0.3177 | 0.5200 | 101 | Retand\_18 | 0.2817 | 0.6850 |
| 5 | Angela\_2 | 0.2702 | 0.6510 | 103 | Retand\_19 | 0.3941 | 0.3370 |
| 14 | Angela\_3 | 0.5073 | 0.1180 | 112 | Retand\_20 | 0.4008 | 0.3000 |
| 15 | Angela\_4 | 0.2170 | 0.8160 | 117 | Retand\_21 | 0.3912 | 0.3590 |
| 55 | Angela\_5 | 0.2384 | 0.7530 | 132 | Retand\_22 | 0.3261 | 0.4750 |
| 81 | Angela\_6 | 0.2473 | 0.7380 | 160 | Retand\_23 | 0.4118 | 0.3610 |
| 86 | Angela\_7 | 0.2889 | 0.6420 | 178 | Retand\_24 | 0.5538 | 0.0470 |
| 92 | Angela\_8 | 0.2993 | 0.6190 | 180 | Retand\_25 | 0.4416 | 0.1580 |
| 115 | Angela\_9 | 0.2473 | 0.7680 | 223 | Retand\_26 | 0.4754 | 0.1160 |
| 167 | Ikeros | 0.4735 | 0.1360 | 23 | Tekay\_1 | 0.3267 | 0.4720 |
| 13 | SIRE\_1 | 0.2846 | 0.6170 | 25 | Tekay\_2 | 0.4040 | 0.3530 |
| 16 | SIRE\_2 | 0.3148 | 0.5330 | 50 | Tekay\_3 | 0.2894 | 0.5810 |
| 40 | SIRE\_3 | 0.3128 | 0.5040 | 63 | **Tekay\_4** | **1.3463** | **0.0040** |
| 43 | SIRE\_4 | 0.3197 | 0.5320 | 90 | Tekay\_5 | 0.1691 | 0.9050 |
| 52 | SIRE\_5 | 0.2477 | 0.7700 | 108 | Tekay\_6 | 0.4487 | 0.2940 |
| 68 | SIRE\_6 | 0.2165 | 0.8290 | 118 | Tekay\_7 | 0.4218 | 0.3150 |
| 95 | SIRE\_7 | 0.3357 | 0.4620 | 129 | Tekay\_8 | 0.2556 | 0.7410 |
| 98 | SIRE\_8 | 0.3081 | 0.5600 | 220 | Tekay\_9 | 0.5207 | 0.1700 |
| 122 | SIRE\_9 | 0.3181 | 0.5200 |  |  |  |  |

**Table 5.3.\_** Phylogenetic signal *Fine leaved* group obtained with Blomberg’s K and Pagel’s lambda tests. Significant values are highlighted in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **N. Cluster** | **Cluster Name** | **Phylogenetic signal on combined tree** | | **N. Cluster** | **Cluster Name** | **Phylogenetic signal on combined tree** | |
| **K** | **p-value** | **K** | **p-value** |
| 18 | LTR\_1 | 0.5850 | 0.3040 | 178 | Ivana | 0.6122 | 0.2780 |
| 124 | LTR\_10 | 0.4946 | 0.5210 | 1 | SIRE\_1 | 0.4255 | 0.6880 |
| 36 | LTR\_2 | 0.3961 | 0.7580 | 10 | SIRE\_2 | 0.4795 | 0.5640 |
| 52 | LTR\_3 | 0.4874 | 0.4790 | 17 | SIRE\_3 | 0.4726 | 0.5560 |
| 61 | LTR\_4 | 0.3825 | 0.7960 | 20 | SIRE\_4 | 0.5103 | 0.4530 |
| 79 | LTR\_5 | 0.6444 | 0.1800 | 22 | SIRE\_5 | 0.4442 | 0.6720 |
| 82 | LTR\_6 | 0.5286 | 0.4160 | 33 | SIRE\_6 | 0.6636 | 0.1920 |
| 92 | LTR\_7 | 0.5928 | 0.2790 | 43 | SIRE\_7 | 0.4188 | 0.6890 |
| 107 | LTR\_8 | 0.6859 | 0.1720 | 58 | SIRE\_8 | 0.4299 | 0.6800 |
