

TMM output for: liposarcoma-clean

Date: 2017-05-18 16:48:52.612

Comments on iteration:

liposarcoma, correct pathway, final test

Inputs:

Iteration dir: C:\Dropbox\Bioinformatics_Group\The_telomere_project\telomere_network\alt-tert-networks\tmm_tests\liposarcoma-clean

Gene expression matrix:

C:\Dropbox\Bioinformatics_Group\The_telomere_project\telomere_network\alt-tert-networks\tmm_0.1_example\Liposarcoma_gene_expression_mat.txt

Options:

Number of samples: 21

PSF summary file:

C:\Dropbox\Bioinformatics_Group\The_telomere_project\telomere_network\alt-tert-networks\tmm_tests\liposarcoma-clean\psf_summary.xls

Number of bootstrap cycles: 200

Mode: Validation

TMM labels file:

C:\Dropbox\Bioinformatics_Group\The_telomere_project\telomere_network\alt-tert-networks\tmm_0.1_example\Liposarcoma_tmm_labels.txt

Validation results

Classification accuracy: 0.62

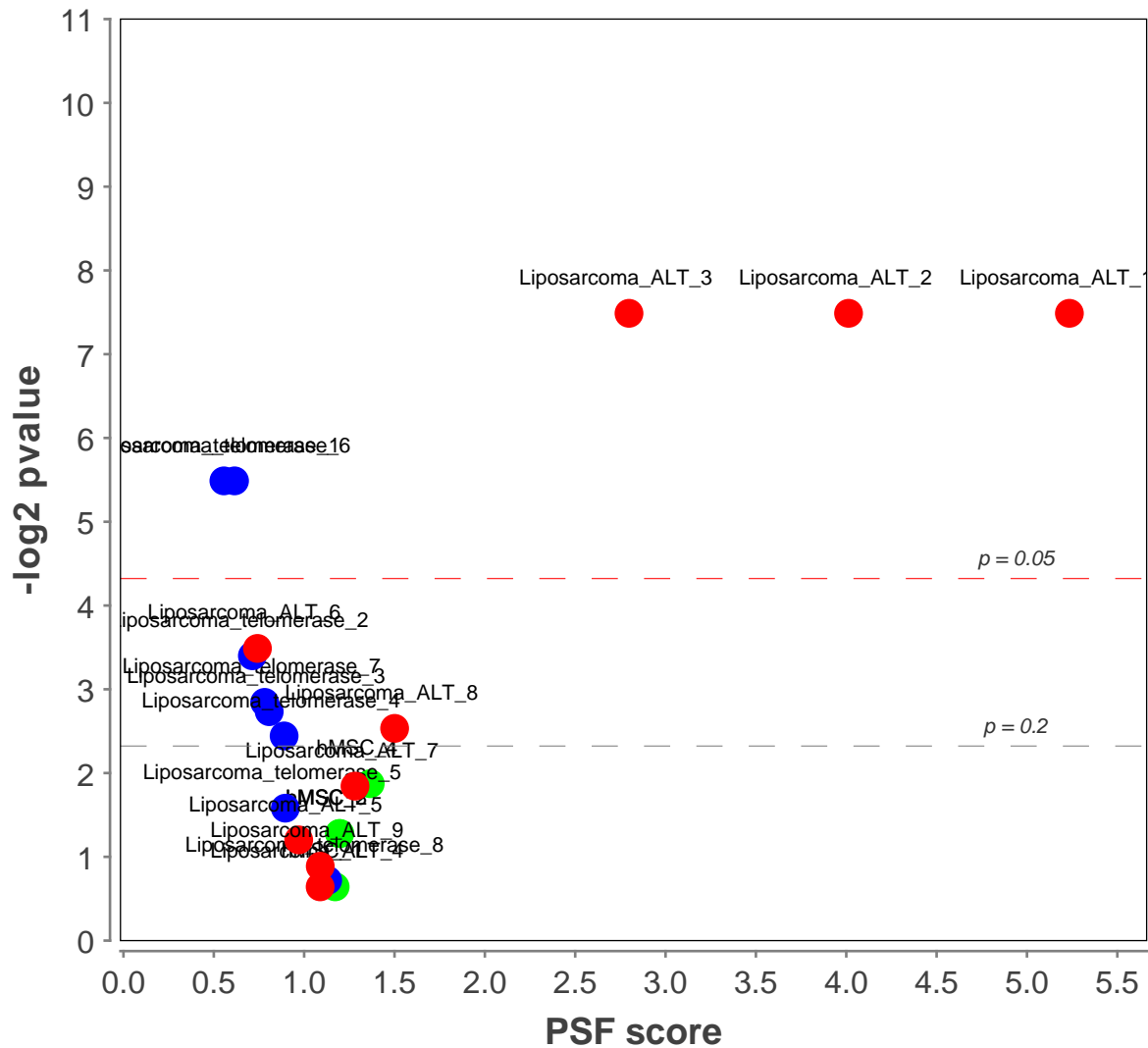
Median differences and p values

Overall p value (Kruskal-Wallis rank sum test): 0.004

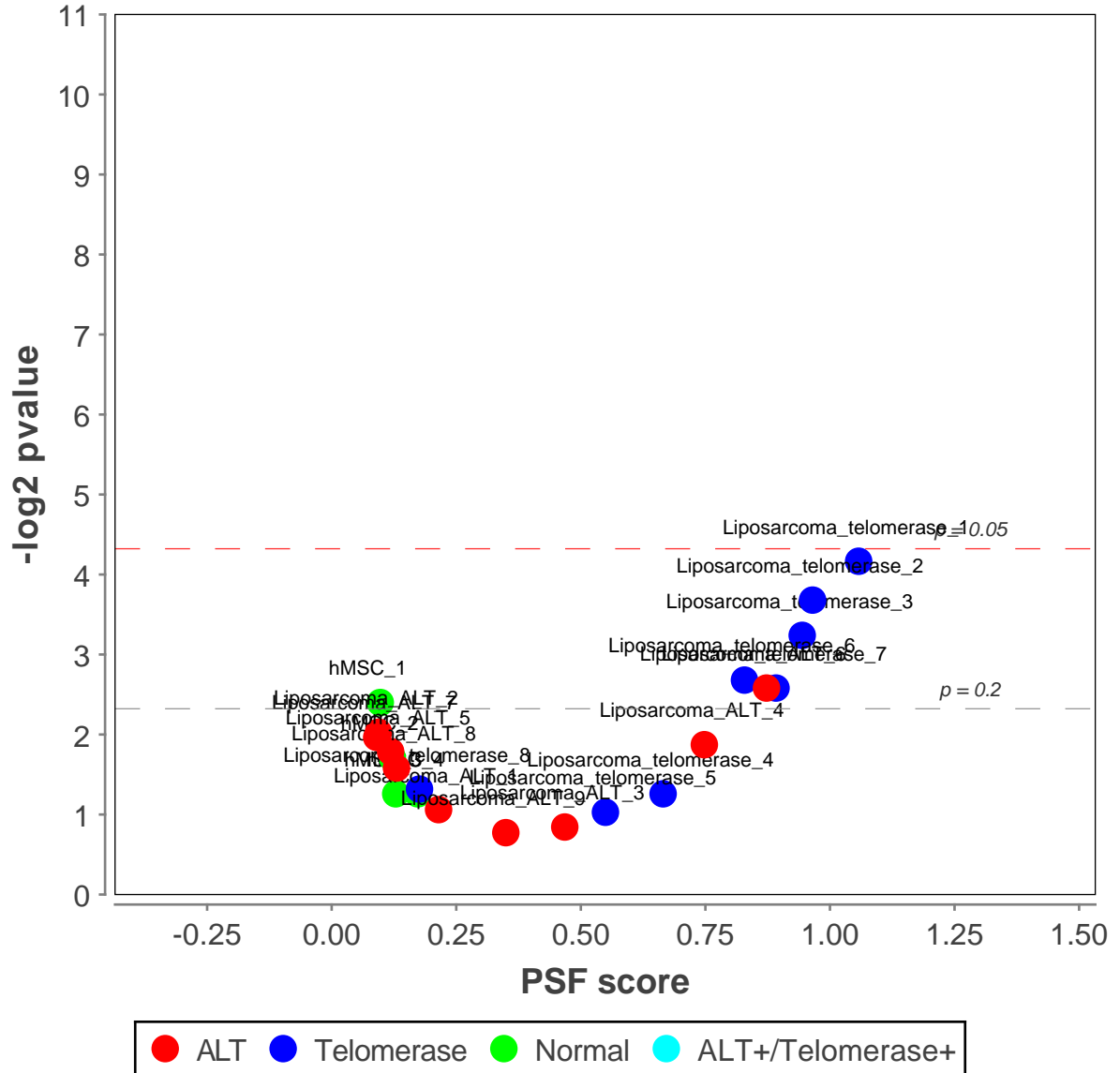
ALT versus normal: Median difference: 0.089 p value 0.414

