**Supplementary Data**

Abbreviations: Arabidopsis thaliana (A), Solanum tuberosum (S), Oryza sativa (O), Hordeum vulgare (H), Physcomitrella patens (P) and Chlamydomonas reinhardtii (C), PtLnc-BXE model built on training data of species X (Model\_X), long non-coding RNAs (lncRNAs), protein coding transcripts (pcts)

**Supplementary Table S0.** Optimal feature subsets for six species.

|  |  |
| --- | --- |
| Species (amount) | Features |
| A  (89) | 'A', 'A0', 'A1', 'A2', 'AAA', 'AAC', 'AAG', 'AAT', 'ACA', 'ACC', 'ACG', 'ACT', 'AG', 'AGC', 'ATG', 'C0', 'C2', 'C3', 'C4', 'CAG', 'CCA', 'CCC', 'CCG', 'CCT', 'CGG', 'CGT', 'CTG', 'CTT', 'Fop', 'G', 'G1', 'GAG', 'GAT', 'GCA', 'GCG', 'GGA', 'GGG', 'GTC', 'GTT', 'Gravy', 'Instability', 'ORF-coverage', 'RCB', 'RSCU\_AAA', 'RSCU\_AAC', 'RSCU\_AAG', 'RSCU\_ACA', 'RSCU\_ACC', 'RSCU\_ACT', 'RSCU\_AGA', 'RSCU\_ATG', 'RSCU\_ATT', 'RSCU\_CAA', 'RSCU\_CAC', 'RSCU\_CAT', 'RSCU\_CCC', 'RSCU\_CCG', 'RSCU\_CCT', 'RSCU\_CGC', 'RSCU\_CGT', 'RSCU\_CTC', 'RSCU\_CTT', 'RSCU\_GAA', 'RSCU\_GCA', 'RSCU\_GCG', 'RSCU\_GCT', 'RSCU\_GGG', 'RSCU\_GGT', 'RSCU\_GTA', 'RSCU\_TAC', 'RSCU\_TAT', 'RSCU\_TCA', 'RSCU\_TCT', 'RSCU\_TGT', 'RSCU\_TTC', 'RSCU\_TTG', 'RSCU\_TTT', 'SCUO', 'T', 'T0', 'TAT', 'TCT', 'TG', 'TGT', 'TTA', 'TTG', 'TTT', 'fickett', 'transcript length' |
| S  (93) | 'A0', 'A3', 'A4', 'AAA', 'AAC', 'AAT', 'AC', 'ACA', 'ACG', 'ACT', 'AG', 'AGA', 'AGC', 'AGG', 'AGT', 'ATA', 'ATC', 'C', 'C0', 'C1', 'C4', 'CAA', 'CAC', 'CAG', 'CAT', 'CCC', 'CCT', 'CGA', 'CGG', 'CTA', 'EW', 'G', 'G3', 'G4', 'GAC', 'GAG', 'GCT', 'GGA', 'GGT', 'Gravy', 'Instability', 'ORF-coverage', 'ORF-integrity', 'RCB', 'RSCU\_AAA', 'RSCU\_AAG', 'RSCU\_ACA', 'RSCU\_ACC', 'RSCU\_AGA', 'RSCU\_AGC', 'RSCU\_AGT', 'RSCU\_ATA', 'RSCU\_ATC', 'RSCU\_ATG', 'RSCU\_CAT', 'RSCU\_CCA', 'RSCU\_CCC', 'RSCU\_CCG', 'RSCU\_CGG', 'RSCU\_CGT', 'RSCU\_CTA', 'RSCU\_GAG', 'RSCU\_GCA', 'RSCU\_GCG', 'RSCU\_GCT', 'RSCU\_GGA', 'RSCU\_GGG', 'RSCU\_GGT', 'RSCU\_GTA', 'RSCU\_GTT', 'RSCU\_TCA', 'RSCU\_TCC', 'RSCU\_TCT', 'RSCU\_TGG', 'RSCU\_TGT', 'RSCU\_TTG', 'RSCU\_TTT', 'T1', 'T3', 'TAA', 'TAG', 'TAT', 'TCC', 'TCG', 'TCT', 'TGG', 'TGT', 'TTA', 'TTG', 'TTT', 'Frame Entropy', 'FF-score', 'fickett' |
| O  (87) | 'A0', 'A1', 'A2', 'A4', 'AAA', 'AAT', 'ACA', 'AG', 'AGC', 'AGT', 'AT', 'ATC', 'C4', 'CAA', 'CAC', 'CAG', 'CAT', 'CGC', 'CGG', 'CGT', 'CTT', 'EW', 'Fop', 'G0', 'G2', 'GAC', 'GC', 'GCA', 'GCC', 'GGA', 'GGC', 'GGG', 'GTC', 'GTG', 'Instability', 'ORF', 'ORF-integrity', 'RSCU\_AAA', 'RSCU\_AAT', 'RSCU\_ACT', 'RSCU\_AGA', 'RSCU\_AGC', 'RSCU\_ATC', 'RSCU\_ATT', 'RSCU\_CAC', 'RSCU\_CAT', 'RSCU\_CCC', 'RSCU\_CCG', 'RSCU\_CCT', 'RSCU\_CGA', 'RSCU\_CGC', 'RSCU\_CTA', 'RSCU\_CTG', 'RSCU\_GAA', 'RSCU\_GCA', 'RSCU\_GCC', 'RSCU\_GCG', 'RSCU\_GCT', 'RSCU\_GGA', 'RSCU\_GGG', 'RSCU\_GGT', 'RSCU\_GTA', 'RSCU\_GTG', 'RSCU\_GTT', 'RSCU\_TAT', 'RSCU\_TCT', 'RSCU\_TGC', 'RSCU\_TTC', 'SCUO', 'T', 'T0', 'T1', 'T2', 'T3', 'T4', 'TAT', 'TC', 'TCA', 'TCC', 'TG', 'TGC', 'TTA', 'TTC', 'TTG', 'TTT', 'Frame Entropy', 'Numbers of hits' |
