

SUPPLEMENTAL MATERIAL

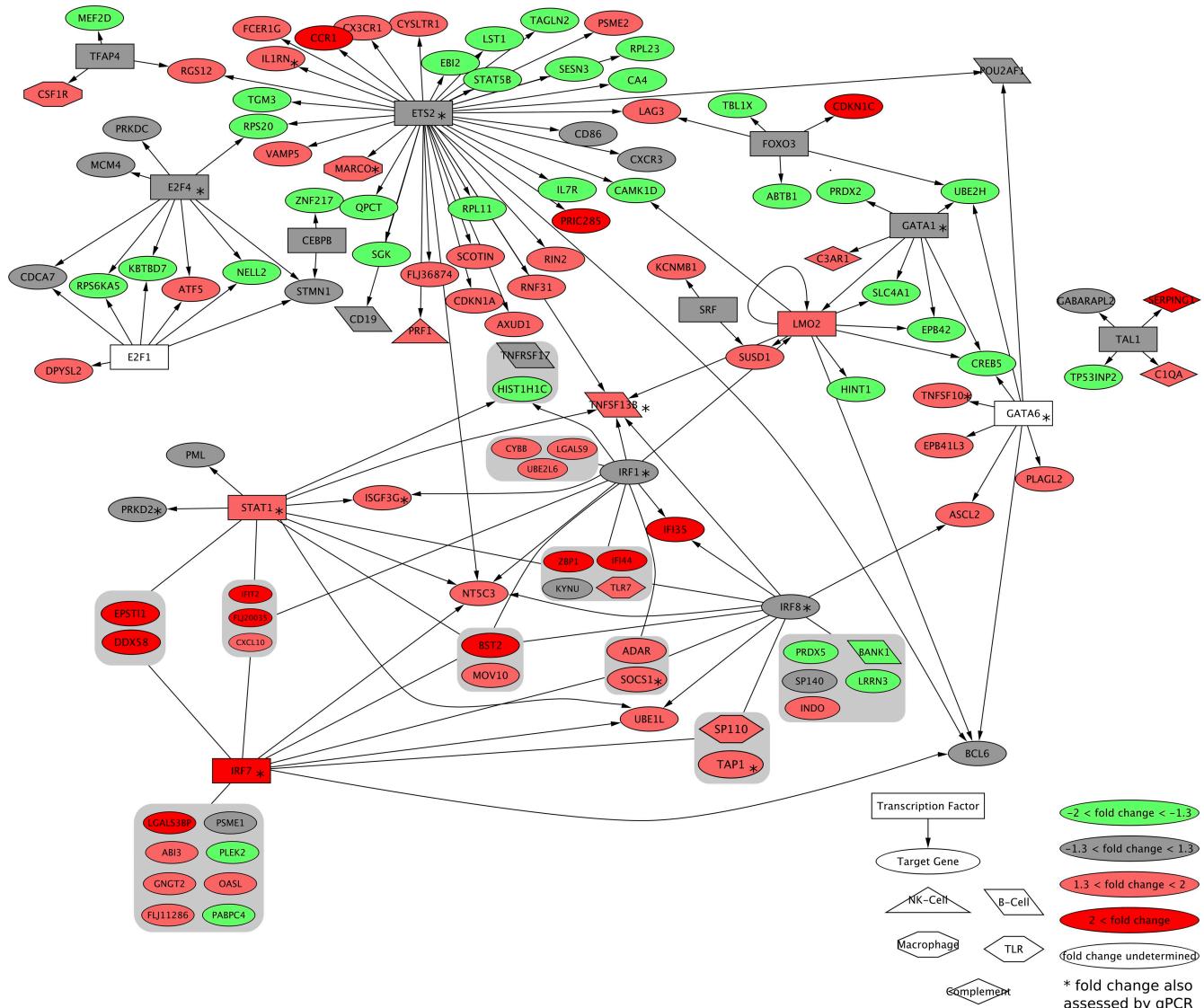
Gaucher et al., <http://www.jem.org/cgi/content/full/jem.20082292/DC1>

Figure S1. Transcriptional network of differentially expressed genes after YF17D vaccination, as inferred by gene set enrichment. Network representation of inferred transcription factors (Xie, X., J. Lu, E.J. Kulbokas, T.R. Golub, V. Mootha, K. Lindblad-Toh, E.S. Lander, and M. Kellis. 2005. *Nature*. 434:338–345) and predicted target genes that are significantly modulated. Node colors indicate fold change of gene expression between day 0 and 7, in $n = 11$ volunteers. Rectangular nodes indicate transcription factors identified by gene enrichment; the different shapes indicate genes in the different functional categories of Fig. 3 (a–e). Genes in gray boxes are grouped to enhance readability. Genes that were subsequently evaluated by RT-PCR are identified by an asterisk.

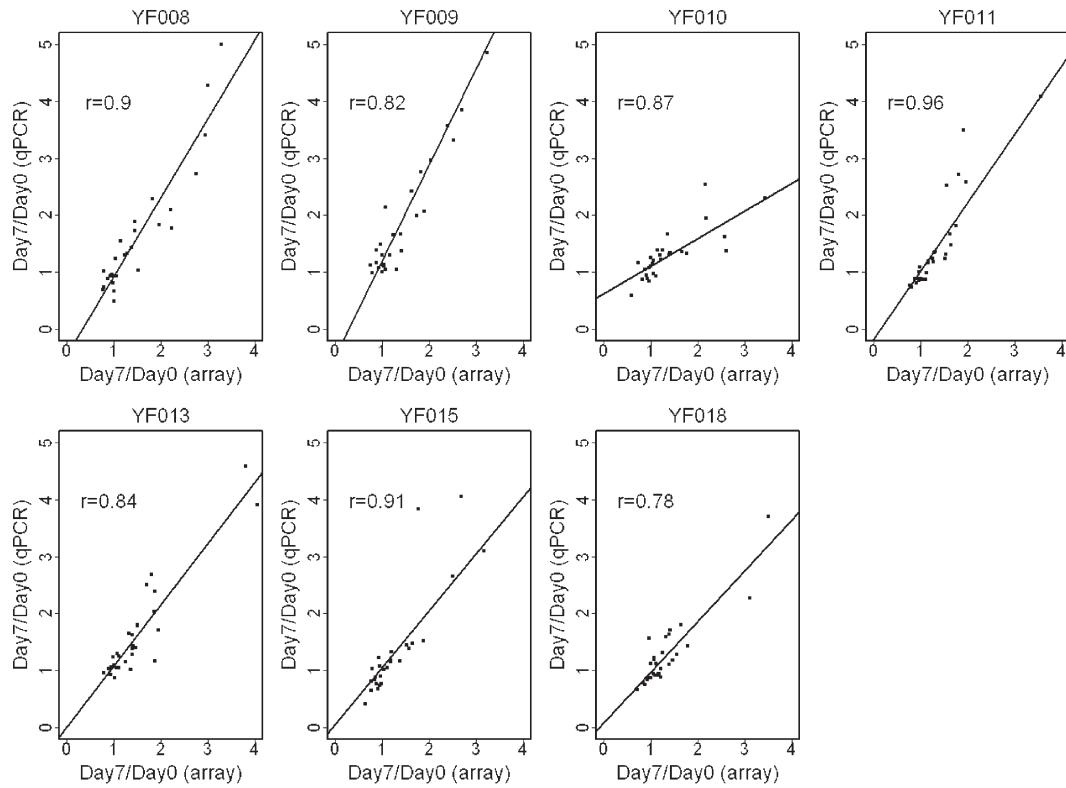


Figure S2. Correlation of gene expression, at day7/day0, showing fold change between Illumina array and qPCR data (Montreal cohort), using the common genes between the Illumina probe set and the qPCR gene list. r represents the Spearman correlation coefficient.

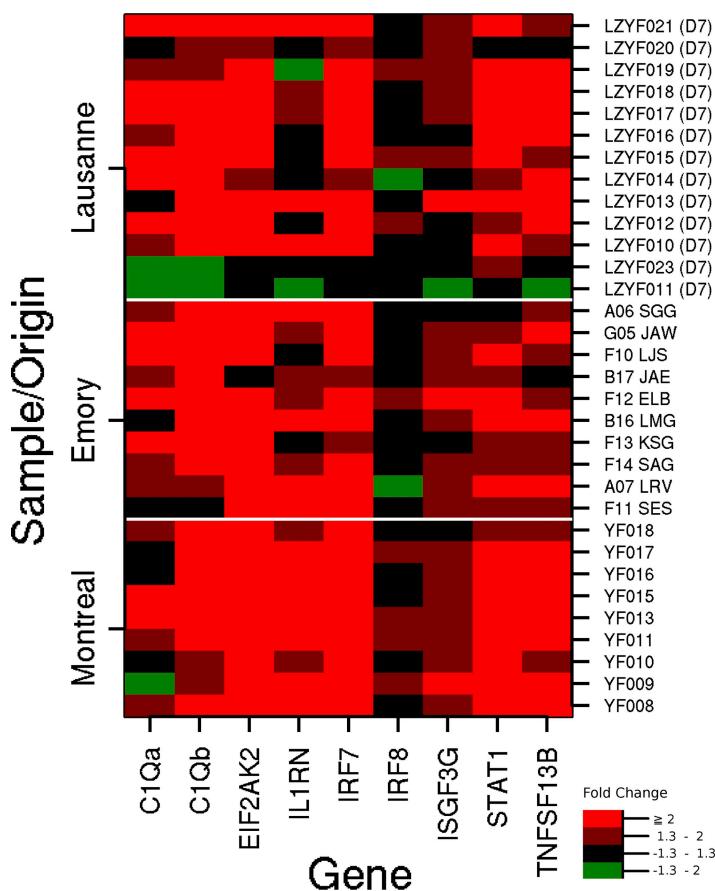


Figure S3. Heat map of fold change gene expression (all 43 genes tested) between day 0 and day 3 or 7 after YF17D vaccination as measured by qPCR. All fold changes reported for the Montreal and the Emory data are between day 0 and 7; for the Lausanne data, the sample labels indicate D3 or D7 for day 3 or 7, respectively.

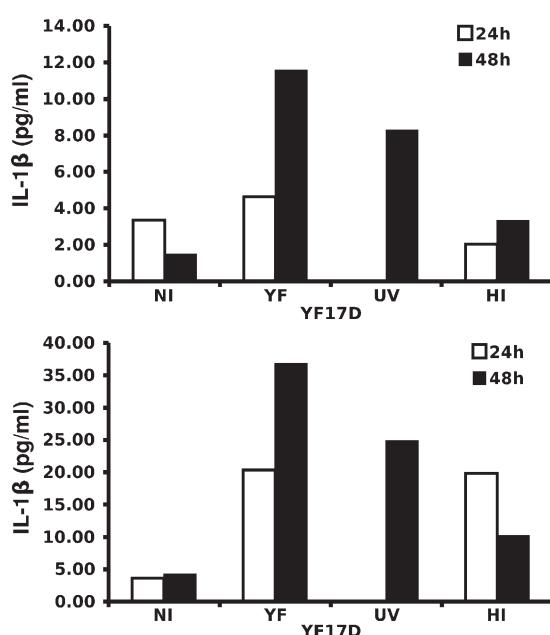


Figure S4. YF17D virus induces IL-1 β production by DCs. Monocyte-derived DCs were generated and incubated with live (YF), UV-inactivated (UV), or heat-inactivated (HI) YF17D. NI, noninfected cells. After 24 or 48 h, the supernatants were harvested and the levels of IL-1 β secreted by the cells were determined by ELISA. In both experiments, there is no 24 h sample for DCs incubated with UV-attenuated virus. This depicts the results from two representatives out of three separate experiments. The results for the third experiment are shown in Fig. 5 b.

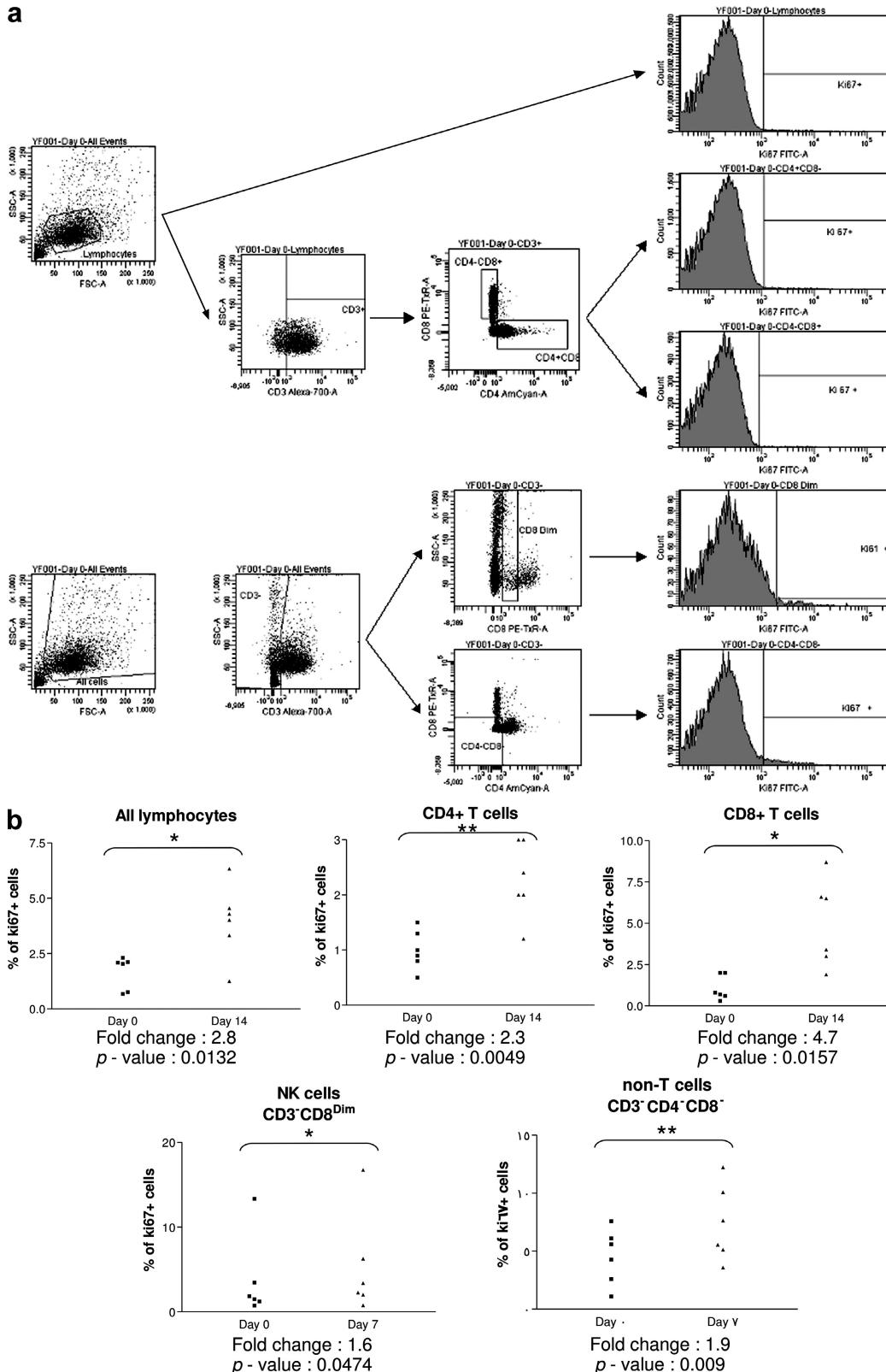


Figure S5. Analysis of Ki67 expression in different subsets of PBMCs. (a) Gating strategy to identify lymphocytes, CD4⁺ T cells, CD8⁺ T cells, NK cells (CD3⁻CD8^{Dim}) and non-T cells (CD3⁻CD4⁻CD8⁻) by flow cytometry. (b-f) PBMCs sampled at day 0, 3, 7, 10, 14, and 28 after vaccination from 6 volunteers were stained with anti-Ki67 and other specific antibodies to identify the distinct cell subsets described in a. Significant percentages of Ki67-positive cells in each subset were then analyzed by a paired Student's *t* test. Data for the most significant time points are presented. Each point represents individual volunteer. *P < 0.05, **P < 0.01.

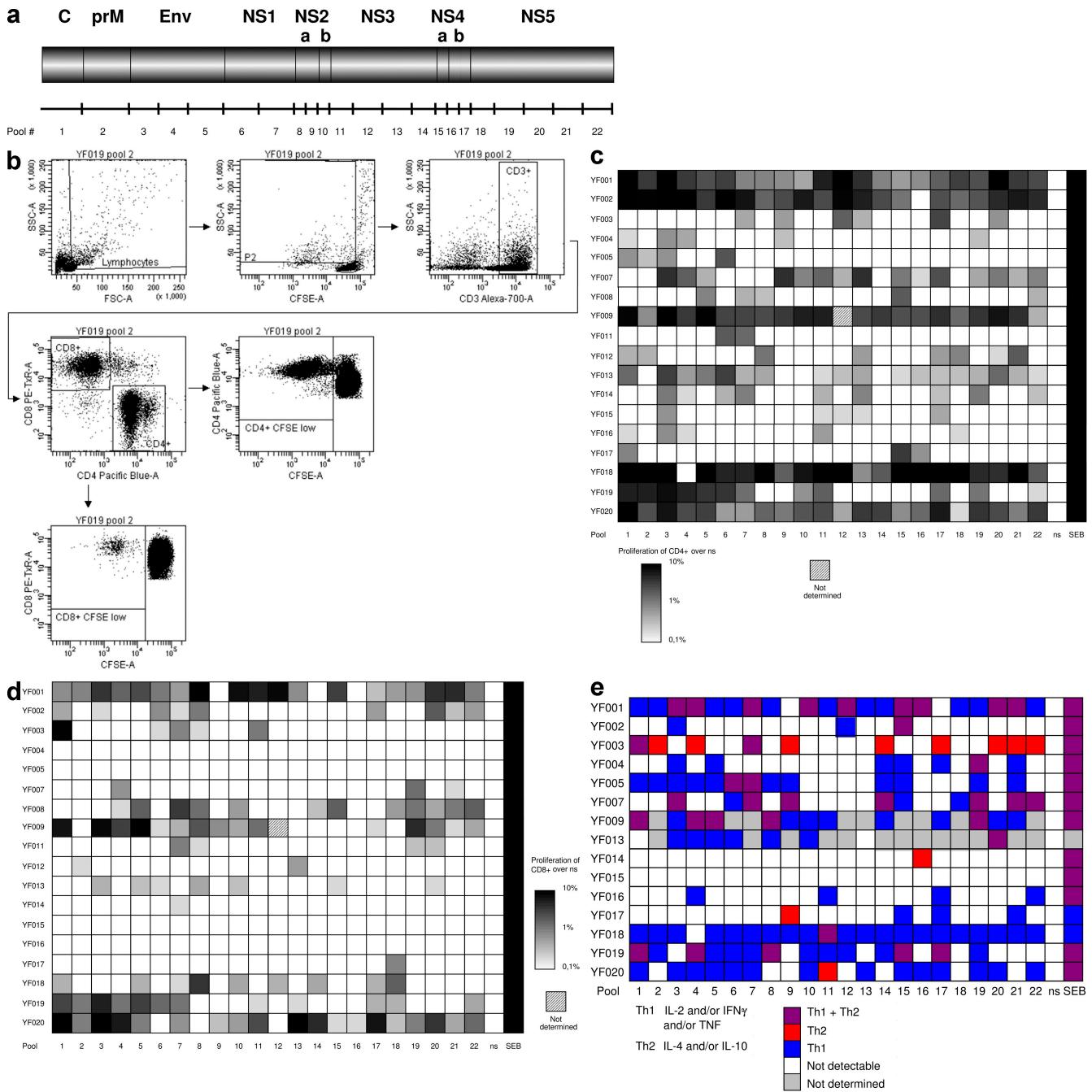


Figure S6. YF17D vaccination induces antigen-specific CD4 $^{+}$ and CD8 $^{+}$ T cell responses. (a) Schematic representation of the 22 YF17D-derived peptide pools used in this study. A total of 851 overlapping (by 11 amino acids) peptides, spanning the entire YF17D proteome, were obtained from the Emery Vaccine Center, Atlanta. These 15-mer peptides were grouped in 22 pools (containing 28–46 peptides each), according to the YF17D protein they were derived from. PBMCs from 18 volunteers from day 60 after vaccination were labeled with CFSE and stimulated for 6 d with the YF17D-derived peptide pools, and then analyzed by FACS for their proliferative response. The gating strategy is described in b. (c and d) The heat maps represent the percentage of cell proliferation over background for CD4 $^{+}$ T cells and CD8 $^{+}$ T cells, respectively. Positive pools were defined as pools stimulating $\geq 0.2\%$ proliferation over nonstimulated values. (e) At 24 h of culture, supernatants were analyzed by CBA to determine the Th1/Th2 cytokine secretion profile of PBMCs from each volunteer, in response to each peptide pool. The heat maps represent the data for the same six volunteers. The Th1/Th2 profiles determined this way for all the volunteers and pools are shown in e.