ALT versus telomerase Median difference: -0.478 p value 0.011

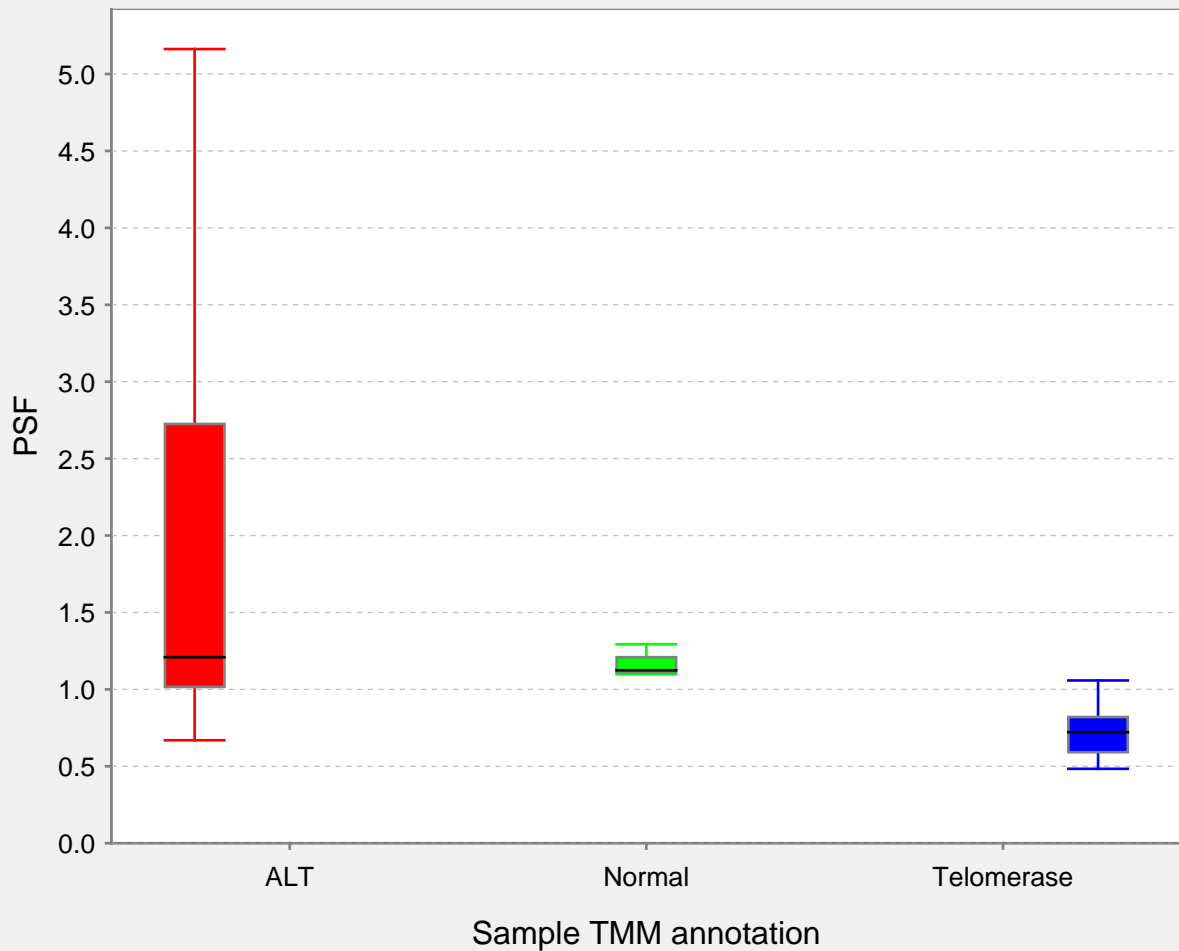
ALT volcano plot



Telomerase volcano plot



ALT PSF boxplot