| H  (95) | 'A', 'A0', 'A1', 'A2', 'A4', 'AAG', 'ACA', 'ACT', 'AGC', 'AGG', 'AT', 'ATT', 'C', 'C0', 'C1', 'C2', 'CAG', 'CCA', 'CCC', 'CCG', 'CCT', 'CGA', 'CTA', 'CUB', 'EW', 'Fop', 'G', 'G2', 'G4', 'GAG', 'GAT', 'GC', 'GCT', 'GGA', 'GTA', 'GTC', 'Instability', 'ORF', 'ORF-coverage', 'PI', 'RSCU\_AAA', 'RSCU\_AAG', 'RSCU\_AAT', 'RSCU\_ACA', 'RSCU\_ACC', 'RSCU\_ACG', 'RSCU\_AGC', 'RSCU\_AGG', 'RSCU\_AGT', 'RSCU\_ATG', 'RSCU\_CAA', 'RSCU\_CAC', 'RSCU\_CAG', 'RSCU\_CCA', 'RSCU\_CCC', 'RSCU\_CGA', 'RSCU\_CGG', 'RSCU\_CTC', 'RSCU\_CTT', 'RSCU\_GAC', 'RSCU\_GAG', 'RSCU\_GCA', 'RSCU\_GCC', 'RSCU\_GCG', 'RSCU\_GGA', 'RSCU\_GGT', 'RSCU\_GTG', 'RSCU\_GTT', 'RSCU\_TAT', 'RSCU\_TCA', 'RSCU\_TCC', 'RSCU\_TGC', 'RSCU\_TGG', 'RSCU\_TGT', 'RSCU\_TTA', 'RSCU\_TTT', 'SCUO', 'T', 'T0', 'T1', 'T2', 'TAC', 'TC', 'TCC', 'TCT', 'TG', 'TGG', 'TTA', 'TTC', 'TTG', 'TTT', 'Total bit score', 'Frame Entropy', 'FF-score', 'fickett' |
| P  (90) | 'A', 'A0', 'A1', 'A2', 'A3', 'AAG', 'AC', 'ACA', 'ACT', 'AG', 'AGA', 'AGC', 'AGG', 'ATA', 'ATC', 'ATG', 'C1', 'C2', 'CAA', 'CCC', 'CCG', 'CCT', 'CGC', 'CTA', 'CTG', 'Fop', 'G+C', 'GAA', 'GAC', 'GAT', 'GC', 'GCG', 'GCT', 'GTC', 'GTG', 'Gravy', 'Instability', 'ORF', 'RSCU\_AAA', 'RSCU\_AAG', 'RSCU\_AAT', 'RSCU\_ACT', 'RSCU\_AGA', 'RSCU\_AGG', 'RSCU\_ATC', 'RSCU\_CAA', 'RSCU\_CAC', 'RSCU\_CCA', 'RSCU\_CCC', 'RSCU\_CCG', 'RSCU\_CCT', 'RSCU\_CGA', 'RSCU\_CGC', 'RSCU\_CGT', 'RSCU\_CTA', 'RSCU\_CTT', 'RSCU\_GAG', 'RSCU\_GAT', 'RSCU\_GCC', 'RSCU\_GGA', 'RSCU\_GGC', 'RSCU\_GGG', 'RSCU\_GGT', 'RSCU\_GTA', 'RSCU\_GTC', 'RSCU\_GTT', 'RSCU\_TAC', 'RSCU\_TAT', 'RSCU\_TCC', 'RSCU\_TCG', 'RSCU\_TGG', 'RSCU\_TTA', 'RSCU\_TTT', 'T', 'T0', 'T3', 'TAA', 'TAC', 'TAT', 'TC', 'TCA', 'TG', 'TTA', 'TTC', 'TTG', 'Frame Entropy', 'Significance score', 'Numbers of hits', 'FF-score', 'fickett' |
| C  (88) | 'A', 'A0', 'A4', 'AC', 'ACC', 'ACG', 'AG', 'AGA', 'AGC', 'AT', 'ATC', 'ATT', 'C0', 'C2', 'CAC', 'CCC', 'CCG', 'CCT', 'CGC', 'CGG', 'CTA', 'CTC', 'CTT', 'CUB', 'EW', 'Fop', 'G', 'G+C', 'G1', 'G2', 'G3', 'GAA', 'GAG', 'GAT', 'GCA', 'GCG', 'GCT', 'GGC', 'GGT', 'GTC', 'GTG', 'GTT', 'Gravy', 'Instability', 'ORF', 'PI', 'RSCU\_AAA', 'RSCU\_AAC', 'RSCU\_ACT', 'RSCU\_AGA', 'RSCU\_AGC', 'RSCU\_ATA', 'RSCU\_CAA', 'RSCU\_CCA', 'RSCU\_CGC', 'RSCU\_CGG', 'RSCU\_CTA', 'RSCU\_CTC', 'RSCU\_CTG', 'RSCU\_CTT', 'RSCU\_GCA', 'RSCU\_GCC', 'RSCU\_GCG', 'RSCU\_GCT', 'RSCU\_GGA', 'RSCU\_GGC', 'RSCU\_GGG', 'RSCU\_GGT', 'RSCU\_TAT', 'RSCU\_TCA', 'RSCU\_TCC', 'RSCU\_TCG', 'RSCU\_TCT', 'RSCU\_TGG', 'RSCU\_TGT', 'RSCU\_TTG', 'RSCU\_TTT', 'T', 'T0', 'T1', 'TC', 'TGT', 'TTA', 'TTG', 'Frame Entropy', 'FF-score', 'transcript length', 'hexamer' |