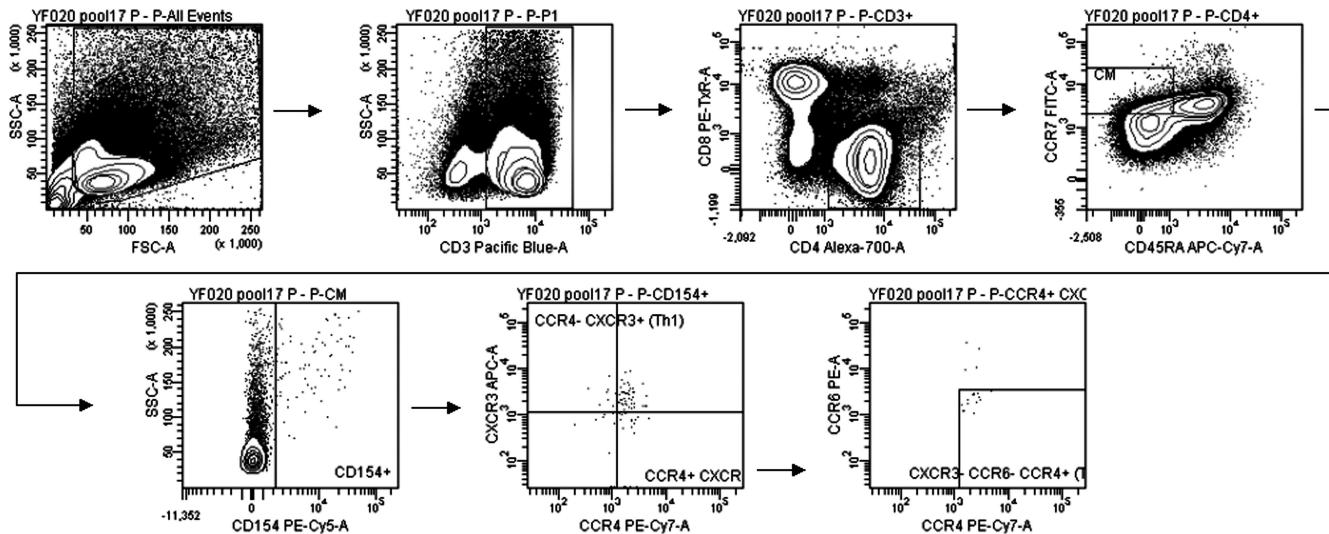


Figure S7. Gating strategy used to identify central memory Th1 and Th2 cells by flow cytometry. PBMCs from vaccinated volunteers (day 365 after vaccination) were stimulated and restimulated with immunostimulatory YF17D-derived peptide pools. Cells were harvested and stained for flow cytometry with antibodies against CD3, CD4, CD8, CCR7, CD45RA, CD154, CXCR3, CCR4, and CCR6. CD3⁺CD4⁺ cells (T helper cells) that do not express CD45RA but are positive for CCR7 (central memory T helper cells) were first identified. Of those, the antigen-specific cells (CD154⁺) were gated on, and Th1 cells were identified as being CXCR3⁺ CCR4⁻. Th2 cells were identified as CXCR3⁻CCR4⁺CCR6⁻.

Supplemental Document 1: YF17D vaccination regulates the transcription of numerous genes in total blood cells. Volunteers were vaccinated with YF17D and their total blood was collected at Days 0, 3, 7, 10, 14, 28 and 60 post-vaccination. Total RNA was isolated from the blood samples, amplified and hybridized to Illumina Human RefSeq-8 v2. Samples from 11-15 volunteers per time point were used for analysis. This list enumerates all the modulated genes with a fold change value < -1.3 or > 1.3 (time point compared to Day 0), with or without a p value < 0.05.

ProbeID	Symbol	NCBI Gene symbol	P-value						Fold change						Description		Ontology	
			D3/D0	D7/D0	D10/D0	D14/D0	D28/D0	D60/D0	D3/D0	D7/D0	D10/D0	D14/D0	D28/D0	D60/D0				
6620711	RSA2D	RSA2D	-6E-11	8E-15	1E-08	0.753599	0.0943	0.19702	8.37	15.97	5.38	1.06	1.61	1.48	radical S-adenosyl methionine domain containing 2	catalytic activity		
7200258	IFH4	IFH4	-6E-11	1E-16	1E-08	0.57246	0.0541	0.19358	9.21	15.84	4.92	1.05	1.6	1.38	interferon-induced protein 44-like			
101038	ISG15	ISG15	-6E-11	1E-16	1E-08	0.57246	0.0541	0.19358	9.21	15.84	4.92	1.05	1.6	1.38	interferon-induced protein 44	immune response		
5870221	IFI44	IFI44	-5E-11	1E-16	1E-08	0.391746	0.0813	0.58861	9.34	9.67	3.92	-1.02	1.65	1.37	interferon-induced protein 44	response to virus		
1780632	IFI11	IFI11	-6E-10	4E-13	4E-06	0.59085	0.0507	0.24084	5.78	9.41	3.45	-1.01	1.63	1.38	interferon-induced protein with tetrapeptide repeats 1	immune response		
4220436	OAS3	OAS3	-2E-10	3E-16	4E-07	0.5902	0.0766	0.42464	4.73	8.37	3.02	1.12	1.46	1.40	2-5'-oligoadenylate synthetase 3, 100kDa	immune response		
1710259	HERC5	HERC5	-6E-09	5E-13	3E-05	0.91391	0.1124	0.23469	3.57	6.8	2.45	-1.02	1.41	1.32	helicase domain and RLD 5	ubiquitin cycle		
2690452	IFI3	IFI3	-2E-09	1E-12	1E-07	0.59062	0.0741	0.27195	3.87	6.39	3.03	-1.12	1.48	1.29	interferon-induced protein with tetrapeptide repeats 3	immune response		
2490325	LY6G	LY6G	-5E-10	1E-12	1E-07	0.59074	0.0748	0.42626	3.87	6.21	3.50	1.45	1.45	1.15	lymphocyte antigen 6 complex, locus E	defense response		
62063	EPSTI1	EPSTI1	-1E-09	1E-12	1E-07	0.59077	0.0748	0.42626	3.87	6.21	3.50	1.24	1.45	1.22	EPSTI1	defense response		
4210291	IFI3M	IFI3M	-1E-09	1E-08	7E-06	0.59341	0.0546	0.42638	4.51	5.9	2.22	-1.15	1.45	1.35	interferon induced transmembrane protein 3	immune response		
5220477	IFI27	IFI27	-1E-09	1E-10	4E-05	0.7515	0.5397	1.302	5.96	4.61	1.08	1.16	1.00	interferon, alpha-inducible protein 27	immune response			
3940731	OAS1	OAS1	-9E-11	2E-16	2E-07	0.39457	0.1287	0.58576	3.76	5.64	2.55	1.16	1.30	1.30	2-5'-oligoadenylate synthetase 1, 40kDa	response to virus		
6370035	OASL	OASL	-7E-09	1E-13	7E-06	0.39222	0.0116	0.25716	5.19	5.58	2.42	1.18	1.65	1.27	2-5'-oligoadenylate synthetase-like	immune response		
2630110	MX1	MX1	-1E-10	1E-15	1E-08	0.43332	0.0498	0.60598	3.34	5.2	2.06	1.14	1.36	1.28	influenza influenza A virus) resistance 1, interferon-inducible protein p	response to virus		
4820725	HES4	HES4	-3E-09	1E-11	1E-08	0.59071	0.0507	0.35346	2.46	5.22	2.16	1.12	1.23	1.29	hair and enhancer of 3 complex	regulation of transcription		
3700243	OAS2	OAS2	-6E-09	3E-16	2E-06	0.40547	0.2743	0.289	2.71	4.98	2.08	1.14	1.18	1.19	interferon-induced protein with tetrapeptide repeats 1	olfaction	sensory perception of sound	
1740341	BIRC4BP	XAF1	-1E-10	1E-13	1E-08	0.89832	0.1841	0.03054	2.43	5.25	1.99	1.02	1.24	1.15	XMAP associated factor 1			
1240754	OAS2	OAS2	-6E-09	3E-16	2E-06	0.40547	0.2743	0.289	2.71	4.98	2.08	1.14	1.18	1.19	2-5'-oligoadenylate synthetase 2, 69kDa	immune response		
4390575	SERPING1	SERPING1	-7E-07	1E-09	1E-06	0.87889	0.0562	0.561	2.68	4.93	2.41	1.03	1.42	1.47	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	complement activation, classical pathway		
5810709	DNAPTP6	LCC26010	-1E-06	1E-14	1E-06	0.00016	0.93466	0.2791	2.23	4.36	1.77	1.01	1.18	1.20	DNA polymerase-transactivated protein 6			
6760048	MT2A	MT2A	-6E-07	9E-13	1E-05	0.70676	0.04784	0.27484	2.27	3.73	1.94	1.06	1.22	1.12	metallothionein 2A	copper ion homeostasis		
3330707	HERC6	HERC6	-6E-07	9E-16	1E-05	0.75974	0.0759	0.23493	2.10	3.71	1.82	1.06	1.25	1.17	helicase domain and RLD 6	ubiquitin cycle		
3303242	IFI27	IFI27	-6E-07	1E-12	1E-05	0.75974	0.0759	0.23493	2.10	3.71	1.82	1.06	1.25	1.17	interferon-induced protein with tetrapeptide repeats 2	immune response		
4040532	OAS1	OAS1	-6E-08	1E-01	1E-06	0.00064	0.93664	0.65427	3.769	4.718	2.08	1.05	1.25	1.15	2-5'-oligoadenylate synthetase 1, 40kDa	response to virus		
5870047	IRF7	IRF7	-2E-07	4E-14	1E-06	0.00012	0.75772	0.1313	0.36153	2.20	3.54	1.63	-1.04	1.21	1.13	interferon regulatory factor 7	passive viral induction of host immune response	
430021	IFI3	IFI3	-6E-08	1E-06	1E-05	0.0051	0.70952	0.6474	3.5289	3.31	1.92	-1.09	1.12	1.18	interferon-induced protein with tetrapeptide repeats 3	immune response		
1190349	Eif2AK2	Eif2AK2	-6E-07	2E-12	1E-06	0.00018	0.75682	0.1511	0.25519	1.77	2.08	1.72	-1.06	1.22	1.19	eukaryotic translation initiation factor 2-alpha kinase 2	immune response	
5420215	SAMD9L	SAMD9L	-6E-07	3E-11	1E-05	0.67948	0.6502	0.5822	2.11	3.37	1.86	-1.07	1.07	1.27	sterile alpha motif domain containing 9-like			
4503272	OAS2	OAS2	-6E-07	1E-05	1E-05	0.69798	0.0785	0.219	2.18	3.33	1.72	1.02	1.11	1.22	2-5'-oligoadenylate synthetase 2, 69kDa	immune response		
5100434	IFI1	IFI1	-6E-07	1E-09	1E-06	0.00019	0.56539	0.6177	0.3309	2.29	3.35	1.86	1.02	1.11	1.23	interferon-induced protein with tetrapeptide repeats 35	immune response	
2100308	IFI1	IFI1	-6E-07	1E-09	1E-06	0.00019	0.56539	0.6177	0.3309	2.29	3.35	1.86	1.02	1.11	1.23	interferon-induced protein with tetrapeptide repeats 35	immune response	
2350377	PRIC285	PRIC285	-2E-07	1E-12	1E-06	0.00043	0.91942	0.114	0.1002	1.78	2.83	1.38	-1.01	1.22	1.25	erccosomal proliferator-activated receptor α interacting complex 28	regulation of transcription	
1260681	TIMM10	TIMM10	-1E-06	1E-13	1E-05	0.7277	0.4205	0.06082	1.85	2.50	1.66	1.04	1.10	1.23	hypothetical protein	FLJ20305	nucleic acid binding	
3830041	IFI3	IFI3	-7E-07	1E-09	1E-06	0.00097	0.90463	0.4649	0.19801	1.65	2.56	1.62	1.01	1.14	1.28	interferon-induced protein with tetrapeptide repeats 3	immune response	
4920719	TRIM22	TRIM22	-6E-07	1E-11	1E-05	0.58569	0.6672	0.3558	1.78	2.63	1.82	-1.07	1.05	1.13	tripartite motif-containing 22	response to virus		
6260215	GPR1	GPR1	-6E-08	1E-07	1E-05	0.57628	0.4179	0.20911	1.54	2.56	1.07	-1.08	1.22	1.07	guanylate binding protein 1, interferon-inducible 67kDa	immune response		
770364	MT1A	MT1A	-1E-08	1E-10	1E-05	0.47426	0.2234	0.56568	1.97	3.09	1.71	1.17	1.08	1.08	metallothionein 1A	metal ion binding		
4590035	LAP3	LAP3	-6E-08	1E-06	1E-05	0.58465	0.75608	0.14698	1.74	2.08	1.56	-1.09	1.05	1.25	leucine-rich aminopeptidase 3	protein metabolism		
316274	PARP9	PARP9	-6E-08	1E-03	1E-05	0.46458	0.3918	0.41662	1.60	2.43	1.80	-1.19	1.11	1.12	poly (ADP-ribose) polymerase family, member 9	protein amino acid ADP-ribosylation		
4180546	TIMM10	TIMM10	-1E-06	1E-05	1E-05	0.59303	0.8933	0.35464	1.38	2.33	1.75	1.01	1.02	1.14	translocase of inner mitochondrial membrane 10 homolog	protein import into mitochondrial inner membrane		
5960717	STAT2	STAT2	-9E-10	4E-13	4E-06	0.48414	0.3137	0.04042	1.51	2.31	1.49	-1.07	1.10	1.23	signal transducer and activator of transcription 2, 113kDa	response to virus		
3840376	DDX58	DDX58	-1E-06	1E-09	1E-05	0.02163	0.72912	0.56062	0.6892	1.68	2.59	1.33	-1.05	1.10	1.18	DEAD box-Gli3bp-Asp box peptide 58	nucleotide binding	
2320070	CTSL	CTSL	-6E-08	1E-09	1E-05	0.00597	0.22912	0.50626	0.6892	1.68	2.59	1.33	-1.06	1.10	1.18	cathepsin L	proteolysis and peptidolysis	
4203167	SCD2	SCD2	-6E-08	1E-09	1E-05	0.02915	0.6315	0.7	0.68902	1.58	2.25	1.32	-1.04	1.12	1.19	junctional plakophilin	cell junction	
4060674	IL1RN	IL1RN	-6E-08	1E-09	1E-05	0.00884	0.3285	0.03641	0.5713	1.67	2.22	1.40	-1.03	1.03	1.09	SCC catenin, alpha 1, receptor antagonist	inflammation	
1070564	MABP	MABP	-6E-08	1E-09	1E-05	0.06179	0.05726	0.08062	0.76966	1.52	2.18	1.25	-1.27	1.03	1.27	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B	regulation of transcription	
1850538	LGALS3B	LGALS3B	-2E-08	1E-09	1E-05	0.08945	0.28527	0.25201	1.50	2.1	1.33	1.10	1.12	1.12	lectin, galactose-binding, soluble 1	protein amino acid ADP-ribosylation		
6290672	BLVRA	BLVRA	-6E-08	1E-09	1E-05	0.00043	0.02442	0.4402	1.47	2.07	1.59	-1.02	1.07	1.22	lectin, galactose-binding, A	electroneutral transport		
1850093	TNFSF10	TNFSF10	-6E-08	1E-07	1E-05	0.00051	0.2554	0.42337	1.43	2.05	1.54	-1.16	1.14	1.16	tumor necrosis factor [ligand] superfamily, member 10	positive regulation of 1-kappaB kinase/NF-kappaB cascade		
3310243	TOR1B	TOR1B	-1E-08	1E-09	1E-05	0.03159	0.291	0.6019	1.36	1.94	1.20	-1.06	1.10	1.15	torsin family 1, member B	protein folding		
5960035	GPRB1	GPRB1	-3E-08	1E-07	1E-05	0.04729	0.60603	0.06591	0.0571	1.67	1.94	1.25	-1.06	1.24	1.28	G-protein coupled receptor signaling pathway		
60482	IFI6	IFI6	-6E-08	1E-07	1E-05	0.02166	0.42771	0.6784	0.36491	1.45	1.93	1.32	-1.04	1.12	1.12	interferon, gamma-inducible protein 16	response to virus, monocytic differentiation	
5720743	PART10	PART10	-6E-08	1E-07	1E-05	0.02068	0.42771	0.6784	0.36491	1.45	1.93	1.32	-1.04	1.12	1.12	poly (ADP-ribose) polymerase family, member 10	protein amino acid ADP-ribosylation	
4390500	EPB41	EPB41	-6E-08	1E-07	1E-05	0.02059	0.42771	0.6784	0.36491	1.45	1.93	1.32	-1.04	1.12	1.12	epithelial growth factor receptor-like 1	cellular proliferation	
6840750	FAM464A	FAM464A	-6E-08	1E-10	1E-05	0.00043	0.51024	0.20343	1.34	1.84	1.24	-1.06	1.11	1.15	family with sequence similarity 46, member A	apoptosis		
6840750	AUD1	AUD1	-6E-08	1E-07	1E-05	0.00043	0.51024	0.20343	1.34	1.84	1.24	-1.07	1.12	1.18	AXIN1 up-regulated 1	apoptosis		
2500045	FLJ128	FLJ128	-6E-08	1E-														

