

ONLINE SUPPLEMENTARY MATERIAL

Supplementary Table 1. Genes with RA-associated expression at the pre-pregnancy baseline among women who subsequently improve during pregnancy

Fold-changes (FCs) in expression and q values (to 1 decimal place) are shown for the 89 genes differentially expressed ($FC \leq -2$ or $FC \geq 2$, $q < 0.05$) between RA_{improved} vs healthy women at the pre-pregnancy (T0) baseline and at the 3rd trimester (T3). FCs corresponding to a decrease in expression are shown as negative values. The genes (n=24) that remained differentially expressed between RA_{improved} vs healthy women at the 3rd trimester are shown in italics.

Gene	RA _{improved} vs healthy at T0		RA _{improved} vs healthy at T3	
	Fold-change	q value	Fold-change	q value
ANKRD34B	2.4	1.6E-03	1.5	1.8E-01
ANXA3	2.0	2.1E-02	1.2	6.1E-01
BLVRB	2.0	1.5E-04	1.5	7.7E-02
BOLA2B	2.1	3.6E-02	1.0	9.4E-01
<i>C4BPA</i>	2.5	<i>1.2E-04</i>	2.9	<i>1.6E-06</i>
C8orf88	2.0	2.7E-03	1.6	8.2E-02
CAMP	4.1	2.2E-04	1.7	3.3E-01
CBS	2.1	2.8E-02	-1.1	8.7E-01
CD177	5.1	5.7E-04	2.2	1.7E-01
<i>CENPK</i>	2.0	<i>4.0E-04</i>	2.7	<i>3.2E-08</i>
CMPK2	-2.8	4.9E-03	1.1	9.0E-01
CRISP3	4.1	2.3E-04	1.7	3.1E-01
DDX11L10	-2.0	9.5E-03	-1.4	3.1E-01
<i>DDX11L9</i>	<i>-2.1</i>	<i>2.2E-02</i>	-2.3	<i>1.1E-02</i>
DDX60	-2.0	2.2E-03	1.2	6.2E-01
EPB42	2.2	4.9E-04	1.5	1.3E-01
<i>EPHB2</i>	<i>-2.1</i>	<i>4.6E-03</i>	-2.0	<i>1.1E-02</i>
EPSTI1	-2.1	4.6E-02	1.3	5.7E-01
<i>FADS2</i>	<i>-2.3</i>	<i>2.2E-07</i>	-2.3	<i>2.1E-07</i>
FGFR2	-2.2	4.9E-04	-1.7	5.0E-02
HERC5	-2.9	3.4E-03	-1.1	9.3E-01
HIST1H4E	2.1	1.5E-04	1.3	3.2E-01
<i>HLA-DQA2</i>	<i>3.1</i>	<i>1.4E-10</i>	3.5	<i>8.7E-14</i>

IFI44	-2.9	6.2E-03	1.1	8.9E-01
IFI44L	-3.2	5.0E-03	1.0	9.8E-01
<i>IFITM3</i>	-2.5	<i>1.3E-02</i>	-2.5	<i>1.5E-02</i>
<i>IGHA1</i>	-2.8	<i>8.6E-03</i>	-2.6	<i>1.9E-02</i>
IGHG1	-3.8	1.8E-02	-1.9	4.1E-01
IGHV3-23	-2.1	9.8E-03	-1.3	5.9E-01
IGHV3-7	-2.1	8.3E-05	-1.3	4.8E-01
IGHV5-51	-2.1	2.5E-03	-1.9	2.8E-02
IGLC2	-2.1	3.0E-02	-1.6	2.6E-01
<i>IGLC3</i>	-2.8	<i>5.3E-03</i>	-2.8	<i>7.0E-03</i>
IGLV2-14	-2.0	1.2E-02	-1.5	2.6E-01
<i>IGLV3-21</i>	-3.3	<i>8.9E-03</i>	-3.6	<i>7.0E-03</i>
IL1RL1	-2.2	5.3E-05	-1.6	8.2E-02
<i>IL5RA</i>	-2.4	<i>1.7E-02</i>	-2.5	<i>1.0E-02</i>
<i>ITGA2B</i>	-2.0	<i>1.1E-02</i>	-2.2	<i>4.0E-03</i>
ITGB3	-2.0	6.6E-03	-1.5	2.5E-01
ITLN1	2.0	1.3E-03	1.5	4.8E-02
KLF1	2.1	1.1E-02	1.8	4.8E-02
KRT1	2.4	1.8E-04	1.7	4.3E-02
LGALS2	2.1	1.6E-02	1.3	5.4E-01
<i>LRRC7</i>	2.0	<i>2.5E-03</i>	2.9	<i>7.4E-08</i>
LY6E	-2.1	1.9E-02	-1.5	3.9E-01
<i>MAOA</i>	3.1	<i>9.2E-06</i>	3.1	<i>3.2E-08</i>
MMP8	3.1	1.3E-02	1.6	4.2E-01
MT-ND6	-2.3	1.4E-02	-1.2	7.5E-01
MX1	-2.6	1.6E-02	-1.2	8.3E-01
MYL6	2.0	4.9E-04	1.4	2.5E-01
<i>NEBL</i>	-2.0	<i>5.2E-05</i>	-2.1	<i>1.4E-05</i>
NKX3-1	-2.0	1.1E-02	-1.9	3.6E-02
OAS1	-2.2	3.1E-02	-1.0	9.6E-01
OAS2	-2.3	1.3E-03	1.1	8.9E-01
OAS3	-3.4	1.8E-03	-1.2	8.4E-01
OLFM4	5.3	9.0E-05	2.6	5.1E-02
<i>OLIG2</i>	-3.8	<i>8.4E-05</i>	-5.1	<i>1.0E-06</i>
ORM1	3.0	3.9E-03	1.2	7.7E-01
<i>PAQR9</i>	2.2	<i>2.7E-02</i>	2.3	<i>1.1E-02</i>
PCSK5	-3.1	2.5E-06	-1.5	2.9E-01
PDZK1IP1	2.0	3.0E-03	1.6	1.0E-01
<i>PF4V1</i>	-2.4	<i>7.4E-07</i>	-2.2	<i>1.4E-05</i>
PLEK2	2.0	3.3E-05	1.6	1.1E-02
PPFIA4	2.2	9.6E-05	1.2	5.3E-01
PRDX5	2.0	1.4E-04	1.3	4.0E-01
<i>PTGDR2</i>	-2.5	<i>3.6E-02</i>	-2.5	<i>3.2E-02</i>

