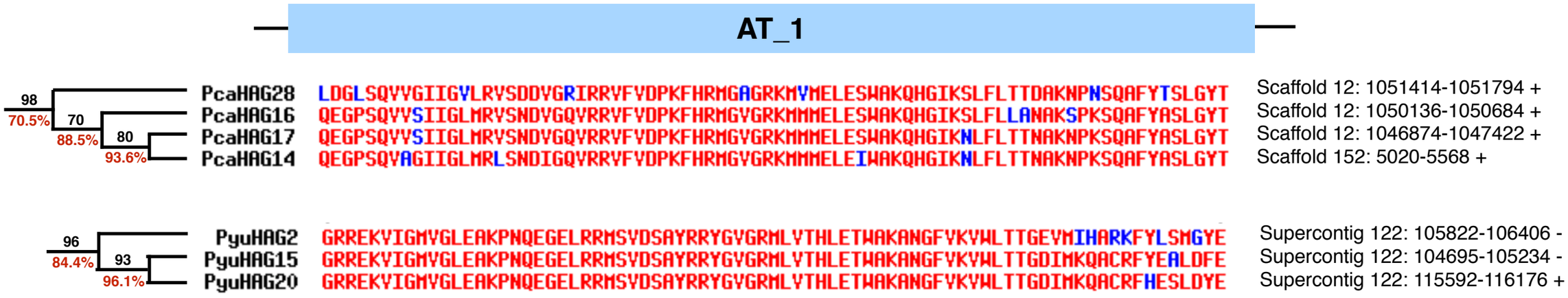
A


AT_1
98
70.5%
70
88.5%
80
93.6%
PcaHAG28 LDGLSQVVGIIGVLRVSDDVGRIRRVFVDPKFHRMGAGRKMVMELESWAKQHGIKSLFLTTDAKNPNSQAFYTSLGYT Scaffold 12: 1051414-1051794 +
PcaHAG16 QEGPSQVVSIIGLMRVSNDVGQVRRVFVDPKFHRMGVGRKMMMELESWAKQHGIKSLFLLANAKSPKSQAFYASLGYT Scaffold 12: 1050136-1050684 +
PcaHAG17 QEGPSQVVSIIGLMRVSNDVGQVRRVFVDPKFHRMGVGRKMMMELESWAKQHGIKNLFLTTNAKNPKSQAFYASLGYT Scaffold 12: 1046874-1047422 +
PcaHAG14 QEGPSQVAGIIGLMRLSNDIGQVRRVFVDPKFHRMGVGRKMMMELEIWAKQHGIKNLFLTTNAKNPKSQAFYASLGYT Scaffold 152: 5020-5568 +
96
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93
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PyuHAG2 GRREKVIGMVGLEAKPNQEGELRRMSVDSAYRRYGVGRMLVTHLETWAKANGFVKVWLTTGEVMIHARKFYLSMGYE Supercontig 122: 105822-106406 -
PyuHAG15 GRREKVIGMVGLEAKPNQEGELRRMSVDSAYRRYGVGRMLVTHLETWAKANGFVKVWLTTGDIMKQACRFYEALDFE Supercontig 122: 104695-105234 -
PyuHAG20 GRREKVIGMVGLEAKPNQEGELRRMSVDSAYRRYGVGRMLVTHLETWAKANGFVKVWLTTGDIMKQACRFHESLDYE Supercontig 122: 115592-116176 +

B


86
30.8%
45
39.5%
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99
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SpaHAT9 ASERELTAASLSQHDPSGRFLCIHSVVVEAAHRRDGLGTALLRAYLAHVQQHHPSVDAIVLLAKPALVQWYVRCGF Supercontig 1: 605109-605647 +
SpaHAG19 MAYARLLGPGAK--HATQQRPMIGRVLTAPSARGKGLGKALVTRAIAECRARWPN-EAIEIGAQSYLRSFYEDFGF Supercontig 1: 6055906-606481 -
SpaHAG7 MAYARLLGPGTK--GASQQLPMIGRVLTSPKHRGGGLGKQLMQEAIAECSRRWPD-KGIEISAQVYLEAFYKSLGF Supercontig 1: 614439-615074 -
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34
13.7%
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