TMM output for: v2.0_cl2_ds0.9_fcGlobalMean_mult_validation

Date: 2021-02-01 16:00:44.206

Comments on iteration:
No comment supplied

Inputs:
Iteration dir:
E:\Dropbox\TMM\resources\tmm_runs\v2.0_cl2_ds0.9_fcGlobalMean_mult_validation
Gene expression matrix: E:\Dropbox\TMM\resources\data\cl2_ds0.9\gene_expression.txt

Options:
Number of samples: 28
Fold change mode: fcGlobalMean
PSF option: mult
PSF summary file:
E:\Dropbox\TMM\resources\tmm_runs\v2.0_cl2_ds0.9_fcGlobalMean_mult_validation\psf_summ
ary.xls
Number of bootstrap cycles: 200
Label mode: Validation
TMM labels file: E:\Dropbox\TMM\resources\data\cl2_ds0.9\tmm_labels.txt

Validation results
Classification accuracy: 0.71

Median differences and p values

ALT PSF: overall p value (Kruskal-Wallis rank sum test):   0.0
ALT versus norm: Median difference: 0.692   p value   0.0
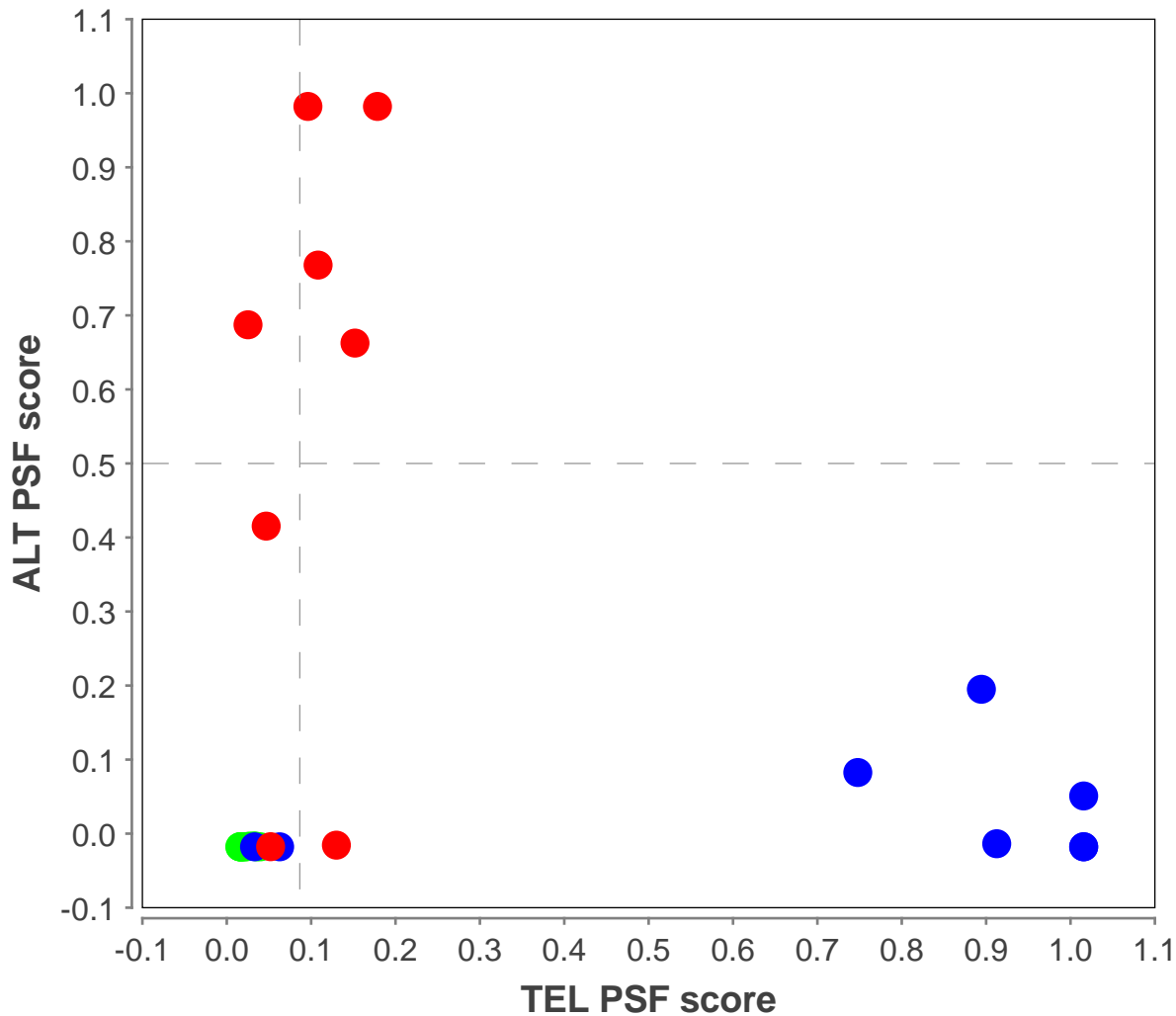ALT versus Tel-ase: Median difference: 0.678   p value   0.01

