

hNFATc1 MPSTSFVPVSKFPLGPAAAVFGRGETLGPAPRAGGTMKSAEEEHYGYASSNVSPALPLPTAHSTLPAPCH 70

hNFATc2 ---MNAPERQPPDQ-----GDAPGHEPFGSPQDELDFSI LFDYELNPNNEEPNAHKVASFPSPGPA 59

mNFATc3 MTTANCGAHDELDFK---LVFGEDGAPAPVSVSRPADLEPDDCASIIYIFNVDPSPSTLNSSLGLPHHGL 67

mNFATc4 MGAASC-EDEELEFK---LVFGEEKEPPLGPGGPEELDSEDTPPCRLALGEP LYPYGAAPIGIPRPPP 66

hNFATc1-ca MPSTSFVPVSKFPLGPAAAVFGRGETLGPAPRAGGTMKSAEEEHYGYASSNVSPALPLPTAHSTLPAPCH 70

hNFATc1 NLQTSTPGIIPPADHPSGYGAALDGGPAGYFLSSGHTRPDGAPALESPRIEITSSCLGLYHNNNQFFHDVE 140

hNFATc2 YPDDVLDYGLKPYSPLASLSGEPGR-----FGEPRVGPQKFLSAAKPAGASGLSPRIEITPSHELIQ 123

mNFATc3 LQS--HSSVLSPSFQLQGYKNEYGTGDISSES---KYSPLGGPKPFCEPSIQITSSISPNCHQGTDAHEDDL 132

mNFATc4 PRPGMHSPPPRPAPSPGTWESQPARSVRLGGPGGNAGGAGGRRVLECP SIRITSSISPTPDPPPTSLEDTSE 136

hNFATc1-ca NLQTSTPGIIPPADHPSGYGAALDGGPAGYFLSSGHTRPDGAPALESPRIEITSSCLGLYHNNNQFFHDVE 140

hNFATc1 VEDVLPSSKRSPSTATLSLPSLEAYRDPSC LSPAS---SLSSRSCNSEASSYESNYSYPYASP----- 200

hNFATc2 AVGPLMRDAGLLVEQP--PLAGVAASPRFTLPVPGFEGYREPLCLSPASSGSSASFISDTFS----- 191

mNFATc3 HINDPEREYLERPSRDHLYLPLEPSYRESSLSPS-ASSISSRWFSDASSCESLSHIYDDVDSELNEAA 201

mNFATc4 TWGDGSPRDYPPPEGFGGYREAGGQGGGAFFSPSPGSSSLSSWFFSDASDEAALYAACDEVESELNEAA 206

hNFATc1-ca VEDVLPSSKRSPSTATLSLPSLEAYRDPSC LSPAA---ALAA RACN EAAAYEANYAYPYAAP----- 200

hNFATc1 ----QTS PWQSPCVSPKTTDPEEGFPRGLGACTLLGSPRHSPSTSPRASVTEESWLGAR-----SSRPA 260

hNFATc2 -----PYTSPCVSPNNGGDDLCQPFQ-IPAHYSPRTSPIMSPRTSLAEDSCLGRHSPVPRPASRSS 246

mNFATc3 ARFTLGSPLTSPGGSPGGCPGEESWHQYQYSGHSL-SPRQSPCHSPRSSITDENWLSRPASG-PSSRPT 269

mNFATc4 SRFGLSPLSPRASPRPWTPEDPWSLYGPSSGGR-APEDS-----WLLSAPGPVP-ASRPA 263

hNFATc1-ca ----QTAPWQAPCVAPKTTDPEEGFPRGLGACTLLGAPQHAPSTSPRASVTEESWLGAR-----SSRPA 260

hNFATc1 SPCNKRRKYS L NGRQPP----YSPHHSPTPSPHGSPRVSVTDDSWLGNTTQYTSSAIVAAINALTTDSSLD 326

hNFATc2 SPGAKRRHS SCAEALVALPPGAS PQRSRSPSPQPSHSHVAPQDHGSPAGYPPVAG---SAVIMDALNSLATD 313

mNFATc3 SPCGKRRHS SAEVCYAGS--LSPHHSVPVSPHSPRGSVTEDTWL-TAPVHTGSGLS PAFPFFQYCVETD 336

mNFATc4 SPCGKRRYS SSGTPSS-----ASPALSRRGSLGEEGPEPPPP-PPLPLVRDPSSPGPFDYVGAPTE 324

hNFATc1-ca SPCNKRRKYS L NGRQPP----YAPHHAPTAPHGAPRVSVTDDSWLGNTTQYTSSAIVAAINALTTDSSLD 326

hNFATc1 LGDGV PVKSRKTTLEQPPSVALKVEPVGEDLGSPPPADFAPE D-YSSFQHIRKGGFCQYLAVPQHPYQ 395

hNFATc2 SPCGIPPKMWKTS PDPSVSA-----APSKAGLPRHIYPAVEFLG PCEQGERRNSAPESILLVPP-TWP 376

mNFATc3 ----IPLKTRKTS EDQAAILPGKLEICSDDQGNLSPSRETSVDDGLGSQYPLKKDSSGDQFLSVPS-PFT 401

mNFATc4 S---IPQKTRRTS SEQAVALP-----RSEPPSCNGKLPSTGEDSVAAPGALRKEVAGMDYLAVPS-PLA 385

hNFATc1-ca LGDGV PVKSRKTTLEQPPSVALKVEPVGEDLGSPPPADFAPE D-YSSFQHIRKGGFCQYLAVPQHPYQ 395

hNFATc1 WAKPKPL-SPTS YMSPTLPALDWQ----- 418

hNFATc2 KPLVPAIPIC SIPVTASLPPLEWPLSSQSGS 407

mNFATc3 WSKPKPG-HTPIFR TSSLPPLDWPLPHFGQ 431

mNFATc4 WSKARIGGHSP IFR TSSALPPLDWPLPSQYEQ 416

hNFATc1-ca WAKPKPL-SPTS YMSPTLPALDWQ----- 418

Supplemental Figure 3

Amino acid alignment of the N-terminal regions of NFATc1, NFATc2, NFATc3, NFATc4, and the constitutively active form of NFATc1. Asterisk (*) indicates fully conserved serine or threonine residues and the colon (:) indicates serine or threonine residues conserved among NFATc1, c2, c3, and c4. Alanine residues replacing serine residues in the constitutively active NFATc1 are shown in red.