

File S2 Alignment of the RM11-1a and S288C *BUD32*, *GON7*, *KAE1*, and *PCC1* nucleotide sequences.

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RM11-1a BUD32      ATGACGCAAGAATTCATTGATAAAGTATCTTCCTACCTGACTCCTGATGTGGACATTGCA 60
S288C BUD32        ATGACGCAAGAATTCATTGATAAAGTATCTTCCTACCTGACTCCTGATGTGGACATTGCA 60
*****

RM11-1a BUD32      CCTATTTCTCAAGGTGCAGAAGCCATTGTTTTCACAACGACTACTCACCATATCTCCCA 120
S288C BUD32        CCTATTTCTCAAGGTGCAGAAGCCATTGTTTTCACAACGACTACTCACCATATCTCCCA 120
*****

RM11-1a BUD32      AGAGCAAAGGATTCTCATCAAAAGTATATTATCAAATATAGGCCACCAAAGCGTTATAGA 180
S288C BUD32        AGAGCAAAGGATTCTCATCAAAAGTATATTATCAAATATAGGCCACCAAAGCGTTATAGA 180
*****

RM11-1a BUD32      CATCCACAAATAGACCAGGCACTAACAAAACATCGTACGTTGAATGAGTCGCGTTTATTG 240
S288C BUD32        CATCCACAAATAGACCAGGCACTAACAAAACATCGTACGTTGAATGAGTCGCGTTTATTG 240
*****

RM11-1a BUD32      GCCAAATTATACTTGATTCCAGGGCTATGTGTCCCTCAACTGATAGCGTGTGATCCATAC 300
S288C BUD32        GCCAAATTATACTTGATTCCAGGGCTATGTGTCCCTCAACTGATAGCGTGTGATCCATAC 300
*****

RM11-1a BUD32      AATGGATTTCATTTGGTTAGAGTTCCTTGGAGAAGATCTTCCCGGAGGGCACGGTTTTAGT 360
S288C BUD32        AATGGATTTCATTTGGTTAGAGTTCCTTGGAGAAGATCTTCCCGGAGGGCACGGTTTTAGT 360
*****

RM11-1a BUD32      AACCTAAAGAACTTCCTTTGGATGCATGACCAAGATCCATATAGTGATCTTGTAGCAACT 420
S288C BUD32        AACCTAAAGAACTTCCTTTGGATGCATGACCAAGATCCATATAGTGATCTTGTAGCAACT 420
*****

RM11-1a BUD32      ACACTACGGAAAGTGGGGCGCCAAATTGGGTTGTTGCACTGGAATGACTACTGTCATGGT 480
S288C BUD32        ACACTACGGAAAGTGGGGCGCCAAATTGGGTTGTTGCACTGGAATGACTACTGTCATGGT 480
*****

RM11-1a BUD32      GATTTGACAAGTTCTAACATTGTTCTCGTGCGAGATGGTGCGAGATGGACGCCTCATTG 540
S288C BUD32        GATTTGACAAGTTCTAACATTGTTCTCGTGCGAGATGGTGCGAGATGGACGCCTCATTG 540
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RM11-1a BUD32	ATTGATTTCGGTCTGGGCTCAGTTTCAAACCTGGTCGAAGATAAAGGCGTCGATTTATAC	600
S288C BUD32	ATTGATTTCGGTCTGGGCTCAGTTTCAAACCTGGTCGAAGATAAAGGCGTCGATTTATAC	600

RM11-1a BUD32	GTCTTAGAGAGAGCTATTTTAAGTACACATTCGAAGCATGCGGAAAAATACAATGCTTGG	660
S288C BUD32	GTCTTAGAGAGAGCTATTTTAAGTACACATTCGAAGCATGCGGAAAAATACAATGCTTGG	660

RM11-1a BUD32	ATCATGGAGGGGTTCGAAGAGGTCTATCGTGAACAAGGTGCGAAAGGTGCCAAGAACTG	720
S288C BUD32	ATCATGGAGGGGTTCGAAGAGGTCTATCGTGAACAAGGTGCGAAAGGTGCCAAGAACTG	720

RM11-1a BUD32	AAAGAAGTTACCAAAAGATTCTGAAGAGGTCAGGTTGCGTGGTCGTAAGAGAAGTATGCTA	780
S288C BUD32	AAAGAAGTTACCAAAAGATTCTGAAGAGGTCAGGTTGCGTGGTCGTAAGAGAAGTATGCTA	780

RM11-1a BUD32	GGATAA	786
S288C BUD32	GGATAA	786

RM11-1a GON7	ATGAAACTACCGGTAGCACAGTACAGTGCACCAGATGGTGTGGAAAAAAGTTTGCACCA	60
S288C GON7	ATGAAACTACCGGTAGCACAGTACAGTGCACCAGATGGTGTGGAAAAAAGTTTGCACCA	60

