

TABLE 2. DESCRIPTION OF THE 44 PROGNOSTIC GENES OF THE METAGENE ASSOCIATED WITH SURVIVAL

Operon ID	HUGO Short Name	Gene Name	Chr. Position	Hazard Ratio*	P Value†	Bhattacharjee <i>et al.</i> (2001) (2)	Beer <i>et al.</i> (2002) (4)	Tomida <i>et al.</i> (2004) (7)	Bild <i>et al.</i> (2006) (22)
<b>H300013783</b>	<b>ARPC2</b>	actin-related protein 2/3 complex, subunit 2	2q36.1	6.27	6.6E-03	<b>0.025</b>	0.56	0.16	0.08
H200017863	FOXQ1	forkhead box q1	6p25	6.26	5.7E-04				0.26
<b>H200012139</b>	<b>SDF2</b>	stromal cell-derived factor 2	17q11.2	5.66	6.9E-03	0.33	<b>0.017</b>	0.11	0.88
H200009657	MOSPD3	motile sperm domain containing 3	7q22	0.18‡	3.4E-03				0.08
H200017969	PMS2L9	postmeiotic segregation increased 2-like3	7q11.23	0.19‡	4.0E-04				
H200014047	MUT	methylmalonyl coenzyme a mutase	6p21	5.08	4.2E-04	0.49	0.54		0.46
H200008119	NOC4	neighbor of cox4	16q24	4.61	4.8E-04				
H300003690	NA	—		4.59	3.2E-03				
H200007113	NDUFC1	nadh dehydrogenase (ubiquinone) 1	4q28.2	4.55	9.5E-03	0.58			0.32
H300021867	KIAA2010	kiaa2010	14q32	4.32	2.1E-02				0.24
<b>H200005989</b>	<b>AP3D1</b>	adaptor-related protein complex 3, delta 1 subunit	19p13.3	4.31	1.5E-03	<b>0.013</b>	0.53		<b>0.002</b>
H300005457	XP_372900.2	—	22q13.2	4.16	2.3E-03				
<b>H200014959</b>	<b>MRPL44</b>	mitochondrial ribosomal protein l44	2q36.1	4.13	1.8E-03				<b>0.02</b>
H300018776	CHCHD2	coiled-coil-helix-coiled-coil domain containing 2	7p11.2	4.10	2.1E-03				0.98
H300008134	SLC37A2	solute carrier family 37, member 2	11q24.2	0.24‡	2.5E-02				0.29
H200017073	ACTR10	actin-related protein 10 homolog (s. cerevisiae)	14q23.1	4.07	5.1E-03				0.75
H300012698	Q6PIE2	Kiaa0220-like protein	16p11.2	0.25‡	3.0E-03				
H200014044	TCEB3	transcription elongation factor b, polypeptide 3	1p36.1	3.97	1.5E-02	0.088	0.72	0.18	0.07
H200004476	INO80	ino80 homolog (yeast)	15q15.1	3.91	5.2E-02				
<b>H200006915</b>	<b>MYO1E</b>	myosin ie	15q21	3.90	9.9E-03	0.29	0.3	0.99	<b>0.04</b>
H300012071	LOC90410	intraflagellar transport protein ift20	17q11.2	3.87	3.1E-02				
H300013306	APG5L	apg5 autophagy 5-like (s. cerevisiae)	6q21	3.73	5.6E-03				
H300007836	MGC33302	hypothetical protein mqc33302	4q28.1	3.71	5.7E-03			0.7	0.31
H200003249	FTSJ1	ftsj homolog 1 (e. coli)	Xp11.23	3.70	1.2E-02	0.2			0.67
<b>H200006553</b>	<b>VEGFB</b>	vascular endothelial growth factor b	11q13	0.28‡	9.0E-04	<b>0.022</b>	<b>0.002</b>	<b>0.002</b>	0.054
H200014122	RNF103	ring finger protein 103	2p11.2	3.60	1.8E-02	0.7	0.75		0.51
H200013667	CYB561D2	cytochrome b-561 domain containing 2	3p21.3	3.59	6.5E-03	0.082			0.53
<b>H200017355</b>	<b>OPTN</b>	optineurin	10p13	0.28‡	3.4E-03	<b>0.016</b>		0.63	0.62
H300010368	MAT2B	ddtp-4-keto-6-deoxy-d-glucose 4-reductase	5q13.2	0.28‡	1.7E-02				
<b>H200011731</b>	<b>HEBP2</b>	heme binding protein 2	6q24	3.50	4.3E-03	<b>0.016</b>			0.77
H300003194	LRRC9	leucine rich repeat containing 9	14q23.1	3.47	8.1E-04				
H300010348	NA	—		3.44	9.2E-03				
<b>H300013688</b>	<b>CSNK1A1</b>	casein kinase 1, alpha 1	5q32	3.43	2.6E-03	0.84	0.5	0.22	<b>0.04</b>
H300015410	NA	—		3.41	1.3E-02				
<b>H200004109</b>	<b>CLIP1</b>	restin	12q24.3	3.35	3.6E-03	0.89	0.6		<b>0.0004</b>
<b>H200009361</b>	<b>MUS81</b>	mus81 endonuclease homolog (yeast)	11q13	0.30‡	1.5E-02				<b>0.0003</b>
<b>H200008089</b>	<b>ARG2</b>	arginase, type ii	14q24.1	3.32	2.6E-03	0.46	<b>0.005</b>		0.78
<b>H200014666</b>	<b>SNAP29</b>	synaptosomal-associated protein	22q11.21	3.29	4.7E-02			<b>0.048</b>	0.11
H300006812	LOC91661	hypothetical protein bc001610	19q13.42	0.30‡	2.7E-02				
H300018503	NYREN18	nedd8 ultimate buster-1	7q36	0.31‡	6.1E-03				
H200004564	MGC10067	ubiquitin-like domain containing ctd phosphatase 1	5q33.3	3.22	1.1E-02				
H300021626	RMI1	chromosome 9 open reading frame 76	9q21.32	3.19	2.5E-03				
H200006229	MBTPS1	membrane-bound transcription factor peptidase, site 1	16q24.1	3.17	1.2E-02	0.57	0.95	0.74	0.48
H300022216	CBWD2	hypothetical protein from clone 1659351	2q14.1	3.13	7.6E-03				0.43

Definition of abbreviations: Chr. = chromosomal; NA = not available; UICC = International Union Against Cancer.

The genes were refined using four independent data sets (the boldfaced genes were included in the 13-gene refined metagene). The P values presented in the last four columns were obtained by testing (log-ratio test of a univariate Cox proportional hazards model) the association between each of these genes and survival.

\* Hazard ratios are reported for each gene included in the metagene. Cox proportional hazards models were fitted gene by gene including the information of UICC stages as single covariate.

† P values for the hazard ratios were estimated by Cox regression analysis.

‡ Protective genes have a hazard ratio between 0 and 1. Genes with a hazard ratio greater than 1 are risk genes.