SUPPLEMENTARY APPENDIX

Transcription factor nuclear factor erythroid-2 mediates expression of the cytokine interleukin 8, a known predictor of inferior outcome in patients with myeloproliferative neoplasms

Julius Wehrle, Thalia S. Seeger, Sven Schwemmers, Dietmar Pfeifer, Alla Bulashevska, and Heike L. Pahl

Department of Hematology/Oncology, Center for Clinical Research, University Hospital Freiburg, Freiburg, Germany

©2013 Ferrata Storti Foundation. This is an open-access paper. Haematologica 2013;98. doi:10.3324/haematol.2012.071183

Online Supplementary Table 1. Genes whose expression levels are modulated by changes in NF-E2 levels.

TABLES

Rank	Affymetrix ID	SYMBOL	DESCRIPTION	ACC	effect size	NF-E2	adj.p.	p - value	known target of NF-E2	NRF2
1	3456666	NFE2	nuclear factor (erythroid-derived 2), 45kDa	NM_001136023	2,93	0,54	0,003	0,0000002	i.	
2	3819609				0,47	1,44	0,012	0,000002		
3	2731332	IL8	interleukin 8	NM_000584	1,91	0,55	0,012	0,000002		
4	2372719	RGS18	regulator of G-protein sigling 18	NM_130782	1,14	0,62	0,364	0,0001		Shen et al. / 2006
5	3834379	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6	NM_002483	0,55	1,09	0,387	0,0001		
6	2831968				0,34	1,12	0,508	0,0002		
7	3252577	VDAC2	voltage-dependent anion channel 2	NM_003375	0,64	1,04	0,508	0,0002		
8	2980516	CNKSR3	CNKSR family member 3	NM_173515	0,85	0,62	0,509	0,0005		
9	3676670	1			0,60	1,10	0,509	0,0006		
10	3090436	NEFM	neurofilament, medium polypeptide	NM_005382	0,52	0,56	0,509	0,0007		
11	2366422	ATP1B1	ATPase, +/K+ transporting, beta 1 polypeptide	NM_001677	0,87	0,60	0,509	0,0007		
12	3069082	TFEC	transcription factor EC	NM_012252	0,80	0,51	0,509	0,0008		
13	2840728				0,55	0,96	0,509	0,0008		
14	3089102	EPB49	erythrocyte membrane protein band 4.9 (dematin)	NM_001978	1,00	0,60	0,509	0,0009	Steiner et al. / 2009	
15	3275510				0,71	0,94	0,509	0,0010		
16	2453307	CD34	CD34 molecule	NM_001773	0,68	0,99	0,509	0,0010		
17	3434562	UNC119B	unc-119 homolog B (C. elegans)	NM_001080533	0,71	1,02	0,509	0,0010		
18	3869784	ZNF28	zinc finger protein 28	NM_006969	0,89	0,70	0,509	0,0011		
19	2482211	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	NM_001008708	0,61	0,88	0,509	0,0012		
20	3740483	5			0,64	0,78	0,509	0,0012		
21	2793310	C4orf27	chromosome 4 open reading frame 27	NM_017867	0,59	0,83	0,509	0,0012		
22	2758870	CYTL1	cytokine-like 1	NM_018659	0,94	0,56	0,509	0,0013		
23	2949118	LTB	lymphotoxin beta (TNF superfamily, member 3)	NM_002341	1,34	0,99	0,509	0,0014		
24	2746269	LSM6	LSM6 homolog, U6 small nuclear R associated	NM_007080	0,60	0,81	0,509	0,0015		
25	3764245	MPO	myeloperoxidase	NM_000250	0,70	1,00	0,509	0,0015		
26	2420790	C1orf52	chromosome 1 open reading frame 52	NR_024113	0,74	0,71	0,509	0,0016		
27	2510464	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	NM_007115	1,03	0,67	0,509	0,0017		
28	3995392	ZNF185	zinc finger protein 185 (LIM domain)	NM_007150	1,21	0,68	0,509	0,0017		
29	3431553	C12orf24	chromosome 12 open reading frame 24	NM_013300	0,65	0,93	0,509	0,0017		
30	3212298			1010A	0,70	1,07	0,509	0,0017		
31	3319319				0,78	1,44	0,509	0,0018		

