

Figure 1

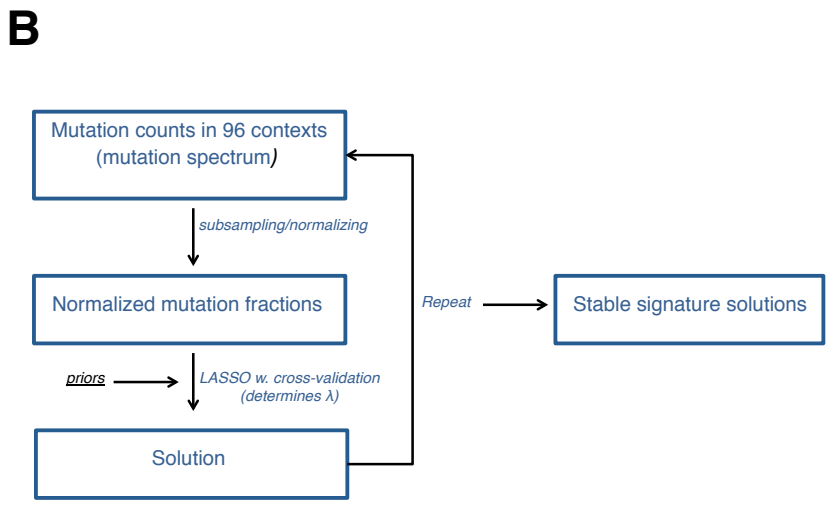
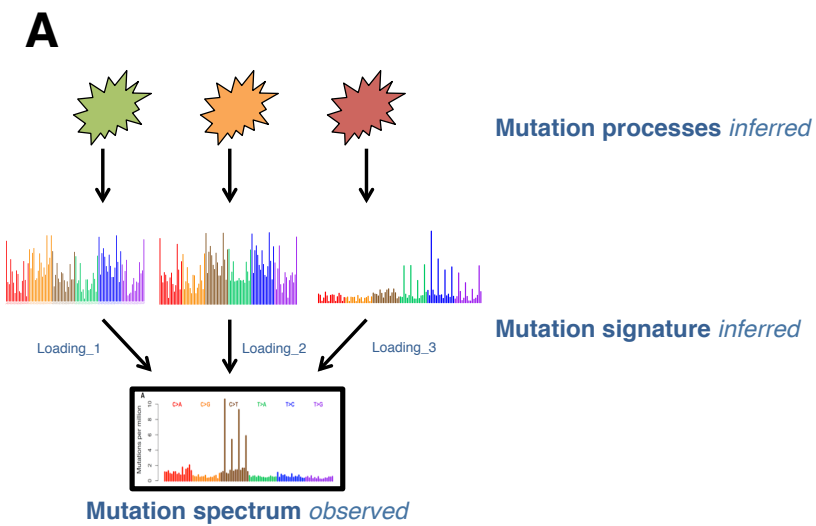
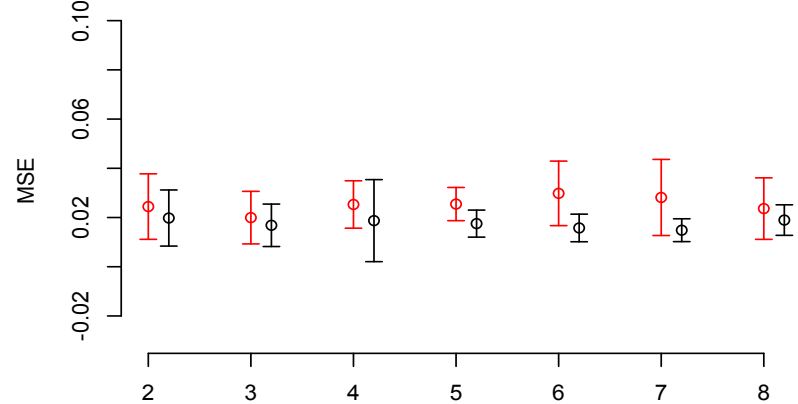
