Supplemental file 2

>c1026\_g1

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>c15246\_g1

MATDHLTIADFSLLTTVTVLNLVVPVVADKWPKLTAWLENMKQLPYYEKANAKGLEALVEKFKPALEKLKA\*

>c28406\_g1

MPASNALRQTNLAVSYSIRLPKLWRPSRRRGKERKQANSKNPFLACIEVGYVVILEAACISSMSILKIQ\*

>c51927\_g1

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>c53084\_g1

MTPCTRKTPRSVLSSINCSSSISPQYIAPLLTHMSNNTSSRKKSMQRSTRQSIQLLNS\*

>c53248\_g1

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>c54345\_g1

MIWPWFERTEMLKYLLPEKFELDKERFSKLVAWRDLMINDQAVKGHYLNGETHAKFMKARRDNVHDYNMLVLDA\*

>c54811\_g1

MGKIVLYGIEASPPVRSVLLTLNALDLPYEFIDVDLFAKANKSEEFLKINPGGTVPALLDDGQAILDSHAIIAYLASKYGKDDSLYPKDLVKRSVVDHRLFFEASMAFERALRGTTKPIIFDNETNVPQQKNRQYY\*

>c56749\_g1

MEIQNYDCCFRYLADKGQFSEQLYPKALEQRARVDEFLEWQHLGVRLGCATYFLDMWLLPMNGIKPKPSAEKAAILSKNMESQLKILEEIWLKDTPFVVDNKMTVADLFGACEVEQTKLAHYDVGKKFPKIAEWMQRVREQASPHYDAAHEFIYKKSGMKPSNSKL\*

>c56998\_g1

MAAKDLISFDNEVFSAYVFWSAVLVLKLLFMSLLTAIQRFRTKTFANPEDLMDKRLKVKFDNPDVERVRRAHRNDLENILPFFIIGFLYVLIDPTPGLAINLFRAVGIARIVHTIVYAVVVVPQPSRALAFFVALGATVYMGFQVVIAAL\*

>c57533\_g1

MSSKLILYGTKKSAPTRTVLLTLKALDLDFEFREVNIWAKEQMQPEFVEKNPQHTVPTLEDGAHILVDSHAIAGYLVRKYGKDDTLYPADFYARAVVDHRLYYEAATLFATCMKQITGPLFQQNITDIPKEKFEQIRNAYTLLETFLTKSAYMAGEHLTIADFSIVSTVSVLSATFVAVDSNKWPKLAEWLKRLEALPYYAEISDAALKEYAELVHSKLPKQYEKLWKKAYEEIKSSRQ\*

>c57582\_g1

MDFYYVGGSSPCRSVIMTAKALNVNLNKKILNLMAGEHLKPEFLKINPQHTIPTLVDNGFALWESRAIMVYLVEKYGKDDALYPKCPKKKALINQRLYFDMGTLYKSYSDYYFPQLFAKAPADPELYKKIETAFELLDTFLEGHSYVAGDALSLADIAVLATVSTFDVSGFDFSKYANVAKWYANAKQVVPGFDENWQGCLEFKAKFFH\*

>c58056\_g1

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>c58209\_g1

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>c58506\_g1

MDFYYDLVSAPCRSVLLLSKALGLELNRKTLDLSKGEHLAAEFLKLNPEHTIPTLVDNGFSVWESRVILIYLVEKYGKDDSLYPKSPKERTIVNQRIFFDLNLYAVFSNYYYPIARDKLPPVPEDLTKLEDKLEILNSFLEAQTYVANNSLSIADFTSYATVSTIATCLDYDLSKYPNIARWFAHLSKTLAGADENQKGCDLFKVYVW\*

>c58506\_g2

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>c58670\_g2

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>c58799\_g1

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>c59002\_g1

MDFYYMPASAPCRAVLLTAKCVGIELNKILLDLRAGEHLTPEFLKINPQHTIPTLVDKDFALWESRAIMIYLVEQYAKTDSLYSQCPEMRALINQRLYFDMNLALTFGKYFYKPVMSKTPFDPEQRKQLETQLELFNTLLAGNNFVIGETLTLADLALLATISTIDVAQCLKDFNVNVRKYAHIQKWYENMRAVTPGFKENQEGCLEMKKFFEGQ\*

>c59375\_g1

MSGGKHLAKGSQKPELPDDGVLRLYSMRFCPYAHRAHLVLDAKNIPHHTIYINLTEKPEWLTEVSPLGKVPALQLPKEEGNPSLIESLIIAEYLDEKYPEVPLFPKDPLKKAQDKILIERFNAVTSAMYKVFLGGSEAAPGALTEISTGLDIFEKELNSRGTPYFGGDKPGMLDYMIWPWCERSAMLKYLLPDKYEMDKERFGKLIAWRDLMINDPAVKVFYLDGETHAKFMKARRENVHDYNMLVNDAKRQRTC\*