32	3742424				0,85	0,68	0,509	0,0021		
33	2424102	CNN3	calponin 3, acidic	NM_001839	0,75	0,81	0,509	0,0021		
34	3831284			and the second second second	0,73	1,04	0,509	0,0022		
35	3740499				0,69	0,85	0,509	0,0022		
36	2908509				0,72	0,91	0,509	0,0023		
37	2499234	CCDC138	coiled-coil domain containing 138	NM_144978	0,68	0,91	0,509	0,0023		
38	2614142	NR1D2	nuclear receptor subfamily 1, group D, member 2	NM_005126	0,71	0,78	0,509	0,0025		
39	3737874	BAHCC1	BAH domain and coiled-coil containing 1	NM_001080519	0,75	1,17	0,509	0,0025		
40	2384705	URB2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	NM_014777	0,74	0,91	0,509	0,0025		
41	2794408	HPGD	hydroxyprostaglandin dehydrogese 15-(D)	NR_027332	1,17	0,79	0,509	0,0025		
42	2735598	TIGD2	tigger transposable element derived 2	NM_145715	0,71	0,77	0,509	0,0026		
43	3360456	HBE1	hemoglobin, epsilon 1	NM_005330	1,50	1,06	0,509	0,0027	Gui et al. / 2003	
44	2993647				0,70	0,82	0,509	0,0028		
45	2995254	C7orf41	chromosome 7 open reading frame 41	NM_152793	0,99	0,66	0,509	0,0029		
46	3089360	SLC39A14	solute carrier family 39 (zinc transporter), member 14	NM_001128431	0,74	0,93	0,509	0,0029		Shen et al. / 200
47	2645906	PLS1	plastin 1 (I isoform)	NM_001145319	0,69	0,89	0,509	0,0029		
48	3815223	PRTN3	proteise 3	NM_002777	0,74	0,97	0,509	0,0029		
49	2474341	CAD	carbamoyl-phosphate synthetase 2	NM_004341	0,76	0,95	0,509	0,0030		
50	2930753	C6orf72	chromosome 6 open reading frame 72	AY358952	0,57	0,78	0,509	0,0031		
51	2991860	ITGB8	integrin, beta 8	NM_002214	1,18	0,74	0,509	0,0031		
52	2999485	STK17A	serine/threonine kise 17a	NM_004760	0,94	0,71	0,509	0,0031		
53	3699759				0,75	1,08	0,509	0,0031		
54	2761842	PROM1	prominin 1	NM_001145847	0,65	0,82	0,509	0,0031		
55	3862077	EID2	EP300 interacting inhibitor of differentiation 2	NM_153232	0,72	0,92	0,509	0,0031		
56	2409613	ERI3	exoribonuclease 3	NM_024066	0,67	0,88	0,509	0,0032		
57	3416500				0,67	0,96	0,509	0,0033		
58	4016308	BEX1	brain expressed, X-linked 1	NM_018476	0,61	0,85	0,509	0,0034		
59	3322071				0,62	0,97	0,509	0,0035		
60	3455946	EIF4B	eukaryotic translation initiation factor 4B	NM_001417	0,80	1,45	0,509	0,0035		
61	2406783	CSF3R	colony stimulating factor 3 receptor (granulocyte)	NM_156039	0,73	0,91	0,509	0,0036		
62	2781138	LEF1	lymphoid enhancer-binding factor 1	NM_016269	0,76	1,14	0,509	0.0037		
63	3519309		sprouty homolog 2 (Drosophila)	NM_005842	0,72	0,98	0,509	0,0038		
64	3453386	000000000		Contraction of the Contraction o	0,65	0,75	0,509	0,0039		
65	3309345	SFXN4	sideroflexin 4	NM_213649	0,65	0,96	0,509	0,0040		
66	3249043		receptor accessory protein 3		0,71	1,07	0,509	0,0042		

