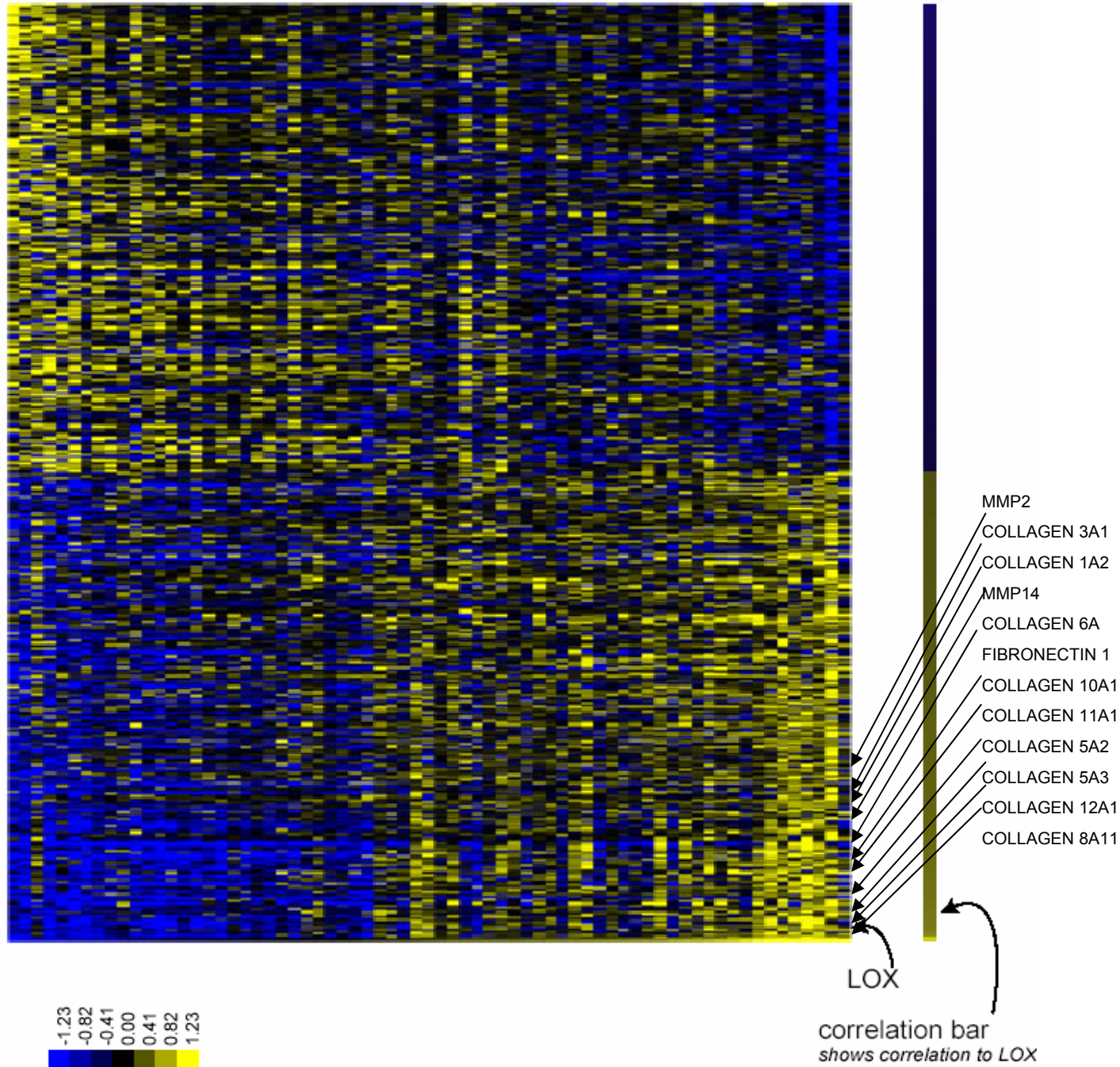


NKI ER NEGATIVE TUMORS ONLY

SAMPLE.28
 SAMPLE.29
 SAMPLE.308
 SAMPLE.378
 SAMPLE.374
 SAMPLE.144
 SAMPLE.310
 SAMPLE.109
 SAMPLE.350
 SAMPLE.270
 SAMPLE.149
 SAMPLE.8
 SAMPLE.396
 SAMPLE.135
 SAMPLE.130
 SAMPLE.226
 SAMPLE.222
 SAMPLE.268
 SAMPLE.186
 SAMPLE.269
 SAMPLE.181
 SAMPLE.103
 SAMPLE.402
 SAMPLE.333
 SAMPLE.307
 SAMPLE.265
 SAMPLE.141
 SAMPLE.177
 SAMPLE.321
 SAMPLE.274
 SAMPLE.312
 SAMPLE.312
 SAMPLE.330
 SAMPLE.76
 SAMPLE.7
 SAMPLE.195
 SAMPLE.158
 SAMPLE.236
 SAMPLE.335
 SAMPLE.237
 SAMPLE.246
 SAMPLE.257
 SAMPLE.217
 SAMPLE.202
 SAMPLE.147
 SAMPLE.341
 SAMPLE.277
 SAMPLE.276
 SAMPLE.175
 SAMPLE.136
 SAMPLE.98
 SAMPLE.126
 SAMPLE.164
 SAMPLE.344
 SAMPLE.194
 SAMPLE.113
 SAMPLE.238
 SAMPLE.228
 SAMPLE.241
 SAMPLE.71
 SAMPLE.338
 SAMPLE.179
 SAMPLE.75
 SAMPLE.153
 SAMPLE.197
 SAMPLE.230
 SAMPLE.12
 SAMPLE.215



Supplementary Figure 3: Genes with strong correlation to LOX in human breast cancer patients bearing ER-negative tumors.

Generated employing previously published dataset10 only for patients with ER-negative tumors. Genes with standard deviation of >70% of all possible standard deviations were isolated and correlated with LOX. Only genes either in the top 95th percentile (ie most correlated) or bottom 5th percentile of all correlations to LOX were retained. Genes were then sorted by their correlation to LOX to generate a pcl file displayed here as a heatmap where blue indicates most anticorrelated and yellow indicates most strongly correlated. Genes were not mean centered. Genes of interest from the top 50 most correlated genes are highlighted with arrows. Full list available online (Excel Book2).