

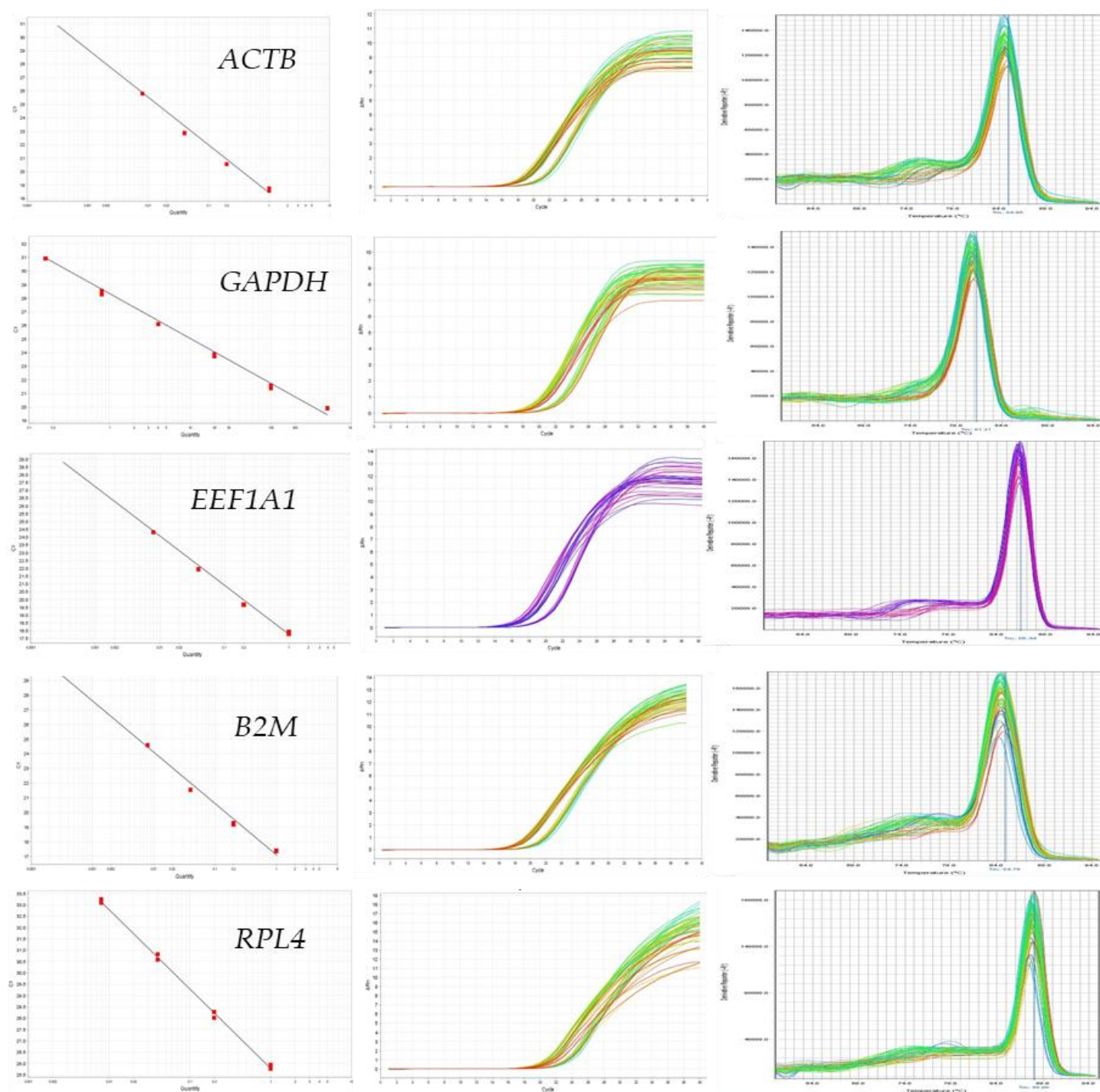


Fig. S1 qPCR standard curve, Amplification curve and melting peaks for RGs: *ACTB*, *GAPDH*, *EEF1A1*, *B2M* and *RPL4* in LAY-Fb and SAC-Fb

