Additional file 3. Alignment of *Cryptons* and *Crypton*-derived genes in Saccharomycetaceae fungi in fasta format.

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----------EEDSYVATIDRAIPAVAEK----LRALSSQQTAANLWTERAFVE-----L----------
RQQVQRLEKKMEELAKASYTITISPGRSTVTQRVGMPKRGRPRAPGRAPTATAM----------
----
----------ATAPRDDST--APVPPSSSN
AAEAERGAVLQPDTATRL-----PL----------PPVAPSVPSAPSAP-------SVPRFEVPL-DIRRIPDLWHLWRY--GRAGMPSVESLEARYG-
AAWR----PKSQKSVFCGRKAIVDFIL--------RKSRERDGLQ----SAAEHAPRV----------IAQMEEL-----CPKWSLDK-----V----------
----------TK--AIKNGDLERRWPPEA----------

>CryF2_CGlo
M----------DSDLTYTARLREVVERCLLESQQQTPENTRRAGFASIPE----------GWPATHVPGRPLPE
DLVDEGKLLLFMADEVVSRAPRTGSRVAQERRKRRETEQAGGI--AKRKKLQGHGKDEVAEWSEDCIVVHTVPADADDADSGDV
ESSF--ESSLK--------LQYNTVRSY-------VSAIQKLYDVQRTRGI--------NPAPRPQSVALKAMQKSILRTTWARKRSEYADRGENTIKDS
Y----TP-SQIPVHTSAVWNES----------KQIACALRTQVYFLLGNHMLLR-SSNRRPLELPDCFCLELP-NEGVKNKDNITRAFVVVMNQ

GKT--------NQHGRLEYGACLRHRDPLACLVGALGFWLFYRWHVEK-ES-------FPSFSRRKD----------WYDLKILRRSINEPKDV
LTPQTANDWTRRFYEKSGI-KTTKASHAPRVA---------SSQNADIAGVHEGQIRRAGRWNNGDQMTGC-------YLTSLPLEFMRAVAD
FDPEWSGSY-----FIARSTAKPPGRLLARVFPGLDYWKEQHDAPESS----------PFAATVQQDKAAGAFLELLAWLREVV--
----LQDAAFLKPLFPNHPIFRD--------PLFQDPEFEQY----------AARVRDICSQA----------
----------HEDSHQTAIEKTIPSVAEK----LRSISTQQVAQNALNQRRHEE-----T----------VQALRK
LERKLDLLANTRYTVTISPEGKHLEQRVELPRGRRVHRRRRESSLSPC----------

----------SPPPHASSLASTTAAASSSNTEHLLR
TGNEKPVGQHIPTVSPSKA----------PGVAVVGPEDDESP---------PRFRFPQ-SVRTVMELWRLWRH--GLPPMPSIQSLEERWG-AR
WR----ARGDRQYFSIRRRIFDEIV--------RRSQARDQPE----EVS----------AREMDIERG-----KISLDK-----F----------
----------SK--ALRAQRGQGTG----------

>MarCry1_FO
M----------AADDSYTAADERARAARRAGLQAKKDEQPANTARSYAAKQREWKAHGSLYSWPDG----------
--------ELVTPDKLAAWLKEDILLRRVAPPQKKPRARGKGKGKGKAVQLRRQLEQEQLEAAALAEAESLAEALEVPLAEAAELLADD
REGYVPPTALAPAAADLAEGSLLTRGTIDAY------IAAVIELWRLQVAHGN--------ANTENPRGAAVRGFLEQRGRQRGKHDRASFK
DRGTDGIQAGY----SP-DEWLRVQDLLLSGA---------AYMPQNLRTRVDLLFGHYYLLR-GENRRKMELADLSLLDYPSSEGPT----PC
GCLVTLLRDGKL--------NKTAKKEFMGALRHKDPLFCTQGALAQLFFWRWHVAG-EP-------SPSFRRRQD----------WYRIKVLV
--GRDREQELSYPTQLQETWRIFGAAGL-MASKKTHLPRRV---------GAQDAETHGTSLAQISQAGRW-NQSVLCQA-------YLTRLPRQ
FMRIVAGFSA-SPGDY-----FLARAAHEPPYVLQKQLWPWIEEWEPRFEARARR----------QCWAEGGLDDDDLAADGFLKL
MRRLRIVL------LQDLAVLQPRYPSLPFFAY--------APFNGPEWDEF----------AVAVRSDAV
G----------ATEPLSLLVQRALPELSGV----LESTREAVLQNSQRLAIRL----------
-EARLEGIQGGLDALLQGKVPVTFTGHFGAGP----------

