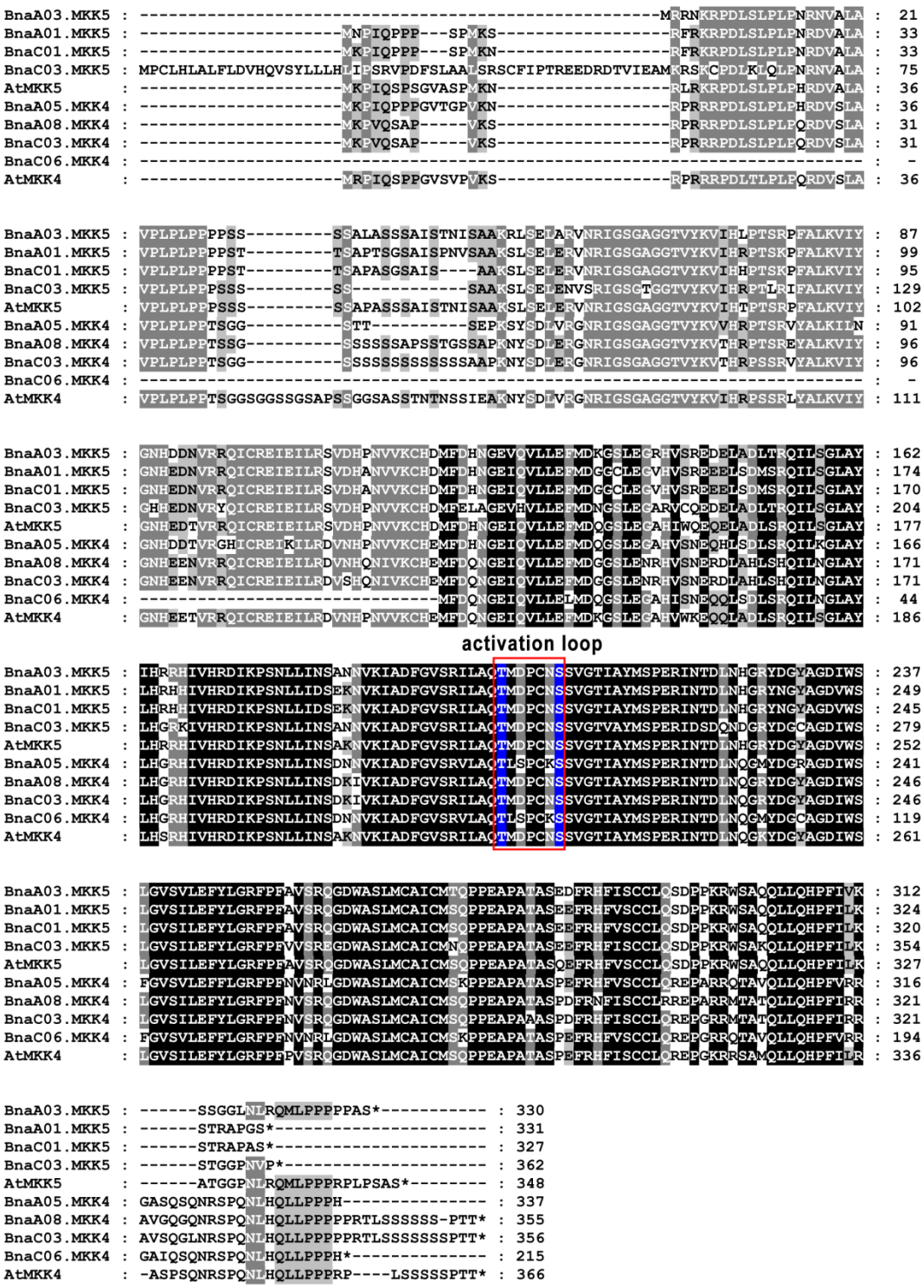

Figure S1: Sequence alignment of identified MPK4/5 copies in *Brassica napus* and *Arabidopsis*. Amino acid sequences were used for alignment, and the identical amino acids and similar amino acids were displayed with black and grey shading respectively. The activation loop was marked with red square frame, and conserved Ser/Thr was highlighted in blue.