RM11-1a GON7	ATACGCGATGACCCTCGATACATGACCACAGAGGGAAGGACAACCTGGGCCAGTGACCAT	120
S288C GON7	ATACGCGATGACCCTCGATACATGACCACAGAGGGAAGGACAACCTGGGCCAGTGACCAT	120

RM11-1a GON7	GTGCTAAACGCTGGCCAAATCGATAGAGACAAACCTTCAGAACCGBAACGCACAAAAGAT	180
S288C GON7	GTGCTAAACGCTGGCCAAATCGATAGAGACAAACCTTCAGAACCGBAACGCACAAAAGAT	180

RM11-1a GON7	GGCTCACAACCTGACATACTTAGGCCAGCTGCGCACGCAGCTGACGGGGCTACAGGACGAT	240
S288C GON7	GGCTCACAACCTGACATACTTAGGCCAGCTGCGCACGCAGCTGACGGGGCTACAGGACGAT	240

RM11-1a GON7 ATTAACGAGTTTTTGACAGGAAGAATGGAATTGGCAAAAAATAAGAAGAAAGCCGGCGCA 300
S288C GON7 ATTAACGAGTTTTTGACAGGAAGAATGGAATTGGCAAAAAATAAGAAGAAAGCCGGCGCA 300

RM11-1a GON7 GACGAGAAGCGGATCCAGGAAGAGATTAATCAGCTATTAGATGGTGGTGATGGTGACGAA 360
S288C GON7 GACGAGAAGCGGATCCAGGAAGAGATTAACCAGCTATTAGATGGTGGTGACGGTGACGAA 360

RM11-1a GON7 GATGCTGTTTAG 372
S288C GON7 GATGCTGTTTAG 372

RM11-1a KAE1 ATGGTCAACTTGAACACTATCCCACCCAAAAATGGCAGGGACTACTACATTGCGCTTGA 60
S288C KAE1 ATGGTCAACTTGAACACTATCCCACCCAAAAATGGCAGGGACTACTACATTGCGCTTGA 60

RM11-1a KAE1 CTCGAAGGTTCTGCAAATAAACTGGGCGTTGGTATAGTTAAGCATCCGCTTCTGCCTAAA 120
S288C KAE1 CTTGAAGGTTCTGCAAATAAACTGGGCGTTGGTATAGTTAAGCATCCGCTTCTGCCTAAA 120

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RM11-1a KAE1 CATGCCAACAGCGATCTATCTTATGATTGCGAAGCTGAGATGCTTTCTAATATTAGAGAC 180
S288C KAE1 CATGCCAACAGCGATCTATCTTATGATTGCGAAGCTGAGATGCTTTCTAATATTAGAGAC 180

RM11-1a KAE1 ACATATGTCACACCTCCTGGGGAGGGATTTTTGCCTCGAGACACGGCAAGGCATCACAGA 240
S288C KAE1 ACATATGTCACACCTCCTGGGGAGGGATTTTTGCCTCGAGACACGGCAAGGCATCACAGA 240

RM11-1a KAE1 AATTGGTGCATAAGACTCATAAAACAAGCACTGGCCGAAGCTGACATCAAAAACCCGACA 300
S288C KAE1 AATTGGTGCATAAGACTCATAAAACAAGCACTGGCCGAAGCTGACATCAAAAAGCCCGACA 300

RM11-1a KAE1 CTAGACATTGATGTAATTTGCTTTACCAAAGGTCCCGGCATGGGGGCCCTCTGCATTCA 360
S288C KAE1 CTAGACATTGATGTAATTTGCTTTACCAAAGGTCCCGGCATGGGGGCCCTCTGCATTCA 360

RM11-1a KAE1 GTTGTTCATCGCCGCCAGAACGTGCTCCTTACTGTGGGACGTGCCACTGGTGGGAGTAAAC 420
S288C KAE1 GTTGTTCATCGCCGCCAGAACGTGCTCCTTACTGTGGGACGTGCCACTGGTGGGAGTAAAC 420

RM11-1a KAE1 CACTGCATTGGTCACATCGAAATGGGGAGAGAAATCACTAAAGCTCAAAATCCTGTGGTA 480
S288C KAE1 CACTGCATTGGTCACATCGAAATGGGGAGAGAAATCACTAAAGCTCAAAATCCTGTGGTA 480

RM11-1a KAE1 CTGTATGTAAGTGGTGGAAATACACAGGTTATTGCATACTCGGAAAAAAGGTACCGTATC 540
S288C KAE1 CTGTATGTAAGTGGTGGAAATACACAAGTTATTGCATACTCGGAAAAAAGGTACCGTATC 540

RM11-1a KAE1 TTTGGTGAAACGCTTGATATTGCTATCGGTAATTGTCTTGATAGATTGCAAGAACTCTG 600
S288C KAE1 TTTGGTGAAACGCTTGATATTGCTATCGGTAATTGTCTTGATAGATTGCAAGAACTCTG 600