**Supplementary Table S1.** Common preferred features (dimensions) among three species or more

|  |  |  |
| --- | --- | --- |
| Species | Amount | Features |
| A S O H P C | 7 | RSCU\_AAA RSCU\_GGT TTA Instability AGC TTG A0 |
| A S O H P | 2 | RSCU\_CCC ACA |
| A S O H C | 2 | RSCU\_GCA RSCU\_GCG |
| A S O P C | 3 | RSCU\_GGG RSCU\_AGA AG |
| A S H P C | 3 | RSCU\_TTT CCT CCC |
| A O H P C | 5 | Fop T0 T GTC RSCU\_TAT |
| S O H P C | 2 | Frame entropy RSCU\_GGA |
| A H O S | 3 | GGA CAG TTT |
| A O P S | 3 | RSCU\_GTA RSCU\_CCG TAT |
| A C O S | 3 | CGG RSCU\_GCT RSCU\_TCT |
| A H P S | 3 | RSCU\_AAG ACT Fickett |
| A C H S | 5 | C0 GAG RSCU\_TCA RSCU\_TGT G |
| A C P S | 1 | Gravy |
| A H O P | 4 | A1 RSCU\_CAC TG A2 |
| A C O P | 2 | RSCU\_CGC RSCU\_ACT |
| A C H P | 6 | CCG GAT RSCU\_CAA C2 RSCU\_CTT A |
| H O P S | 1 | RSCU\_GTT |
| C H O S | 4 | T1 EW RSCU\_AGC A4 |
| C O P S | 2 | ATC RSCU\_CTA |
| C H P S | 6 | RSCU\_CCA FF-score RSCU\_TGG CTA GCT RSCU\_TCC |
| C H O P | 3 | RSCU\_GCC ORF TC |
| A O S | 4 | AAA AAT RSCU\_CAT C4 |
| A H S | 5 | ORF-coverage RSCU\_ACC RSCU\_ATG RSCU\_ACA TCT |
| A P S | 1 | RSCU\_CGT |
| A C S | 3 | RSCU\_TTG TGT ACG |
| A H O | 1 | SCUO |
| A O P | 1 | RSCU\_CCT |
| A C O | 2 | CTT GCA |
| A H P | 1 | AAG |
| A C H | 1 | RSCU\_CTC |
| A C P | 1 | GCG |
| H O S | 1 | TCC |
| O P S | 4 | T3 CAA GAC RSCU\_ATC |
| C O S | 1 | CAC |
| H P S | 3 | C1 RSCU\_GAG AGG |
| C H S | 1 | RSCU\_CGG |
| C P S | 2 | AC AGA |
| H O P | 4 | RSCU\_CGA GC TTC RSCU\_AAT |
| C H O | 2 | AT G2 |
| C O P | 2 | GTG CGC |

**Supplementary Table S2**. Comparison of cross-validation performance (AUC) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 99.27% | 95.78% | 99.09% |
| 1:2 | 99.27% | 96.00% | 99.19% |
| 1:3 | 99.31% | 96.29% | 99.24% |
| 1:5 | 99.30% | 96.41% | 99.23% |
| Model\_S | 1:1 | 98.60% | 94.09% | 96.99% |
| 1:2 | 98.61% | 94.51% | 97.17% |
| 1:3 | 98.62% | 94.71% | 97.42% |
| 1:5 | 98.67% | 94.97% | 97.51% |
| Model\_O | 1:1 | 96.22% | 92.08% | 93.86% |
| 1:2 | 96.37% | 92.77% | 94.61% |
| 1:3 | 96.74% | 92.86% | 94.80% |
| 1:5 | 96.74% | 92.85% | 94.77% |
| Model\_H | 1:1 | 96.29% | 91.70% | 95.63% |
| 1:2 | 95.91% | 91.58% | 95.72% |
| 1:3 | 96.35% | 91.95% | 96.11% |
| 1:5 | 96.15% | 92.04% | 96.02% |
| Model\_P | 1:1 | 97.68% | 93.43% | 96.52% |
| 1:2 | 96.70% | 92.80% | 95.66% |
| 1:3 | 97.17% | 93.45% | 96.13% |
| 1:5 | 97.29% | 93.96% | 96.40% |
| Model\_C | 1:1 | 99.26% | 98.19% | 98.87% |
| 1:2 | 99.29% | 98.35% | 99.04% |
| 1:3 | 99.27% | 98.32% | 98.89% |
| 1:5 | 99.34% | 98.42% | 99.01% |

**Supplementary Table S3**. Comparison of cross-validation performance (ACC) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 96.60% | 87.98% | 95.73% |
| 1:2 | 96.58% | 88.45% | 96.11% |
| 1:3 | 96.60% | 90.33% | 96.66% |
| 1:5 | 97.07% | 92.55% | 96.97% |
| Model\_S | 1:1 | 94.07% | 87.16% | 91.94% |
| 1:2 | 93.76% | 87.43% | 91.91% |
| 1:3 | 94.33% | 88.44% | 92.52% |
| 1:5 | 95.41% | 90.19% | 94.02% |
| Model\_O | 1:1 | 90.63% | 84.19% | 87.93% |
| 1:2 | 89.91% | 84.83% | 87.71% |
| 1:3 | 91.09% | 85.88% | 88.76% |
| 1:5 | 92.55% | 88.67% | 90.58% |
| Model\_H | 1:1 | 90.87% | 84.53% | 89.97% |
| 1:2 | 89.82% | 83.64% | 89.37% |
| 1:3 | 90.76% | 84.92% | 90.56% |
| 1:5 | 91.54% | 87.53% | 91.51% |
| Model\_P | 1:1 | 92.90% | 86.70% | 92.76% |
| 1:2 | 91.54% | 85.57% | 91.04% |
| 1:3 | 92.19% | 86.67% | 90.98% |
| 1:5 | 92.87% | 87.69% | 91.30% |
| Model\_C | 1:1 | 96.05% | 92.90% | 94.58% |
| 1:2 | 96.19% | 93.18% | 95.03% |
| 1:3 | 96.36% | 94.01% | 95.36% |
| 1:5 | 96.82% | 95.16% | 96.27% |

**Supplementary Table S4**. Comparison of cross-validation performance (AUPR) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 99.08% | 95.65% | 98.85% |
| 1:2 | 98.36% | 92.52% | 98.02% |
| 1:3 | 97.72% | 90.38% | 97.47% |
| 1:5 | 96.25% | 86.30% | 95.92% |
| Model\_S | 1:1 | 98.54% | 93.46% | 96.25% |
| 1:2 | 97.32% | 89.55% | 93.84% |
| 1:3 | 96.16% | 86.26% | 92.54% |
| 1:5 | 94.54% | 82.04% | 90.00% |
| Model\_O | 1:1 | 95.48% | 91.13% | 91.38% |
| 1:2 | 92.19% | 85.51% | 87.85% |
| 1:3 | 90.70% | 81.41% | 84.62% |
| 1:5 | 86.16% | 73.53% | 78.80% |
| Model\_H | 1:1 | 95.12% | 89.81% | 94.30% |
| 1:2 | 90.21% | 81.47% | 90.09% |
| 1:3 | 88.17% | 76.60% | 87.66% |
| 1:5 | 81.33% | 67.76% | 81.82% |
| Model\_P | 1:1 | 97.10% | 91.59% | 94.63% |
| 1:2 | 91.70% | 82.89% | 87.16% |
| 1:3 | 90.40% | 79.21% | 84.59% |
| 1:5 | 86.28% | 72.66% | 79.77% |
| Model\_C | 1:1 | 99.22% | 98.08% | 98.73% |
| 1:2 | 98.46% | 96.66% | 97.97% |
| 1:3 | 97.77% | 95.12% | 96.60% |
| 1:5 | 96.90% | 93.44% | 95.52% |