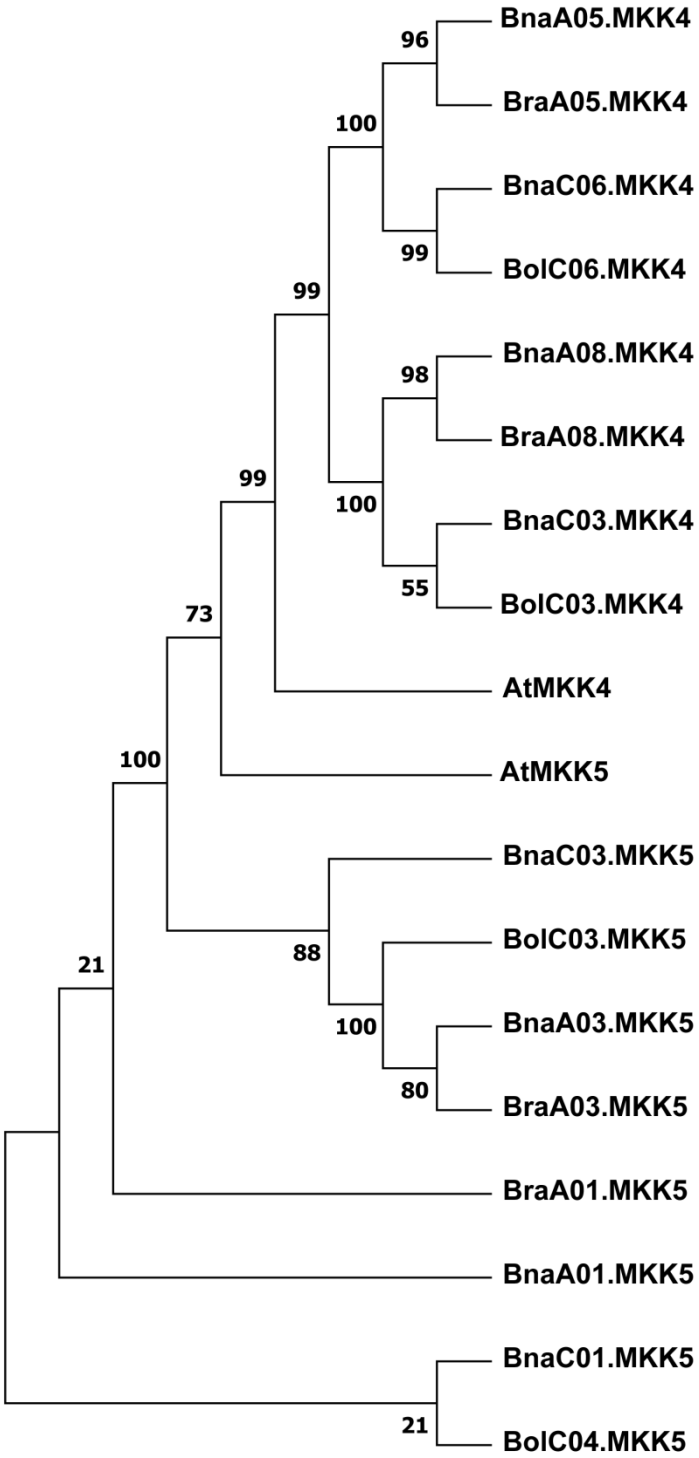

Figure S2: Phylogenetic analysis showing the relationship between each copy of B. napus MKK5 and MKK4/5 in *Brassica* species, as well as MKK4/5 in *Arabidopsis*.

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BnaA06.MPK3 : MNNAGGQ----------------------YPDFPAVQTHGGQFISYDIFGSLFEVTSKYRPPIVPIG :  45
BnaC03.MPK3 : MNNAGGQ----------------------YPDFPAVQTHGGQFISYDIFGSLFEVTSKYRPPIVPIG :  45
BnaC04.MPK6 : MDGNAGQPAADTEMSEAP--SQPSPQMPGVENIPATLSHGGKFIQYNIFGNIFEVTAKYKPPIMPIG :  65
BnaA05.MPK6 : MDGNAGQPAADTEMSEAP--SNPSPQVPGIENIPATLSHGGKFIQYNIFGNIFEVTVKYKPPIMPIG :  65
BnaA03.MPK6 : MDGGTGQPAADTEMSEATGGAAPSQPMPGIENIPATLSHGGMFIQYNIFGNIFEVTAKYSPPIMPIG :  67
BnaC03.MPK6 : MDGGTGQPAADTEMSEASGGAVASQPMPGKENIPATLSHGGRFIQYNIFGNIFEVTAKYNPPIMPIG :  67

BnaA06.MPK3 : RGAYGIVCSVLDSETNELVAMKKIANAFDNHMDAKRTLREIKLLRHLDHENIIAIRDVVPPPLRRQF : 112
BnaC03.MPK3 : RGAYGIVCSVLDSETNELVAMKKIANAFDNHMDAKRTLREIKLLRHLDHENIIAIRDVVPPPLRREF : 112
BnaC04.MPK6 : KGAYGIVCSAMNSETNESVAIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRDIIPPPLRNAF : 132
BnaA05.MPK6 : KGAYGIVCSAMNSETNESVAIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRDIIPPPLRNAF : 132
BnaA03.MPK6 : KGAYGIVCSAMNSETNESVAIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRDIIPPPLRTAF : 134
BnaC03.MPK6 : KGAYGIVCSAMNSETNESVAIKKIANAFDNKIDAKRTLREIKLLRHMDHENIVAIRDIIPPPLRTAF : 134

