Comparing effects of transforming growth factor b1 on microglia from rat and mouse: Transcriptional profiles and potassium channels

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Supplementary Table 1. Rat target sequences for nCounter Assay CodeSet

Gene	Accession #	Target sequence
Adora1	NM_017155.2	TGTCCTCATCCTCACCCAGAGCTCCATTCTGGCTCTGCTCGCCATTGCTG
		TGGATCGATACCTCCGAGTCAAGATCCCTCTCCGGTACAAGACAGTGGTG
Adora2a	NM_053294.3	CCCTGGAGAAGTCATGATTTTGGGAGATGCAGAGTCGTCTGTGAGAACGT
		CTTCGGGGAGCTCTCTCTGGGAACGCTCGTGGCTCTTGTGAGGAAAGGGC
Aif1 (Iba1)	NM_017196.2	ATCGATATTATGTCCTTGAAGCGAATGCTGGAGAAACTTGGGGTTCCCAA
		GACCCATCTAGAGCTGAAGAAATTAATTAGAGAGGTGTCCAGTGGCTCCG
Arg1	NM_017134.2	ACGGGAAGGTAATCATAAGCCAGAGACTGACTACCTTAAACCACCGAAAT
		AAATGTGAATACATCGCATAAAAGTCATCTGGGGCATCACAGCAAACCGA
Calm	NM_031969.2	GCTACATCAGTGCGGCAGAACTGCGCCACGTCATGACAAACCTCGGGGAA
		AAGCTAACAGATGAAGAAGTAGACGAAATGATCAGAGAAGCAGATATTGA
Casp1 (ICE)	NM_012762.2	AGATTCTAAGGGAGGACATCCTTTCTCCTCAGAAACAAAAGAAAAACTGA
		ACAAAGAAGGTGGCGCATTTCCTGGACCGAGTGGTTCCCTCAAGTTTTGC
Ccl3	NM_013025.2	ACGGCAAATTCCACGAAAATTCATTGCTGACTATTTTGAGACCAGCAGCC
		TTTGCTCCCAGCCGGGTGTCATTTTCCTGACCAAGAGAAACCGGCAGATC
Ccl22	NM_057203.1	TACATCCGTCACCCTCTGCCACCACGTTTCGTGAAGGAGTTCTACTGGAC
		CTCAAAGTCCTGCCGCAAGCCTGGCGTCGTTTTGATAACCATCAAGAACC
Ccr2	NM_021866.1	ATTCTCTATTTCCAAGAAGTATCCAAGAGCTTGATGAGGGGGCCACCACA
		CCGTATGACTATGATGATGGTGAACCTTGTCATAAAACCAGTGTGAAGCA
Ccr5	NM_053960.3	AGGACATGAAGAGAATGGTCAAGGCCGAATCCTAAGGCATCATATCAGCA
		TTGCTTCTTCAGAGTTATGAGCATGGTGGGGAGCACCTAGACAGGTTTGT
Cd68 (ED1)	NM_001031638.1	CTCTCATTCCCTTACGGACAGCTTACCTTTGGATTCAAACAGGACCGACA
		TCAGAGCCACAGTACAGTCTACCTTAACTACATGGCAGTGGAATACAATG
Cd163	NM_001107887.1	CCTCTGTAATTTGCTCAGGAAACCAATCGCATACACTGTTGCCATGTAGT
		TCATCATCTTCGGTCCAAACAACAAGTTCTACCATTGCAAAGGACAGTGA
Csf1r	NM_001029901.1	ACCTACCTAGGGCCGTTCTTTGAAGACCCACACAATCTTGAGTTTAGAAC
		CCAATGGACCACATACAGCTACTCATTCAAACTCCACCTGAACCGTGTAA
Cx3cr1	NM_133534.1	ATGTGCAAGCTCACGACTGCTTTCTTCTTCATTGGCTTCTTTGGGGGCAT
		ATTCTTCATCACCGTCATCAGCATCGACCGGTACCTCGCCATCGTCCTGG
Cybb (Nox2)	NM_023965.1	CAGTACCAAAGTTTGCCGGAAACCCTCCTATGACTTGGAAATGGATCGTG
