hiPSCore Report ECTODERM - 2025-06-17

hiPSCore

the key to iPSC quality

The hiPSCore is a machine learning-based thoroughly validated functional pluripotency test. By analyzing hiPSC-derived undifferentiated, endoderm-, ectoderm-, and mesoderm-differentiated samples using qPCR, the automated hiPSCore classification assesses differentiation potential of hiPSCs with high accuracy, sensitivity, and specificity. Successfully validated cell lines are truly pluripotent according to the Standards of the International Society for Stem Cell Research (ISSCR) and may be used for research. The following report contains detailed analysis and description of the results.

Report Parameters

Selected Parameters

These parameters were selected to be included in the report:

- **gl_plot**
- **sample_summary_report**
- **mean_ct_table**
- **mean_dct_table**
- **subtest_table**
- **gl_table**
- **duo_score**

These samples were analyzed:

- **Mesoderm_h216**
- **Ectoderm_h212**
- **Endoderm_h214**
- **Pluripotency_h210**

Scoring Model Version: **0.3**

Report

hiPSCore Results Plot

hiPSCore Cell Fate Results Plot

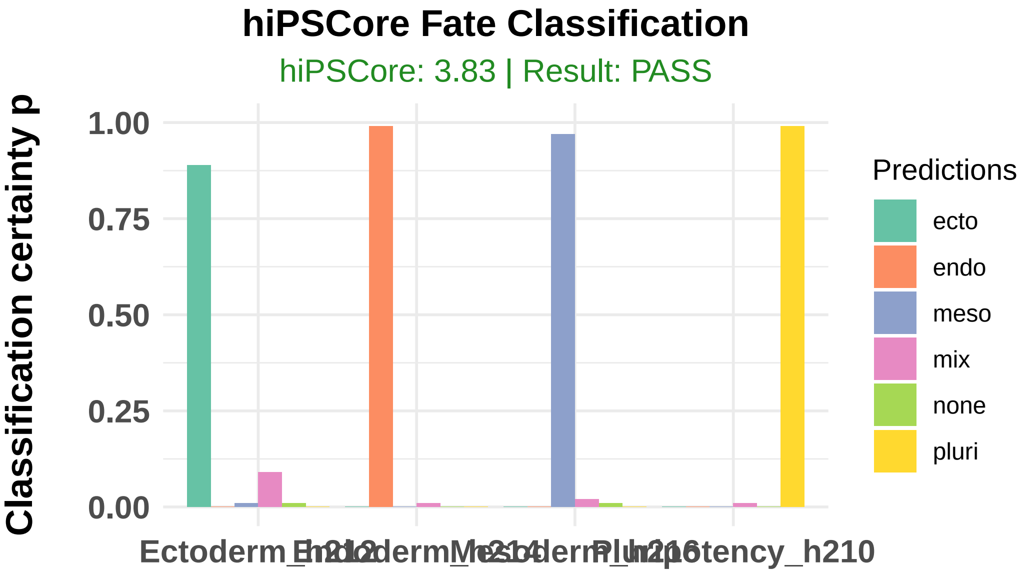

Figure 1: This graph shows the results of the hiPSCore GL/Cell Fate classification model. Here, samples are classified as either undifferentiated iPSCs, endoderm, ectoderm, mesoderm, or none of the before, or a mix of the before. The certainty p of classification is given for each sample with high values above 0.8 indicating high quality pure samples. Lower values or high values for none or mix classes indicate bad sample quality and warrant reanalysis of the samples.

Sample Summary

The sample summary indicates individual per sample quality and takes into the account both the cell fate classification and the cell fate-specific subtest. Only if both are consistent a sample is regarded as good quality!

Ectoderm_h212	Endoderm_h214	Mesoderm_h216	Pluripotency_h210
Ectoderm_h212 is ecto with a certainty of 0.88. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (ecto) has a certainty p of 1. This represents a high confidence/likelihood that Ectoderm_h212 contains cells of the origin ecto. The combined hiPSCore score is 1.88 indicating Good Quality of your Sample. For details consult the individual tables generated.	Endoderm_h214 is endo with a certainty of 0.99. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (endo) has a certainty p of 1. This represents a high confidence/likelihood that Endoderm_h214 contains cells of the origin endo. The combined hiPSCore score is 1.99 indicating Good Quality of your Sample. For details consult the individual tables generated.	Mesoderm_h216 is meso with a certainty of 0.97. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (meso) has a certainty p of 1. This represents a high confidence/likelihood that Mesoderm_h216 contains cells of the origin meso. The combined hiPSCore score is 1.97 indicating Good Quality of your Sample. For details consult the individual tables generated.	Pluripotency_h210 is pluri with a certainty of 0.99. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (pluri) has a certainty p of 0.97. This represents a high confidence/likelihood that Pluripotency_h210 contains cells of the origin pluri. The combined hiPSCore score is 1.96 indicating Good Quality of your Sample. For details consult the individual tables generated.