PTMS	2.2	3.2E-02	1.1	8.3E-01
<i>RGPD2</i>	2.2	1.3E-08	2.5	4.8E-13
RGS1	-2.3	4.8E-03	-1.2	6.5E-01
RPL11	2.0	2.7E-03	1.3	3.8E-01
RPL36AL	2.0	4.3E-02	1.6	2.1E-01
RPS3	2.0	6.3E-03	1.2	5.8E-01
RPS6	2.0	2.5E-03	1.5	1.9E-01
RSAD2	-3.2	2.2E-02	1.4	6.8E-01
S100A12	2.0	4.6E-02	1.1	9.1E-01
SELENBP1	2.0	5.0E-04	1.2	6.2E-01
<i>SEPTIN3</i>	2.4	2.1E-05	2.5	4.3E-05
SIGLEC1	-3.8	7.5E-04	-1.4	6.1E-01
SNRPD2	2.1	9.2E-03	1.5	2.6E-01
TMC5	2.0	1.3E-04	1.3	2.5E-01
TRBV12-4	2.2	1.4E-02	1.9	5.8E-02
<i>TREML4</i>	-2.3	9.5E-03	-3.5	3.3E-07
TRIM10	2.2	2.4E-06	1.7	5.2E-03
TRPC6	-2.5	2.5E-04	-1.9	3.3E-02
<i>TUBB2A</i>	2.0	2.2E-02	2.4	2.6E-03
TXNDC5	-2.1	1.7E-03	-1.2	6.6E-01
UBB	3.5	4.4E-06	1.7	1.7E-01
USP18	-2.4	4.8E-02	1.1	9.1E-01
<i>VWF</i>	-2.0	1.7E-02	-2.5	5.0E-04

Supplementary Table 2. Genes with RA-associated expression at the pre-pregnancy baseline among women who subsequently improve or worsen during pregnancy

Fold-changes (FCs) in expression and q values (to 1 decimal place) are shown for the genes differentially expressed ($FC \leq -2$ or $FC \geq 2$, $q < 0.05$) at the pre-pregnancy (T0) baseline between RA_{improved} and healthy women and between RA_{worsened} and healthy women. FCs corresponding to a decrease in expression are shown as negative values. Genes that overlap between the two RA expression signatures (n=19) are shown in bold. Remaining genes present in the RA_{improved} signature are in black font and those in the RA_{worsened} signature are in blue font.

Gene	RA _{improved} vs healthy at T0		RA _{worsened} vs healthy at T0	
	Fold-change	q value	Fold-change	q value
ANKRD34B	2.4	1.6E-03	-2.9	2.7E-03
FADS2	-2.3	2.2E-07	-3.3	1.2E-07
HLA-DQA2	3.1	1.4E-10	-3.4	1.1E-06
IGLC3	-2.8	5.3E-03	-4.9	3.6E-07
IGLV2-14	-2.0	1.2E-02	-2.2	1.1E-03
IL1RL1	-2.2	5.3E-05	-2.0	6.5E-03
KRT1	2.4	1.8E-04	3.1	5.5E-03
NKX3-1	-2.0	1.1E-02	-3.3	6.4E-06
OLFM4	5.3	9.0E-05	2.7	8.7E-03
ORM1	3.0	3.9E-03	2.6	1.9E-04
PF4V1	-2.4	7.4E-07	-3.3	1.5E-04
PTMS	2.2	3.2E-02	4.7	2.4E-09
RGPD2	2.2	1.3E-08	3.7	9.8E-20
SEPTIN3	2.4	2.1E-05	2.0	1.7E-02
TMC5	2.0	1.3E-04	2.4	2.0E-03
TRBV12-4	2.2	1.4E-02	2.1	3.3E-02
TREML4	-2.3	9.5E-03	3.1	3.6E-06
TUBB2A	2.0	2.2E-02	2.7	2.2E-02
UBB	3.5	4.4E-06	2.9	1.4E-02
ANXA3	2.0	2.1E-02	2.0	2.1E-01
BLVRB	2.0	1.5E-04	1.3	6.6E-01
BOLA2B	2.1	3.6E-02	1.8	5.1E-02
C4BPA	2.5	1.2E-04	1.1	8.2E-01
C8orf88	2.0	2.7E-03	1.5	2.9E-01
CAMP	4.1	2.2E-04	1.3	6.5E-01
CBS	2.1	2.8E-02	1.6	3.9E-01