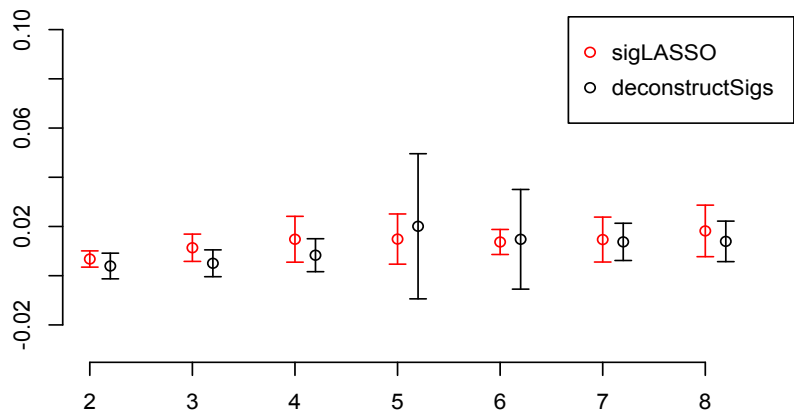
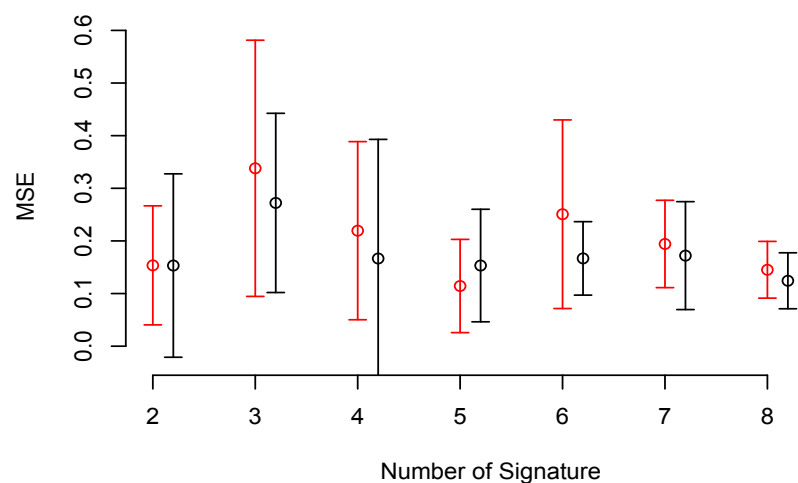
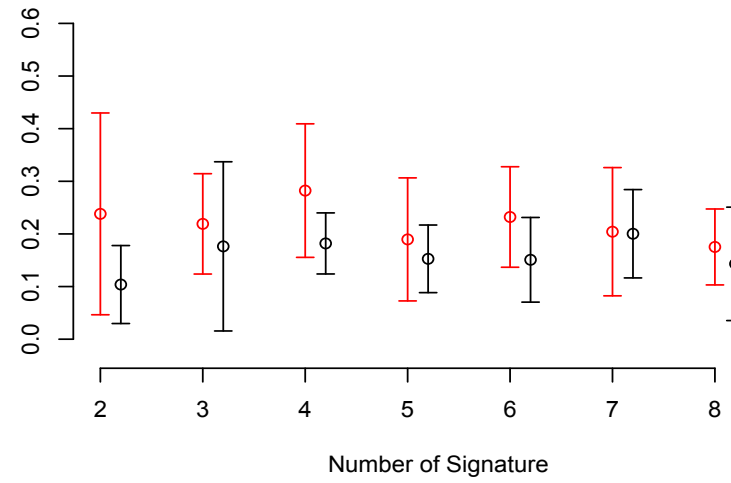


