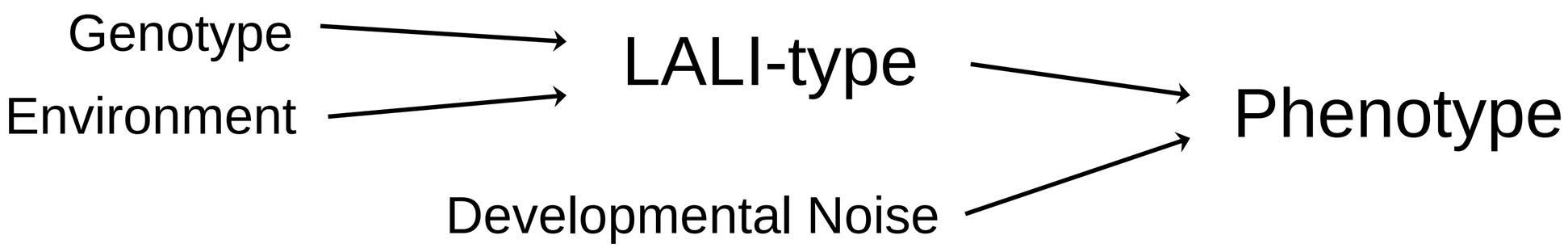
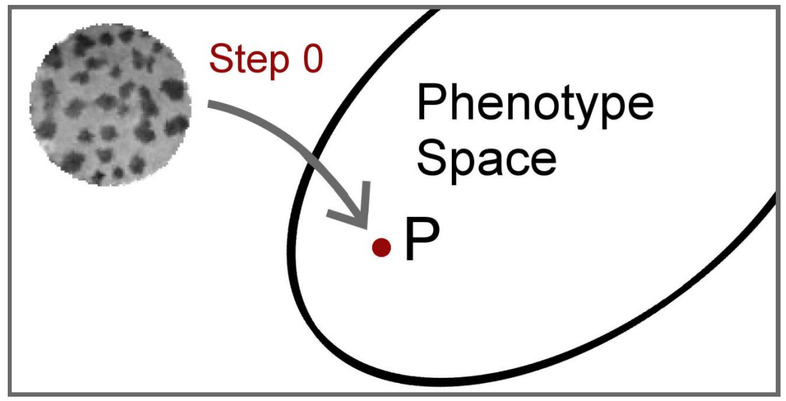
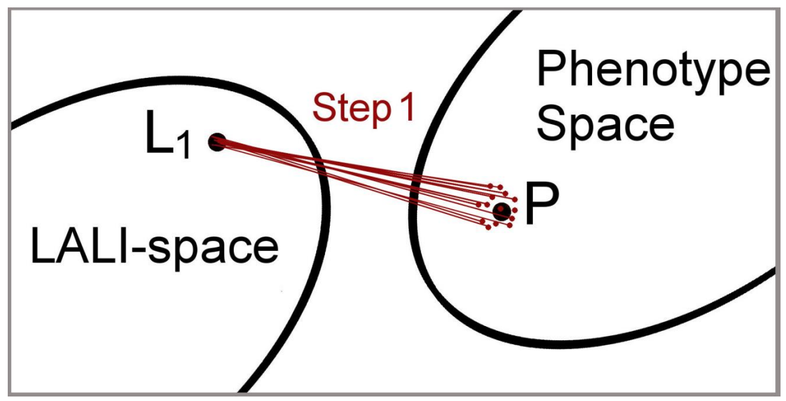
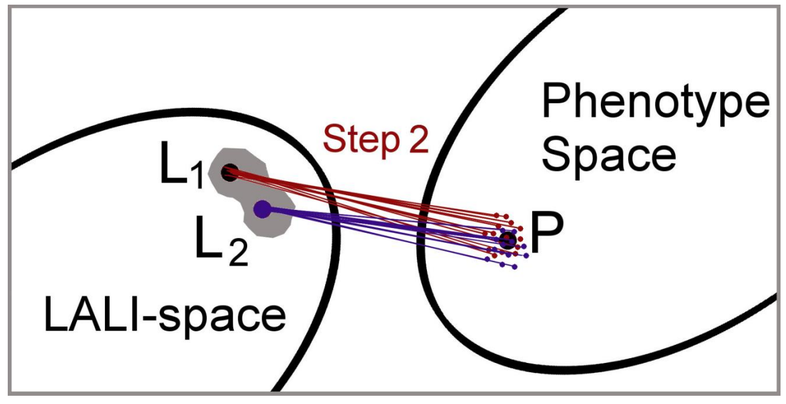
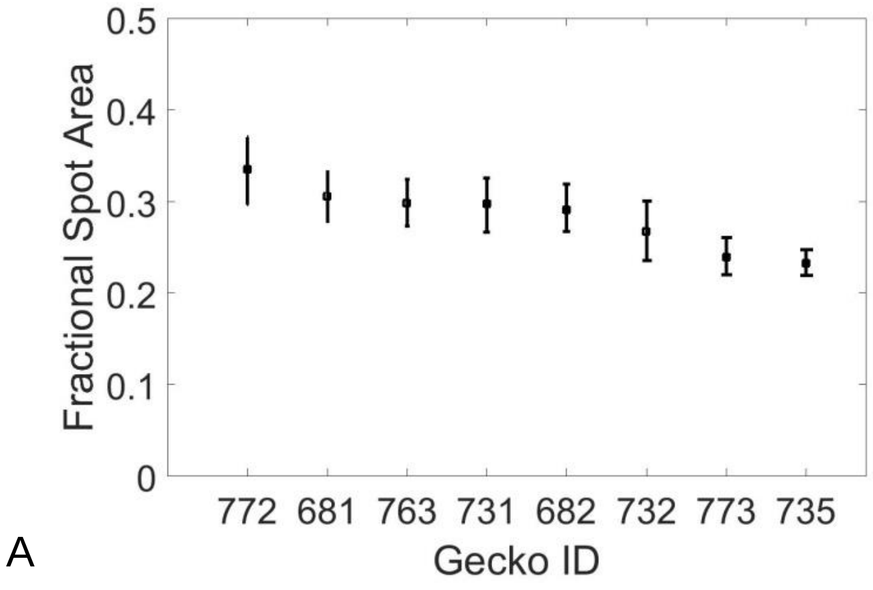
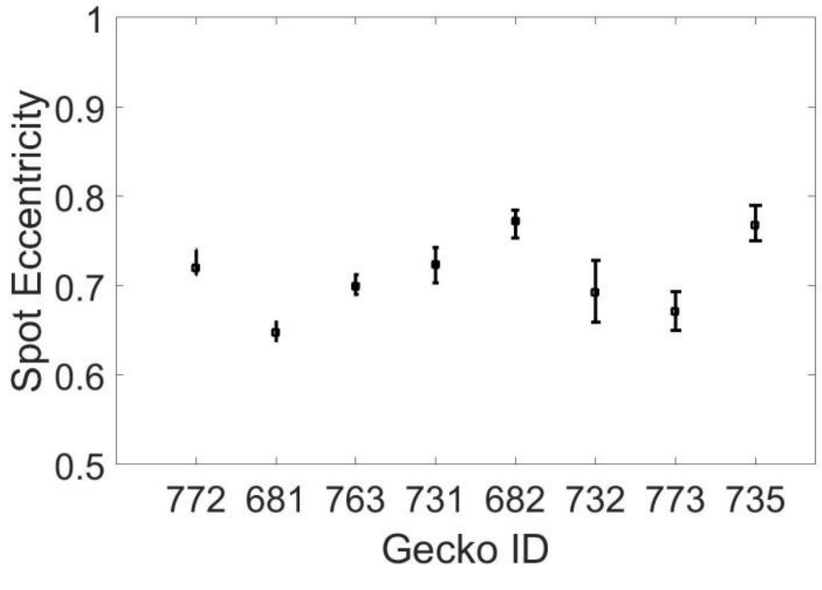