3360246	TMEM51	TMEM51	0.1055	TFE09	0.1088	0.78278	0.6955	0.14705	1.17	1.52	1.16	1.03	1.05	1.17	transmembrane protein 51	integral to membrane		
6040539	AIM2	AIM2	0.00085	DE004	0.00053	0.8228	0.3704	0.1113	1.26	1.27	1.03	1.12	1.26	1.15	absent in melanoma 2	immune response		
5570181	SP140	SP140	0.00085	DE007	0.00073	0.00676	0.1612	0.07904	1.25	1.51	1.31	1.25	1.12	1.17	SP140 nuclear body protein	regulation of transcription, defense response		
510128	DUSP5	DUSP5	0.0141	DE06	0.01623	0.0104	0.8462	0.38725	1.27	1.50	1.25	1.28	-1.02	1.09	dual specificity phosphatase 5	protein amino acid dephosphorylation		
150703	ATF3	ATF3	0.5151	DE09	0.02671	1	0.8223	0.18728	1.05	1.60	1.16	1.00	1.02	1.11	activating transcription factor 3	regulation of transcription		
20110	UBE2L6	UBE2L6	0.0928	DE047	0.0947	0.29395	0.52579	0.8238	0.68416	1.31	1.60	1.17	-1.11	-1.04	1.07	ubiquitin-conjugating enzyme E2L 6	ubiquitin cycle	
5560280	CERCR1	CERCR1	0.0001	DE06	0.35901	0.63524	0.4838	0.02487	1.59	1.59	1.08	1.02	1.07	1.26	cat eye syndrome chromosome region, candidate 1	purine ribonucleotide monophosphate biosynthesis		
5390058	NYSCOR18	NYSCOR18	0.0001	DE06	0.10783	0.10783	0.10783	0.10783	0.10783	1.26	1.26	1.20	1.14	1.14	1.15	transmembrane protein 51	integral to membrane	
1410521	RRAS	RRAS	0.0001	DE06	0.00049	0.05557	0.05557	0.05557	0.05557	0.05557	1.26	1.26	1.01	1.10	1.13	1.13	related RAS oncogene homolog	intracellular protein transport
2370240	TAP2	TAP2	0.0481	DE06	0.00017	0.47496	0.12	0.05548	1.19	1.56	1.29	1.06	1.14	1.20	transporter 2, ATP-binding cassette, sub-family B	intracellular protein transport		
6270725	HAVCR2	HAVCR2	0.00002	DE08	0.00032	0.5152	0.0825	0.02167	1.34	1.58	1.23	1.05	1.14	1.21	hepatitis A virus cellular receptor 2	receptor activity		
4060100	MICB	MICB	0.0028	DE10	0.005	0.32478	0.07	0.03644	1.26	1.58	1.29	1.06	1.12	1.15	MHC class I polypeptide-related sequence B	antigen presentation, cellular defense response		
1010343	TRIM21	TRIM21	0.0079	DE05	0.00692	0.88163	0.1642	0.10302	1.32	1.57	1.30	1.02	1.15	1.12	tripartite motif-containing 21	metal ion binding		
6510024	ISGF3G	ISGF3G	0.0001	DE09	0.00012	0.86995	0.05766	0.157	1.28	1.06	1.15	1.15	1.15	1.15	interferon-stimulated transcription factor 3, gamma 48kDa	response to virus		
1101023	BCL2	BCL2	0.0128	DE06	0.0001	0.4851	0.05557	0.05557	0.05557	0.05557	1.08	1.08	1.00	1.13	1.13	1.13	basis for leptomeningeal carcinomatosis	regulation of transcription
1103038	ADAR	ADAR	0.0001	DE09	0.00053	0.05105	0.0469	0.19041	1.23	1.25	1.15	1.04	1.05	1.10	adenosine deaminase, RNA-specific	mRNA processing		
6590564	TCN2	TCN2	0.0008	DE08	0.1166	1	0.3104	0.20254	1.04	1.55	1.11	1.00	1.07	1.10	transcobalamin II, macrocytic anemia	ion transport		
670180	ZNF91X1	ZNF91X1	0.0233	DE06	0.07245	0.046821	0.1804	0.08146	1.21	1.54	1.02	1.06	1.12	1.17	zinc finger, NXF1-type containing 1	regulation of transcription		
5130735	C9orf91	C9orf91	0.00028	DE10	0.00232	0.99567	0.1688	0.00629	1.21	1.54	1.20	-1.00	1.09	1.20	chromosome 9 open reading frame 91	activation of transcription		
6040358	ATF5	ATF5	0.034	DE08	0.0002	0.96546	0.0594	0.5762	1.26	1.54	1.05	1.00	-1.01	1.07	activating transcription factor 5	regulation of cell cycle		
3290091	NAGK	NAGK	0.0001	DE08	0.00012	0.66874	0.058	0.02555	1.30	1.54	1.17	-1.03	1.14	1.19	N-acetylglucosamine kinase	N-acetylglucosamine metabolism		
5390058	NYSCOR18	NYSCOR18	0.0001	DE06	0.0001	0.07083	0.07083	0.07083	0.07083	0.07083	1.26	1.26	1.00	1.13	1.13	1.13	transmembrane protein 51	integral to membrane
5870138	TTTH3	TTTH3	0.0001	DE06	0.00071	0.56202	0.118	0.05557	1.26	1.26	1.14	1.06	1.14	1.23	twenty homeobox	response to virus		
6229433	OSBP1	OSBP1	0.0001	DE07	0.0003	0.4656	0.2251	0.07026	1.26	1.53	1.20	1.05	1.09	1.03	osmolyte binding protein-like 5	steroid metabolism		
5582092	LOC441168	LOC441168	0.0793	DE09	0.00315	0.15637	0.0715	0.07159	1.30	1.53	1.34	-1.24	-1.01	1.34	hypothetical protein LOC441168	regulation of transcription		
3450328	GRN	GRN	0.0005	DE02	0.14692	0.18964	0.0823	0.18303	1.48	1.53	1.16	1.00	1.21	1.17	granulin	cytokine activity		
4590189	SIDT2	SIDT2	0.0005	DE05	0.31982	0.05267	0.4935	0.05497	1.40	1.52	1.09	1.00	1.06	1.21	SID1 transmembrane family member 2	integral to membrane		
2900463	GNLY	GNLY	0.0001	DE03	0.2318	0.13501	0.722	0.8924	1.22	1.54	1.21	1.20	-1.06	1.06	granulin	defense response to bacteria		
4804436	PTEN	PTEN	0.0001	DE06	0.00021	0.18819	0.0814	0.04628	1.26	1.54	1.25	1.05	1.04	1.05	perform 1 (pore-forming protein)	virus-infected cell apoptosis		
1010347	PSME2	PSME2	0.0001	DE06	0.0001	0.37478	0.05557	0.05557	0.05557	0.05557	1.26	1.26	1.04	1.15	1.15	1.15	proteasome, some subunit 2	protein transport
3120612	CHMP5	CHMP5	0.0022	DE08	0.00054	0.41456	0.6261	0.13365	1.24	1.51	1.30	-1.01	1.06	1.23	chaperone-modifying protein 5	protein transport		
6590736	SRC	SRC	0.0001	DE06	0.00033	0.93441	0.05557	0.05557	0.05557	0.05557	1.26	1.26	1.15	1.15	1.15	1.15	v-src sarcoma (Schmidt-Ruppin A) viral oncogene homolog	protein amino acid phosphorylation
2320037	ANKFY1	ANKFY1	0.0043	DE07	0.04429	0.7391	0.7832	0.15602	1.16	1.51	1.05	-1.02	1.02	1.11	ankyrin repeat and FVE domain containing 1	endocytosis, metal ion binding		
4780220	CYBB	CYBB	0.0008	DE06	0.01841	0.27444	0.12	0.0105	1.26	1.50	1.20	-1.09	1.09	1.33	cytchrome b-245, beta polypeptide (chronic granulomatous disease)	ion transport		
1700019	ISG20	ISG20	0.0001	DE04	0.12404	0.07167	0.12416	0.07155	0.63335	1.09	1.50	1.11	1.03	1.08	1.08	interferon stimulated exonuclease gene 20kDa	cell proliferation, response to virus	
7565441	LMO2	LMO2	0.0001	DE06	0.00051	0.25051	0.05557	0.05557	0.05557	0.05557	1.26	1.26	1.04	1.15	1.15	1.15	complement component 3a receptor 1	cellular defense response, complement component C3a receptor activity
1260048	FNS	C11orf75	0.00087	DE06	0.0028	0.45141	0.4687	0.04837	1.26	1.50	1.18	-1.08	1.08	1.25	LM domain, domain 2 (homophilic-like)	metal ion binding		
2940653	TTC12A1	TTC12A1	0.1202	DE08	0.13626	0.05283	0.4628	0.04977	1.10	1.49	1.09	1.01	1.05	1.07	tetratricopeptide repeat domain 21A	F5N protein		
5560273	LILRB1	LILRB1	0.00147	DE06	0.12653	0.54640	0.5024	0.15117	1.26	1.54	1.13	-1.06	1.06	1.14	leukocyte immunoglobulin-like receptor, subfamily B, member 1	binding		
580445	NEXN	NEXN	0.0107	DE10	0.01038	0.87897	0.884	0.04072	1.09	1.48	1.14	-1.01	-1.01	1.05	nefelin (F5 binding protein)	response to virus		
5050086	CSFR1	CSFR1	0.00005	DE06	0.0006	0.5012	0.27352	0.9607	0.80901	1.49	1.48	1.07	-1.13	-1.01	1.23	transferrin	muscle development	
3190200	AGLN	AGLN	0.0001	DE06	0.0001	0.8223	0.05557	0.05557	0.05557	0.05557	1.26	1.26	1.04	1.15	1.15	1.15	transferrin	muscle development
4595458	RPL32	RPL32	0.0001	DE06	0.0001	0.77443	0.4518	0.07234	1.26	1.50	1.14	1.02	1.06	1.09	ribosomal protein L32	positive regulation of cell proliferation		
4810204	CYSLTR1	CYSLTR1	0.00001	DE05	0.00013	0.98554	0.1192	0.1203	0.132	1.42	1.46	1.00	1.05	1.15	1.12	cysteinyl leukotriene receptor 1	defense response, leukotriene receptor activity	
2630189	FFAR2	FFAR2	0.0002	DE03	0.15892	0.26429	0.147	0.03689	1.30	1.47	1.18	-1.06	1.19	-1.01	fast fatty acid receptor 2	signal transduction		
2260593	ASCL2	ASCL2	0.00016	DE06	0.01664	0.79687	0.1982	0.05487	1.27	1.47	1.20	-1.02	1.11	1.05	achaeloate complex-like 2	regulation of transcription		
5550195	CST3	CST3	0.00035	DE05	0.0582	0.99971	0.0964	0.07822	1.39	1.47	1.17	1.06	1.15	1.18	cystatin C (amyloid angiopathy and cerebral hemorrhage)	cysteine protease inhibitor activity		
4767030	VAMP5	VAMP5	0.0703	DE04	0.00045	0.41799	0.5678	0.09922	1.00	1.46	1.03	1.06	1.06	1.20	vesicle-associated membrane protein 5 (myoelin)	cell differentiation		
2907435	FRMD3	FRMD3	0.0001	DE06	0.0001	0.39505	0.04874	0.04874	0.04874	0.04874	1.26	1.26	1.03	1.15	1.15	1.15	frizzled-like receptor 3	positive regulation of F4 kappaB kinase/NF-kappaB cascade
1260437	FRMD3	FRMD3	0.0001	DE06	0.0001	0.38247	0.04874	0.04874	0.04874	0.04874	1.26	1.26	1.02	1.12	1.12	1.12	frizzled-like receptor 3	positive regulation of F4 kappaB kinase/NF-kappaB cascade
840750	PML	PML	0.0589	DE08	0.0055	0.39774	0.8774	0.38928	1.12	1.44	1.13	-1.00	1.02	1.05	promyelocytic leukemia	induction of apoptosis		
830162	SCOTIN	SCOTIN	0.0002	DE06	0.00178	0.44386	0.0179	0.02053	1.32	1.44	1.17	1.06	1.19	1.01	scotin	positive regulation of F4 kappaB kinase/NF-kappaB cascade		
8402523	PLAC8	PLAC8	0.0128	DE05	0.04333	0.37181	0.09309	0.07863	1.26	1.50	1.17	-1.04	1.06	1.02	placenta-specific 8	lipoprotein receptor-like 2		
5590216	RG312	RG312	0.0001	DE06	0.0001	0.40343	0.32426	0.05756	0.05881	0.05881	1.26	1.26	1.02	1.15	1.15	1.15	GTP cyclohydrolase (copper-responsive dynatrin)	nitric oxide synthase
2140141	SNTB1	SNTB1	0.0001	DE07	0.00079	0.75330	0.33144	0.15656	1.16	1.36	1.16	-1.02	1.06	1.15	beta 1 integrin-associated protein 1, 59kDa, basic comp.	muscle contraction, actin binding		
2340349	HDL-DR8	HDL-DR8	0.0444	DE07	0.22733	0.74854	0.2592	0.18262	1.26	1.51	1.18	-1.02	1.12	1.16	capase 3, apoptosis-related cysteine peptidase	regulation of apoptosis		
5080566	CASP5	CASP5	0.1196	DE07	0.02277	0.83787	0.2857	0.18262	1.26	1.50	1.18	-1.02	1.12	1.16	death effector protease	regulation of apoptosis		
6290358	FLJ25084	FLJ25084	0.00029	DE03	0.00011	0.37944	0.04948	0.04676	1.26	1.39	1.01	1.23	1.09	1.09	SkA3Poric Protease	fatty acid biosynthesis		
1090064	CD74	CD74	0.0744	DE01	0.00024	0.07247	0.281	0.04161	1.05	1.38	1.17	1.14	1.14	1.28	CD74 antigen	cell proliferation, T cell selection, negative regulation of apoptosis		
4040436	DKF2671E19	DKF2671E19	0.00001	DE06	0.00012	0.07245	0.05263	0.05263	0.05263	0.05263	1.26	1.26	1.07	1.17	1.17	1.17	induction of apoptosis by intracellular signals	cellular defense response
5080566	SRBD1	SRBD1	0.0001	DE06	0.0001	0.35798	0.68492	0.1599	0.13141	1.22	1.27	1.10</td						

