

Supplementary Information

An endometrial gene expression signature accurately predicts recurrent implantation failure after IVF.

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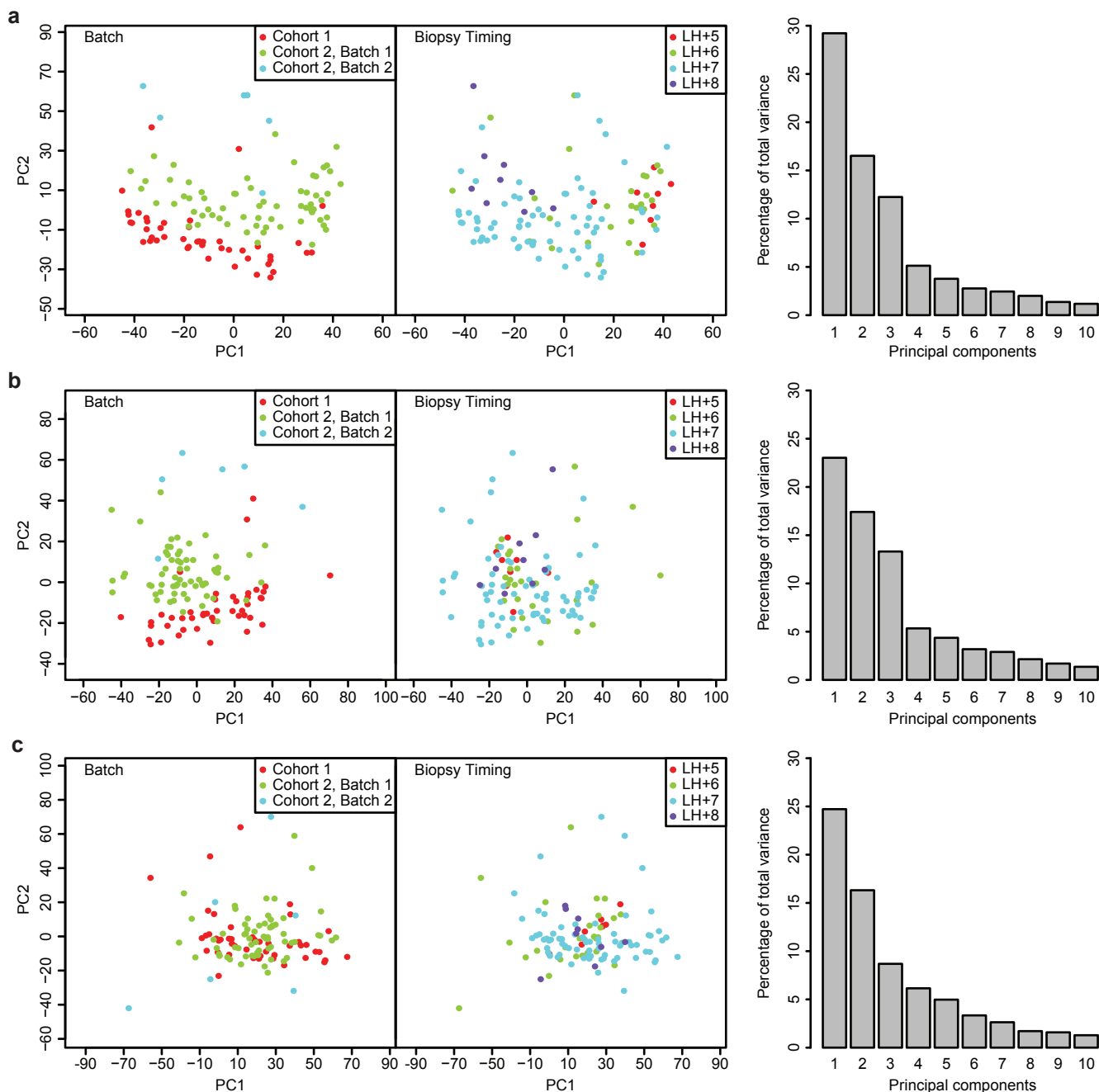
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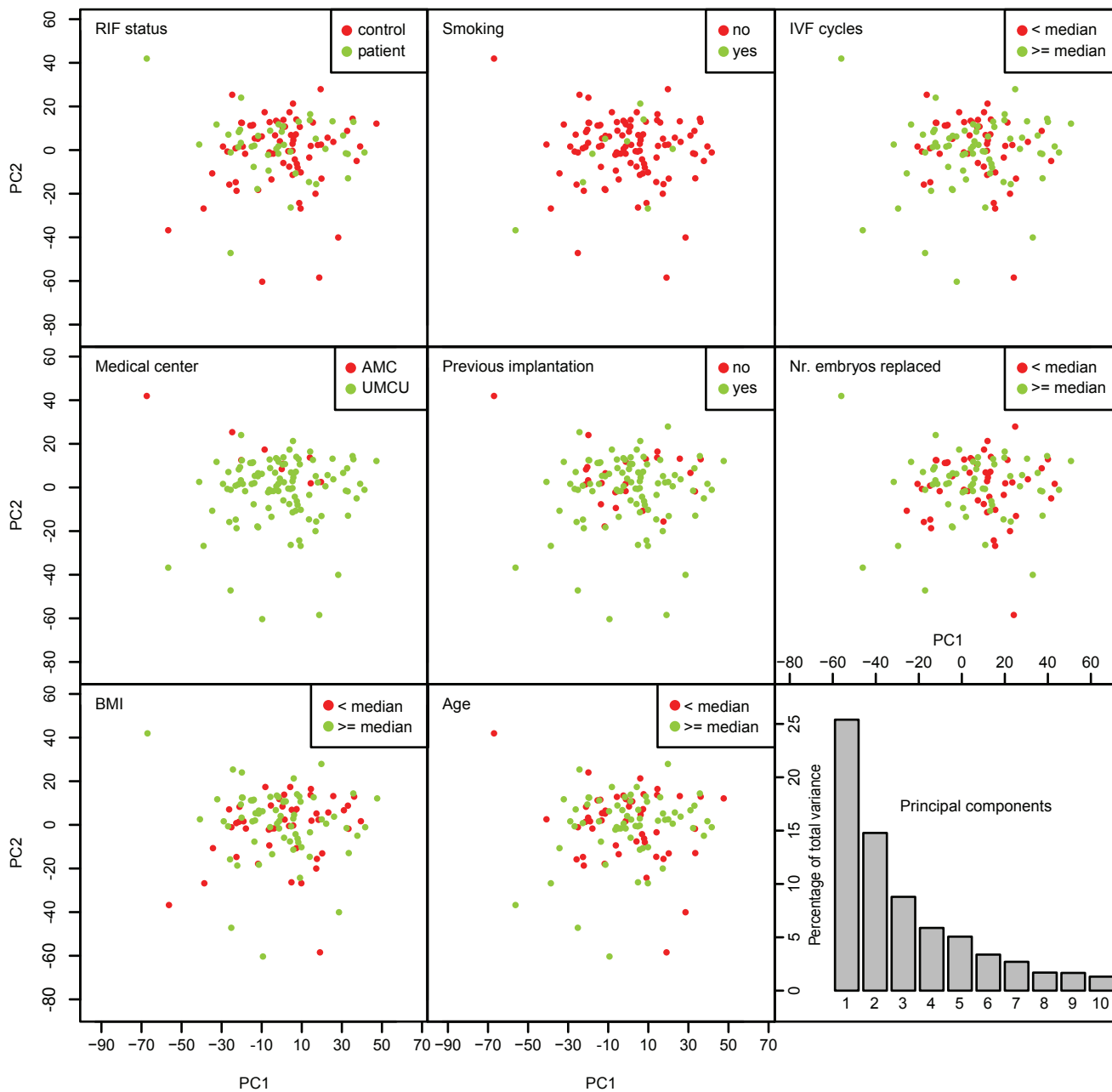
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Supplementary Figure 1