----------AVSLAPAPAPSTAPTLNFNTA
PA----------PAPEPPVPG----------MPVVAALA-KVFTVRDVWKEWEE--GIAGQPAVRVLEETWG-SRWRP---GNGIRVQFCRRKVIW
DEL---------LARTASGKSE----EEA----------VAELELLRA-----GRSLNR-----L----------
----------VD--ELKQRRRRGQGQGRIRVQVGTPVPDDPGPGPRPTRGQGHRGRWARLGRRRTAPRRR----------
----
>CryF1_CI
M----------ATPTLNSQSALMVEMEARVRHALDSALDARPKKTRMQYESRQEEWRHFCRTKGFQNG--------
----------ELVTEQKLLWFLSECVVGC---PAKRSCHSRDRTNENGEPVVQ----------T--------LGQPSIKAY----
---KTAIVNLWSYQRSCRT--------NSYPHPVGQAVRALLETHSRQEHERKKAEFVDCGTGTLLDGY----HE-KDIVQLVEYCWQGW----S
ESKKGQSVEPHLRTAVDFLMGHSMLLR-GESRRTAQLADLFTLELT-NEGPT----PCFPMVLIMGNGKT--------NQMGWIEYATVMH
HRNLLLCTMAQTAFYLFYRWDIVR-EP-------PPQFHNHQD----------WYQLHLIK--RDDVRKPLSYKTQLDWIRCIYSGTGL-SG
LKKTHAGRAA---------GARHAEQVGVSEGQICRAGRW-NSDALSQC-------YLTNIPRKFVQAMAGFDSRTPGNF-----YLPRARVPVPE
SLERAVWPWVDDWMRWFESYDAQDPNSCLQGPELRRFSDQSGPWDQPRGPSAVQLDRDDLAAQEFLRLLHHLHTVL------LQD
SVILQPLFPSHPLWTS--------PVFMREDYRQF----------AEAVQMANTH----------
----------KEELYEMQLQQTVPMVADQ----LRIVQQDLGVACGHLHTAL----------ETGLQKINNQ
LEALTSGQVSFLVRAFPAGQRMM----------

----------TAAAAFEDKDEERDSGSTASREAQAPACSLEIAPA--
----------SASASV--------PATYQLSR-TITTVPDLWQEWTV--GLGGGPSVQSLDALYG-AKWRP---GGTERMFYSRRKVIIDYI-------
--NRQRQGSASG----SAA----------VEELELVRQ---RGKLSLNR-----L----------
----------SR--MLATGSGHCVEVQTMFRCRTQGLYD----------

>CryF1_CP
M----------ATPTLNSQSALMVEMEARIQHALDSALDARPKKTRMQYESRQEEWRHFCRTKGFQDG--------
----------ELVTEQKLLWFLSECVVGR---PAKRSCHSRDRTNENGEPVVQ----------T--------LGQPSIKAY-----
--KAAIVNLWSYQQSCRT--------NPHPHPVGQAIQALLETHSRQEHERKKAEFVDHSTGTLLDGY----HE-KDIVRLVEYCWQGW----S
ESKKGQSVEPHLRTAVDFLMGHSMLLR-SESRRTAQLADLFTLELT-NEGPT----PCFPMVLIMGNGKT--------NQMGRIEYATVMRH
RNPLLCTMAQTAFYLFYRWDIVQ-EP-------PPQFHNRQD----------WYQLHLIK--RDDVRKPLSYETQLDWIRRIYSGTGL-SGL
KKTHAGRAA---------GARHAEQVGVSEGQIRRAGRW-NSDALSQC-------YLTNIPRKFVQAMAGFDSRTPGNF-----YLPRARVPVPES
LERAVWPWVDDWMRWFESYDAQDPNSCLQGPELRRFSDQSGSWDQPRGPSAVRLDRDDLAAQGFLRLLHHLRTVL------LQDSV
ILQPLFPGHPLWTS--------PVFMREDYHQF----------AEAVRVANTH----------
-----KEEPYEMQLQQTVPMVADQ----LRIVQQDLGVACGHLHTAL----------ETGLQKINNQLE
ALTSGQVSFLVRAFPAGQRMM----------