7400669	HLA-A	HLA-A	00008 02-05	00065 082842 08865 028574 1.21 1.35	1.20 1.12 1.12 1.08	major histocompatibility complex, class I, A	antigen presentation
5690193	GORASP1	GORASP1	00008 02086 065081 071439 04866 027912 1.18 1.35	1.03 -1.02 1.00 1.08	-1.07	poly(A)-specific ribonuclease 1, 65kDa	protein transport
6900367	MARCKS	MARCKS	0.1882 00472 00473 033661 013459 08928 03995 0.114 -1.35	1.09 -1.16 -1.01 1.09	1.09	myristoylated alanine-rich protein kinase C substrate	cell motility
3800427	ALDH3B1	ALDH3B1	0.00008 0.0033 0.92698 0.96361 0.2253 0.37966 1.39 -1.35	-1.01 1.00 1.12 1.02	1.09	aldehyde dehydrogenase 3 family, member B1	metabolism
6040088	MOBK2C	MOBK2C	0.1891 03-05 054337 099786 0.598 0.37568 1.09 1.30	1.04 -1.00 1.03 1.02	1.02	M6CB1, Mps One Binder kinase activator-like 2C	kinase activity
6250576	FLJ36874	PA1L1	0.1392 03-06 026551 0.95046 0.7749 0.08671 1.08 1.33	1.06 -1.00 1.02 1.11	1.11	PLJ36874 protein	signal transduction
2260040	GINS12	GINS12	0.00008 01006 01071 0.59177 0.59205 0.53594 1.24 1.32	1.15 1.03 1.06 1.06	1.06	cleotide binding protein (G protein), gamma transducing activity polypeptide	signal transduction
4000001	ANXA10	ANXA10	0.1252 02-05 0.92730 0.95046 0.612 0.37568 1.24 1.35	1.21 1.04 1.06 1.08	1.24	ANXA10, annexin A10	cell adhesion
1400220	RAF88A	RAF88A	0.1688 01-08 0.00018 0.71739 0.1078 0.07945 1.22 1.35	1.24 1.04 1.02 1.07	1.09	RAB8A, member RAS oncogene family	regulation of transcription
1440408	PPM1K	PPM1K	0.5726 02-05 0.91690 0.37054 0.1381 0.59061 1.04 1.32	1.01 -1.06 -1.11 -1.04	1.04	protein phosphatase 1K (PP2C domain containing)	protein amino acid dephosphorylation
2650228	FLJ20698	FLJ20698	0.03789 0.0111 0.07592 0.84507 0.1859 0.37379 1.19 1.32	1.15 1.02 1.11 -1.03	1.03	hypothetical protein FLJ20698	binding
10070	EMILIN2	EMILIN2	0.0516 0054 0.0084 0.80834 0.56746 0.581 0.04063 1.20 1.32	-1.02 -1.00 1.06 1.24	1.08	elastin microfibril interfacer 2	cell adhesion
5870673	NMI	NMI	0.1849 0.0304 0.0182 0.13169 0.8595 0.82695 1.13 -1.32	1.23 -1.15 1.02 1.04	1.04	N-myc (and STAT) interactor	inflammatory response
1090703	RIPK3	RIPK3	0.0078 03-07 010388 0.58782 0.301 0.1005 1.14 1.32	1.12 1.03 1.14 1.09	1.09	receptor-interacting serine-threonine kinase 3	protein amino acid phosphorylation
5690194	ERBB3	ERBB3	0.00008 01006 01071 0.59177 0.59205 0.53594 1.24 1.32	1.04 1.03 1.06 1.07	1.07	proto-oncogene (prospective oncogene) activator subunit 1	immune response
3130474	HSPC117	C22orf28	0.2685 01-06 0.10597 0.04574 0.5779 0.04465 1.06 1.35	1.08 -1.01 1.11 1.12	1.12	hypothetical protein C22orf28	intracellular transport
5670274	APOL3	APOL3	0.1611 03-06 00005 0.96575 0.2953 0.07042 1.08 1.32	1.20 1.01 1.06 1.17	1.17	apolipoprotein L 3	lipoprotein metabolism
4230538	LDLR	LDLR	0.1174 00001 0.91904 0.42589 0.7671 0.04328 1.11 1.31	1.09 1.05 1.02 1.06	1.06	low density lipoprotein receptor (familial hypercholesterolemia)	lipid metabolism
4490445	SIGLEC5	SIGLEC5	0.0449 0.0141 0.4763 0.59456 0.1038 0.49934 1.24 1.31	1.08 1.06 -1.04 1.08	1.08	sialic acid binding Ig-like lectin 5	cell adhesion
6373628	GNA15	GNA15	0.00004 0.016 0.60315 0.82607 0.1489 0.09119 1.24 1.31	1.04 -1.02 1.13 1.16	1.16	guanine nucleotide binding protein (G protein), alpha 15	protein amino acid ADP-ribosylation
5910762	NPC2	NPC2	0.0028 04-06 00028 0.77816 0.0822 0.0233 1.18 1.31	1.11 1.02 1.10 1.14	1.14	Niemann-Pick disease, type C2	
6801110	SLC16A1	SLC16A1	0.1453 01-06 0.03433 0.97079 0.259 0.23896 1.08 1.35	1.08 -1.00 1.01 1.04	1.04	membrane carrier family 2 (anion exchanger), member 1	ion homeostasis
6840414	NAPA	NAPA	0.00008 02-05 0.92630 0.23482 0.1704 0.0256 1.18 1.31	1.13 -1.06 1.07 1.07	1.07	N-ethylnitroso-sarcosine factor attachment protein, alpha	intracellular transport
4570735	KYNU	KYNU	0.0745 00891 0.27183 0.21684 0.7038 0.04527 1.19 1.31	1.11 -1.13 1.04 1.24	1.24	kyurenimono L (kyurenimono hydrolase)	NAD biosynthesis
1050258	CARD15	NOD2	0.3639 00485 0.08972 0.76716 0.1735 0.03913 1.08 1.35	1.16 -1.04 1.13 1.22	1.22	capsule recruitment domain family, member 15	defense response, regulation of apoptosis
3830544	OGRF	OGRF	0.00044 0.0084 0.35878 0.40181 0.0286 0.16673 1.23 1.31	1.06 1.06 1.17 1.11	1.11	opioid growth factor receptor	regulation of cell growth
7570338	PHACTR2	PHACTR2	0.1774 00002 0.07369 0.84959 0.5293 0.05261 1.09 1.30	1.12 -1.01 1.04 1.05	1.05	phosphatase and actuator regulator 2	actin binding
6960441	KCNMB1	KCNMB1	0.0034 0.0078 0.07373 0.42642 0.1209 0.01818 1.19 1.30	1.09 -1.04 1.06 1.14	1.14	large conductance calcium-activated channel, subfamily M, beta 4	smooth muscle contraction
6801112	SLC16A1	SLC16A1	0.1453 01-06 0.03433 0.97079 0.259 0.23896 1.08 1.35	1.08 -1.00 1.01 1.04	1.04	solute carrier family 2 (anion exchanger), member 6	carbohydrate transport
4020114	USAP3	USAP3	0.1215 01-06 0.03433 0.97079 0.259 0.23896 1.08 1.35	1.08 -1.00 1.02 1.04	1.04	USAP3, USAP3	
5910528	MCMV	MCMV	0.5226 004 00045 0.95008 0.259 0.56065 1.05 1.36	1.26 -1.05 -1.05 1.05	1.05	MCMV, marmosete maintenance deficient 4	regulation of transcription
2360520	ACOT7	ACOT7	0.1736 01-06 0.05 0.046 0.5474 0.81705 1.03 1.32	1.05 -1.04 1.05 1.06	1.06	acyl-CoA thioesterase 7	lipid metabolism
6860477	PRAM1	PRAM1	0.00031 0.0377 0.81928 0.67336 0.0347 0.35845 1.34 1.23	1.02 1.04 1.23 1.17	1.17	PM1_RARA regulatory adaptor molecule 1	
3360400	C19orf10	C19orf10	0.2322 0.0344 0.37214 ##### 0.37214 0.46768 1.10 1.20	1.07 -1.04 1.07 1.06	1.06	chromosome 19 open reading frame 10	
2350026	CERCR	CERCR	0.4381 0.157 0.94572 0.93224 0.980 0.37156 1.14 1.20	1.01 -1.00 1.03 1.12	1.12	cat eye syndrome chromosome region, candidate 6	
5450025	PSD-95	PSD-95	0.00008 0.0042 0.95034 0.95034 0.2182 0.37156 1.14 1.20	1.05 -1.04 1.06 1.05	1.05	thyroperoxidase	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
4076881	CENPF	CENPF	0.1703 01-06 0.02688 0.95034 0.2182 0.37156 1.14 1.20	1.05 -1.04 1.06 1.05	1.05	chromosome 22 open reading frame 18	regulation of transcription
7200156	TNNOCS1	TNNOCS1	0.0801 0.036 0.05124 0.95034 0.2182 0.37156 1.14 1.20	1.05 -1.04 1.06 1.05	1.05	thioredoxin domain containing 5	anti-apoptosis
5670707	TUBG1	TUBG1	0.1023 0011 0.00028 0.3909 0.688 0.02878 1.08 1.21	1.19 -1.04 1.04 1.02	1.02	tubulin, gamma 1	microtubule nucleation
5670040	SDFL2L1	SDFL2L1	0.7851 00008 0.0256 ##### 0.0256 0.4538 0.74611 1.02 1.18	1.22 -1.06 1.05 1.02	1.02	stromal cell-derived factor 2-like 1	hydrolase activity
270068	CDCA7	CDCA7	0.6773 0.156 0.8116 0.8116 0.0391 0.81705 1.03 1.21	1.05 -1.04 1.07 1.07	1.07	cell division cycle associated 7	metal ion binding
5670435	P2RX1	P2RX1	0.1215 01-06 0.03433 0.97079 0.259 0.23896 1.08 1.35	1.03 -1.04 1.07 1.07	1.07	purinergic receptor P2X, ligand-gated ion channel, 1	ion transport
6560239	CDCC45	CDCC45	0.1208 0.106 0.02688 0.95034 0.2182 0.37156 1.14 1.20	1.05 -1.04 1.06 1.05	1.05	L76/PLAUR domain containing 2	
1770360	CCNB2	CCNB2	0.1525 0.008 0.00012 0.888 0.0882 0.101 1.05 1.25	1.15 -1.05 -1.05 1.05	1.05	cell division cycle 5	mitotic chromosome condensation
2060273	TNNOCS1	TNNOCS1	0.0801 0.036 0.05124 0.95034 0.2182 0.37156 1.14 1.20	1.05 -1.04 1.06 1.05	1.05	thioredoxin domain containing 5	regulation of cell cycle
6510275	SRM	SRM	0.1469 0.0493 0.09591 0.6884 0.08019 1.00 1.14	1.11 -1.04 1.06 1.02	1.02	sperrmine synthase	sperrmine biosynthesis
2450603	UBE2C2	UBE2C2	0.946 0.0815 0.0915 0.0915 0.0532 0.0532 1.05 1.20	1.02 -1.00 -1.00 -1.02	1.02	ubiquitin-conjugating enzyme E2C	cyclin catalysis, ubiquitin cycle
3420274	TK1	TK1	0.9845 0.0727 0.00013 ##### 0.00013 0.82657 1.00 1.13	1.29 -1.09 1.01 1.01	1.01	thymidine kinase 1, soluble	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
10458	PTEN	PTEN	0.8915 0.015 0.95034 0.95034 0.0505 0.0505 1.11 1.25	1.01 -1.02 1.01 1.02	1.02	ubiquitin-converting protein PTEN finger domain containing 1	regulation of transcription
5390277	DHFR	DHFR	0.1703 0.113 0.02678 0.02678 0.6802 0.6802 1.05 1.25	1.05 -1.04 1.05 1.05	1.05	proto-oncogene DHFR	electron transport
7230341	MLCS1A	MLCS1A	0.7281 0.0654 0.00011 0.888 0.0882 0.101 1.05 1.25	1.14 -1.05 1.01 1.01	1.01	MLCS1A, myelin basic protein 1	mitotic development
6450672	IGJ	IGJ	0.9393 0.6379 0.03277 ##### 0.03277 0.58537 1.02 1.18	1.05 -1.04 1.01 1.01	1.01	linker protein for immunoglobulin alpha and mu	antigen binding
7550445	CXR3	CXR3	0.5432 0.652 0.13764 0.8086 0.0576 0.0576 1.05 1.25	1.06 -1.04 1.03 1.02	1.02	chemokine	chemotaxis
5220239	STMN1	STMN1	0.8719 0.175 0.00006 0.00006 0.9294 0.9294 1.01 1.25	1.07 -1.04 1.05 1.05	1.05	stathmin	microtubule depolymerization
6280730	FKBP11	FKBP11	0.8366 0.2131 0.07036 ##### 0.07036 0.3647 1.02 1.10	1.04 -1.03 1.05 1.08	1.08	FK506 binding protein 11, 19 kDa	protein folding
5620239	KBP1	KBP1	0.9678 0.0311 0.00008 0.00008 0.6592 0.6592 1.00 1.25	1.08 -1.03 1.04 1.04	1.04	x-box binding protein 1	immune response, regulation of transcription
6560237	PRB1	PRB1	0.7268 0.276 0.00008 0.00008 0.4282 0.4282 1.02 1.25	1.08 -1.03 1.04 1.02	1.02	proto-oncogene PRB1	regulation of apoptosis
5690194	MARCH2	MARCH2	0.0362 0.0809 0.05089 0.05089 0.7671 0.7671 1.11 -1.23	1.09 -1.04 1.04 1.02	1.02	membrane-associated ring finger	protein ubiquitination
3140603	ARRHGP24	ARRHGP24	0.1057 0.107 0.00035 0.00035 0.3515 0.3515 1.02 1.25	1.11 -1.04 1.01 1.01	1.01	Rho GTPase activating protein 24	GTPase activation
2630647	SERPINA13	SERPINA13	0.3514 0.1637 0.31597 0.7849 0.82009 0.82009 1.07 1.25	1.07 -1.04 1.01 1.02	1.02	serine/threonine-protein kinase, alpha (alpha-1 antiprotease, antitrypsin), me	peptidase activity
5312010	CSDA	CSDA	0.4968 0.043 0.05363 0.05363 0.3078 0.3078 1.05 1.25	1.05 -1.04 1.02 1.01	1.00	coiled-coil domain containing 1	regulation of transcription
520315	OR2735	OR2735	0.3809 0.0489 0.4849 0.4849 0.25815 0.25815 1.05 1.25	1.05 -1.04 1.02 1.01	1.01	epithelial olfactory receptor, 27, subfamily 1, member 3	olfactory receptor
7050285	DHFR	DHFR	0.1247 0.1247 0.00008 0.00008 0.6592 0.6592 1.04 1.25	1.05 -1.04 1.01 1.01	1.01	dhfr	transport
4563164	CDC14B	CDC14B	0.8782 0.0489 0.28513 0.28513 0.2851 0.2851 1.00 -1.26	1.16 -1.08 1.04 1.02	1.02	CDC14 cell division cycle 14 homolog B	protein amino acid dephosphorylation
5390047	GPIR175	GPIR175	0.3192 0.0344 0.0007 0.81015 0.8159 0.8159 1.11 -1.17	1.02 -1.02 1.02 -1.05	1.05	phosphoinositide cluster sorting protein 1	protein binding
5720576	ST6GalNAc4	ST6GalNAc4	0.3474 0.0247 0.47251 0.61027 0.6363 0.6363 1.13 -1.18	1.08 -1.06 1.08 -1.05	1.05	F5K06 binding protein 8, 38Da	protein folding
3440392	FLJ20273	FLBMM7	0.0316 0.008 0.02792 0.02792 0.4055 0.4055 1.04 -1.20	1.08 -1.05 1.06 -1.07	1.07	RNA-binding protein	protein folding
1770280	ANPEP	ANPEP	0.1247 0.1247 0.00008 0.00008 0.6593 0.6593 1.04 -1.20	1.05 -1.04 1.01 1.01	1.01	laminin, gamma 1 chain	positive regulation of cell adhesion
1660291	CD19	CD19	0.0876 0.1624 0.4187 0.4187 0.552 0.552 1.05 -1.20	1.08 -1.07 1.06 -1.07	1.07	CD19 antigen-binding protein	cellular defense response
3850687	NARF	NARF	0.0003 0.0189 0.1366 0.1366 0.2043 0.2043 1.01 -1.20	1.11 -1.03 1.01 1.01	1.01	nuclear prelaminin recognition factor	electron transport
4570474	EPB49	EPB49	0.1944 0.0314 0.47833 0.5378 0.6486 0.6486 1.30 -1.21	1.13 -1.05 1.09 -1.04	1.04	erythrocyte membrane protein band 4.9	cytoskeleton organization and biogenesis
5130436	ROPN1B	ROPN1B	0.3242 0.0367 0.16132 0.16132 0.8987 0.8987 1.01 -1.20	1.12 -1.06 1.06 -1.06	1.06	ropnophin, ropnophin associated protein B	sperm motility
50563	BCL6	BCL6	0.00064 0.00064 0.00064 0.00064 0.62458 0.62458 1.06 -1.23	1.13 -1.07 1.01 1.03	1.03	B-cell Lymphoma 6 (c-finger protein 51)	regulation of transcription
4260332	HBQ1	HBQ1	0.5478 0.2896 0.46744 0.46744 0.61229 0.61229 1.03 -1.24	1.14 -1.08 1.06 1.04	1.04	hemoglobin, theta	oxygen transport
4490674	C5orf4	C5orf4	0.3383 0.2564 0.00443 0.00433 0.5061 0.5061 1.21 -1.24	1.07 -1.06 1.04 1.04	1.04	mediator of RNA polymerase II transcription, subunit 2, regulatory	metabolism
7550678	FAM46C	FAM46C	0.4673 0.2388 0.45				