Tel-ase PSF: overall p value (Kruskal-Wallis rank sum test):   0.0
Tel-ase versus norm: Median difference: 0.878   p value   0.0
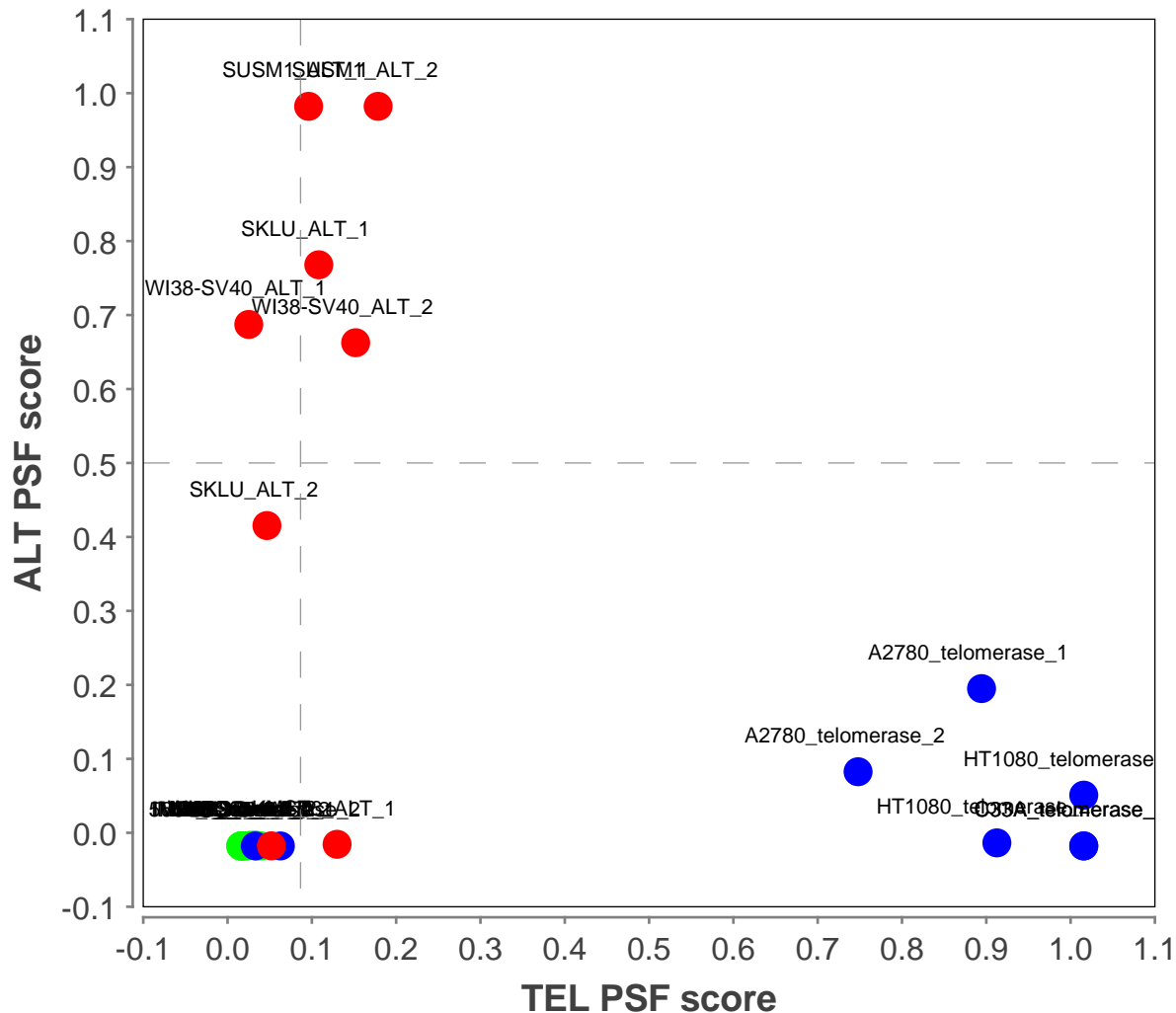Tel-ase versus ALT: Median difference: 0.801   p value   0.037
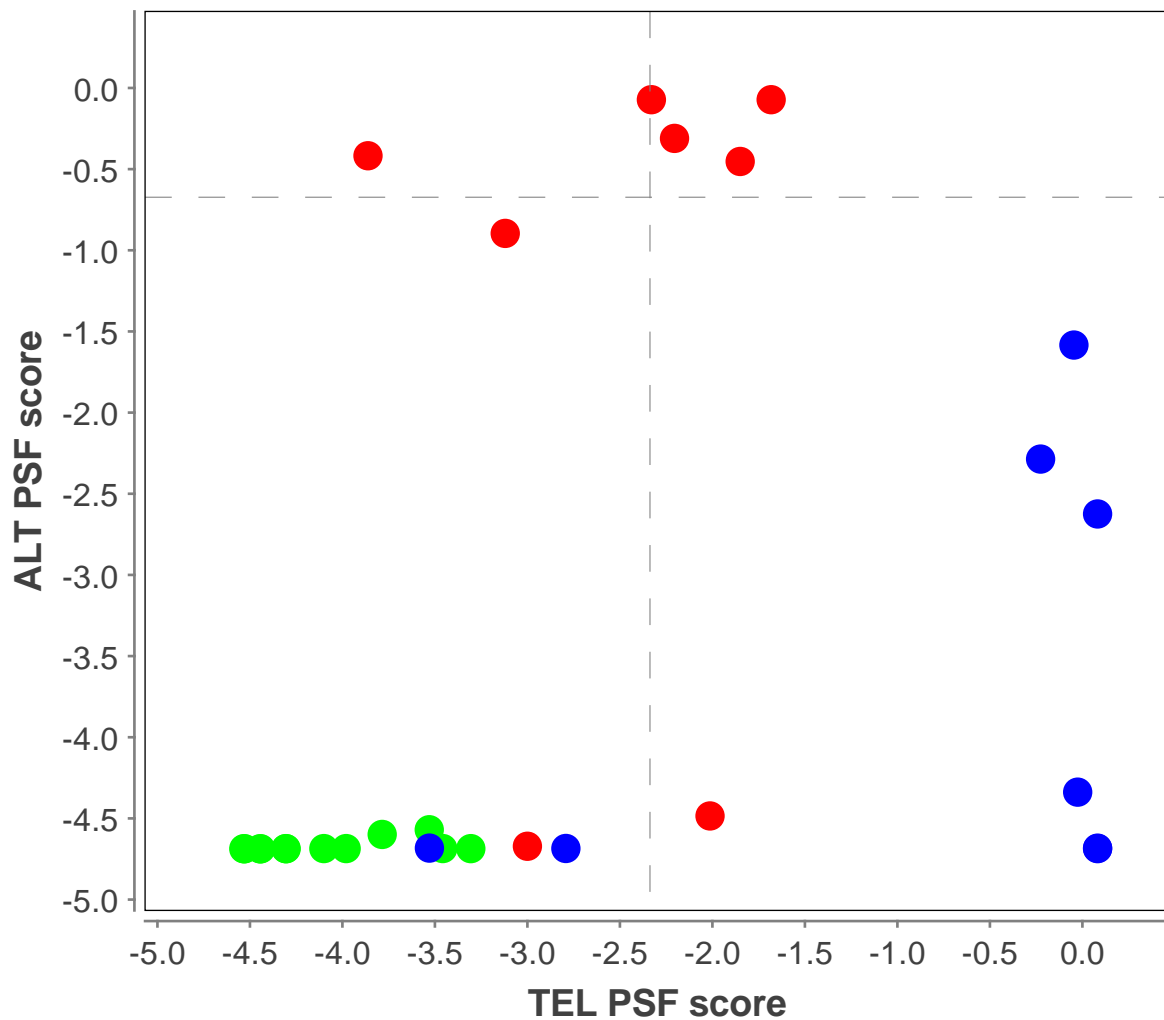
TMM scores 2D plot

