

Prediction performance of gender according to an independent gene set consisting of genes located on chromosomes 1-22 and X.

| Features | Genes | Machine learning algorithms | | | | | | | | Support samples | |
|----------|--------|-----------------------------|--------|---------------|--------|---------------|--------|----------------|--------|-----------------|-------|
| | | Support vector machine | | Decision tree | | Random forest | | Neural network | | | |
| | | accuracy | AUC | accuracy | AUC | accuracy | AUC | accuracy | AUC | Train | Test |
| Gender | 12,883 | 0.9825 | 0.9825 | 0.9634 | 0.9635 | 0.9133 | 0.9915 | 0.9662 | 0.9963 | 5,479 | 2,349 |

| Features | Classes | Machine learning algorithms | | | | | | | | | | | | Support samples | |
|----------|---------|-----------------------------|--------|----------|---------------|--------|----------|---------------|--------|----------|----------------|--------|----------|-----------------|------|
| | | Support vector machine | | | Decision tree | | | Random forest | | | Neural network | | | | |
| | | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | Train | Test |
| Gender | Female | 0.98 | 0.98 | 0.98 | 0.97 | 0.96 | 0.96 | 0.97 | 0.98 | 0.96 | 0.99 | 0.95 | 0.97 | 2774 | 1272 |
| | Male | 0.98 | 0.98 | 0.98 | 0.96 | 0.97 | 0.96 | 0.96 | 0.97 | 0.96 | 0.94 | 0.99 | 0.97 | 2705 | 1077 |

Prediction performance of gender according to an independent gene set consisting of significant genes located on chromosomes 1-22 and X selected through statistical analysis.

| Features | Genes | Machine learning algorithms | | | | | | | | Support samples | |
|----------|-------|-----------------------------|--------|---------------|--------|---------------|--------|----------------|--------|-----------------|-------|
| | | Support vector machine | | Decision tree | | Random forest | | Neural network | | | |
| | | accuracy | AUC | accuracy | AUC | accuracy | AUC | accuracy | AUC | Train | Test |
| Gender | 5,790 | 0.9834 | 0.9833 | 0.9613 | 0.9613 | 0.9137 | 0.9915 | 0.9483 | 0.9950 | 5,479 | 2,349 |

| Features | Classes | Machine learning algorithms | | | | | | | | | | | | Support samples | |
|----------|---------|-----------------------------|--------|----------|---------------|--------|----------|---------------|--------|----------|----------------|--------|----------|-----------------|------|
| | | Support vector machine | | | Decision tree | | | Random forest | | | Neural network | | | | |
| | | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | Train | Test |
| Gender | Female | 0.98 | 0.99 | 0.98 | 0.97 | 0.96 | 0.96 | 0.97 | 0.98 | 0.98 | 0.99 | 0.91 | 0.95 | 2774 | 1272 |
| | Male | 0.99 | 0.98 | 0.98 | 0.96 | 0.96 | 0.96 | 0.98 | 0.97 | 0.97 | 0.91 | 0.99 | 0.95 | 2705 | 1077 |

Prediction performance of gender according to independent gene set consisting of genes located on chromosomes 1-22 and X by top five ranked cancer type

| Cancer type | Features | Machine learning algorithms | | | | | | | | Support samples | |
|-------------|----------|-----------------------------|--------|---------------|--------|---------------|--------|----------------|--------|-----------------|------|
| | | Support vector machine | | Decision tree | | Random forest | | Neural network | | | |
| | | accuracy | AUC | accuracy | AUC | accuracy | AUC | accuracy | AUC | Train | Test |
| BRCA | Gender | 0.9861 | 0.5000 | 1.0000 | 1.0000 | 0.9861 | 0.5000 | 0.9861 | 0.7676 | 669 | 288 |
| KIRC | Gender | 0.9808 | 0.9741 | 0.9423 | 0.94 | 0.8077 | 0.7578 | 0.6987 | 0.889 | 363 | 156 |
| HNSC | Gender | 0.9866 | 0.9823 | 0.9866 | 0.991 | 0.7785 | 0.5897 | 0.7919 | 0.8281 | 347 | 149 |
| LGG | Gender | 1.0000 | 1.0000 | 0.9863 | 0.9859 | 0.8630 | 0.8756 | 0.7534 | 0.8469 | 340 | 146 |
| LUAD | Gender | 1.0000 | 1.0000 | 0.9920 | 0.9907 | 0.7280 | 0.7555 | 0.6960 | 0.7160 | 291 | 125 |

| Cancer type | Features | Classes | Machine learning algorithms | | | | | | | | | | | | Support samples | |
|-------------|----------|---------|-----------------------------|--------|----------|---------------|--------|----------|---------------|--------|----------|----------------|--------|----------|-----------------|------|
| | | | Support vector machine | | | Decision tree | | | Random forest | | | Neural network | | | | |
| | | | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | precision | recall | f1-score | Train | Test |
| BRCA | Gender | Female | 0.98 | 1.00 | 0.99 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 0.97 | 1.00 | 0.99 | 662 | 284 |
| | | Male | 0 | 0 | 0 | 1.00 | 0.80 | 0.89 | 1.00 | 0.80 | 0.89 | 0 | 0 | 0 | 7 | 4 |
| KIRC | Gender | Female | 0.96 | 0.90 | 0.93 | 0.89 | 0.90 | 0.89 | 0.91 | 0.95 | 0.93 | 0.90 | 0.40 | 0.55 | 125 | 58 |
| | | Male | 0.94 | 0.98 | 0.96 | 0.94 | 0.93 | 0.93 | 0.97 | 0.94 | 0.95 | 0.68 | 0.97 | 0.80 | 238 | 98 |
| HNSC | Gender | Female | 1.00 | 0.88 | 0.93 | 0.98 | 0.94 | 0.96 | 1.00 | 0.96 | 0.98 | 0.50 | 0.03 | 0.06 | 94 | 38 |
| | | Male | 0.94 | 1.00 | 0.97 | 0.97 | 0.99 | 0.98 | 0.98 | 1.00 | 0.99 | 0.68 | 0.99 | 0.81 | 253 | 111 |
| LGG | Gender | Female | 1.00 | 1.00 | 1.00 | 0.97 | 0.99 | 0.98 | 0.97 | 0.99 | 0.98 | 1.00 | 0.02 | 0.04 | 157 | 61 |
| | | Male | 1.00 | 1.00 | 1.00 | 0.99 | 0.97 | 0.98 | 1.00 | 0.97 | 0.99 | 0.54 | 1.00 | 0.70 | 183 | 85 |
| LUAD | Gender | Female | 0.95 | 1.00 | 0.97 | 0.92 | 0.97 | 0.95 | 0.96 | 0.97 | 0.95 | 0.66 | 0.51 | 0.57 | 160 | 71 |
| | | Male | 1.00 | 0.93 | 0.96 | 0.96 | 0.89 | 0.92 | 1.00 | 0.95 | 0.97 | 0.55 | 0.69 | 0.61 | 131 | 54 |