1580538	GYPC	GYPC	0.4012	0.076	0.24462	0.69588	0.4709	0.0729	1.13	-1.1	-1.18	1.88	-1.11	1.69	glycophorin C	protein amino acid O-linked glycosylation	
5910730	MGC39518	FAM126B	0.0029	0.065	0.10908	0.26002	0.5203	0.62601	-1.24	-1.3	-1.16	-1.11	1.06	-1.05	hypothetical protein MGC39518		
6980201	NAPL1	NAPL1	0.0683	0.013	0.47368	0.03095	0.0247	0.52025	-1.16	-1.31	-1.06	-1.18	-1.20	-1.06	nucleosome assembly protein 1-like	positive regulation of cell proliferation	
5900411	CAMK1D	CAMK1D	0.0048	0.0001	0.05	0.85123	0.8795	0.98047	-1.22	-1.32	-1.25	-1.01	1.01	-1.05	calcium/calmodulin-dependent protein kinase ID	protein amino acid phosphorylation	
5550040	FIS1	FIS1	0.8745	0.053	0.13143	0.95955	0.566	0.3683	1.01	-1.32	-1.14	1.06	-1.06	-1.24	calmodulin/CaM-dependent protein kinase ID	apoptosis	
6900164	DDX3X	DDX3X	0.0004	0.0004	0.00768	0.00729	0.0748	0.36405	-1.27	-1.32	-1.16	-1.22	-1.14	-1.07	fission 1 (mitochondrial outer membrane) homolog	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	
1601324	CREB5	CREB5	0.0268	0.001	0.11425	0.23116	0.9535	0.59004	-1.27	-1.32	-1.18	-1.14	1.04	-1.07	CAMP responsive element binding protein 5	ATP-dependent RNA helicase activity	
7000247	KIF3A	KIF3A	0.0004	0.0004	0.00768	0.00729	0.0748	0.36405	-1.27	-1.32	-1.17	-1.14	-1.16	-1.12	microtubule-associated protein 1A	positive regulation of transcription	
5000242	PLVAP	PLVAP	0.4277	0.1813	0.03766	0.91455	0.4504	0.55527	-1.17	-1.32	-1.02	-1.02	-1.16	-1.14	plasmalogens-binding protein	integral to membrane	
2190475	DHRS8	HSD17B11	0.0825	0.086	0.02394	0.02177	0.1047	0.45537	-1.19	-1.32	-1.24	-1.27	-1.18	-1.08	dehydrogenase/reductase (SDR family) member 8	steroid biosynthesis	
520228	UBE2H	UBE2H	0.8801	0.0159	0.01554	0.85435	0.1685	0.16644	-1.02	-1.32	-1.29	-1.02	-1.16	-1.18	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	ubiquitin cycle	
2690181	SERF2	SERF2	0.4643	0.047	0.01913	0.40694	0.198	0.06909	-1.07	-1.32	-1.23	-1.01	-1.13	-1.12	small ERK-rich factor 2		
430324	PTO1V1	PTO1V1	0.0026	0.05	0.01688	0.74684	0.4872	0.67558	-1.22	-1.32	-1.16	-1.02	1.05	-1.03	prostate tumor overexpressed gene 1	RNA aminoacylation for protein translation	
7560446	ZNF217	ZNF217	0.0128	0.0001	0.00768	0.3045	0.65808	-1.19	-1.32	-1.20	-1.15	1.07	-1.01	zinc finger protein 217	regulation of transcription		
5000245	PLXNC1	PLXNC1	0.0004	0.0004	0.00768	0.00729	0.0748	0.36405	-1.22	-1.32	-1.03	-1.01	-1.04	-1.05	PLXNC1 protein	structural constituent of ribosome	
5900671	C1orf74	FAM129A	0.0007	0.01813	0.01784	0.76284	0.528	0.74985	-1.28	-1.32	-1.00	1.06	1.05	-1.03	chromosome 1 open reading frame 74	protein folding	
5810681	ICAM3	ICAM3	0.003	0.06	0.00768	0.763	0.757	0.38573	-1.24	-1.32	-1.28	-1.01	1.02	-1.06	intercellular adhesion molecule 3	cell-cell adhesion	
990435	TP53NP2	TP53NP2	0.0008	0.0001	0.00768	0.976	0.1649	0.4851	-1.26	-1.32	-1.20	-1.00	1.05	-1.05	tumor protein p53 inducible nuclear protein 2	nucleus	
7550519	FLJ11151	FLJ11151	0.0014	0.004	0.00768	0.1138	0.3102	0.62185	-1.31	-1.32	-1.23	-1.14	-1.09	1.01	hypothetical protein FLJ11151	DNA repair	
4780672	QPC7	QPC7	0.5593	0.002	0.00768	0.94769	0.3659	0.48272	-1.07	-1.32	-1.02	-1.01	1.11	-1.09	glutamyl-peptide cyclotransferase (glutaminyl cyclase)	protein modification	
70390	HDC	HDC	0.4452	0.031	0.00768	0.28928	0.8022	0.902	-1.11	-1.32	-1.31	-1.15	-1.03	1.02	histidine decarboxylase	histidine metabolism	
5011647	KIF3A	KIF3A	0.0004	0.0004	0.00768	0.94769	0.3659	0.48272	-1.07	-1.32	-1.23	-1.01	1.05	-1.03	microtubule-associated protein 1A	protein ubiquitination during ubiquitin-dependent protein catabolism	
50187	DPHOSPHO1	DPHOSPHO1	0.2610	0.0999	0.00431	0.32881	0.881	0.45359	-1.28	-1.32	-1.22	-1.11	1.02	-1.23	phosphatase, ornithine 1	metabolism	
3800612	RPS25	RPS25	0.0128	0.0007	0.13613	0.77191	0.107	0.39588	-1.22	-1.32	-1.12	-1.02	1.14	-1.08	ribosomal protein S25	structural constituent of ribosome	
2360242	MBP	MBP	0.1709	0.0143	0.05091	0.30835	0.33109	-1.16	-1.32	-1.23	-1.12	-1.09	-1.12	myelin basic protein	immune response		
2320239	KHL2	KHL2	0.0002	0.048	0.46196	0.06933	0.9964	0.87605	-1.30	-1.32	-1.07	-1.19	1.00	1.02	kelch-like 2, Mayven		
7380019	PABPC1	PABPC1	0.0881	0.003	0.02073	0.83906	0.1007	0.4367	-1.13	-1.32	-1.18	-1.02	1.13	-1.06	poly	positive regulation of translation	
5360403	PIP5K2A	PIP5K2A	0.3287	0.1187	0.01784	0.75942	0.5282	0.82657	-1.19	-1.32	-1.16	-1.12	1.04	-1.09	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	glycerophospholipid metabolism	
2710057	RNBP1	RNBP1	0.0004	0.0004	0.00768	0.94769	0.3659	0.48272	-1.07	-1.32	-1.23	-1.00	1.05	-1.03	ring finger protein 11	protein ubiquitination during ubiquitin-dependent protein catabolism	
501110	CD200	CD200	0.0004	0.0004	0.00768	0.94769	0.3659	0.48272	-1.07	-1.32	-1.24	-1.00	1.05	-1.03	cysteine-rich protein 242	cell cycle arrest	
4880202	PINK1	PINK1	0.0841	0.002	0.00768	0.64738	0.9788	0.6588	-1.00	-1.32	-1.27	-1.04	1.00	-1.14	PTEN induced putative kinase 1	negative regulation of lymphocyte proliferation	
6550142	PABPC4	PABPC4	0.0113	0.06	0.00768	0.0047	0.24241	0.011	0.24472	-1.17	-1.32	-1.24	-1.07	-1.17	-1.08	leukocyte specific transcript 1	RNA catalysis
3450685	LGALS3	LGALS3	0.451	0.075	0.02463	0.23199	0.2637	0.58744	-1.12	-1.32	-1.40	-1.21	-1.19	-1.10	lectin, galactoside-binding, soluble, 3 (galectin 3)	lectin, galactoside-binding, soluble, 3 (galectin 3)	
5670424	ABTB1	ABTB1	0.0073	0.058	0.0069	0.07989	0.3659	0.38381	-1.11	-1.32	-1.17	-1.07	1.02	1.02	ankyrin repeat and BTB domain-containing protein 1	protein binding	
7000247	ZFP32	ZFP32	0.0004	0.0004	0.00768	0.94769	0.3659	0.48272	-1.07	-1.32	-1.27	-1.04	1.05	-1.06	zinc finger protein 32	regulation of transcription	
1450246	RCBP2	RCBP2	0.4146	0.0659	0.02463	0.84789	0.6911	0.22274	-1.15	-1.32	-1.28	-1.02	1.05	-1.14	RCBP2, RBP2, RBP2, RBP2	poly(A) binding protein 2	
4040699	LDBH	LDBH	0.1465	0.0681	0.07232	0.70654	0.2097	0.63188	-1.18	-1.32	-1.03	-1.04	-1.16	-1.16	leucine-rich, histidine-rich protein 8	mRNA metabolism	
4590301	LMBRD1	LMBRD1	0.0004	0.0004	0.00768	0.0659	0.5544	0.58772	-1.25	-1.32	-1.17	-1.15	-1.05	-1.05	LMBRD1 domain containing 1	anaerobic glycolysis	
3450148	Elt1	Elt1	0.0741	0.067	0.00576	0.08642	0.0146	0.2132	-1.21	-1.32	-1.20	-1.06	-1.16	-1.14	hypothetical protein El1		
6220672	ERGIC1	ERGIC1	0.001	0.004	0.00768	0.79436	0.6308	0.34603	-1.30	-1.32	-1.25	-1.02	-1.04	-1.08	endoplasmic reticulum-golgi intermediate compartment	transport	
5720441	NPL	NPL	0.3739	0.079	0.00549	0.55539	0.8466	0.23753	-1.04	-1.32	-1.20	-1.02	-1.13	-1.13	N-acetylneuraminate pyruvate lyase (hydrolipidolipase)	lysase activity	
4780205	FCE1R1	FCE1R1	0.0173	0.014	0.00768	0.88776	0.5547	0.45218	-1.16	-1.32	-1.27	-1.04	1.09	-1.05	FC fragment of IgE, heavy affinity 1 receptor, for alpha polypeptide	immunity response, IgE binding	
4040693	CD200	CD200	0.0004	0.0004	0.00768	0.94769	0.3659	0.48272	-1.04	-1.32	-1.27	-1.04	1.05	-1.05	CD200	protein binding	
380561	TBC1D14	TBC1D14	0.0004	0.0001	0.00768	0.04519	0.3189	0.68881	-1.21	-1.32	-1.23	-1.00	1.07	-1.03	TBC1 domain family, member 14		
130100	SLC25A37	SLC25A37	0.6274	0.0182	0.00768	0.05236	0.55996	0.8951	-1.05	-1.32	-1.07	-1.02	-1.03	-1.03	solute carrier family, member 37		
4260379	STM3N1	STM3N1	0.0043	0.004	0.00768	0.02548	0.36532	0.00627	0.04312	-1.18	-1.32	-1.07	-1.19	-1.19	-1.19	stathmin-like 3	intracellular signaling cascade
6280040	CENTD3	CENTD3	0.0105	0.005	0.00768	0.04817	0.5479	0.84841	-1.23	-1.32	-1.06	-1.05	1.05	-1.02	centaurin, delta 3	centaurin, delta 3	
3800010	ALK8H7	ALK8H7	0.0074	0.045	0.00768	0.1176	0.29084	0.0695	0.0659	-1.26	-1.32	-1.16	-1.11	-1.13	-1.13	alkB, alkyl ester alkylation, repair	alkB, alkyl ester alkylation, repair
361024	C20orf13	C20orf13	0.0004	0.0004	0.00768	0.04597	0.3659	0.48272	-1.06	-1.32	-1.27	-1.04	1.05	-1.06	chromosome 20 open reading frame 13	protein biosynthesis	
2190474	FOXP1A1	FOXP1A1	0.0004	0.0004	0.00768	0.04597	0.3659	0.48272	-1.06	-1.32	-1.27	-1.04	1.05	-1.06	B1-Birky-Reilly-McKenna-Schochetman syndrome	protein biosynthesis	
5720655	SNURF1	SNURF1	0.122	0.050	0.0504	0.2453	0.058	0.15084	-1.18	-1.32	-1.21	-1.13	-1.25	-1.18	SNURF1 upstream reading frame	protein biosynthesis	
4880431	PRDX2	PRDX2	0.8863	0.0105	0.00768	0.04982	0.0825	0.0105	-1.02	-1.32	-1.26	-1.02	-1.23	-1.20	peroxiredoxin 2	protein biosynthesis	
1090494	RPL7A	RPL7A	0.0004	0.0004	0.00768	0.04597	0.3659	0.48272	-1.06	-1.32	-1.26	-1.07	-1.05	-1.05	ribosomal protein L7	protein biosynthesis	
4040259	ITM2A	ITM2A	0.2741	0.081	0.00768	0.42839	0.528	0.08955	-1.16	-1.32	-1.09	-1.22	-1.26	-1.26	ITM2A	protein binding	
5670601	RPL35A	RPL35A	0.0304	0.016	0.07845	0.35988	0.2467	0.76304	-1.28	-1.32	-1.08	-1.11	-1.14	-1.04	ribosomal protein L35A	structural constituent of ribosome	
3130437	RP51A	RP51A	0.0028	0.0105	0.06126	0.43017	0.1815	0.91728	-1.27	-1.32	-1.15	-1.11	-1.11	-1.01	ribosomal protein S14	structural constituent of ribosome	
6590553	CPD	CPD	0.0004	0.004	0.00768	0.04845	0.14396	0.9336	-1.29	-1.32	-1.17	-1.14	-1.01	1.04	carboxypeptidase D	metallopeptidase activity	
4980028	RPL22	RPL22	0.0012	0.07	0.00768	0.02688	0.0196	0.0157	0.0157	-1.25	-1.32	-1.09	-1.10	-1.21	-1.11	ribosomal protein L22	structural constituent of ribosome
4902009	RPS6	RPS6	0.0117	0.009	0.00768	0.04943	0.30638	0.0729	0.02975	-1.27	-1.32	-1.14	-1.11	-1.19	-1.02	ribosomal protein S6	structural constituent of ribosome
2200262	KIF3A	KIF3A	0.0004	0.0004	0.00768	0.04943	0.30638	0.0729	-1.27	-1.32	-1.17	-1.14	-1.16	-1.04	KIF3A	structural constituent of ribosome	
10279	SYNA12	SYNA12	0.0004	0.0004	0.00768	0.04943	0.30638	0.0729	-1.27	-1.32	-1.17	-1.14	-1.16	-1.04	SYNA12	structural constituent of ribosome	
4040259	RP51B	RP51B	0.2212	0.081	0.00768	0.42839	0.528										

6510309	RPL13A	RPL13A	00103	00002	020484	01182	00848	027205	-1.32	-1.55	-1.14	-1.11	-1.21	-1.03	ribosomal protein L13a	structural constituent of ribosome
7400703	EEF1B2	EEF1B2	00137	00047	017171	016782	05538	045918	-1.44	-1.56	-1.05	-1.06	-1.09	-1.13	eukaryotic translation elongation factor 1 beta 2	translational elongation
4180142	EIF3EIP	EIF3EIP	0E-043	0E-010	066935	00621	011066	0136	-1.29	-1.03	-1.12	-1.02	-1.04	-1.04	eukaryotic translation initiation factor 3, subunit 6 interacting protein	protein biosynthesis
2340408	LOC349114	LOC349114	01063	00032	000055	077182	04101	005058	-1.26	-1.56	-1.32	-1.04	-1.13	-1.04	hypothetical protein LOC349114	
6840092	SNCA	SNCA	04054	00761	004708	01694	04301	01624	1.22	-1.56	-1.61	1.06	-1.21	-1.51	synuclein, alpha (non A4 component of amyloid precursor)	anti-apoptosis
4060114	CYP27A1	CYP27A1	04056	00078	001001	046452	00833	00975	-1.14	-1.57	-1.39	-1.13	-1.07	-1.00	cytochrome P450, family 27, subfamily A, polypeptide 1	structural constituent of ribosome
1170400	HISP1	HISP1	04056	00078	001001	046452	00833	00975	-1.14	-1.57	-1.39	-1.13	-1.07	-1.00	cytochrome P450, family 27, subfamily A, polypeptide 1	electron transport, steroid hydroxylase activity
4070139	PGLYRP1	PGLYRP1	02507	00017	01235	037194	01708	04817	-1.23	-1.57	-1.31	-1.18	-1.28	-1.17	peptidoglycan recognition protein 1	innate immune response
6660300	GLS	GLS	00008	1E-006	000498	015691	07031	020698	-1.25	-1.57	-1.18	-1.13	-1.03	-1.12	glutaminase	glutamine catabolism
3290068	EIF4B	EIF4B	00001	7E-007	004384	047438	047428	034767	-1.31	-1.57	-1.20	-1.03	-1.10	-1.01	eukaryotic translation initiation factor 4B	regulation of translational initiation
4120707	RPL23	RPL23	01228	00028	008207	012149	02773	054168	-1.38	-1.58	-1.00	1.08	-1.25	1.15	ribosomal protein L23	ribosomal protein import into nucleus
6350364	PPBP	PPBP	07746	00104	01372	012328	01273	05822	-1.05	-1.59	-1.28	-1.31	-1.31	-1.11	pro-platelet basic protein	cell proliferation, immune response, chemotaxis
2320403	RPL27	RPL27	00254	00022	005269	01359	04518	075283	-1.38	-1.60	-1.09	-1.14	-1.12	-1.05	ribosomal protein L27	structural constituent of ribosome
6110205	C12orf5	C12orf5	00001	1E-005	000001	000001	000001	000001	-1.08	-1.20	-1.04	-1.04	-1.04	-1.04	chromosome 12 open reading frame 45	
470424	RPL31	RPL31	01283	00017	00317	036509	050067	030967	-1.30	-1.56	-1.01	-1.22	-1.15	-1.17	ribosomal protein L31	structural constituent of ribosome
3992296	CA4	CA4	01711	00024	00034	037528	01842	047015	-1.23	-1.52	1.06	1.14	-1.22	-1.12	carbonic anhydrase IV	one-carbon compound metabolism
1820044	RPS27A	RPS27A	00004	3E-005	010307	02417	01077	048681	-1.32	-1.62	-1.18	-1.13	-1.19	-1.08	ribosomal protein S27a	protein modification
4290202	RPS23	RPS23	02881	00058	025143	017154	04303	038347	-1.25	-1.62	-1.26	-1.06	-1.18	-1.22	ribosomal protein S23	structural constituent of ribosome
3890372	TSPAN5	TSPAN5	06465	00393	000074	018101	0108	0163	-1.07	-1.20	-1.50	-1.25	-1.50	-1.45	tetraspanin 5	integral to membrane
4730612	RPS17	RPS17	00787	0011	0172365	038315	05544	057072	-1.08	-1.38	-1.06	-1.17	-1.12	-1.12	ribosomal protein S17	structural constituent of ribosome
5650444	SUPT6H	SUPT6H	00001	1E-005	000001	000001	000001	000001	-1.16	-1.20	-1.04	-1.04	-1.04	-1.04	solute carrier family 1 member 1	cell communication
4850767	RPS3A	RPS3A	01255	00172	008111	029567	049493	049493	-1.24	-1.56	-1.08	-1.24	-1.09	-1.16	ribosomal protein S3A	structural constituent of ribosome
430328	ERAF	ERAF	05915	00383	02013	085653	07115	000698	-1.14	-1.57	1.04	1.05	-1.09	-1.54	erythroid-associated factor	protein folding
1030754	EMR3	EMR3	05205	2E-008	01106	034129	01685	044388	-1.38	-1.56	-1.08	-1.04	-1.07	-1.07	egf-like module containing, mucin-type like, hormone receptor-like 3	signal transduction
4640647	ORM1	ORM1	01111	00733	002747	0598	01373	04022	-1.63	-1.70	-1.11	-1.05	-1.17	-1.07	ormosoucin 1	acute-phase response, inflammatory response
6660193	RPL4	RPL4	00045	4E-006	005601	044746	01427	060208	-1.46	-1.70	-1.08	-1.17	-1.02	-1.02	ribosomal protein L4	structural constituent of ribosome
1170400	C12orf57	C12orf57	00005	1E-006	016422	037984	00684	045189	-1.41	-1.51	-1.10	-1.21	-1.14	-1.14	chromosome 12 open reading frame 57	
50161	SLC16A1	SLC16A1	00001	1E-006	016422	037984	00684	045189	-1.41	-1.51	-1.23	-1.23	-1.23	-1.04	tumor protein, translationally-controlled 1	anti-apoptosis
53651	RPLP0	RPLP0	00416	00001	012641	031624	00684	045189	-1.38	-1.56	-1.23	-1.23	-1.23	-1.04	ribosomal protein P0	ribosomal proteins and assembly
780365	RPS15A	RPS15A	00881	00088	005378	030608	04165	048443	-1.38	-1.56	-1.09	-1.22	-1.17	-1.04	ribosomal protein S15a	structural constituent of ribosome
6290274	RPS4X	RPS4X	00114	9E-006	001407	037585	00882	047081	-1.35	-1.57	-1.21	-1.04	-1.22	-1.09	ribosomal protein S4-X-linked	structural constituent of ribosome
940246	FAM101B	FAM101B	00007	1E-007	00057	017913	08919	026558	-1.39	-1.56	-1.03	1.01	-1.12	-1.12	family with sequence similarity 101, member B	
4250398	HIST1H4C	HIST1H4C	01012	9E-005	006076	076986	0142	049786	-1.40	-1.56	-1.07	1.04	-1.20	-1.10	histone 1, H4c	nitrogen compound metabolism, cell motility
1490639	LOC10192	LOC10192	00001	1E-002	000001	000001	000001	000001	-1.00	-1.00	-1.00	-1.00	-1.00	-1.00	peptidase inhibitor 3, skin-derived	senes-centrifugal factor, inhibitor of apoptosis
2510767	P15	P15	00045	00018	00006	022117	017125	048181	-1.38	-1.56	-1.20	-1.08	-1.08	-1.01	alkaline phosphatase, liver/bone/kidney	hydrolase activity
6890164	ALPL	ALPL	00004	1E-005	00008	060548	0837	030524	-1.58	-2.10	-1.75	-1.08	-1.03	-1.04	alkaline phosphatase, liver/bone/kidney	electron transport
1510736	TXND12	TXND12	00001	2E-009	000107	089954	04256	023037	-1.65	-2.38	-1.50	1.02	-1.11	-1.18	thioredoxin domain containing 12	
50598	FCGR3A	FCGR3A	02462	75151	023031	09743	08323	007703	-1.22	-1.06	-1.21	-1.01	1.04	1.38	Fc fragment of IgG, low affinity IIIa, receptor	immune response
60162	BCL2L1	BCL2L1	00001	1E-002	000001	000001	000001	000001	-1.00	-1.16	-1.02	-1.02	-1.02	-1.02	BCL2-like 1	regulation of apoptosis
610241	C16orf32	C16orf32	00001	1E-002	000001	000001	000001	000001	-1.20	-1.36	-1.04	-1.13	-1.04	-1.04	coiled-coil domain containing 72	
609500	KRT1	KRT1	03577	01342	017003	094539	03398	010441	-1.19	-1.36	-1.04	-1.04	-1.04	-1.04	chromosome 16 open reading frame 35	
1112028	SNCA	SNCA	04658	01214	006693	045878	0587	013427	-1.18	-1.36	-1.08	-1.08	-1.08	-1.08	brevilinidine B (flavin reductase)	nucleotide-sugar metabolism
1340598	CGI-69	CGI-69	01898	05166	000001	000001	000001	000001	-1.03	-1.29	-1.06	-1.06	-1.06	-1.06	CGI-69 protein	complement activation, lecithin pathway
1450309	RNASE2	RNASE2	01479	0067	000913	097182	0194	037012	-1.32	-1.49	-1.01	1.02	-1.21	-1.21	ribonuclease, RNase A, family 2	RNA catabolism
1470554	ELA2	ELA2	01287	01587	017277	008504	09465	048426	-1.06	1.19	1.11	-1.07	1.02	1.02	elastase, 2, neutrophil	proteolysis and peptidolysis
1660303	ITAM2	ITAM2	01264	02433	019348	094924	094912	015052	-1.12	-1.30	-1.03	-1.03	-1.03	-1.03	adrenoreceptor, alpha-2	activation of MAPK activity
1690364	RPL22	RPL22	00001	1E-002	000001	000001	000001	000001	-1.03	-1.20	-1.03	-1.03	-1.03	-1.03	ribosomal protein S22-like	structural constituent of ribosome
1780477	TMOD1	TMOD1	01432	01638	019384	032132	05821	016863	-1.09	-1.28	-1.24	-1.24	-1.24	-1.24	microtubule-associated protein 1B	structural constituent of ribosome
2000205	RPL26	RPL26	01528	01325	006177	028362	038355	047366	-1.30	-1.46	-1.04	-1.12	-1.05	-1.19	ribosomal protein S26	structural constituent of ribosome
2030441	TNN1T1	TNN1T1	00739	01698	049683	038945	04164	053987	-1.04	1.37	1.05	-1.03	1.20	1.16	troponin T type 1	regulation of muscle contraction
2140497	PRK2	PRK2	01283	02749	017399	067487	017089	047042	-1.15	-1.31	-1.02	1.05	-1.05	-1.12	prokinin 2	chemotaxis, anti-apoptosis, inflammatory response
2340110	MGC13057	MGC13057	01715	00873	004026	079391	09958	010975	-1.07	-1.30	-1.03	-1.03	-1.03	-1.03	hypothetical protein MGC13057	
2570379	PTPRC	PTPRC	01248	02455	005551	068880	048461	008461	-1.09	-1.31	-1.22	-1.07	-1.11	-1.04	protein tyrosine phosphatase, receptor type C	T cell receptor signaling pathway
3206356	AL2R2	AL2R2	00001	1E-002	000001	000001	000001	000001	-1.03	-1.20	-1.02	-1.02	-1.02	-1.02	protein amino acid phosphorylation	
3310091	DEFA3	DEFA3	00737	04837	016974	015653	050218	068695	-1.13	-1.36	-1.17	-1.14	-1.14	-1.14	ankyrin repeat domain containing 1A	defense response to bacteria
3440510	RNF10	RNF10	01295	01925	03934	0645	0645	06352	-1.13	-1.39	-1.13	-1.07	-1.07	-1.07	defensin, alpha-1, neutrophil-specific	metal ion binding
3520338	CSFR3	CSFR3	00832	06728	054845	06096	05278	05247	-1.19	-1.31	-1.11	-1.12	-1.16	-1.16	colony stimulating factor 3 receptor (granulocyte)	defense response
3520468	SLC6A8	SLC6A8	04477	02255	036783	033422	05733	010516	-1.12	-1.34	-1.23	-1.06	-1.06	-1.06	urate carrier family 6 (neurotransmitter transporter, creatine), member 8	ion transport
3520474	GYPE	GYPE	05623	04954	03344	051233	048277	03501	-1.23	-1.44	-1.22	-1.22	-1.22	-1.22	glycophorin E	integral to plasma membrane
5560446	GPR56	GPR56	03268	06812	032109	037043	059763	1.15	-1.34	1.14	-1.04	-1.04	-1.04	Ras-induced senescence 1	regulated by transcription	
5700541	LOC440313	LOC440313	00784	01704	029811	0646	07588	010788	-1.16	-1.37	-1.05	-1.05	-1.05	-1.05	CD40 ligand	signaling
5720372	HBZ	HBZ	02084	06855	048688	023099	02331	089068	-1.04	-1.24	-1.04	-1.04	-1.04	-1.04	hemoglobin, zeta	oxygen transport
597129	ALM2	ALM2	00001	1E-002	000001	000001	000001	000001	-1.03	-1.20	-1.03	-1.03	-1.03	-1.03	lysophosphatidylethanolamine	signaling
6320176	HBEB1	HBEB1	018305	007891	016216	04701	0819	065639	-1.05	-1.36	-1.32	-1.13</td				