		GGTCCCATGTTCCTGTATCTGTGTGAGAGGCTGGTGCGGTTTTGGCGATC
Fcgr1a	NM_001100836.1	TGATGGATCATACTGGTGCGAGGTAGCCACGGAGGACGGCCGTGTCCTTA
		AGCGCAGCACCAAGTTGGAGCTATTTGGTCCCCAGTCATCAGATCCTGTC
Fcgr2b	NM_175756.1	CTGGTCCAAGGAATGCTGTAGATATGAAAGAAAACATCTAGAGTCCCTTC
		TGTGAGTCCTGAAACCAACAGACACTACGATATTGGTTCCCAATGGTTGA
Fcgr3a	NM_207603.1	GACTCTTGTTTGCAATAGACACAGTGCTGTATTTCTCGGTGCAGAGGAGT
		CTTCAAAGTTCCGTGGCAGTCTATGAGGAACCCAAACTTCACTGGAGCAA
Gusb	NM_017015.2	TCATTTGATCCTGGATGAGAAACGAAAAGAATATGTCATCGGAGAGCTCA

		TCTGGAATTTTGCTGACTTCATGACGAACCAGTCACCACTGAGAGTAACA
Hprt1	NM_012583.2	AGCTTCCTCCTCAGACCGCTTTTCCCGCGAGCCGACCGGTTCTGTCATGT CGACCCTCAGTCCCAGCGTCGTGATTAGTGATGATGAACCAGGTTATGAC
Hvcn1	XM_006249369.2	ACCAAGAGGATGAGCAGGTTCTTGAAGCACTTCACAGTGGTGGGGGACGA CTACCACACCTGGAATGTCAACTACAAGAAGTGGGAGAACGAGGAGGATG
Ifng	NM_138880.2	AAGGACGGTAACACGAAAATACTTGAGAGCCAGATTATCTCTTTCTACCT CAGACTCTTTGAAGTCTTGAAAGACAACCAGGCCATCAGCAACAACATAA
Ifngr1	NM_053783.1	CCTGTTACACATTCGACTACACTGTGTTTGTGAAACATTACAGGAGTGGG GAGATCCTACATACAGAACATAGCGTCCTAAAAGAAGATTGTAGCGAAAC
Ifngr2	NM_001108313.1	TTTCTTAAGTTACACTTAGTAAAGCAGATGAGTCCGCAGGAGACTTCAGC AAGAAAGAAGTTCCTACCGTCTCATCCCTTAGTTCTTCAAAGCCAAAGGA
Il1b	NM_031512.1	TGCACTGCAGGCTTCGAGATGAACAACAAAAATGCCTCGTGCTGTCTGAC CCATGTGAGCTGAAAGCTCTCCACCTCAATGGACAGAACATAAGCCAACA
Il1r1	NM_013123.3	CTCATATTCTGGAGACTGCACACGTACGGTTAGTATACCCAGTTCCTGAC TTCAAGAATTACCTCATCGGGGGCTTTGCCATCTTCACAGCTACAGCCGT
Il1rn	NM_022194.2	TCATTGCTGGGTACTTACAAGGACCAAATACCAAACTAGAAGAAAAGATA GACATGGTGCCTATTGACTTTCGGAATGTGTTCTTGGGCATCCACGGGGG
Il4	NM_201270.1	TGCTGTCACCCTGTTCTGCTTTCTCATATGTACCGGGAACGGTATCCACG GATGTAACGACAGCCCTCTGAGAGAGATCATCAACACTTTGAACCAGGTC
Il4r	NM_133380.2	GGGTGTCAGCATCTCCTGCATCTGCATCCTATTGTTTTGCCTGACCTGTT ACTTCAGCATTATCAAGATTAAGAAGATATGGTGGGACCAGATTCCCACT
Il6	NM_012589.1	GGAACAGCTATGAAGTTTCTCTCCGCAAGAGACTTCCAGCCAGTTGCCTT CTTGGGACTGATGTTGTTGACAGCCACTGCCTTCCCTACTTCACAAGTCC
Il10	NM_012854.2	ACAACATACTGCTGACAGATTCCTTACTGCAGGACTTTAAGGGTTACTTG GGTTGCCAAGCCTTGTCAGAAATGATCAAGTTTTACCTGGTAGAAGTGAT
Il10ra	NM_057193.2	TGTTTACATGTCACGACGGAGCATTATTTCACCGTGACCAACCTCAGCAT TTTCTTCTTATCCATCCTGATACTCTGTGGAGCCCTGGTCTGCCTGGTTC
