hiPSCore Report DU546 - 2026-03-25

hiPSCore

the key to iPSC quality

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Report Parameters

Selected Parameters

These parameters were selected to be included in the report:

- **hiPSCore Plot**
- **hiPSCore GL Plot**
- **Sample Summary Report**
- **hiPSCore GL Table**
- **hiPSCore Duo Score Table**
- **hiPSCore Subtest Table**
- **Mean dCt Table**

These samples were analyzed:

- **undiff**
- **endo**
- **ecto**
- **meso**

Scoring Model Version: **V2**

Report

hiPSCore Results Plot

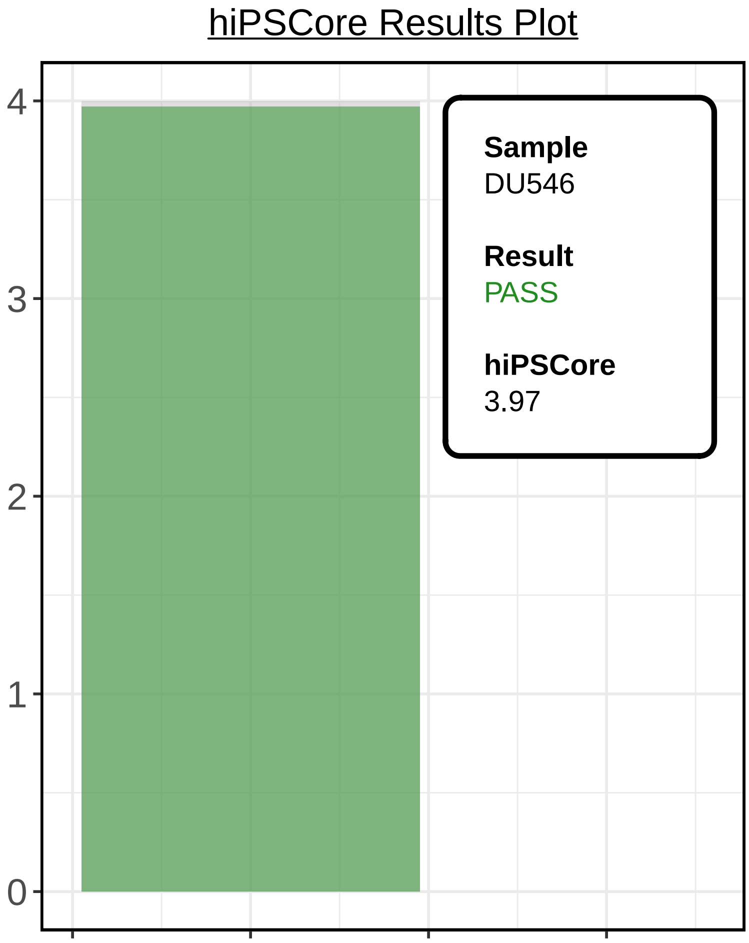

Figure 1: This graph shows the results of the canonical hiPSCore classification model based on the classification of iPSC-derived undifferentiated, endoderm, ectoderm, and mesoderm samples. A score above 3 indicates successful individual subtests and validate the tested iPSC lines functional pluripotency, i.e. the capacity of undifferentiated iPSCs to differentiate into each of the three primary germ layers.

