Discriminating gene set	**Cluster 1**	**Cluster 2**	**Accuracy**	**MCC**[a]	***P* value**[b]
18 up-regulated genes	85N+35M	72N+57M	57.0%	0.1555	0.0141
18 up-regulated genes + *NKAIN1*	83N+28M	74N+64M	59.4%	0.2178	0.0006
NKAIN1+CYP4Z2P+WNT5A+TMC5	83N+27M	74N+65M	59.4%	0.2286	0.0003
NKAIN1+CYP4Z2P+WNT5A+MAPT+MSX2+TFAP2B	83N+27M	74N+65M	59.4%	0.2286	0.0003
NKAIN1+CYP4Z2P+NRIP3+SEC14L2+TFAP2B	82N+26M	75N+66M	59.4%	0.2334	0.0002

[a] Matthews' correlation coefficient.
[b] Chi-square test.