67	2334314	HPDL	4-hydroxyphenylpyruvate dioxygese-like	NM_032756	0,73	0,88	0,509	0,0042	
68	3275268				0,72	1,30	0,509	0,0043	
69	2700365	TM4SF1	transmembrane 4 L six family member 1	NM_014220	0,97	0,62	0,509	0,0043	
70	3470370			10.10	0,69	0,94	0,509	0,0043	
71	2874686	HINT1	histidine triad nucleotide binding protein 1	NR_024610	0,58	0,83	0,509	0,0044	
72	3844039				0,52	0,84	0,509	0,0044	
73	2487696	PCYOX1	prenylcysteine oxidase 1	NM_016297	0,71	0,73	0,509	0,0044	
74	2882098	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	NM_003118	0,73	0,84	0,509	0,0044	
75	2820865	ARSK	arylsulfatase family, member K	NM_198150	0,70	0,82	0,509	0,0045	
76	3475106				0,72	1,04	0,509	0,0045	
77	3386217	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	NM_012124	0,48	0,92	0,509	0,0046	Kwak et al. 2003
78	2347732	TMEM56	transmembrane protein 56	NM_152487	0,66	0,81	0,509	0,0047	
79	3441685	VWF	von Willebrand factor	NM_000552	1,09	0,65	0,509	0,0047	
80	2443450	SELL	selectin L	NM_000655	0,75	1,07	0,509	0,0048	
81	2791197	PDGFC	platelet derived growth factor C	NM_016205	0,70	0,77	0,509	0,0048	
82	2361761	NTRK1	neurotrophic tyrosine kise, receptor, type 1	NM_001007792	0,94	0,77	0,509	0,0049	
83	3044938	RP9P	retinitis pigmentosa 9 pseudogene	NR_003500	0,70	0,74	0,509	0,0049	
84	3527684	RSE3	ribonuclease, Rse A family, 3 (eosinophil cationic protein)	NM_002935	0,63	0,88	0,509	0,0049	
85	3401099	FKBP4	FK506 binding protein 4, 59kDa	NM_002014	0,73	0,94	0,509	0,0050	
86	3205586	EXOSC3	exosome component 3	NM_016042	0,74	0,98	0,509	0,0050	
87	3665846	THAP11	THAP domain containing 11	NM_020457	0,72	0,91	0,509	0,0050	
88	2773434	CXCL2	chemokine (C-X-C motif) ligand 2	NM_002089	1,17	0,50	0,509	0,0051	
89	2349402	AMY2B	amylase, alpha 2B (pancreatic)	NM_020978	0,71	0,70	0,509	0,0051	
90	2599907				0,69	0,64	0,509	0,0051	
91	2601499	FAM124B	family with sequence similarity 1248	NM_024785	0,80	0,76	0,509	0,0052	
92	2595252	SUMO1	SMT3 suppressor of mil two 3 homolog 1 (S. cerevisiae)	NM_003352	0,66	0,89	0,509	0,0052	
93	2514516	KLHL23	kelch-like 23 (Drosophila)	NM_144711	0,64	0,92	0,509	0,0052	
94	3556238				0,75	0,44	0,509	0,0052	
95	2476510	LTBP1	latent transforming growth factor beta binding protein 1	NM_206943	1,04	0,67	0,509	0,0053	
96	2807886	FBXO4	F-box protein 4	NM_012176	0,72	0,82	0,509	0,0053	
97	2560704	C2orf3	chromosome 2 open reading frame 3	NM_003203	0,71	0,83	0,509	0,0053	
98	2418929	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	NM_005482	0,67	0,79	0,509	0,0054	
99	3891342	TUBB1	tubulin, beta 1	NM_030773	1,38	0,57	0,509	0,0054	Lecine et al. 2000
100	3304970	SH3PXD2A	SH3 and PX domains 2A	NM_014631	0,65	1,17	0,509	0,0054	

Depicted are the rank order, the most deregulated gene being placed on rank 1; the Affymetrix ID; a brief description of the gene function, if known; the GenBank accession code; the regulation by NF-E2, shown as effect size, either up- or down-regulation; the FDR adjusted p-value; the p-value; and whether the gene is known to be a NF-E2 or Nrf2 target, the appropriate references are given.