Figure 2

High mutations (WGS)



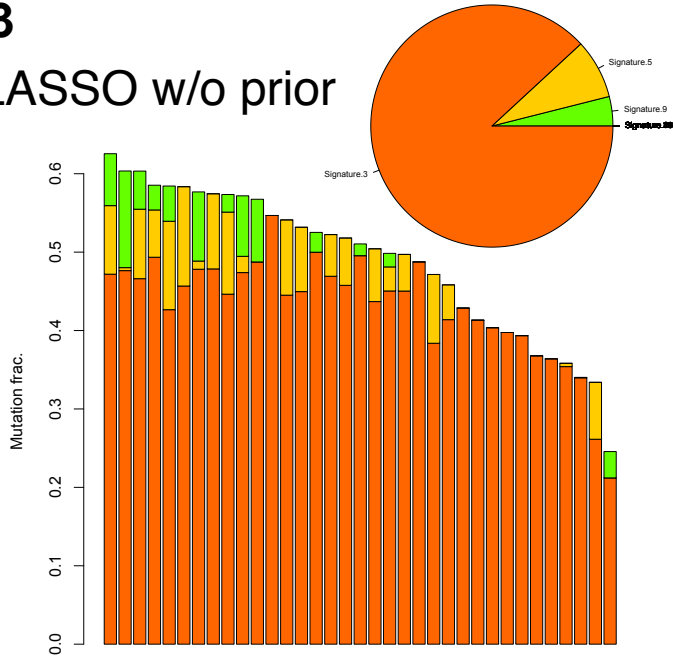
Low mutations (WXS)



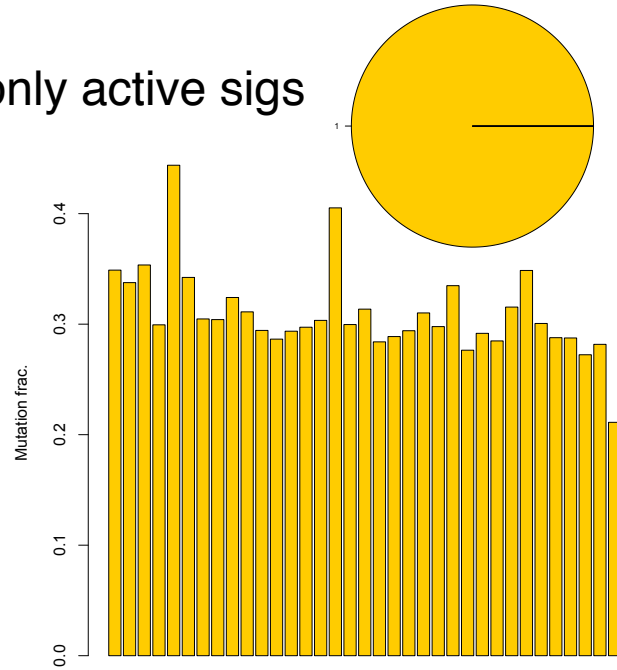
10 random simulations for each signature number, 5000/50 mutations, 0.1/0.2 noise respectively. Error bars indicate ne SD