CD177	5.1	5.7E-04	2.9	1.7E-01
CENPK	2.0	4.0E-04	1.5	9.9E-02
CMPK2	-2.8	4.9E-03	1.3	8.0E-01
CRISP3	4.1	2.3E-04	2.0	1.6E-01
DDX11L10	-2.0	9.5E-03	-1.3	6.6E-01
DDX11L9	-2.1	2.2E-02	1.5	4.3E-01
DDX60	-2.0	2.2E-03	1.2	8.6E-01
EPB42	2.2	4.9E-04	1.2	7.7E-01
EPHB2	-2.1	4.6E-03	1.3	6.8E-01
EPSTI1	-2.1	4.6E-02	1.5	6.2E-01
FGFR2	-2.2	4.9E-04	-1.3	5.1E-01
HERC5	-2.9	3.4E-03	1.5	7.4E-01
HIST1H4E	2.1	1.5E-04	1.1	8.6E-01
IFI44	-2.9	6.2E-03	1.2	8.9E-01
IFI44L	-3.2	5.0E-03	1.2	8.7E-01
IFITM3	-2.5	1.3E-02	1.7	5.5E-01
IGHA1	-2.8	8.6E-03	-1.3	7.4E-01
IGHG1	-3.8	1.8E-02	-1.1	9.4E-01
IGHV3-23	-2.1	9.8E-03	1.1	8.5E-01
IGHV3-7	-2.1	8.3E-05	1.0	9.9E-01
IGHV5-51	-2.1	2.5E-03	-1.3	6.1E-01
IGLC2	-2.1	3.0E-02	-1.3	6.8E-01
IGLV3-21	-3.3	8.9E-03	-2.9	1.2E-01
IL5RA	-2.4	1.7E-02	-1.6	1.6E-01
ITGA2B	-2.0	1.1E-02	-1.1	9.3E-01
ITGB3	-2.0	6.6E-03	-2.4	7.8E-02
ITLN1	2.0	1.3E-03	1.4	4.9E-01
KLF1	2.1	1.1E-02	1.7	4.1E-01
LGALS2	2.1	1.6E-02	1.5	3.8E-01
LRRC7	2.0	2.5E-03	1.9	2.2E-02
LY6E	-2.1	1.9E-02	1.9	3.5E-01
MAOA	3.1	9.2E-06	1.0	9.7E-01
MMP8	3.1	1.3E-02	2.2	9.4E-02
MT-ND6	-2.3	1.4E-02	1.6	5.8E-01
MX1	-2.6	1.6E-02	1.4	7.8E-01
MYL6	2.0	4.9E-04	1.7	5.6E-02
NEBL	-2.0	5.2E-05	1.1	7.1E-01
OAS1	-2.2	3.1E-02	1.4	7.4E-01
OAS2	-2.3	1.3E-03	1.1	9.1E-01
OAS3	-3.4	1.8E-03	1.2	9.3E-01
OLIG2	-3.8	8.4E-05	-1.1	9.2E-01
PAQR9	2.2	2.7E-02	1.5	4.7E-01
PCSK5	-3.1	2.5E-06	1.2	8.7E-01

PDZK1IP1	2.0	3.0E-03	1.7	3.0E-01
PLEK2	2.0	3.3E-05	1.4	4.3E-01
PPFIA4	2.2	9.6E-05	1.4	4.5E-01
PRDX5	2.0	1.4E-04	1.9	6.8E-03
PTGDR2	-2.5	3.6E-02	-2.0	1.1E-01
RGS1	-2.3	4.8E-03	-1.3	5.1E-01
RPL11	2.0	2.7E-03	1.4	4.7E-01
RPL36AL	2.0	4.3E-02	1.3	6.1E-01
RPS3	2.0	6.3E-03	1.6	2.7E-01
RPS6	2.0	2.5E-03	1.6	3.4E-01
RSAD2	-3.2	2.2E-02	1.4	8.0E-01
S100A12	2.0	4.6E-02	1.5	5.5E-01
SELENBP1	2.0	5.0E-04	1.9	2.1E-01
SIGLEC1	-3.8	7.5E-04	-1.3	8.6E-01
SNRPD2	2.1	9.2E-03	1.7	2.5E-01
TRIM10	2.2	2.4E-06	1.6	3.1E-01
TRPC6	-2.5	2.5E-04	-1.9	6.3E-02
TXNDC5	-2.1	1.7E-03	-1.3	5.5E-01
USP18	-2.4	4.8E-02	2.0	4.9E-01
VWF	-2.0	1.7E-02	-1.1	9.4E-01
A2M	-1.3	8.5E-01	20.0	2.4E-36
ABCD1	-1.0	1.0E+00	2.2	1.5E-02
ABCF2	1.4	4.2E-01	2.0	2.3E-02
ABHD1	1.1	9.4E-01	2.3	4.9E-04
ABHD12B	-1.1	9.8E-01	2.1	3.8E-03
ABI3	-1.1	9.6E-01	2.6	4.6E-08
ABI3BP	-1.1	9.6E-01	2.2	3.6E-06
AC001226.2	-1.2	7.9E-01	5.3	1.3E-32
AC005726.1	-1.2	9.0E-01	2.2	2.7E-03
AC015802.6	1.1	9.4E-01	2.2	2.4E-07
AC018755.2	1.1	9.4E-01	3.4	6.6E-04
AC069368.1	1.7	3.0E-01	2.9	1.4E-02
AC072022.2	1.2	8.5E-01	8.2	1.1E-26
AC091959.3	1.7	5.3E-02	2.1	1.6E-02
AC104389.6	2.6	5.4E-02	8.1	4.6E-10
AC107871.1	1.1	9.6E-01	2.1	4.4E-03
ACO1	-1.1	9.5E-01	6.0	1.1E-06
ACOT13	-1.0	9.9E-01	2.3	8.3E-09
ADAMTS2	1.6	4.7E-01	3.2	2.7E-06
ADAMTS5	-1.3	6.6E-01	-2.5	2.4E-02
ADAMTSL4	1.0	9.9E-01	5.8	8.1E-09
ADGRG2	1.0	9.9E-01	2.5	6.0E-05
ADGRL1	1.1	9.6E-01	2.4	1.2E-04

