

Supplemental Information for the manuscript: Population genomics of the invasive Argentine ant (*Linepithema humile*) - adaptive evolution in the introduced population
Ida Holmberg, Jenni Paviala, Jes Sørensen, Heikki Helanterä, Lumi Viljakainen

S15. 20 kbp genomic windows with the highest F_{ST} values.

Please note that Catalonia was excluded from this step.

HIGHEST 1%

Sample pair 20 kbp window (name of the window + position)

Native & Chile NW_012158321.1+110000, NW_012158321.1+130000, NW_012158820.1+30000, NW_012160018.1+50000, NW_012160079.1+30000

Native & European NW_012158181.1+50000, NW_012158181.1+70000, NW_012160180.1+110000, NW_012160180.1+250000, NW_012160181.1+50000

European Main & C NW_012158181.1+50000, NW_012158181.1+70000, NW_012159286.1+30000, NW_012159286.1+70000, NW_012159286.1+90000,

HIGHEST 5%

Sample pair 20 kbp window (name of the window + position)

Native & Chile NW_012158181.1+130000, NW_012158181.1+210000, NW_012158181.1+310000, NW_012158321.1+110000, NW_012158321.1+130000

Native & European NW_012158181.1+50000, NW_012158181.1+70000, NW_012158321.1+110000, NW_012158820.1+130000, NW_012160077.1+30000

European Main & C NW_012158181.1+210000, NW_012158181.1+310000, NW_012158181.1+50000, NW_012158181.1+70000, NW_012158321.1+150000

0, NW_012160079.1+50000, NW_012160100.1+270000, NW_012160179.1+30000, NW_012160179.1+50000, NW_012160181.1+110000, NW_012160186.
0, NW_012160181.1+70000, NW_012160185.1+70000, NW_012160185.1+90000, NW_012160188.1+430000, NW_012160191.1+70000, NW_012160210.1
NW_012159963.1+50000, NW_012160002.1+70000, NW_012160176.1+130000, NW_012160176.1+30000, NW_012160186.1+10000, NW_012160190.1+2

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+230000, NW_012160333.1+1070000, NW_012160333.1+1130000, NW_012160333.1+430000, NW_012160333.1+890000, NW_012160333.1+910000, NW
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1590000, NW_0121606
70000, NW_01216054

NW_012160213.1+17
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S15. Genes with the highest F_{ST} values.

Please note that Catalonia was excluded from this step.

HIGHEST 1%

Sample pair	Genes
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Native & Chile	LOC105667341, LOC105667615, LOC105667687, LOC105667764, LOC105667777, LOC105667866, LOC105668737, LOC105668790, LOC10566881
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Native & Europea	LOC105667782, LOC105668707, LOC105668737, LOC105668782, LOC105668783, LOC105668954, LOC105669391, LOC105669469, LOC10566952
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European Main &	LOC105667349, LOC105667351, LOC105667776, LOC105668525, LOC105668533, LOC105668537, LOC105668540, LOC105668761, LOC10566884
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HIGHEST 5%

Sample pair	Genes
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Native & Chile	LOC105667323, LOC105667326, LOC105667341, LOC105667349, LOC105667351, LOC105667615, LOC105667625, LOC105667667, LOC10566768
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Native & Europea	LOC105667341, LOC105667587, LOC105667666, LOC105667706, LOC105667748, LOC105667755, LOC105667776, LOC105667781, LOC10566778
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European Main &	LOC105667323, LOC105667326, LOC105667341, LOC105667349, LOC105667351, LOC105667442, LOC105667615, LOC105667666, LOC10566768
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