Supplemental Document 2: Lists of genes selected to make up the "TLR-associated and IFN-induced genes", "complement-associated genes", "macrophage-associated genes", "NK cell-associated genes" and "B cell-associated genes" gene sets used for Figures 3a, b, c, d and e, respectively. The document also includes the "immunomodulator genes", gene set used for Figure 4. The gene symbol is the standard gene symbol used by the HGNC, the gene symbol and name (as of February 2008) and known synonyms are provided for each gene. At least one reference supporting the assignment of each gene to its respective set is also given.

Immune chip	Official Symbol	Official name	Aliases/Synonyms	References
Complement-associated genes				
C1QA	C1QA	complement component 1, q subcomponent, A chain [Homo sapiens]	Cutter, A. J. et al. T-cell-dependent immune response in C1q-deficient mice: defective interferon gamma production by antigen-specific T cells. <i>J. Exp. Med.</i> 187 , 1789-97 (1998).	
C1QB	C1QB	complement component 1, q subcomponent, B chain [Homo sapiens]	Kojouharova, M. S., Panchev, I. D., Tchorbadjieva, M. I., Reid, K. B. & Hoppe, H. J. Differential binding of IgG and of a HIV gp41 peptide by the B chain and A chain globular head sequences of C1q, respectively. <i>J. Immunol.</i> 161 , 4325-31 (1998).	
C3AR1	C3AR1	complement component 3a receptor 1 [Homo sapiens]	Guttmann, R. et al. Human plasmacytoid dendritic cells express receptors for complement proteins C3a and C5a. <i>J. Invest. Dermatol.</i> 126 , 2422-6 (2006).	
SERPING1	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angiogenesis, hereditary) [Homo sapiens]	Liu, D. et al. C1 inhibitor-mediated protection from sepsis. <i>J. Immunol.</i> 179 , 3966-72 (2007).	
TLR-associated and IFN-induced genes				
ADAR	ADAR	adenosine deaminase, RNA-specific [Homo sapiens]	Zahn, R. C., Scheid, I., Utermohlen, O. & von Laer, D. A-to-G hypermutation in the genome of lymphocytic choriomeningitis virus. <i>Virology</i> 81 , 457-64 (2007).	
AIM2	AIM2	absent in melanoma 2 [Homo sapiens]	Johnstone, R. W. & Tewari, M. J. A family of proteins. <i>Mol. Cell Biol.</i> 19 , 5833-8 (1999).	
G1P2	ISG15	ISG15 ubiquitin-like modifier [Homo sapiens]	Zhou, C., Denissenko, C., Hultgren, J. M., Gog, S. & Krup, R. M. Human ISG15 conjugation targets both IFN-induced and constitutively expressed proteins functioning in diverse cellular pathways. <i>Proc. Natl. Acad. Sci. U. S. A.</i> 103 , 1538-43 (2006).	
G1P3	IFI6	interferon, alpha-inducible protein 6 [Homo sapiens]	Kelly, J. M. et al. Characterization of a human gene inducible by alpha- and beta-interferons and its expression in mouse cells. <i>Embo J.</i> 5 , 1601-6 (1986).	
GBP1	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa [Homo sapiens]	Cheng, Y. S., Becker-Manley, M. F., Chow, T. & Horan, D. C. Affinity purification of an interferon-induced human guanylate-binding protein and its characterization. <i>J. Biol. Chem.</i> 260 , 15834-9 (1985).	
GBP2	GBP2	guanylate binding protein 2, interferon-inducible [Homo sapiens]	Neun, R., Richter, M. F., Staeheli, P. & Schwemmle, M. GP1Pse protein is a novel, interferon-induced human guanylate-binding protein. <i>FEBS Lett.</i> 390 , 69-72 (1996).	
IFI27	IFI27	interferon, alpha-inducible protein 27 [Homo sapiens]	Rasmussen, L. B. et al. Identification of a new interferon-alpha-inducible gene (p27) on human chromosome 14q32 and its expression in breast carcinomas. <i>Cancer Res.</i> 53 , 4096-101 (1993).	
IFI30	IFI30	interferon, gamma-inducible protein 30 [Homo sapiens]	Arinachalem, B., Phan, U. T., Gezzi, H. J. & Creswell, P. Enzymatic reduction of disulfide bonds in lysosomes: characterization of a gamma-interferon-inducible lysosomal thiol reductase (GLT). <i>Proc. Natl. Acad. Sci. U. S. A.</i> 97 , 745-50 (2000).	
IFI44	IFI44	interferon-induced protein 44 [Homo sapiens]	Hallen, L. C. et al. Antiproliferative activity of the human IFN-alpha-inducible protein IF44. <i>J. Interferon Cytokine Res.</i> 27 , 675-80 (2007).	
IFI11	IFI11	interferon-induced protein with tetra-tripeptide repeats 1 [Homo sapiens]	Blyatman, H. A. et al. Structure, chromosome localization, and regulation of expression of the interferon-regulated mouse IFN54/IF56 gene family. <i>Genomics</i> 24 , 137-48 (1994).	
IFI11L	IFI11L	interferon-induced protein with tetra-tripeptide repeats 1-like [Homo sapiens]	Wathelet, M. G. et al. Cloning and chromosomal location of human genes inducible by type I interferon. <i>Somat. Cell Mol. Genet.</i> 14 , 415-26 (1988).	
IFI12	IFI12	interferon-induced protein with tetra-tripeptide repeat 2 [Homo sapiens]	Blyatman, H. A. et al. Structure, chromosome localization, and regulation of expression of the interferon-regulated mouse IFN54/IF56 gene family. <i>Genomics</i> 24 , 137-48 (1994).	
IFI13	IFI13	interferon-induced protein with tetra-tripeptide repeats 3 [Homo sapiens]	Wathelet, M. G. et al. Cloning and chromosomal location of human genes inducible by type I interferon. <i>Somat. Cell Mol. Genet.</i> 14 , 415-26 (1988).	
IFI15	IFI15	interferon-induced protein with tetra-tripeptide repeats 5 [Homo sapiens]	Wathelet, M. G. et al. Cloning and chromosomal location of human genes inducible by type I interferon. <i>Somat. Cell Mol. Genet.</i> 14 , 415-26 (1988).	
IFI17M1	IFI17M1	interferon induced transmembrane protein 1 (9-27) [Homo sapiens]	Yang, G., Xu, Y., Chen, X. & Hu, G. IFITM1 plays an essential role in the antiproliferative action of interferon-gamma. <i>Oncogene</i> 26 , 594-603 (2007).	
IFI17M3	IFI17M3	interferon induced transmembrane protein 3 (1-8U) [Homo sapiens]	Bren, R., Oraszlan-Szovik, J., Fosser, S., Bohmann, B. & Certo, U. Inhibition of proliferation by 1-U and 10-U interferon-alpha-responsive and non responsive cell lines. <i>Cell. Mol. Life Sci.</i> 60 , 1235-48 (2003).	
IKBKE	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon [Homo sapiens]	RP11-34M12, 18K, IKKE, IKK1, KIAA0151, MGC125294, MGC125295, MGC125297	
IL15	IL15	interleukin 15 [Homo sapiens]	IL-15, MGC9721	
IRAK1	IRAK1	interleukin-1 receptor-associated kinase 1 [Homo sapiens]	IRAK, pelle	
IRAK4	IRAK4	interleukin-1 receptor-associated kinase 4 [Homo sapiens]	IPDI, NY-REN-46, RENCA	
IRF3	IRF3	interferon regulatory factor 3 [Homo sapiens]	RP11-34M12, 18K, IKKE, IKK1, KIAA0151, MGC125294, MGC125295, MGC125297	
IRF5	IRF5	interferon regulatory factor 5 [Homo sapiens]	Jung, Y. O. et al. Toll-like receptor 2 and 4 combination engagement upregulates the expression of type I interferon-regulated synovial fibroblasts. <i>Immunol. Lett.</i> 108 , 21-7 (2007).	
IRF7	IRF7	interferon regulatory factor 7 [Homo sapiens]	Uematsu, S. et al. Interleukin-1 receptor-associated kinase-1 plays an essential role in type I interferon (IFN)-induced gene expression. <i>Nature</i> 434 , 777-7 (2005).	
MX1	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) [Homo sapiens]	IFI78K, IFI78, MX, Mxa	
MX2	MX2	myxovirus (influenza virus) resistance 2 [Homo sapiens]	MXB	
MYD88	MYD88	myeloid differentiation primary response gene (88) [Homo sapiens]	Takada, A. et al. Integral role of IRF-5 in the gene induction programme activated by Toll-like receptors. <i>Nature</i> 434 , 243-9 (2005).	
OAS1	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa [Homo sapiens]	Honda, K. et al. IRF-7 is the master regulator of type-I interferon-induced immune responses. <i>Nature</i> 434 , 777-7 (2005).	
OAS2	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa [Homo sapiens]	Marie, J., Galan, J., Svab, J. & Horwitz, A. G. Preparation and characterization of 2'-5'-oligoadenylates specific for 69 and 100 kDa forms of human 2'-S' synthetase. <i>Somat. Cell Mol. Genet.</i> 14 , 123-31 (1988).	
OAS3	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa [Homo sapiens]	Melen, K. et al. Human Myb protein, an interferon-alpha-inducible GTPase, is a nuclear transcription factor that binds to a heterochromatin region beneath the nuclear envelope. <i>J. Biol. Chem.</i> 271 , 7478-86 (1996).	
OASL	OASL	2'-5'-oligoadenylate synthetase-like [Homo sapiens]	Hoover, D. B. & Robert, R. A. A universal role for MyoB8 in TLK/L-1R-mediated signaling. <i>Trends Biochem. Sci.</i> 27 , 474-82 (2002).	
SP110	SP110	SP110 nuclear body protein [Homo sapiens]	Wathelet, M. G. et al. Cloning and chromosomal location of human genes inducible by type I interferon. <i>Somat. Cell Mol. Genet.</i> 14 , 415-26 (1988).	
TBK1	TBK1	TANK-binding kinase 1 [Homo sapiens]	IPDI, NY-REN-46, RENCA	
TICAM1	TICAM1	toll-like receptor adaptor molecule 1 [Homo sapiens]	RP11-34M12, 18K, IKKE, IKK1, KIAA0151, MGC125294, MGC125295, MGC125297	
TIRAP	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein [Homo sapiens]	FLJ42105, Mai, wyat	
TLR1	TLR1	toll-like receptor 1 [Homo sapiens]	CD281, DK1Zp747016062, KIAA0012, MGC10940, OPN506 (2006).	
TLR2	TLR2	toll-like receptor 2 [Homo sapiens]	Lien, E. et al. Toll-like receptor 2 functions as a pattern recognition receptor for diverse bacterial products. <i>J. Biol. Chem.</i> 274 , 33419-25 (1999).	
TLR3	TLR3	toll-like receptor 3 [Homo sapiens]	Matsuhashi, M., Kikkawa, S., Kohase, M., Miyake, K. & Saya, T. Establishment of a monoclonal antibody against human Toll-like receptor 3 that blocks double-stranded RNA-mediated signaling. <i>Biochem. Biophys. Res. Commun.</i> 295 , 101-5 (2002).	
TLR4	TLR4	toll-like receptor 4 [Homo sapiens]	Tapping, R. I., Akashi, S., Miyake, K., Godowski, P. J. & Tobita, P. S. Toll-like receptor 4, but not toll-like receptor 2, is a signaling receptor for Escherichia coli lipopolysaccharide. <i>J. Biol. Chem.</i> 276 , 57867-7000 (2001).	
TLR5	TLR5	toll-like receptor 5 [Homo sapiens]	Hayashi, T. et al. The innate immune response to bacterial flagellin is mediated by toll-like receptor 5. <i>Nature</i> 410 , 1099-103 (2001).	
TLR6	TLR6	toll-like receptor 6 [Homo sapiens]	Takeuchi, O. et al. TLR6: A novel member of an expanding toll-like receptor family. <i>J. Biol. Chem.</i> 271 , 5045-5 (1996).	
TLR7	TLR7	toll-like receptor 7 [Homo sapiens]	Tripathi, S. et al. TLR7 and TLR8 are involved in the host's immune response to human parvovirus 1. <i>Eur. J. Immunol.</i> 35 , 2416-23 (2005).	
TLR8	TLR8	toll-like receptor 8 [Homo sapiens]	CD288, MGC11999, MGC119600	
TLR9	TLR9	toll-like receptor 9 [Homo sapiens]	CD289, MGC104967, MGC126398, MGC126399	
TLR10	TLR10	toll-like receptor 10 [Homo sapiens]	CD290, MGC104967, MGC126398, MGC126399	
TLR11	TLR11	toll-like receptor 11 [Homo sapiens]	CD291, MGC104967, MGC126398, MGC126399	
TLR12	TLR12	toll-like receptor 12 [Homo sapiens]	CD292, MGC104967, MGC126398, MGC126399	
TLR13	TLR13	toll-like receptor 13 [Homo sapiens]	CD293, MGC104967, MGC126398, MGC126399	
TLR14	TLR14	toll-like receptor 14 [Homo sapiens]	CD294, MGC104967, MGC126398, MGC126399	
TLR15	TLR15	toll-like receptor 15 [Homo sapiens]	CD295, MGC104967, MGC126398, MGC126399	
TLR16	TLR16	toll-like receptor 16 [Homo sapiens]	CD296, MGC104967, MGC126398, MGC126399	
TLR17	TLR17	toll-like receptor 17 [Homo sapiens]	CD297, MGC104967, MGC126398, MGC126399	
TLR18	TLR18	toll-like receptor 18 [Homo sapiens]	CD298, MGC104967, MGC126398, MGC126399	
TLR19	TLR19	toll-like receptor 19 [Homo sapiens]	CD299, MGC104967, MGC126398, MGC126399	
TLR20	TLR20	toll-like receptor 20 [Homo sapiens]	CD300, MGC104967, MGC126398, MGC126399	
TLR21	TLR21	toll-like receptor 21 [Homo sapiens]	CD301, MGC104967, MGC126398, MGC126399	
TLR22	TLR22	toll-like receptor 22 [Homo sapiens]	CD302, MGC104967, MGC126398, MGC126399	
TLR23	TLR23	toll-like receptor 23 [Homo sapiens]	CD303, MGC104967, MGC126398, MGC126399	
TLR24	TLR24	toll-like receptor 24 [Homo sapiens]	CD304, MGC104967, MGC126398, MGC126399	
TLR25	TLR25	toll-like receptor 25 [Homo sapiens]	CD305, MGC104967, MGC126398, MGC126399	
TLR26	TLR26	toll-like receptor 26 [Homo sapiens]	CD306, MGC104967, MGC126398, MGC126399	
TLR27	TLR27	toll-like receptor 27 [Homo sapiens]	CD307, MGC104967, MGC126398, MGC126399	
TLR28	TLR28	toll-like receptor 28 [Homo sapiens]	CD308, MGC104967, MGC126398, MGC126399	
TLR29	TLR29	toll-like receptor 29 [Homo sapiens]	CD309, MGC104967, MGC126398, MGC126399	
TLR30	TLR30	toll-like receptor 30 [Homo sapiens]	CD310, MGC104967, MGC126398, MGC126399	
TLR31	TLR31	toll-like receptor 31 [Homo sapiens]	CD311, MGC104967, MGC126398, MGC126399	
TLR32	TLR32	toll-like receptor 32 [Homo sapiens]	CD312, MGC104967, MGC126398, MGC126399	
TLR33	TLR33	toll-like receptor 33 [Homo sapiens]	CD313, MGC104967, MGC126398, MGC126399	
TLR34	TLR34	toll-like receptor 34 [Homo sapiens]	CD314, MGC104967, MGC126398, MGC126399	
TLR35	TLR35	toll-like receptor 35 [Homo sapiens]	CD315, MGC104967, MGC126398, MGC126399	
TLR36	TLR36	toll-like receptor 36 [Homo sapiens]	CD316, MGC104967, MGC126398, MGC126399	
TLR37	TLR37	toll-like receptor 37 [Homo sapiens]	CD317, MGC104967, MGC126398, MGC126399	
TLR38	TLR38	toll-like receptor 38 [Homo sapiens]	CD318, MGC104967, MGC126398, MGC126399	
TLR39	TLR39	toll-like receptor 39 [Homo sapiens]	CD319, MGC104967, MGC126398, MGC126399	
TLR40	TLR40	toll-like receptor 40 [Homo sapiens]	CD320, MGC104967, MGC126398, MGC126399	
TLR41	TLR41	toll-like receptor 41 [Homo sapiens]	CD321, MGC104967, MGC126398, MGC126399	
TLR42	TLR42	toll-like receptor 42 [Homo sapiens]	CD322, MGC104967, MGC126398, MGC126399	
TLR43	TLR43	toll-like receptor 43 [Homo sapiens]	CD323, MGC104967, MGC126398, MGC126399	
TLR44	TLR44	toll-like receptor 44 [Homo sapiens]	CD324, MGC104967, MGC126398, MGC126399	
TLR45	TLR45	toll-like receptor 45 [Homo sapiens]	CD325, MGC104967, MGC126398, MGC126399	
TLR46	TLR46	toll-like receptor 46 [Homo sapiens]	CD326, MGC104967, MGC126398, MGC126399	
TLR47	TLR47	toll-like receptor 47 [Homo sapiens]	CD327, MGC104967, MGC126398, MGC126399	
TLR48	TLR48	toll-like receptor 48 [Homo sapiens]	CD328, MGC104967, MGC126398, MGC126399	
TLR49	TLR49	toll-like receptor 49 [Homo sapiens]	CD329, MGC104967, MGC126398, MGC126399	
TLR50	TLR50	toll-like receptor 50 [Homo sapiens]	CD330, MGC104967, MGC126398, MGC126399	
TLR51	TLR51	toll-like receptor 51 [Homo sapiens]	CD331, MGC104967, MGC126398, MGC126399	
TLR52	TLR52	toll-like receptor 52 [Homo sapiens]	CD332, MGC104967, MGC126398, MGC126399	
TLR53	TLR53	toll-like receptor 53 [Homo sapiens]	CD333, MGC104967, MGC126398, MGC126399	
TLR54	TLR54	toll-like receptor 54 [Homo sapiens]	CD334, MGC104967, MGC126398, MGC126399	
TLR55	TLR55	toll-like receptor 55 [Homo sapiens]	CD335, MGC104967, MGC126398, MGC126399	
TLR56	TLR56	toll-like receptor 56 [Homo sapiens]	CD336, MGC104967, MGC126398, MGC126399	
TLR57	TLR57	toll-like receptor 57 [Homo sapiens]	CD337, MGC104967, MGC126398, MGC126399	
TLR58	TLR58	toll-like receptor 58 [Homo sapiens]	CD338, MGC104967, MGC126398, MGC126399	
TLR59	TLR59	toll-like receptor 59 [Homo sapiens]	CD339, MGC104967, MGC126398, MGC126399	
TLR60	TLR60	toll-like receptor 60 [Homo sapiens]	CD340, MGC104967, MGC126398, MGC126399	
TLR61	TLR61	toll-like receptor 61 [Homo sapiens]	CD341, MGC104967, MGC126398, MGC126399	
TLR62	TLR62	toll-like receptor 62 [Homo sapiens]	CD342, MGC104967, MGC126398, MGC126399	
TLR63	TLR63	toll-like receptor 63 [Homo sapiens]	CD343, MGC104967, MGC126398, MGC126399	
TLR64	TLR64	toll-like receptor 64 [Homo sapiens]	CD344, MGC104967, MGC126398, MGC126399	
TLR65	TLR65	toll-like receptor 65 [Homo sapiens]	CD345, MGC104967, MGC126398, MGC126399	
TLR66	TLR66	toll-like receptor 66 [Homo sapiens]	CD346, MGC104967, MGC126398, MGC126399	
TLR67	TLR67	toll-like receptor 67 [Homo sapiens]	CD347, MGC104967, MGC126398, MGC126399	
TLR68	TLR68	toll-like receptor 68 [Homo sapiens]	CD348, MGC104967, MGC126398, MGC126399	
TLR69	TLR69	toll-like receptor 69 [Homo sapiens]	CD349, MGC104967, MGC126398, MGC126399	
TLR70	TLR70	toll-like receptor 70 [Homo sapiens]	CD350, MGC104967, MGC126398, MGC126399	
TLR71	TLR71	toll-like receptor 71 [Homo sapiens]	CD351, MGC104967, MGC126398, MGC126399	
TLR72	TLR72	toll-like receptor 72 [Homo sapiens]	CD352, MGC104967, MGC126398, MGC126399	
TLR73	TLR73	toll-like receptor 73 [Homo sapiens]	CD353, MGC104967, MGC126398, MGC126399	
TLR74	TLR74	toll-like receptor 74 [Homo sapiens]	CD354, MGC104967, MGC126398, MGC126399	
TLR75	TLR75	toll-like receptor 75 [Homo sapiens]	CD355, MGC104967, MGC126398, MGC126399	
TLR76	TLR76	toll-like receptor 76 [Homo sapiens]	CD356, MGC104967, MGC126398, MGC126399	
TLR77	TLR77	toll-like receptor 77 [Homo sapiens]	CD357, MGC104967, MGC126398, MGC126399	
TLR78	TLR78	toll-like receptor 78 [Homo sapiens]	CD358, MGC104967, MGC126398, MGC126399	
TLR79	TLR79	toll-like receptor 79 [Homo sapiens]	CD359, MGC104967, MGC126398, MGC126399	
TLR80	TLR80	toll-like receptor 80 [Homo sapiens]	CD360, MGC104967, MGC126398, MGC126399	
TLR81	TLR81	toll-like receptor 81 [Homo sapiens]	CD361, MGC104967, MGC126398, MGC126399	
TLR82	TLR82	toll-like receptor 82 [Homo sapiens]	CD362, MGC104967, MGC126398, MGC126399	
TLR83	TLR83	toll-like receptor 83 [Homo sapiens]	CD363, MGC104967, MGC126398, MGC126399	
TLR84	TLR84	toll-like receptor 84 [Homo sapiens]	CD364, MGC104967, MGC126398, MGC126399	
TLR85	TLR85	toll-like receptor 85 [Homo sapiens]	CD365, MGC104967, MGC126398, MGC126399	
TLR86	TLR86	toll-like receptor 86 [Homo sapiens]	CD366, MGC104967, MGC126398, MGC126399	
TLR87	TLR87	toll-like receptor 87 [Homo sapiens]	CD367, MGC104967, MGC126398, MGC126399	
TLR88	TLR88	toll-like receptor 88 [Homo sapiens]	CD368, MGC104967, MGC126398, MGC126399	
TLR89	TLR89	toll-like receptor 89 [Homo sapi		