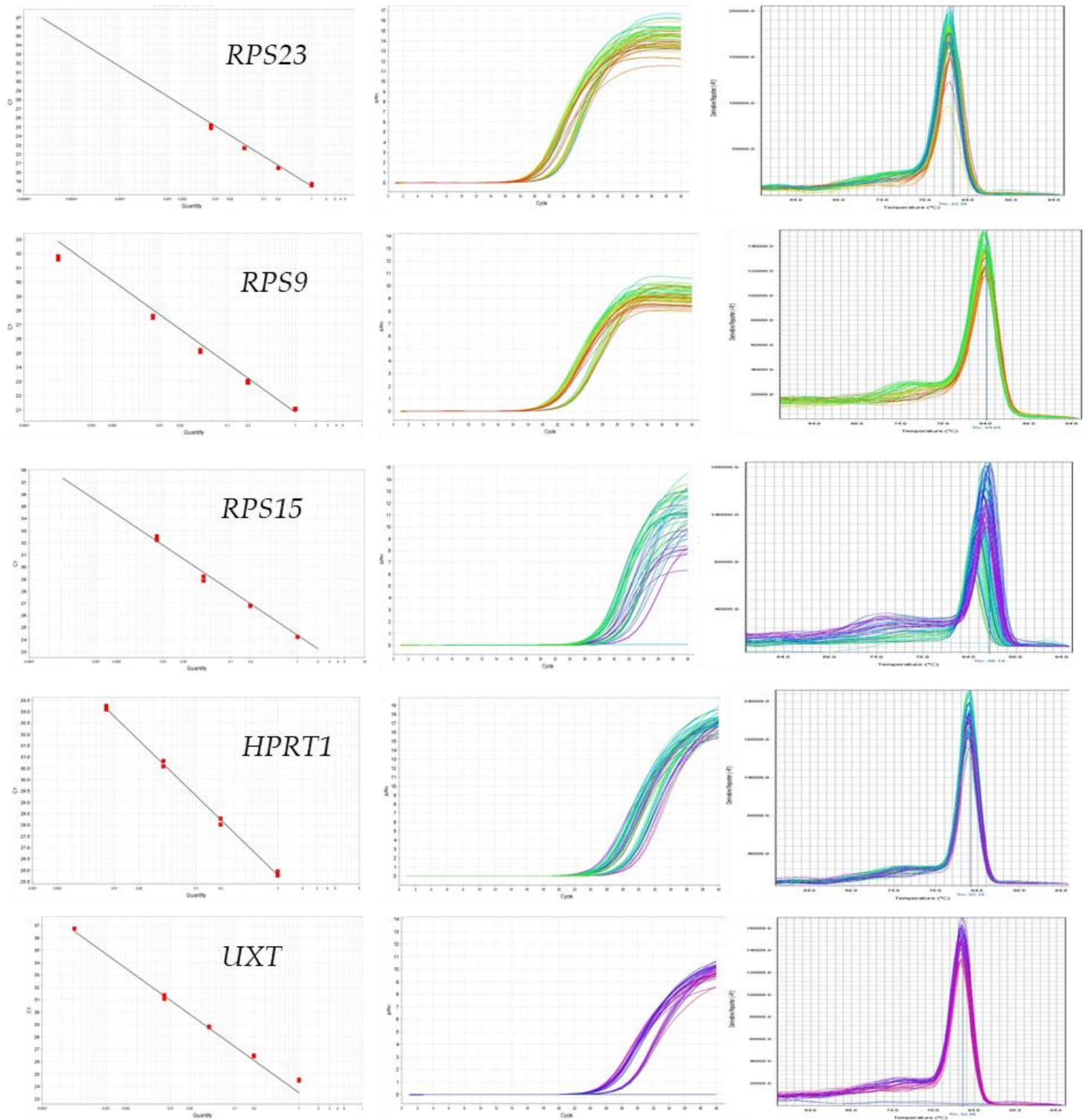


Fig. S2 qPCR standard curve, Amplification curve and melting peaks for RGs: *RPS23*, *RPS9*, *RPS15*, *HPRT1* and *UXT* in LAY-Fb and SAC-Fb