Genotype
Environment
LALI-type
Phenotype
Developmental Noise

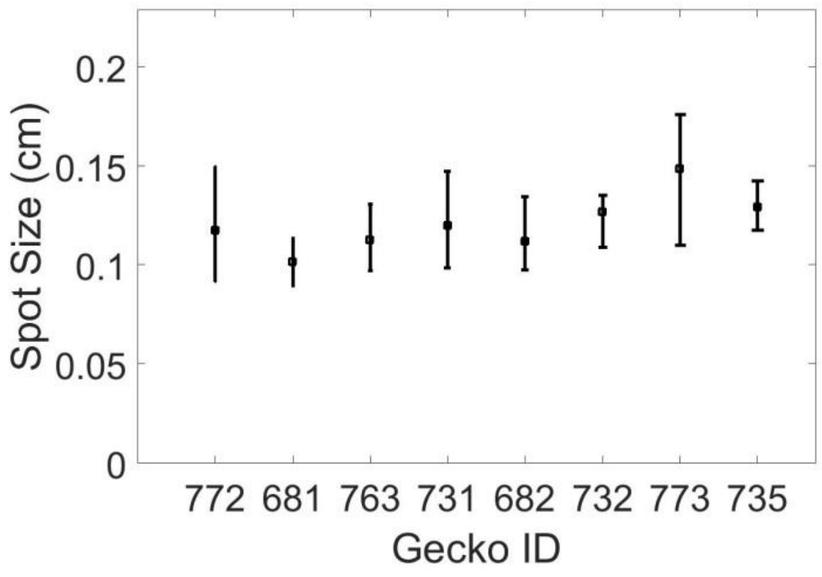
Step 0	**Identifying the location of gecko phenotypes in phenotype space** *We measure the fractional area and eccentricity of each gecko pattern to find its location in [FA,EE] phenotype space.*	
Step 1	**Generating the phenotype cloud of a single LALI-type L** *Through numerical simulations with fixed LALI-type L_1 (same genotype and environment for each LALI-type), but varied random initial conditions. In this way, we obtained the set of phenotypes generated by a single LALI-type due to developmental noise (red lines), thus determining the 'phenotype cloud' of L_1 (red points).*	
Step 2	**Generating the *r* % neutral region of a phenotype P** *We systematically search a larger region of LALI-space to find all the LALI-types L (variation in genotype and environmental conditions, e.g. L_1 and L_2) likely to yield phenotype P. The set of LALI-types containing the phenotype P in their r% phenotype cloud is the "r% neutral region of P" (sketched in gray, with two example LALI-types L_1 and L_2).*	


