Table 1. Summary of results based on the 5-fold cross validation on the training dataset.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Outcome | Quality measure | Baseline result | Design 1 | Design 2 | Design 3 | Best Design |
| DNA | Sensitivity | 6.9 |  |  |  |  |
| Specificity | 99.3 |  |  |  |  |
| Accuracy | 95.2 |  |  |  |  |
| **MCC** | **0.132** |  |  |  |  |
| RNA | Sensitivity | 39.6 |  |  |  |  |
| Specificity | 98.9 |  |  |  |  |
| Accuracy | 95.3 |  |  |  |  |
| **MCC** | **0.501** |  |  |  |  |
| DRNA | Sensitivity | 4.5 |  |  |  |  |
| Specificity | 100.0 |  |  |  |  |
| Accuracy | 99.7 |  |  |  |  |
| **MCC** | **0.122** |  |  |  |  |
| nonDRNA | Sensitivity | 98.6 |  |  |  |  |
| Specificity | 29.8 |  |  |  |  |
| Accuracy | 91.3 |  |  |  |  |
| **MCC** | **0.428** |  |  |  |  |
| **averageMCC** | | **0.296** |  |  |  |  |
| *accuracy4labels* | | 90.8 |  |  |  |  |

Confusion matrix that corresponds to the baseline result (also useful to validate your calculations)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | | **predicted** | | | |
|  | | DNA | RNA | DRNA | nonDRNA |
| **actual** | DNA | 27 | 20 | 0 | 344 |
| RNA | 21 | 207 | 1 | 294 |
| DRNA | 0 | 2 | 1 | 19 |
| nonDRNA | 36 | 71 | 1 | 7751 |