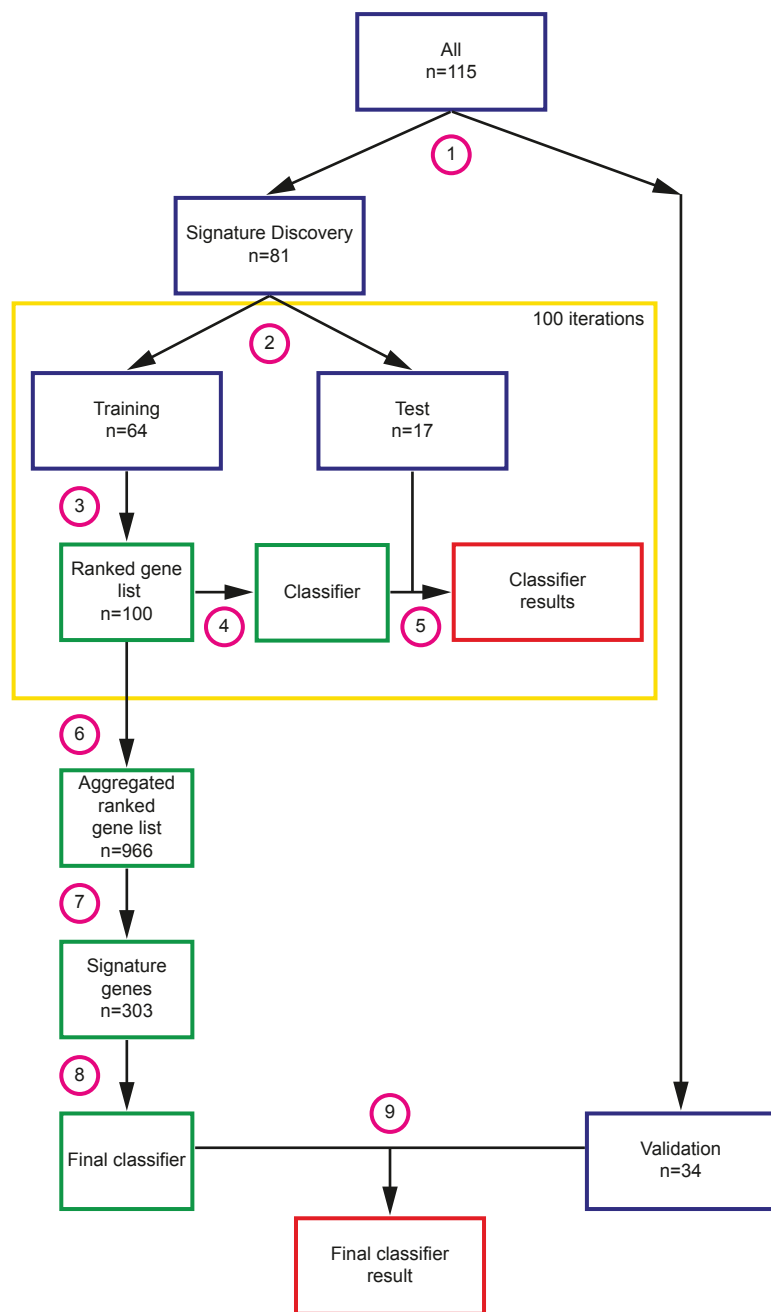
Supplementary Figure 1. Correction of biopsy timing and batch effect. A shows PCA plots for the uncorrected profiles of all samples ($n=115$) with batches (left) and biopsy timing (middle) superimposed. The right plot shows the amount of variation in the data explained by each of the first ten principal components. B shows the same plots but after correcting for the biopsy timing effect. C shows the results after also correcting for the batch effect.

Supplementary Figure 2



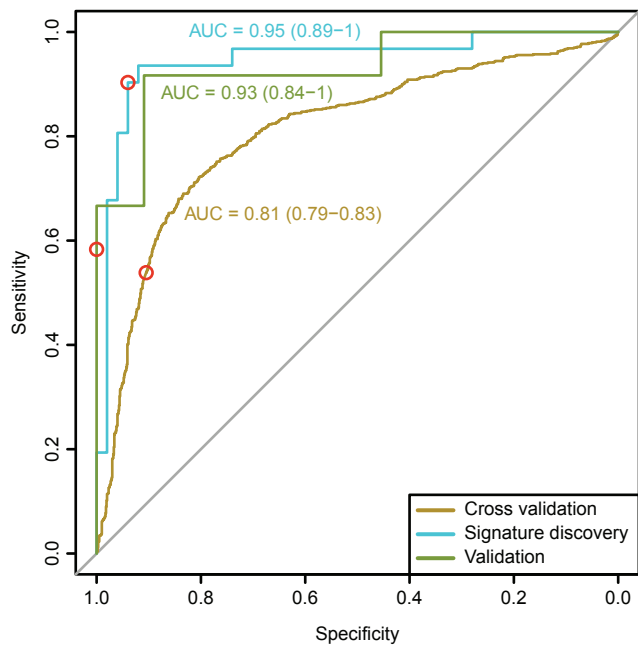
Supplementary Figure 2. PCA plots with patient characteristics and treatment variables. This figure shows PCA plots with 8 different patient characteristics and treatment variables superimposed. Continuous variables were dichotomized into below and above/equal to median value. The lower right plot shows the amount of variation in the data that is explained by each of the first ten principal components.

