

Supplementary Information

P04637	-----MEEPQSDPSVEPP-----LSQETFSDLWK	24
Q9H3D4	MNFETSRCATLQYCPDPYIQRFVETPAHFSWKESYYRSTMSQSTQTNEFLSPEVFQHIWD	60
	: * : * * *	** * . * . : *
P04637	LLPE-----NNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP-----	60
Q9H3D4	FLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQSDSLSDPMWPQYTNLGLLSNM	120
	: * : * * . * . * : : * * * . : : . * *	
P04637	-----DEAPRMEAAAPVAPAPAAPTPAAPAPAPSWPLSS--VPSQKTYQGSYGFRLG	112
Q9H3D4	DQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTTFDALSPSPAIPSNNTDYPGPHSFVDS	180
 * : . : : * * * * . * : * : . * * . : * . : .	
P04637	FLHSGTAKSVTCTYSPALNKMFCQLAKTCVPQLWVDSTPPPGTRVRAMAIYKQSQHMTEV	172
Q9H3D4	FQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPQGAIVIRAMPVYKKAHVTEV	240
	* : * . * * * . * * * . * : : : * : * * * * : * : * * * : * : * : * : * : * *	
P04637	VRRCPHHERCSDSD--GLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDDCT	230
Q9H3D4	VKRCPNHELSTREFNEGQIAPPQHLIRVEGNLHAQYVEDPITGRQSVLVPYEPQVGTEFT	300
	* : * * : * * . : : : * * * . * * * * * : : : * * * : * * * : * * * : * * : *	
P04637	TIHYNMCMNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLR	290
Q9H3D4	TVLYNFMCMNSSCVGGMNRRPILIIIVTLETRDQVLGRRCFEARICACPGDRDKADEDSIR	360
	* : * : * * * * : * * * * * * * * : * : * * . * . * : * * * * * : : : : *	
P04637	KKGEPHHELPPGSTKRALPNNTS--SSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEA	347
Q9H3D4	KQQVSDSTKNGDGTKRPFRRQNTTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKES	420
	* : . . . * * * : : * * . . * : . * * : * : * * * : * : : * : *	
P04637	LELKD-----AQAGKEPGGSRAHSS-----HLKSKKG	374
Q9H3D4	LELMQYLPQHTIETIRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQ	480
	* * * : * : . . . * : * * . : * * . : * * .	
P04637	QSTSRHKKLMFKTEGPDSD-----	393
Q9H3D4	LINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTSHCTPP	540
	. . : : : : : * * *	
P04637	-----	
Q9H3D4	PPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLALSKIPEQFRHAIWKG	600
P04637	-----	
Q9H3D4	ILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDEWND	660
P04637	-----	
Q9H3D4	FNFDMDARRNKQORIKEEGE	680

(A)

Figure S1. Cont.

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Q9H3D4      MNFETSRCATLQYCPDPYIQRFVETPAHFWSKESYYRSTMSQSTQTNEFLSPEVFQHIWD 60
O15350      -----MAQSTATSPDGG-TTFEHLWS 20
              *:*** * . . :*:*.

Q9H3D4      FLEQPICSVQPIDLNFDPESEDGATNKIEISMDCIRMQSDSLSDPMWFPQYTNLGLLSNM 120
O15350      SLEP---DSTYFDLPQSSRGNNE-VVGTDSSMDVFHLEG--MTTSVMAQFN---LLSST 71
              ** . :** .. .: : *** :::. :. :.*. **.

Q9H3D4      DQQIQNGSSSTSPYNTDHAQNVSAPTAPSYAQPSSTFDALSPSPAIPSNSTDYPGPFSFDVS 180
O15350      MDQMSSRAASASPYPTEHAA-SVPTHSPYAQPSSTFTMSPAPVIPSNSTDYPGPFFHEVT 130
              :*:.. :*:**.**:** **: *****::*:*.***** *:*:

Q9H3D4      FQQSSTAQSATWTYSTELKKLYCQIAKTCPQIKVMTPPPQGAVIRAMPVYKKAHVTEV 240
O15350      FQQSSTAQSATWTYSPLKKLYCQIAKTCPQIKVSTPPPGTAIRAMPVYKKAHVTDV 190
              ***** . ***** **** *:*****:

Q9H3D4      VKRCPNHELSEFNEGQIAPPShLIRVEGNASHAQYVEDPITGRQSVLVPEPPQVGTEFT 300
O15350      VKRCPNHELGRDFNEGQSAPASHLIRVEGNNSQYVDDPVTGRQSVVPEPPQVGTEFT 250
              ***** *.***** *.***** .:****:*****.*****

Q9H3D4      TVLYNFMCNSSCVGMNRRPILIIIVTLETDRGQVLGRRCFEARICACFGRDRKADEDSIR 360
O15350      TILYNFMCNSSCVGMNRRPILIIITLEMRDGQVLGRSFEGRICACFGRDRKADEDHYR 310
              *.*****:**** ******.*****

Q9H3D4      KQQVS--DSTKNGDGTRKPRFRQNTHTGIQMT--SIKKRRSPDELLEYLVRGRETYEMLLK 416
O15350      EQQALNESSAKNGAASKRAFQSQPPAVPALGAGVKRRHGDEDTYYLQVRGRENFEILMK 370
              :*. .*:*** .:*.*:.. .: .:**** *: * *****.:*:

Q9H3D4      IKESLELMQYLPHQHTIETYRQQQQQHQLLQKQTSIQSPSSYGNSPPLNKMN-SMNKL 475
O15350      LKESLELMELVPQPLVDYSYRQQQ-----LLQRPSHLQFPS-YGPVLFPMNVHGMNKL 424
              :*****: ** ::***** ***: :*.** *. .:***: .****

Q9H3D4      PSVSQLIN--PQQRNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPS 533
O15350      PSVNQLVGQPPPHSSAATPNLGPVPGPM-LNNHGHAVPANGEMS-----SSHSAQSMVS 477
              ***.***. * : .* ** . * * : * :* ** . : .. **

Q9H3D4      TSHCTPPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPSEQF 593
O15350      GSHCTPPPPYHADPSLVSLTLGLGPCNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQY 537
              ***** : * *****: ***.***:*****: *****: *****:

Q9H3D4      RHAIWKGLDHRQLHEFSSPSHLLRTFSSASTVSVGS-ETRGERVIDAVRFTLRQTISF 652
O15350      RMTIWRGLQDLKGHDYSTAQQLRS-SNAATISIGSGELQRQRVMEAVHFRVRHTITI 596
              * :***: * : * *:***:*****: *.***:*. * : :***:***: *:***:

Q9H3D4      PPR-----DEWNDFNFDMDARRNQQRKEEGE----- 680
O15350      PNRRGGPGGPDWADFGFDLPDCKARKQPIKEEFTEAEIH 636
              * * *****: : * ****
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(B)

Figure S1. Cont.

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P04637      MEEPQSDPSVEPPLSQETFSDLWKLLENVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP 60
P79820      -----MDPVPDLPEQSQSFQELWETVS-YPPLETSLPTVNEPTGSWVATGDMFLDQDL 54
              ** : * ** :*.:**.:.      *..*.: : : : * : * * .

P04637      DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRGLFHLHSGTAK 120
P79820      SGTFFDDKIFDIPIEPVPTN-----EVNPPP-----TTVPVTTDYPGSYELELRFQKSGTAK 105
              . :          *: *.*:          *. *          :*: * . * *** :.* * :*****

P04637      SVTCTYSPALNKMFCQLAKTCFVQLWVDSTPPPGTRVRAMAIYKQSQHMTTEVVRRCPHHE 180
P79820      SVTSTYSETLNKLYCQLAKTSPIEVRVSKPEPKGAILRATAVYKKEHVADVVRRCPHHQ 165
              ***.*** :***.:*****.*.: : *.. ** * : ** *:***.: : : :*****:

P04637      RCSDSGLAPPQHILIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDDCTTIHNYMCNS 240
P79820      ---NEDSVEHRSHLIRVEGSQLAQYFEDPYTKRQSVTVPYEPPQPGSEMTTILLSYMCNS 222
              :.*.: .*****. .: : * * *:*.*****: ** : *** .*****

P04637      SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLRKKGEPPHHELP 300
P79820      SCMGGMNRRPILTILTLET-EGVLVGRRCFEVRICACPGDRDRKTEESRQKTQPKKRKVT 281
              *****:*** . * :***..*****:*****:****. :*. : : : .