----------TAAAAFEDKDEERDSGSTASREAQAPACSLEIAPA------
----------SASASV--------PATYQLSR-TITTVPDLWQEWTV--GLGGGPSVQSLDALYG-AKWRP---GGTERMFYSRRKVIIDYI---------N
RQRQGSASG----SAA----------VEELELVRQ---RGKLSLNR-----L----------
----------SR--MLRVKKKLP----------
>CryF1_MC
M----------FLQEEVMYR---EIRPSRYKKSRT
NIEGESVKQ----------T--------LSEASIKAY-------IAALVDLWGVQVSMRT--------NTHASPRGALVKGLIRT
RRQQESKRKREQYEDRGLNSLQDGY----TS-AEFVRLIRFCWSSGYNVS------GQLEPFLRTAADLLLAHTLLLR-GEVRRKVQMADL
FTLTLD-NEGPT----PCHAMVVLIDNGKT--------NQDGRREYGTAVRHKNPLLCTMASIGFYFFMRWNIMG-ET-------PPNFQRREL---
----------WYDLLVIK--GQSNVKPIAYETQLQWSNRVYKGIGL-GIKKKTHAGRSQ---------GAKFAELAGVNEGQIRRAGRW-NSDS
LTTS-------YLTNIPRKFVRAMAGFQPVETGAY-----YLPRTKIEPPASLKQALWPWVDEWLLWQASYTGSGSEDVQLPPESVRF--------
-----DSGKVDHGDLASQGFLYLLDYLRTVI-----LQDSVLFMQEFPGHPIWSH--------SLFARDDYLCF----------
----------SQLVRDSLID----------VEEPQDVQLRRTVPAIATR----LQTIEQSIVQTLKVSEERN----------
----------VGFLQTIDRNIKDIVDGTVSFTVRANAPGSPLS----------

----------AAATATAT
AASTPYATPRCMHGAIPHPSLSPSCSPH----------PPSSSAVAAAPHTG----PPPLSMGFSQSR-TIGTVMDLWREWAE--GLGGRP
SVRSMEEAYG-PRWRR-H-RPGESMMFSRRKVVVDEIV--------RRQRVQKKSL----SVV----------IEELETNMD---WCVASLASPP
PSFLLLFLLLLSLFHVHVRIEYQDRFQSISTPILFLSSFFSSFEMPFNNNTAGDGMALVLYDRQIARMTDTPGILRVGGQELAPYVH
NDLGRAVLSLPGLHVRYVPYSIDARQILSHRASYINGLLVQSRGRPEVHACTDCRGRTGLRPFTECVRLPGHFGGACGNCKWRDR
ASHCSVRDEIQQARTEVIVLDDDSGDDRQVIDLTGDGPVRRPRARITGGGNGSSASRAIVLL----------
>CryF1_TS
MQCGVTEIDALSRIAAGLIVRVDYAMDRLLSLLPRTAPLQIQVPDIATTEIEPPRPEDIAIQKALDEVLEYHRVHRPKNTTKNYEPK
QKEWKAWCKKMGFKEG----------GRYLPGDYVDEGKLLLFIKEEVASRPPRRGQRLKAERKRKRT-AAAEVLSEGPPSKRKREK---