**Supplementary Table S5**. Comparison of cross-validation performance (Sensitivity) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 97.68% | 87.94% | 98.66% |
| 1:2 | 95.53% | 80.91% | 97.02% |
| 1:3 | 93.57% | 76.14% | 95.11% |
| 1:5 | 90.71% | 68.46% | 91.12% |
| Model\_S | 1:1 | 95.82% | 88.92% | 94.47% |
| 1:2 | 91.77% | 75.22% | 89.89% |
| 1:3 | 89.25% | 64.65% | 85.81% |
| 1:5 | 84.13% | 47.78% | 77.97% |
| Model\_O | 1:1 | 92.86% | 86.25% | 93.39% |
| 1:2 | 84.85% | 70.28% | 85.04% |
| 1:3 | 79.80% | 58.91% | 76.59% |
| 1:5 | 71.25% | 43.27% | 61.58% |
| Model\_H | 1:1 | 93.82% | 88.76% | 95.27% |
| 1:2 | 87.55% | 73.52% | 90.27% |
| 1:3 | 82.55% | 61.06% | 85.11% |
| 1:5 | 72.55% | 42.19% | 72.97% |
| Model\_P | 1:1 | 95.83% | 93.08% | 97.82% |
| 1:2 | 90.72% | 79.07% | 93.47% |
| 1:3 | 87.31% | 63.45% | 85.80% |
| 1:5 | 76.89% | 33.90% | 67.05% |
| Model\_C | 1:1 | 97.17% | 92.63% | 97.56% |
| 1:2 | 95.15% | 88.43% | 94.42% |
| 1:3 | 93.28% | 86.29% | 92.06% |
| 1:5 | 89.42% | 81.55% | 87.47% |

**Supplementary Table S6**. Comparison of cross-validation performance (Specificity) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 95.53% | 88.03% | 92.79% |
| 1:2 | 97.11% | 92.23% | 95.65% |
| 1:3 | 97.61% | 95.07% | 97.18% |
| 1:5 | 98.34% | 97.37% | 98.14% |
| Model\_S | 1:1 | 92.31% | 85.41% | 89.40% |
| 1:2 | 94.75% | 93.54% | 92.92% |
| 1:3 | 96.03% | 96.37% | 94.75% |
| 1:5 | 97.67% | 98.68% | 97.23% |
| Model\_O | 1:1 | 88.39% | 82.13% | 82.47% |
| 1:2 | 92.45% | 92.11% | 89.05% |
| 1:3 | 94.85% | 94.87% | 92.81% |
| 1:5 | 96.81% | 97.75% | 96.38% |
| Model\_H | 1:1 | 87.93% | 80.30% | 84.68% |
| 1:2 | 90.96% | 88.70% | 88.93% |
| 1:3 | 93.49% | 92.88% | 92.37% |
| 1:5 | 95.34% | 96.60% | 95.21% |
| Model\_P | 1:1 | 89.96% | 80.31% | 87.69% |
| 1:2 | 91.95% | 88.83% | 89.82% |
| 1:3 | 93.81% | 94.41% | 92.71% |
| 1:5 | 96.06% | 98.45% | 96.16% |
| Model\_C | 1:1 | 94.92% | 93.16% | 91.60% |
| 1:2 | 96.71% | 95.55% | 95.34% |
| 1:3 | 97.39% | 96.59% | 96.46% |
| 1:5 | 98.30% | 97.88% | 98.03% |

**Supplementary Table S7**. Comparison of cross-validation performance (MCC) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 93.23% | 75.99% | 91.61% |
| 1:2 | 92.35% | 73.82% | 91.45% |
| 1:3 | 90.95% | 73.57% | 91.23% |
| 1:5 | 89.40% | 71.58% | 89.10% |
| Model\_S | 1:1 | 88.20% | 74.39% | 83.98% |
| 1:2 | 86.06% | 71.18% | 82.01% |
| 1:3 | 84.96% | 67.50% | 80.15% |
| 1:5 | 83.23% | 60.30% | 77.84% |
| Model\_O | 1:1 | 81.39% | 68.49% | 76.32% |
| 1:2 | 77.36% | 65.06% | 72.92% |
| 1:3 | 75.91% | 59.86% | 69.84% |
| 1:5 | 72.02% | 53.21% | 63.64% |
| Model\_H | 1:1 | 81.90% | 69.33% | 80.39% |
| 1:2 | 77.50% | 62.87% | 77.12% |
| 1:3 | 75.53% | 57.74% | 75.57% |
| 1:5 | 69.07% | 48.47% | 69.05% |
| Model\_P | 1:1 | 86.06% | 74.09% | 85.95% |
| 1:2 | 81.41% | 67.73% | 80.91% |
| 1:3 | 79.70% | 62.68% | 76.64% |
| 1:5 | 74.04% | 47.28% | 67.13% |
| Model\_C | 1:1 | 92.13% | 85.81% | 89.31% |
| 1:2 | 91.49% | 84.57% | 88.97% |
| 1:3 | 90.35% | 83.87% | 87.75% |
| 1:5 | 88.49% | 82.11% | 86.44% |