AFDN	-1.3	3.8E-01	-2.1	2.5E-04
AGBL5	-1.1	9.5E-01	2.1	1.2E-05
AK1	1.5	1.6E-01	2.7	1.8E-04
AKAP5	-1.0	1.0E+00	2.0	2.8E-03
AKT2	1.3	4.2E-01	-4.8	2.4E-08
AL121594.1	1.2	8.6E-01	-2.2	1.2E-02
AL358113.1	1.0	1.0E+00	2.5	1.0E-05
AL591806.4	-1.1	9.6E-01	3.5	4.4E-05
AL669918.1	1.4	8.0E-01	4.0	2.1E-08
AL807752.6	1.8	5.1E-01	4.0	3.0E-03
ALDH1A2	1.3	8.6E-01	3.1	2.9E-05
ALG1L2	-1.1	9.6E-01	-2.0	4.1E-02
ALOX12	-1.1	9.1E-01	2.6	2.0E-06
AMDHD1	1.1	9.4E-01	2.3	8.8E-04
AMT	1.1	9.4E-01	2.1	1.9E-04
ANKDD1A	1.5	1.4E-01	2.5	4.4E-05
ANKUB1	1.0	9.9E-01	2.5	2.2E-05
AP002990.1	1.3	7.9E-01	2.4	4.9E-03
ARG1	1.8	2.4E-01	2.1	1.1E-02
ARHGEF26	-1.1	9.3E-01	2.1	1.6E-03
ARHGEF35	1.4	2.0E-01	2.1	7.7E-04
ARHGEF39	1.2	9.3E-01	2.0	4.8E-02
ARHGEF4	1.0	9.9E-01	2.5	9.7E-04
ARL2BP	-1.1	9.6E-01	-2.4	6.4E-06
ARMC5	1.1	8.5E-01	2.7	8.1E-09
ASAH2B	1.2	8.0E-01	2.9	2.0E-07
ATP2C2	1.4	7.2E-01	2.3	7.9E-03
ATP5PD	1.3	4.5E-01	2.9	2.8E-10
ATP6V1F	1.1	9.4E-01	2.1	3.9E-04
ATP8B1	-1.3	8.8E-01	3.5	1.2E-08
B3GALT2	1.1	9.6E-01	4.0	1.1E-16
B3GNT7	-1.1	9.7E-01	2.1	1.1E-03
BAIAP3	1.3	6.6E-01	2.0	1.3E-02
BBS5	-1.1	9.5E-01	2.3	1.4E-03
BIVM	1.3	3.6E-01	2.4	1.1E-03
BTBD2	-1.0	9.9E-01	2.1	2.4E-04
BYSL	-1.2	7.4E-01	2.0	3.2E-03
C10orf105	1.1	9.5E-01	3.2	1.2E-04
C1orf56	1.0	1.0E+00	3.9	2.5E-14
C1orf74	-1.1	8.6E-01	2.5	2.5E-06
C3orf52	-1.1	9.4E-01	2.2	2.7E-03
C9orf131	1.0	1.0E+00	2.5	3.6E-05
CA6	1.0	9.9E-01	2.5	3.9E-05

