**Table 1:** **Comparison of feature selection performance of L1MSVM, RF, and RL1MSVM.** Three sets of 196 lncRNAs were selected by three approaches. SVM is used to classify the breast cancer samples into five subtypes using the selected features. Values of four performance metrics, including Accuracy, Precision, Recall, and f1 Score, are evaluated. Last column reports the time required by L1MSVM, RF, and RL1MSVM, in selecting 196 lncRNAs.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Model Name** | **# of features** | **Accuracy** | **Precision** | **Recall** | **f1 Score** | **Cost (sec.)** |
| L1MSVM | 196 | 0.90 (+/- 0.02) | 0.83 (+/- 0.04) | 0.82 (+/- 0.04) | 0.82 (+/- 0.03) | 0.67 |
| RF | 196 | 0.84 (+/- 0.02) | 0.78 (+/- 0.05) | 0.76 (+/- 0.03) | 0.76 (+/- 0.03) | 10.83 |
| **RL1MSVM** | **196** | **0.92 (+/- 0.02)** | **0.87 (+/- 0.03)** | **0.85 (+/- 0.03)** | **0.85 (+/- 0.02)** | **0.64** |
| Key features | 91 | 0.83 (+/- 0.03) | 0.78 (+/- 0.03) | 0.75 (+/- 0.03) | 0.75 (+/- 0.04) | 0.42 |
| Novel | 26 | 0.80 (+/- 0.04) | 0.71 (+/- 0.04) | 0.64 (+/- 0.04) | 0.69 (+/- 0.04) | 0.29 |

A picture containing text, indoor

Description automatically generated

**Figure 1:** Clustering capability using the expression profiles of discovered 196 lncRNAs by: heatmap (a) L1MSVM (b) RF (c) RL1MSVM

Chart, scatter chart

Description automatically generated

**Figure 2:** Clustering capability using the expression profiles of discovered 196 lncRNAs by: t-SNE plot (a) L1MSVM (b) RF (c) RL1MSVM

Calendar

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**Figure 3:** Confusion matrix derived from the classification using the expression profiles of discovered 196 lncRNAs by: (a) L1MSVM (b) RF (c) RL1MSVM (d) 91 key lncRNAs

Graphical user interface

Description automatically generated

**Figure 4:** Performance using the expression profiles of novel 26 lncRNAs: (a) tSNE plot (b) Heatmap (c) Confusion matrix