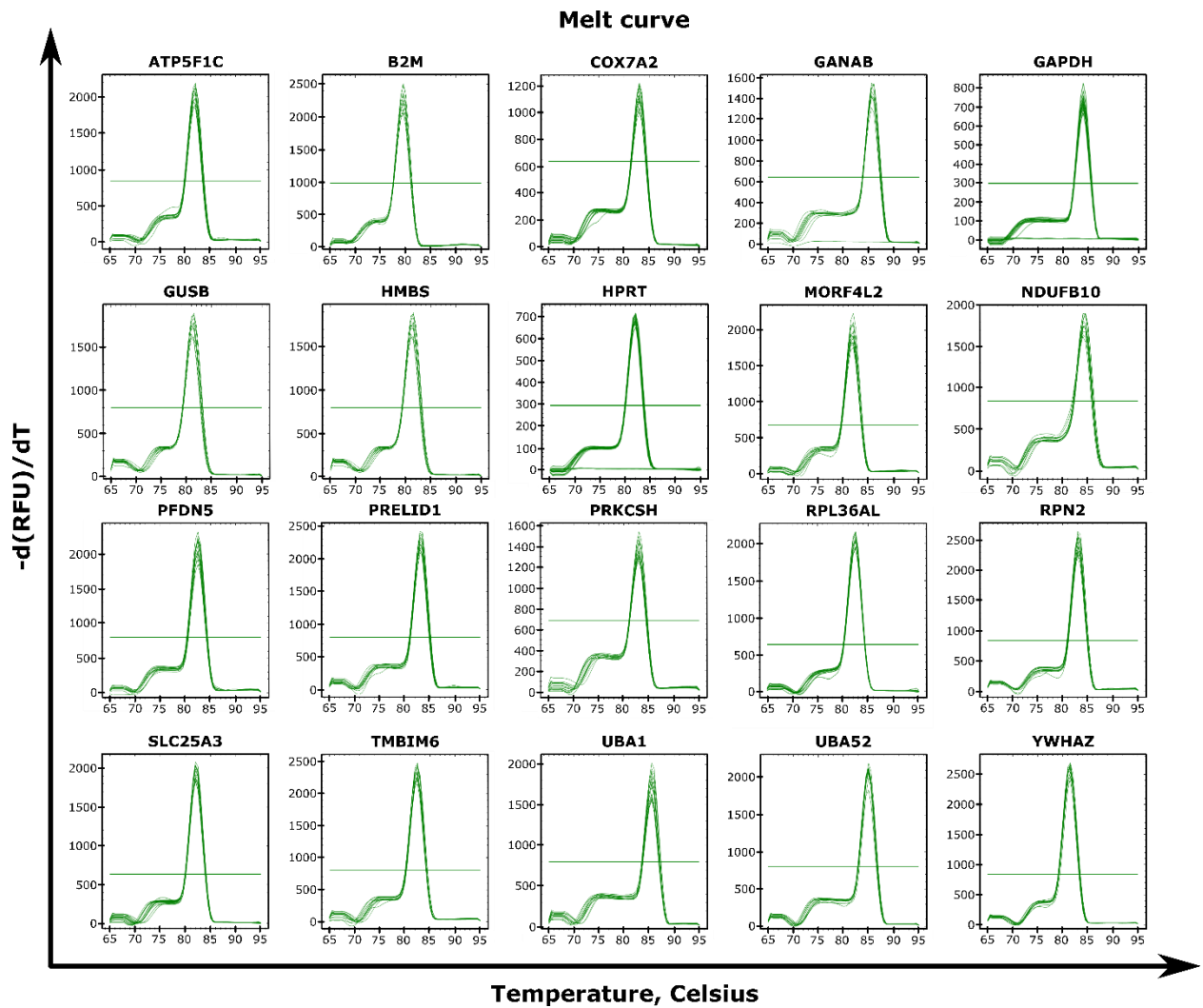


Identification of stable housekeeping genes for induced pluripotent stem cells and -derived endothelial cells for drug testing

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Supplementary information



Supp Figure 1. Melt curve of selected housekeeping genes. Melt curves of 20 housekeeping genes were plotted using serial dilutions of qRT-PCR were run on each primer pair. All 20 housekeeping genes shows a high specificity of primers as all of their melt curve peaks at the same point.

