

Appendix 4 – microarray probe sequences

Part A, genes of interest

Identity	Probe
12-lopky:2259	GGCCACCCACTTTCTACCACAATTACTTAGCTTTCTCACTATACCACTAG
12-lopky:2024	CTTATGAATACCTCAAGCCCAGCCGCATAGAGAACAGTATCACCATCTGA
ABC1:7627	ACTTTTCAAATACATTAGATCCTCCTAAGCAGCAAAGATTAGCAGCCAA
ABC1:6829	CCTTTTGCAGGATGAGAAAGTGAAGAAAGTTATGTATGAAGAATCCCG
BDNF:597	GTATCCAAAGGCCAACTGAAGCAGTATTTCTACGAGACCAAGTGTATCC
BDNF:782	AGACACTTCCTGTGTATGTACACTGACCATTAAAAGGGGAAGATAGTGGGA
C1qAlpha:513	AACCTCCAAGTGATCTCCAAGTGGGACCTTTGTCTGTTTATCAAGTCTTC
C1qAlpha:500	CTTCTATTACTTCAACTTCCAAGTGATCTCCAAGTGGGACCTTTGTCTGT
C1qR:2939	CAGGTTACTCTCCTCCTTAGAGCTACAACATAACATTTCTGAGGGGAGTCA
C1qR:1910	TTATCATAAACGGAGAGCCAAGAAGGAGGAGATAAAAGAGAAGAAGCCT
Catalase:1779	TGATGACTTTAAACGATAATCCGGGCTTCTAGAGTGAATGATAACCATG
Catalse:1787	TTAAAACGATAATCCGGGCTTCTAGAGTGAATGATAACCATGCTTTTGAT
cathepsinD:1011	GGTCTACCTGAAGCTAGGAGGCCAAAACTATGAACACACCCAGACAAGT
CathepsinD:1481	CTTCAAAGGCCCTACTGGTTTAAAGCTGCTGAGATGGATTGTCTTGTC
Caveolin:439	GTCTACTCCATCTACGTCCATACCTTCTGCGATCCACTCTTTGAAGCTAT
Caveolin:454	GTCCATACCTTCTGCGATCCACTCTTTGAAGCTATTGGCAAGATATTCAG
CD14:260	GCAGTTCACTGATATTATCAAGTCTCTGTCCTTAAAGCGGCTTACGGTGC
CD14:1200	AAATCTTAATCCACGATGTAAGGAAAGAAAGGCAGTCAAGATGGTTCAGT
CD36:2164	GCAACTGTGAGCAGATGGCATAAGTATAACATCTTGAAAGACTTAAGAAT
CD36:1298	GTATATTTGCGTCCACATTTCTCATGCAAGTCCAGATGTTTCAGAAC
CD36L2:1356	AGATCAACACTTACGTTAGGAAACTGGATGACTTTGTTGAAACGGGAGAC
CD36L2:1001	CTGTACCTCTTCCCGTCAGACTTGTGCGAGGTACGTACATATCACTTTCAG
CD40:1467	CCTAAAATGGATGTGGTGGTGTATTGTAGAAATTTAATCCGCCCTGG
CD40:1196	ATTATTTATACAATGGCATCTCAGAACTCTAGCAGGTGGGGCAGAAAAAC
CD40L:1028	AACCCCACTGATTACAGACAACCCAGAAAAAGACAAAGCCATAATACACAGAT
CD40L:505	GAAGGACTCTATTATGTCTACACTCAAGTCACCTTCTGCTCTAATCGGGA
CD68:614	GATTCAAACAGGACCTACATCAGAGCCCGAGTACAGTCTACCTGGACTAC
CD68long:1116	ATCTCTTCACCATGCCACTGACTCAACAGTTACCTTCTCTCTGTCTTT
CD200:1413	CGCCAGTGTGTTTCCCTGTTGTTTGAGTATCTAGTTGACTACCTGTTACT
CD200:1691	CAATAACACTTTCTTTGAGGCCATTCTGAATCCTGTCTCGTGAATGATA
CD200R:635	CCTGCATTGTCTCTCATTTGACTGGTAACCAATCTCTGTCCATAGAAGT
CD200R:368	ATGAGGGGACTTACACATGTGAGACAGTAACACCTGAAGGGAATTTTGAA
Clecsf12:2192	CCACTGAATTGTTCTCTTGAAAAATGATTGGGTTTATGTCACTTTCATCTC
Clecsf12:2133	GGGGATCTGTTTATAGCTTTCTCAGACTAATCAATATGTGGGCAGAAATT