**Supplementary Table S8**. Comparison of cross-validation performance (F1-score) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 96.64% | 87.97% | 95.85% |
| 1:2 | 94.91% | 82.36% | 94.32% |
| 1:3 | 93.22% | 79.73% | 93.44% |
| 1:5 | 91.15% | 75.38% | 90.92% |
| Model\_S | 1:1 | 94.17% | 87.38% | 92.14% |
| 1:2 | 90.74% | 79.93% | 88.10% |
| 1:3 | 88.73% | 73.61% | 85.15% |
| 1:5 | 85.94% | 61.88% | 81.29% |
| Model\_O | 1:1 | 90.82% | 84.48% | 88.56% |
| 1:2 | 84.84% | 75.52% | 82.19% |
| 1:3 | 81.74% | 67.53% | 77.30% |
| 1:5 | 76.13% | 55.92% | 68.54% |
| Model\_H | 1:1 | 91.14% | 85.16% | 90.48% |
| 1:2 | 85.15% | 74.98% | 84.99% |
| 1:3 | 81.70% | 66.94% | 81.84% |
| 1:5 | 74.09% | 52.98% | 74.11% |
| Model\_P | 1:1 | 93.14% | 87.55% | 93.11% |
| 1:2 | 87.74% | 78.49% | 87.42% |
| 1:3 | 84.82% | 70.35% | 82.63% |
| 1:5 | 78.22% | 47.73% | 71.99% |
| Model\_C | 1:1 | 96.09% | 92.87% | 94.73% |
| 1:2 | 94.34% | 89.62% | 92.69% |
| 1:3 | 92.76% | 87.81% | 90.84% |
| 1:5 | 90.36% | 84.87% | 88.66% |

**Supplementary Table S9**. Comparison of cross-validation performance (Precision) of PtLnc-BXE models with existing tools

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | PtLnc-BXE | PLIT | PLncPRO |
| Model\_A | 1:1 | 95.63% | 88.03% | 93.19% |
| 1:2 | 94.31% | 83.90% | 91.77% |
| 1:3 | 92.88% | 83.74% | 91.83% |
| 1:5 | 91.63% | 83.94% | 90.72% |
| Model\_S | 1:1 | 92.58% | 85.91% | 89.92% |
| 1:2 | 89.76% | 85.37% | 86.39% |
| 1:3 | 88.24% | 85.59% | 84.50% |
| 1:5 | 87.83% | 87.84% | 84.91% |
| Model\_O | 1:1 | 88.92% | 82.82% | 84.19% |
| 1:2 | 84.97% | 81.75% | 79.52% |
| 1:3 | 83.82% | 79.27% | 78.03% |
| 1:5 | 81.85% | 79.56% | 77.27% |
| Model\_H | 1:1 | 88.60% | 81.86% | 86.14% |
| 1:2 | 82.90% | 76.51% | 80.30% |
| 1:3 | 80.88% | 74.08% | 78.81% |
| 1:5 | 75.73% | 71.29% | 75.30% |
| Model\_P | 1:1 | 90.70% | 82.73% | 88.82% |
| 1:2 | 84.98% | 78.09% | 82.11% |
| 1:3 | 82.63% | 79.40% | 79.68% |
| 1:5 | 79.79% | 81.04% | 77.72% |
| Model\_C | 1:1 | 95.04% | 93.13% | 92.07% |
| 1:2 | 93.56% | 90.88% | 91.02% |
| 1:3 | 92.28% | 89.41% | 89.66% |
| 1:5 | 91.39% | 88.52% | 89.87% |

**Supplementary Table S10.** Performance comparison (AUC) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 99.27% | 96.58% | 89.91% | 89.98% | 96.27% | 95.20% |
| 1:2 | 99.27% | 96.65% | 90.13% | 89.57% | 96.43% | 94.44% |
| 1:3 | 99.31% | 96.71% | 90.32% | 89.87% | 96.59% | 95.19% |
| 1:5 | 99.30% | 96.64% | 90.20% | 89.71% | 96.43% | 95.25% |
| Model\_S | 1:1 | 99.15% | 98.60% | 93.64% | 91.79% | 96.38% | 99.13% |
| 1:2 | 99.24% | 98.61% | 93.36% | 91.55% | 96.62% | 99.16% |
| 1:3 | 99.23% | 98.62% | 93.39% | 91.26% | 96.51% | 99.09% |
| 1:5 | 99.22% | 98.67% | 93.46% | 91.26% | 96.44% | 99.11% |
| Model\_O | 1:1 | 97.45% | 95.82% | 96.22% | 92.58% | 93.31% | 98.33% |
| 1:2 | 97.59% | 96.06% | 96.37% | 92.04% | 92.96% | 98.46% |
| 1:3 | 97.55% | 96.25% | 96.74% | 92.29% | 92.77% | 98.41% |
| 1:5 | 97.63% | 95.96% | 96.74% | 92.22% | 92.96% | 98.32% |
| Model\_H | 1:1 | 98.61% | 96.78% | 92.90% | 96.29% | 95.73% | 97.77% |
| 1:2 | 98.65% | 97.04% | 93.03% | 95.91% | 95.76% | 97.85% |
| 1:3 | 98.63% | 96.86% | 92.98% | 96.35% | 95.90% | 97.86% |
| 1:5 | 98.68% | 96.94% | 92.76% | 96.15% | 96.03% | 97.77% |
| Model\_P | 1:1 | 98.54% | 95.87% | 92.79% | 92.49% | 97.68% | 97.69% |
| 1:2 | 98.66% | 96.04% | 91.42% | 92.54% | 96.70% | 97.61% |
| 1:3 | 98.83% | 96.24% | 91.43% | 92.28% | 97.17% | 96.48% |
| 1:5 | 98.82% | 96.06% | 90.63% | 92.33% | 97.29% | 96.38% |
| Model\_C | 1:1 | 96.32% | 91.25% | 89.79% | 90.17% | 88.60% | 99.26% |
| 1:2 | 96.52% | 92.67% | 90.13% | 90.53% | 89.25% | 99.29% |
| 1:3 | 97.07% | 93.79% | 90.47% | 90.73% | 90.16% | 99.27% |
| 1:5 | 96.83% | 92.84% | 90.04% | 90.52% | 89.80% | 99.34% |