Supplementary Table S1. Mean Ct, STD and CV% of 20 HKG

Gene	Mean Ct	STD	CV(%)
COX7A2	21.54	0.30	1.40
HPRT1	24.51	0.36	1.47
YWHAZ	20.52	0.37	1.79
PRDN5	21.34	0.42	1.94
RPL36AL	19.09	0.42	2.21
ATP5F1C	21.80	0.48	2.22
UBA52	18.99	0.49	2.61
NDUFB10	22.18	0.53	2.38
PRELID1	21.37	0.59	2.76
MORF4L2	20.70	0.60	2.90
SLC25A3	20.55	0.63	3.05
GUSB	23.02	0.66	2.86
TMBIM6	21.31	0.71	3.33
GAPDH	19.61	0.88	4.47
RPN2	21.40	0.95	4.44
HMBS	25.52	1.02	3.99
GANAB	24.72	1.09	4.39
B2M	22.32	1.11	4.96
UBA1	25.08	1.66	6.60
PRKCSH	25.49	1.78	6.98

Supp Table 2. Housekeeping genes and primer sequences

Gene	Name	Accession Number	Forward primer sequence	Reverse primer sequence	Amplicon size (bp)	R ²
ATP5F1C	ATP synthase F1 subunit gamma	NM_001001973.3	TGAGCAGAGTGCCAGGATGACA	TGTGATGACAGCTTGGCGGGTA	109	1.00
B2M	Beta-2-Microglobulin	NM_004048.4	CTATCCAGCGTACTCCAAAG	TCAATGTCGGATGGATGAAA	109	1.00
COX7A2	cytochrome c oxidase subunit 7A2	ENSG00000112695	TGGTCAGTAACAGCCAAGATG	TTTTAAAATGCCTGCGGGAAG	94	1.00
GANAB	glucosidase II alpha subunit	NM_198334.3	GCTTGGCTTCTAAGAGGCGGAA	CAGCCCTCATAGTCAGAGCCAT	139	0.99
GAPDH	Glyceraldehyde-3-Phosphate Dehydrogenase	NM_002046.7	GAGTCAACGGATTTGGTCGT	TTGATTTTGGAGGGATCTCG	238	1.00
GUSB	Glucuronidase Beta	NM_000181.4	ACCAGGATCCACCTCTGATG	GAAATCGGCAAAATTCCAAA	128	1.00
HMBS	Hydroxymethylbilane Synthase	NM_000190.4	AGGATGGGCAACTGTACCTG	ATGGTAGCCTGCATGGTCTC	82	1.00
HPRT1	Hypoxanthine Phosphoribosyltransferase 1	NM_000194.3	CATTATGCTGAGGATTTGGAAAGG	CTTGAGCACACAGAGGGCTACA	129	0.98
MORF4L2	mortality factor 4 like 2	NM_012286.3	CTTGAACCAGCTCTCCCAGGAA	TACTGCCACCATCTCCGTTTCC	121	1.00
NDUFB10	NADH:ubiquinone oxidoreductase subunit B10	NM_004548.3	GGAAGGACAGAACTACCAGCAG	ACTTCCTGGCAGAACTGTAGGC	116	1.00
PFDN5	prefoldin subunit 5	NM_002624.4	TGTGGAAGCCAAGGACTGTCTG	GAGCACGTGTTCCACATCATGC	121	1.00
PRELID1	PRELI domain containing 1	NM_013237.4	GGAGGACTCTATTGTGGACCCA	CAGTCCAGCCACTGTTGTCAGA	131	1.00
PRKCSH	protein kinase C substrate 80K-H	NM_001289104.2	GCGTCATCTGTGAGAACACCTG	CGTGCCTTCTTCCAGTCCTCAA	130	1.00
RPL36AL	ribosomal protein L36a like	NM_001001.5	ATCGGAAGCAGAGTGGCTATGG	CAGCATCCTCTTGGATCTGCAG	125	1.00
RPN2	ribophorin II	NM_002951.5	AGCCACCAGAACTTCGCCTTGT	CGGCAACAAACACCACTTCCTG	127	0.99
SLC25A3	solute carrier family 25 member 3	NM_002635.4	CTGGCTCCTATGGAAGCTGCTA	GTCTCATCCAGAGAGGAGCAAC	142	1.00
TMBIM6	transmembrane BAX inhibitor motif containing 6	NM_003217.3	GCTGATGGCAACACCTCATAGC	GTTGACAGCAATACAAAACCTCCAG	121	1.00
UBA1	ubiquitin like modifier activating enzyme 1	NM_003334.4	TCCTCACAGAGGACAAGTGCCT	CTTGAGCAGCTCACAGCCAATG	143	0.99
UBA52	ubiquitin A-52 residue ribosomal protein fusion product 1	NM_001033930.3	GCCTGCGAGGTGGCATTATTGA	TTCTTGCGGCAGTTGACAGCAC	124	0.98
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta	NM_145690.3	ACCGTTACTTGGCTGAGGTTGC	CCCAGTCTGATAGGATGTGTTGG	130	1.00

Commonly used housekeeping genes are highlighted in grey.

Supp Table 3. Other primer sequences

Gene	Forward primer sequence	Reverse primer sequence	Amplicon size (bp)
FOSB	AGCAGCAGCTAAATGCAGGA	CCAAGTCTGTCTCCGCC	71
SERPINE1	AGAGCGCTGTCAAGAAGACC	TGAAGTTCTCAGAGGTGCCT	115
SERPINE1-FOSB	AGAGCGCTGTCAAGAAGACC	GAAGAGATGAGGGTGGGTTG	223