

Agilent probe ID	P (Corr)	FC	Gene Symbol	GeneName	RefSeqAcc
A_23_P163025	0.00001	2.36	RNASE3	ribonuclease, RNase A family, 3	NM_002935
A_32_P1712	0.00001	2.39	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	NM_002934
A_23_P151637	0.00003	2.44	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	NM_002934
A_24_P261929	0.019	1.43	IFI27L1	interferon, alpha-inducible protein 27-like 1	NM_206949
A_23_P78134	0.022	1.24	EMC6	ER membrane protein complex subunit 6	NM_001014764
A_23_P328511	0.022	1.40	HSBP1	heat shock factor binding protein 1	NM_001537
A_23_P78563	0.022	1.43	UBL5	ubiquitin-like 5	NM_024292
A_23_P53298	0.022	1.48	BLOC1S1	biogenesis of lysosomal organelles complex-1, subunit 1	NM_001487
A_23_P417632	0.022	1.94	ECRP	ribonuclease, RNase A family, 2 pseudogene	NR_033909
A_23_P75769	0.025	2.17	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4A	NM_024021
A_23_P130642	0.027	-1.24	GBP6	guanylate binding protein family, member 6	NM_198460
A_24_P88505	0.027	1.44	ZCCHC17	zinc finger, CCHC domain containing 17	NM_016505
A_23_P20384	0.027	1.45	LSM1	LSM1, U6 small nuclear RNA associated	NM_014462
A_23_P76488	0.028	1.93	EMP1	epithelial membrane protein 1	NM_001423
A_23_P358555	0.030	1.31	NAA38	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	NM_032356
A_23_P209347	0.030	-1.36	ANKRD44	ankyrin repeat domain 44	NM_153697
A_23_P25735	0.030	1.56	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	NM_002791
A_23_P81690	0.030	1.59	COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	NM_001865
A_32_P98313	0.030	1.79	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NM_002489
A_23_P52647	0.031	-1.27	EHD1	EH-domain containing 1	NM_006795
A_23_P154832	0.031	1.47	ATP5J	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	NM_001003703
A_23_P425932	0.032	-1.27	VTI1A	vesicle transport through interaction with t-SNAREs 1A	XM_005269544
A_32_P168247	0.032	1.34	COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	NM_004373
A_23_P15493	0.032	1.21	PTRH2	peptidyl-tRNA hydrolase 2	NM_016077
A_23_P98382	0.032	1.66	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	NM_012459
A_23_P74114	0.034	-1.22	ZNF713	zinc finger protein 713	NM_182633
A_23_P140146	0.034	1.47	IFI27L2	interferon, alpha-inducible protein 27-like 2	NM_032036
A_23_P159650	0.035	2.01	COX7B	cytochrome c oxidase subunit VIIb	NM_001866
A_23_P1254	0.036	1.35	GSTO1	glutathione S-transferase omega 1	NM_004832

A_24_P113815	0.036	-1.36	SLC35E2	solute carrier family 35, member E2	NM_182838
A_23_P132644	0.036	1.40	NCEH1	neutral cholesterol ester hydrolase 1	NM_020792
A_23_P41114	0.036	2.08	CSTA	cystatin A (stefin A)	NM_005213
A_32_P131377	0.037	1.26	REEP5	receptor accessory protein 5	NM_005669
A_23_P127533	0.037	1.39	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5	NM_032299
A_24_P186379	0.037	1.34	FUOM	fucose mutarotase	NM_198472
A_23_P145777	0.038	1.76	NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	NM_002489
A_32_P43217	0.038	1.52	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	NM_002791
A_23_P213718	0.038	1.77	UQCQRQ	ubiquinol-cytochrome c reductase, complexIII	NM_014402
A_24_P304051	0.039	1.35	GSTO1	glutathione S-transferase omega 1	NM_004832
A_23_P170233	0.039	1.91	CSTA	cystatin A (stefin A)	NM_005213
A_23_P59877	0.039	1.49	FABP5	fatty acid binding protein 5 (psoriasis-associated)	NM_001444
A_23_P59022	0.040	-1.20	TRERF1	transcriptional regulating factor 1	NM_033502
A_23_P201497	0.040	-1.43	RASSF5	Ras association (RalGDS/AF-6) domain family member 5	NM_182663
A_23_P128734	0.040	1.47	ERH	enhancer of rudimentary homolog (Drosophila)	NM_004450
A_32_P205553	0.040	1.51	RPL26L1	ribosomal protein L26-like 1	NM_016093
A_23_P380848	0.040	1.54	TXNDC17	thioredoxin domain containing 17	NM_032731
A_23_P344973	0.040	1.55	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	NM_079423
A_23_P326080	0.040	4.47	DEFA4	defensin, alpha 4, corticostatin	NM_001925
A_23_P26413	0.040	-1.32	RBL2	retinoblastoma-like 2	NM_005611
A_32_P187827	0.040	-1.38	NPIPB9	nuclear pore complex interacting protein family, member B9	NM_001287251
A_23_P79199	0.040	1.64	DBI	diazepam binding inhibitor	NM_020548
A_23_P114929	0.041	1.18	MPC2	mitochondrial pyruvate carrier 2	NM_015415
A_23_P127467	0.041	1.22	EIF1AD	eukaryotic translation initiation factor 1A domain containing	NM_032325
A_23_P114282	0.041	1.47	MCTS1	malignant T cell amplified sequence 1	NM_014060
A_23_P353014	0.041	1.37	CACNA2D4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	NM_172364
A_23_P371613	0.041	1.32	CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1	NM_203298
A_23_P380240	0.041	3.85	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	NM_001816
A_23_P42375	0.043	1.26	RAB32	RAB32, member RAS oncogene family	NM_006834
A_23_P15705	0.043	1.32	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	NM_002798

A_23_P71148	0.044	1.42	BLVRA	biliverdin reductase A	NM_000712
A_24_P23245	0.044	1.57	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	NM_002490
A_23_P54179	0.045	1.15	ZNF410	zinc finger protein 410	NM_021188
A_23_P103282	0.048	1.22	TMEM59	transmembrane protein 59	NM_004872
A_23_P7087	0.048	-1.14	CTBP1-AS2	CTBP1 antisense RNA 2 (head to head)	NR_033339
A_23_P326170	0.048	1.28	CALM2	calmodulin 2 (phosphorylase kinase, delta)	NM_001743
A_23_P63178	0.049	1.26	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_005644
A_23_P7697	0.049	1.28	SNX2	sorting nexin 2	NM_003100
A_23_P97005	0.049	-1.42	JAK1	Janus kinase 1	NM_002227
A_23_P205281	0.050	1.39	C14orf2	chromosome 14 open reading frame 2	NM_004894

Additional file 2: Transcripts differentially expressed in ABA/MTX responders (R) vs non-responders (NR). Only Agilent's probes with accession number (RefSeqAcc) are reported in this table (69 out of 87 transcripts). Fold change (FC) is the ratio of relative abundance of transcripts in NR *versus* R. Positive FC means an up-regulation of the corresponding transcript in NR patients and conversely. *P* values were determined by t-test with Benjamini-Hochberg correction for false discovery rate estimation ($p < 0.05$).