**Supplementary Table S11**. Performance comparison (ACC) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 96.60% | 89.68% | 75.18% | 76.81% | 87.42% | 86.73% |
| 1:2 | 96.58% | 91.30% | 78.54% | 78.95% | 88.89% | 86.89% |
| 1:3 | 96.60% | 92.30% | 81.06% | 81.59% | 90.45% | 89.27% |
| 1:5 | 97.07% | 93.12% | 83.37% | 83.15% | 91.65% | 90.12% |
| Model\_S | 1:1 | 95.22% | 94.07% | 83.79% | 83.92% | 90.95% | 96.32% |
| 1:2 | 96.86% | 93.76% | 87.14% | 85.94% | 92.99% | 96.50% |
| 1:3 | 97.10% | 94.33% | 88.74% | 85.50% | 93.27% | 96.36% |
| 1:5 | 97.17% | 95.41% | 90.60% | 85.69% | 93.87% | 95.53% |
| Model\_O | 1:1 | 87.42% | 82.08% | 90.63% | 85.40% | 84.88% | 95.11% |
| 1:2 | 91.35% | 86.42% | 89.91% | 86.64% | 87.35% | 94.38% |
| 1:3 | 92.72% | 90.07% | 91.09% | 87.15% | 88.94% | 93.75% |
| 1:5 | 93.73% | 91.43% | 92.55% | 87.11% | 89.87% | 91.89% |
| Model\_H | 1:1 | 92.35% | 88.30% | 81.23% | 90.87% | 88.60% | 93.85% |
| 1:2 | 94.75% | 91.98% | 85.57% | 89.82% | 90.73% | 93.96% |
| 1:3 | 95.44% | 92.87% | 87.42% | 90.76% | 91.77% | 93.82% |
| 1:5 | 95.91% | 93.59% | 89.36% | 91.54% | 92.80% | 92.94% |
| Model\_P | 1:1 | 94.17% | 90.50% | 84.94% | 86.84% | 92.90% | 94.64% |
| 1:2 | 95.82% | 92.68% | 86.31% | 87.82% | 91.54% | 93.57% |
| 1:3 | 96.36% | 93.86% | 88.53% | 87.90% | 92.19% | 93.49% |
| 1:5 | 95.71% | 93.81% | 90.13% | 88.01% | 92.87% | 91.55% |
| Model\_C | 1:1 | 82.31% | 68.17% | 69.88% | 78.19% | 77.83% | 96.05% |
| 1:2 | 85.11% | 71.60% | 75.67% | 81.52% | 80.95% | 96.19% |
| 1:3 | 87.84% | 75.10% | 77.94% | 82.63% | 82.13% | 96.36% |
| 1:5 | 89.25% | 78.15% | 81.65% | 83.71% | 83.69% | 96.82% |

**Supplementary Table S12**. Performance comparison (AUPR) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 99.08% | 83.15% | 32.44% | 60.10% | 63.49% | 78.17% |
| 1:2 | 98.36% | 82.74% | 34.53% | 59.14% | 65.26% | 75.66% |
| 1:3 | 97.72% | 82.03% | 33.97% | 59.18% | 66.77% | 78.64% |
| 1:5 | 96.25% | 81.65% | 32.68% | 58.86% | 65.11% | 77.23% |
| Model\_S | 1:1 | 92.01% | 98.54% | 48.57% | 60.96% | 58.38% | 95.63% |
| 1:2 | 92.67% | 97.32% | 45.37% | 58.48% | 60.02% | 95.85% |
| 1:3 | 92.58% | 96.16% | 46.10% | 59.18% | 58.93% | 95.59% |
| 1:5 | 92.58% | 94.54% | 47.61% | 59.37% | 56.78% | 95.62% |
| Model\_O | 1:1 | 81.82% | 70.39% | 95.48% | 63.76% | 42.45% | 90.85% |
| 1:2 | 80.98% | 69.91% | 92.19% | 62.05% | 36.77% | 91.33% |
| 1:3 | 80.41% | 71.61% | 90.70% | 62.93% | 35.27% | 91.53% |
| 1:5 | 81.49% | 69.91% | 86.16% | 62.75% | 39.97% | 90.99% |
| Model\_H | 1:1 | 88.53% | 77.55% | 39.97% | 95.12% | 55.84% | 87.16% |
| 1:2 | 89.01% | 81.38% | 39.92% | 90.21% | 57.83% | 87.70% |
| 1:3 | 88.73% | 77.57% | 39.11% | 88.17% | 58.15% | 87.44% |
| 1:5 | 88.86% | 78.79% | 37.19% | 81.33% | 59.40% | 86.81% |
| Model\_P | 1:1 | 87.27% | 73.32% | 45.11% | 63.24% | 97.10% | 87.56% |
| 1:2 | 88.63% | 78.37% | 38.18% | 64.63% | 91.70% | 85.67% |
| 1:3 | 89.80% | 78.66% | 38.57% | 64.06% | 90.40% | 85.53% |
| 1:5 | 90.12% | 76.94% | 36.65% | 64.84% | 86.28% | 85.21% |
| Model\_C | 1:1 | 71.48% | 59.09% | 34.82% | 55.96% | 26.82% | 99.22% |
| 1:2 | 74.41% | 69.63% | 36.93% | 57.45% | 27.78% | 98.46% |
| 1:3 | 78.46% | 73.47% | 37.99% | 57.97% | 30.42% | 97.77% |
| 1:5 | 76.87% | 70.22% | 34.03% | 56.78% | 29.38% | 96.90% |

