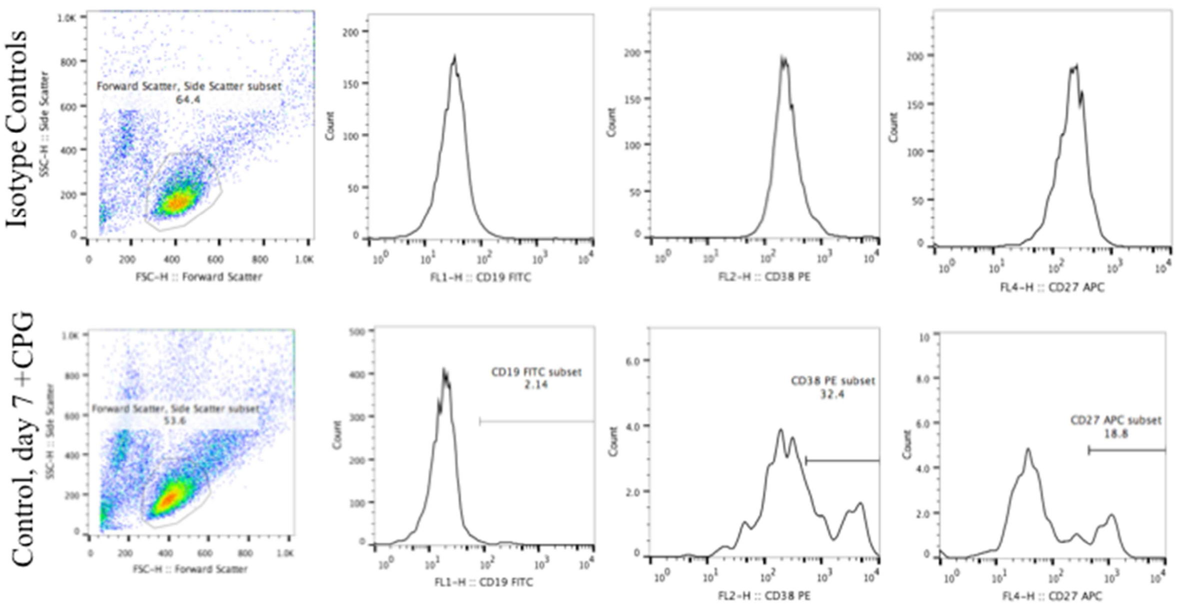
Supplemental Figures

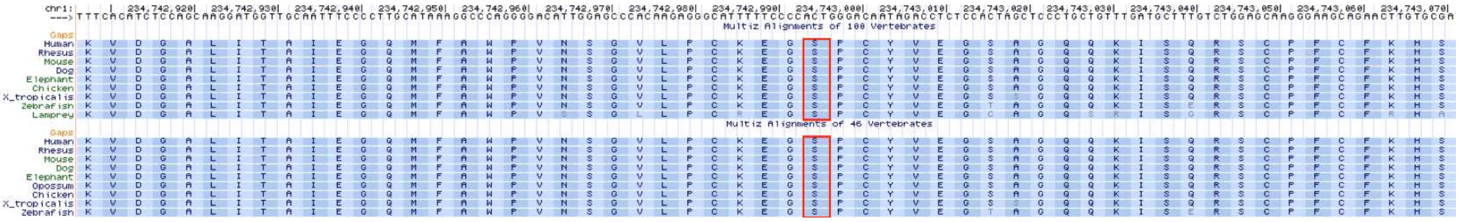
S1. RT-PCR primers for IRF2BP2:

Isoforms 1 and 2:
Forward: AGTTCTGCTTCCCTTGCTCC
Reverse: AGGATGGTTGCAATTTCCCC

Isoform 2 only:
Forward: CAGGTTGTTGGGTTTCGAGG
Reverse: GATCTTGAGCCCCTCTGTGG


Isotype Controls
Control, day 7 +CPG
Forward Scatter, Side Scatter subset
64.4
SSC-H :: Side Scatter
FSC-H :: Forward Scatter
FL1-H :: CD19 FITC
FL2-H :: CD38 PE
FL4-H :: CD27 APC
Count
Forward Scatter, Side Scatter subset
53.6
CD19 FITC subset
2.14
CD38 PE subset
32.4
CD27 APC subset
18.8