Supplementary Figure 3



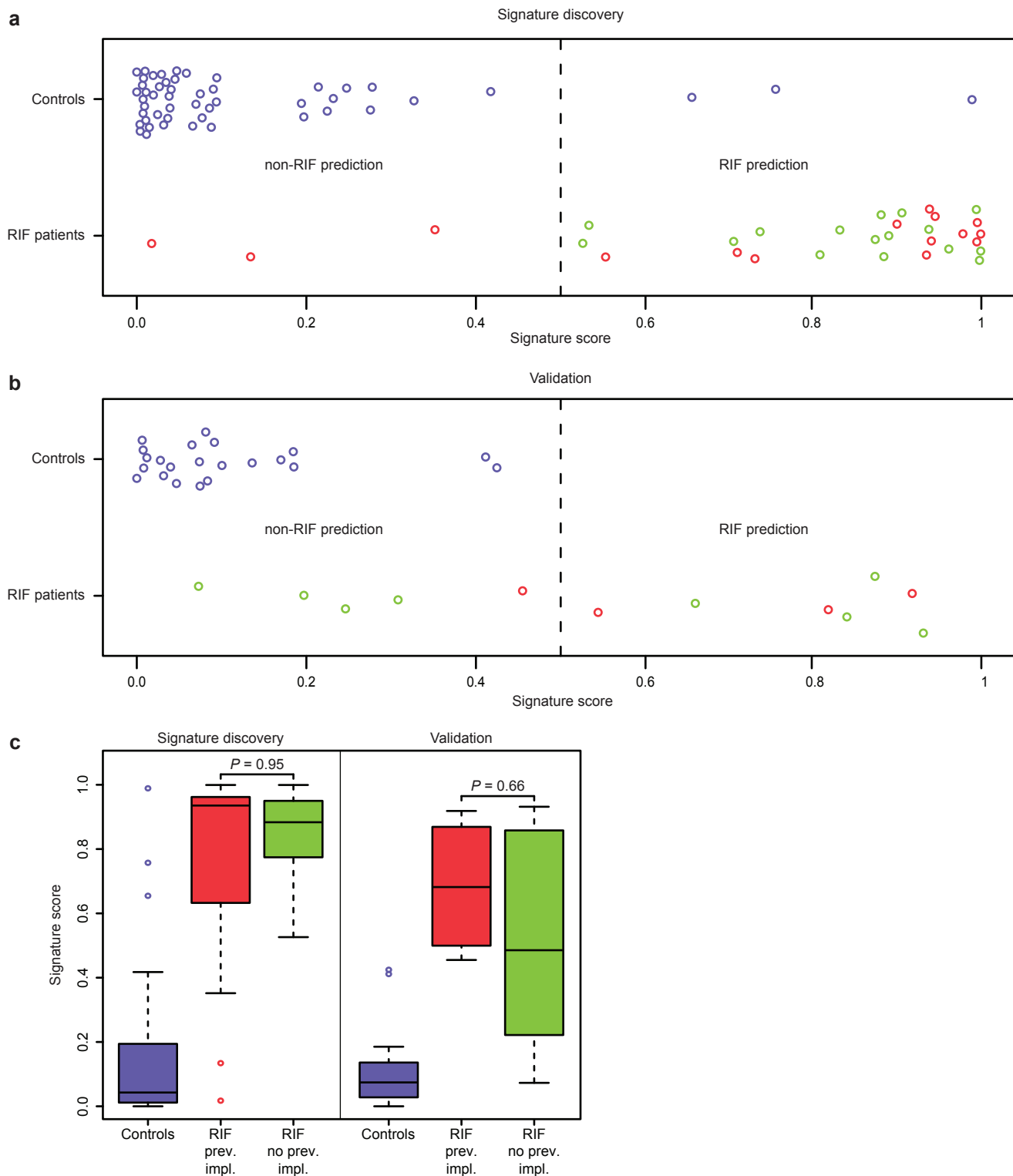
Supplementary Figure 3. Signature discovery algorithm. Diagram depicting the data used (blue boxes), analyses performed (numbered circles), output generated (green boxes) and performance measured (red boxes) during signature discovery and validation. In the first step the data is split between a signature discovery set and a validation set, step 2 involves splitting the signature discovery set into a training and test set. The training data is used to identify the 100 genes that best distinguish between RIF patient and controls (step 3). These 100 genes are employed to build a SVM classifier (step 4) which then attempts to predict the class of the samples in the test set (step 5). Step 2 to 5 are repeated 100 times which results in 100 separate 100-gene lists. These 100 lists are combined in a single list which is ranked by the occurrence of individual genes in the 100 lists (step 6). All genes which occur 10 times or more are included in the final signature (step 7) which is used to build a SVM classifier (step 8). The ninth and last step is to use the final classifier to classify the samples in the validation set.

Supplementary Figure 4



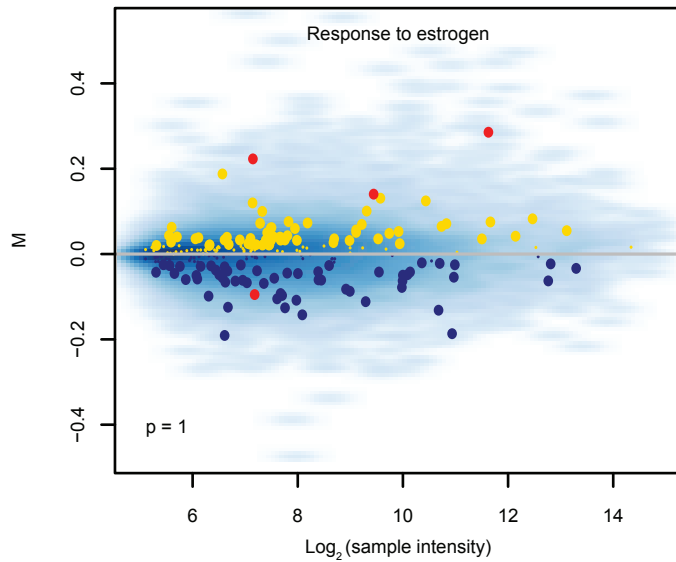
Supplementary Figure 4. Classifier ROC curves. This figure shows ROC curves for classifier performance. It is similar to Fig. 1C (blue and green curves) with an extra curve added (yellow) for the results of the 100 iterations of the cross validation procedure during signature discovery (step 5 in Supplementary Fig. S3). The Area Under the Curve (AUC) with the 95% CI is shown next to the curves. The dots indicate the point of the ROC curve that corresponds with the actual threshold used for classification (0.5).

Supplementary Figure 5



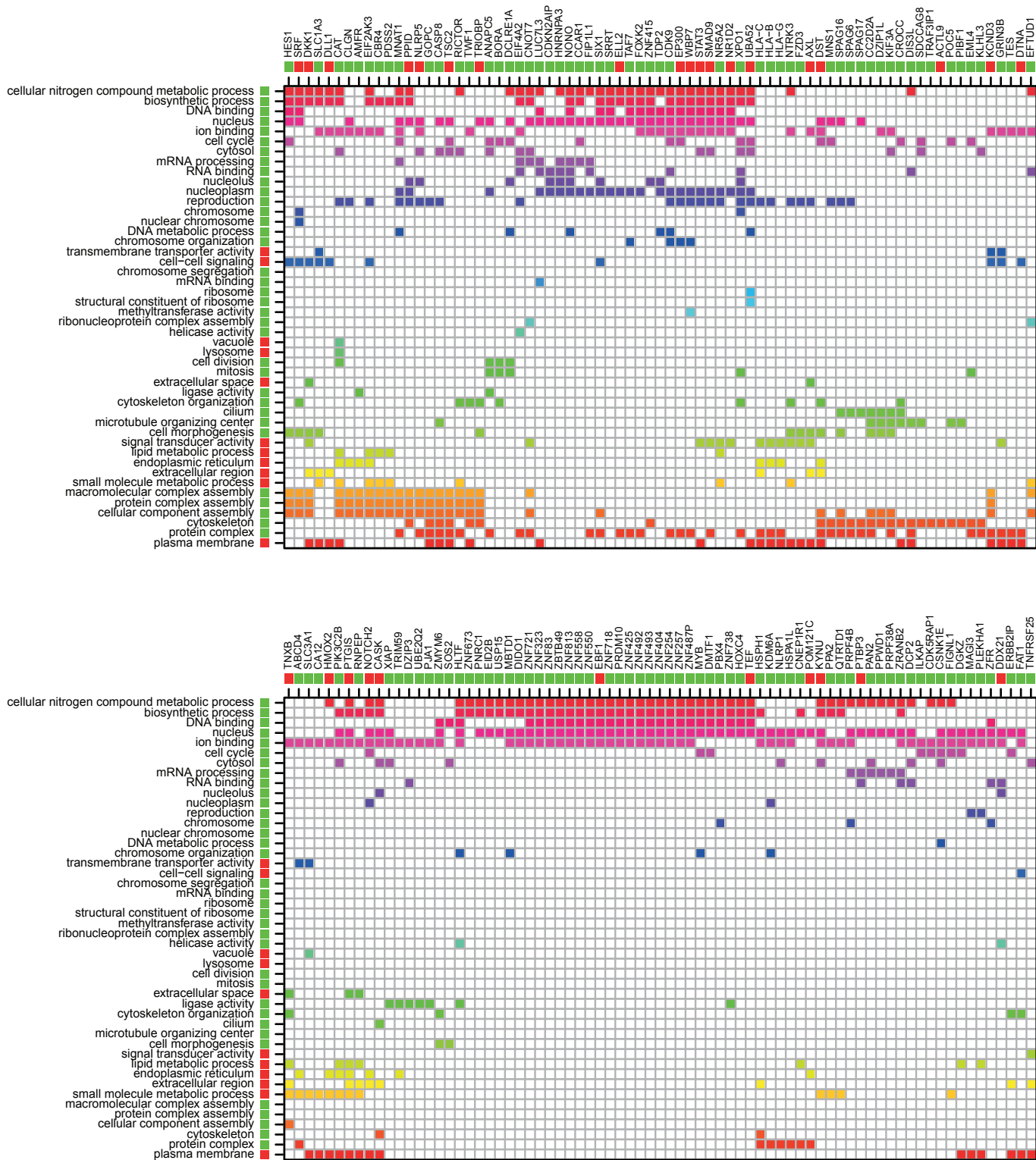
Supplementary Figure 5. Impact of previous implantation events on classifier outcome. This figure is similar to Figs. 1A and B, additionally dividing RIF patients into those with an implantation event prior to the endometrial biopsy and those without. A shows the signature scores for all RIF patients with previous implantation (red) and without previous implantation (green) and controls (blue). The signature scores are based on a classifier trained on all samples in the signature discovery set with the exception of the sample that is predicted (leave one out cross validation). All samples with a signature score below 0.5 are predicted to be controls, those with a signature score of 0.5 or higher are predicted to be RIF patients (the threshold is shown as a dotted line). B is similar to A. The samples shown are from the validation set which were scored based on a classifier trained on all samples in the signature discovery set. C shows boxplots of the signature scores of three groups; controls (blue), RIF patients with (red) and without previous implantation (green). P was calculated with a two-sided Mann-Whitney test.