TRAF3	TRAF3	TNF receptor-associated factor 3 [Homo sapiens]	CAP-1, CD40Rp, CRAF1, LAP1	Hoebe, K., Beutler, B., and Reiter, J.: A new component of the TLR-signaling apparatus. <i>Trends Mol. Med.</i> 12 , 187-97 (2006).
TRAF6	TRAF6	TNF receptor-associated factor 6 [Homo sapiens]	MGC3310, RNFS8	Gohari, J., Matsumura, T., & Inoue, J.: Cutting edge: TNFR-associated factor (TRAF) 6 is essential for MyD88-dependent pathway but not IL1R-associated pathway in TLR signaling. <i>J. Immunol.</i> 173 , 2913-7 (2004).
TICAM2	TICAM2	toll-like receptor adaptor molecule 2 [Homo sapiens]	MGC129876, MGC129877, TICAM-2, TRAP, TIRP, TRAM	Yamamoto, M., et al.: TRAM is specifically involved in the Toll-like receptor-4-mediated MyD88-independent signaling pathway. <i>Nat. Immunol.</i> 4 , 114-50 (2003).
TRIM21	TRIM21	tripartite motif-containing 21 [Homo sapiens]	RNFI1, R052, SSA, SSAT	Orimo, A., et al.: Molecular cloning of ring finger protein 21 (RNFI21)/interferon-responsive finger protein (ifn1), which possesses two NLS and a B box-coded coil domains in tandem. <i>Genomics</i> 69 , 143-9 (2003).
TRIM22	TRIM22	tripartite motif-containing 22 [Homo sapiens]	GPSTAF50, RNFI94, STAF5	Tissé, C., & Mechti, N.: Molecular cloning of a new interferon-induced gene, GPSTAF50, encoding a tripartite motif protein that has a long terminal repeat exon. <i>J. Biol. Chem.</i> 270 , 14841-8 (1995).
TRIM5	TRIM5	tripartite motif-containing 5 [Homo sapiens]	RNFI88, TRIM5alpha	Sakuma, R., Maed, A., & Ikeda, Y.: Alpha interferon enhances expression of the human TRIM5 gene in human and rhesus monkey cells. <i>J. Virol.</i> 71 , 17071-17077 (1997).
WARS	WARS	tryptophanyl-tRNA synthetase [Homo sapiens]	GAMMA-2, IFI53, IFP53	Tolstrup, A. B., Bejder, A., Fleckner, J., & Justesen, J.: Transcriptional regulation of the interferon-gamma-inducible tryptophanyl-tRNA synthetase involves alternative splicing. <i>J. Biol. Chem.</i> 270 , 397-403 (1995).
Macrophage-associated genes				
CD36	CD36	CD36 molecule (fibrinopronid receptor) [Homo sapiens]	CHD57, FAT, GP3B, GPI4, GPIV, PAVIV, SCARB3	Sampson, M. J., Davies, J. R., Brascia, S., Ivory, K., Hughes, D. A.: Increased expression of a scavenger receptor (CD36) is monocytose from subjects with Type 2 diabetes. <i>Atherosclerosis</i> 167 , 129-34 (2003).
CD68	CD68	CD68 molecule [Homo sapiens]	DKZP768618236, GP10, SCARD1	Holmes, C., & L. Simmons, D. L.: Molecular cloning of CD68, a human membrane marker related to lysosomal glycoproteins. <i>Blood</i> 81 , 1607-13 (1993).
CD163	CD163	CD163 molecule [Homo sapiens]	MI30, MM130	Hogger, P., Dreier, J., Drost, A., Buck, F., & Sorg, C.: Identification of the integral membrane protein RM3/3 on human monocytes as a member of the scavenger receptor class B type I receptor/lectin-rich family (CT116). <i>J. Immunol.</i> 161 , 1583-90 (1998).
CFS1R	CFS1R	colony stimulating factor 1 receptor, formerly McDonagh feline sarcoma viral (v-fms) oncogene homolog [Homo sapiens]	C-FMS, CD115, CSFR, FIM, FMS	Shery, C., J.: Regulation of monocyte/macrophage proliferation by colony stimulating factor-1. <i>J. Cell. Cloning</i> 8 Suppl. 1 , 46-60; discussion 60-2 (1999).
IFI16	IFI16	interferon-gamma-inducible protein 16 [Homo sapiens]	IFNCH1, MGC9466, PTIH2N	Daulby, J., Mouchiroud, G., & Bourret, R. P.: The interferon-inducible gene, IFNCH1, is transcriptionally activated in response to TNF-CSF, and its product, IFNCH1, is expressed in myeloid progenitor cells. <i>J. Interferon Res.</i> 79 , 173-83 (2000).
MARCO	MARCO	macrophage receptor with collagenous structure [Homo sapiens]	SCARA2	Elomas, O., et al.: Structure of the human macrophage MARCO receptor gene and identification of its bacterial binding region. <i>J. Biol. Chem.</i> 273 , 4735-8 (1998).
CARD15	NOD2	nucleotide-binding oligomerization domain containing 2 [Homo sapiens]	ACUG, BLAU, CARD15, C5, CLR16.3, IBD1, NLRC2, NO28, PSORAS1	Ogura, Y., et al.: Nod2, an Ile108Asp family member that is restricted to intestinal epithelial cells and activates NF-kappaB. <i>J. Biol. Chem.</i> 276 , 4812-8 (2001).
STAB1	STAB1	stabin 1 [Homo sapiens]	CLEVER-1, FEEL-1, FEEL-2, FEX1, KIAA0246, STAB-1	Kathyjkowska, J., et al.: Stabin-1 localizes to endosomes and the trans-Golgi network in human macrophages and interacts with GGA adaptors. <i>J. Interferon Res.</i> 78 , 1151-61 (2004).
Dendritic cell-associated genes				
CD86	CD86	CD86 molecule [Homo sapiens]	B7-2, B70, CD28LG2, LAB72, MCG34413	Cao, C., et al.: B7/B7-2 is identical to CD86 and is their major functional ligand for CD28 expressed on human dendritic cells. <i>J. Exp. Med.</i> 180 , 1841-7 (1994).
MICB	MICB	MHC class I polypeptide-related sequence B [Homo sapiens]	DAQB2-7H16.3, PERB11.2	Leiberman, M., et al.: Critical role of MHC class I-related chain A and B expression in TNF-alpha-stimulated dendritic cells in NK cell activation: impairment in chronic hepatitis C virus infection. <i>J. Immunol.</i> 170 , 1745-54 (2003).
NK cell-associated genes				
GNLY	GNLY	granzulin [Homo sapiens]	S19, D269R, LAG-2, LAG2, NGK5, TL519	Kaspar, A., et al.: A distinct pathway of cell-mediated apoptosis initiated by granzulin. <i>J. Immunol.</i> 167 , 3556-6 (2001).
CD160	CD160	CD160 molecule [Homo sapiens]	BY55, FLJ46513, NK1, NK2	Barkanay, A., et al.: Cutting edge: engagement of CD160 by its HLA-C physiological ligand triggers a unique cytokine profile secretion in the human peripheral blood NK cell subset. <i>J. Immunol.</i> 173 , 539-54 (2004).
CD244	CD244	CD244 molecule, natural killer cell receptor [Homo sapiens]	2B4, NAII, NKR2B4, Nmrl, SLAM4	Nakajima, M., et al.: Colony, M., 2B4: an NK cell activating receptor with Ig-like domains and signal transduction mechanism. <i>Hum. Immunol.</i> 61 , 16-24 (2000).
KLRK1	KLRK1	killer cell lectin-like receptor subfamily K, member 1 [Homo sapiens]	CD114, D12S2489E, KLR-KNG2-D, NKG2D, NKKG2D	Warren, H. S.: The Eighth Human Leucocyte Differentiation Antigen (HLA-E): natural killer cell section report. <i>Cell. Immunol.</i> 176 , 17-20 (2002).
NCR3	NCR3	natural cytotoxicity triggering receptor 3 [Homo sapiens]	DASS-280D6.6, IC7, CD333	Pende, D., et al.: Identification of molecular characterization of Nkp30, a natural killer cell receptor involved in cell recognition mediated by human natural killer cells. <i>J. Exp. Med.</i> 190 , 1505-16 (1999).
GZMB	GZMB	granzyme B (granzyme B, cytotoxic T-lymphocyte-associated serine esterase 1) [Homo sapiens]	CPLC, CGL-1, CGLL, CSPB, CT1A1, CTGSL1, HLP, SECT	Dahli, C. A., et al.: Isolation of a cDNA clone encoding a novel form of granzyme B from human NK cells and mapping to chromosome 14. <i>Hum. Genet.</i> 84 , 465-70 (1990).
GZMK	GZMK	granzyme K (granzyme K, tryptase II) [Homo sapiens]	TRY2P	Hameed, A., Lowrey, D. M., Lichtenheld, M., & Piroick, E. R.: Characterization of three serine esterases isolated from human IL-2-activated killer cells. <i>J. Immunol.</i> 144 , 3447-53 (1990).
KIR2DL3	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3 [Homo sapiens]	CD158B, CD158B, KIR-7.7b, KIR-10A3	Przekat, M., Yost, B., Schmidt, F. B.: Cloning of cDNA for human granzyme K. <i>FEBS Lett.</i> 364 , 268-71 (1995).
KIR2DL4	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 [Homo sapiens]	CD158D, GPR, KIR103, KIR-10A3	Selvakumar, A., Steffens, U., & Dupont, B.: NK cell receptor gene of the KIR family with two Ig domains but highest homology to KIR receptors with three Ig domains. <i>Tissue Antigens</i> 48 , 285-94 (1996).
KIR3DL1	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 [Homo sapiens]	CD158E1, KIR, MGC19723, MGC19728, MGC126509P, MGC261591, NKAT2A, NKAT2B, NKIR	Wu, M., et al.: Increase in the expression of killer cell inhibitory receptors on peritoneal natural killer cells in women with endometriosis. <i>Fertil. Steril.</i> 74 , 1187-91 (2000).
KLRC2	KLRC2	killer cell lectin-like receptor subfamily C, member 2 [Homo sapiens]	CD159c, MGC138244, NK2G2, C, NK2G2	Warren, H. S.: The Eighth Human Leucocyte Differentiation Antigen (HLA-E): natural killer cell section report. <i>Cell. Immunol.</i> 216 , 17-20 (2001).
PRF1	PRF1	perforin 1 (pore forming protein) [Homo sapiens]	RP11-701A11.3, FLI2, HPL2, MGC65093, PI, PIP	Lown, B., Beermann, F., Schmidt, A., & Tschoep, J.: A mutation in perforin gene impairs cytolytic T lymphocytes and natural killer cell-mediated cytotoxicity. <i>Proc. Natl. Acad. Sci. U. S. A.</i> 91 , 11571-5 (1994).
B cell-associated genes				
POU2AF1	POU2AF1	POU class 2 associating factor 1 [Homo sapiens]	BOB1, OBFI-1, OBFI, OCAM	Shieh, M., Neafsey, J. W., & Mathews, P.: OBFI-1, a new of B cell-specific co-factor that stimulates immunoglobulin production by myeloma through association with octamer-binding proteins. <i>Cell</i> 80 , 497-506 (1995).
BANK1	BANK1	B-cell scaffold protein with ankyrin repeats 1 [Homo sapiens]	BANK, FLJ20706, FLJ54204	Yokoyama, K., et al.: BANK regulates BCR-induced calcium mobilization by promoting tyrosine phosphorylation of IP3(3) receptor. <i>Embo J.</i> 21 , 177-86 (2002).
CD19	CD19	CD19 molecule [Homo sapiens]	B4, MGC12802	Tedder, T. F., & Isaacs, C.: Isolation of cDNAs encoding the CD19 antigen of human and mouse B lymphocytes. A new member of the immunoglobulin superfamily. <i>Science</i> 243 , 710-3 (1991).
IGJ	IGJ	immunoglobulin I polypeptide, linker protein for immunoglobulin alpha and mu polypeptides [Homo sapiens]	IGCJ, JCH	Tedder, T. F., & Isaacs, C.: Isolation of cDNAs encoding the CD19 antigen of human and mouse B lymphocytes. A new member of the immunoglobulin superfamily. <i>J. Immunol.</i> 143 , 712-7 (1989).
PIK3AP1	PIK3AP1	phosphoinositide-3-kinase adapter protein 1 [Homo sapiens]	BCAP, RP1-34E5.3	Okada, T., Maeda, A., Iwamoto, A., Gotoh, K., & Kurasaki, T.: BCAP: the phosphoinositide-3-kinase activation. <i>Immunity</i> 13 , 207-22 (2000).
TNFRSF13B	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B [Homo sapiens]	CD267, CVID, FLJ39942, MGC13324, MGC39952, TAC1, TNFRSF14B	Sakurai, D., et al.: TAC1 regulates Ig production by APRIL in collaboration with HSPG. <i>Biof. Lett.</i> 169 , 2961-7 (2007).
TNFRSF17	TNFRSF17	tumor necrosis factor receptor superfamily, member 17 [Homo sapiens]	BCM, BCM4, CD269	Lashi, Y., et al.: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed. <i>Nucleic Acids Res.</i> 29 , 1147-54 (1994).
Inflammasome-associated genes				
CASP1	CASP1	caspase 1, apoptosis-related cysteine peptidase [interleukin 1, beta, converter] [Homo sapiens]	ICE, IL1B, P45	Matzinger, P., Burnet, K., & Zychlinsky, J.: The inflammasome: a molecular platform triggering activation of inflammatory caspases and processing of pro-IL1beta. <i>Mol. Cell.</i> 10 , 47-56 (2001).
CASP3	CASP3	caspase 3, apoptosis-related cysteine peptidase [Homo sapiens]	ICE/ced-3, ICE/R1, ICE-1, Mch-3, MGC14196	Martinson, F., Burns, K., & Tschoop, J.: The inflammasome: a molecular platform triggering activation of inflammatory caspases and processing of pro-IL1beta. <i>Mol. Cell.</i> 10 , 47-56 (2001).
PYCARD	PYCARD	PYD and CARD domain containing [Homo sapiens]	ASC, CARD, MGC10332	Martinson, F., Burns, K., & Tschoop, J.: The inflammasome: a molecular platform triggering activation of inflammatory caspases and processing of pro-IL1beta. <i>Mol. Cell.</i> 10 , 47-56 (2001).
NALP1	NLRP1	NLR family, pyrin domain containing 1 [Homo sapiens]	CD123, CLR17.1, DECAF1, DECAF1-2, DECAF1-3, DECAF1-4, DEZF1, DEZF1-2, DEZF1-3, DEZF1-4, KIAA0413, NALP1, P91/114, SV1, YV1, YV4, YV5	Srinivasula, S. M., et al.: The PYD/CARD protein ASC is an activating adaptor for caspase-1. <i>J. Biol. Chem.</i> 277 , 21119-22 (2002).
IL1B	IL1B	interleukin 1, beta [Homo sapiens]	IL-1, IL-1BETA, IL1F2	Martinson, F., Burns, K., & Tschoop, J.: The inflammasome: a molecular platform triggering activation of inflammatory caspases and processing of pro-IL1beta. <i>Mol. Cell.</i> 10 , 47-56 (2001).
IL18	IL18	interleukin 18 (interferon-gamma-inducing factor) [Homo sapiens]	IGF, IL-18, IL-1g, IL1F4, MGC12320	Fantuzzi, G., Purén, A., Harding, M. W., Livingston, D. J., & Dinarello, C. A.: Interleukin-18 regulation of interferon gamma production and cell proliferation as shown by a recombinant interleukin-18-converting enzyme (IL-18c)-deficient mouse. <i>Proc. Natl. Acad. Sci. U. S. A.</i> 91 , 2118-23 (1994).
IL33	IL33	interleukin 33 [Homo sapiens]	C026r, DKF258560H0532	Schmitz, J., et al.: IL-33, an interleukin-1-like cytokine that signals via the IL-1 receptor-related protein ST2 and induces T helper type 2-associated cytokines. <i>Immunity</i> 23 , 479-90 (2005).
IL1R1	IL1R1	interleukin 1 receptor, type I [Homo sapiens]	CD121A, D2S1473, IL-1R, alpha, IL1R1, IL1RA, PRO	Dinarello, C. A.: Interleukin-1, interleukin-1 receptors and interleukin-1 receptor antagonist. <i>Int. Rev. Immunol.</i> 16 , 457-99 (1997).
IL1R2	IL1R2	interleukin 1 receptor, type II [Homo sapiens]	CD121B, IL1RB, MGC47723	Dinarello, C. A.: Interleukin-1, interleukin-1 receptors and interleukin-1 receptor antagonist. <i>Int. Rev. Immunol.</i> 16 , 457-99 (1997).
IL1RN	IL1RN	interleukin 1 receptor antagonist [Homo sapiens]	ICIL-1, IL1RA, IL1RAP, MGC10340	Dinarello, C. A.: Interleukin-1, interleukin-1 receptors and interleukin-1 receptor antagonist. <i>Int. Rev. Immunol.</i> 16 , 457-99 (1997).
Plasmacytoma-associated genes				
TRAF3	TRAF3	TNF receptor-associated factor 3 [Homo sapiens]	CAP-1, CD40Rp, CRAF1, LAP1	Fleckenstein, J., Baumgaertner, H. H., & Justesen, J.: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamma 2) homologous to rabbit peptide chain release factor and bovine tryptophanyl-tRNA synthetase. <i>Proc. Natl. Acad. Sci. U. S. A.</i> 88 , 11520-4 (1991).