| 121 | LTR\_9 | 0.4593 | 0.6240 | 66 | SIRE\_9 | 0.4203 | 0.7200 |
| 51 | 45S\_rDNA\_1 | 0.5162 | 0.4370 | 68 | SIRE\_10 | 0.6319 | 0.2110 |
| 112 | 45S\_rDNA\_2 | 0.6238 | 0.2660 | 71 | SIRE\_11 | 0.5350 | 0.3940 |
| 183 | 5S\_rDNA | 0.5924 | 0.2420 | 86 | SIRE\_12 | 0.5048 | 0.4990 |
| 16 | **Repeat\_1** | **1.0080** | **0.0250** | 114 | SIRE\_13 | 0.4121 | 0.7350 |
| 24 | Repeat\_2 | 0.4221 | 0.7190 | 15 | TAR | 0.5817 | 0.3120 |
| 67 | Repeat\_3 | 0.3501 | 0.8790 | 145 | Tork | 0.6339 | 0.1990 |
| 140 | Repeat\_4 | 0.4277 | 0.7000 | 25 | Athila\_1 | 0.3757 | 0.8400 |
| 34 | Satellite\_1 | 0.5174 | 0.4740 | 27 | Athila\_2 | 0.4745 | 0.5670 |
| 96 | Satellite\_2 | 0.3895 | 0.7970 | 32 | Athila\_3 | 0.4377 | 0.6350 |
| 6 | EnSpm\_CACTA\_1 | 0.4334 | 0.6900 | 39 | Athila\_4 | 0.3759 | 0.8270 |
| 9 | EnSpm\_CACTA\_2 | 0.4903 | 0.4900 | 40 | Athila\_5 | 0.5311 | 0.3540 |
| 46 | EnSpm\_CACTA\_3 | 0.4561 | 0.6060 | 47 | Athila\_6 | 0.4955 | 0.4820 |
| 49 | EnSpm\_CACTA\_4 | 0.4501 | 0.5980 | 54 | Athila\_7 | 0.4510 | 0.5860 |
| 55 | EnSpm\_CACTA\_5 | 0.5194 | 0.4530 | 81 | Athila\_8 | 0.4363 | 0.6530 |
| 60 | EnSpm\_CACTA\_6 | 0.4620 | 0.6040 | 131 | Athila\_9 | 0.4843 | 0.4760 |
| 64 | EnSpm\_CACTA\_7 | 0.6836 | 0.2210 | 135 | Athila\_10 | 0.4966 | 0.4560 |
| 73 | EnSpm\_CACTA\_8 | 0.4144 | 0.7190 | 138 | Athila\_11 | 0.6256 | 0.1840 |
| 80 | EnSpm\_CACTA\_9 | 0.4872 | 0.5390 | 149 | Athila\_12 | 0.3980 | 0.7520 |
| 105 | EnSpm\_CACTA\_10 | 0.5294 | 0.4210 | 187 | Athila\_13 | 0.4041 | 0.7130 |
| 125 | EnSpm\_CACTA\_11 | 0.4066 | 0.7510 | 42 | CRM\_1 | 0.6362 | 0.2460 |
| 144 | EnSpm\_CACTA\_12 | 0.5082 | 0.4910 | 59 | CRM\_2 | 0.3588 | 0.8750 |
| 157 | EnSpm\_CACTA\_13 | 0.5125 | 0.4800 | 100 | CRM\_3 | 0.3510 | 0.8600 |
| 45 | MuDR\_Mutator\_1 | 0.5426 | 0.3880 | 103 | CRM\_4 | 0.3466 | 0.8890 |
| 101 | MuDR\_Mutator\_2 | 0.5144 | 0.4370 | 116 | CRM\_5 | 0.6577 | 0.2860 |
| 219 | MuDR\_Mutator\_3 | 0.7445 | 0.2030 | 126 | CRM\_6 | 0.3726 | 0.8240 |
| 229 | MuDR\_Mutator\_4 | 0.6158 | 0.3420 | 136 | CRM\_7 | 0.6476 | 0.2630 |
| 197 | PIF\_Harbinger | 0.5061 | 0.4370 | 170 | CRM\_8 | 0.4988 | 0.4740 |
| 3 | Angela\_1 | 0.7349 | 0.1480 | 171 | CRM\_9 | 0.7605 | 0.0920 |
| 7 | Angela\_2 | 0.6601 | 0.2330 | 152 | Ogre\_1 | 0.6782 | 0.2880 |
| 11 | Angela\_3 | 0.7251 | 0.1630 | 184 | Ogre\_2 | 0.4720 | 0.5490 |