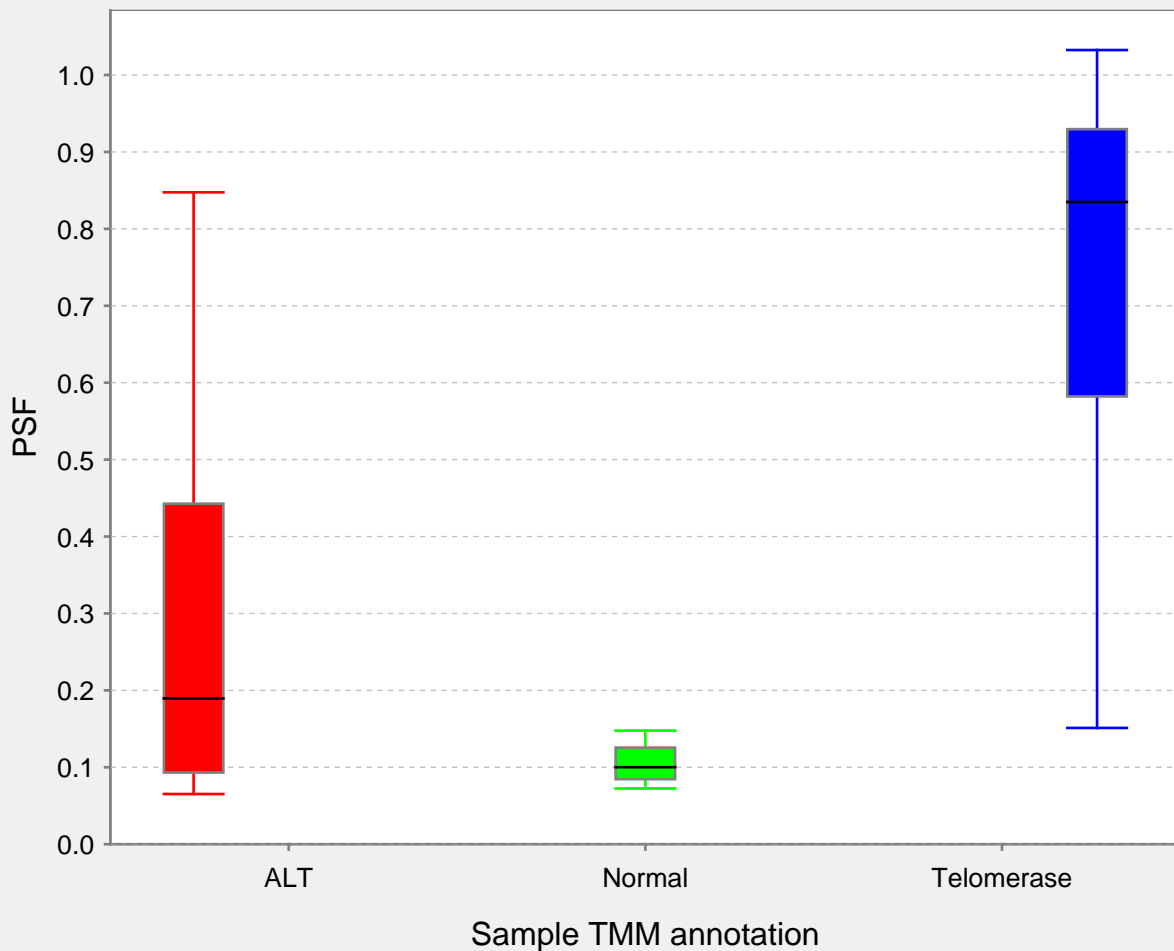
Statistics

Overall p value: 0.004

ALT vs normal	Median Diff: 0.09	p value: 0.94
ALT vs telomerase	Median Diff: 0.52	p value: 0.006