**Supplementary Table S13**. Performance comparison (Sensitivity) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 97.68% | 92.85% | 93.70% | 92.81% | 97.02% | 92.37% |
| 1:2 | 95.53% | 89.80% | 90.38% | 88.52% | 94.80% | 88.62% |
| 1:3 | 93.57% | 87.57% | 87.19% | 84.10% | 92.16% | 84.73% |
| 1:5 | 90.71% | 83.04% | 82.47% | 78.58% | 87.98% | 75.55% |
| Model\_S | 1:1 | 98.15% | 95.82% | 90.64% | 88.12% | 92.58% | 89.41% |
| 1:2 | 95.44% | 91.77% | 82.95% | 79.12% | 84.40% | 84.28% |
| 1:3 | 92.52% | 89.25% | 76.69% | 71.44% | 76.73% | 81.33% |
| 1:5 | 87.50% | 84.13% | 67.51% | 61.53% | 65.47% | 71.91% |
| Model\_O | 1:1 | 98.07% | 97.39% | 92.86% | 88.06% | 94.88% | 81.60% |
| 1:2 | 96.11% | 95.78% | 84.85% | 76.97% | 87.47% | 68.29% |
| 1:3 | 92.95% | 91.82% | 79.80% | 68.62% | 75.36% | 62.41% |
| 1:5 | 87.83% | 86.38% | 71.25% | 56.19% | 63.77% | 47.01% |
| Model\_H | 1:1 | 98.87% | 95.62% | 94.14% | 93.82% | 96.68% | 83.15% |
| 1:2 | 95.66% | 90.00% | 88.33% | 87.55% | 90.71% | 75.65% |
| 1:3 | 93.32% | 86.22% | 82.16% | 82.55% | 85.68% | 70.56% |
| 1:5 | 85.92% | 76.25% | 72.06% | 72.55% | 72.29% | 60.94% |
| Model\_P | 1:1 | 97.00% | 91.68% | 88.02% | 85.75% | 95.83% | 80.57% |
| 1:2 | 89.68% | 84.02% | 81.64% | 80.01% | 90.72% | 70.43% |
| 1:3 | 79.08% | 71.69% | 74.77% | 71.78% | 87.31% | 66.68% |
| 1:5 | 69.94% | 61.65% | 62.31% | 57.87% | 76.89% | 48.04% |
| Model\_C | 1:1 | 98.39% | 98.05% | 95.15% | 93.55% | 95.91% | 97.17% |
| 1:2 | 95.84% | 95.76% | 90.42% | 86.11% | 89.77% | 95.15% |
| 1:3 | 95.07% | 94.02% | 87.49% | 82.38% | 85.93% | 93.28% |
| 1:5 | 91.58% | 88.51% | 79.45% | 74.08% | 74.77% | 89.42% |

**Supplementary Table S14**. Performance comparison (Specificity) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 95.53% | 89.32% | 73.95% | 73.65% | 86.66% | 85.77% |
| 1:2 | 97.11% | 91.48% | 77.75% | 77.06% | 88.43% | 86.60% |
| 1:3 | 97.61% | 92.85% | 80.65% | 81.10% | 90.32% | 90.04% |
| 1:5 | 98.34% | 94.29% | 83.43% | 84.05% | 91.94% | 92.61% |
| Model\_S | 1:1 | 94.85% | 92.31% | 83.33% | 83.09% | 90.82% | 97.50% |
| 1:2 | 97.05% | 94.75% | 87.42% | 87.28% | 93.66% | 98.58% |
| 1:3 | 97.68% | 96.03% | 89.54% | 88.27% | 94.56% | 98.92% |
| 1:5 | 98.40% | 97.67% | 92.14% | 90.45% | 96.10% | 99.57% |
| Model\_O | 1:1 | 86.07% | 80.30% | 88.39% | 84.88% | 84.10% | 97.42% |
| 1:2 | 90.75% | 85.33% | 92.45% | 88.55% | 87.34% | 98.83% |
| 1:3 | 92.69% | 89.87% | 94.85% | 90.81% | 90.01% | 99.11% |
| 1:5 | 94.48% | 92.01% | 96.81% | 93.21% | 91.92% | 99.56% |
| Model\_H | 1:1 | 91.52% | 87.45% | 80.37% | 87.93% | 87.97% | 95.68% |
| 1:2 | 94.63% | 92.21% | 85.39% | 90.96% | 90.73% | 97.09% |
| 1:3 | 95.71% | 93.64% | 87.77% | 93.49% | 92.25% | 97.80% |
| 1:5 | 97.18% | 95.60% | 90.51% | 95.34% | 94.41% | 98.41% |
| Model\_P | 1:1 | 93.82% | 90.36% | 84.74% | 87.06% | 89.96% | 97.04% |
| 1:2 | 96.60% | 93.69% | 86.62% | 89.36% | 91.95% | 97.53% |
| 1:3 | 98.55% | 96.44% | 89.45% | 91.08% | 93.81% | 98.07% |
| 1:5 | 98.98% | 97.54% | 91.97% | 93.95% | 96.06% | 98.98% |
| Model\_C | 1:1 | 80.26% | 64.70% | 68.21% | 75.15% | 76.42% | 94.92% |
| 1:2 | 83.75% | 68.80% | 74.69% | 80.62% | 80.26% | 96.71% |
| 1:3 | 86.92% | 72.90% | 77.30% | 82.68% | 81.83% | 97.39% |
| 1:5 | 88.95% | 76.95% | 81.80% | 85.61% | 84.39% | 98.30% |

**Supplementary Table S15**. Performance comparison (MCC) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 93.23% | 63.64% | 35.58% | 50.99% | 54.92% | 63.17% |
| 1:2 | 92.35% | 66.08% | 37.30% | 51.45% | 56.71% | 61.85% |
| 1:3 | 90.95% | 67.82% | 38.61% | 52.96% | 58.89% | 64.96% |
| 1:5 | 89.40% | 68.55% | 39.32% | 52.79% | 60.04% | 63.56% |
| Model\_S | 1:1 | 80.99% | 88.20% | 43.68% | 58.44% | 60.24% | 85.49% |
| 1:2 | 85.93% | 86.06% | 45.30% | 57.97% | 62.33% | 85.59% |
| 1:3 | 86.30% | 84.96% | 45.35% | 53.86% | 60.07% | 84.84% |
| 1:5 | 85.89% | 83.23% | 45.05% | 50.08% | 57.70% | 81.10% |
| Model\_O | 1:1 | 62.86% | 52.94% | 81.39% | 60.84% | 49.79% | 80.14% |
| 1:2 | 69.98% | 58.74% | 77.36% | 58.45% | 50.44% | 75.84% |
| 1:3 | 72.17% | 64.04% | 75.91% | 56.21% | 47.86% | 72.82% |
| 1:5 | 73.31% | 65.04% | 72.02% | 51.44% | 44.28% | 63.45% |
| Model\_H | 1:1 | 73.37% | 62.05% | 41.99% | 81.90% | 56.97% | 76.26% |
| 1:2 | 78.82% | 67.88% | 45.21% | 77.50% | 58.90% | 75.10% |
| 1:3 | 80.38% | 68.91% | 45.42% | 75.53% | 59.36% | 73.79% |
| 1:5 | 80.35% | 67.82% | 44.40% | 69.07% | 56.63% | 69.07% |
| Model\_P | 1:1 | 77.54% | 64.94% | 44.12% | 62.42% | 86.06% | 78.30% |
| 1:2 | 80.81% | 67.58% | 43.28% | 62.05% | 81.41% | 72.81% |
| 1:3 | 81.14% | 67.42% | 44.00% | 59.12% | 79.70% | 71.97% |
| 1:5 | 77.00% | 64.38% | 41.26% | 54.47% | 74.04% | 61.62% |
| Model\_C | 1:1 | 55.06% | 38.83% | 31.94% | 53.05% | 41.44% | 92.13% |
| 1:2 | 57.98% | 40.62% | 34.54% | 53.83% | 42.08% | 91.49% |
| 1:3 | 62.28% | 43.10% | 35.37% | 53.73% | 41.75% | 90.35% |
| 1:5 | 63.55% | 43.67% | 35.71% | 51.68% | 38.45% | 88.49% |