| 21 | Angela\_4 | 0.5692 | 0.3330 | 2 | Retand\_1 | 0.3831 | 0.7980 |
| 26 | Angela\_5 | 0.5260 | 0.4440 | 4 | Retand\_2 | 0.4944 | 0.5290 |
| 30 | Angela\_6 | 0.5605 | 0.3710 | 5 | Retand\_3 | 0.5164 | 0.4030 |
| 35 | Angela\_7 | 0.5329 | 0.3950 | 14 | Retand\_4 | 0.4230 | 0.7090 |
| 41 | Angela\_8 | 0.7546 | 0.1210 | 19 | Retand\_5 | 0.6771 | 0.1810 |
| 48 | Angela\_9 | 0.7401 | 0.1350 | 37 | Retand\_6 | 0.3956 | 0.7640 |
| 75 | **Angela\_10** | **0.8110** | **0.0830** | 89 | Retand\_7 | 0.5288 | 0.4010 |
| 76 | Angela\_11 | 0.4887 | 0.5130 | 193 | Retand\_8 | 0.7818 | 0.1380 |
| 78 | Angela\_12 | 0.5210 | 0.3690 | 23 | Tekay\_1 | 0.5026 | 0.5260 |
| 117 | Angela\_13 | 0.5121 | 0.4270 | 85 | **Tekay\_2** | **1.1647** | **0.0900** |
| 120 | Angela\_14 | 0.4530 | 0.6090 | 97 | **Tekay\_3** | **1.2022** | **0.0780** |
| 153 | Angela\_15 | 0.4987 | 0.4770 |  |  |  |  |

**Table 5.4.\_** Phylogenetic signal *Broad leaved* group obtained with Blomberg’s K and Pagel’s lambda tests. Significant values are highlighted in bold.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **N. Cluster** | **Cluster Name** | **Phylogenetic signal on combinate tree** | | **N. Cluster** | **Cluster**  **Name** | **Phylogenetic signal on combinate tree** | |
| **K** | **p-value** | **K** | **p-value** |
| 40 | Repeat\_1 | 0.3435 | 0.5850 | 1 | Tekay\_1 | 0.5706 | 0.1220 |
| 57 | Repeat\_2 | 0.4259 | 0.3090 | 4 | **Tekay\_2** | **1.0530** | **0.0080** |
| 58 | Repeat\_3 | 0.3954 | 0.4410 | 7 | **Tekay\_3** | **0.6307** | **0.0730** |
| 70 | Repeat\_4 | 0.4548 | 0.2880 | 8 | Tekay\_4 | 0.3789 | 0.4640 |
| 84 | Repeat\_5 | 0.3713 | 0.4890 | 10 | **Tekay\_5** | **0.7060** | **0.0780** |
| 108 | Repeat\_6 | 0.2951 | 0.7690 | 19 | **Tekay\_6** | **0.9883** | **0.0230** |
| 110 | Repeat\_7 | 0.3704 | 0.5180 | 27 | Tekay\_7 | 0.6976 | 0.0370 |
| 179 | Repeat\_8 | 0.4154 | 0.3740 | 43 | Tekay\_8 | 1.1727 | 0.0040 |
| 189 | Repeat\_9 | 0.3301 | 0.6560 | 46 | Tekay\_9 | 0.3280 | 0.6190 |
| 218 | Repeat\_10 | 0.2661 | 0.8800 | 49 | **Tekay\_10** | **0.9624** | **0.0080** |
| 100 | LINE\_1 | 0.3406 | 0.6240 | 62 | **Tekay\_11** | **1.0418** | **0.0080** |
| 12 | **LTR\_1** | **1.0796** | **0.0050** | 65 | **Tekay\_12** | **1.0957** | **0.0020** |
| 256 | Ale\_1 | 0.2603 | 0.7670 | 114 | **Tekay\_13** | **0.8371** | **0.0230** |