Figure 3

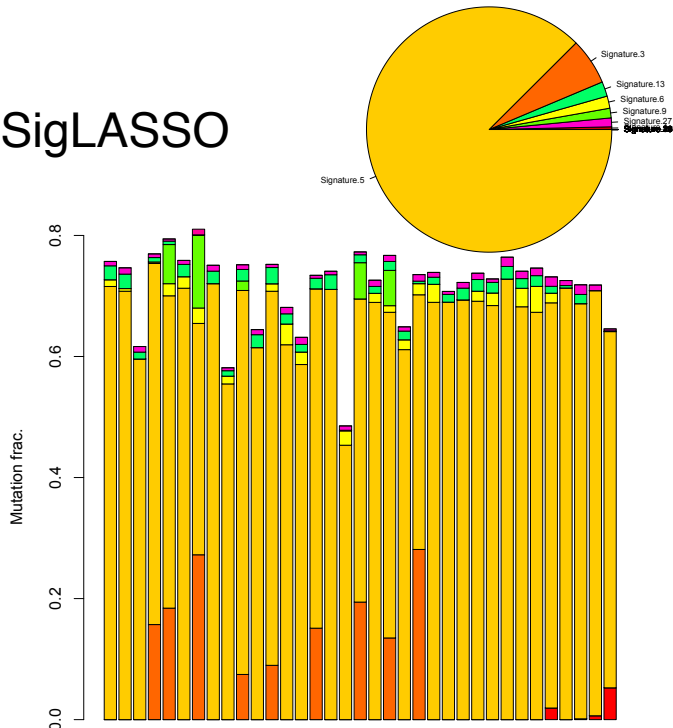
SigLASSO w/o prior



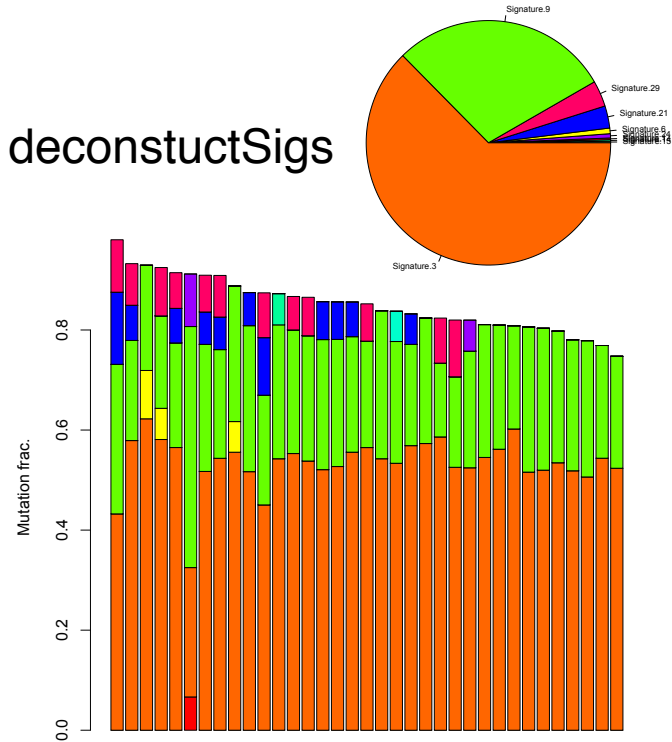
only active sigs



SigLASSO

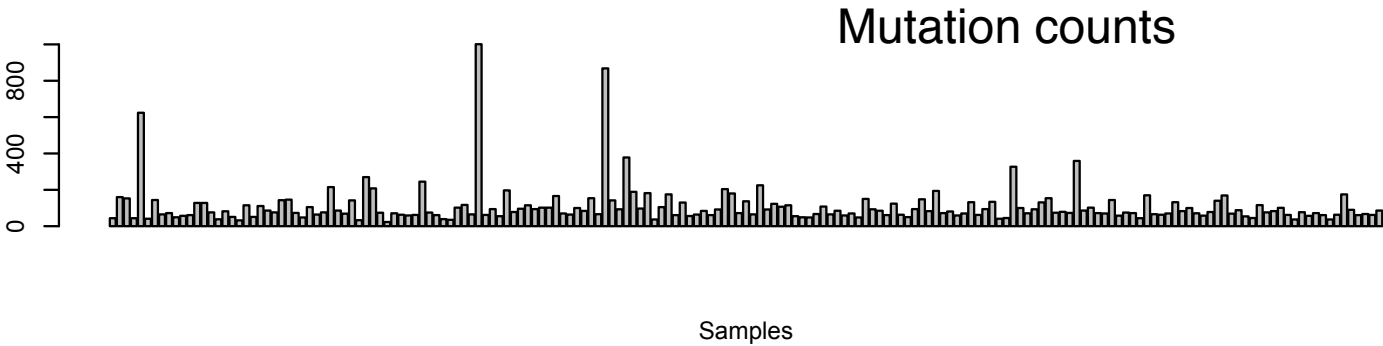