Il10rb	NM_001107111.1	CCTCCCTGGATCGTGGCCATCATCCTTATAGCCTCCGTCTTGATAGTCTT CCTCTTCCTACTGGGCTGCTTCAGCATGGTGTGGTTCATTTACAAGAAGA
Il13ra1	NM_145789.2	TAACGAATTTGAGTGTCTCTGTCGAAAATCTCTGCACAATAGTGTGGACA TGGAGTCCTCCTGAGGGAGCCAGTCCAAATTGCAGTCTCAGATATTTTAG
Itgam (Cd11b)	NM_012711.1	CATCCCTTCCTTCAACAGTAAAGAAATATTCAACGTCACCCTCCAGGGCA ATCTGCTATTTGACTGGTACATCGAGACTTCTCATGACCACCTCCTGCTT
Itgb2	NM_001037780.2	CAATATCAGGTGCAACGGAGTCAACTGTCTCCACAAAAAGTGACCCTTAA CTTGCGACCAGGGCAGGCTGCTGCATTCAATGTGACTTTCCGACGGGCCA
Kcna2 (Kv1.2)	NM_012970.3	GCCGGCCAGGATCATAGCCATTGTATCTGTGATGGTCATTCTGATCTCGA TCGTCAGCTTCTGTCTGGAAACCTTGCCCATCTTCCGGGATGAGAACGAG
Kcna3 (Kv1.3)	NM_019270.3	GCCACCTTCTCCAGAAATATCATGAACCTGATAGACATTGTAGCCATCAT CCCTTATTTTATTACTCTGGGCACTGAGCTGGCTGAGCGACAGGGTAATG
Kcna5 (Kv1.5)	NM_012972.1	ATCAGAAGGGGTAGCTGTCCTCTAGAAAAGTGTCACCTCAAGGCCAAGAG CAACGTGGACTTGCGGAGGTCCCTGTATGCCCTCTGTCTGGACACTAGCC
Kcnj2 (Kir2.1)	NM_017296.1	GTTCTTTGGCTGTGTGTTTTGGTTGATAGCTCTGCTCCACGGGGATCTGG ATGCTTCTAAAGAGAGCAAAGCGTGTGTGTCTGAGGTCAACAGCTTCACG
Kcnma1 (Bk)	NM_031828.1	TGATATCTGCCCAGACACTGACTGGCAGAGTCCTGGTTGTGTTAGTCTTT GCTCTCAGCATTGGTGCCCTTGTAATATACTTCATAGACTCATCAAACCC
Kcnn3 (SK3)	NM_019315.2	AGAGAAAGCGACTGAGTGACTATGCTCTGATTTTTGGGATGTTTGGAATT GTTGTTATGGTGATAGAGACCGAACTGTCTTGGGGTTTGTACTCAAAGGA

Kcnn4 (SK4)	NM_023021.2	TACGTCTCTACCTGGTGCCTCGCGCGGTACTTCTGCGTAGCGGGGTCCTG CTCAACGCGTCTTACCGCAGCATCGGGGCGCTCAACCAAGTCCGATTCCG
Mrc1 (CD206)	NM_001106123.1	CTTTGGAATCAAGGGCACAGAGCTATATTTTAACTATGGCAACAGGCAAG AAAAGAATATCAAGCTTTACAAAGGTTCCGGTTTGTGGAGCAGATGGAAG
Msr1 (SR-A)	NM_001191939.1	CACGTTCCATGACAGCATCCCTTCCTCACAACACTATAAATGGCTCCTCC GTTCAGGAGAAACTGAAGTCCTTCAAAGTTGCCCTCGTCGCTCTCTACCT
Myc	NM_012603.2	ACCGAGGAAAACGACAAGAGGCGGACACACAACGTCTTGGAACGTCAGAG GAGAAACGAGCTGAAGCGTAGCTTTTTTGCCCTGCGCGACCAGATCCCTG
Ncf1	NM_053734.2	TCCATTCCCAGCATCCCATAATTGGGCTTGTCCGTGTTCCAACATCTGGG CGGAATTTCACAGCCAAAGGTCAAGAGGACTGCTGTTACGTTCAAGGTCG
Nfkbia (IκBα)	NM_001105720.2	TATTGTGCTTTTGGTTGAACCGCCATAGACTGTAGCTGACCCCAGTGTGC CCTCTCACGTAAGAACCAGGTGTTCAGTGGTATGTGCTTAAGTCATCCCC