>c59762\_g1

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>c60363\_g1

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>c60394\_g1

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>c60989\_g1

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>c60989\_g2

MDTLYKSFADYYYPHLFFKKPLVPELYKNMETAMELLNTFLEGNKYVAGDQLSVADLSILASVSIFDVANFDLSKYANVA\*

>c61180\_g1

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>c62360\_g3

MAKPVLYYATLSPPSRAVLLTANLLGLDLELRPVNLLKGEQLTDDFIKMNPQHTIPTMIDADGAVVYDSHAICGYLVDKYGEDDKLYPKDLVKRAQVNARLHFDSGHLFARLRFLYEPILYSGSTDCSMDKIAYIQKTYEIMEEMLKEHPYVCGEDLTIADLCCVATITSVDEVAPIDEFKFPKLLAWMKRLSELPNYQKINQEGADELKKVFKEILTNNRTKQK\*

>c62712\_g1

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>c63495\_g1

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>c63558\_g1

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>c65183\_g1

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>c70029\_g1

MFANNSNYNVRPILYYDDINPHSRAVLMILNMLDVDIELRAVEMIKGEHLKPAYAKINPALTVPTMVHKDLIITGNAIFSYVCENNDNEKANQLIALKCYKRHCCVLSRLFFESQVLHRIHGHLMTDLVRKTIYQTDVDYHQKKVEHAYDVMEAYLSDSQFMAGSVLTAADISFVACLGALDMMFPIDGDRKRWEKLNDWYRRMRSLSIQKINEFGIEKQRQIVEYFAKFQFKSDIKRFTTGLRESQIPGFPSRPDRCSVSIQTVSGAEPTLDILSIKNNIGKITYLEEQPAMEVTDERNVIMQPNTLKEGVAPKIVNEINKIAKTKINQILNEELEKELARFSEPNFLPPPIPEEPNPSKTSVTVLNDMDKSIAFSETPKDETPILTDRSLGGAHKERPPVPPRRKRYLPSKVENSQDLTNIAENVQKPDATEASEDTMKAFENNDLMNQSQEHKLSRLNGGVESTILLEKIEENEIRLQSAAASPLKPSINSTEINKVSPKTSETIKIAKINRSNSNITHLSEASPLIAACISREPEKVSQIGTTATKPNSCAKNHATRKLKPTDTLLPEGLPINGQQAALSYTRGVVAPNLLLPAPPPSPENYSQDEEFPPPPSELLIPKTNPRAKTTPTTRLVNCKPTVEPNERLGKKKSVKPKTDVAVESTVKLLRKKSGDLRSLPGRKSLAPESKVCKLTQKLNSGGLFASGTRSPCSNRSQGSIVPARCKKVPNTSNVSKAIQNLTANTKLFPNAKRLDKKIQKLKSDSVGTMVESSDSSTNIIQKLIRHSSKFSATNQLKVPNIGNQLRVEGGGHETPSLAAEGQNEFQQPTVIVVKSKTMMKMGNEHRYEERWQQKPPKSPKPRPKTPSNLTNKEMKPASQNFVARSKQKTYPTPTRFQTKNFKTVGSPQPTKFFDTSPSKPGQSFNTQQPKLVVEKKPAIKNKKKSGTKAHNDNMVNKTPPPMNEALPTPTSLLGTNATLQCAPEHATPQSAVGTVSSTLKTLTETIHISPKLTSPPTSSSDDTITANVPVKVGLVAKALQTLNVANSNFRPPSYNTSKELTLESPPLPPPPSYNTSKEIPSATHPLPAPASYNISKELTSATPPLPAQPSNNISKELTSATPPHPPLPPPNHRYLAAPTPPSLPVKDILPLAGTVAKALQSLSAVTSEANPLCGSVKPFRKVDLRMKFMETARASEVTDKALTKNITSNADEKIDARPLAEILTATVKQVNKESSDDTKSTTLSDGIKEMLLKMRTLPDKDGTPVVIVNSMTESTKPFQSTLITPSTSVITGLENSADKMIVESEPNNALLTAPPLLNIQNLPESAVPPILCEPVQALLPTKKVSIAEPYDMAKSYPSWAAHTEASILSASDVKSSKEEKNKLEASKSKRYVIDRTMINDGIIDMEPTPLPCQPNIIITGYTPMEPKNVAPLFVGTSRPLGNMIAPALRRPTNSPRTHGPSANVVISTFGYTPMSDLDTIPEHLIHMLNKPIFIEQQTAPPTPVLSAAAAPVTTVGEERTHVPRRKGDRPYPTAHRSGSQRRTDQSINIRGRVM\*

>c74100\_g1

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