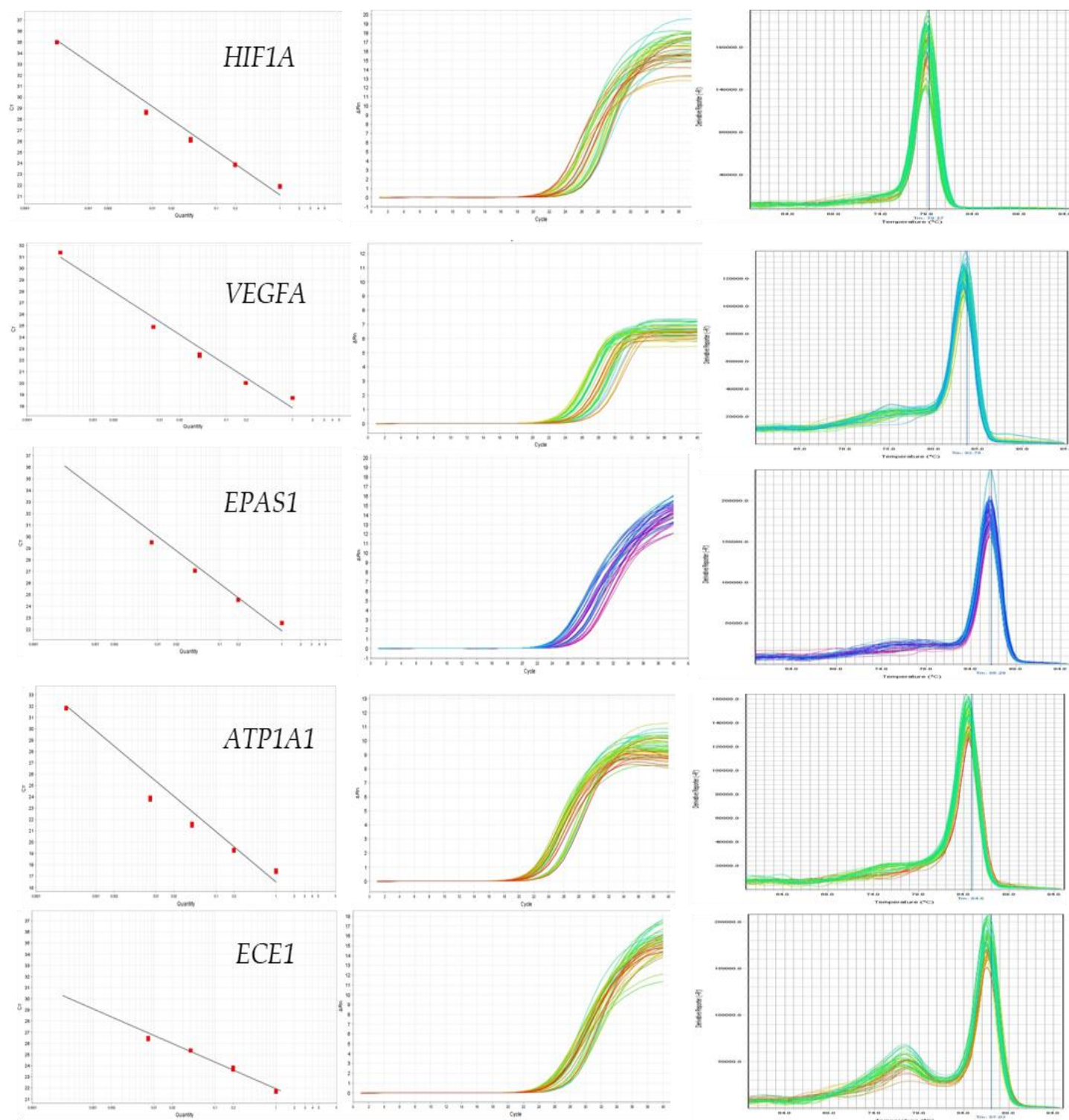


Fig. S3 qPCR standard curve, amplification plot and melting peak for *HIF1A*, *VEGFA*, *EPAS1*, *ATP1A1* and *ECE1* in LAY-Fb and SAC-Fb