Fractional Spot Area
0.5
0.4
0.3
0.2
0.1
0
772 681 763 731 682 732 773 735
Gecko ID

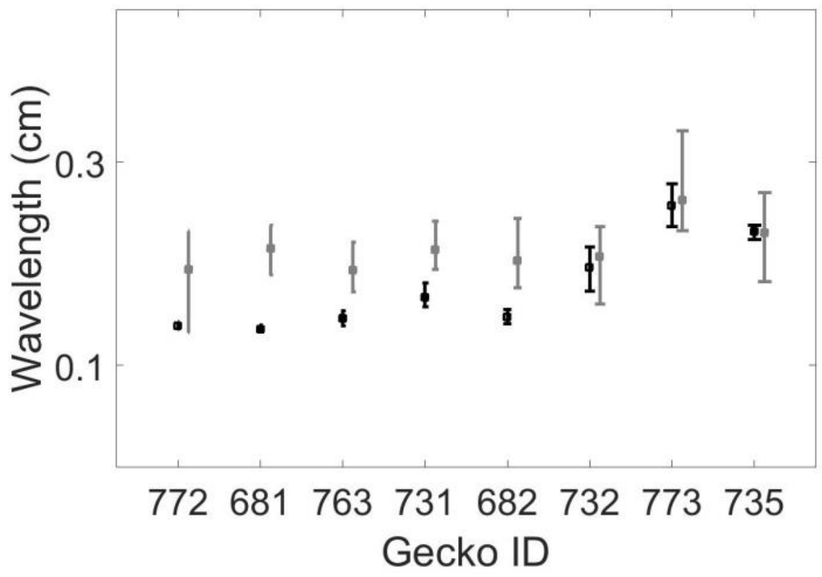
A


Spot Eccentricity
1
0.9
0.8
0.7
0.6
0.5
772 681 763 731 682 732 773 735
Gecko ID

B

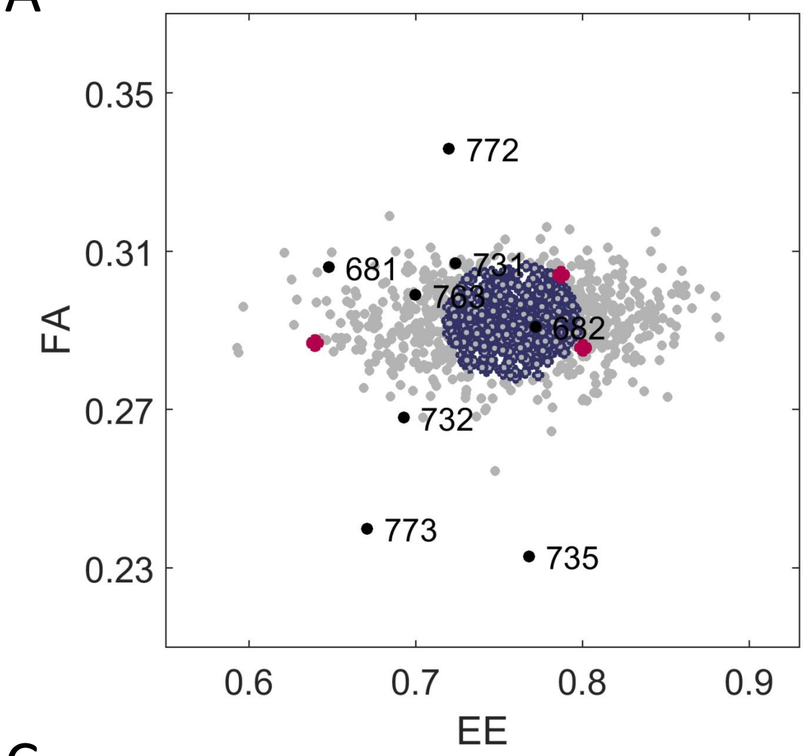

Spot Size (cm)
0.2
0.15
0.1
0.05
0
772 681 763 731 682 732 773 735
