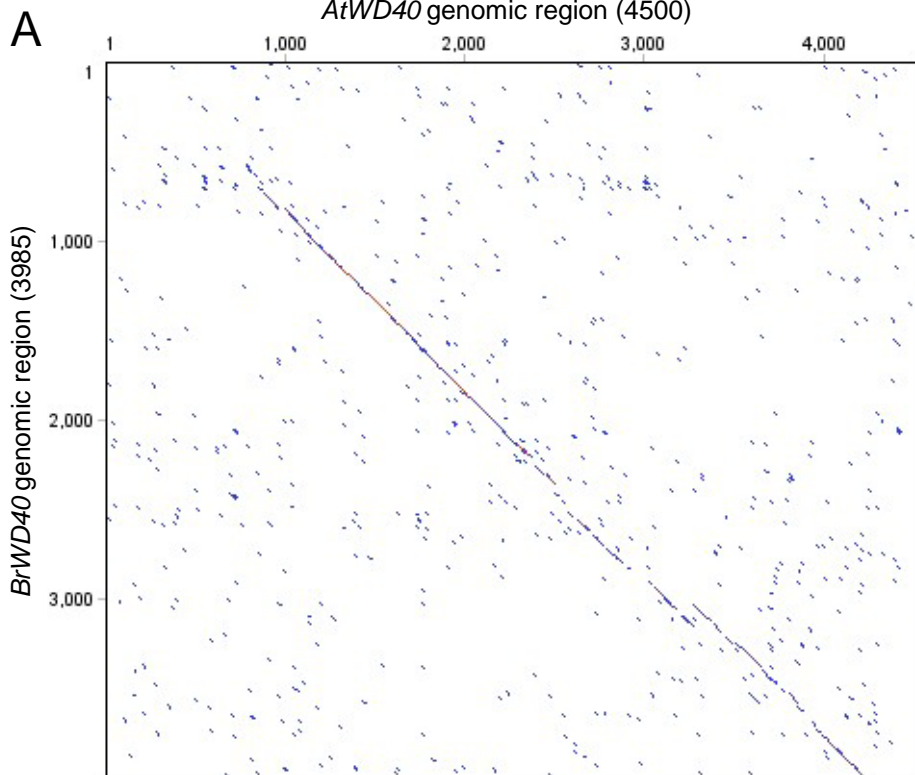


AtWD40 genomic region (4500)



B Identities = 373/425 (87%), Positives = 396/425 (93%), Gaps = 9/425 (2%)

AtWD40	1	MVRSIQEG--VLMSSSSSSTTSNSN--DSDGSLSP-SASTKSFVLNLTLPITGAYKPLA	55
		MVRSIQEG ++MSSSSSSTT+++N DSD SLSP SAS+KSFVL TL PPITGAYKPLA	
BrWD40	1	MVRSIQEGGVLMSSSSSSTTSNNGTSDSDSLSPSSASSKSFVLTLPITGAYKPLA	60
AtWD40	56	VLSAHVGSVSSLALCGEFLLSASQGKDIIVWQQPDLKIPAKFGQGDGSVKALVSVGSKVF	115
		VLSAHVGSVSSLALCGEFLLSASQGKDIIVWQQPDLKIP KFGQGDGSVKALVSVGSKVF	
BrWD40	61	VLSAHVGSVSSLALCGEFLLSASQGKDIIVWQQPDLKIPKFGQGDGSVKALVSVGSKVF	120
AtWD40	116	TAHQDSRIRVWVKSRRRSENAFRLVDTLPTTKDYLKGFPMKQSNYVQTRRNHKLWIEHAD	175
		TAHQDSRIRVWVKSRRR+SENAFRLVD+LPTTKDYLKGFPMKQSNYVQTRRNHKLWIEHAD	
BrWD40	121	TAHQDSRIRVWVKSRRRSENAFRLVDSLPTTKDYLKGFPMKQSNYVQTRRNHKLWIEHAD	180
AtWD40	176	SISCLAVHAGIIYSGSWDKTLKVVRLSDLKLCLESIKAHDDAINGLVAGDGRVYSASADGK	235
		SISCLAVHAGIIYSGSWDKTLKVVRLSDLKLCLESIKAHDDAINGLVAG+GRVYSASADGK	
BrWD40	181	SISCLAVHAGIIYSGSWDKTLKVVRLSDLKLCLESIKAHDDAINGLVAGEGRVYSASADGK	240
AtWD40	236	VKIWGKEKRRKQIESTSSSSSS--LHVLKATLEGRAEVSVNSVTVSGDGNWVYGGGSDGFV	293
		+KIWGKEKRRK+ +S+ SSSSS HVLKATLEG AEVSVNSVTVSG+G WYVYGGGSDGFV	
BrWD40	241	IKIWGKEKRRKADSSLSSSSSSWSHVLKATLEGHAEVSVNSVTVSGEGKMWYGGGSDGFV	300
AtWD40	294	IGWEKKEKEGDFEEWRLGFEETRGNMAVLCMCVVGEMVCSGSADKSIGLWRREVTGMLCK	353
		+GWE+ EK GDFEEWRLGFE RGH MAVLCMCVVGEMVCSGSADKSIGLW+RE +G LCK	
BrWD40	301	MGWERSEKGGDFEEWRLGFEMRGHKMAVLCMCVVGEMVCSGSADKSIGLWKREESGRICK	360
AtWD40	354	FGVIHGHEGVPVKLQASPNNVGAGFMLYSGGLDKSLRVWVVPKQDNLEE--KKSSFKTLTLL	411
		FGVIHGHEGVPVKLQASPNNVGAGFMLYSG LDKS+RVWVWV KQD +EE KK+SF+TLL	
BrWD40	361	FGVIHGHEGVPVKLQASPNNVGAGFMLYSGSLDKSIRVWVWVSKQDCVEEEKKTSFRTLL	420
AtWD40	412	TQKE* 416	
		Q+ *	
BrWD40	421	MQQG* 425	