Clecsf10:1140	GGTCTTGCCCTGGTTTCTTTCTATGAACTGCTGTTACTTGAAAGTATAAG
Clecsf10:674	GTTTCAATAGTTTACTGGAATCCTTCGAAATGGGGCTGGAATGATGTTTT
Cleccsf9:2201	TTCTGTCTTGGGTTTATTTGCATGGTTTCATTACACTCCTTGACTTGAT
Clecsf9:2135	GCTTCATATTTAAAGATTCTGAATTCCATCAAAGGGCACACAAAGAAATC
Clecsf5:694	ATTAGTTGTGACTGAAACCAGCCCAGGAAATATAGAGCATCAAAGACTGT
Clecsf5:682	CTAGCAAAGGAGATTAGTTGTGACTGAAACCAGCCCAGGAAATATAGAGC
CR1:1694	TAAATTATAAAGAAGACAGCTGTGTCGCCCTTCAGTCTCTGCTCACAAGT
CR1:933	TTGATTGGGATACTGAGGACCTATTTGTGAGTGGATTCTTGTGAGATAC
CR2:2052	GGGCTCAGCACTTATCATTTTGATGAGTGTGCGCTTCTGTATGATATTAA
CR2:2017	CGGTCAACTATTCTCTTATTTGTGGTATTTCTGTGGGCTCAGCACTTAT
CR3:3335	CTGTGAAGTACGCCATCTACATGATTGTCACCAAGTATGAGAGTTCTATC
CR3:4094	CAACACCGAAGCTAGTGACACATATGTTGTTGCTGTGATGTCTTATACAA
CRP:213	GTCAAAGAAGCCACTGAACACCTTTACTGTGTGTCTCCATTTCTACACTG
CRP:1431	CAGCCACTGATTACCTCTAGCTCTTCATATAGGGTTCTGTCTTTGTGAAA
CRP-Ductin:6420	GCCAAGTTTTCCAGGATCTATCAGACTGAAGGCTAGGAAGAAATGTCATA
CRP-Ductin:5915	CCCTCAGTGTACCTGCAGTGTAAGTGGTAGTATGTCGAGCGTATGATA
Cryst.A2:1098	TGATTGAAAACTGTGACTAGTGTGAAGCTTATTAATGCTAAGGGCTGG
Cryst.A2:403	TAAAACCCCTGACCTCACCATTCAGAAAGCTTCAGAAGACTGCATATATA

Identity	Probe
CrystB2:327	GGACAGCCAAGAGCACAAGATCATCTTATATGAGAACCCCAACTTTACTG
CrystB2:367	AACTTTACTGGCAAGAAGATGGAGATTGTAGACGACGATGTGCCAGCTT
CNTFfull:1391	CAATACATACTCTTACGCTCCAAGTTTCTGCCTTCGCCTACCAGCTAGAG
CNTFfull:1151	GTTTCAGACCTGACTGCTCTTATGGAATCTTATGTAAAACATCAAGGCCTG
Cxcr3:1522	TGAATGTGCCCATCTCAGTATCTCAATATTTGCCCAATTTTATTTCTAGA
Cxcr3:1368	ATTACTGTGCCTTAGCTGCCATGCCCTATCTTGCTGTTTTAGAACTAGCT
Doppell:2940	CAACGATCACTTGTATAATTTTGTCTCTGCGGTTTGTAATTCCTGATT
Doppell:2212	ACAGTTTACCCCTTGCACGCCATTTAAATATCAGACAATAAAGAAGGAA
FasL:1264	GCCAAGAGAATTTTAACCATTTGAAGAAGACACCTTTACACTCACTTCCAG
FasL:1445	CCATCTTTACTGTTACCTAATGTTTTCTGAGCCGACCTTTGATCCTAACG
Fgf2:301	TTCTTCTTTGAACGACTGGAATCTAATAACTACAATACCTACCGGTCACG
Fgf2:244	CTTGCTATGAAGGAAGATGGACGGCTGCTGGCTTCTAAGTGTGTTACAGA
Fpr:825	ATTGCCAGTTATCATTCGTTTGACCACAGTCCCTAATAGTAGACTTGGAC
Fpr:787	GTAATCATCGTACCCTGGATTTGTGCATTTCTTCTTACATTGCCAGTTAT
FPRL1:1041	GACTCTGGTCATATCAGTGATACAAGAACCAATTTGGCTTCACTTCCCTGA
Fpr-rs1:515	GTAGATTGAGCTTTGTATCCTGGGGCAACTCTGTTGAGGAAAGGTTGAAC
Fpr-rs2long:873	CCTTTTGGGCACAGTCTGGTTTAAAGAGACATTGCTTAGTGGTAGTTATA