Gecko ID

C

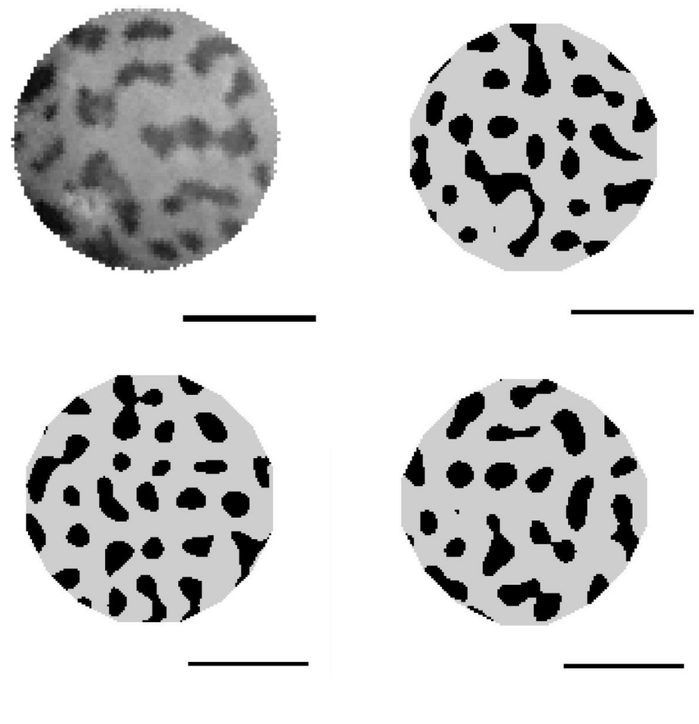

Wavelength (cm)
0.3
0.1
772 681 763 731 682 732 773 735
Gecko ID

D

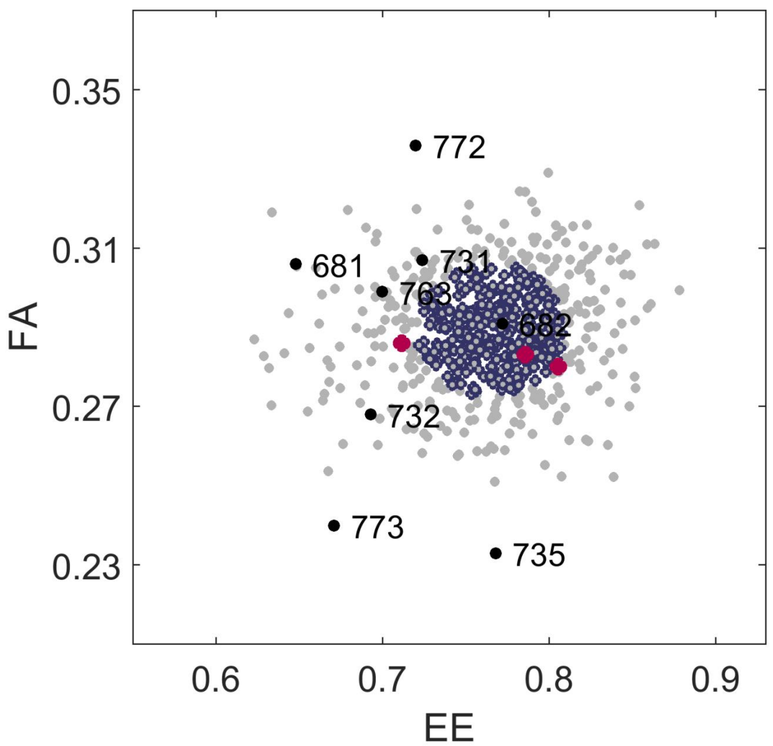
A


0.35
0.31
0.27
0.23
FA
772
681
731
763
682
732
773
735
0.6
0.7
0.8
0.9
EE

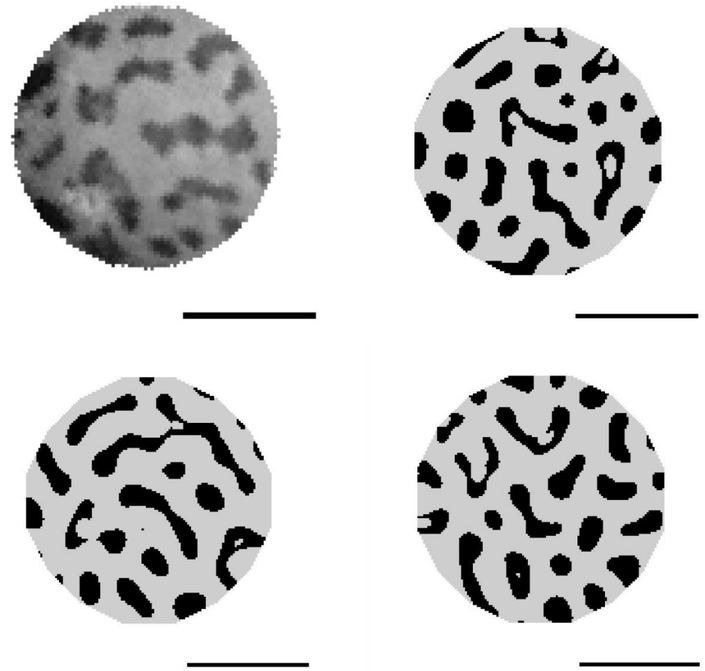
B

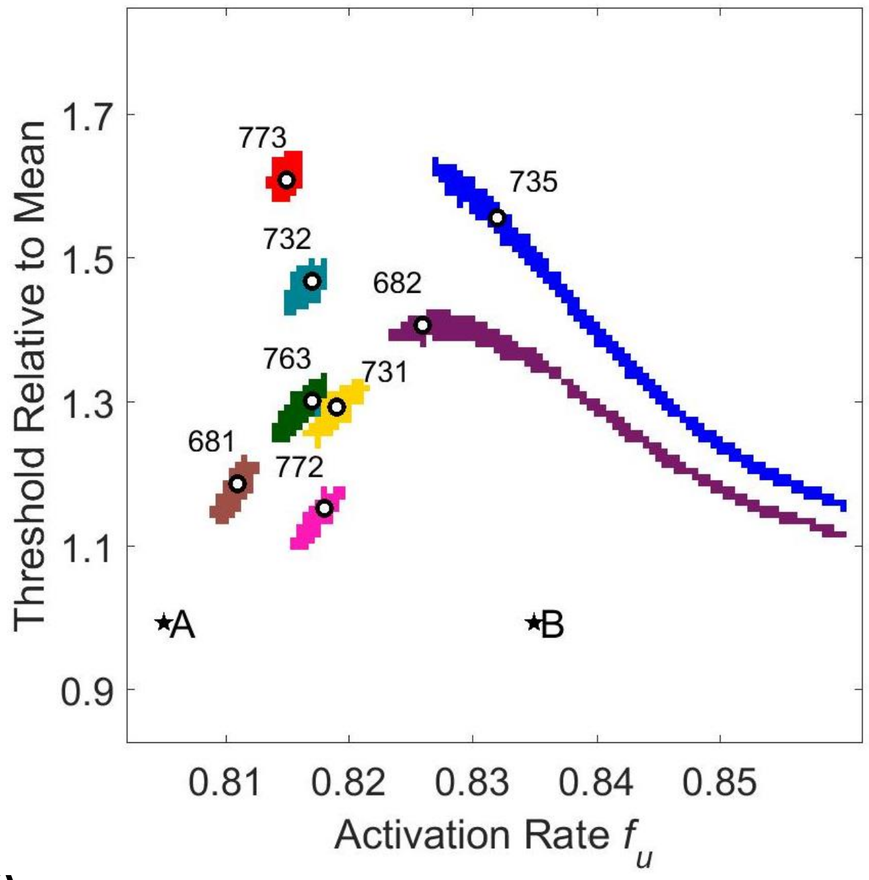