P04637      PGSTKRALPNNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG 360
P79820      PNTSSSKRKKSHSSGEEEDNR---EVFHFVYGRERYEFLKKINDGLELLEKESK--- 333
              *.: : . : ** . : : : * * : : : *****:*****:*** : : :

P04637      GSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD 393
P79820      -SKNKDS-----GMVPSSGKKLKS----- 352
              * : :.*      * . * *** :


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(C)

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P04637      MEEPQSDPSVEPPLSQETFSDLWKLLENVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP 60
Q9N6D8      -----MYISQPMS-----WHKESTDEDDSTEVDIKEDIPKTVEVSGSELTEP-- 44
              :. *: *      *: . :. . : : :*: : : . : * : *

P04637      DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRGLFHLHSGTAK 120
Q9N6D8      --MAFLQGLNSGNLMQFSQQSVLREMMLQDIQIQANTLPKLENHNIGGYCFSMVLDEPPK 102
              . :      . : :      . : : : . : . * : : : : . ..*

P04637      SVTCTYSPALNKMFCQLAKTCFVQLWVDSTPPPGTRVRAMAIYKQSQHMTTEVVRRCPHHE 180
Q9N6D8      SL-WMYSIPLNKLYIRMNKA FNVDVQFKSKMPIQP-LNLRVFLCFSNDVSAPVVRQCQNLH 160
              *: ** .***: : : *: * : : .*. * . :. : : *: : : * ** : *

P04637      RCS--DSDGLAPPQHILIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDDCTTIHNYMCNS 231
Q9N6D8      SVEPLTANNAKMRESLLRSENPNVSVYCGNAQKGKISERFSVVVPLNMSRSVTRSGLTRQT 220
              . : : . : ** * . * : : . : *.***** : . . * *

P04637      IHYNYMCNSSCMGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLRK 291
Q9N6D8      LAFKFVCQNSCIG---RKETSLVFCLEKACGDIVGQHVHVICTCPKRDRIQDERQLNS 277
              : : : :*:***: * : : * : : : : : : : : :*:*** ** * : : : .

P04637      KG-----EPHHELP PGSTKRALPNNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNE 346
Q9N6D8      KKRKSVPEAAEEDPSKVRRCIAIKTEDTESNDSRDCDDSAEWNVS-RTPDGDYRLAIT 336
              *      *. * *...*: :. : : : *.. : : * : *

P04637      ALELKDAQAGKEPGGSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD-- 393
Q9N6D8      CPNKEWLLQSIEGMIKEAAAEVLRNPNQENLRRHANKLLSLKKRAYELP 385
              . : : . * ..* :. * : : : ** : : : : :

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(D)

Figure S1. Pair-wise sequence alignment. “*”, “:”, “.”, and “-” stand for identical amino acids, highly similar amino acids, similar amino acids, and gaps, respectively. **(A)** Human P53 (Uniprot ID: P04637) vs. human P63 (Uniprot ID: Q9H3D4); **(B)** Human P63 (Uniprot ID: Q9H3D4) vs. human P73 (Uniprot ID: O15350); **(C)** Human P53 (Uniprot ID: P04637) vs. fish P53 (Uniprot ID: P79820); **(D)** Human P53 (Uniprot ID: P04637) vs. Fly P53 (Uniprot ID: Q9N6D8).