Nme2 (NDPK-B)	NM_031833.2	TGATTCAGTGGAGAGTGCCGAGAAAGAGATCGGTCTATGGTTTAAGCCCG AAGAACTGATTGACTATAAGTCTTGTGCCCATGACTGGGTGTATGAGTAG
Nos2	NM_012611.2	ACGGGACACAGTGTCGCTGGTTTGAAACTTCTCAGCCACCTTGGTGAGGG GACTGGACTTTTAGAGACGCTTCTGAGGTTCCTCAGGCTTGGGTCTTGTT
Nox1	NM_053683.1	CCGAGAAAGAAGATTCTTGGCTAAATCCCATCCAGTCTCCAAACGTGACA GTGATGTATGCAGCATTTACCAGTATTGCTGGCCTTACTGGAGTGGTCGC
Nox4	NM_053524.1	TGTTGGACAAAAGCAAGACTCTACATATCACCTGTGGCATAACTATTTGT ATTTTCTCAGGTGTGCATGTAGCTGCCCACTTGGTGAACGCCCTGAACTT
Nr3c1 (GR)	NM_012576.2	AGCTTTCCTTGAAGCGTATAAAGAGCCATGCTCCTTTAGTATGTGGGGAA GAAGAGAGCTGTCATAGTTTTGAGTACAGTGAGAAGATGCGGTACTGTCT
Orai1	NM_001013982.1	GCCTTCTCCACCGTCATCGGGACGCTGCTTTTCCTGGCCGAAGTCGTGCT GCTCTGCTGGGTGAAGTTCTTACCGCTCAAGAGGCAGGCGGGACAGCCAA
Orai3	NM_001014024.1	ACCTGTAATGTGCTTTACAGTTGGCATCCTGGGAGAGATTTTACATAGGC TCCTCAGATGAACCACTTTACACTTGGTGACTTGTGGTGGTGTGTCCCAC
P2rx7	NM_019256.1	ACTTTAAGAGGTCACATTAACCAGACTAGAAGCCATCGCATCTAACCGCA TACCAGACACAGTCTGACGCCTCATTGCTATGCTATGGTTCTAAGTGACT
P2ry2	NM_017255.1	GAGCTCTTTAGCCATTTTGTGGCTTACAGCTCTGTCATGCTGGGTCTGCT TTTTGCTGTGCCCTTTTCCATCATCCTGGTCTGTTACGTGCTCATGGCCC
P2ry12	NM_022800.1	TGATAACCATTGACCGATACCTGAAGACCACCAGACCATTTAAAACTTCC AGCCCCAGCAATCTTTTGGGTGCGAAGATTCTTTCTGTTGCCATCTGGGC
Phtp1	NM_001106558.2	CCTGTGTTCTCCTTTTGTACCTTGGGCAACACACCACCTGCCAGGCCTTA GAGGCCAGAGCAATCTGATCCATAGGAATTAAAGTATTGATATGCCTACT
Pparg	NM_013124.1	TTTATAGCTGTCATTATTCTCAGTGGAGACCGCCCAGGCTTGCTGAACGT GAAGCCCATCGAGGACATCCAAGACAACCTGCTGCAGGCCCTGGAACTCC
Ptgs2 (Cox2)	NM_017232.3	TTCGGAGGAGAAGTGGGTTTTAGGATCATCAACACTGCCTCAATTCAGTC TCTCATCTGCAATAATGTGAAAGGGTGTCCCTTTGCCTCTTTCAATGTGC
Ptk2b (Pyk2)	NM_017318.2	GCAGTGATCATGAAGAATCTTGACCACCCTCACATCGTCAAGCTGATTGG CATCATTGAAGAGGAACCCACATGGATCGTCATGGAACTGTATCCTTATG
Ptpn6 (SHP-1)	NM_053908.1	GCAGAGTCACTGCTGCAGGCCAAGGGCGAGCCCTGGACATTTCTTGTGCG TGAGAGTCTCAGCCAACCTGGTGATTTTGTGCTCTCTGTGCTCAATGACC
Rest	NM_031788.1	GCTGAGCTGGCTGCTCCCATGGAATCTACCAGTGCTTTATCCTCTGAACA AAGCTCAAATGCACCAGATGGTGAAACATTACACAGCGAGTGTCAGGCTG
Retnla (Fizz1)	NM_053333.1	AGGAACTTCTAGCCCATCAAGATAACTATCCCTCTGCTGTAAGGAAGACC CTCTCATGCACTAATGTCAAGTCTATGAGCAAATGGGCCTCCTGCCCTGC