C

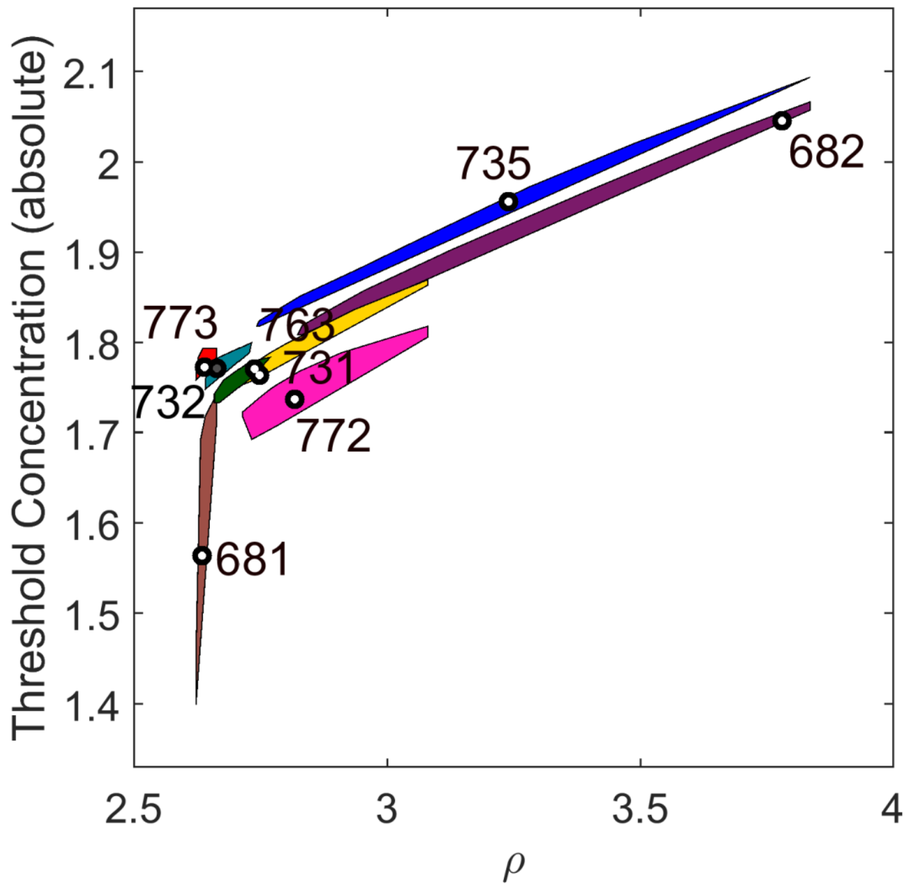

0.35
0.31
0.27
0.23
FA
772
681
731
763
682
732
773
735
0.6
0.7
0.8
0.9
EE

D

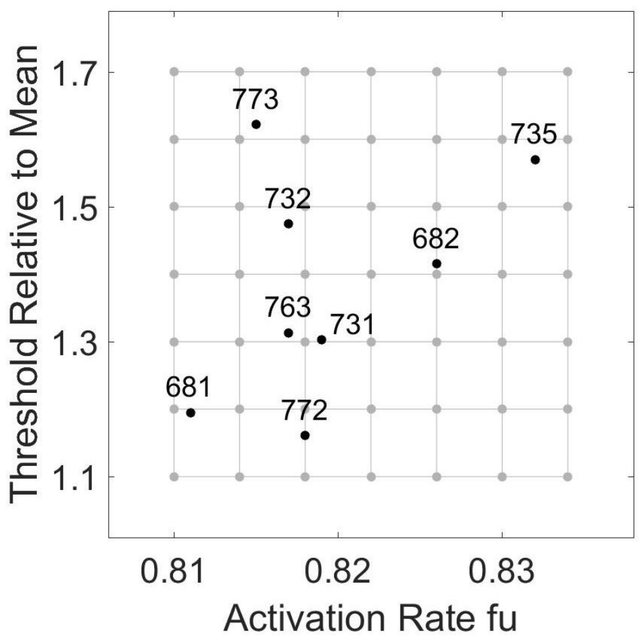



1.7
1.5
1.3
1.1
0.9
Threshold Relative to Mean
773
735
732
682
763
731
681
772
A
B
0.81
0.82
0.83
0.84
0.85
Activation Rate f_u