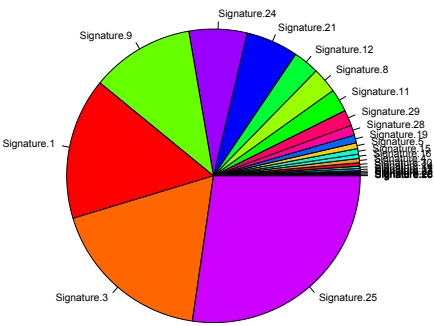
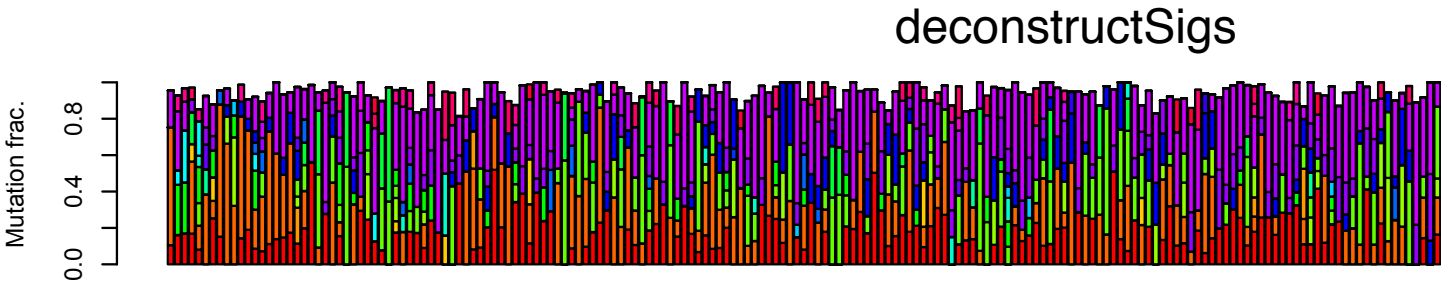
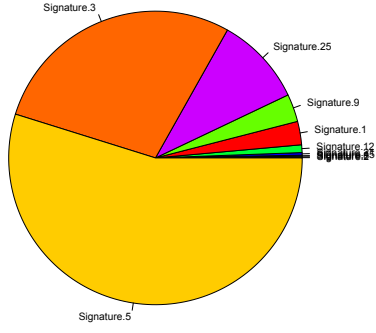
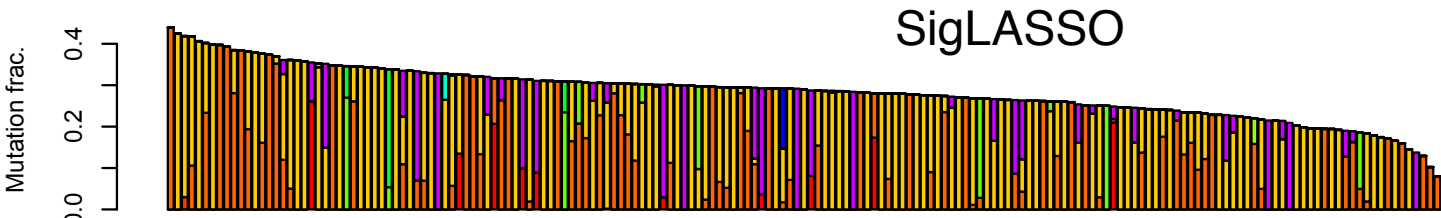