Fpr-rs2long:1014	CTTTCGTGAGAGATTTATTCAATCCCTGCCTTATAGTCTTGAGAGAGCCC
Fpr-rs3:603	GAATCATCAGTTTTATTAAATGCTTCAGCCTACCCATGTCCTTCAATTGCC
Fpr-rs3:615	TTTTATTAAATGCTTCAGCCTACCCATGTCCTTCAATGCCGCTGCTATG
Fpr-rs4long:875	AGATGCAAGAGGGGATGTGTACTGTATATCTAAATTTGAATCCTGGGTG
Fpr-rs4long:468	CTCTTTATAACCTTTGTCCTCGGTGTTCTAGGTAATGGGCTTGTGATTTG
Frac.:2918	AGAATGTGGGCCGTAACAACTGAGGAGGACTTTAAAAGTTGTTGATCCT
Frac.:1939	ATAACCTATGGCCCTGACATCATCACTTTCTCTGAGATCCTTGTCTCCAC
Gdnf:2992	AAGAGGTAAAAGTTACTAGGTATCCTTTCCCTTCCGTGGCCCTAAAGAC
Gdnf:2952	GGCCTCTCTCGAATAGTCATGTCAAATTTTCAAAGTAACCAAGAGGTAAA
Gfap:1921	CACTGGTAGAGATCATTTGGACACTCGGAGTTGAAAGTTACAGGCAATCT
Gfap:1371	GCTTCATAGATGGCATAGATGGCATATACCTTCACTTCAACTAACAGG
GMFb:3760	GGTTCGTGAGCTGAATATTTCTTGGTAGGCCATGTGACACTTCAGATCAGT
GMFb:4067	TTTCTGCTAGTTCATACCGCATGTTATTTTGAGTCTTTTGGTAAGCAT
GPX1:863	CTGTGTCATTGTCACCTTTTGGATAGCCTCATAGTCAGGGATAAGGAAC
GPX1:348	AGCCCAATTTTACATTGTTTGAGAAGTGCGAAGTGAATGGTGAGAAAGCT
GSR:1244	AAGACAATGTGAAAACTACTCGACTGCCTTTACCCCGATGTATCAGCCT
GSR:1231	CATAAGTATGGGAAAGACAATGTGAAAATCTACTCGACTGCCTTTACCCC
GSS:1299	GTATTTTGGAGTCTATGTGACAGAGGAACAACACTGGTGATGAACAAG
GSS:624	CTAATGCGGTGGTGCTACTGATTGCTCAAGAGAAGGAAAGGAACATATTT
GST-Pi:707	CTTCTGTCCCCGTTTCCCAGCACTAATAAAGTTTGTAAAGACAGAAAAA
GST-Pi:702	AAGAGCTTCTGTCCCCGTTTCCCAGCACTAATAAAGTTTGTAAAGACAG
HemeOx.:1429	GGGGTGGGTGGGAAAGAATTATTTAATAGTTGTAACCTTGGTCTCTAACT
HemeOx.:1314	TTCTGTCTCGTATTCTGTCTGTTTTTATTATTTCCCCAGTTCTACCA
HM74:1863	GGGCGGTTCACTTACTTGGGTTTCTGTACTTTAACATCTACCATTTCAATA
HM74:1212	GAACAGGGTAACATCTTCAGATTTGGCTTACGCTTTCTTGGAACTTCTAG
Hsp25:745	CAATCTGTGCGCTCTTTGATACATACATTTACCTGCTGTTTTCTCAAA
Hsp25:736	CCTCTGTCAATCTGTGCGCTCTTTTGATACATACATTTACCTGCTGTT
IFNa4:232	ATCCTTGTGCTAAGAGATCTTACCCAGCAGATTTTGAACCTCTTCACATC
IFNa4:29	TCCTAGTAATGATGAGCTACTACTGGTCAGCCTGTTCTCTAGGATGTGAC
IFNb:457	AAAGGTACCTTAAACTCATGAAGTACAACAGCTACGCCTGGATGGTGGTC
IFNb:507	CGAGCAGAGATCTTCAGGAACCTTCTCATCATTCGAAGACTTACCAGAAA
IFNg:773	ATTATTTCTTCTGACTAATTAGCCAAGACTGTGATTGCGGGGTTGTATCT
IFNg:862	TGTAGCTTGTACCTTTACTTCACTGACCAATAAGAAACATTCAGAGCTGC
IGF2:3007	ATTAGGACCCCAATTTATGCCAATGATCTATTCCTCTTTTATTTCT
IGF2:4032	TCAAAGAGTAAATTGTTATAATTGGAGACTATGAATTGGCCTGGTATCCA
IL-10:692	TAACGGAAACAACCTCTGGAAAACCTCGTTGTACCTCTCTCCGAAATA

Identity	Probe