CRELD2	1.3	8.1E-01	2.9	1.1E-03
CRYBG2	1.1	9.2E-01	2.7	3.6E-06
CTNNA2	-1.0	9.9E-01	-2.1	3.5E-02
CTRL	1.5	3.8E-01	2.1	2.6E-02
CXCL5	-1.7	2.5E-03	-2.2	1.5E-02
CYBC1	1.2	6.2E-01	2.0	2.1E-02
CYP27A1	-1.5	1.5E-01	-2.1	1.8E-04
CYP46A1	-1.2	7.2E-01	2.1	1.4E-05
CYP4F8	-1.3	7.7E-01	2.2	5.6E-03
CYREN	-1.0	1.0E+00	2.2	1.3E-03
DAAM2	2.0	2.5E-01	4.4	4.1E-06
DACT3	1.3	4.3E-01	2.1	6.3E-04
DAXX	-1.0	1.0E+00	2.8	2.5E-06
DDTL	1.4	3.4E-01	2.1	3.1E-03
DEDD	-1.1	9.7E-01	2.0	5.9E-03
DEFA3	2.7	2.7E-01	3.3	2.1E-02
DERPC	-1.4	7.3E-01	-2.5	1.2E-03
DIPK1B	-1.3	7.1E-01	2.1	3.5E-03
DNAH14	1.0	1.0E+00	2.6	2.9E-06
DOK6	1.0	9.9E-01	4.1	9.4E-16
DPCD	1.5	2.4E-01	2.0	3.1E-03
DRAP1	-1.1	9.5E-01	3.2	1.1E-03
DSP	1.1	9.6E-01	2.9	3.7E-06
ECSIT	1.2	7.3E-01	2.3	3.4E-07
EFCAB10	1.0	1.0E+00	2.0	1.5E-02
EFCAB6	-1.2	7.5E-01	2.0	8.7E-04
ELMO3	1.4	3.6E-01	2.3	4.5E-04
ELOF1	1.5	1.1E-02	2.2	1.0E-04
ENC1	1.1	9.4E-01	-2.0	6.7E-04
ENG	-1.1	9.6E-01	2.0	4.6E-03
EPHB4	1.5	4.8E-02	2.4	6.4E-06
ERCC6L	-1.2	7.6E-01	2.1	3.2E-03
ERP29	1.4	2.4E-01	2.7	7.1E-08
ESR1	-1.3	4.5E-01	2.4	1.7E-06
ESR2	-1.0	9.9E-01	3.0	7.5E-06
ETFBKMT	-1.1	9.5E-01	2.0	2.8E-04
EYS	-1.0	9.8E-01	2.3	6.8E-06
FABP5	-1.2	8.7E-01	2.1	2.9E-03
FAM181B	-1.1	9.5E-01	2.9	3.5E-06
FAM20A	-1.1	9.4E-01	11.3	7.2E-50
FAM47E-STBD1	1.1	9.7E-01	2.1	3.9E-02
FAM83A	1.5	7.9E-01	8.6	4.8E-12

FAM86B1	1.1	9.7E-01	2.0	1.5E-02
FARP1	-1.0	1.0E+00	2.9	4.4E-10
FAT4	-1.5	1.0E-01	-2.2	3.2E-04
FBN2	1.0	9.9E-01	-2.1	1.8E-04
FBXL16	1.1	9.2E-01	2.0	1.4E-02
FBXO10	-1.1	9.8E-01	2.2	2.5E-03
FBXO17	-1.1	9.6E-01	2.2	1.4E-02
FCER2	1.4	5.6E-01	3.5	4.2E-08
FGF7	1.0	1.0E+00	2.4	6.1E-04
FIZ1	1.0	1.0E+00	2.7	4.1E-06
FLACC1	1.1	8.3E-01	2.2	2.5E-05
FLOT2	1.3	6.7E-01	2.5	7.4E-03
FRMD4A	1.1	9.8E-01	2.8	3.2E-08
FSD2	1.1	9.5E-01	2.5	4.8E-06
G0S2	1.8	7.5E-02	2.0	2.1E-02
GADD45B	1.1	9.1E-01	2.3	3.5E-02
GALM	-1.2	6.7E-01	2.3	3.3E-02
GHRL	-1.1	9.7E-01	2.1	1.8E-03
GLRX5	1.6	3.9E-02	2.1	1.6E-02
GNAL	1.2	9.4E-01	3.8	3.0E-11
GOLGA6L1	1.6	6.4E-01	4.0	1.4E-04
GPM6B	-1.1	9.4E-01	6.1	2.4E-24
GPR18	-1.1	9.0E-01	2.2	1.1E-06
GPR68	-1.0	9.9E-01	2.6	4.4E-06
GPS2	1.3	2.7E-01	2.7	1.9E-09
GPSM3	1.1	9.0E-01	2.8	5.8E-05
HDGFL3	-1.0	9.9E-01	2.2	9.5E-06
HEPACAM	1.2	8.8E-01	2.6	2.5E-04
HEXIM2	-1.0	9.9E-01	4.3	3.0E-13
HHLA1	-1.5	3.9E-01	2.5	9.9E-03
HLA-C	1.3	5.2E-01	3.5	2.5E-04
HMGA1	-1.3	4.5E-01	2.2	6.4E-06
HRAS	1.3	6.2E-01	2.0	1.2E-02
HSD17B1	-1.0	9.9E-01	3.7	1.5E-15
ICA1L	-1.1	9.6E-01	2.0	6.1E-04
IGHV4-39	1.5	3.9E-01	2.8	2.6E-03
IL23R	-1.4	4.1E-01	-2.3	7.9E-03
IL7	1.1	9.6E-01	2.2	2.6E-03
INMT	-1.1	9.6E-01	3.4	1.9E-05
INSL6	1.0	9.9E-01	2.4	1.1E-06
ISG20	1.0	9.9E-01	2.5	2.6E-02
ISYNA1	1.1	9.6E-01	2.0	7.8E-03
KCNE4	-1.2	6.0E-01	2.0	1.8E-04