deconstuctSigs



35 WGS pRCC samples

Figure 4A



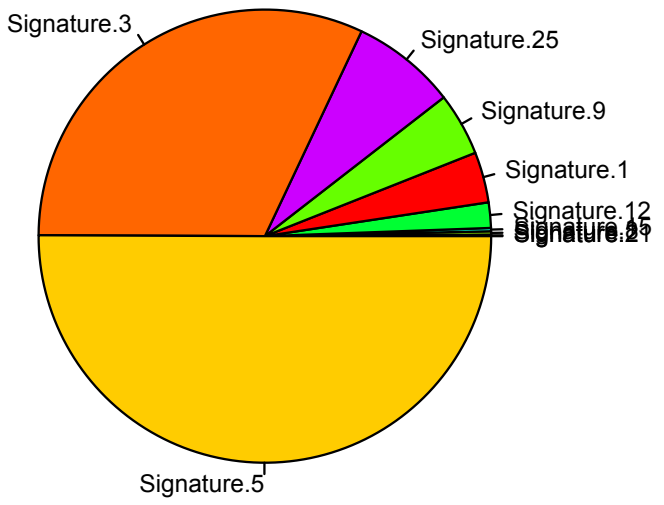
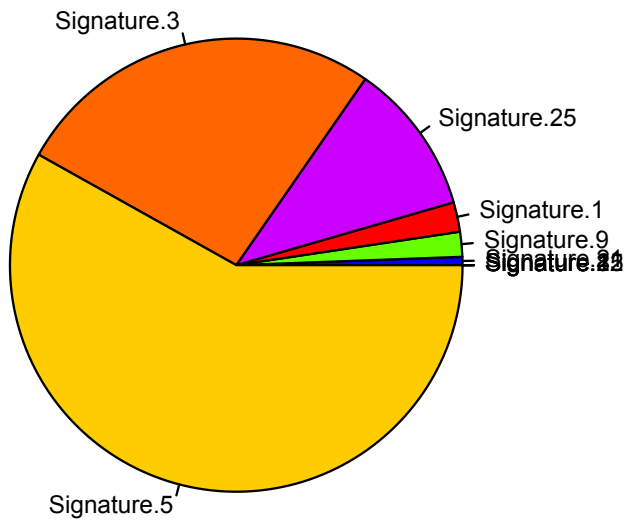
181 WXS ESCA samples...(mutation counts >20)

Figure 4B

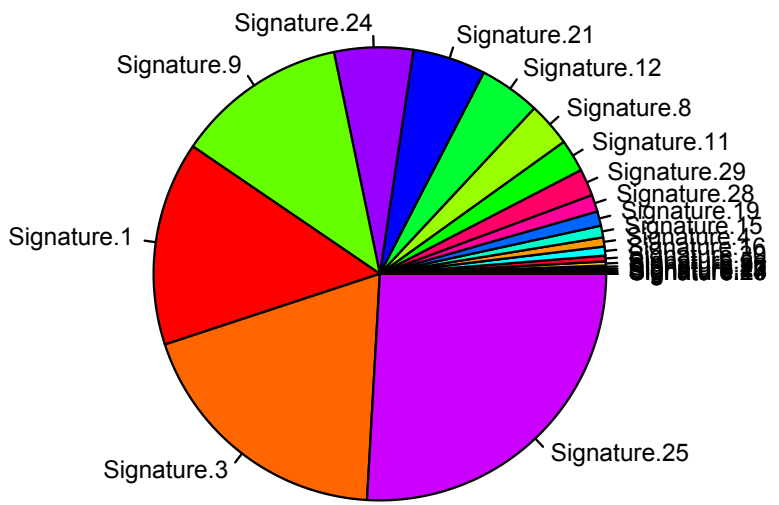
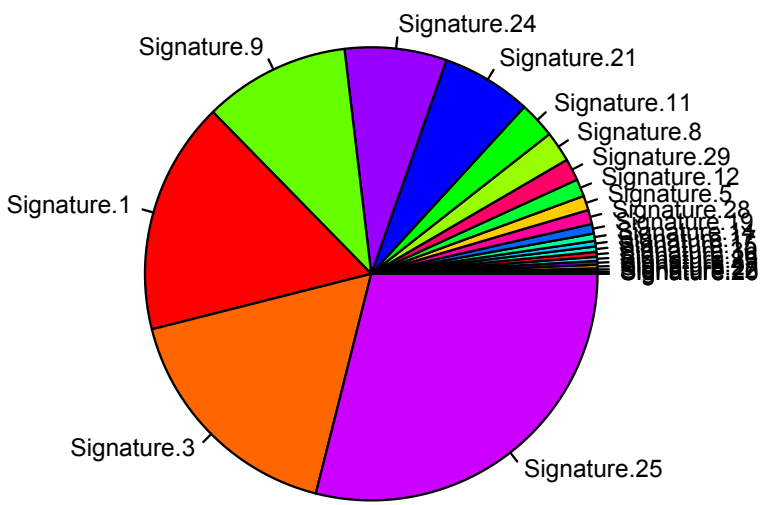
Adeno