Supplementary Figure 6



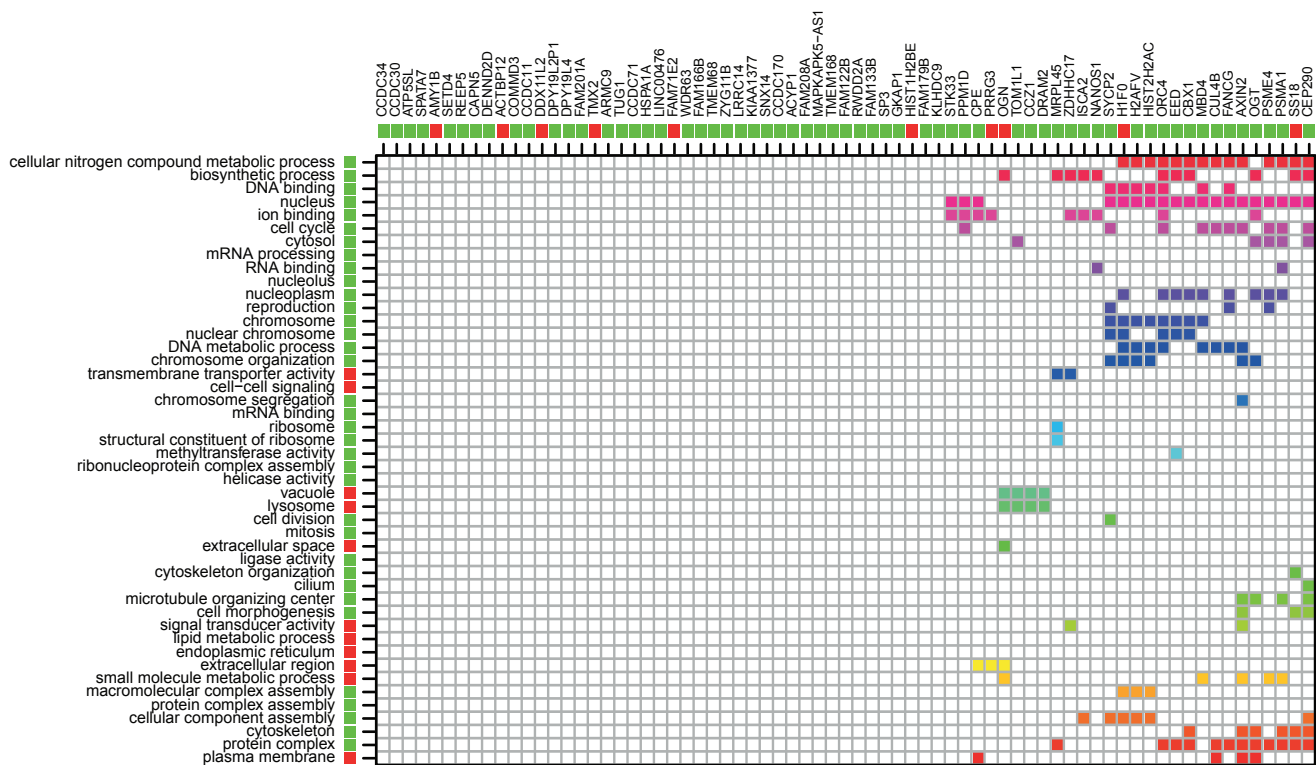
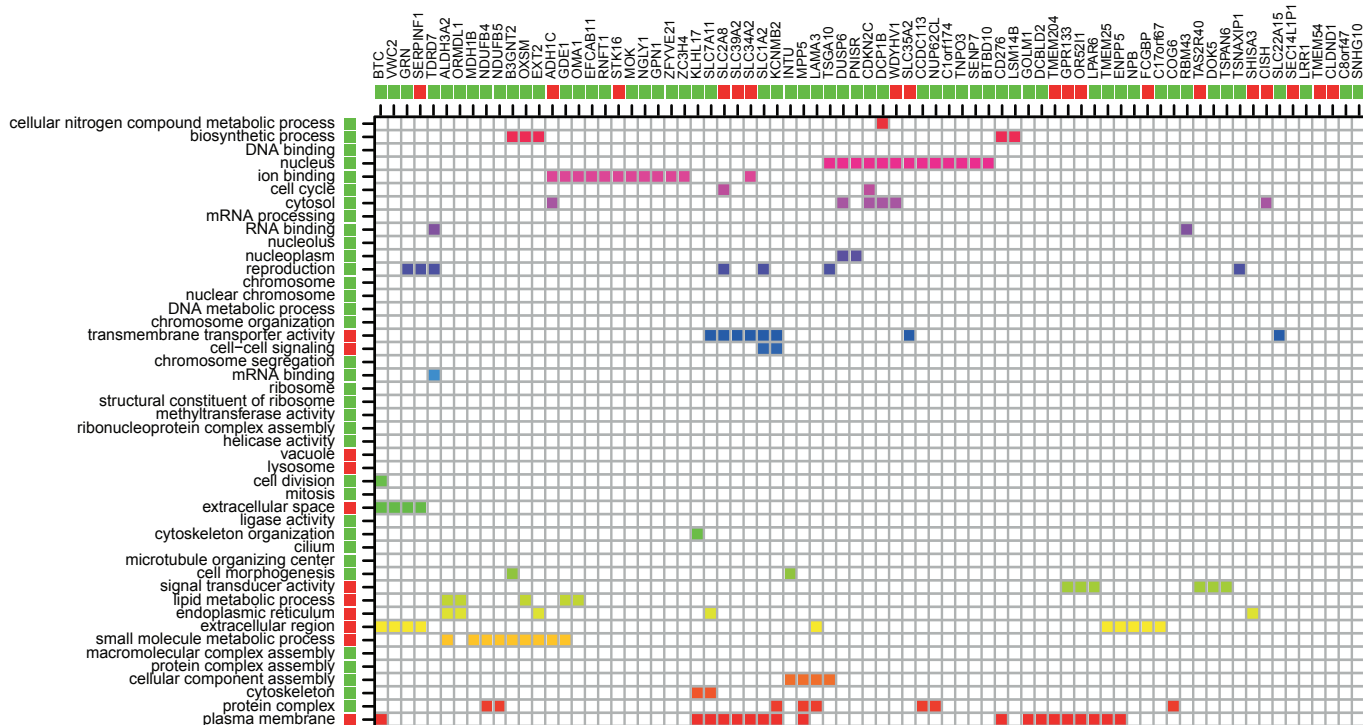
Supplementary Figure 6. Estrogen response enrichment analysis. This figure shows the gene expression of RIF patients compared against controls (log₂ fold change or M) and the average expression across all samples (log₂ sample intensity). Genes in the GO term 'response to estrogen' (GO:0043627) which are up-regulated in RIF patients are shown in yellow, genes down-regulated in blue. Shown in red are the genes which are also part of the 303-gene signature. Genes that are not part of the GO term are shown as a blue density map where darker blue indicates higher gene density.