ALT PSF score / TEL PSF score

Classification accuracy: 0.71

ALT ● TEL ● Normal ● ALT+/TEL+ ●

TMM scores 2D plot: labeled

Classification accuracy: 0.71

ALT   TEL   Normal   ALT+/TEL+

TMM scores 2D plot (log2 scale)

ALT PSF score

TEL PSF score

Classification accuracy: 0.71

ALT   TEL   Normal   ALT+/TEL+

TMM scores 2D plot: labeled (log2 scale)

Classification accuracy: 0.71
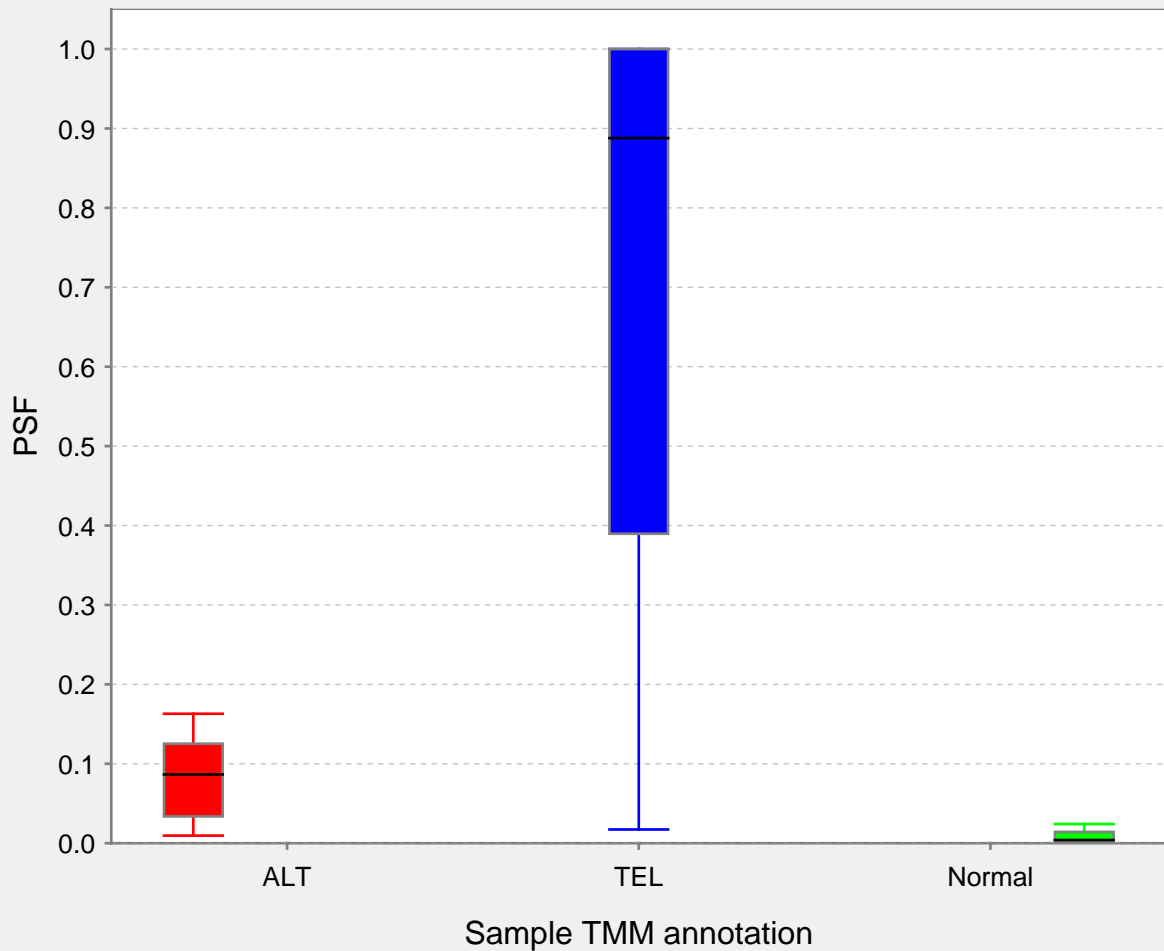
ALT   TEL   Normal   ALT+/TEL+