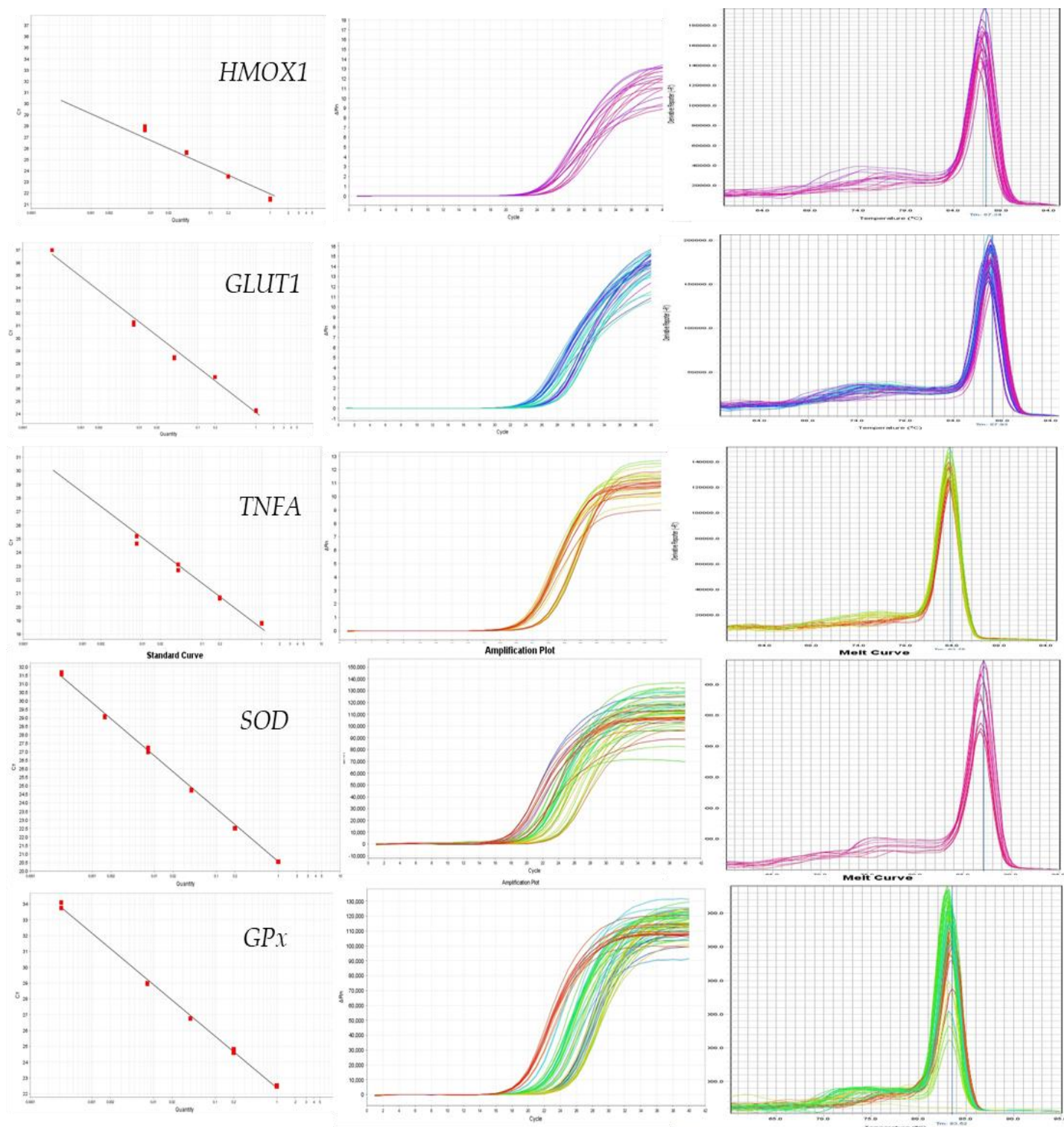


Fig. S4 qPCR standard curve, amplification plot and melting peak for *HMOX1*, *GLUT1*, *TNFA*, *GPx* and *SOD* in LAY-Fb and SAC-Fb

Table S1 Parameters based quantitative cycle (Ct) values for candidate RGs LAY-Fb