Report Tables – Underlying Data & Analysis

hiPSCore Germlayer Table

This table displays the results of the hiPSCore germlayer model which classifies cell types according to their cell fate as either undifferentiated iPSCs, endoderm, ectoderm, mesoderm, or none of the before, or a mix of the before. The prediction_val indicates the top, i.e. most likely cell fate of analyzed samples. Individual prediciton values for each of the six classes (pluri = undifferentiated iPSCs, endo = endoderm, ecto = ectoderm, meso = mesoderm, none = neither of the first four, mix = mix of two or more of the first four) are given and indicate the likelihood of a prediction to be correct or not. High (≥ 0.8) values indicate high certainty of classification whereas medium (≥ 0.5 & ≤ 0.8) and low (≥ 0.49) values indicate that an analyzed sample is not pure and of overall bad quality.

Sample	.pred	pluri	endo	ecto	meso	none	mix
Ectoderm_h212	ecto	0.00	0.00	0.88	0.01	0.01	0.09
Endoderm_h214	endo	0.00	0.99	0.00	0.00	0.00	0.01
Mesoderm_h216	meso	0.00	0.00	0.00	0.97	0.01	0.02
Pluripotency_h210	pluri	0.99	0.00	0.00	0.00	0.00	0.01

hiPSCore duo Score Table

This table shows the result of the hiPSCore duo score which is an enhanced stricter implementation combining both the power of the multi-class classification and the binary classification backing the individual subtests. The forward implementation first classifies the cell fate and then backs this classification up by performing the respective subtest. The result is a continuous score between 0 and 2, with ≥ 1.6 indicating a good quality sample, between 1.3 and 1.6 issuing a low score flag, between 1.1 and 1.3 issuing a warning and ≤ 1.1 indicating a sample of bad quality.

sample_ID	pred.	gl_p	subtest_p	duo_hiPSCore	FLAG
Mesoderm_h216	meso	0.97	1.00	1.97	PASS
Ectoderm_h212	ecto	0.88	1.00	1.88	PASS
Endoderm_h214	endo	0.99	1.00	1.99	PASS
Pluripotency_h210	pluri	0.99	0.97	1.96	PASS

Mean C_t Table

This table displays the mean C_t values ($\pm \sigma$) of each gene target for each sample and gives an indication of the qPCR run quality.

Sample Name	Target Name	mean	sd
Ectoderm_h212	ACTB	16.1	0.1
Ectoderm_h212	APLNR	26.8	0.1
Ectoderm_h212	CER1	31.1	0.5
Ectoderm_h212	CNMD	26.4	0.0
Ectoderm_h212	EOMES	31.3	1.1
Ectoderm_h212	GAPDH	15.7	0.1
Ectoderm_h212	HAND1	32.1	0.3
Ectoderm_h212	HES5	27.0	0.1

Sample Name	Target Name	mean	sd
Ectoderm_h212	HOXB7	32.4	0.1
Ectoderm_h212	NANOG	27.2	0.3
Ectoderm_h212	PAX6	22.0	0.1
Ectoderm_h212	SPP1	25.4	0.1
Endoderm_h214	ACTB	15.0	0.0
Endoderm_h214	APLNR	32.9	10.0
Endoderm_h214	CER1	14.7	0.1
Endoderm_h214	CNMD	29.8	0.1
Endoderm_h214	EOMES	18.4	0.0
Endoderm_h214	GAPDH	16.5	0.0
Endoderm_h214	HAND1	29.9	0.2
Endoderm_h214	HES5	33.9	0.6
Endoderm_h214	HOXB7	32.4	0.3
Endoderm_h214	NANOG	22.9	0.0
Endoderm_h214	PAX6	28.1	0.2
Endoderm_h214	SPP1	24.8	0.0
Mesoderm_h216	ACTB	16.8	0.1
Mesoderm_h216	APLNR	22.7	0.1
Mesoderm_h216	CER1	32.6	0.1
Mesoderm_h216	CNMD	26.3	0.0
Mesoderm_h216	EOMES	31.6	0.5
Mesoderm_h216	GAPDH	16.1	0.1
Mesoderm_h216	HAND1	23.5	0.1
Mesoderm_h216	HES5	35.4	0.6
Mesoderm_h216	HOXB7	26.2	0.0
Mesoderm_h216	NANOG	28.3	0.2
Mesoderm_h216	PAX6	39.5	0.6
Mesoderm_h216	SPP1	29.9	0.1
Pluripotency_h210	ACTB	15.8	0.0
Pluripotency_h210	APLNR	30.9	0.1
Pluripotency_h210	CER1	22.5	0.0
Pluripotency_h210	CNMD	23.1	0.1
Pluripotency_h210	EOMES	26.8	0.1
Pluripotency_h210	GAPDH	16.0	0.1
Pluripotency_h210	HAND1	32.6	0.0
Pluripotency_h210	HES5	32.0	0.4
Pluripotency_h210	HOXB7	35.1	0.7
Pluripotency_h210	NANOG	20.5	0.1
Pluripotency_h210	PAX6	33.5	0.8
Pluripotency_h210	SPP1	21.7	0.0