Socs1	NM_145879.1	CGGCCGCTGCAGGAGCTGTGTCGCCAGCGCATCGTGGCCGCCGTGGGTCG

		CGAGAACCTGGCACGCATCCCTCTTAACCCGGTACTCCGTGACTACCTGA
Socs3	NM_053565.1	GGAAGACTGTCAACGGTCACCTGGACTCCTATGAGAAAGTGACCCAGCTG CCTGGACCCATTCGGGAGTTCCTGGACCAGTATGATGCTCCACTTTAAAG
Stim1	NM_001108496.2	TATCTATCGTGATTGGTGTGGGTGGCTGCTGGTTTGCCTATATCCAGAAC CGTTACTCTAAGGAGCACATGAAGAAAATGATGAAGGATCTGGAAGGATT
Tgfb1	NM_021578.2	CGCCTGCAGAGATTCAAGTCAACTGTGGAGCAACACGTAGAACTCTACCA GAAATATAGCAACAATTCCTGGCGTTACCTTGGTAACCGGCTGCTGACCC
Tgfbr1	NM_012775.2	GTCTGCATTGCACTTATGCTGATGGTCTATATCTGCCATAACCGCACTGT CATTCACCACCGCGTACCAAATGAAGAGGATCCCTCACTAGATCGCCCTT
Tgfbr2	NM_031132.3	CCAGCAGTCCTGACCTGTTGCTGGTCATTATCCAAGTGACGGGCGTCAGC CTCCTGCCTCCGCTGGGGATTGCCATAGCTGTCATTGCCATCTTCTACTG
Tlr2	NM_198769.2	TTTACAAACCCTTAGGGTAGGAAATGTTGACACTTTCAGTGAGATAAGGA GAATAGATTTTGCTGGGCTGACCTCTCTCAACGAACTTGAAATTCAGGTA
Tlr4	NM_019178.1	GTCAGTGTGCTTGTGGTAGCCACTGTAGCATTTCTGATATACCACTTCTA TTTTCACCTGATACTTATTGCTGGCTGTAAAAAGTACAGCAGAGGAGAAA
Tnf	NM_012675.2	GGTGATCGGTCCCAACAAGGAGGAGAAGTTCCCAAATGGGCTCCCTCTCA TCAGTTCCATGGCCCAGACCCTCACACTCAGATCATCTTCTCAAAACTCG
Tnfrsf1a (TNFR1)	NM_013091.1	TATTCTTTATCTGCATCAGTCTACTGTGCCGATATCCCCAGTGGAGGCCC AGGGTCTACTCCATCATTTGTAGGGATTCAGCTCCTGTCAAAGAGGTGGA
Tnfrsf1b (TNFR2)	NM_130426.4	AGGAGTTCAGATTCTTCCCATGGCAGCCACGGGACCCATGTCAACGTCAC CTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCTCTCAGTGTTCTT
Trem1	NM_001106885.1	TCAAATGACTGACCTTCAAGTGACAGACTCTGGATTATATCGTTGTGTGA TTTACCATCCTCCGAACGACCCTGTTCTGCTCTTCCATCCCGTCCGCCTG
Trem2	NM_001106884.1	TCCGGCTGGCTGAGGAAGGGTGCCATGGAACCTCTCCACGTGTTTGTCCT GTTGCTGGTCACAGAGCTGTCCCAAGCCCTCAACACCACAGTGCTGCAGG
Trpm2	NM_001011559.1	GTGAGCCTCCGGTCTCTCTATAAGCGATCAACAGGCCACGTTACCTTCAC CATTGACCCAGTCCGCGATCTTCTCATTTGGGCCATCATCCAGAACCACA
Trpm4	NM_001136229.1	AACTATTCTGCTTTCTTCTTGGTGGATGATGGTACCTATGGCCGCATGGG TGGTGAGAACCGCTTCCGCCTTCGGTTTGAGTCCTATGTGGCTCAGCAGA
Trpm7	XM_001056331.1	TTCTCTTCATTCAGAAACAGAGAGCTGTAGTAGAAGAGCGTCGACAGAAG ACTCTCCGGACGTAGATTCCAGAGCAGCTTTGTTGCCGGATTGGTTACGA
Tspo	NM_012515.1	GCTGCCCGCTTGCTGTATCCTTACCTGGCCTGGCTGGCCTTTGCCACCAT GCTCAACTACTATGTATGGCGTGATAACTCTGGTCGGCGAGGGGGCTCCC