

Table S2: The complete list of genes participating in the 2,922 non-redundant and maximally predictive molecular signatures discovered by TIE* in the data of Zaas *et al.* [1] for discriminating between Candidemia-infected samples and healthy controls.

<i>Probe set ID</i>	<i>Gene symbol</i>	<i>Gene title</i>	<i>Percentage of signatures participated in</i>
1420330_at	<i>Clec4e</i>	C-type lectin domain family 4, member e	100.00%
1424132_at	<i>Hras1</i>	Harvey rat sarcoma virus oncogene 1	100.00%
1427747_a_at	<i>Lcn2</i>	lipocalin 2	100.00%
1417293_at	<i>Hs6st1</i> /// <i>LOC100047260</i>	heparan sulfate 6-O-sulfotransferase 1 /// similar to heparan sulfate 6-sulfotransferase 1	73.51%
1426739_at	<i>Donson</i>	downstream neighbor of SON	72.25%
1427011_a_at	<i>Lancl1</i>	LanC (bacterial lantibiotic synthetase component C)-like 1	71.42%
1427925_at	<i>Stx17</i>	syntaxin 17	71.36%
1452197_at	<i>Smc4</i>	structural maintenance of chromosomes 4	71.01%
1428357_at	<i>2610019F03Rik</i>	RIKEN cDNA 2610019F03 gene	70.71%
1416378_at	<i>Pnkp</i>	polynucleotide kinase 3'-phosphatase	69.75%
1452504_s_at	<i>Ctbs</i>	chitinase, di-N-acetyl-	66.80%
1417933_at	<i>Igfbp6</i>	insulin-like growth factor binding protein 6	56.71%
1422438_at	<i>Ephx1</i>	epoxide hydrolase 1, microsomal	52.05%
1416524_at	<i>Spop</i>	speckle-type POZ protein	46.68%
1418012_at	<i>Sh3glb1</i>	SH3-domain GRB2-like B1 (endophilin)	41.75%
1424754_at	<i>Ms4a7</i>	membrane-spanning 4-domains, subfamily A, member 7	33.85%
1427030_at	<i>Ccdc52</i>	coiled-coil domain containing 52	33.57%
1429800_at	<i>9130221H12Rik</i> /// <i>Zfp526</i>	RIKEN cDNA 9130221H12 gene /// zinc finger protein 526	32.58%
1416988_at	<i>Msh2</i>	mutS homolog 2 (E. coli)	32.27%
1451092_a_at	<i>Rangap1</i>	RAN GTPase activating protein 1	29.23%
1417164_at	<i>Dusp10</i>	dual specificity phosphatase 10	20.91%
1423466_at	<i>Ccr7</i>	chemokine (C-C motif) receptor 7	20.84%
1454722_at	<i>Pten</i>	phosphatase and tensin homolog	18.24%
1448361_at	<i>Ttc3</i>	tetratricopeptide repeat domain 3	16.91%
1460551_at	<i>Ran</i>	RAN, member RAS oncogene family	16.77%
1416226_at	<i>Arpc1b</i>	actin related protein 2/3 complex, subunit 1B	14.82%
1449945_at	<i>Ppargc1b</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	11.33%
1416359_at	<i>Snx18</i>	sorting nexin 18	7.91%
1448129_at	<i>Arpc5</i>	actin related protein 2/3 complex, subunit 5	7.73%
1424369_at	<i>Psmf1</i>	proteasome (prosome, macropain) inhibitor subunit 1	5.30%
1423371_at	<i>Pole4</i>	polymerase (DNA-directed), epsilon 4 (p12 subunit)	5.13%
1419833_s_at	<i>Arap3</i>	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	3.87%
1418396_at	<i>Gpsm3</i>	G-protein signalling modulator 3 (AGS3-like, <i>C. elegans</i>)	2.67%
1423539_at	<i>Pms2</i>	postmeiotic segregation increased 2 (<i>S. cerevisiae</i>)	2.67%
1416759_at	<i>Mical1</i>	microtubule associated monooxygenase, calponin and LIM domain containing 1	2.22%
1422637_at	<i>Rassf5</i>	Ras association (RalGDS/AF-6) domain family member 5	2.22%
1434998_at	<i>Iqgap1</i>	IQ motif containing GTPase activating protein 1	2.22%
1416629_at	<i>Slc1a5</i>	solute carrier family 1 (neutral amino acid transporter), member 5	1.81%
1460436_at	<i>Ndst1</i>	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1.27%
1433507_a_at	<i>Hmgn2</i>	high mobility group nucleosomal binding domain 2	1.10%

Genes highlighted in bold are those that also comprised a 14-gene signature developed by applying GLL in the same data.

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Table S2: Continued from the previous page.

<i>Probe set ID</i>	<i>Gene symbol</i>	<i>Gene title</i>	<i>Percentage of signatures participated in</i>
1418634_at	<i>Notch1</i>	Notch gene homolog 1 (Drosophila)	1.06%
1449883_at	<i>Fxyd2</i>	FXYD domain-containing ion transport regulator 2	1.06%
1436180_at	<i>Dnajc5</i>	DnaJ (Hsp40) homolog, subfamily C, member 5	0.62%
1419810_x_at	<i>Arhgap9</i>	Rho GTPase activating protein 9	0.41%
1421038_a_at	<i>Kcnn4</i>	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	0.41%
1424526_a_at	<i>Tgds</i>	TDP-glucose 4,6-dehydratase	0.41%
1436838_x_at	<i>Cot11</i>	coactosin-like 1 (Dictyostelium)	0.41%
1448407_at	<i>4632428N05Rik</i>	RIKEN cDNA 4632428N05 gene	0.41%
1449111_a_at	<i>Grb2</i>	growth factor receptor bound protein 2	0.41%
1434561_at	<i>Asxl1</i>	additional sex combs like 1 (Drosophila)	0.38%
1426212_s_at	<i>Tmem161a</i>	transmembrane protein 161A	0.34%
1437773_x_at	<i>Ddx17</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	0.34%
1419731_at	<i>Cyp2b19</i>	cytochrome P450, family 2, subfamily b, polypeptide 19	0.31%
1428736_at	<i>Gramd3</i>	GRAM domain containing 3	0.31%
1451125_at	<i>Paip2b</i>	poly(A) binding protein interacting protein 2B	0.31%
1417171_at	<i>Itk</i>	IL2-inducible T-cell kinase	0.03%
1417597_at	<i>Cd28</i>	CD28 antigen	0.03%
1418468_at	<i>Anxa11 /// Gm2260 /// Gm2274</i>	annexin A11 /// predicted gene 2260 /// predicted gene 2274	0.03%
1419193_a_at	<i>Gmfg</i>	glia maturation factor, gamma	0.03%
1423150_at	<i>Scg5</i>	secretogranin V	0.03%
1423897_at	<i>Rnf187</i>	ring finger protein 187	0.03%
1424168_a_at	<i>Capzb</i>	capping protein (actin filament) muscle Z-line, beta	0.03%
1427108_at	<i>9530068E07Rik</i>	RIKEN cDNA 9530068E07 gene	0.03%
1451181_at	<i>Tmem121</i>	transmembrane protein 121	0.03%
1460555_at	<i>Fam65b</i>	family with sequence similarity 65, member B	0.03%

References

1. Zaas AK, Aziz H, Lucas J, Perfect JR, Ginsburg GS (2010) Blood gene expression signatures predict invasive candidiasis. *Sci Transl Med* 2: 21ra17.