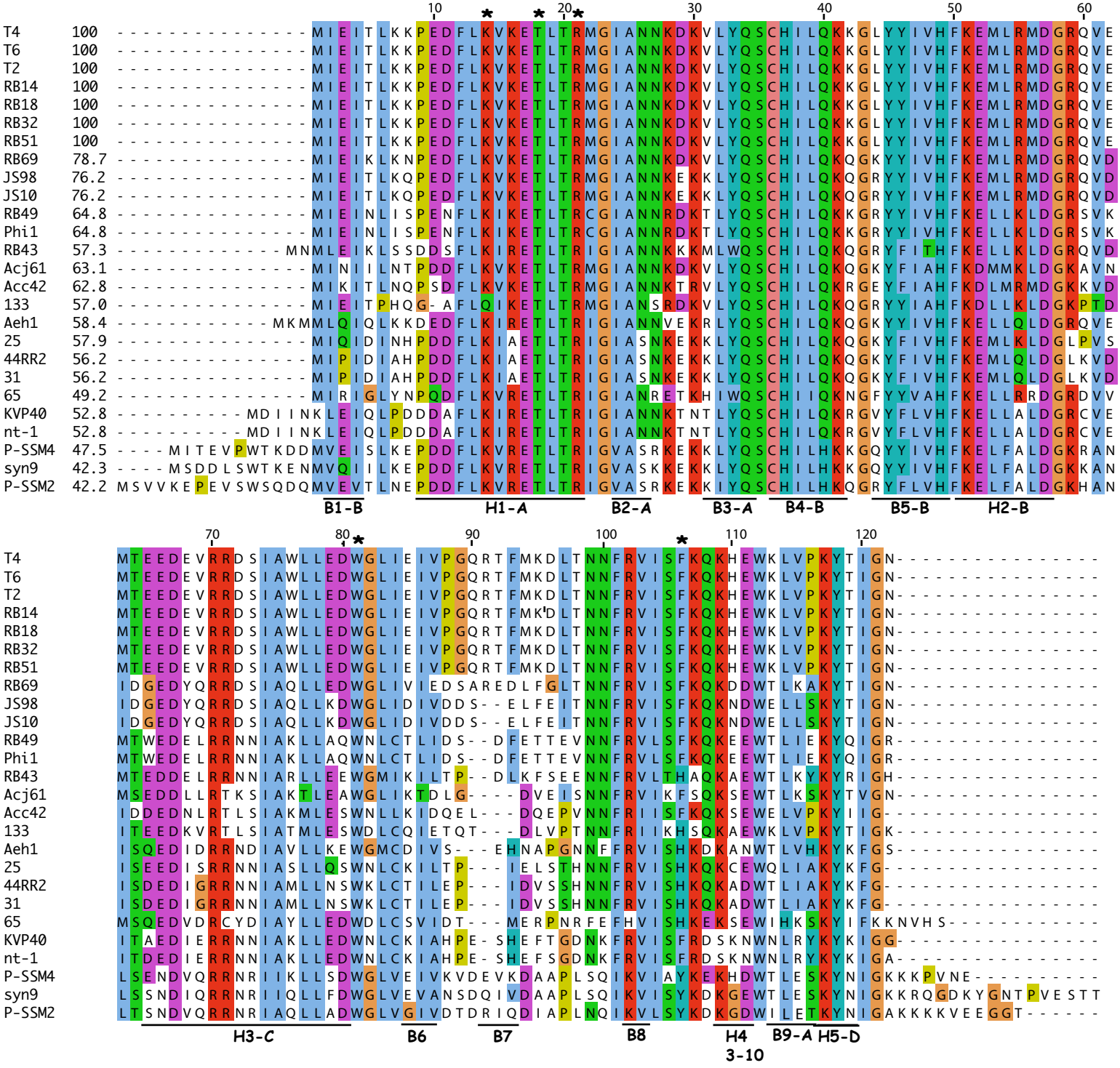
T4 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
T6 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
T2 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
RB14 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
RB18 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
RB32 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
RB51 100 MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVE
RB69 78.7 MIEIKLKNPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKQGKYYIVHFKEMLRMDGRQVD
JS98 76.2 MIEITLKQPEDFLKVKETLTRMGIANNKEKKLYQSCHILQKQGRYYIVHFKEMLRMDGRQVD
JS10 76.2 MIEITLKQPEDFLKVKETLTRMGIANNKEKKLYQSCHILQKQGRYYIVHFKEMLRMDGRQVD
RB49 64.8 MIEINLISPENFLKIKETLTRCGIANNRDKTLYQSCHILQKKGRYYIVHFKELLKLDGRSVK
Phi1 64.8 MIEINLISPENFLKIKETLTRCGIANNRDKTLYQSCHILQKKGRYYIVHFKELLKLDGRSVK
RB43 57.3 MNMLEIKLSSDDSFLKIRETLTRIGIANNKKKMLWQSCHILQKQGRYFITHFKELLKLDGRQVD
Acj61 63.1 MINIILNTPDDFLKVKETLTRMGIANNKDKVLYQSCHILQKQGKYFIAHFKDMMKLDGKAVN
Acc42 62.8 MIKITLNQPSDFLKVKETLTRMGIANNKTRVLYQSCHILQKRGEYFIAHFKDLMRMDGKKVD
133 57.0 MIEITPHQG-AFLQIKETLTRMGIANSRDKVLYQSCHILQKQGRYYIAHFKDLLKLDGKPTD
Aeh1 58.4 MKMMLQIQLKKDEDFLKIRETLTRIGIANNVEKRLYQSCHILQKQGKYYIVHFKELLQLDGRQVE
25 57.9 MIQIDINHPDDFLKIAETLTRIGIASNKEKKLYQSCHILQKQGKYFIVHFKEMLKLDGLPVS
44RR2 56.2 MIPIDIAHPDDFLKIAETLTRIGIASNKEKKLYQSCHILQKQGKYFIVHFKEMLQLDGLKVD
31 56.2 MIPIDIAHPDDFLKIAETLTRIGIASNKEKKLYQSCHILQKQGKYFIVHFKEMLQLDGLKVD
65 49.2 MIRIGLYNPQDFLKVRETLTRIGIANRETKHIWQSCHIIQKNGFYYVAHFKELLRRDGRDVV
KVP40 52.8 MDIINKLEIQLPDDDAFLKIRETLTRIGIANNKTNTLYQSCHILQKRGVYFLVHFKELLALDGRCVE
nt-1 52.8 MDIINKLEIQLPDDDAFLKIRETLTRIGIANNKTNTLYQSCHILQKRGVYFLVHFKELLALDGRCVE