IL-10:889	GTATTTAAAGGGAGATTATATTATATGATGGGAGGGGTTCTTCTTGGGA
IL-12b:1446	TTACATTTGTATACCAAGATGTATTGAATATTTTCATGTGCTTGTGGCCT
IL-12b:1562	TCAGGGCTTCGTAGGTACATTAGCTTTTGTGACAACCAATAAGAACATAA
IL-1aii:1027	GCAAACCCTAGTGGAGGCCACCCCGACATATGATACTATCTGTTATTTTAA
IL-1aii:1836	TGAAGTTTCTTTCTAGAATGTAATCAGTGTTCCTCGGATTCCAATTT
IL-1b:1125	TTAAGTTGATTCAAGGGGACATTAGGCAGCACTCTCTAGAACAGAACCTA
IL-1b:612	CTCAAAGGAAAGAATCTATACCTGTCTGTGTAATGAAAGACGGCACACC
IL-6:514	TAAAAAGTCTTCTACCCCAATTTCCAATGCTCTCTAACAGATAAGC
IL-6:149	ACTCCCAACAGACCTGTCTATACCACTTCACAAGTCGGAGGCTTAATTAC
Integ.aV:3226	GCTACTGGCTGTGTTGGTATTTGTAATGTACAGGATGGGCTTTTCAAAC
Integ.aV:3061	GTCATCTGCTTCTTTAATATCATAGAAATCCCTTACAAGAACCTGCCAA
Integ.b3:2506	GGGCTGGAAGAATGTCAAGTATGTGGGAATGTATCTCTGTGTGTACTTA
Integ.b3:2367	CTTCACCAATATCACCTACCGGGGGGACTTAATGAGACCACTTCAGATGAC
Integ.b5:2246	GCTTCTACAAAAGTCTAAGGACTGCGTTATGATGTTTCTAGCTACACAGAA
Integ.b5:1204	TTTGCTGTGACGAAGAACCCTATATGCTCTACAAGAATTTTACAGCCCT
IDO:1312	CTATCAGGGCAGCAAAAACACCTTCATCCTGTCTAGTCTCATTTAAATCAG
IDO:1107	TGAGAAAAGTTCCACCTCGCAATAGTAGATACTTACATTATGAAACCTTCG
LamR:676	ATCTTTACTTCTACAGAGACCCAGAGGAGATTGAGAAGGAGGAGCAGGCT
LamR:664	AGGTCATGCCTGATCTTTACTTCTACAGAGACCCAGAGGAGATTGAGAAG
Lox-1:3423	TGGAATTACAGACGTTTTTGAACAATCCTATAGACTCTGGGAAGTGAACC
Lox-1:2872	TGGATCTATAGTGTCAATTTGTATCTGTGTAATTTGTTGATGCCATTTGGG
LBP:1401	AGGCATTCTTAACCTACTACCTTCTCAACAGCCTCTACCTGATGTCAAT
LBP:1111	ATACAAAAAGTATCCCGACATGAAATTGGAGCTCCTTAGAACAGTGGTCT
M130:2853	GATCATCTGTGACAACAAAAAAGACTCCAGGAAGGGGCATACAGACTGTT
M130:3823	TAAATTTCTGGTTGGTTTTCTGACGTTTTAGGGTTTCGTGAATATAAA
MARCO:1446	CAACAGAGGCCGAGCTGAAGTTTACTATAACAATGAGTGGGGGACAATTT
MARCO:137	TTGGCCACCTATAAAGCTTAGCAATGGGAAGTAAAGAAGCTCTCAAGAG
Mbl1:400	GAGAAGCTGGCAAATATGGAGGCAGAGATAAGGATCCTGAAATCAAAACT
Mbl1:51	CAGAAGCTGGACTCGAGACATAGTTTCTCTTCCACTGCTCCTTACTCTA
Mbl2:955	TGACGTCCGCAGTTTGTCTGAAAAATAAAATATGGGAAAAATATAAACAA
Mbl2:939	CTTGATTCTTTAGGGTACTCCTGACGTCCGCAGTTTGTCTGAAAAATAA
Mrc1:4829	TTCAGGACCTCCCAGAGATATGTTATACACCGAATGTGAATTCACATTT
Mrc1:4659	AAAACAGAAGAGGGGATAATAATGTTGATTGTTGATTGCCACTTTTGAAGA
Mrc2:2784	GAGAGTGACGGACGCTTCAGGTGGACAGATGGTTCTATTATAAACTTCAT
Mrc2:4501	ACATTCTGGTGTCTGACATGGAAATGAACGAACAGCAAGAATAGAGCCAA
NCF1long:1179	CCCTAGACGGCTCCTATCCCTATCTCTGTATATACTTGTGTATAGCCTCA
