

**Table S10.** Ten-fold cross-validation accuracies of gene-pair classifiers composed of genes that encode extracellular products.

		Predicted phenotype (%) <sup>a</sup>							total	
		EPN	GBM	MDL	MNG	OLG	PA	normal		UC <sup>b</sup>
Actual phenotype	EPN	<b>83.3</b>	2.9	4.9	4.9	2.0	1.0	0.0	1.0	102
	GBM	2.2	<b>72.3</b>	0.4	1.3	20.3	0.9	0.0	2.6	231
	MDL	1.0	1.0	<b>94.1</b>	1.0	2.0	0.0	0.0	1.0	101
	MNG	0.0	1.2	0.6	<b>97.5</b>	0.0	0.0	0.0	0.6	161
	OLG	0.0	16.4	0.0	0.0	<b>75.4</b>	3.3	1.6	3.3	61
	PA	1.6	1.6	0.0	0.0	3.2	<b>91.9</b>	0.0	1.6	62
	normal	0.0	1.0	0.0	0.0	1.5	0.0	<b>96.6</b>	1.0	203

<sup>a</sup>Accuracies reflect average performance in ten-fold cross-validation conducted ten times. The main diagonal gives the average classification accuracy of each class (bold), and the off-diagonal elements show the erroneous predictions.

<sup>b</sup>UC (Unclassified samples). When using the node classifiers, expression profiles that did not exert a signature of any phenotype (i.e., did not percolate down to at least one positive terminal node) were rejected from classification. In this case, the Unclassified sample is treated as a misclassification.