RM11-1a KAE1 AAGATACCTAATGAGCCCTCGCCTGGCTACAACATCGAGCAGTTAGCTAAAAAAGCCCCT 660
S288C KAE1 AAGATACCTAATGAGCCCTCGCCTGGCTACAACATCGAGCAGTTAGCTAAAAAAGCCCCT 660

RM11-1a KAE1 CACAAAGAAAACCTTGGTAGAACTTCCCTATACAGTAAAGGGGATGGATCTTTCGATGAGT 720
S288C KAE1 CACAAAGAAAACCTTGGTAGAACTTCCCTATACAGTAAAGGGGATGGATCTTTCGATGAGT 720

RM11-1a KAE1 GGTATATTGGCTTCCATCGATTTACTTGCCAAGGATCTATTTAAGGGCAATAAGAAAAAT 780
S288C KAE1 GGTATATTGGCTTCCATCGATTTACTTGCCAAGGATCTATTTAAGGGCAATAAGAAAAAT 780

RM11-1a KAE1 AAGATCCTATTCGACAAGACAACGGGCGAGCAAAAAGTCACTGTAGAGGATCTTTGCTAC 840
S288C KAE1 AAGATCCTATTCGACAAGACAACGGGCGAGCAAAAAGTCACTGTAGAGGATCTTTGCTAC 840

RM11-1a KAE1 TCTCTGCAAGAGAACCTATTCGCCATGCTAGTTGAAATAACAGAAAGAGCTATGGCTCAC 900
S288C KAE1 TCTCTGCAAGAGAACCTATTCGCCATGCTAGTTGAAATAACAGAAAGAGCTATGGCTCAC 900

RM11-1a KAE1 GTTAACTCCAATCAAGTTTTGATCGTAGGCGGTGTTGGTTGTAACGTGCGATTACAAGAG 960

S288C KAE1 GTTAACTCCAATCAAGTTTTGATCGTAGGCGGTGTTGGTTGTAACGTGCGATTACAAGAA 960

RM11-1a KAE1 ATGATGGCGCAAATGTGTAAAGACAGGGCCAATGGGCAAGTACATGCTACAGATAATAGG 1020

S288C KAE1 ATGATGGCGCAAATGTGTAAAGACAGGGCCAATGGGCAAGTACATGCTACAGATAATAGG 1020

RM11-1a KAE1 TTTTGTATCGATAACGGAGTTATGATTGCCCAAGCAGGACTACTAGAGTATAGAATGGGT 1080

S288C KAE1 TTTTGTATCGATAACGGAGTTATGATTGCCCAAGCAGGACTACTAGAGTATAGAATGGGT 1080

RM11-1a KAE1 GGGATCGTGAAGGACTTTTCTGAAACTGTTGTTACGCAGAAATTCAGAACCGATGAAGTA 1140

S288C KAE1 GGGATCGTGAAGGACTTTTCTGAAACTGTTGTTACGCAGAAATTCAGAACCGATGAAGTA 1140

RM11-1a KAE1 TACGCAGCCTGGCGTGATTAA 1161

S288C KAE1 TACGCAGCCTGGCGTGATTAA 1161

RM11-1a PCC1 ATGACAAGCAAACGGGAAAAGTCACTGGATCACACATTGTAAGTAGAAGCAGTTTTTCAA 60

S288C PCC1 ATGACAAGCAAACGGGAAAAGTCACTGGATCACACATTGTAAGTAGAAGCAGTTTTTCAA 60

RM11-1a PCC1 TGGAAGACCGCACTGCATAGTTTACTAACTATTTAACTTTCCAAACATTAGAGAACTA 120

S288C PCC1 TGGAAGACCGCACTGCATAGTTTACTAACTATTTAACTTTCCAAACATTAGAGAACTA 120

RM11-1a PCC1 AAGATACCGTTTGAAACGGAGCGACAAGCGACCATAGCAACCAAAGTCCTATCTCCGGAC 180

S288C PCC1 AAGATACCGTTTGAAACGGAGCGACAAGCGACCATAGCAACCAAAGTCCTATCTCCGGAC 180

RM11-1a PCC1 CCGATTTTGAAGCCACAAGATTTTCAAGTAGACTACAGTCCGAGAAAAATGTCATGCTA 240

S288C PCC1 CCGATTTTGAAGCCACAAGATTTTCAAGTAGACTACAGTCCGAGAAAAATGTCATGCTA 240

RM11-1a PCC1	GTCCAGTTCAGAAGCATTGATGATAGGGTGCTTCGAGTGGGAGTTAGCAGTATCATAGAC	300
S288C PCC1	GTCCAGTTCAGAAGCATTGATGATAGGGTGCTTCGAGTGGGAGTTAGCAGTATCATAGAC	300

RM11-1a PCC1	AGTATCAAAACCATTGTGGAAGCCATGGACGTTCTATCATAA	342
S288C PCC1	AGTATCAAAACCATTGTGGAAGCCATGGACGTTCTATCATAA	342