NCF1:145	GGAGAAGGTGGTCTACAGAAAAATCACCGAGATCTACGAGTCCATAAAA
NCF2:1664	GAGAAGTCTAGGATACAAAGCTGAAGCAAAGTGTGTTTTTCCCTTG
NCF2:343	AGAATGGAGAAGTACGACCTTGCTATCAAAGACCTTAAAGAGGCCTTGAC
NGFb:772	AGTGCTGGCCGAGGTGAACATTAACAACAGTGATTACAGACAGTACTTTT
NGFb:287	GTGCATAGCGTAATGTCCATGTTGTTCTACACTCTGATCACTGCGTTTTT
Nod1:1451	GACAGTTGGAATGTTGCAGATAACGTGTTCTTTGCCAGTTCATTTGTTA
Nod1:964	CATGGTTATTCTGAGTCTCTCTCTCTGCTTAGTCCCTCTCACTGTACA
Nos1:4287	GTCACCCCTCAGAACATATGAAGTGACCAACCGCCTTAGATCTGAGTCCAT
Nos1:3936	GTCTTCGGGTGTGCAATCCAAGATAGATCATATCTACAGAGAGGAGAC
Nos2:3932	CACCATGCCGCCGCTCTAATACTTAGCTGCACTATGTACAGATATTTATA
Nos2:3519	AGAGCCAGAAACGTTATCATGAAGATATCTTCGGTGCAGTCTTTTCTAT
NT3:563	AACAATATTTTTATGAAACGAGATGTAAAGAAGCCAGGCCGGTCAAAAAAC
NT3:3	GTCCATCTTGTTTTATGTGATATTTCTTGCTTATCTCCGTGGCATCCAAG
Osi:1835	ATGTGAAGCCGAATGAAGGATCTTATCTTATACTGTCCCCCTTTCTAATG
Osi:1747	AATAAAGCCATTATGTTAAGAGGGGACTGTCCATAGTGAGTGAAAGGTGG
P2AGA4A:2201	TCAACACACTGAACAACATTGATGTGATAAAGGATGCCATTGTTGAGAGC
P2AG4A:1715	CACTGGATGTCAAAAAGTAAGAAGATTCATGTGGTAGATAGTGGGCTCACA
PafR:1091	AGCCAACCAGACTCCTATTGTGTGCTGAAAAATTAATCTCTGCTTATTA

Identity	Probe
PafR:132	TCTGAGTTTCGATACACGCTCTTTCCGATTGTTTACAGTGTCATCTTTAT
Pgrp:529	AAAGCTGGGAACACTACCGAGAGTGAGAGACCTTGAGACCTAGTGAGAAT
Pgrp533	CTGGGAACACTACCGAGAGTGAGAGACCTTGAGACCTAGTGAGAATCCCC
Pgrp-L:1734	GAGGTATTATCCCTGATGATCCTTTGAGCAACCACAGACCTCCAATAAAG
Pgrp-L:1697	AACTAAGAACTCCTTTGAGAGACCCTTGAAGATCCAGGAGGTATTATCCC
Pmp:1824	AGACATAAACTGCGATAGCTTCAGCTTGACACTGGGATTCTGTATAGA
Pmp:1473	AGGGCACTAGAATGATCTTTAGCCTTGCTTGGATTGAAGTAGGAGATCTT
ProtoCadg:4240	GTAGAATAGCCAATAGTATAGTGTGGTGTGCTTTTACGTGATGGCGAGTG
ProtiCadg:4180	ATAGAACTTCCTCTGCCCTAGCCCTTACAGTAGTGTAGAAGATCCCCCTC
PSR:1081	TGGCACAAGACGGTAAGAGGGAGACCAAAGTTATCAAGGAAGTGGTATAG
PSR:629	TGGAAGACTACAAGGTGCCCAAGTTTTTCACAGATGATCTTTTCCAATAC
Ptgs-1:2595	GTCAAGGCAGTAAGGTGTTCTTGGGAGCCACACTTAGACTCTTTCCAAAG
Ptgs-1:1259	AGTTTTTATTTAACACTTCTATGCTGGTGGACTATGGGGTTGAGGCACTG
Ptgs-2:3181	CGCTGATTGGGTTTTCGTAGCTGTGTTACCAGGTTTTTAGTATCAGAACT
Ptgs-2:3843	TGCATAGGATCCAATATTGACTGACCCAAGCATGTTATAAAGACTGACAT
RAGE:1296	CCTTCTCCAACCAGAGCCCATGATCCATGCTGAGTAAACATTTGATAC
RAGE:486	AAACTTCTGATTCCCGATGGCAAAGAAACACTCGTGAAGGAAGAGACCAG
Rp105:2828	TACATCCATCATCTGTCTTTTTAAATGTAATTGTGCCCTCGTGTCTGTCT