ALT PSF boxplot

Statistics

```
Overall p value:     0.0
ALT vs norm      Median Diff:   0.69    p value:  0.0
ALT vs Tel-ase   Median Diff:   0.68    p value:  0.01
```

TEL PSF boxplot
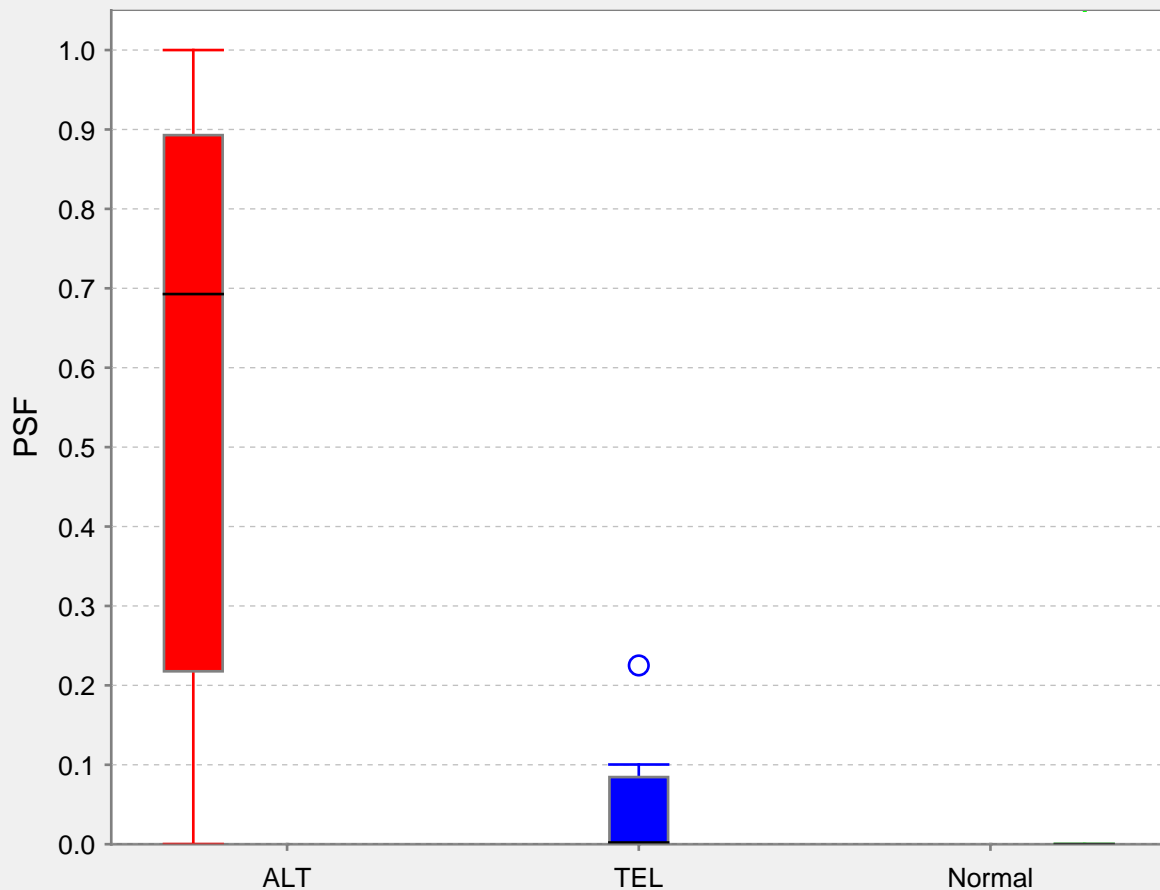
PSF vs Sample TMM annotation