**Supplementary Table S16**. Performance comparison (F1-score) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 96.64% | 65.18% | 31.97% | 56.88% | 52.84% | 67.01% |
| 1:2 | 94.91% | 68.22% | 34.40% | 58.08% | 55.36% | 66.37% |
| 1:3 | 93.22% | 70.30% | 36.43% | 60.09% | 58.39% | 69.73% |
| 1:5 | 91.15% | 71.52% | 38.17% | 60.58% | 60.51% | 69.06% |
| Model\_S | 1:1 | 82.25% | 94.17% | 41.04% | 64.36% | 59.79% | 87.63% |
| 1:2 | 87.29% | 90.74% | 44.54% | 64.97% | 63.62% | 87.54% |
| 1:3 | 87.80% | 88.73% | 45.90% | 61.88% | 62.35% | 86.69% |
| 1:5 | 87.48% | 85.94% | 47.22% | 58.62% | 60.83% | 82.45% |
| Model\_O | 1:1 | 63.77% | 53.05% | 90.82% | 66.53% | 47.71% | 82.97% |
| 1:2 | 71.50% | 59.46% | 84.84% | 65.51% | 50.12% | 77.99% |
| 1:3 | 74.23% | 65.79% | 81.74% | 63.77% | 49.76% | 74.46% |
| 1:5 | 75.96% | 67.69% | 76.13% | 58.97% | 47.78% | 62.85% |
| Model\_H | 1:1 | 74.46% | 62.95% | 38.44% | 91.14% | 55.21% | 79.79% |
| 1:2 | 80.43% | 70.01% | 43.25% | 85.15% | 58.70% | 78.53% |
| 1:3 | 82.20% | 71.54% | 44.84% | 81.70% | 60.22% | 76.93% |
| 1:5 | 82.59% | 71.22% | 45.75% | 74.09% | 59.34% | 71.58% |
| Model\_P | 1:1 | 78.98% | 66.74% | 42.12% | 68.23% | 93.14% | 81.42% |
| 1:2 | 82.87% | 70.49% | 42.61% | 68.40% | 87.74% | 76.18% |
| 1:3 | 83.05% | 70.84% | 44.81% | 66.16% | 84.82% | 74.92% |
| 1:5 | 78.61% | 67.43% | 44.00% | 61.40% | 78.22% | 62.39% |
| Model\_C | 1:1 | 55.65% | 39.05% | 28.23% | 58.56% | 38.61% | 96.09% |
| 1:2 | 59.23% | 41.22% | 31.63% | 60.56% | 40.65% | 94.34% |
| 1:3 | 63.82% | 43.98% | 33.05% | 60.98% | 41.14% | 92.76% |
| 1:5 | 65.79% | 45.73% | 35.03% | 59.98% | 39.98% | 90.36% |

**Supplementary Table S17**. Performance comparison (Precision) of PtLnc-BXE models in cross-species lncRNA identification

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Model | LncRNAs:pcts | A | S | O | H | P | C |
| Model\_A | 1:1 | 95.63% | 50.21% | 19.27% | 41.00% | 36.31% | 52.57% |
| 1:2 | 94.31% | 55.01% | 21.24% | 43.22% | 39.10% | 53.05% |
| 1:3 | 92.88% | 58.72% | 23.02% | 46.75% | 42.73% | 59.25% |
| 1:5 | 91.63% | 62.81% | 24.84% | 49.29% | 46.11% | 63.59% |
| Model\_S | 1:1 | 70.78% | 92.58% | 26.53% | 50.69% | 44.15% | 85.92% |
| 1:2 | 80.43% | 89.76% | 30.44% | 55.11% | 51.06% | 91.05% |
| 1:3 | 83.54% | 88.24% | 32.75% | 54.58% | 52.51% | 92.82% |
| 1:5 | 87.46% | 87.83% | 36.30% | 55.98% | 56.80% | 96.63% |
| Model\_O | 1:1 | 47.24% | 36.45% | 88.92% | 53.46% | 31.86% | 84.39% |
| 1:2 | 56.93% | 43.11% | 84.97% | 57.02% | 35.12% | 90.89% |
| 1:3 | 61.78% | 51.25% | 83.82% | 59.56% | 37.14% | 92.27% |
| 1:5 | 66.92% | 55.65% | 81.85% | 62.03% | 38.20% | 94.80% |
| Model\_H | 1:1 | 59.72% | 46.92% | 24.15% | 88.60% | 38.64% | 76.69% |
| 1:2 | 69.38% | 57.28% | 28.63% | 82.90% | 43.39% | 81.63% |
| 1:3 | 73.45% | 61.13% | 30.83% | 80.88% | 46.42% | 84.55% |
| 1:5 | 79.50% | 66.81% | 33.51% | 75.73% | 50.33% | 86.74% |
| Model\_P | 1:1 | 66.61% | 52.47% | 27.69% | 56.65% | 90.70% | 82.30% |
| 1:2 | 77.03% | 60.71% | 28.83% | 59.73% | 84.98% | 82.95% |
| 1:3 | 87.43% | 70.02% | 31.99% | 61.36% | 82.63% | 85.49% |
| 1:5 | 89.75% | 74.41% | 34.01% | 65.38% | 79.79% | 88.98% |
| Model\_C | 1:1 | 38.80% | 24.38% | 16.57% | 42.62% | 24.17% | 95.04% |
| 1:2 | 42.86% | 26.26% | 19.17% | 46.71% | 26.27% | 93.56% |
| 1:3 | 48.04% | 28.71% | 20.37% | 48.41% | 27.05% | 92.28% |
| 1:5 | 51.33% | 30.83% | 22.47% | 50.39% | 27.29% | 91.39% |