hiPSCore subtest Table

This table displays the individual hiPSCore subtest results and gives an indication on which cell types are contained within analyzed samples. A high (≥ 0.8) X1 prediction value indicates that a given cell type is highly likely present in the analyzed sample, whereas medium (≥ 0.5 & ≤ 0.8) and low (≤ 0.49) values indicate that a given cell type is unlikely to be present in the analyzed sample.

X0	X1	Sample	test	eval
1.00	0.00	Ectoderm_h212	undifferentiated	FAIL
0.98	0.02	Endoderm_h214	undifferentiated	FAIL
1.00	0.00	Mesoderm_h216	undifferentiated	FAIL
0.03	0.97	Pluripotency_h210	undifferentiated	PASS
1.00	0.00	Ectoderm_h212	endoderm	FAIL
0.00	1.00	Endoderm_h214	endoderm	PASS
1.00	0.00	Mesoderm_h216	endoderm	FAIL
0.99	0.01	Pluripotency_h210	endoderm	FAIL
0.00	1.00	Ectoderm_h212	ectoderm	PASS
1.00	0.00	Endoderm_h214	ectoderm	FAIL
0.92	0.08	Mesoderm_h216	ectoderm	FAIL
1.00	0.00	Pluripotency_h210	ectoderm	FAIL
1.00	0.00	Ectoderm_h212	mesoderm	FAIL
1.00	0.00	Endoderm_h214	mesoderm	FAIL
0.00	1.00	Mesoderm_h216	mesoderm	PASS
1.00	0.00	Pluripotency_h210	mesoderm	FAIL

Mean ΔC_t Table

This table displays the mean ΔC_t values normalized to the reference genes for each sample.

Sample Name	genes	dct
Ectoderm_h212	APLNR	10.92
Ectoderm_h212	CER1	15.18
Ectoderm_h212	CNMD	10.52
Ectoderm_h212	EOMES	15.37
Ectoderm_h212	HAND1	16.23
Ectoderm_h212	HES5	11.14
Ectoderm_h212	HOXB7	16.54
Ectoderm_h212	NANOG	11.33
Ectoderm_h212	PAX6	6.14

Sample Name	genes	dct
Ectoderm_h212	SPP1	9.49
Endoderm_h214	APLNR	17.19
Endoderm_h214	CER1	-0.99
Endoderm_h214	CNMD	14.10
Endoderm_h214	EOMES	2.66
Endoderm_h214	HAND1	14.13
Endoderm_h214	HES5	18.13
Endoderm_h214	HOXB7	16.69
Endoderm_h214	NANOG	7.19
Endoderm_h214	PAX6	12.34
Endoderm_h214	SPP1	9.05
Mesoderm_h216	APLNR	6.22
Mesoderm_h216	CER1	16.17
Mesoderm_h216	CNMD	9.81
Mesoderm_h216	EOMES	15.13
Mesoderm_h216	HAND1	7.02
Mesoderm_h216	HES5	18.99
Mesoderm_h216	HOXB7	9.74
Mesoderm_h216	NANOG	11.83
Mesoderm_h216	PAX6	23.09
Mesoderm_h216	SPP1	13.47
Pluripotency_h210	APLNR	15.00
Pluripotency_h210	CER1	6.58
Pluripotency_h210	CNMD	7.21
Pluripotency_h210	EOMES	10.89
Pluripotency_h210	HAND1	16.68
Pluripotency_h210	HES5	16.05
Pluripotency_h210	HOXB7	19.16
Pluripotency_h210	NANOG	4.62
Pluripotency_h210	PAX6	17.64
Pluripotency_h210	SPP1	5.82