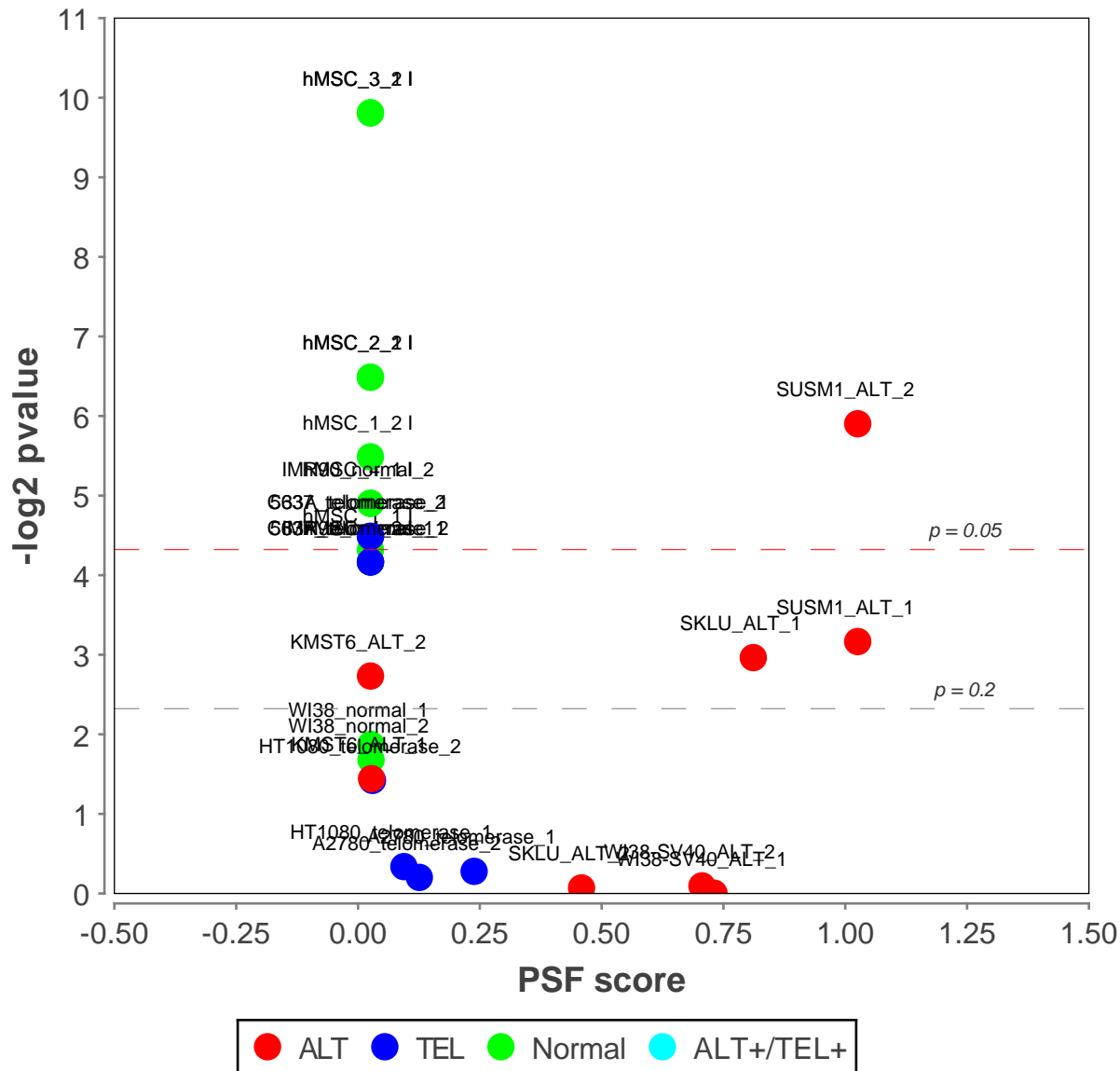**Statistics**

Overall p value: 0.0
Tel-ase vs norm   Median Diff: 0.88   p value: 0.0
Tel-ase vs ALT   Median Diff: 0.8   p value: 0.037

Legend: ALT TEL Normal

TEL volcano plot

ALT · TEL · Normal · ALT+/TEL+