Supplementary Figure 7



Supplementary Figure 7. Functional characterisation 303-gene signature. This figure is similar to Fig. 2E but now showing all signature genes (n=296) present in the GO database.

Supplementary Figure 7 continued



TableS1. PCA of biopsy timing and batch effect corrections

(A) Before correction				
	<i>P</i>			
	PC1	PC2	PC3	PC4
Biopsy timing				
LH+5	4.2 X 10 ⁻⁵	0.178	0.382	0.047
LH+6	2.0 x 10 ⁻⁵	0.157	0.623	0.490
LH+7	4.2 x 10 ⁻⁵	3.4 x 10 ⁻⁴	0.058	0.016
LH+8	0.003	0.003	0.069	0.171
Batch				
Cohort 1	4.2 x 10 ⁻⁵	9.7 x 10 ⁻¹²	1.3 x 10 ⁻⁷	0.866
Cohort 2, Batch 1	2.0 x 10 ⁻⁵	6.2 x 10 ⁻⁷	2.0 x 10 ⁻⁸	0.403
Cohort 2, Batch 2	0.593	1.4 x 10 ⁻⁴	0.342	0.136
(B) After correction for biopsy timing				
Biopsy timing				
LH+5	0.320	0.072	0.779	0.342
LH+6	0.091	0.591	0.546	0.825
LH+7	0.432	0.006	0.110	0.399
LH+8	0.767	0.016	0.097	0.330
Batch				
Cohort 1	3.0 x 10 ⁻⁴	1.4 x 10 ⁻¹²	5.1 x 10 ⁻⁷	0.306
Cohort 2, Batch 1	1.6 x 10 ⁻⁴	1.7 x 10 ⁻⁷	1.0 x 10 ⁻⁷	0.086
Cohort 2, Batch 2	0.628	1.2 x 10 ⁻⁴	0.389	0.114
(C) After correction for batch				
Biopsy timing				
LH+5	0.407	0.081	0.438	0.520
LH+6	0.079	0.815	0.002	0.699
LH+7	0.137	0.158	0.098	0.263
LH+8	0.482	0.599	0.286	0.426
Batch				
Cohort 1	0.580	0.175	0.938	0.588
Cohort 2, Batch 1	0.426	0.144	0.763	0.575
Cohort 2, Batch 2	0.576	0.777	0.619	0.955

P was calculated using a two-sided Mann-Whitney test contrasting the PC values of samples with a particular variable value against the rest (i.e. PC1 values of LH+5 vs. LH+6/7/8); PC1-4, principal component 1-4; LH+X, biopsy was taken X days after luteinizing hormone (LH) surge.

TableS2. Variable association with principal components

Variables	<i>P</i>			
	PC1	PC2	PC3	PC4
RIF status (patient/control)	0.577	0.692	0.561	0.209
Medical center (UMCU/AMC)	0.556	0.002	0.606	0.979
BMI (median)	0.349	0.315	0.507	0.157
Smoking (yes/no)	0.571	0.549	0.760	0.744
Implantations (median)	0.618	0.183	0.855	0.910
Age (median)	0.768	0.913	0.750	0.953
IVF cycles (median)	0.845	0.233	0.468	0.292
Nr. embryos replaced (median)	0.430	0.791	0.949	0.313

P was calculated using a two-sided Mann-Whitney test contrasting the PC values of one group against the other group (i.e. PC1 values of smokers vs. non-smokers); PC1-4, principal component 1-4; Median, the median value was used to dichotomize the covariates (< median & ≥ median); BMI, body mass index.

Table S3. Signature genes

Probe ID	Gene symbol	Description	M
HSAE000532	PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1	-0.19
HSAE022203	POC5	POC5 centriolar protein homolog (Chlamydomonas)	-0.17
HSAE022471	CSNK1E	casein kinase 1, epsilon	-0.12
HSAE019770	FAM179B	family with sequence similarity 179, member B	-0.19
HSAE005427	CPE	carboxypeptidase E	-0.48
HSAE006018	DCP1B	DCP1 decapping enzyme homolog B (<i>S. cerevisiae</i>)	-0.11
HSAE010975	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	-0.15
HSAE014616	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	-0.24
HSAE021377	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	-0.11
HSAE021192	OXSM	3-oxoacyl-ACP synthase, mitochondrial	-0.12
HSAE008217	EP300	E1A binding protein p300	0.19
HSAE030183	TNXB	tenascin XB	0.12
HSAE011196	KLHDC9	kelch domain containing 9	-0.15
HSAE007316	EID2B	EP300 interacting inhibitor of differentiation 2B	-0.10
HSAE000275	CAT	Catalase	-0.17
HSAE020379	CBR4	carbonyl reductase 4	-0.16
HSAE003961	TMEM25	transmembrane protein 25	-0.13
HSAE007811	SLC22A15	solute carrier family 22, member 15	-0.11
HSAE002494	CUL4B	cullin 4B	-0.12
HSAE004566	FCGBP	Fc fragment of IgG binding protein	0.14
HSAE012530	CASP8	caspase 8, apoptosis-related cysteine peptidase	-0.07
HSAE001942	OMA1	OMA1 zinc metallopeptidase homolog (<i>S. cerevisiae</i>)	-0.11
HSAE014904	CCZ1	CCZ1 vacuolar protein trafficking and biogenesis associated homolog (<i>S. cerevisiae</i>)	-0.05
HSAE031372	ZNF257	zinc finger protein 257	-0.13
HSAE002376	H2AFV	H2A histone family, member V	-0.14
HSAE016014	CCDC113	coiled-coil domain containing 113	-0.20
HSAE032669	ZNF415	zinc finger protein 415	-0.18
HSAE013562	ZMYM6	zinc finger, MYM-type 6	-0.12
HSAE015519	RP1-152L7.5	RP1-152L7.5	-0.11
HSAE002271	DZIP3	DAZ interacting protein 3, zinc finger	-0.17
HSAE004693	ZNF673	zinc finger family member 673	-0.13
HSAE011062	TDP2	tyrosyl-DNA phosphodiesterase 2	-0.12
HSAE033287	ZNF487P	zinc finger protein 487, pseudogene	-0.15
HSAE020170	ZNF738	zinc finger protein 738	-0.19
HSAE031067	KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	-0.19
HSAE011386	LAMA3	laminin, alpha 3	-0.25
HSAE026892	NLRP1	NLR family, pyrin domain containing 1	-0.23
HSAE007958	DIDO1	death inducer-obliterator 1	-0.10
HSAE018217	RP5-1129J21.3	RP5-1129J21.3	-0.18
HSAE002930	TNXB	tenascin XB	0.11
HSAE023427	CTD-2116N17.1	CTD-2116N17.1	0.19
HSAE024971	HIST1H2BE	histone cluster 1, H2be	0.09
HSAE022135	AC007292.6	AC007292.6	0.12
HSAE011646	GKAP1	G kinase anchoring protein 1	-0.17
HSAE006812	SP3	Sp3 transcription factor	-0.20
HSAE007705	DZIP1L	DAZ interacting protein 1-like	-0.21
HSAE000804	CCAR1	cell division cycle and apoptosis regulator 1	-0.10
HSAE016921	INTU	inturned planar cell polarity effector homolog (<i>Drosophila</i>)	-0.15
HSAE012539	FAM133B	family with sequence similarity 133, member B	-0.10
HSAE013456	ZRANB2	zinc finger, RAN-binding domain containing 2	-0.17
HSAE002193	ZFYVE21	zinc finger, FYVE domain containing 21	-0.10
HSAE021606	RP11-706O15.3	RP11-706O15.3	-0.07

