**Table 2 (full) Compilation of correlation estimates between individual measures of inbreeding from empirical data in scenarios where molecular estimators are obtained assuming allele frequencies from the current generation**

| | $F_{VR1}$ | $F_{VR2}$ | $F_{YA2}$ | $F_{LH1}$ or $F_{HOM}$ | $F_{LH2}$ | $F_{ROH}$ |
|---|---|---|---|---|---|---|
| $F_{PED}$ | **0.21**<br>0.13[2], 0.39[2], 0.10[3], 0.35[12], 0.07[11], 0.23[18] | **−0.09**<br>0.21[6], −0.26[8], −0.21[8], −0.21[8], −0.01[11], −0.08[16], −0.07[17] | **0.42**<br>0.47[3], 0.72[4], 0.29[5], 0.26[5], 0.68[8], 0.43[8], 0.32[8], 0.43[12], 0.15[17] | **0.50**<br>0.66[1], 0.10[2], 0.35[2], 0.77[3], 0.67[4], 0.45[5], 0.41[5], 0.45[6], 0.68[7], 0.78[8], 0.60[8], 0.37[8], 0.32[11], 0.59[15], 0.31[16], 0.43[17] | **0.32**<br>0.32[17] | **0.50**<br>0.63[1], 0.07[2], 0.37[2], 0.77[4], 0.53[5], 0.51[5], 0.44[6], 0.73[8], 0.46[8], 0.49[8], 0.37[11], 0.92[12], 0.60[15], 0.35[16], 0.47[17], 0.25[18] |
| $F_{VR1}$ | | **0.91**<br>0.83[9], 0.94[10], 0.97[11], 0.88[13] | **0.84**<br>0.88[3], 0.71[9], 0.92[10], 0.84[12], 0.87[13] | **0.42**<br>1.0[2], 0.28[3], 0.11[9], 0.63[10], −0.13[11], 0.62[13] | | **0.57**<br>0.99[2], −0.13[11], 0.73[12], 0.70[18] |
| $F_{VR2}$ | | | **0.52**<br>0.29[8], 0.42[8], 0.54[8], 0.26[9], 0.75[10], 0.66[13], 0.72[17] | **−0.21**<br>0.27[6], −0.61[8], −0.48[8], −0.95[8], −0.38[9], 0.35[10], −0.32[11], 0.36[13], −0.23[16], −0.06[17] | **−0.64**<br>−0.64[17] | **0.01**<br>0.22[6], 0.09[8], 0.14[8], 0.003[8], −0.26[11], 0.16[14], −0.21[16], −0.07[17] |
| $F_{YA2}$ | | | | **0.64**<br>0.70[3], 0.92[4], 0.72[5], 0.66[5], 0.58[8], 0.60[8], −0.24[8], 0.74[9], 0.88[10], 0.91[13], 0.54[17] | **−0.04**<br>−0.04[17] | **0.78**<br>0.87[4], 0.65[5], 0.62[5], 0.95[8], 0.92[8], 0.81[8], 0.92[12], 0.77[14], 0.50[17] |
| $F_{LH1}$ or $F_{HOM}$ | | | | | **0.72**<br>0.72[17] | **0.83**<br>0.97[1], 0.99[2], 0.86[4], 0.90[5], 0.91[5], 0.80[6], 0.71[8], 0.76[8], 0.31[8], 0.90[11], 0.80[14], 0.86[15], 0.95[16], 0.93[17] |
| $F_{LH2}$ | | | | | | **0.66**<br>0.66[17] |

The compilation is not intended to be exhaustive, but to give a general picture of the empirical correlations found in different studies with several marker-based estimators of inbreeding: $F_{VR1}$ and $F_{VR2}$: Estimators described by VanRaden [19]. $F_{YA1}$ and $F_{YA2}$: Estimator proposed by Yang et al. [36] and modified by Zhang et al. [34]. $F_{LH1}$ and $F_{LH2}$: Estimators derived from Li and Horvitz [16]. $F_{HOM}$: Average marker homozygosity. Correlations with estimates from ROH are included for completeness. Averages are shown at the start of each cell in bold face.

REFERENCES: [1]Saura et al. ([14]; Guadyerbas pig strain). [2]Yoshida et al. ([51], pure lines of farmed coho salmon). [3]Alemu et al. ([42]; Dutch Holstein cattle). [4]Bérénos et al. ([49]; Soay sheep). [5]Pryce et al. ([13]; Holstein and Jersey dairy cattle). [6]Rodríguez-Ramilo et al. ([52]; Rabbits). [7]Saura et al. ([66]; Iberian pigs). [8]Zhang et al. ([39], Holstein, Jersey and Danish Red Cattle breeds, sequence data). [9]Morales-González et al. ([43]; Turbot). [10]Solé et al. ([50]; Belgian Blue cattle). [11]Brito et al. ([41]; Goat breeds). [12]Polak et al. ([57]; Polish cold-blooded horses). [13]Villanueva et al. ([12]; Guadyerbas pig strain). [14]Nosrati et al. ([58]; Average for 68 sheep populations). [15]Antonios et al. ([53]; Dairy Sheep). [16]Shi et al. ([54]; Pigs). [17]Schiavo et al. ([55]; seven Pig breeds). [18]Adams et al ([56]; three Turkey lines).