KCNMA1	1.3	9.3E-01	2.9	1.2E-02
KCNRG	-1.4	6.3E-01	2.5	9.8E-04
KIAA1211L	1.6	4.4E-01	2.1	2.5E-02
KIAA1324	1.2	6.5E-01	-2.0	7.1E-03
KIF19	1.4	6.7E-01	2.6	3.6E-06
KIF24	1.1	9.4E-01	2.4	1.3E-06
KY	-1.0	9.9E-01	17.5	4.6E-28
LCAT	1.4	5.6E-01	3.1	5.7E-06
LCTL	1.0	9.9E-01	2.0	1.6E-02
LGALS3BP	-1.2	8.3E-01	2.0	1.6E-02
LGR6	1.2	9.1E-01	2.3	5.5E-03
LHPP	1.2	8.0E-01	2.2	1.9E-04
LIMS2	1.4	7.0E-01	6.2	1.7E-15
LINGO3	1.3	6.0E-01	12.9	3.5E-57
LRP10	1.2	8.2E-01	2.4	9.3E-03
LRRC34	1.0	9.9E-01	2.3	1.2E-04
LRRC75A	1.4	1.4E-01	3.7	3.2E-12
LRTOMT	1.0	9.9E-01	2.9	1.7E-09
LSM2	1.1	9.7E-01	2.2	3.1E-02
LSR	1.2	7.3E-01	2.4	3.7E-05
LYSMD1	1.2	8.6E-01	4.5	1.5E-15
LYVE1	1.3	7.0E-01	2.0	8.6E-04
MAB21L3	-1.1	9.4E-01	2.0	4.9E-04
MAMDC4	1.0	9.9E-01	3.9	1.8E-07
MAP7D1	1.4	4.4E-01	2.2	6.9E-03
MAPK12	-1.0	9.9E-01	3.0	1.4E-04
MAPT	-1.1	9.9E-01	2.5	1.4E-03
MARCKSL1	-1.1	9.7E-01	2.1	7.0E-04
MAS1	-1.2	8.4E-01	2.4	3.2E-04
MCC	1.0	9.9E-01	3.5	1.1E-09
MDGA1	-1.2	8.4E-01	-2.4	1.5E-03
ME1	-1.3	5.2E-01	-2.1	1.6E-02
MFSD2A	-1.5	1.2E-01	-2.0	6.9E-03
MFSD4A	-1.2	8.0E-01	2.1	1.0E-03
MIEN1	1.3	5.6E-01	2.3	6.3E-05
MLANA	1.0	1.0E+00	2.0	7.9E-05
MLLT11	-1.0	9.8E-01	5.7	1.0E-29
MPV17L	1.1	9.7E-01	2.5	8.6E-09
MS4A14	-1.4	1.4E-01	-2.9	3.1E-07
MST1	-1.1	9.5E-01	2.5	3.5E-05
MTFR1	-1.0	9.9E-01	3.0	7.3E-10
MTRNR2L6	-1.2	9.4E-01	-4.6	3.3E-03
MTRNR2L8	-1.2	9.6E-01	-3.7	3.9E-02

MYH10	1.1	9.4E-01	11.6	6.5E-38
MYH11	-1.1	9.9E-01	3.4	5.8E-08
MYH7B	1.0	1.0E+00	2.2	4.1E-03
MYL4	1.6	6.1E-02	2.6	9.1E-04
MYL5	-1.0	1.0E+00	2.5	1.6E-06
MYO16	1.2	8.9E-01	2.2	1.0E-02
MYOM2	-1.9	2.3E-02	-2.3	3.1E-03
NDUFB1	1.3	6.6E-01	3.1	7.4E-07
NECTIN2	1.5	3.6E-01	2.2	3.3E-04
NEXN	-1.2	7.9E-01	2.3	4.1E-06
NFE2L3	-1.2	7.4E-01	3.4	2.6E-14
NFIX	1.6	5.7E-02	3.0	1.3E-03
NFKBIL1	1.2	8.5E-01	2.0	1.4E-03
NKD1	-1.1	9.4E-01	2.3	4.3E-03
NKG7	-1.0	9.9E-01	2.3	1.6E-03
NLRP6	1.1	9.3E-01	2.9	1.5E-03
NOCT	-1.2	8.6E-01	2.2	7.0E-05
NR1H2	1.1	9.4E-01	2.3	4.4E-06
NRM	1.1	9.8E-01	3.5	4.6E-09
NRSN1	1.7	5.4E-01	175.6	2.4E-39
NUDT13	-1.4	3.6E-01	2.0	3.1E-04
NUTM2D	-1.2	9.0E-01	2.1	6.1E-04
ODF3B	-1.3	7.6E-01	2.3	1.8E-02
OMG	1.1	9.5E-01	3.1	4.0E-05
OR2B11	-1.0	9.9E-01	2.4	1.4E-04
OR2V1	1.2	8.1E-01	2.1	2.7E-02
OR7A5	-1.1	9.7E-01	2.8	1.3E-06
OS9	1.3	5.4E-01	2.2	5.8E-03
PAPLN	1.0	9.9E-01	2.2	1.9E-03
PARP3	1.1	9.6E-01	2.2	6.0E-04
PCDH12	-1.5	2.3E-01	2.7	2.9E-05
PDLIM1	-1.2	6.2E-01	-2.1	2.2E-02
PDZD2	-1.1	9.6E-01	2.7	5.0E-08
PFDN1	-1.0	1.0E+00	2.1	4.0E-03
PFN2	-1.1	9.4E-01	2.5	6.2E-06
PGGHG	1.3	5.0E-01	2.0	1.1E-02
PGLYRP1	1.9	1.8E-01	3.3	5.9E-04
PHACTR3	-1.1	9.5E-01	2.0	7.7E-04
PHOSPHO1	1.3	4.2E-01	2.2	5.4E-03
PIGC	1.9	3.8E-07	2.0	9.0E-04
PIM2	-1.2	6.2E-01	2.0	1.3E-02
PKD1L3	-1.2	8.6E-01	2.1	1.2E-02
PKM	1.1	8.7E-01	2.2	2.4E-04

