

Intermodel Comparisons

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Models

```
##
## Call:
## glm(formula = prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 +
##      CCL28 + CD86 + C5 + DCK + age_c + gender + stage + trans_class_bin,
##      family = binomial(link = logit), data = melanoma, weights = tile_count)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -20.965  -2.737   1.597   4.357  13.876
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.8139387  0.0277942  29.285 < 2e-16 ***
## KLRD1          -0.2020518  0.0107349 -18.822 < 2e-16 ***
## RFX5           -0.0930217  0.0087148 -10.674 < 2e-16 ***
## DDX58           0.1175686  0.0107460  10.941 < 2e-16 ***
## EIF2AK2        -0.0846684  0.0091883  -9.215 < 2e-16 ***
## CCL28          -0.0939413  0.0076328 -12.308 < 2e-16 ***
## CD86            0.1155478  0.0121146   9.538 < 2e-16 ***
## C5             -0.0285333  0.0077891  -3.663 0.000249 ***
## DCK            -0.1072896  0.0083370 -12.869 < 2e-16 ***
## age_c          -0.0013434  0.0004914  -2.733 0.006267 **
## gendermale     -0.1239559  0.0154758  -8.010 1.15e-15 ***
## stage           0.0512536  0.0097432   5.260 1.44e-07 ***
## trans_class_bin -0.2667031  0.0185781 -14.356 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10648.2  on 239  degrees of freedom
## Residual deviance:  8308.8  on 227  degrees of freedom
## AIC: 9688.6
##
## Number of Fisher Scoring iterations: 4
##
## Call:
## glm(formula = prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 +
##      CCL28 + CD86 + C5 + DCK + IL17RB + TLR4 + CCL28 + IL17C +
```

```
##      age_c + gender + stage + trans_class_bin, family = binomial(link = logit),
##      data = melanoma, weights = tile_count)
##
## Deviance Residuals:
##      Min        1Q      Median        3Q        Max
## -22.621   -2.365    1.405    4.173   13.984
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.8448045  0.0282245  29.932 < 2e-16 ***
## KLRD1         -0.1246878  0.0121209 -10.287 < 2e-16 ***
## RFX5          -0.1050638  0.0091662 -11.462 < 2e-16 ***
## DDX58         0.1116777  0.0107894  10.351 < 2e-16 ***
## EIF2AK2      -0.0487247  0.0093523  -5.210 1.89e-07 ***
## CCL28        -0.0961490  0.0077877 -12.346 < 2e-16 ***
## CD86         0.0999596  0.0149022   6.708 1.98e-11 ***
## C5           -0.0187436  0.0078313  -2.393  0.0167 *
## DCK          -0.1297524  0.0088088 -14.730 < 2e-16 ***
## IL17RB       -0.0709636  0.0067864 -10.457 < 2e-16 ***
## TLR4         -0.1196973  0.0089653 -13.351 < 2e-16 ***
## IL17C        0.0831964  0.0082053  10.139 < 2e-16 ***
## age_c        -0.0005047  0.0005010  -1.007  0.3138
## gendermale   -0.1390903  0.0155396  -8.951 < 2e-16 ***
## stage        0.0415409  0.0100592   4.130 3.63e-05 ***
## trans_class_bin -0.2549694  0.0188277 -13.542 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 10648.2  on 239  degrees of freedom
## Residual deviance:  7822.3  on 224  degrees of freedom
## AIC: 9208.2
##
## Number of Fisher Scoring iterations: 4
```

LRTs

```
## Likelihood ratio test
##
## Model 1: prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 + CCL28 + CD86 +
##      C5 + DCK + IL17RB + TLR4 + CCL28 + IL17C + age_c + gender +
##      stage + trans_class_bin
## Model 2: prop_infiltrated ~ KLRD1 + RFX5 + DDX58 + EIF2AK2 + CCL28 + CD86 +
##      C5 + DCK + age_c + gender + stage + trans_class_bin
##      #Df LogLik Df  Chisq Pr(>Chisq)
## 1   16 -4588.1
## 2   13 -4831.3 -3  486.48 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Deviances

```
## [1] 8308.781
```

```
## [1] 7822.299
```

Hosmer-Lemeshow

```
##  
## Hosmer and Lemeshow goodness of fit (GOF) test  
##  
## data: melanoma$prop_infiltrated, fitted(model1)  
## X-squared = 1.4817, df = 8, p-value = 0.993
```

```
##  
## The Hosmer-Lemeshow goodness-of-fit test  
##
```

##	Group	Size	Observed	Expected
##	1	7939	3904	374.4
##	2	8372	4870	474.7
##	3	8414	5426	521.9
##	4	8270	4801	523.7
##	5	8302	5682	544.5
##	6	8504	5730	588.6
##	7	8264	5859	567.6
##	8	8362	5816	597.5
##	9	8496	6308	634.4
##	10	8726	6792	706.0

```
##  
## Statistic = 478562.2  
## degrees of freedom = 8  
## p-value = < 2.22e-16
```

```
##  
## Hosmer and Lemeshow goodness of fit (GOF) test  
##  
## data: melanoma$prop_infiltrated, fitted(model2)  
## X-squared = 1.9201, df = 8, p-value = 0.9834
```

```
##  
## The Hosmer-Lemeshow goodness-of-fit test  
##
```

##	Group	Size	Observed	Expected
##	1	8545	3923	413.6
##	2	8599	5122	509.7
##	3	8463	4908	531.7
##	4	8549	6118	566.0
##	5	8482	5691	573.7
##	6	8423	5412	579.3
##	7	8218	5641	563.1
##	8	8270	5772	586.5
##	9	8246	6229	606.0
##	10	7854	6372	579.0

```
##  
## Statistic = 482072.1
```

```
## degrees of freedom = 8
##           p-value = < 2.22e-16
```