

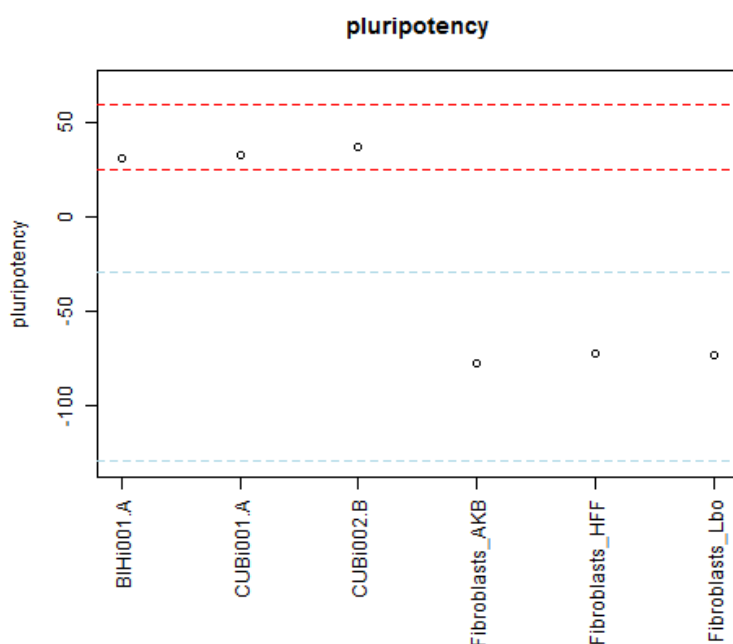
cell line name/passage	CUBi001-A Passage: 22
Name operator	Harald Stachelscheid
Date of testing	05.08.2016
Sample	A: BIHi001.A (positive control) B: CUBi001.A C: CUBi002.B D: Fibroblasts_AKB E: Fibroblasts_HFF (negative control) F: Fibroblasts_Lbo

Results

with ILLUMINA Microarray

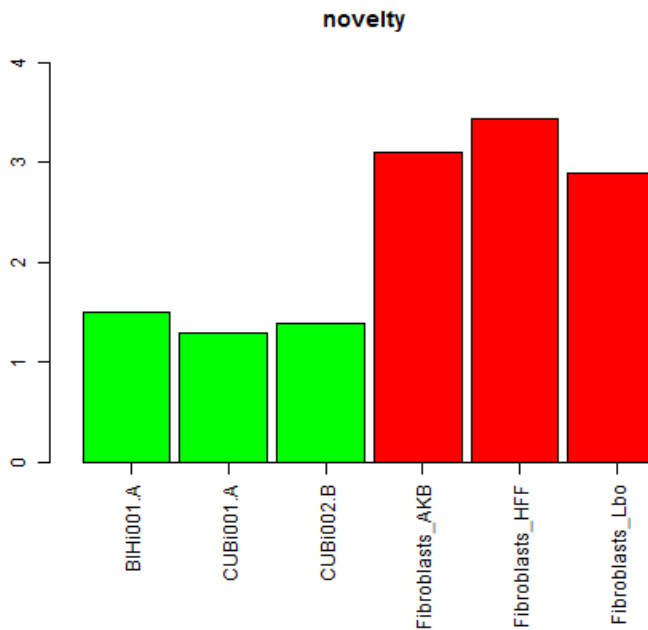
	pluri-raw	pluri logit-p	novelty	novelty logit-p	RMSD
BIHi001.A	31.32	1.00	1.50	0.02	0.44
CUBi001.A	32.75	1.00	1.30	0.00	0.40
CUBi002.B	37.23	1.00	1.38	0.01	0.42
Fibroblasts_AKB	-77.92	0.00	3.11	1.00	0.84
Fibroblasts_HFF	-72.17	0.00	3.44	1.00	0.86
Fibroblasts_Lbo	-73.01	0.00	2.90	1.00	0.80

Model-Based Multi-Class Pluripotency Score:

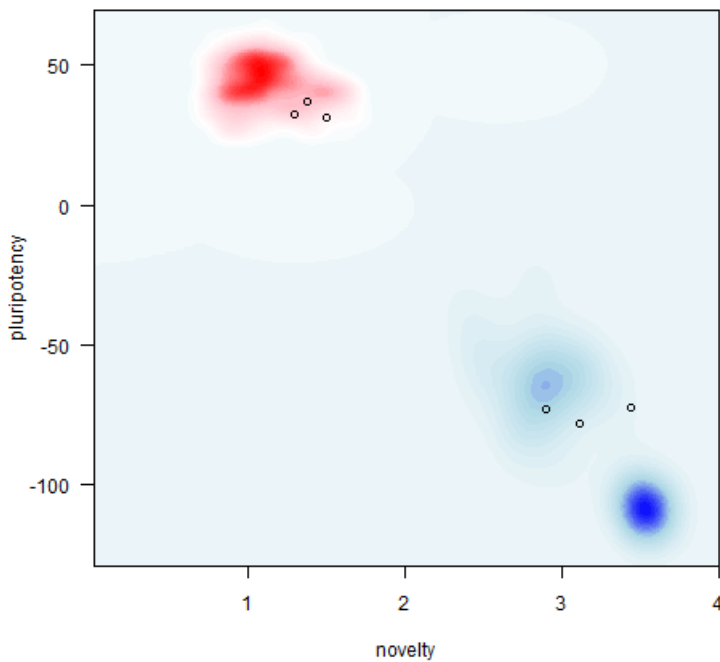


A score that is based on all samples (pluripotent cells, somatic cells and tissues) in the stem cell model matrix. Samples with positive values are more similar to the pluripotent samples in the model matrix than to all other classes of samples in the matrix. The area between the red lines indicates the range that contains approximately 95 percent of the pluripotent samples tested. The *Pluripotency Score* gives an indication if a sample contains a pluripotent signature, but not necessarily if the cell preparation is a normal, bona-fide hESC or iPSC.

Novelty score:



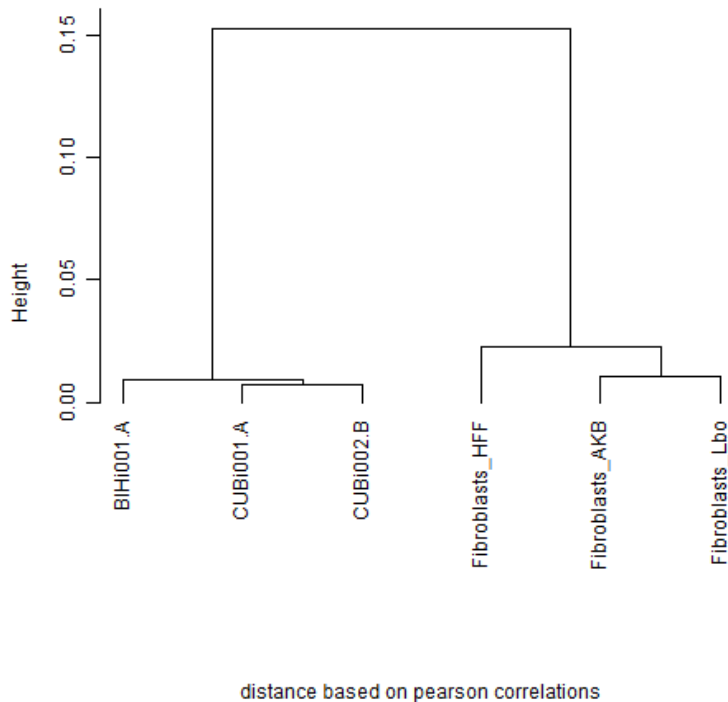
A score that is based on well-characterized pluripotent samples in the stem cell model matrix. Samples are color-coded green (pluripotent), orange, red (not-pluripotent) based on the probabilities given from the logistic regression model. Orange and red samples are more dissimilar to the pluripotent samples in the model matrix than the other pluripotent samples in the matrix. A low Novelty Score indicates that the test sample can be well reconstructed based on existing data from other well-characterized iPSC and ESC lines.



Combines the Pluripotency Score on the y-axis with the Novelty Score on the x-axis. The red and blue background hint to the empirical distribution of the pluripotent (red) and non-pluripotent samples (blue) in the test data set.

Quality Control: Hierarchical Clustering:

Clustering of vst-transformed samples



A plot generated by the Lumi package after the samples were transformed with a variance stabilizing transformation (VST) and before robust spline normalization (RSN). Outlier arrays with too much technical variation might be spotted if they do not cluster with their respective technical or biological replicates from the same sample or sample type.

Conclusion

The cell line CUBi001/A p.22 is tested positive for pluripotency.

Responsible person / date: Harald Stachelscheid / 05.08.2016