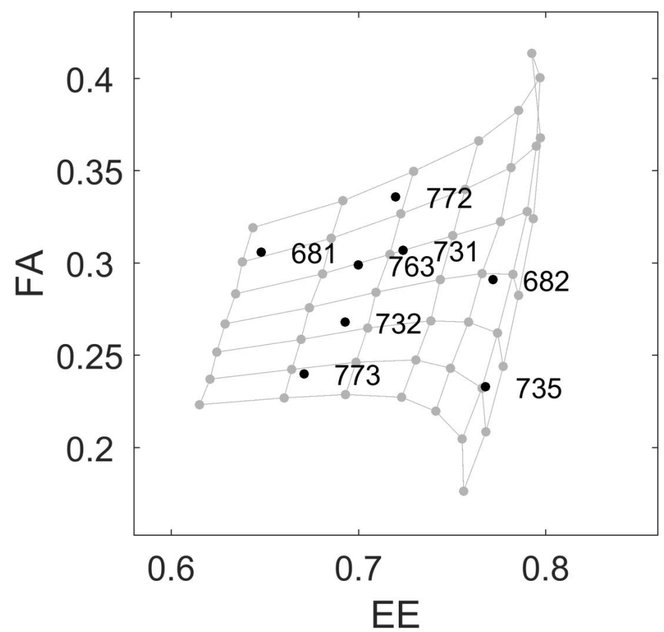
A


2.1
2
1.9
1.8
1.7
1.6
1.5
1.4
Threshold Concentration (absolute)
735
682
773
763
731
732
772
681
2.5
3
3.5
4
ρ

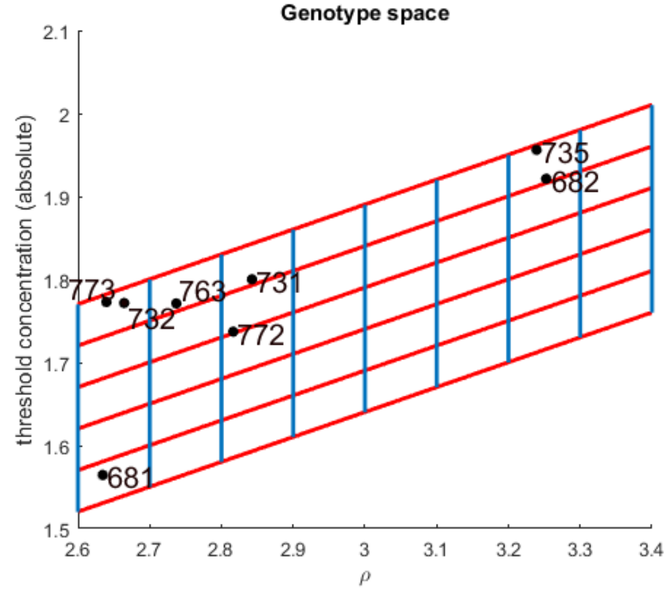
B


Threshold Relative to Mean
1.7
1.5
1.3
1.1
773
735
732
682
763
731
681
772
0.81
0.82
0.83
Activation Rate fu