BnaA06.MPK3 : SDVYIATELMDTDLHQIIRSNQGLSEEHCQYFLYQLLRGLKYIHSAKVIHRDLKPSNLLLNANCDLK : 179
BnaC03.MPK3 : SDVYIATELMDTDLHQIIRSNQGLSEEHCQYFLYQLLRGLKYIHSAKVIHRDLKPSNLLLNANCDLK : 179
BnaC04.MPK6 : NDVYIAYELMDTDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLK : 199
BnaA05.MPK6 : NDVYIAYELMDTDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLK : 199
BnaA03.MPK6 : NDVYIAYELMDTDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLK : 201
BnaC03.MPK6 : NDVYIAYELMDTDLHQIIRSNQGLSEEHCQYFLYQILRGLKYIHSANVLHRDLKPSNLLLNANCDLK : 201

BnaA06.MPK3 : ICDFGLARPTSENEFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMNRKPLFPGKDHVH : 246
BnaC03.MPK3 : ICDFGLARPTSENEFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMNRKPLFPGKDHVH : 246
BnaC04.MPK6 : ICDFGLARVTSESDFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMDRKPLFPGRDHVH : 266
BnaA05.MPK6 : ICDFGLARVTSESDFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMDRKPLFPGRDHVH : 266
BnaA03.MPK6 : ICDFGLARVNSESDFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMDRKPLFPGRDHVH : 268
BnaC03.MPK6 : ICDFGLARVNSESDFMTEYVVTRWYRAPELLLNSSDYTAAIDVWSVGCIFMELMDRKPLFPGRDHVH : 268

BnaA06.MPK3 : QMRLLTELLGTPTESDLGFTHNEDAKRYIRQLPNFPRQPLAKLFSHVNPLAIDLVDRMLTFDPSKRI : 313
BnaC03.MPK3 : QMRLLTELLGTPTESDLGFTHNEDAKRYIRQLPNFPRQPLAKLFSHVNSLAIDLVDRMLTFDPNKRI : 313
BnaC04.MPK6 : QLRLLMELIGTPSEEELEFLN-ENAKRYIKQLPPYPRQSLTDKFPNVHPLAIDLIEKMLTFDPRRRI : 332
BnaA05.MPK6 : QLRLLMELIGTPSEEELEFLN-ENAKRYIKQLPPYPRQSLTDKFPNVHPLAIDLIEKMLMFDPRRRI : 332
BnaA03.MPK6 : QLRLLMELIGTPSEQEVEFLN-ENAKRYIRQLPPYPRQSITDKFPNVHPLAIDLIEKMLTFDPRRRI : 334
BnaC03.MPK6 : QLRLLMELIGTPSEQEVEFLN-ENAKRYIRQLPPYPRQSITDKFPNVHPLAIDLIEKMLTFDPRRRI : 334

                      common docking site
BnaA06.MPK3 : TVEEALNHPYLAFLHDPNDEPICLKPFSFDFEQQPLDEEQIKEMIYREAIALNPTYA*---- : 370
BnaC03.MPK3 : TVEEALNHPYLAFLHDPNDEPICLKPFSFDFEQQPLDEEQIKEMIYREAIALNPTYA*---- : 370
BnaC04.MPK6 : TVLDALAHPYLNSLHDISDEPECTVPFNFDFEQHALSEEQMKELIYHEALAFNPEYQQIV*- : 392
BnaA05.MPK6 : TVLDALAHPYLNSLHDISDEPECTVPFNFDFEQHALSEEQMKELIYREALAFNPEYQQIV*- : 392
BnaA03.MPK6 : TVLDALAHPYLNSLHDISDEPECTIPFNFDFEQHALSEEQMKELIYREALAFNPEYQTAIA* : 395
BnaC03.MPK6 : TVLDALAHPYLNSLHDISDEPECTIPFNFDFEQHALSEEQMKELIYREALAFNPEYQPAIA* : 395
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Figure S3: Sequence alignment of *B. napus* MPK3/6 copies. The identical amino acids and similar amino acids were displayed with black and grey shading respectively. TEY motif was marked with red; common docking site was marked with red square frame, and two adjacent acidic residues was highlighted in blue.