HSAE019450	ZNF254	zinc finger protein 254	-0.14
HSAE030937	FOXP2	forkhead box K2	-0.06
HSAE002268	CISH	cytokine inducible SH2-containing protein	0.22
HSAE012322	DCBLD2	discoidin, CUB and LCCL domain containing 2	-0.20
HSAE000881	SOS2	son of sevenless homolog 2 (Drosophila)	-0.10
HSAE001077	EIF4A2	eukaryotic translation initiation factor 4A2	-0.12
HSAE009803	ELL2	elongation factor, RNA polymerase II, 2	0.07
HSAE034109	PPA2	pyrophosphatase (inorganic) 2	-0.12
HSAE009179	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	-0.10
HSAE009528	EED	embryonic ectoderm development	-0.20
HSAE005215	RWDD2A	RWD domain containing 2A	-0.08
HSAE013680	SENP7	SUMO1/sentrin specific peptidase 7	-0.23
HSAE001761	BTBD10	BTB (POZ) domain containing 10	-0.06
HSAE032952	TNPO3	transportin 3	-0.03
HSAE012052	KYNU	kynureninase	0.52
HSAE014369	CA12	carbonic anhydrase XII	-0.47
HSAE008008	CNEP1R1	CTD nuclear envelope phosphatase 1 regulatory subunit 1	-0.03
HSAE010272	SPAG16	sperm associated antigen 16	-0.11
HSAE015672	C17orf67	chromosome 17 open reading frame 67	-0.09
HSAE033077	KIF3A	kinesin family member 3A	-0.09
HSAE011415	ZNF404	zinc finger protein 404	-0.29
HSAE013758	EML4	echinoderm microtubule associated protein like 4	-0.11
HSAE023428	OGN	osteoglycin	0.21
HSAE008504	ZFR	zinc finger RNA binding protein	-0.10
HSAE010484	FANCG	Fanconi anemia, complementation group G	-0.11
HSAE027480	KDM6A	lysine (K)-specific demethylase 6A	-0.09
HSAE016847	ZNF493	zinc finger protein 493	-0.13
HSAE001943	OMA1	OMA1 zinc metallopeptidase homolog (S. cerevisiae)	-0.06
HSAE022240	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	0.14
HSAE005948	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	-0.26
HSAE018195	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	0.09
HSAE018201	MBTD1	mbt domain containing 1	-0.12
HSAE002138	SS18	synovial sarcoma translocation, chromosome 18	0.03
HSAE027412	DST	dystonin	0.06
HSAE015476	PTGIS	prostaglandin I2 (prostacyclin) synthase	0.19
HSAE011055	OGN	osteoglycin	0.19
HSAE020336	FAM122B	family with sequence similarity 122B	-0.22
HSAE015317	TMEM168	transmembrane protein 168	-0.14
HSAE004016	USP15	ubiquitin specific peptidase 15	-0.16
HSAE006357	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	-0.10
HSAE000600	TES	testis derived transcript (3 LIM domains)	-0.03
HSAE000934	TOM1L1	target of myb1 (chicken)-like 1	-0.05
HSAE011421	PBX4	pre-B-cell leukemia homeobox 4	-0.08
HSAE014003	CBX1	chromobox homolog 1	-0.14
HSAE001338	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-0.16
HSAE014032	C1orf174	chromosome 1 open reading frame 174	-0.06
HSAE019250	MDH1B	malate dehydrogenase 1B, NAD (soluble)	-0.18
HSAE011842	MAPKAPK5-AS1	MAPKAPK5 antisense RNA 1	-0.06
HSAE001836	EIF2AK3	eukaryotic translation initiation factor 2-alpha kinase 3	-0.09
HSAE013221	ZC3H4	zinc finger CCCH-type containing 4	-0.10
HSAE010205	FAM208A	family with sequence similarity 208, member A	-0.08
HSAE021043	PSME4	proteasome (prosome, macropain) activator subunit 4	-0.14
HSAE013883	SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-0.14
HSAE002020	DUSP6	dual specificity phosphatase 6	-0.19
HSAE003248	ACYP1	acylphosphatase 1, erythrocyte (common) type	-0.12
HSAE011498	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	-0.08
HSAE018659	ETV6	ets variant 6	-0.10