Rp105:2124	AAGAGTTGATTTTCTCCAGTTAGTACAGAATGCTATGGCAATTGGTGTGG
SAP:923	TGTGAACATCTTGATACATATCTGCCAAATAAAAACTCTCTCCAATTCC
SAP:764	TGAATTGGCAGGCTCTTAACTATGAAATAAATGGCTACGTAGTCATCAGG
Scya3:636	CTCCCAGTTGTTACACTGTTTGGTGACAGCTATTCTAGGTAGACATGAT
Scya3:472	GCTGCCAAGTAGCCACATCGAGGGACTCTTCACTTGAAATTTTATTTAAT
Scya4:451	GATTTCTGCCCTCTTCTTAATTTAAATCTCTGTGTAGACTTTGTTTTG
Scya4:431	GTCCTTGCTCCTCACGTTTCAGATTTCTGCCCTCTTCTTAATTTAAATC
Scyb9:1098	TTTGCCTCTTCAATAAACTCTCCTAGAAGGTTGTGGCTGTAGCTTAGTG
Scyb9:956	ATTGTGTCTCAGAGATGGTGCTAATGGTTTTGGGGTTCTACAGTGGAGAC
Scyb10:786	TCCCAAGGGGTTATCAAGATACTCAGAGGAACCTGAAAATGTATGTGTAA
Scyb10:267	ATCCGGAATCTAAGACCATCAAGAATTTAATGAAAGCGTTAGCCAAAAA
Sialoadhesin:6600	AAAAATTTGGCGTTTCCCTAGGTGTCTTACTTACTGTTCTTTTGCTGTGAG
Sialoadhesin:6487	ATGTTGAAGAGAGTGGCATTATTAGGCTAGGGTCTGAATTAGTGTTCCGA
SLC:658	GGGGTAGACCTAGAGAGTCAGAAAGAAAGAGTGTCTCCAGGGAATGAGGA
SLC:158	AGAAAAATCCCTACAGTATTGTCCGAGGCTATAGGAAGCAAGAACCAAGT
SLC1A1	TTCCCGAAGATGGCTTATAAAAGTCTACACTTCTGTCTCATCTGTAAA
SLC1A1	CTGCCTGTCTTTCTCCTGCTAATTTCCCGAAGATGGCTTATAAAAGTCTAC
SLC1A2:1591	TTTACGACGACAAGAACCACAGGGAAAGCAACTCTAATCAGTGTGTCTAT
SLC1A2:1953	CAAGAAATGGTGGTGTGTCAGAACTTTAATGGCCTTCAGATATTCTCTCC
SLC1A3:172	ATATAAGTGAATAACAAGCGTGAACTGGTCTACGGAGCAAAAACAAAG
SLC1A3:146	TCTCAGGTCTGATTTTGCCTTTCTAATATAAGTGAACATAACAAGGCGTG
SOD-1:375	AAGATGACTTGGGCAAGGTGGAAATGAAGAAAGTACAAAGACTGGAAAT
SOD-1:153	AGTATGGGGACAATACACAAGGCTGTACCAGTGCAGGACCTCATTTTAAT
SOD-2:605	TGGGAGCACGCTTACTACCTCAGTATAAAAACGTCAGACCTGACTATCT
SOD-2:407	GAGGCTATCAAGCGTGACTTTGGGTCTTTTGAGAAGTTTAAGGAGAAGCT
SRA-I:1505	TTTCTCAAATACAAATAGAGATTGAAATAGGGGTCTGTCCATCCATTCA
SRA-I:1024	GACAAAAGGGAGAGAAGGGGAGTGATGGCGGATCAAGATCAGTATAACTC
SRA-II:2139	GCCAAAGTCACACAGTCAGAAGTAAGTACTACTAACCAGGATCATGAA
SRA-II:1983	TCTAACAAAGCACATACAACAAAAGAACTCTCAGTGCCTGTTTCTTCT
SRB-I:2222	GCGCTTTTCTATCGTCTCTGCTATGTCACTGAATTAACCACTGTACGTG
SRB-I:908	GACTCAGCAAGATCGATTATTGGCATTCAGAGCAGTGAACATGATCAAT
SRCL:2536	GGACTGAATCGCATAGATTTTCTCAGCCATTAACCATAGAAATTTATGCAA
SRCL:2277	TTTCAATTTGTGAGAAGGAAAGGGAGGCAGTACCATCATCCATATTATAGCA
TGFb:1371	GGAAGTCTACCAGAAATATAGCAACAATTCCTGGCGTTACCTTGGTAACC
TGFb:714	GCTGCTTTCTCCCTCAACCTCAAAATTTTTCAGGACTATCACCTACCTTTC
TNFa:1495	ATTTATCTAACCAATTTGTCTTAATAACGCTGATTTGGTGACCAGGCTGT
