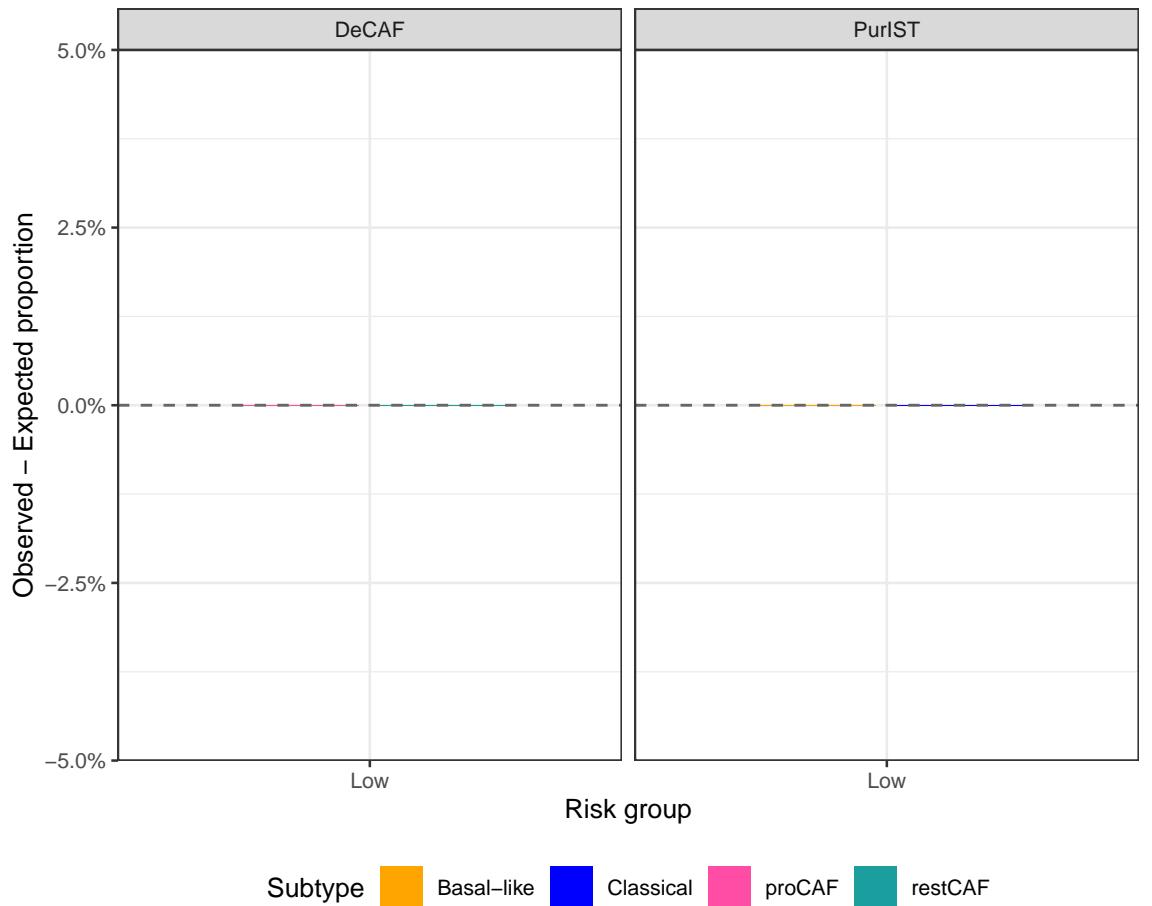
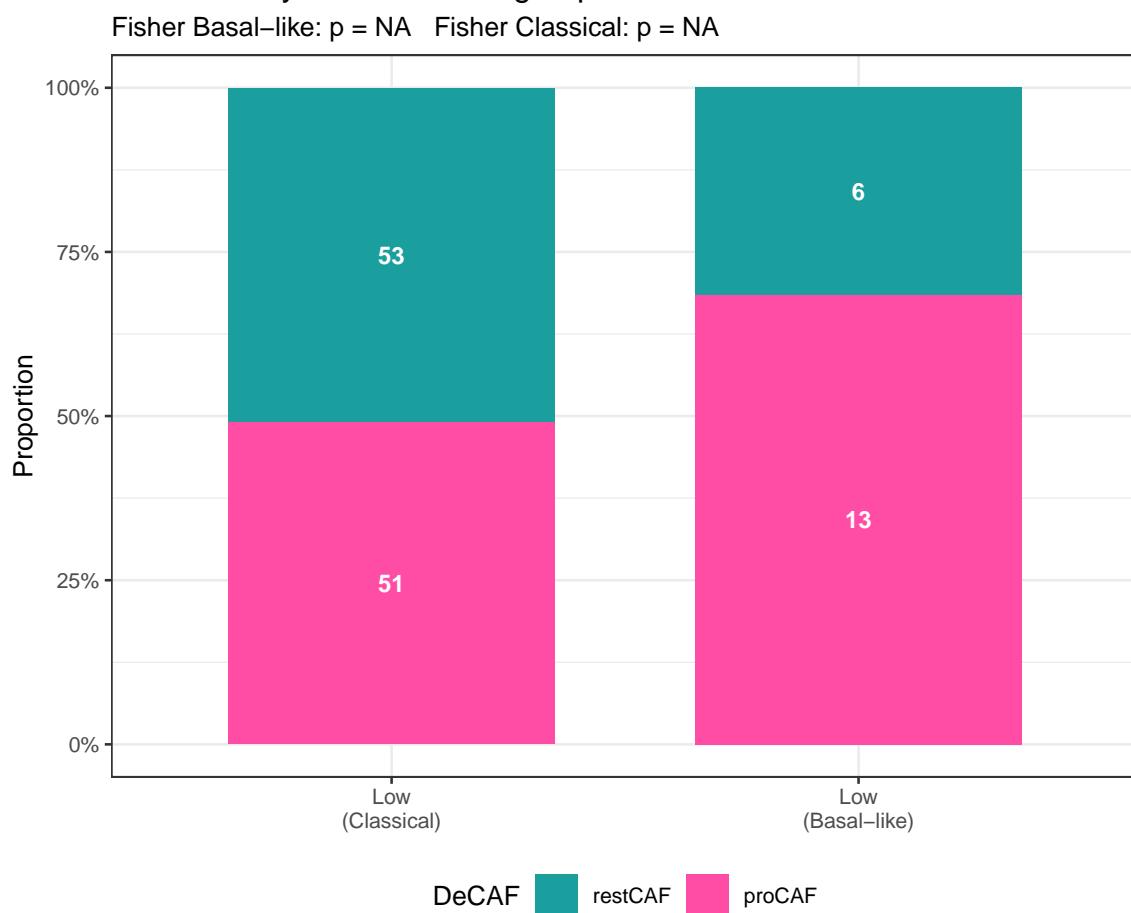


Moffitt_GEO_array Factor 1 (logrank cutpoint)

A. Enrichment relative to marginal



B. DeCAF by PurlST x Risk group



C. Sample counts

	High	Low
Classical / restCAF	0	53
Classical / proCAF	0	51
Basal-like / restCAF	0	6
Basal-like / proCAF	0	13

The table shows sample counts for different gene expression patterns across High and Low risk groups. The counts are: Classical / restCAF (53), Classical / proCAF (51), Basal-like / restCAF (6), and Basal-like / proCAF (13).