HSAE001585	ORC4	origin recognition complex, subunit 4	-0.10
HSAE022833	CCDC170	coiled-coil domain containing 170	-0.25
HSAE003644	GPN1	GPN-loop GTPase 1	-0.08
HSAE004788	NGLY1	N-glycanase 1	-0.11
HSAE010725	MOK	MOK protein kinase	-0.11
HSAE005403	SNX14	sorting nexin 14	-0.13
HSAE004343	SYCP2	synaptonemal complex protein 2	-0.15
HSAE002779	ZNF492	zinc finger protein 492	-0.10
HSAE018198	KIAA1377	KIAA1377	-0.15
HSAE002663	ISCA2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	-0.07
HSAE029538	DTNA	dystrobrevin, alpha	0.15
HSAE015424	LRRC10B	leucine rich repeat containing 10B	-0.18
HSAE014744	LRRC14	leucine rich repeat containing 14	-0.14
HSAE005719	ERBB2IP	erbb2 interacting protein	-0.12
HSAE008692	ZYG11B	zyg-11 homolog B (C. elegans)	-0.10
HSAE020721	DGKZ	diacylglycerol kinase, zeta	-0.09
HSAE016618	ZNF425	zinc finger protein 425	-0.05
HSAE001849	TMEM68	transmembrane protein 68	-0.05
HSAE016437	RP11-686D22.8	RP11-686D22.8	-0.11
HSAE004102	FAM166B	family with sequence similarity 166, member B	-0.07
HSAE001830	BTC	betacellulin	-0.06
HSAE008612	WDR63	WD repeat domain 63	-0.12
HSAE014596	FAM71E2	family with sequence similarity 71, member E2	0.12
HSAE000694	MRPL45	mitochondrial ribosomal protein L45	-0.05
HSAE019606	LINC00476	long intergenic non-protein coding RNA 476	-0.11
HSAE001712	KLHL3	kelch-like 3 (Drosophila)	-0.15
HSAE000571	HSPA1A	heat shock 70kDa protein 1A	-0.16
HSAE009957	CCDC71	coiled-coil domain containing 71	-0.04
HSAE024874	HOXC4	homeobox C4	-0.13
HSAE007783	PRRG3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	0.15
HSAE003836	PIK3C2B	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 beta	-0.17
HSAE017699	PRDM10	PR domain containing 10	-0.12
HSAE033212	Unknown	Unknown	-0.22
HSAE029507	TUG1	taurine upregulated 1 (non-protein coding)	-0.16
HSAE005634	H1F0	H1 histone family, member 0	0.32
HSAE018292	TRIM59	tripartite motif containing 59	-0.21
HSAE004297	ARMC9	armadillo repeat containing 9	-0.17
HSAE029390	MAGI3	membrane associated guanylate kinase, WW and PDZ domain containing 3	-0.13
HSAE002178	WBP7	Histone-lysine N-methyltransferase MLL4	0.07
HSAE018961	PDSS2	prenyl (decaprenyl) diphosphate synthase, subunit 2	-0.03
HSAE010367	NDUFB4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa	-0.05
HSAE001227	ZNF718	zinc finger protein 718	-0.06
HSAE012481	TMX2	thioredoxin-related transmembrane protein 2	0.07
HSAE013709	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	-0.08
HSAE001201	TDRD7	tudor domain containing 7	-0.06
HSAE005355	CDKN2AIP	CDKN2A interacting protein	-0.14
HSAE032816	KLHL17	kelch-like 17 (Drosophila)	-0.10
HSAE012522	EBF1	early B-cell factor 1	0.04
HSAE022046	NOTCH2	notch 2	0.12
HSAE030479	OR52I1	olfactory receptor, family 52, subfamily I, member 1	0.08
HSAE010170	DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	-0.05
HSAE019411	RP11-689P11.2	RP11-689P11.2	-0.12
HSAE030182	FAM201A	family with sequence similarity 201, member A	-0.07
HSAE017450	DPY19L4	dpy-19-like 4 (C. elegans)	-0.12
HSAE021251	XIAP	X-linked inhibitor of apoptosis	-0.11
HSAE027237	ALDH3A2	aldehyde dehydrogenase 3 family, member A2	-0.17

HSAE012753	DPY19L2P1	dpy-19-like 2 pseudogene 1 (<i>C. elegans</i>)	-0.13
HSAE001450	SLC39A2	solute carrier family 39 (zinc transporter), member 2	0.06
HSAE017691	DDX11L2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 like 2	0.17
HSAE010102	PAN2	PAN2 poly(A) specific ribonuclease subunit homolog (<i>S. cerevisiae</i>)	-0.12
HSAE030728	NR5A2	nuclear receptor subfamily 5, group A, member 2	-0.13
HSAE007702	CCDC11	coiled-coil domain containing 11	-0.12
HSAE024253	LUC7L3	LUC7-like 3 (<i>S. cerevisiae</i>)	-0.21
HSAE010180	HES1	hairy and enhancer of split 1, (<i>Drosophila</i>)	-0.13
HSAE003618	TSGA10	testis specific, 10	-0.13
HSAE014580	POM121C	POM121 transmembrane nucleoporin C	0.02
HSAE006626	NUP62CL	nucleoporin 62kDa C-terminal like	-0.16
HSAE001620	EXT2	exostosin 2	-0.13
HSAE009603	GDE1	glycerophosphodiester phosphodiesterase 1	-0.08
HSAE024589	NDUFB5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa	-0.12
HSAE010188	TSC2	tuberous sclerosis 2	0.13
HSAE016743	PRPF38A	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	-0.10
HSAE032880	ZNF730	Zinc finger protein 730	-0.21
HSAE009304	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	-0.04
HSAE005110	SLC2A8	solute carrier family 2 (facilitated glucose transporter), member 8	0.10
HSAE023646	TMEM204	transmembrane protein 204	0.12
HSAE008410	SHISA3	shisa homolog 3 (<i>Xenopus laevis</i>)	0.23
HSAE017269	TRAF3IP1	TNF receptor-associated factor 3 interacting protein 1	-0.08
HSAE006817	FZD3	frizzled family receptor 3	-0.18
HSAE001956	COMMD3	COMM domain containing 3	-0.10
HSAE005511	LPAR6	lysophosphatidic acid receptor 6	-0.16
HSAE019557	CD276	CD276 molecule	-0.08
HSAE011219	DMTF1	cyclin D binding myb-like transcription factor 1	-0.14
HSAE019844	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	-0.21
HSAE007934	CNOT7	CCR4-NOT transcription complex, subunit 7	-0.11
HSAE020945	SLC7A11	solute carrier family 7 (anionic amino acid transporter light chain, xc-system), member 11	-0.21
HSAE030082	HLA-B	major histocompatibility complex, class I, B	-0.27
HSAE017421	Unknown	Unknown	-0.07
HSAE025366	CC2D2A	coiled-coil and C2 domain containing 2A	-0.18
HSAE003728	CLGN	calmegin	-0.21
HSAE014978	NANOS1	nanos homolog 1 (<i>Drosophila</i>)	-0.07
HSAE024968	GPR133	G protein-coupled receptor 133	0.08
HSAE001491	TSNAXIP1	translin-associated factor X interacting protein 1	-0.14
HSAE010427	HSPA1L	heat shock 70kDa protein 1-like	-0.06
HSAE023884	GRN	granulin	-0.06
HSAE000025	HMOX2	heme oxygenase (decycling) 2	0.08
HSAE005268	BORA	bora, aurora kinase A activator	-0.14
HSAE008114	DOK5	docking protein 5	-0.17
HSAE013693	DRAM2	DNA-damage regulated autophagy modulator 2	-0.08
HSAE001682	SLC34A2	solute carrier family 34 (sodium phosphate), member 2	0.28
HSAE033332	Unknown	Unknown	0.09
HSAE012471	NONO	non-POU domain containing, octamer-binding	-0.09
HSAE032360	ACTBP12	actin, beta pseudogene 12	0.12
HSAE004298	ARMC9	armadillo repeat containing 9	-0.13
HSAE011189	DENND2D	DENN/MADD domain containing 2D	-0.10
HSAE030948	CAPN5	calpain 5	-0.13
HSAE004030	ANAPC5	anaphase promoting complex subunit 5	-0.08
HSAE008084	XPO1	exportin 1 (CRM1 homolog, yeast)	-0.10
HSAE002092	AMFR	autocrine motility factor receptor, E3 ubiquitin protein ligase	-0.33
HSAE006303	LSM14B	LSM14B, SCD6 homolog B (<i>S. cerevisiae</i>)	-0.03
HSAE014463	SRF	serum response factor (c-fos serum response element-binding transcription factor)	0.06
HSAE001396	STK33	serine/threonine kinase 33	-0.15