TNFa:1508	AATTGTCTTAATAACGCTGATTTGGTGACCAGGCTGTGCTACATCACTG

Identity	Probe
TNFa:1326	ATTATTTGCTTATGAATGTATTTATTTGGAAGGCCGGGGTGTCTGGAG
TLR1full:2431	GCTGCTCTGGGGAGTTCTAATAATAGTACCATTATATCAGCAAGAACCT
TLR1full:2416	CACCTCAATGATGTTGCTGCTCTGGGGAGTTCTAATAATAGTACCATTCA
TLR2:2626	GCAGGAAGTGTGTTGGGTAAATCTGAGAACTGCAATAAAGTCCTAGGTTC
TLR2:2621	GGCCAGCAGGAAGTGTGTTGGGTAAATCTGAGAACTGCAATAAAGTCCTA
TLR3:2740	ATCTCGGAATTCAGCACATTAAACTCATTTGAAGATTTGGAGTCGGTAAA
TLR3:2727	AAGTAGCACTTGGATCTCGGAATTCAGCACATTAAACTCATTTGAAGATT
TLR4:3513	TAACATCCTTTTCCTTCATCATTCTCATTTCTGGACATGCCTTGTGAGAT
TLR4:3412	TCACATAGCTGAATGACAAGACTACATATGCTGCAACTGATGTTCTTCT
TLR5:4226	CCTTCTTTCTTCCCCACAACATATAACAAGAGCTGTTGCAACCACTGAAAAA
TLR5:4048	CACAAGTGATAAGAAGTTGGACAGATAGACAGATAGCAGCAGTCCCATTG
TLR5:4038	CACCTAAGTGACAAGTGATAAGAAGTTGGACAGATAGACAGATAGCAGC
TLR6:2400	ATGAAGTTAGCCTTAGTCAATGAGGATGATGTGAAAACCTTGAAACTTGGG
TLR6:2490	ACTGTGGTTTTTCAGTTCTACCTGGAGGTACTTCTGTTGTGGTGTCTTAG
TLR7:2942	CTGAGAGTTTAAAGATGGCATTTTATTTGTCTCATCAGAGGCTCCTGGAT
TLR7:3157	GACAATCATGTGGCTTATAGTCAAATGTTCAAGGAAACAGTCTAGCTCTC
TLR8:2706	CTGTTACTGACTGGGTAATCAATGAACTGCGCTACCACCTTGAAGAGAGT
TLR8:2630	TTAAAAGGCTACAGGACTTCATCCACATCCCAAACCTTTCTATGATGCTTA
TLR9:2081	CTGAGCCTCCGAGACAACCTACCTATCTTTCTTTAACTGGACCAGTCTGTC
TLR9:3386	GAGAGTGAAGATAGACACCAGACCCACACAGAACAGGACTGGAGTTCATT
TREM-1:713	GAAGCTATACAATAGTGACCTTCAGCGGTGTCTATTTACAGGAGGAGCT
TREM-1:482	TATTACCACAAAATACTACCCAGTGACACAACCTACAACCCGATCCCTAC
TREM-2:754	AATTCTGAGTGGGAGGAGAACTACAGCTTAAGTCCAGCCAGGAGTCAATC
TREM-2:741	AGGTACGTGAGAGAAATCTGAGTGGGAGGAGAACTACAGCTTAAGTCCAG
TREM-3:707	CTTCCTACATTCTCCTTGTGAACTCTAGTTAGCACATGATACTCCCAGAG
TREM-3:633	CTACAAGCTGTGAGCACACCTTCCCTTATCTATTAACAACATACCAGATG

Appendix 4, probe sequences
Part B, Control probes

Identity	Probe
EF-1a:1469	GGAAGAACGGTCTCAGAACTGTTTGTCTCAATTGGCCATTTAAGTTTAAT
EF-1a:1143	ATGCAAGTTTGCTGAGCTTAAAGAAAAGATCGATCGTCGTTCTGGTAAGA
c-yes:4384	CACCAGAAACGAAAGTTGTTAAAAGCAGCCTTCTAGCACAAACACTTTTT
c-yes:4338	TTTTCAACAGCTTTCATCTGTATTGTCTTAACGTGGAACTTTAACACACC
Zeta-p:607	TTGCAAGAAGTTTACCATAAGTCTATGACTCTGAAGGAGGCCATCAAGTC
Zeta-p:184	ATCCAGACCTCAGAGGGTGTATGTCTAGCTGTGGAGAAGAGAATTACCTC
PP1cg:2050	AACAACACTGTCCTATACGAGTGACCGATAATGCTTTCTTTGGCTACATT