PLA2G7	-1.2	8.0E-01	-2.0	1.5E-03
PLCE1	-1.1	9.4E-01	2.1	1.5E-05
PLD5	1.1	9.7E-01	2.5	1.6E-03
PLEKHG6	1.2	8.4E-01	4.5	6.6E-11
PLEKHO2	1.1	9.5E-01	2.3	1.5E-02
PLLP	1.4	7.6E-01	19.0	4.8E-13
PLN	-1.1	9.2E-01	2.2	7.0E-05
PLSCR3	-1.0	1.0E+00	2.2	2.2E-04
PODXL	-1.3	5.6E-01	4.0	1.1E-13
POLR2E	1.1	8.4E-01	2.0	5.8E-05
POTEC	-1.1	9.4E-01	2.2	1.1E-03
POTEM	-1.2	7.7E-01	2.2	8.7E-06
PPAN-P2RY11	1.4	6.2E-01	2.0	1.1E-02
PPEF2	1.3	9.1E-01	60.2	2.1E-18
PPIAL4H	-1.2	8.9E-01	-2.1	8.7E-03
PPP1R15A	1.3	5.8E-01	2.0	1.8E-02
PPP2R3A	-1.0	9.9E-01	3.1	7.7E-14
PPP5D1	-1.1	9.8E-01	2.6	4.2E-05
PRR13	1.1	8.8E-01	2.3	1.2E-03
PRSS53	1.0	9.9E-01	2.0	2.3E-02
PRUNE2	1.5	3.4E-01	5.1	1.5E-13
PTPN6	1.2	7.6E-01	2.4	2.6E-03
PTPRZ1	-1.3	5.7E-01	2.0	3.9E-02
RAB15	-1.0	9.9E-01	2.8	5.0E-07
RAB36	1.1	9.4E-01	2.0	1.4E-02
RAB43	1.0	9.8E-01	2.1	1.9E-02
RAD23A	1.2	6.1E-01	2.6	1.9E-04
RAD9B	-1.0	9.9E-01	2.4	4.6E-05
RAP1GAP	-1.9	9.4E-02	3.3	4.7E-04
RAVER2	-1.0	9.9E-01	2.0	5.7E-05
RBP5	-1.0	9.9E-01	2.4	6.1E-04
RGPD1	1.0	9.9E-01	2.2	5.5E-03
RGS9	1.0	9.9E-01	2.9	2.9E-05
RHBDF2	-1.1	9.6E-01	2.1	3.7E-02
RHD	-1.2	5.7E-01	2.7	2.7E-09
RIPOR3	-1.3	7.3E-01	2.9	4.3E-09
RNF167	1.1	8.8E-01	2.1	1.1E-03
RNF175	-1.1	9.4E-01	8.2	3.9E-13
RNF187	1.2	7.4E-01	2.1	6.1E-05
RP1	1.6	1.9E-01	5.7	2.3E-09
RPLP1	1.1	9.7E-01	-2.1	1.5E-03
RPUSD1	-1.0	9.9E-01	2.0	1.3E-03
RSPH9	-1.4	4.0E-01	2.6	7.4E-03

