## Survival prediction with mRMR genes on TCGA-KIRC PCA with mRMR genes on TCGA-KIRC test samples a (66% train / 33% test / auc\_uno: 0.79) Groups High Moderate Low Strata + risk=High + risk=Moderate + risk=Low 5.0 -Survival probability 2.5 -0.0 - 0.0 - 2.5 - - 2.5 p-val: $5.08 \times 10^{-9}$ 0.00 -1000 2000 3000 4000 Time Nº at risk (nº of deceased) Alive **Deceased** -5.0 **-**27 High 32 59 (0) 28 (23) 7 (29) 1 (32) 0 (32) Strata Moderate 17 41 58 (0) 29 (10) 11 (15) 6 (16) 0 (17) Low 58 59 (0) 40 (1) 18 (1) 4 (1) 1 (1) -7.5 **-**2000 4000 1000 3000 Time Dim1 (15.3%) Survival prediction with mRMR genes PCA with mRMR genes on ICGC-RECA C (train TCGA-KIRC / test ICGC-RECA / auc uno: 0.66) Groups High Moderate Low Strata → risk=High → risk=Moderate → risk=Low Survival probability Dim2 (6.9%) p-val: 0.00958 0.00 -500 1000 1500 2000 Time Nº at risk (nº of deceased) Alive **Deceased** -3 **-**High 14 16 21 (8) 15 (13) 5 (16) 30 (0) 24 (6) Moderate 22 8 30 (0) 27 (2) 25 (3) 22 (5) 7 (8) Low 25 6 31 (0) 29 (1) 25 (4) 23 (5) 9 (6) 500 1000 1500 2000 Dim1 (14.5%) Time