Squamous

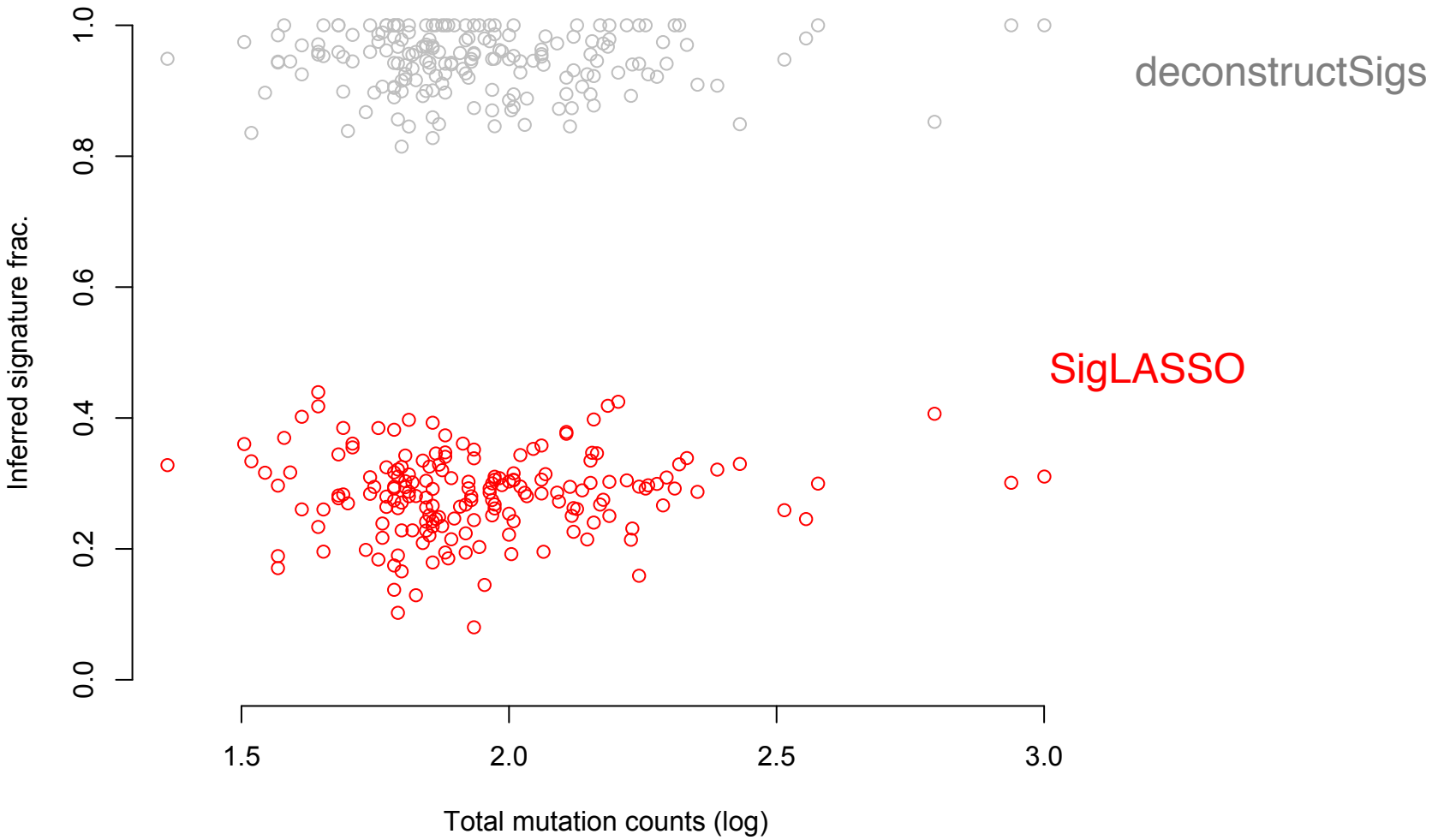
SigLASSO



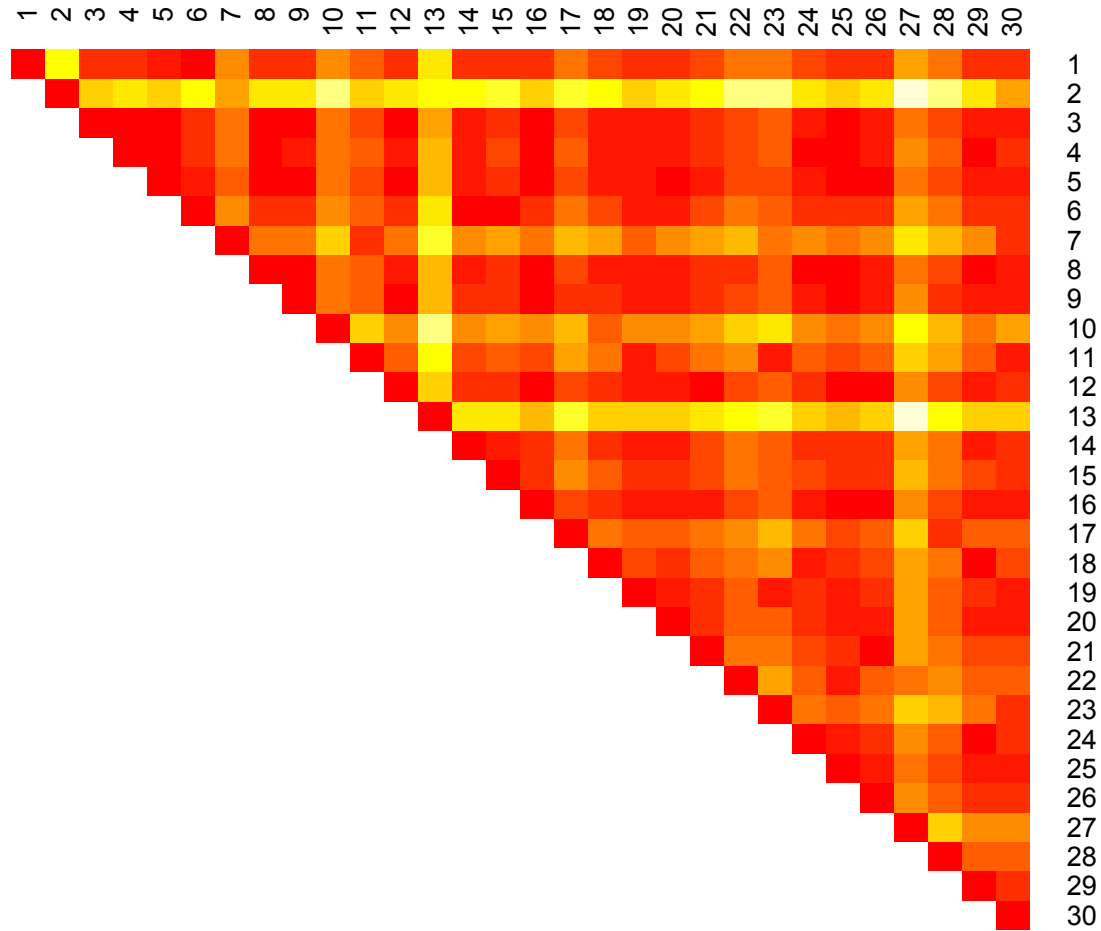
deconstructSigs



Supplement 1



SigLASSO is more conservative and sensitive to total mutation counts (cor: 0.07 versus 0.01 in deconstructSigs)



Euclidean distances between signature