

# Supplemental Figure 1

Factors predicted within a dissimilarity margin less or equal than 15 % :

8	TFE-1 [T00824]	1	STAT4 [T01577]	3	c-Ets-1 [T00112]	3	GR-beta [T01920]	4	ATF3 [T01313]	5	GR-alpha [T00337]	6	C/EBPbeta [T00581]	7	HNF-1C [T01851]
9	HNF-1B [T01950]	9	NFI/CTF [T00094]	10	FOXP3 [T04280]	11	c-Myb [T00137]	12	Elk-1 [T00250]	13	GCF [T00320]	14	RNR-alpha [T01345]	15	RAR-beta [T00721]
16	NF-1 [T00539]	17	NF-AT2 [T01945]	18	NF-AT1 [T01948]	19	STAT1beta [T01573]	20	ER-B [T00686]	21	ER-A [T01661]	22	E2F-1 [T01542]	23	ETF [T00270]
24	Pax-5 [T00070]	25	p53 [T00671]	26	Sp1 [T00739]	27	Egr-3 [T00243]	28	YY1 [T00915]	29	XBP-1 [T00902]	30	PEA3 [T00685]	31	c-Ets-2 [T00113]
32	IRF-1 [T00423]	33	HNF-3alpha [T02512]	34	NF-AT1 [T00150]	35	c-Jun [T00133]	36	MAZ [T00490]	37	WT1 [T00889]	38	NF-kappaB1 [T00592]	39	ENKTF-1 [T00255]
40	SRY [T00997]	41	TCF-4E [T02878]	42	GR [T05076]	43	AP-2alphaA [T00035]	44	C/EBPalpha [T00105]	45	CTF [T00174]	46	NF-Y [T00150]	47	AP-1 [T00029]
48	Ahr [T01795]	49	PPAR-alpha/RXR-alpha [T05221]	50	YDR [T00885]	51	PXR-1/RXR-alpha [T05671]	52	T3R-beta1 [T00851]	53	AR [T00040]	54	LEF-1 [T02905]	55	USF2 [T00878]
56	TFHD [T00820]	57	EBF [T05427]	58	c-Fos [T00123]										

Zoom    [Data \(txt\)](#)

	1	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200																	
FP002142 FLVCR1_1 :+U EU:NC; range -499 to 100.		0 1 2 3	4	5	6 7 8	9 10 11	12 13	14	15 16 17	18	19 20 21	22 23	24 25 26	27 28 29	30 31 32	33 34 35	36 37 38	39 40 41	42 43 44	45 46 47	48 49 50	51 52 53	54 55 56	57 58 59	60 61 62	63 64 65	66 67 68	69 70 71	72 73 74	75 76 77	78 79 80	81 82 83	84 85 86	87 88 89	90 91 92	93 94 95	96 97 98	99 100

	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400
	0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100																			

	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610
	0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100																				

Supplemental FIG 1 The EPDnew (1) eukaryotic promoter database was used to identify the *Flvcr* promoter sequence from -499 to +100 base pairs relative to the transcription start site. This sequence was queried for human transcription factor (TF) binding sites using PROMO (2) and the resulting output is shown above. Of the TF binding sites identified, many are known to be expressed in macrophages and activated by LPS signaling.