

## SUPPLEMENTARY MATERIAL 2

### Taxon abbreviations/Database:

Co: *Capsaspora owczarzaki* (BROAD INSTITUTE-Origins of Multicellularity)

Mb: *Monosiga brevicollis* (JGI)

Ac: *Acanthamoeba castellanii* (own assembly)

Am: *Allomyces macrogynus* (own assembly)

Ap: *Amoebidium parasiticum* (NCBI scaffolds)

Tt: *Thecamonas trahens* (own assembly)

Sp: *Spyzellomyces punctatus* (BROAD INSTITUTE-Origins of Multicellularity)

### Rel/NFkappaβ

>Co\_NFkappaB GU985464 (predicted CAOG\_01632)

```
MDLSELSGWDPNLSLQEHETANLLAMDDSTMAAMILHSDGLSLFRDMGLYNSVSTSLDISGIPKFPFPPQO
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NILGHPVRSVSANTSMVGLPDDLGFSPPTGMDLITITATSPATADSSASATAFPAASPIASPSVSTSSGPV
TVGGTSAALAAALTPDRINRLLSAAEAAAEGAATLVEDLLMVTEEPAQFARFRYMSEQRERSLAGENSFPT
LMVNPKYARVVPPEMALVTAVLVTKMPDPHTGRQQKHWHHLGGI PAAPLEGPQRIARFDNIAVIMDKANNK
DKDKSKAPVRSKDDQRCVRIMFELVVFVSGNTQFYGRAISQPIYNAKLAI TKISHSSGPVTGGNEVIMLCS
KIRKGVTVGVRMTDPTQWSVQAPSGSAWELNPTLKADCNVPGANLFFHHQYAVVLTLPPTYHTQTITAPVT
VRISILDTDDETESQYVEYTYLPAEAAVRNAELAARKRRRDDSMRDFMDFDGS DGGNGSGSGRGNNGGH
DGS DANNGRGGGGSSSSSKGGDEPFNFNSLIPMHQHKLHQLALSTVRAVQGF AASGDARYLLALHRQLL
AAPNENGDSPLHTAVAQGNLRSTMALLPLLAEDLQSVNDMGETVLHSAVIEKRAAIARLLL VAGADLGO
SNARNFNRLSLHYLARHGDRATAMAVFGVFGSAQAPPANTNTPAQAPAGETKPKPADLRLLLARIQAQAIK
ALLACELETGATPAHLAIRGGHWHVFEACAKLAASAPIPKAAGSLLSMVAEKSSGHSLLHSCVLANNEQA
VRL LINLGASGNARDFGKNTPLHLAARQGHIGIAALLVEAGATLSLNAVSTPLDVL TSEGSLSRDQLR
ALVAVLRGELKYADMRGRPTLRMPHAEHLSTAAALTSASPGAVSLADFYAGKKASRSPAPLGASSLLS
STGASAAGASAP TIAAVHAASATPVERTSMNND D YVLEK DAPY PVEQQPHGKR NKHSHRFRTRSSHGS
QDKDELKDKDDPKKEKEPKELSKFTLKEAFVDGTFWELTRKFAGKKKMASASTGEMEPLSPERPLSPT
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### Runx

>Co\_Runx1 GU985462

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>Co\_Runx2 GU985463

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HPPHHQQPQGHGTPLPTPMSATLHFNFASARETAMLEESANVSRCSMIVETQLTGLSQRANALNACTH  
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*T-box*

>Co\_Bra-like GU985459  
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>Co\_Dtbox GU985460  
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>Co\_Tbox3 GU985461  
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IQQGSTAFPFTTLPASPKRARLDHSQGLRSITSLGGGARKLSFESMYSSDFSDLLLLDAQRMFSNANARN  
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>Sp\_Tbox SPPG\_06782  
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>Ap\_Tbox\_partial manually annotated  
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### *Churchill*

>Co\_Churchill CAOG\_05736 reannotated  
MCRNCLKEDTPARGTTCLDTGAYLVNFKGCAQCQSFEFPREQDRKVEDEDETGEETVTFTHVCKQCNHVI  
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>Ac\_Churchill1 manually annotated  
MCRRCLVHVCPQRDRCLSSGSYLLNFKGCGEGKMEFIKIAELEKNETETDETVTYQHQCSECSHKIAD  
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>Ac\_Churchill2\_partial manually annotated  
RARRRARWSHLIIRHRITSKLKSVAANTRDAAAKALAKKTLKLVKKFALNGCGEGKMEFIKIAELEKNE  
TETDETVTYQHQCSECSHKIADHEYTFTIDGEYQEYAMNCVLCGYGEDRVSIMPDDPEKIAQYDMY

>Tt\_Churchill MSG\_09514  
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### *P53*

>Co\_p53 CAOG\_00511  
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### *Stat*

>Co\_STAT CAOG\_04636  
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SDASGAAAHQLAECVRIA AHKAQATLHHLVGDQHVDELKRLQMQEYFVIQYQEFQQLQAVLQRSPRS  
DAARGQIELVKRRKQEVGTTLSTEANNI IALMQSLNRQLQANMGDIAELQTLVLPDALQAWQRAQRLES  
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FATMDRAPFEVPEVVSWPDMLTALQHHSFSLATQQPLSQRDLEYLTKASDLI INESITWKRLTKEALPDR  
TFTFDWDFGAEDVIKRHMLETWQDGLIMGFCNKQQAHDLLINCVPGTFLLRFS DSEIGGLTVAVITEDE  
RGMQRQVFNLHPWFAKDFAIRALADRIHDLPLQLQFLFPDTPKDAVFGRHYSVETAHVTSNNPDYVRSSIAA

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>Tt\_STAT1 MSG\_03678

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>Tt\_STAT2 MSG\_02036

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SPHMRALWADSLVAGFVPGSGVGGMLSAVPSGSFLLRFADSLGALSISYVWDDSRGRQVVHLQPWTLTE  
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>Mb\_STAT JGI38850 reannotated (5' truncated)

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**bZIP**

>Co1 CAOG\_07161