■ ALT ■ Normal ■ Telomerase

Telomerase PSF boxplot

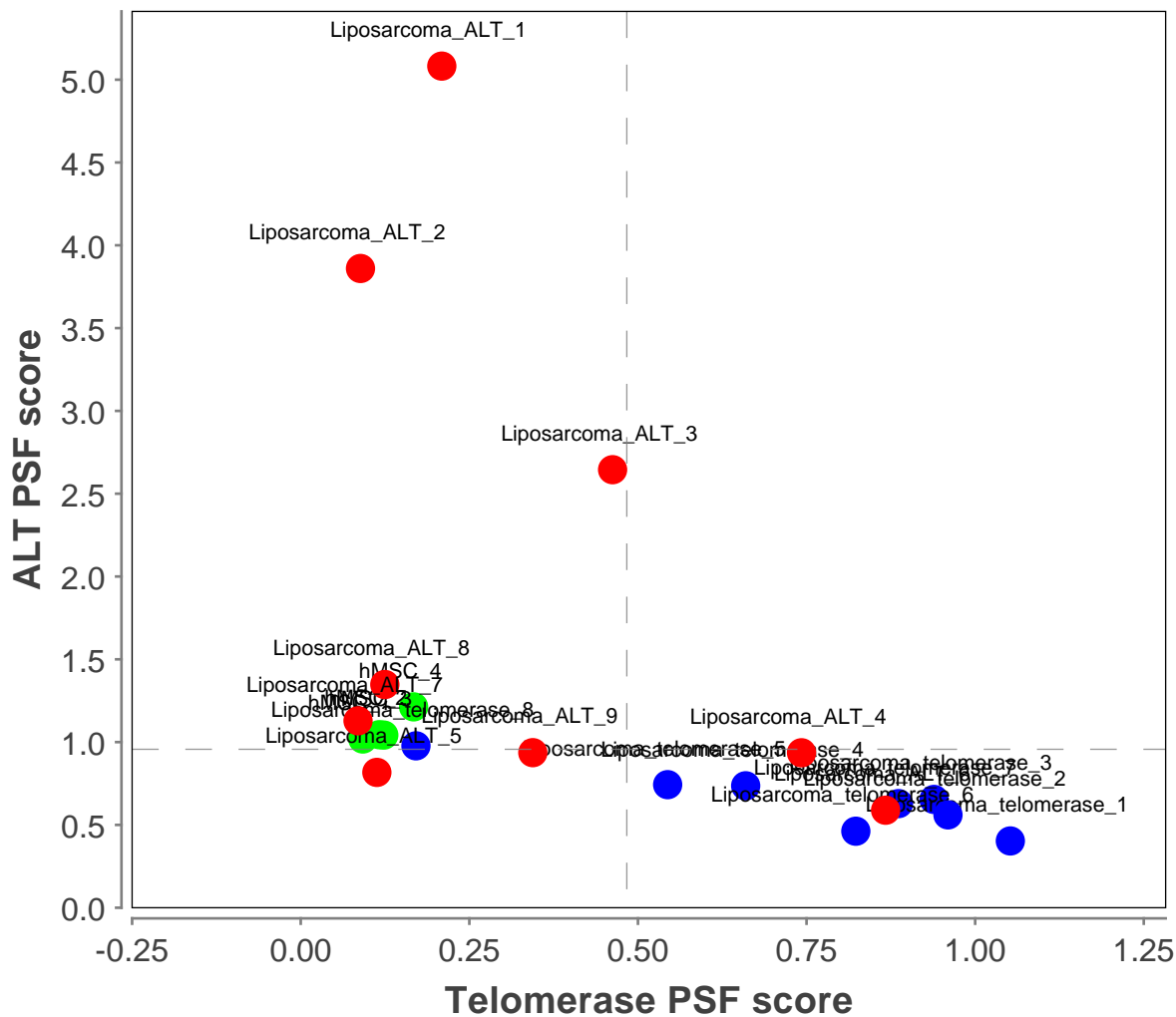


Statistics

Overall p value: 0.004
ALT vs normal Median Diff: 0.09 p value: 0.414
ALT vs telomerase Median Diff: -0.48 p value: 0.011

■ ALT ■ Normal ■ Telomerase

TMM scores 2D plot



Classification accuracy: 0.62