RTEL1-TNFRSF6B	1.3	8.0E-01	2.5	1.9E-05
RUNDC3B	1.2	8.5E-01	2.3	8.2E-04
RUSC1	-1.2	8.7E-01	2.0	4.7E-03
S100A6	1.5	2.4E-01	2.3	4.0E-03
S100Z	-1.1	9.7E-01	-2.1	2.3E-04
SAXO2	-1.0	9.9E-01	3.2	1.2E-09
SCAF1	1.3	7.6E-01	2.0	4.2E-02
SCG3	-1.1	9.0E-01	4.0	7.8E-12
SCN2A	-1.1	9.2E-01	6.5	3.5E-16
SCNM1	1.3	3.6E-01	2.3	1.2E-05
SELENOP	1.1	9.3E-01	2.6	2.9E-05
SEMA5B	1.1	9.8E-01	2.4	4.5E-04
SEPTIN4	-1.0	9.9E-01	2.4	3.5E-02
SERPINB2	-1.1	9.4E-01	-2.1	2.3E-02
SGK1	1.1	9.4E-01	-2.0	4.4E-03
SGTA	1.1	9.4E-01	2.2	6.9E-04
SIGLEC14	-1.1	9.4E-01	4.8	9.3E-05
SLC14A2	-1.0	9.9E-01	2.7	2.6E-06
SLC22A23	1.1	9.4E-01	3.0	1.2E-11
SLC24A1	-1.1	9.2E-01	2.6	3.2E-09
SLC28A2	1.1	9.0E-01	2.3	1.1E-03
SLC35G5	-1.1	9.4E-01	2.0	6.5E-03
SLC48A1	1.1	8.5E-01	2.0	1.1E-03
SLC4A10	-1.4	1.3E-01	-2.2	3.7E-04
SLC6A17	-1.1	9.4E-01	2.1	2.1E-02
SLIT1	-1.0	9.9E-01	2.1	3.8E-03
SLPI	1.8	1.9E-02	2.9	1.4E-02
SNRNP70	1.3	4.5E-01	2.1	8.5E-04
SPATA1	-1.1	9.6E-01	4.9	3.2E-12
SPEG	1.1	9.4E-01	2.0	8.1E-03
SPI1	1.1	8.8E-01	2.5	5.0E-03
SPRYD3	1.1	8.9E-01	2.2	2.7E-05
SPTBN5	1.3	6.6E-01	2.1	1.4E-03
SPTSSB	-1.9	2.2E-02	-2.0	4.9E-02
SRRM4	-1.1	9.1E-01	2.1	2.8E-03
SRSF12	-1.1	9.7E-01	2.5	6.3E-05
SSBP4	1.3	6.8E-01	2.0	4.6E-03
ST13	1.3	1.7E-01	2.0	1.6E-04
ST6GALNAC4	1.1	9.4E-01	2.0	2.2E-02
STARD5	-1.2	8.8E-01	7.7	5.2E-28
SULF2	1.3	2.4E-01	-2.0	1.5E-03
SYCP3	-1.1	9.7E-01	3.1	7.8E-09

SYN3	1.1	9.4E-01	2.4	1.5E-04
TAF1C	1.1	9.4E-01	2.0	9.3E-04
TAF9B	-1.1	9.6E-01	2.2	7.0E-07
TAOK1	1.2	7.8E-01	-2.2	1.3E-02
TBCE	-1.1	9.4E-01	11.9	1.7E-08
TCEA2	1.3	7.6E-01	2.3	4.1E-04
TECRL	-1.0	9.8E-01	3.2	2.1E-07
TIGD3	1.2	8.5E-01	2.3	6.5E-04
TLR9	1.5	4.9E-01	2.5	1.2E-03
TMCC2	1.5	1.7E-01	2.4	1.9E-02
TMEM132A	1.3	7.1E-01	4.9	1.3E-12
TMEM150A	-1.0	1.0E+00	2.0	8.7E-04
TMEM176B	1.0	1.0E+00	3.3	1.3E-10
TMEM266	1.1	9.5E-01	2.0	3.6E-03
TMEM86B	1.4	3.6E-01	2.0	8.6E-03
TMPRSS9	1.1	9.4E-01	2.7	4.0E-04
TNNI2	1.5	4.7E-01	2.2	1.2E-02
TOR2A	-1.1	9.5E-01	2.2	2.5E-05
TPPP	1.2	9.4E-01	2.1	2.9E-02
TRAV1-2	-1.1	9.5E-01	-2.4	8.0E-03
TRAV8-6	-1.1	9.5E-01	-2.0	3.0E-02
TRGV2	-1.4	3.8E-01	2.2	8.0E-04
TRGV3	-1.4	4.0E-01	2.0	4.4E-03
TRIM26	-1.1	9.0E-01	2.0	1.3E-02
TRIR	1.5	2.4E-01	2.3	1.4E-05
TSC22D3	1.1	9.7E-01	2.6	1.1E-03
TSC22D4	1.2	6.6E-01	2.5	1.6E-03
TSPO2	1.4	5.2E-01	2.3	1.6E-03
TVP23A	1.0	9.9E-01	2.5	3.3E-06
UBALD2	1.4	9.8E-03	2.3	1.2E-03
UBE2O	1.5	1.3E-02	2.0	1.6E-02
USP35	1.0	9.9E-01	2.6	1.4E-04
VASH2	-1.0	9.9E-01	3.6	1.4E-11
VAT1	-1.0	9.9E-01	2.7	1.8E-04
VEGFB	-1.0	1.0E+00	2.2	2.3E-03
VSIG4	-1.1	9.8E-01	5.6	3.7E-17
WBP2	1.1	8.7E-01	2.0	3.2E-02
WNK3	1.1	9.4E-01	2.0	7.1E-03
WNT16	-1.0	9.9E-01	2.1	9.0E-03
XRCC3	-1.1	9.8E-01	3.2	3.2E-10
XRRA1	-1.5	6.8E-02	2.1	1.1E-04
YIPF3	1.1	8.3E-01	2.2	5.7E-05
ZNF219	1.2	9.1E-01	3.4	3.1E-08

Online supplement to: The Rheumatoid Arthritis Gene Expression Signature Among Women Who Improve or Worsen During Pregnancy: A Pilot Study. *The Journal of Rheumatology*. doi:10.3899/jrheum.201128

ZNF608	1.3	8.0E-01	2.0	6.6E-04
ZSCAN31	-1.1	9.7E-01	2.1	6.1E-03