PP1cg:2017	AACCCGTCCATTTCAGAAAGCTTCAAATTATAGAAACAACACTGTCCTATA
Tuba1:1522	TTATGAATGATTGATTTTGACAGAGACCCCAAGCTGCCCATTTCACTTAT
Tuba1:1509	TACAGTTACTGACTTATGAATGATTGATTTTGACAGAGACCCCAAGCTGC
Vimentin:1588	GGAGCGCAAGATAGATTTGGAATAGAAAGAAGCTCAGCACTTAACAACCTG
Vimentin:1569	CCTTTACTGCAGTTTTTCAGGAGCGCAAGATAGATTTGGAATAGAAAGAA
GNAS:2241	TGAAAAACCCCTCTTCCCTTCAGCTTGCTTAGATTTCCAAATTTAGTAAG
GNAS:1936	AGTACTTCATTCGGGATGAGTTTCTGAGAATCAGCACTGCTAGTGAGAT
Cofilin:964	TTGTCTGTTTGTCTGTGTGTAAATGAAATGTGGAAATGACCCTCCCTG
Cofilin:459	ATGCCATCAAGAAGAAGCTGACAGGAATCAAGCATGAATTACAAGCTAAC
y-box:1164	TAAGAAATGAACAAAGATTGGAGCTGAAGACCTTAAGTGCTTGCTTTTTG
Y-box:792	AGGAGAGCAAGGTAGACCAGTGAGACAGAATATGTATCGGGGTACAGAC
Lac.dehy:1602	ATTATGTGAGATGTAAGATCTGCATATGGATGATGGAACCAACCACCCAA
Lac.dehy:1491	GTTAAGTCGTATAACCTGGCTCCAGTGTTGTACGTCCATGATGCATATCTT
Pbp:786	GGGGAGGGGTCTAATGTTCTGATGGAGTCATTCTGTTGTTGATATAAAAA
Pbp:661	CTCTCATTGGGAGTTCTTAGCTGTGCTAGGATAGAGGTTTAGGGTGCTT
B-actin:1702	GCCTTAATACTTCATTTTTGTTTTTAATTTCTGAATGGCCAGGTCTGAG
B-actin:1197	AAGTGCTTCTAGGCGGACTGTTACTGAGCTGCGTTTTACACCTTTCTTT
Rheb:763	TATATTCCACCTGAGGAGCAAACCTGCCCGTCATCCTTGAGATAAACTAT
Rheb:473	CATGGCAAGTTGTTGGATATGGTGGGGAAGTGCAGATACCTATTATGTT
Ferritin:468	CTACTGACAAGAATGATCCCCACTTATGTGACTTCATTGAGACGCATTAC
Ferritin:252	AGAACTTTGCCAAATACTTTCTCCATCAATCTCATGAAGAGAGGGAGCAT
GSK3b:1205	AATGTCAAACCTACCAAATGGGCGAGACACACCTGCACTCTTCAACTTTAC
GSK3b:808	TTCATATATCTGTTCTCGGTACTACAGGGCACCAGAGTTGATCTTTGGAG

Identity	Probe
CCR1:843	GAACCCTAGAGCCAAGCCATACAAATTCCTAACCAGAAGATTAAGGACT
CCR1:636	CGGCTCGGCTAAGACTTATGCTAATTTGACTCAAGCTTATGTGGATGTTT
Chlorophyll:355	TGGCATTTTCATTCCAGAAATTCCTAACAAAGATTGGTGTCTTGAACACTC
Chlorophyll:85	AGGAGGTTGTTTTCTTAGTGGAAGGAAATGAGGGTGAAAAAGGAGAGAG
Cellodex.:1215	TCTCCCTCAAACCTCCCTTCTTAACTTTTCAGTATTAAATTTTGCCCAT
Cellodex.:923	AGAAGTACGGCACTACTCTTACTGCGGTGAATACGGTGTGATCGATGTC
CelA:83	CGCTGTTCTTCATTATACCTTTGCTACTCTTATTGGGCCTAGTATCTCGG
Lpo:1188	TTGTCACGGAATATCGGTCTCTGTACTAGAAGTGTTCCTCTCGTGATC
Endotoxin:3357	AGAGAAATCCTTGTGAATTTAACAGAGGGTATAGGGATTACACGCCACTAC
Endotoxin:1808	TTGTTCCGGCAGAAGTAACCTTTGAGGCAGAATATGATTTAGAAAGAGCA
Ald5H:117	CGCTGTTCTTCATTATACCTTTGCTACTCTTATTGGGCCTAGTATCTCGG
Ald5H:1123	AGAGAAAGACTTCGAGAAGCTCACCTACTTGAATGCGTACTGAAGGAAG