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IAGDSHSYIAYSSPQEQYDNEPMAPRKRRRPATTEERQSRRRERNRVAAVVCRQRKQRNEADLKDRVGM  
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>Co3\_CREB CAOG\_04938

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>Co4\_PAR CAOG\_08044

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>Co5\_Oasis CAOG\_01232

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DALSG

>Co8\_At6 CAOG\_04023

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MMVVN SERGVAHVGGRLAVDDQGWGLSVRESSAVGLELPAEATRLSEWQGGPPARVGGQNTGLPLIT  
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>Co9\_C/EBP CAOG\_02294

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>Co10\_C/EBP CAOG\_03823

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>Co13\_At2 CAOG\_06753

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>Mb2\_At f2 JGI37668

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>Mb3\_At f6 JGI22289

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>Mb4\_Oasis JGI30420

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>Mb6\_At f4/5 JGI31254

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>Mb7\_At f4/5 JGI32251

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*bHLH*

>Co1\_MLX/TF4 CAOG\_06632

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>Co17\_MLX/TF4 CAOG\_00266

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>Co18\_MLX/TF4 CAOG\_07309

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>Co28\_MLX/TF4 CAOG\_07309

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>Co19\_MITF CAOG\_03375

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>Co27\_USF CAOG\_02389

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>Co8\_SREBP CAOG\_05901

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>Mb2\_SREBP 32649

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>Co5\_MAX-1 CAOG\_05983

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>Co26\_MAX-2 CAOG\_01784

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>Co6\_MYC-1 CAOG\_06158

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>Co21\_MYC-2 CAOG\_03433

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>Co15\_GroupC-like-1 CAOG\_08129

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>Co31\_GroupC-like-2 CAOG\_06284

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KLRVQHSVQVSNIMTVEITDPDMRYIFVDHMWEIVLGYPKHEVIGRFLKEVVGCPCTPLMQKKAADIREN  
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>Mb7\_GroupC-like-1 26507

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>Mb8\_GroupC-like-2 26679

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*Mef2*

>Co\_Mef2 CAOG00636 reannotated

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>Sp SPPG\_03091

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>Am1 manually annotated

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>Am2 manually annotated

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>Am3 manually annotated

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### Fox

>Cow1 CAOG\_00937

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>Cow2 CAOG\_05750

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>Co\_SSRP-1 CAOG\_07557

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>Co\_SWI/SNF CAOG\_00396

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>Co\_MAT-alpha-like-1 CAOG\_01776

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>Co\_MAT-alpha-like-2 CAOG\_07895

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*Homeobox genes*

>Co1\_TALE-1 CAOG\_08013

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>Co2\_TALE-2 CAOG\_02804





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*LSF/Grainyhead*

>Co\_LSF CAOG\_06888

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>Co\_GRH CAOG\_04897

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LQEQQLQRQQLMQMRPGSGIDDLDLHVD FGPNGSFSGQAFADIRRPSSVASFQSNPASLHHGSVHGIPP  
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LQPHSMVSPSSTPTSAPTSPGGNVLSGVHTGLTSKRSASSASLVDHAAESHTVTSLLPVM DNGIEFVMP  
RTKIVRVVSKKKEPVLTLYL RQEAERYFHSVYLDALTADDLRDKLADLLKLPAA SVREILRR TAKGVLVQ  
MDTKCVEHLENEDDFIVAVELQTDGWYRIVLRS GST