Supplemental Table 1. qPCR analysis of RNA samples from three independent YF17D vaccination studies

		ADORA2A	C1Qa	C1Qb	CTSA	CTSL1	E2F4	EIF2AK2	EOMES	ETS2	GATA1	GATA3	GATA6	IKBKG	IL1B	IL1RN	IL2	IL4	IL18	IRF1	IRF7	RF8	
Up	Montreal	0	5	9	4	9	0	9	1	1	0	1	1	2	3	9	2	3	2	5	9	4	
	Emory	0	8	9	1	8	0	9	4	2	3	0	2	3	4	8	0	2	0	3	10	1	
	Lausanne	0	9	11	1	10	0	11	3	0	4	0	3	0	0	5	2	0	1	1	11	3	
No change	Montreal	7	3	0	5	0	9	0	6	8	6	6	1	6	5	0	1	2	6	4	0	5	
	Emory	7	2	1	8	2	10	1	4	7	4	7	2	5	2	2	7	1	7	4	0	8	
	Lausanne	2	2	0	11	2	9	2	10	4	3	12	4	10	6	6	3	0	11	9	2	9	
Down	Montreal	2	1	0	0	0	0	0	2	0	3	2	6	1	1	0	6	4	1	0	0	0	
	Emory	3	0	0	1	0	0	0	2	1	3	3	6	2	4	0	3	7	3	3	0	1	
	Lausanne	11	2	2	1	1	4	0	0	9	6	1	6	3	7	2	7	0	1	3	0	1	
Total number of samples per study	Montreal	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	
	Emory	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	
	Lausanne	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	12	0	13	13	13	13	
		ISGF3G	MARCO	MMP2	MYD88	NLRC4	NLRP1	NLRP3	NOD2	POU2F1	PRKD2	SH2D3C	SKAP1	SOCS1	STAT1	STAT3	STAT4	STAT6	TAP1	TBX21	TNFSF10	TNFSF13B	TRAF6
Up	Montreal	8	5	3	7	1	1	3	6	3	6	1	0	7	9	4	0	0	9	6	8	9	0
	Emory	8	7	4	8	6	1	3	5	3	0	3	0	3	9	1	0	0	9	5	9	9	0
	Lausanne	7	10	0	3	2	0	4	3	0	3	0	2	10	11	0	2	0	10	7	9	10	0
No change	Montreal	1	3	6	2	8	5	6	3	6	3	8	8	2	0	5	8	6	0	2	1	0	8
	Emory	2	2	2	2	2	7	6	5	6	9	6	7	3	1	9	10	9	1	3	1	1	8
	Lausanne	5	1	0	9	10	8	7	8	12	9	9	9	3	2	10	10	6	3	5	3	2	11
Down	Montreal	0	1	0	0	0	3	0	0	0	0	0	1	0	0	0	1	3	0	1	0	0	1
	Emory	0	1	4	0	2	2	1	0	1	1	1	3	4	0	0	0	1	0	2	0	0	2
	Lausanne	1	2	0	1	1	5	2	2	1	1	4	2	0	0	3	1	7	0	1	1	1	2
Total number of samples per study	Montreal	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	
	Emory	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	Lausanne	13	13	0	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13

RNA samples (day 0 and 7 after vaccination) from three independent YF17D vaccination studies (Montreal, Emory, and Lausanne) were analyzed by qPCR for the expression of 43 genes. Those genes were selected according to our microarray results and to biomedical literature. "Up" samples had a fold change (day 7 vs. day 0) of ≥ 1.3 , whereas "down" samples had a fold change of less than or equal to -1.3 .

Supplemental Table 2. The humoral immune response elicited by YF vaccination is variable

Volunteer	Days post-vaccination									
	0	3	7	10	14	28	60	90	180	360
YF001	0	0	0	0	1/640	1/640	1/1280	1/1280	1/640	1/640
YF002	0	0	0	0	1/640	1/640	1/320	1/320	1/80	1/80
YF003	0	0	0	0	1/80	1/320	1/80	1/80	1/80	1/80
YF004	0	0	0	0	1/320	1/320	1/320	1/640	1/640	1/640
YF005	0	0	0	0	1/320	1/160	1/160	1/320	1/320	1/160
YF006	0	0	0	0	1/320	1/320	1/80	1/80	1/80	1/640
YF007	0	0	0	0	1/160	1/320	1/320	1/320	1/160	1/160
YF008	0	0	0	0	0	1/1280	1/1280	1/1280	1/640	1/640
YF009	0	0	0	0	1/640	1/640	1/640	1/640	1/1280	1/1280
YF010	0	0	0	0	1/2560	1/2560	N/D	N/D	N/D	N/D
YF011	0	0	0	0	1/1280	1/1280	1/1280	1/1280	1/320	1/320
YF012	0	0	0	0	1/640	1/640	1/640	1/640	1/640	320
YF013	0	0	0	0	1/640	1/640	1/640	1/640	1/640	1/640
YF014	0	0	0	0	1/1280	1/1280	1/1280	1/1280	1/640	1/640
YF015	0	0	0	0	1/320	1/320	1/320	1/320	1/160	1/160
YF016	0	0	0	0	1/640	1/640	1/640	1/640	1/640	1/640
YF017	0	0	0	0	1/160	1/160	1/160	1/160	1/80	1/40
YF018	0	0	0	0	1/640	1/640	1/640	1/640	1/640	1/320
YF019	0	0	0	0	1/160	1/160	1/160	1/160	1/160	1/160
YF020	0	0	0	0	1/640	1/640	1/640	1/640	1/320	1/320

YF17D-specific seroconversion by each volunteer after vaccination was assessed by measuring the titer of neutralizing antibodies in all available plasma samples pre- (day 0) and post-vaccination (days 3, 7, 10, 14, 28, 60, 90, 180 and 365). To do so, the plaque reduction neutralization assay (Stefano, I., H.K. Sato, C.S. Pannuti, T.M. Omoto, G. Mann, M.S. Freire, A.M. Yamamura, P.F. Vasconcelos, G.W. Oselka, L.W. Weckx, et al. 1999. Vaccine. 17:1042–1046) was performed in Dr. Rafi Ahmed's laboratory. N/D, Not determined.

Supplemental Table 3. *In vivo* vaccination and *in vitro* primary immune response against YF17D yield similar gene signatures

Whole blood Montreal	Whole blood Lausanne	VaxDesign
BACH1		
BACH2		
		CBFA2T2
CEBPB	CEPB	
	CRX	
	CUTL1	
E2F1		
E2F4		
ETS2	ETS2	ETS2
		FOXF2
		FOXO1A
FOXO3		FOXO3
GATA1	GATA1	
	GATA4	
GATA6		HNF4A
	HSF1	
IRF1	IRF1	IRF1
	IRF2	IRF2
IRF7	IRF7	IRF7
IRF8	IRF8	IRF8
	JUN	JUN
LMO2		
	MLLT7	MLLT7
	POU2F1	
	POU6F1	
	REL	
	RORA	
SRF		
STAT1	STAT1	STAT1
TAL1		
	TBP	
TFAP4		
		TFDP1
		VDR
	VSX1	

Comparison of the transcription factors (with predicted target genes showing a specific modulation) identified by ICA and gene set enrichment analysis. Whole blood (PaxGene tubes) pre- and post-vaccination versus VaxDesign MIMIC system. Transcription factors identified in both analyses are highlighted.

Supplemental Table 4. *In vivo* vaccination and *in vitro* primary immune response against YF17D induce common gene sets

Gene Set Name	q-value		
	Montreal	Lausanne	VaxDesign
GRANDVAUX_IFN_NOT_IRF3_UP	1.31E-012	4.87E-015	1.09E-009
RADAEVA_IFNA_UP	1.33E-016	1.30E-018	6.73E-015
WIELAND_HEPATITIS_B_INDUCED	2.58E-012	4.78E-009	6.11E-011
UV-CMV_UNIQUE_HCMV_6HRS_UP	3.63E-009	4.52E-009	4.15E-005
CMV-UV_HCMV_6HRS_UP	1.01E-012	7.23E-014	2.63E-006
IFNA_UV-CMV_COMMON_HCMV_6HRS_UP	2.14E-015	1.68E-019	1.23E-007
GRANDVAUX_IRF3_UP	2.16E-006	5.41E-007	3.13E-005
DER_IFNB_UP	5.67E-017	1.31E-016	2.70E-008
DER_IFNG_UP	1.01E-007	6.10E-009	2.59E-007
BECKER_IFN_INDUCIBLE_SUBSET_1	2.64E-005	2.17E-005	0.000167804
DER_IFNA_UP	1.17E-016	9.46E-017	9.18E-009
CMV_HCMV_TIMECOURSE_12HRS_UP	1.18E-010	1.28E-012	8.71E-008
HPV31_DN	6.18E-005	0.000621834	9.46E-006
IFNALPHA_NL_HCC_UP	1.10E-007	2.33E-011	6.51E-007
IFNALPHA_NL_UP	2.54E-010	1.04E-013	3.91E-008
DAC_IFN_BLADDER_UP	1.07E-007	1.29E-008	7.30E-009
CMV_8HRS_UP	2.32E-007	3.45E-010	3.78E-006
IFNA_HCMV_6HRS_UP	3.17E-026	6.02E-029	1.89E-009
CMV_ALL_UP	6.50E-006	6.09E-008	0.000205016
REOVIRUS_HEK293_UP	2.17E-006	1.29E-008	2.31E-005
IFNALPHA_HCC_UP	1.74E-008	1.84E-011	1.23E-007
IFN_BETA_UP	5.28E-012	2.43E-010	4.40E-006
IFN_ALPHA_UP	1.31E-012	1.70E-012	8.47E-007
IFN_ANY_UP	3.23E-011	1.27E-010	5.30E-005

Common gene sets identified in the Montreal, Lausanne, and VaxDesign microarray data by ICA and gene set enrichment ($fdr < 0.001$) using the MSigDB c2 "curated gene sets" database.

Supplemental Table 5. Viremia following YF vaccination is variable

Volunteer	Days post-vaccination					
	0	3	7	10	28	60
YF001	21.00	21.00	6920.79	207.72	21.00	N/D
YF002	21.00	24.76	21.00	21.00	21.00	N/D
YF003	21.00	21.00	21.00	21.00	21.00	N/D
YF004	21.00	22.36	1067.59	21.00	21.00	N/D
YF005	21.00	1027.43	616.32	21.00	21.00	N/D
YF006	21.00	21.00	479.03	21.00	21.00	N/D
YF007	21.00	21.00	21.00	74.15	21.00	N/D
YF008	21.00	21.00	21.00	21.00	21.00	N/D
YF009	21.00	21.00	255.35	28.89	21.00	N/D
YF010	21.00	21.00	185.39	21.00	21.00	N/D
YF011	21.00	26.21	1593.71	21.00	21.00	N/D
YF012	21.00	143.65	335.86	21.00	21.00	N/D
YF013	21.00	2580.65	21.00	21.00	21.00	N/D
YF014	21.00	390.06	747.12	70.35	N/D	21.00
YF015	21.00	21.00	331.68	21.00	21.00	N/D
YF016	21.00	21.00	1316.12	21.00	N/D	21.00
YF017	21.00	45.56	108.67	21.00	21.00	N/D
YF018	21.00	21.00	673.54	52.36	21.00	N/D
YF019	21.00	23.01	32.80	21.00	21.00	N/D
YF020	21.00	21.00	34.72	21.00	21.00	N/D

N/D Not determined. Viremia after YF17D vaccination was assessed for each volunteer by determining the number of YF17D viral particles in plasma samples obtained at day 0, 3, 7, 10 and 28. When day 28 samples were not available, day 60 samples were used instead. The method used was the TaqMan real-time PCR assay (Applied Biosystems, Foster City, CA), and was performed in Dr. Rafi Ahmed's laboratory at the Emory Vaccine Center in Atlanta. Numbers are expressed as viral particle per milliliter of plasma. The detection limit of the assay was 21 copies per ml.