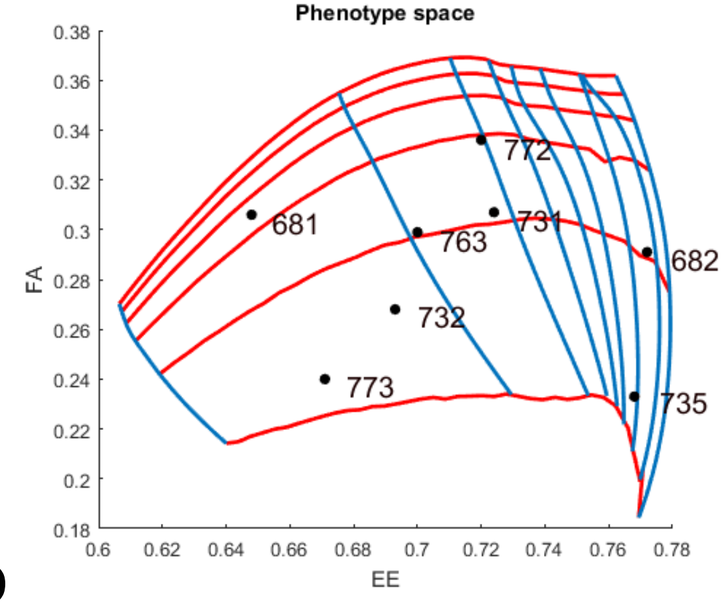
A


FA
0.4
0.35
0.3
0.25
0.2
772
681
731
763
682
732
773
735
0.6
0.7
0.8
EE

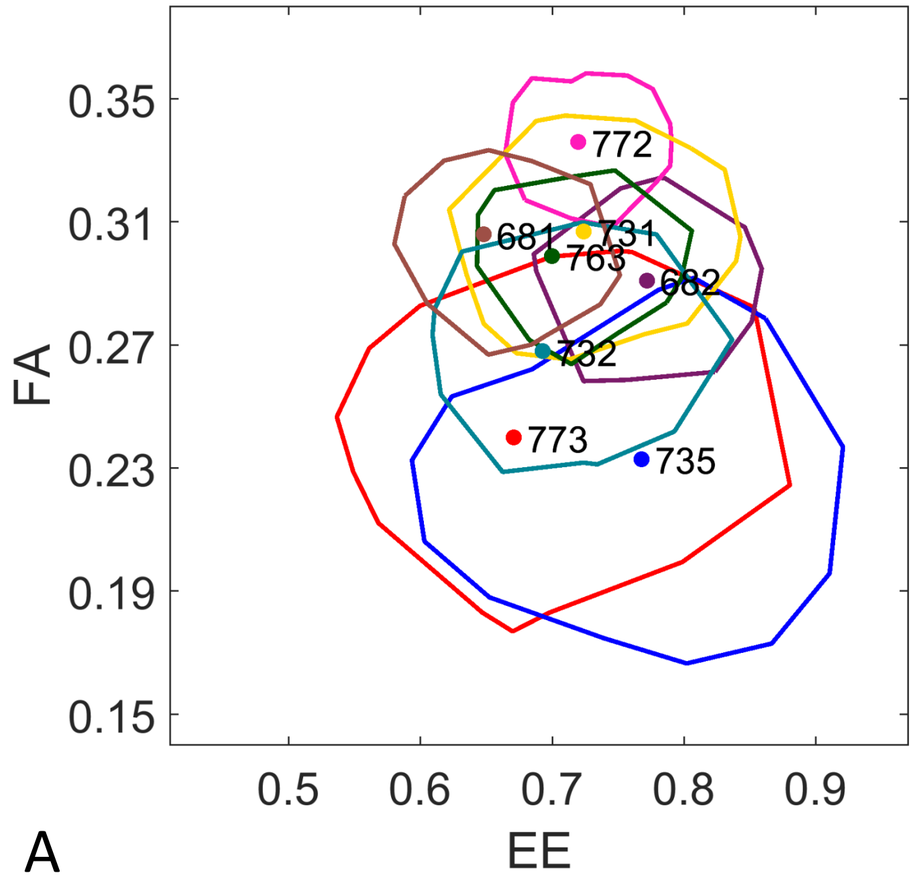
B


Genotype space
threshold concentration (absolute)
2.1
2
1.9
1.8
1.7
1.6
1.5
735
682
773
763
731
732
772
681
2.6
2.7
2.8
2.9
3
3.1
3.2
3.3
3.4
ρ

