

**Table S1:** The complete list of genes participating in the 3,473 non-redundant and maximally predictive molecular signatures discovered by the TIE\* algorithm in the data of Zaas *et al.* [1] for discriminating symptomatic from uninfected samples.

<i>Probe set ID</i>	<i>Gene symbol</i>	<i>Gene name</i>	<i>Percentage of signatures participated in</i>
201065_s_at	<b>GTF2I</b>	general transcription factor Iii	72.93%
213674_x_at	<b>IGHD</b>	immunoglobulin heavy constant delta	72.53%
214511_x_at	<b>FCGR1B</b>	Fc fragment of IgG, high affinity Ib, receptor (CD64)	72.01%
207826_s_at	<b>ID3</b>	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	71.41%
213797_at	<b>RSAD2</b>	radical S-adenosyl methionine domain containing 2	70.66%
217418_x_at	<b>MS4A1</b>	membrane-spanning 4-domains, subfamily A, member 1	69.80%
219471_at	<b>C13orf18</b>	chromosome 13 open reading frame 18	69.39%
219112_at	<b>RAPGEF6</b>	Rap guanine nucleotide exchange factor (GEF) 6	63.29%
219073_s_at	<b>OSBPL10</b>	oxysterol binding protein-like 10	58.71%
219313_at	<b>GRAMD1C</b>	GRAM domain containing 1C	56.29%
204439_at	<b>IFI44L</b>	interferon-induced protein 44-like	42.38%
221234_s_at	<b>BACH2</b>	BTB and CNC homology 1, basic leucine zipper transcription factor 2	28.76%
216950_s_at	<b>FCGR1A, FCGR1C</b>	Fc fragment of IgG, high affinity Ia, receptor (CD64); Fc fragment of IgG, high affinity Ic, receptor (CD64)	27.99%
207431_s_at	<b>DEGS1</b>	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	25.37%
205049_s_at	<b>CD79A</b>	CD79a molecule, immunoglobulin-associated alpha	23.73%
202723_s_at	<b>FOXO1</b>	forkhead box O1	22.40%
44790_s_at	<b>C13orf18</b>	chromosome 13 open reading frame 18	21.83%
203413_at	<b>NELL2</b>	NEL-like 2 (chicken)	19.95%
214059_at	<b>IFI44</b>	Interferon-induced protein 44	19.55%
206025_s_at	<b>TNFAIP6</b>	tumor necrosis factor, alpha-induced protein 6	19.00%
204747_at	<b>IFIT3</b>	interferon-induced protein with tetratricopeptide repeats 3	18.40%
218578_at	<b>CDC73</b>	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	15.38%
207180_s_at	<b>HTATIP2</b>	HIV-1 Tat interactive protein 2, 30kDa	12.44%
210448_s_at	<b>P2RX5</b>	purinergic receptor P2X, ligand-gated ion channel, 5	9.79%
208901_s_at	<b>TOP1</b>	topoisomerase (DNA) I	9.39%
210356_x_at	<b>MS4A1</b>	membrane-spanning 4-domains, subfamily A, member 1	9.39%
203153_at	<b>IFIT1</b>	interferon-induced protein with tetratricopeptide repeats 1	8.49%
205552_s_at	<b>OAS1</b>	2',5'-oligoadenylate synthetase 1, 40/46kDa	8.49%
217719_at	<b>EIF3L</b>	eukaryotic translation initiation factor 3, subunit L	8.12%
219452_at	<b>DPEP2</b>	dipeptidase 2	6.74%
202086_at	<b>MX1</b>	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	6.62%
209582_s_at	<b>CD200</b>	CD200 molecule	5.01%
208975_s_at	<b>KPNB1</b>	karyopherin (importin) beta 1	4.06%
208436_s_at	<b>IRF7</b>	interferon regulatory factor 7	3.80%
205483_s_at	<b>ISG15</b>	ISG15 ubiquitin-like modifier	2.07%
200689_x_at	<b>EEF1G</b>	eukaryotic translation elongation factor 1 gamma	1.99%
209185_s_at	<b>IRS2</b>	insulin receptor substrate 2	1.76%
215621_s_at	<b>IGHD</b>	immunoglobulin heavy constant delta	1.64%
210817_s_at	<b>CALCOCO2</b>	calcium binding and coiled-coil domain 2	1.47%
202748_at	<b>GBP2</b>	guanylate binding protein 2, interferon-inducible	1.41%
219394_at	<b>PGS1</b>	phosphatidylglycerophosphate synthase 1	1.07%

Genes highlighted in bold are those that also comprised the 12-gene panviral signature developed by Statnikov *et al.* [2] by applying GLL on the entire set of samples.

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**Table S1:** Continued from the previous page.

<i>Probe set ID</i>	<i>Gene symbol</i>	<i>Gene name</i>	<i>Percentage of signatures participated in</i>
217986_s_at	<i>BAZIA</i>	bromodomain adjacent to zinc finger domain, 1A	0.98%
204972_at	<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.66%
203038_at	<i>PTPRK</i>	protein tyrosine phosphatase, receptor type, K	0.37%
203939_at	<i>NT5E</i>	5'-nucleotidase, ecto (CD73)	0.35%
205660_at	<i>OASL</i>	2'-5'-oligoadenylate synthetase-like	0.32%
220179_at	<i>DPEP3</i>	dipeptidase 3	0.32%
202100_at	<i>RALB</i>	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	0.26%
204423_at	<i>MKLN1</i>	muskelin 1, intracellular mediator containing kelch motifs	0.26%
212821_at	<i>PLEKHG3</i>	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	0.23%
201739_at	<i>SGK1</i>	serum/glucocorticoid regulated kinase 1	0.03%
204581_at	<i>CD22</i>	CD22 molecule	0.03%
206420_at	<i>IGSF6</i>	immunoglobulin superfamily, member 6	0.03%
209417_s_at	<i>IFI35</i>	interferon-induced protein 35	0.03%
218543_s_at	<i>PARP12</i>	poly (ADP-ribose) polymerase family, member 12	0.03%
219211_at	<i>USP18</i>	ubiquitin specific peptidase 18	0.03%
219364_at	<i>DHX58</i>	DEXH (Asp-Glu-X-His) box polypeptide 58	0.03%
219700_at	<i>PLXDC1</i>	plexin domain containing 1	0.03%
219863_at	<i>HERC5</i>	hect domain and RLD 5	0.03%
221239_s_at	<i>FCRL2</i>	Fc receptor-like 2	0.03%

## References

1. Zaas AK, Chen M, Varkey J, Veldman T, Hero AO, III, Lucas J, Huang Y, Turner R, Gilbert A, Lambkin-Williams R, Oien NC, Nicholson B, Kingsmore S, Carin L, Woods CW, Ginsburg GS (2009) Gene expression signatures diagnose influenza and other symptomatic respiratory viral infections in humans. *Cell Host Microbe* 6: 207-217.
2. Statnikov A, McVoy L, Lytkin N, Aliferis CF (2010) Improving development of the molecular signature for diagnosis of acute respiratory viral infections. *Cell Host Microbe* 7: 100-101.