--------ISVPSMAFEELPVE----SDDDEACSELV--------LMYNTVRSY-------CSAINELWAHQTSLGL--------HNAARPQRVAMTALKTSIA
RGQHQRRRDEFTDRGLATIRDGY----VA-SQIPDLTRKVWAQCLGQ-------NQIEQQFRTQLCFLFGNSMLLR-LSNRLPMELPDLFS
MPLP-NEGPKG---KGWCLVTVMDQGKT--------NQHGRLEYGAALRHRDHQSCLIGALATYFFWRWHCSG-ES-------FPCFRTSQD---
---------------WYNIKVLKRDNNHLTEPLSDSTAASWTRRLYSEAGI-KSSKVTHAGRVS--------GARLAELNGVSEDQIRRGGRW-NAD
QMTGC-------YLTTLPRSFMRGIADFDPDWSSSY-----YLPRETVCPPPALLKRVWPDLDRWQAAHLERTDA----------TE
RVEPNIAAGGFLELLQRLRTVF------LQDSVLWRTEFPSHPIFRD--------PLFQMAEYKAF----------
----------ELDIHMAVTTAM----------EEDPHSIAIQKAIPAVNDR----LRTMTAAIQTGQVTHSQALRS-LEDLM----------
----------VSRIDQLTATINDFIGGTFTCQFVPRGQIVPP----------

----------PITGAAFGPTAPIQ--------LPVTALEKASQAPQYQLWKEWTV--GLNGQLSIERLDELYG-SGWRSGPESSAER
QFYSRRKTLINEIR--------RLATVEDASLGDPCQTV----------VAKLEEERI---RAGASLSKISNPKI----------
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>CryF2_TS
M----------ESISNGLLAEQDRQLELHAKIQLHSQKVAHRIQKNRPAATTRQYDSRQKEFIDFCTKEGFPDG------
----------QVVTEKKLVYFLDHYVINR---PIRPSRYLRNRTDSQGAAVVQ----------T--------LGLPSVKAY---
----TSAIVDLWRFQQSLGT--------NPYPNPRGHLVGAMIKNHQFDETQRKRTQFTDRGFNTLQDGY----TS-ENIRAIVRYCWAGWLS
DQTRGRKPQAQEAYLRTTVDFLFGHNMLLR-GEDRRHLELADLFTLRM--DEGPT----PCWPMILMKLNGKT--------NQFGRLEYM
GVVRHKDPLLCTICHTAFYLFHXWEIMH-EP-------VPQFYQRQQ----------WYKXVLFK--GSDSEHSFSYETQLKWINQVFQSI
GL-NSKKKTHSGRSS---------GARHAELQGVDENSIRRAGHW-NQDSMSNC-------YLSELPRPFIRTLAGFKPTDQGNY-----YLPRAAI
EPPETLVRALWPWIDQWLAWFSPSESN---------PVELSKLDLPPLPLLVQQGVEKCDQDDLAAQSFLKLLSSFRTVI------IQXAVFLQ
QEFPGHSMWTH--------PLFQRSDFQSF----------SQQIIDLVRT----------S
ETPHEIKLRQTIPLVANR----ITTIGENLEHIIQLNHQQT----------QDSIRAIQSQMDQLFSGEV
TFTARLTGSDEKPS----------

----------TPGNTTSQSTEQNTAHTVVQSLQVTPNPIQD----------HPPGIH
LPNEPSGS--------PPFYRMSR-TIQTVRELWEEWHV--GIHGNPSIQSLEDSYG-CRWRS---DNKERVFFSRRKVIIDWI---------QARVS
KGILL----ADA----------IDEIELMRR---NSQRTLYQ-----L----------
----------QA--LLKKGV----------
>CryF1_NF
MESKVTETDALLRSVAGLVVSVDRAMDRLLSLLPRTAP--IQAPEIATPETEAPRPEDIPIRRALDEVLEYHRAHRPKNITKNYEPKQ
KEWKAWCRNMGFKAG----------GRYLPGDYVDDGKLLLFIKDE---------RLKAERERKRTAAAAELTSRAPPSKRKRGK----------TS
APSAASGELPVEGDDADDDDKACSELV--------LMYNTVRSY-------CSAINELWAHQTSSGL--------YNAARPQRVAMTALKTSIAQGQ
HQRRRHEFTDRGLATIRDGY----VA-SRIPDLTRKVWGQCLGQ-------NQVERQFRTQLCFLFGNSMLLR-LSNCLPMELPDLFSMPL
P-NERPKG---RGWCLVTVLDQ----------VLKRDNNHLTEPLSDTTAASWT
QRLYSEAGI-KSPKVTHAGRVS---------GARLAELNGVSEDQIRRGGRW-NADQMTGC-------YLTTLPRAFMRGIADFDPDWSSSY----
YLPREAVCPPPALLNRVWPDLDRWQAAHLERADV----------TERVEPNLAAGGFLRLLQRLRAAF------LQDSVLWRM
EFPGHPIFRD--------PLFETAEYKAF----------ELDVRGAITTAV----------EE
DPHSIAIQKAVPAVNDR----LCTMTAVIQSGQV----------