| 2 | **Angela\_1** | **0.6062** | **0.0830** | 118 | Tekay\_14 | 0.5686 | 0.1650 |
| 3 | Angela\_2 | 0.3894 | 0.4440 | 129 | Tekay\_15 | 0.6237 | 0.1210 |
| 5 | Angela\_3 | 0.3994 | 0.3840 | 132 | Tekay\_16 | 0.3177 | 0.6310 |
| 13 | Angela\_4 | 0.5182 | 0.1780 | 24 | Athila\_1 | 0.2142 | 0.9100 |
| 21 | **Angela\_5** | **0.6538** | **0.0540** | 42 | **Athila\_2** | **0.6794** | **0.0550** |
| 22 | Angela\_6 | 1.2911 | 0.0020 | 48 | Athila\_3 | 0.5150 | 0.1750 |
| 31 | Angela\_7 | 0.5303 | 0.1320 | 55 | Athila\_4 | 0.4772 | 0.2190 |
| 32 | Angela\_8 | 0.5690 | 0.0950 | 60 | **Athila\_5** | **0.6296** | **0.0800** |
| 34 | Angela\_9 | 0.5083 | 0.1890 | 80 | Athila\_6 | 0.2239 | 0.8610 |
| 39 | Angela\_10 | 0.5176 | 0.1500 | 97 | **Athila\_7** | **0.7035** | **0.0540** |
| 53 | Angela\_11 | 0.3974 | 0.3990 | 104 | **Athila\_8** | **0.6905** | **0.0380** |
| 64 | Angela\_12 | 0.4498 | 0.2500 | 185 | Athila\_9 | 0.5642 | 0.1200 |
| 72 | Angela\_13 | 0.4298 | 0.3210 | 11 | Retand\_1 | 0.5333 | 0.1620 |
| 79 | Angela\_14 | 0.4175 | 0.3480 | 45 | EnSpm\_CACTA\_1 | 0.4333 | 0.4040 |
| 81 | **Angela\_15** | **0.7050** | **0.0450** | 47 | EnSpm\_CACTA\_2 | 0.5681 | 0.1320 |
| 95 | Angela\_16 | 0.3509 | 0.5720 | 59 | EnSpm\_CACTA\_3 | 0.4286 | 0.3510 |
| 162 | Angela\_17 | 0.4655 | 0.2330 | 127 | EnSpm\_CACTA\_4 | 0.3997 | 0.4200 |
| 198 | Ikeros\_1 | 0.4370 | 0.2990 | 140 | EnSpm\_CACTA\_5 | 0.5053 | 0.2650 |
| 18 | SIRE\_1 | 0.4566 | 0.2890 | 144 | EnSpm\_CACTA\_6 | 0.4883 | 0.2060 |
| 26 | SIRE\_2 | 0.4068 | 0.3970 | 150 | EnSpm\_CACTA\_7 | 0.4796 | 0.2840 |
| 35 | SIRE\_2.1 | 0.5107 | 0.1750 | 176 | EnSpm\_CACTA\_8 | 0.2484 | 0.8980 |
| 68 | SIRE\_4 | 0.3873 | 0.4810 | 199 | EnSpm\_CACTA\_9 | 0.5272 | 0.1890 |
| 99 | SIRE\_5 | 0.4136 | 0.4120 | 86 | **MuDR\_Mutator\_1** | **0.9483** | **0.0020** |
| 192 | SIRE\_6 | 0.3916 | 0.4380 | 219 | MuDR\_Mutator\_2 | 0.5809 | 0.1410 |
| 28 | TAR\_1 | 0.3529 | 0.5740 | 190 | PIF\_Harbinger\_1 | 0.2860 | 0.7130 |
| 194 | Tork\_1 | 0.3740 | 0.4450 | 98 | 45S\_rDNA\_1 | 0.2531 | 0.8490 |
| 16 | CRM\_1 | 0.3987 | 0.4300 | 133 | 45S\_rDNA\_2 | 0.2497 | 0.8550 |
| 82 | CRM\_2 | 0.6587 | 0.0990 | 236 | 5S\_rDNA\_1 | 0.3941 | 0.4240 |
| 116 | CRM\_3 | 0.5217 | 0.1830 | 107 | Satellite\_1 | 0.5113 | 0.2440 |
| 223 | CRM\_4 | 0.3788 | 0.4460 |  |  |  |  |