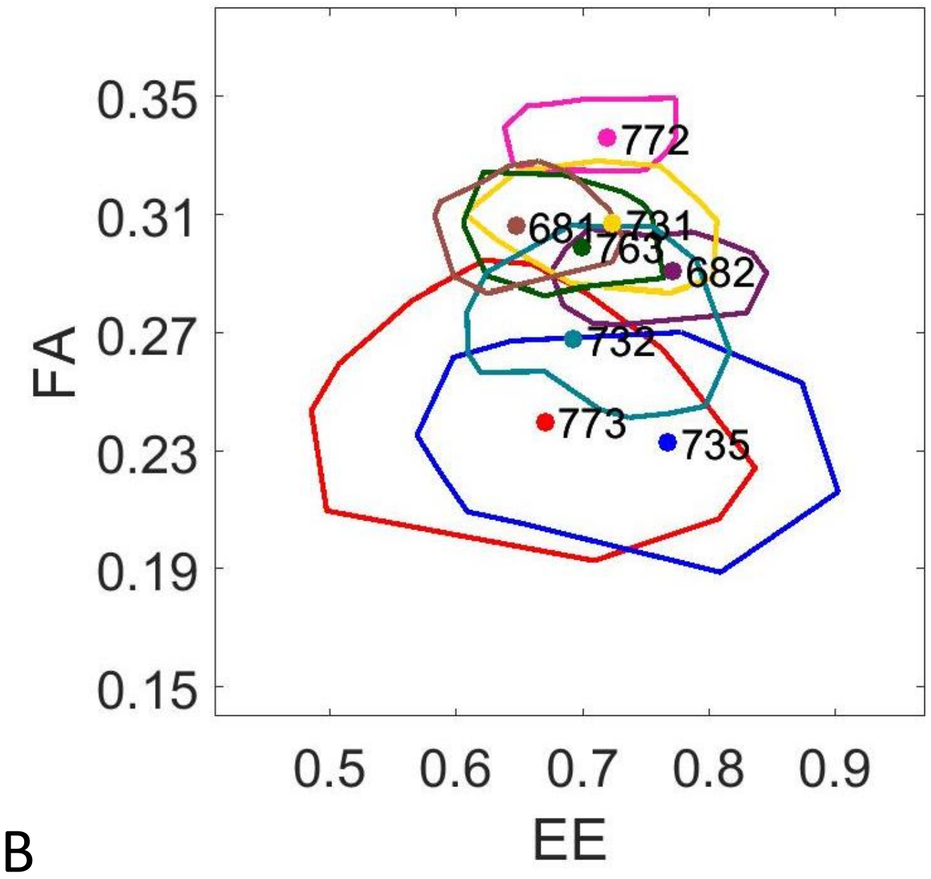
C


Phenotype space
FA
0.38
0.36
0.34
0.32
0.3
0.28
0.26
0.24
0.22
0.2
0.18
772
681
731
763
682
732
773
735
0.6
0.62
0.64
0.66
0.68
0.7
0.72
0.74
0.76
0.78
EE

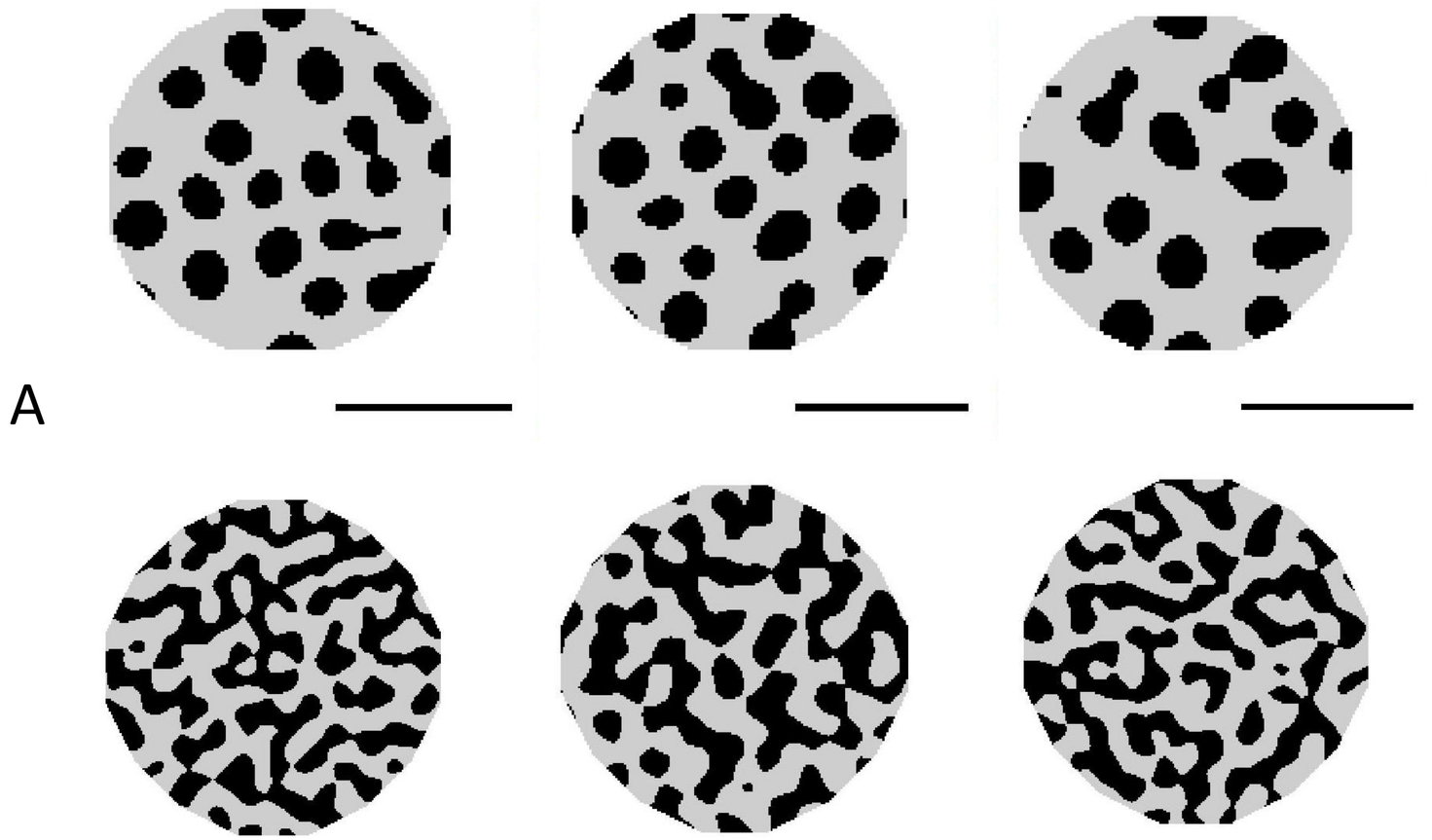
D


0.35
0.31
0.27
0.23
0.19
0.15
FA
772
681
731
763
682
732
773
735
0.5
0.6
0.7
0.8
0.9
EE

A


0.35
0.31
0.27
0.23
0.19
0.15
FA
772
681
731
763
682
732
773
735
0.5
0.6
0.7
0.8
0.9
EE

B


A
B