----------PQYHMSR-TIRTIPDLWQEWTV--RLKGQPSIE
RLDDLYG-SGWRSGPEKSAERQFYSPRKTLITEIR--------RLAAAEDPSLGDPYQKV----------VA----------
---

>CryF1_RO
MSH----------DSNAGPSTRDNDIALPDAEHYEDMIRARLAMDKNTQMVIAENQTYRPKNTTAAYKSKQREWFEWCAN
KEKVAD----G----------TIVYDAKLAFFLKDYVLTR---------GNKFKKNADGSPA----------P--------LGRE
SVLAY------VEA----------GF--------NKHTMARGPIVKRFLDTHTKKEARRKRTEYEDRGKNTLNDGY----TD-QELLRINQYFLI---------
---QNNIFSLRNKVCFSMSHAMLMR-SETALGTQLPDLFIMELK-NQGPS----TCFAIVATITFGKT--------NKDGKIQYGSALRHRDVE
VCPHGAFAQYFFSLFHHQN-LP-------FPNFSTRRD----------WY----------CGV-HSSKLTHINRKS---------AINMVA
NEGVSGDQQRQVGRW-GSDRMVGC-------YLSGLPVDAIKVLAGFTT-RKGDY-----FINRGSIEPSEELRKMVFPWIEYWREKFYGK
EVE----------DDIAGPNFLDLMDYLRTVF------LQDSVVLKGKYPGSFIWSH--------SIFDTDIYKDY----------
----------EERLSSAIAAND----------EKFKMSQHLEVLLPEVAAA----MKTGFDSMNAMLNIV
QSQNQL-----T----------LNAVKQLEAENRTMLADSFL----------

----------QISNMLRQGDENTQIQQTSTILPSSSV----------PLSSIPSPSAANSR-------GLPSFKMSR-SLISVTDVWREYSV--GLAGK
PSIKSMEEQYG-ADWRK-VDNRTESRFFTRRLPLYKKIE--------SLSNERGISC----EEA----------AQFLEFRRV---SDKLSINQ-----
M----------CK--LVADNQI----------

>CryF1_PI
M----------EPPGLQVELEESAHATLDRCREARPANTIRAYAPKQREFKAWCERKGFHET----------T
RYQVTAAKMHLFLQEEVVDRQVRTKGSAR----------K--------VSVATVEMY-------VNAVSDL
YSDQQSRGA--------NSHPHPRNSLIKGLLTSLKRESHAKNKREYADRGVGSLLDGY----CTTNDLVSISRYYMN----------LNTGSDLR
NRMSHFLCHACLLR-GESARNLDLPDLFSVILE-HEGFT----ECRALVMIMEQGKT--------NQFGRREFGSCIRHRNVEVCPVGALAL
YLFWRWSVQK-EA-------VPDFLVPER----------WYDIKLLK-SNKDITTPMTYRAHYDATVKAFSALGM-RSKAKTHAARGS------
---GARMAELAGATESQIRRLGRW-NASAMEGC-------YLSALPREAMRSLAGFPP-DRRTF-----FLDRAAIDPPECLLRDVFPFVETYM
AAYMQQSAP----------HVATGGFLELLLYLRVVL------LQDAVQLRDLHPTHKIWMH--------PPFNSTGFDSF----------
----------ALELKAKMLT----------EKSPQTTHLHEVVPDLMDH----LKQQQQQTI
AHIDNKINEI----------STSINHIATAFSRLTSGSSAVRLTVDWGSAQ----------
---

