Table 1: **Results on the Sotiriou (2003) data set for classification of ER and Grade of the tumor.** In the table we report overall PA (PA), class specific PAs (PA_1, PA_2), g-means, AUC, number of active genes (# gene) and the optimal threshold parameter (λ^*), for different number of ER- or Grade 1 or 2 samples in the training set (n_1). The number of ER+ and Grade 3 samples was kept fixed at 10.

Task	Method	n_1	PA	PA_1	PA_2	g-means	AUC	# genes	λ^*
ER	PAM	10	0.831	0.833	0.829	0.827	0.893	267	2.900
	GM-PAM	10	0.831	0.833	0.827	0.827	0.893	322	2.852
	PAM	20	0.832	0.830	0.836	0.830	0.893	933	2.474
	GM-PAM	20	0.830	0.824	0.843	0.831	0.895	693	2.598
	PAM	30	0.829	0.844	0.808	0.822	0.883	1892	1.799
	GM-PAM	30	0.832	0.831	0.835	0.830	0.896	944	2.266
	PAM	40	0.827	0.856	0.796	0.822	0.875	3132	1.259
	GM-PAM	40	0.831	0.828	0.834	0.828	0.894	1287	2.041
	PAM	50	0.808	0.889	0.757	0.817	0.865	4525	0.703
	GM-PAM	50	0.834	0.846	0.827	0.833	0.896	1527	1.791
	ALP	10	0.829	0.834	0.819	0.823	0.877	70	21.910
	GM-ALP	10	0.829	0.834	0.817	0.822	0.877	90	21.763
	ALP	20	0.848	0.850	0.844	0.845	0.898	333	16.498
	GM-ALP	20	0.846	0.847	0.844	0.844	0.897	342	16.722
	ALP	30	0.845	0.856	0.830	0.841	0.903	1106	11.303
	GM-ALP	30	0.844	0.848	0.838	0.841	0.900	572	13.434
	ALP	40	0.834	0.868	0.798	0.829	0.905	1864	9.099
	GM-ALP	40	0.843	0.858	0.829	0.841	0.907	610	11.590
	ALP	50	0.824	0.883	0.786	0.830	0.906	2755	6.923
	GM-ALP	50	0.840	0.860	0.827	0.841	0.903	594	12.710
	AHP	10	0.854	0.860	0.839	0.847	0.902	212	32.995
	GM-AHP	10	0.854	0.860	0.839	0.847	0.902	212	32.608
	AHP	20	0.863	0.880	0.831	0.853	0.914	212	35.653
	GM-AHP	20	0.862	0.879	0.829	0.851	0.914	272	34.800
	AHP	30	0.860	0.899	0.804	0.848	0.908	399	38.455
	GM-AHP	30	0.861	0.899	0.806	0.849	0.909	324	40.269
	AHP	40	0.859	0.911	0.806	0.855	0.910	381	38.345
	GM-AHP	40	0.860	0.910	0.807	0.856	0.911	351	38.746
	AHP	50	0.833	0.912	0.784	0.842	0.908	336	37.445
	GM-AHP	50	0.836	0.914	0.787	0.845	0.909	303	38.261
Grade	PAM	10	0.599	0.622	0.572	0.585	0.629	508	1.959
	GM-PAM	10	0.600	0.623	0.571	0.586	0.632	536	1.893
	PAM	20	0.616	0.673	0.562	0.607	0.665	1266	1.662
	GM-PAM	20	0.615	0.665	0.566	0.605	0.662	761	1.835
	PAM	30	0.607	0.720	0.529	0.608	0.667	2945	1.110
	GM-PAM	30	0.616	0.673	0.576	0.615	0.667	1014	1.713
	PAM	40	0.566	0.771	0.485	0.601	0.660	4866	0.527
	GM-PAM	40	0.595	0.686	0.559	0.608	0.661	1440	1.566
	ALP	10	0.611	0.637	0.579	0.598	0.656	525	8.190
	GM-ALP	10	0.618	0.647	0.582	0.605	0.661	567	7.471
	ALP	20	0.621	0.690	0.554	0.608	0.662	932	7.907
	GM-ALP	20	0.620	0.675	0.566	0.610	0.662	551	8.224
	ALP	30	0.608	0.740	0.517	0.609	0.684	2219	5.435
	GM-ALP	30	0.610	0.699	0.549	0.613	0.670	871	7.414
	ALP	40	0.571	0.757	0.497	0.603	0.698	3519	3.196
	GM-ALP	40	0.597	0.696	0.558	0.615	0.682	739	6.802
	AHP	10	0.589	0.607	0.566	0.579	0.614	438	13.207
	GM-AHP	10	0.599	0.607	0.588	0.591	0.627	446	11.695
	AHP	20	0.619	0.731	0.510	0.602	0.673	445	10.074
	GM-AHP	20	0.618	0.728	0.510	0.601	0.671	434	10.323
	AHP	30	0.593	0.774	0.470	0.597	0.679	463	9.875
	GM-AHP	30	0.591	0.759	0.476	0.595	0.669	309	10.941
	AHP	40	0.560	0.795	0.466	0.603	0.700	865	9.156
	GM-AHP	40	0.554	0.780	0.463	0.593	0.688	673	10.521

Table 2: **Performance of the classifiers on the Ivshina data set for the multi class classification task.** The table shows overall PA (PA) class specific PAs (PA_1, PA_2, PA_3), g-means, optimal threshold parameter (λ^*) and the number of active genes (# genes) for the prediction of Grade of the tumor. Optimal threshold parameters were estimated with 5-fold CV and the accuracy measures with LOOCV.

Method	λ^*	# genes	PA	PA_1	PA_2	PA_3	g-means
PAM	0.00	22283	0.62	0.76	0.50	0.82	0.68
GM-PAM	0.57	17776	0.62	0.76	0.49	0.84	0.68
ALP	0.00	22283	0.62	0.75	0.51	0.82	0.68
GM-ALP	0.00	22283	0.61	0.75	0.49	0.82	0.67
AHP	0.00	22283	0.62	0.74	0.51	0.82	0.67
GM-AHP	0.00	22283	0.62	0.74	0.51	0.82	0.67