

Supplementary Material 1. The locations and the sequences of primer pairs used in qRT-PCR experiments

Gene	Primer	Length	Position	Tm	%GC	Sequence
JUN	Left	21	270-290	59	52	GCTGGATAAGGGCTCAGAGTT
	Right	20	343-362	59	60	GGCTGTGTCTGTCTGTCTGC
FOS	Left	18	586-603	60	61	GGGGCAAGGTGGAACAGT
	Right	20	695-714	59	50	TCTCCGCTTGGAGTGTATCA
ATF2	Left	20	52-71	59	50	CCTTTAAAGTGCCGTTTCAGC
	Right	25	157-181	59	40	TTTCTCAAGTTTCCATCTAGTACCC
ATF4	Left	19	1028-1046	59	53	TCTCCAGCGACAAGGCTAA
	Right	18	1117-1134	59	56	CCAATCTGTCCCGGAGAA
RELA	Left	19	268-286	60	58	CGAACTGTTCCCTCTATC
	Right	19	327-345	59	47	TTGGGCTGCTCAATGATCT
NFKB	Left	20	3108-3127	59	45	CACCGAAGCAATTGAAGTGA
	Right	19	3150-3168	59	63	GGCCTGAGAGGTGGTCTTC
SMAD3	Left	20	5673-5692	59	60	CTCTCCTCCCAAGGACAGTG
	Right	20	5740-5759	60	50	GCTGAGCCAAAAAGCCACTA
STAT1	Left	23	1673-1695	59	43	GAGCTTCACTCCCTTAGTTTGA
	Right	18	1739-1756	59	61	CACAACGGGCAGAGAGGT
STAT3	Left	21	986-1006	59	43	AACTTCAGACCCGTCACAAA
	Right	20	1036-1055	59	55	GGGTCCCTTTGTAGGAAC
SP1	Left	22	3067-3088	60	36	TCTTTTGTGTTGGGATCAGCTT
	Right	21	3112-3132	60	52	GAGAAGATGAGACGGCAACAG

Supplementary Material 2. Aβ1-42 treatments induced cytotoxicity. The cytotoxicity of Aβ1-42 doses was assessed using an LDH assay. The cytotoxicity levels were as follows: For 24 h of treatments; Control: 0.42±3.56; 0.09 μM Aβ: 8.32±7.74; 10 μM Aβ 24h: 6.36±2.05; For 48 h of treatments; Control: 2.73±5.26; 0.09 μM Aβ 48h: 11.58±8.14; 10 μM Aβ 48h: 45.64±1.92; For 72 h of treatments; Control: 5.07±6.62; 0.09 Aβ: 17.83±7.61; 10 μM Aβ: 19.56±5.71. The data were given as Mean ± SD. After 24 h, LDH levels were found to be higher in both 0.09 μM and 10 μM Aβ1-42 treated groups than that of the untreated control group (p<0.01 and p<0.05, respectively). After 48 h, LDH levels were found to be elevated in the cells treated with 10 μM Aβ1-42 compared to those in the untreated cells and the cells treated with 0.09 μM Aβ1-42 (p<0.0001 and p<0.0001, respectively). Furthermore, LDH release was significantly elevated in both the 0.09 μM and 10 μM Aβ1-42 treated cells in comparison to the control group at 72 h (p<0.05 and p<0.01, respectively).

The following table shows the 25 most relevant pathways sorted by p-value.

<https://reactome.org/PathwayBrowser/#/DTAB=AN&ANALYSIS=MjAyNDQ4MDgyMDQ4NDNfODc2MA253%D253%D>

Supplementary Material 3. Reactome analysis results

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Senescence-Associated Secretory Phenotype (SASP)	5/135	0.006	3.42e-07	3.88e-04	9/22	0.001
Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	3/36	0.002	8.65e-06	0.003	4/11	7.33e-04
Signaling by KIT in disease	3/36	0.002	8.65e-06	0.003	4/26	0.002
TRAF6 mediated NF-κB activation	3/38	0.002	1.02e-05	0.003	2/4	2.67e-04
TRAF6 mediated induction of NFκB and MAP kinases upon TLR7/8 or 9 activation	10/563	0.024	2.62e-05	0.003	28/60	0.004
MyD88 cascade initiated on plasma membrane	11/576	0.024	2.97e-05	0.003	30/70	0.005
Toll Like Receptor 10 (TLR10) Cascade	11/579	0.024	3.06e-05	0.003	30/71	0.005
Toll Like Receptor 5 (TLR5) Cascade	13/586	0.025	3.27e-05	0.003	31/71	0.005
MyD88 dependent cascade initiated on endosome	11/592	0.025	3.46e-05	0.003	30/75	0.005
IkBA variant leads to EDA-ID	2/8	3.35e-04	3.62e-05	0.003	2/2	1.33e-04
Toll Like Receptor 7/8 (TLR7/8) Cascade	11/599	0.025	3.70e-05	0.003	33/85	0.006
Toll Like Receptor 9 (TLR9) Cascade	11/607	0.025	3.98e-05	0.003	33/86	0.006
MyD88: MAL (TIRAP) cascade initiated on plasma membrane	11/626	0.026	4.72e-05	0.003	30/76	0.005
Toll Like Receptor TLR1:TLR2 Cascade	11/630	0.026	4.89e-05	0.003	30/78	0.005
Toll Like Receptor TLR6:TLR2 Cascade	11/632	0.026	4.98e-05	0.003	31/78	0.005
Toll Like Receptor 2 (TLR2) Cascade	11/635	0.027	5.11e-05	0.003	31/80	0.005
Interleukin-21 signaling	2/13	5.44e-04	9.53e-05	0.005	2/5	3.33e-04
Signaling by PDGFRA extracellular domain mutants	2/19	7.95e-04	2.03e-04	0.01	1/7	4.67e-04
Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	2/19	7.95e-04	2.03e-04	0.01	1/7	4.67e-04
Toll Like Receptor 3 (TLR3) Cascade	10/825	0.035	2.14e-04	0.01	29/79	0.005
TRIF (TICAM1)-mediated TLR4 signaling	10/865	0.036	2.76e-04	0.01	29/76	0.005
MyD88-independent TLR4 cascade	10/866	0.036	2.78e-04	0.01	29/78	0.005
Cellular Senescence	10/897	0.038	3.35e-04	0.01	27/90	0.006
MAP kinase activation	10/313	0.013	3.49e-04	0.01	19/32	0.002
Interleukin-6 signaling	3/138	0.006	4.53e-04	0.013	7/20	0.001