hiPSCore Cell Fate Results Plot

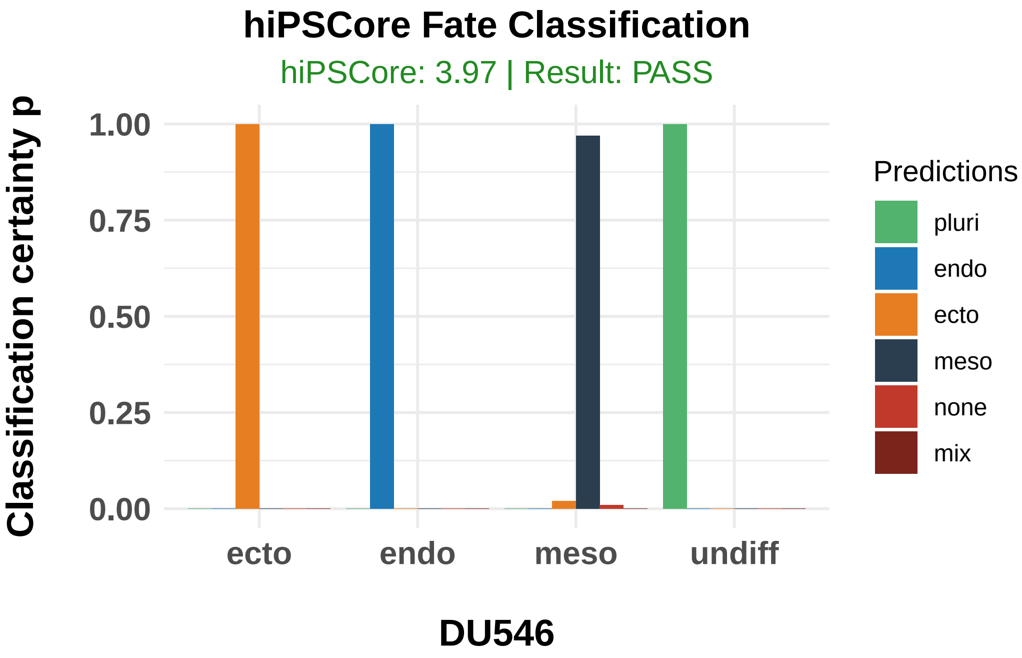

Figure 2: This graph shows the results of the hiPSCore GL/Cell Fate classification model. Here, samples are classified as either undifferentiated iPSCs, endoderm, ectoderm, mesoderm, or none of the before, or a mix of the before. The certainty p of classification is given for each sample with high values 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!

ecto	endo	meso	undiff
undiff is pluri with a certainty of 1. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (pluri) has a certainty p of 0.98. This represents a high confidence/likelihood that undiff contains cells of the origin pluri. The combined hiPSCore score is 1.98 indicating Good Quality of your Sample. For details consult the individual tables generated.	endo is endo with a certainty of 1. 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 endo contains cells of the origin endo. The combined hiPSCore score is 2 indicating Good Quality of your Sample. For details consult the individual tables generated.	ecto is ecto with a certainty of 1. This represents a high confidence/likelihood that the classification is correct.The corresponding subtest (ecto) has a certainty p of 0.99. This represents a high confidence/likelihood that ecto contains cells of the origin ecto. The combined hiPSCore score is 1.99 indicating Good Quality of your Sample. For details consult the individual tables generated.	meso 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 meso 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.

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_class	.pred_pluri	.pred_endo	.pred_ecto	.pred_meso	.pred_mix	.pred_none
undiff	pluri	1	0	0.00	0.00	0	0.00
endo	endo	0	1	0.00	0.00	0	0.00
ecto	ecto	0	0	1.00	0.00	0	0.00
meso	meso	0	0	0.02	0.97	0	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	sub_p	duo_hiPSCore	FLAG	cell_types
undiff	pluri	1.00	0.98	1.98	PASS	undiff
endo	endo	1.00	1.00	2.00	PASS	endo
ecto	ecto	1.00	0.99	1.99	PASS	ecto
meso	meso	0.97	1.00	1.97	PASS	meso

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.

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	0.02	0.98	undiff	undifferentiated	PASS

	X0	X1	Sample	test	eval
2	1.00	0.00	endo	undifferentiated	FAIL
3	0.98	0.02	ecto	undifferentiated	FAIL
4	1.00	0.00	meso	undifferentiated	FAIL
...5	1.00	0.00	undiff	endoderm	FAIL
...6	0.00	1.00	endo	endoderm	PASS
...7	1.00	0.00	ecto	endoderm	FAIL
...8	0.99	0.01	meso	endoderm	FAIL
...9	1.00	0.00	undiff	ectoderm	FAIL
...10	0.98	0.02	endo	ectoderm	FAIL
...11	0.01	0.99	ecto	ectoderm	PASS
...12	1.00	0.00	meso	ectoderm	FAIL
...13	1.00	0.00	undiff	mesoderm	FAIL
...14	0.99	0.01	endo	mesoderm	FAIL
...15	1.00	0.00	ecto	mesoderm	FAIL
...16	0.00	1.00	meso	mesoderm	PASS

Mean ΔC_t Table

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

Sample Name	genes	dct
undiff	SPP1	7.8
undiff	NANOG	6.2
undiff	CNMD	5.1
undiff	EOMES	14.5
undiff	CER1	9.9
undiff	PAX6	17.8
undiff	HES5	16.1
undiff	HAND1	16.3
undiff	APLNR	14.1
undiff	HOXB7	19.7
endo	SPP1	10.6
endo	NANOG	9.9
endo	CNMD	13.7
endo	EOMES	2.9
endo	CER1	-2.7
endo	PAX6	10.8
endo	HES5	19.5
endo	HAND1	12.9

Sample Name	genes	dct
endo	APLNR	11.6
endo	HOXB7	15.4
ecto	SPP1	13.8
ecto	NANOG	12.9
ecto	CNMD	10.6
ecto	EOMES	15.1
ecto	CER1	13.5
ecto	PAX6	4.3
ecto	HES5	3.7
ecto	HAND1	13.5
ecto	APLNR	9.9
ecto	HOXB7	21.1
meso	SPP1	12.4
meso	NANOG	14.8
meso	CNMD	10.5
meso	EOMES	14.1
meso	CER1	13.6
meso	PAX6	20.2
meso	HES5	15.7
meso	HAND1	5.7
meso	APLNR	6.7
meso	HOXB7	5.5