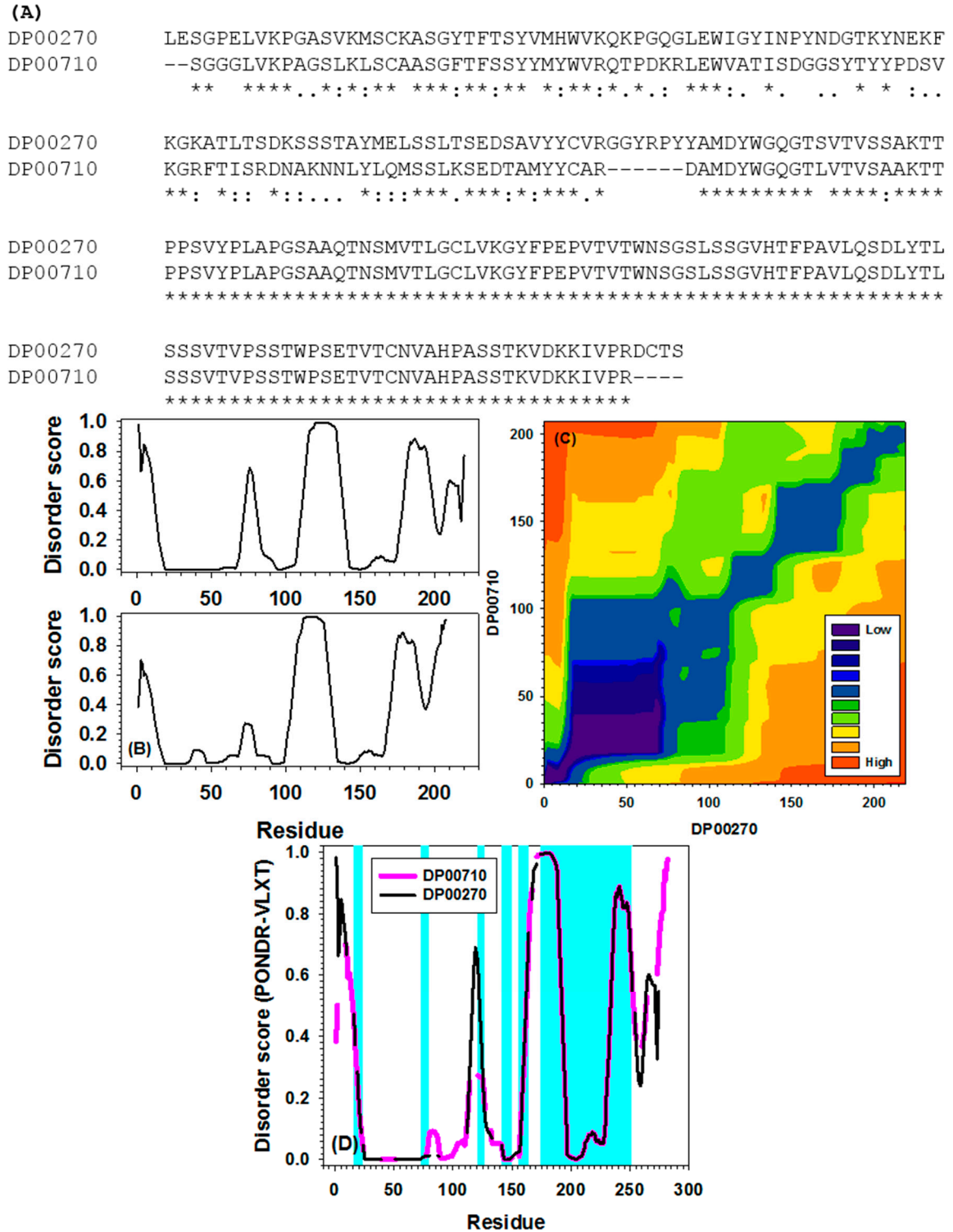


Figure S2. Alignment analysis for DP00270 and DP00710. **(A)** Pair-wise sequence alignment; “*”, “:”, “.”, and “-” stand for identical amino acids, highly similar amino acids, similar amino acids, and gaps, respectively; **(B)** Disorder prediction for DP00270 (**upper** panel) and DP00710 (**lower** panel) by PONDR® VLXT; **(C)** Identified alignment path between DP00270 and DP00710; and **(D)** Alignment of disorder curves between DP00710 (pink) and DP00270 (black) along the alignment path. Only overlapped segment pairs of which the distance between two segments lower than 0.05 were highlighted by cyan.