| Variable Type | Model Name      | F-score | Accuracy | F1_pos | F1_Neg | Recall_pos | Recall_neg | Precison_pos | Precison_neg | TP   | FP  | TN   | FN   |
|---------------|-----------------|---------|----------|--------|--------|------------|------------|--------------|--------------|------|-----|------|------|
| Discrete      | Feature combine | 0.55    | 0.5419   | 0.58   | 0.5    | 0.53       | 0.56       | 0.64         | 0.45         | 1273 | 719 | 902  | 1119 |
|               | Model Combine   | 0.48    | 0.485    | 0.48   | 0.49   | 0.4        | 0.61       | 0.6          | 0.41         | 963  | 637 | 984  | 1429 |
|               | Only Genome     | 0.59    | 0.596    | 0.67   | 0.48   | 0.69       | 0.46       | 0.65         | 0.5          | 1652 | 881 | 740  | 740  |
|               | Only Epigenome  | 0.48    | 0.485    | 0.48   | 0.49   | 0.39       | 0.62       | 0.61         | 0.41         | 942  | 615 | 1006 | 1450 |
| Continuous    | Feature combine | 0.55    | 0.5477   | 0.59   | 0.5    | 0.54       | 0.56       | 0.64         | 0.45         | 1286 | 709 | 912  | 1106 |
|               | Model Combine   | 0.58    | 0.5786   | 0.64   | 0.48   | 0.64       | 0.49       | 0.65         | 0.48         | 1527 | 826 | 795  | 865  |
|               | Only Genome     | 0.59    | 0.596    | 0.67   | 0.48   | 0.69       | 0.46       | 0.65         | 0.5          | 1652 | 881 | 740  | 740  |
|               | Only Epigenome  | 0.49    | 0.4869   | 0.49   | 0.49   | 0.41       | 0.61       | 0.6          | 0.41         | 971  | 638 | 983  | 1421 |
|               |                 |         |          |        |        |            |            |              |              |      |     |      |      |