Locus	Func	Gene	Conserved	sift	polyphen2	Mutation Annotation	ExAC Allele Count	ExAC Allelic Frequency	Related Gene in RAPID database	Description	Function
chr9:11682	nonsynonymous	AMBP	361:Name:lod:39	0	1	uc004bie.3:c.C884T:p.P295L	16	0.0001329		Glycoprotein precursor of both alpha-1-microglobulin, and bikunin (trypsin inhibitor).	
chr1:23474	nonsynonymous	**IRF2BP2**	729:Name:lod:1218	0	0.99	uc001hwf.2:c.G1604A:p.S535N	0	0	IRF8	interferon regulatory factor 2 binding protein 2	Transcriptional corepressor of IRF2
chr10:1050	nonsynonymous	INA	678:Name:lod:756	0.01	1	uc001kws.2:c.C115T:p.R39C	9	0.00009472		internexin neuronal intermediate filament protein, alpha	Subunit of type IV neurofilaments
chr14:5029	nonsynonymous	SDCCAG1	636:Name:lod:512	0.01	1	uc010anq.1:c.C526G:p.H176D	5	0.00004132		nuclear export mediator factor	involved in nuclear export - N terminal export signal.
chr12:1869	nonsynonymous	**PIK3C2G**	613:Name:lod:412	0.01	NA	uc001rdt.2:c.A3466G:p.K1156E	6	0.0001156	PIK3CD	PI3 kinase C2 gamma subunit	PI3K family - specific function not described for this protein
chr22:3130	nonsynonymous	KIAA1664	NA	0	NA	uc011alb.1:c.C2486T:p.P829L	5	0.0001		oxysterol binding protein 2	Binds oxysterols (byproducts of cholesterol biosynth), inhibits cytotoxicity
chr1:10195	nonsynonymous	C1orf159	NA	0	0.400973	uc001acn.2:c.G682A:p.A228T	0	0		chromosome 1 open reading frame 159	Unknown
chr11:1287	nonsynonymous	C11orf45	NA	0	0.392279	uc001qeu.2:c.T181C:p.W61R	29	0.0002391		keratinocyte proline-rich protein	Unknown
chr9:12342	nonsynonymous	MEGF9	374:Name:lod:44	0.06	NA	uc004bkk.3:c.G616A:p.V206M	0	0		multiple EGF-like-domains 9	Unknown
chr14:6824	nonsynonymous	ZFYVE26	502:Name:lod:146	0.12	0.001	uc001xka.2:c.G4943A:p.R1648H	0	0		zinc finger, FYVE domain containing 26	Phosphatidylinositol 3-phosphate-binding protein, mutated in AR spastic paraplegia type 15
chr20:6194	nonsynonymous	COL20A1	371:Name:lod:43	0.24	NA	uc011aav.1:c.T631A:p.S211T	0	0		collagen, type XX, alpha 1	Probable collagen associated protein
chr1:22657	nonsynonymous	**PARP1**	477:Name:lod:116	0.44	0.11	uc001hqd.3:c.G518A:p.R173Q	13	0.0001071		poly (ADP-ribose) polymerase 1	Involved in repair of DNA damage (base excision repair), also may be downstream of MEK/ERK pathway



```
    chr1:    |  234,742,920|  234,742,930|  234,742,940|  234,742,950|  234,742,960|  234,742,970|  234,742,980|  234,742,990|  234,743,000|  234,743,010|  234,743,020|  234,743,030|  234,743,040|  234,743,050|  234,743,060|  234,743,070|
    --->  TTTCACATCTCCAGCAAGGATGGTTGCAATTTCCCCTTGCATAAAGGCCCAGGGGACATTGGAGCCCACAAGAGGGCATTTTTCCCCACTGGGACAATAGACCTCTCCACTAGCTCCCTGCTGTTTGATGCTTTGTCTGGAGCAAGGGAAGCAGAACTTGTGCGA
                                         Multiz Alignments of 100 Vertebrates
        Gaps
       Human  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
      Rhesus  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
       Mouse  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
         Dog  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
    Elephant  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
     Chicken  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
X_tropicalis  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S S G Q Q K I S Q R S C P F C F K H S
   Zebrafish  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G T A G Q Q K I S E R S C P F C F K H S
     Lamprey  K V D G A L I T A I E G Q M F A W P V S S G L L P C R E G S P C Y V E G C A G Q S R I S G R S C P F C F R H A
                                         Multiz Alignments of 46 Vertebrates
        Gaps
       Human  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
      Rhesus  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
       Mouse  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
         Dog  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
    Elephant  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
     Opossum  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
     Chicken  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S A G Q Q K I S Q R S C P F C F K H S
X_tropicalis  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G S S G Q Q K I S Q R S C P F C F K H S
   Zebrafish  K V D G A L I T A I E G Q M F A W P V N S G V L P C K E G S P C Y V E G T A G Q Q K I S E R S C P F C F K H S
```