P-SSM4 47.5 MITEVPWTKDDMVEISLKEPDDFLKVRETLTRIGVASRKEKKLYQSCHILHKKGQYYIVHFKELFALDGKRAN
syn9 42.3 MSDDLSWTKENMVQIILKEPDDFLKVRETLTRIGVASKKEKKLYQSCHILHKKGQYYIVHFKELFALDGKKAN
P-SSM2 42.2 MSVVKEPEVSWSQDQMVEVTLNEPDDFLKVRETLTRIGVASRKEKKIYQSCHILHKQGRYFLVHFKELFALDGKHAN
10
20
30
40
50
60
B1-B
H1-A
B2-A
B3-A
B4-B
B5-B
H2-B
T4 MTEEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN
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RB18 MTEEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN
RB32 MTEEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN
RB51 MTEEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN
RB69 IDGEDYQRRDSIAQLLEDWGLIVIEDSAREDLFGLTNNFRVISFKQKDDWTLKAKYTIGN
JS98 IDGEDYQRRDSIAQLLKDWGLIDIVDDS--ELFEITNNFRVISFKQKNDWELLSKYTIGN
JS10 IDGEDYQRRDSIAQLLKDWGLIDIVDDS--ELFEITNNFRVISFKQKNDWELLSKYTIGN
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Phi1 MTWEDELRRNNIAKLLAQWNLCTLIDS--DFETTEVNNFRVLSFKQKEEWTLIEKYQIGR
RB43 MTEDDELRRNNIARLLEEWGMIKILTP--DLKFSEENNFRVLTHAQKAEWTLKYKYRIGH
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25 ISEEDISRRNNIASLLQSWNLCKILTP---IELSTHNNFRVISHKQKCEWQLIAKYKFG
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31 ISDEDIGRRNNIAMLLNSWKLCTILEP---IDVSSHNNFRVISHKQKADWTLIAKYKFG
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KVP40 ITAEDIERRNNIAKLLEDWNLCKIAHPE-SHEFTGDNKFRVISFRDSKNWNLRYKYKIGG
nt-1 ITDEDIERRNNIAKLLEDWNLCKIAHPE-SHEFSGDNKFRVISFRDSKNWNLRYKYKIGA
P-SSM4 LSENDVQRRNRIIKLLSDWGLVEIVKVDEVKDAAPLSQIKVIAYKEKHDWTLESKYNIGKKKPVNE
syn9 LSSNDIQRRNRIIQLLFDWGLVEVANSDQIVDAAPLSQIKVISYKDKGEWTLESKYNIGKKRQGDKYGNTPVESTT
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70
80
90
100
110
120
H3-C
B6
B7
B8
H4
3-10
B9-A
H5-D