----------SSTSTPVAASQHAP-------LPPTYKLVR-SIKTVQQVWQEWTT--GIHGGPAVRD
LEERYG-SNWRN---SPAEKRFFFRRKRIIDRVT--------LVAQQQHVSE----AQA----------VCILEGQRT---QSQLTLNA-----L----------
----------SE--SLKGRQ----------

>CryF1_PS
M----------QVALKESVQRTYEKATTLRPKNTQRAYSSRQQEFLDWCSEKGAAFN----------NLTR
FTVTGEKLHLFLQERVIGR---------TKRHKSGSTPSDRIE----------T--------VGRSTVNSY-------VAAMVDL
WKQQSRAKV--------NSNPSPRDEAVTTLLKLTEYEEDERKRKIFEDRGADTLLDGY----TTIDQVKEIARYFWTPA----------RDSGKNL

RNLVAFLLSHYALMR-GESARMMELADLHSIVLE-NEGYT---PCRALVMVMRQGKT-------NQVGRIEVGACMRNKHVEICPHGIL
GFYLFWRWHVDG-EA-------FPDFTSSER------------------WYPIKLLK-TGKHPTKPMSYKVHNAAITAALKHVGV-HSKAKTHVGRGS-
--------GSRMADLGGASESQIRRLGRW-NGQSMEKC-------YLTSLPRQAMRTLAGFEP-SIGSF-----FVARASVDPPLALQSMVFPQVE
VWQQAIASGTAE----------------------------------QSLAAGGFLELLQYLRKVV------LQDAVFLQKSAPTHPIWQH--------SIFQSREFTEF-----
---KSEVMQAVDA----------------------------------MEDPTEQRLQKAVPVLNAK----IDGLHQD
FKSSLAQVCSTMRT-----V--QGSLSDVMRVLAPLQGGTAVVQVQLLSGGRE-----------------------
----

--GDGDTAHV-------------VPSASPIAIDVQSD--------RTKYKLRR-GLATVPDLWKEWSV--
GLDGARAVRDLEDQFG-TKWC----SADERRFFNRGRPIYSLVAAVADDILTSARVSDVDAT---NLA------------------VQVLEEYRR---TH
NKSLNW-----I---AK--HAGEIKDAVQAIAVSRCSVST
TSISDPSPND---
>CryF1_SaPa
M--LRPSAADVQEAALAFAMQRSAMETYEMAADKRPKATKAAYSAKAQEYVDWFKAKPGNAN------
----------KLPLVDAQTLHYFIKDKVIGRTARPKTKKDTGAGSTKESTK--V--------IGYATVKQY--
-----VNAIVDLYQEQVRQRA--------NTNPHPRNNLVKTLLKQVSLAEDERKRANYEDRGAGTLIDGY----TTQEQLSQIAKHYWTPA---
-------SFFGVRLRDWLAFALSHYYLLR-GETARMLELADLQSVQLE-NEGCD-----------------------------GVLPFLALARRRRA----------------
------------LPRDDHECR------------------LVRVQAAQ-ERQEPEKEMTYSTHHKAVSDALTATGL-STRAKTHVARGS---------GARMAEMG
GASEAQIRRLGHW-NNQAMEGCYLTKLPRYLTKLPREAMRVMAGFSP-DPRLY-----YLERGQVEPDQELQALVFPDAANWLAKLN
DGKCE----------------------------------ATIAARGFLELLMHLRVVL------LQDSVLLKKLYPAHPMWSA--------PLFSHPLYTAF-------------------
---EIKMEHLLA--LTTSMNLVTSG----LEDVRAVVNNL-----------------
---RTDVAAQGQVVSNLASGRFVMRLEMEPDGAPR--

---------QSPPRATQKPSAKPSTQPTTTASAMSN-------------NPSTTRVAIGNQMS-----------------RVQTLPELWREWFH--GLGDRPSVVSI
EQTPS-ARWR----NDSARRFYNRRRVVIRAVQ--------AYASRTRMPI----DAA------------------VARLEERRL---QQNRTLDW-----I-------------
---AK--HDNTFIHDD--