HSAE017690	FAM126B	family with sequence similarity 126, member	-0.14
HSAE020161	GOLM1	golgi membrane protein 1	-0.05
HSAE002216	EML4	echinoderm microtubule associated protein like 4	-0.18
HSAE006880	REEP5	receptor accessory protein 5	-0.07
HSAE007003	ZNF550	zinc finger protein 550	-0.10
HSAE005704	HIST2H2AC	histone cluster 2, H2ac	-0.17
HSAE013304	SETD4	SET domain containing 4	-0.09
HSAE001016	ORMDL1	ORM1-like 1 (<i>S. cerevisiae</i>)	-0.11
HSAE012469	TEF	thyrotrophic embryonic factor	0.03
HSAE023950	IQCD	IQ motif containing D	-0.05
HSAE029097	AMY1B	amylase, alpha 1B (salivary)	0.48
HSAE017836	SPATA7	spermatogenesis associated 7	-0.12
HSAE002184	ILKAP	integrin-linked kinase-associated serine/threonine phosphatase	-0.04
HSAE005751	FIGNL1	fidgetin-like 1	-0.12
HSAE004529	ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative)	-0.08
HSAE017429	RICTOR	RPTOR independent companion of MTOR, complex 2	-0.13
HSAE005562	ZNF558	zinc finger protein 558	-0.11
HSAE027741	ZNF813	zinc finger protein 813	-0.03
HSAE010738	SIX1	SIX homeobox 1	-0.08
HSAE012506	ZBTB49	zinc finger and BTB domain containing 49	-0.10
HSAE033552	CROCC	ciliary rootlet coiled-coil, rootletin	-0.12
HSAE032557	SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	-0.06
HSAE021990	RNPEP	arginyl aminopeptidase (aminopeptidase B)	-0.07
HSAE032660	NPB	neuropeptide B	-0.08
HSAE000414	ATP5SL	ATP5S-like	-0.04
HSAE014170	HLA-G	major histocompatibility complex, class I, G	-0.18
HSAE032969	HLA-C	major histocompatibility complex, class I, C	-0.19
HSAE016907	RBM43	RNA binding motif protein 43	-0.12
HSAE021891	ZNF83	zinc finger protein 83	-0.14
HSAE008338	PIBF1	progesterone immunomodulatory binding factor 1	-0.09
HSAE003626	TSPAN6	tetraspanin 6	-0.18
HSAE013158	SPAG6	sperm associated antigen 6	-0.26
HSAE024786	SRRT	serrate RNA effector molecule homolog (<i>Arabidopsis</i>)	-0.08
HSAE027749	ACTL9	actin-like 9	0.07
HSAE002971	VWC2	von Willebrand factor C domain containing 2	-0.23
HSAE002682	EFTUD1	elongation factor Tu GTP binding domain containing 1	-0.06
HSAE026502	TRIOBP	TRIO and F-actin binding protein	0.07
HSAE009253	NLRP5	NLR family, pyrin domain containing 5	0.15
HSAE000440	STK16	serine/threonine kinase 16	0.06
HSAE007450	ABCD4	ATP-binding cassette, sub-family D (ALD), member 4	-0.12
HSAE004543	ZNF323	zinc finger protein 323	-0.15
HSAE006633	TAS2R40	taste receptor, type 2, member 40	0.27
HSAE017069	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.22
HSAE012776	SDCCAG8	serologically defined colon cancer antigen 8	-0.02
HSAE013790	HLTF	helicase-like transcription factor	-0.19
HSAE011512	MBD4	methyl-CpG binding domain protein 4	-0.07
HSAE006537	ZNF721	zinc finger protein 721	-0.08
HSAE014584	CCDC30	coiled-coil domain containing 30	-0.10
HSAE010374	FAT1	FAT tumor suppressor homolog 1 (<i>Drosophila</i>)	-0.11
HSAE024319	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	-0.22
HSAE006041	ZDHHC17	zinc finger, DHHC-type containing 17	-0.18
HSAE025704	CCDC34	coiled-coil domain containing 34	-0.19
HSAE007323	CEP290	centrosomal protein 290kDa	-0.15
HSAE027046	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	-0.13
HSAE012714	UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	0.06
HSAE003564	CDK9	cyclin-dependent kinase 9	-0.07

HSAE026293	Unknown	Unknown	0.08
HSAE010971	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.05
HSAE000034	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	0.19
HSAE031007	GRIN3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	-0.14
HSAE004172	RNFT1	ring finger protein, transmembrane 1	-0.10
HSAE011288	HSPH1	heat shock 105kDa/110kDa protein 1	-0.19
HSAE018395	SNHG10	small nucleolar RNA host gene 10 (non-protein coding)	-0.12
HSAE017258	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	0.04
HSAE019166	PJA1	praja ring finger 1, E3 ubiquitin protein ligase	-0.17
HSAE025842	PTBP3	polypyrimidine tract binding protein 3	0.09
HSAE007756	PPID	peptidylprolyl isomerase D	0.02
HSAE006495	C8orf47	chromosome 8 open reading frame 47	-0.14
HSAE002475	AXIN2	axin 2	-0.10
HSAE006190	SPAG17	sperm associated antigen 17	-0.23
HSAE016684	NR1D2	nuclear receptor subfamily 1, group D, member 2	0.12
HSAE002873	CLDND1	claudin domain containing 1	0.08
HSAE016637	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-0.17
HSAE029270	TMEM215	Transmembrane protein 215	-0.07
HSAE009822	GOPC	golgi-associated PDZ and coiled-coil motif containing	-0.15
HSAE017125	PPM1D	protein phosphatase, Mg2+/Mn2+ dependent, 1D	-0.06
HSAE010471	WDYHV1	WDYHV motif containing 1	0.17
HSAE009559	COG6	component of oligomeric golgi complex 6	-0.11
HSAE010643	DCLRE1A	DNA cross-link repair 1A	-0.10
HSAE018343	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	-0.08
HSAE006438	MNS1	meiosis-specific nuclear structural 1	-0.19
HSAE009793	FIP1L1	FIP1 like 1 (<i>S. cerevisiae</i>)	-0.07
HSAE001155	PNISR	PNN-interacting serine/arginine-rich protein	-0.12
HSAE000041	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	0.15
HSAE004908	DKK1	dickkopf 1 homolog (<i>Xenopus laevis</i>)	0.44
HSAE030313	Unknown	Unknown	0.20
HSAE023444	PNRC1	proline-rich nuclear receptor coactivator 1	-0.11
HSAE005572	SMAD9	SMAD family member 9	0.13
HSAE020054	TMEM54	transmembrane protein 54	0.14
HSAE018904	CDK5RAP1	CDK5 regulatory subunit associated protein 1	-0.07
HSAE016335	DCP2	DCP2 decapping enzyme homolog (<i>S. cerevisiae</i>)	-0.13
HSAE024037	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	-0.08
HSAE003487	DLL1	delta-like 1 (<i>Drosophila</i>)	0.10
HSAE004236	AXL	AXL receptor tyrosine kinase	0.06
HSAE024468	TOMM5	Translocase of outer mitochondrial membrane 5 homolog (yeast)	0.06
HSAE021697	LRR1	leucine rich repeat protein 1	-0.14
HSAE031910	SEC14L1P1	SEC14-like 1 pseudogene 1	0.10
HSAE023997	DDX21	DEAD (Asp-Glu-Ala-Asp) box helicase 21	0.07
HSAE001462	EFCAB11	EF-hand calcium binding domain 11	-0.08

M, M-values were calculated as the difference between the average M-value of RIF patients and controls. Unknown, probe could not be mapped to a known gene.