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
n	12	12	12	12	12	12	12	12	12	12
geo Mean [CP]	21.33	20.23	22.34	17.78	24.87	20.33	18.93	27.38	25.03	22.23
AR Mean [CP]	21.36	20.26	22.37	17.84	24.90	20.37	18.97	27.41	25.06	22.26
min [CP]	19.99	18.90	21.09	15.91	23.56	19.13	17.38	25.44	23.47	20.92
max [CP]	23.25	21.86	24.19	20.88	27.07	22.20	20.71	29.48	27.21	23.93
std dev [+/- CP]	0.99	1.00	1.07	1.28	1.16	1.04	1.02	1.08	1.10	1.01
CV [% CP]	4.63	4.94	4.79	7.20	4.66	5.11	5.40	3.94	4.40	4.55
min [x-fold]	-2.54	-2.52	-2.37	-3.67	-2.49	-2.31	-2.94	-3.84	-2.95	-2.49
max [x-fold]	3.78	3.09	3.61	8.57	4.59	3.63	3.43	4.29	4.53	3.23
std dev [+/- x-fold]	1.99	2.00	2.10	2.43	2.24	2.06	2.03	2.11	2.15	2.02

Table S2 Repeated pair-wise correlation among genes and genes with BestKeeper index in LAY-Fb

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
<i>ACTB</i>	0.982	-	-	-	-	-	-	-	-	-
p-value	0.001	-	-	-	-	-	-	-	-	-
<i>RPS9</i>	0.983	0.976	-	-	-	-	-	-	-	-
p-value	0.001	0.001	-	-	-	-	-	-	-	-
<i>EEF1A1</i>	0.756	0.838	0.732	-	-	-	-	-	-	-
p-value	0.004	0.001	0.007	-	-	-	-	-	-	-
<i>RPS15</i>	0.918	0.960	0.945	0.833	-	-	-	-	-	-
p-value	0.001	0.001	0.001	0.001	-	-	-	-	-	-
<i>RPS23</i>	0.988	0.973	0.986	0.766	0.927	-	-	-	-	-
p-value	0.001	0.001	0.001	0.004	0.001	-	-	-	-	-
<i>B2M</i>	0.978	0.997	0.965	0.846	0.949	0.969	-	-	-	-
p-value	0.001	0.001	0.001	0.001	0.001	0.001	-	-	-	-
<i>UXT</i>	0.901	0.843	0.923	0.424	0.786	0.894	0.829	-	-	-
p-value	0.001	0.001	0.001	0.170	0.002	0.001	0.001	-	-	-
<i>HPRT</i>	0.985	0.972	0.957	0.821	0.905	0.985	0.972	0.833	-	-

p-value	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	-	-
<i>RPL4</i>	0.992	0.972	0.971	0.764	0.904	0.983	0.967	0.884	0.986	-
p-value	0.001	0.001	0.001	0.004	0.001	0.001	0.001	0.001	0.001	-

BestKeeper vs.	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
coeff. of corr. [r]	0.988	0.996	0.982	0.833	0.957	0.987	0.993	0.852	0.985	0.985
p-value	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001	0.001

Table S3 Parameters based quantitative cycle (Ct) values for candidate RGs in SAC-Fb

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
N	12	12	12	12	12	12	12	12	12	12
geo Mean [CP]	21.36	20.41	22.67	18.56	25.21	20.51	19.12	27.32	25.28	22.44
AR Mean [CP]	21.39	20.44	22.70	18.62	25.28	20.54	19.15	27.34	25.31	22.47
min [CP]	20.19	19.31	21.44	16.44	23.23	19.43	17.99	25.56	24.01	21.38
max [CP]	23.32	22.46	24.79	21.59	28.96	22.47	21.17	29.39	27.41	24.36
std dev [+/- CP]	1.04	1.00	1.12	1.29	1.60	1.00	1.04	0.98	1.14	0.97
CV [% CP]	4.84	4.90	4.91	6.94	6.34	4.88	5.41	3.58	4.52	4.32
min [x-fold]	-2.25	-2.15	-2.36	-4.33	-3.94	-2.12	-2.18	-3.38	-2.42	-2.09
max [x-fold]	3.88	4.14	4.35	8.17	13.44	3.90	4.15	4.22	4.39	3.77
std dev [+/- x-fold]	2.05	2.00	2.17	2.45	3.04	2.00	2.05	1.97	2.21	1.96

Table S4 Repeated pair-wise correlation among genes and genes with BestKeeper index in SAC-Fb

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
<i>ACTB</i>	0.944	-	-	-	-	-	-	-	-	-
p-value	0.001	-	-	-	-	-	-	-	-	-
<i>RPS9</i>	0.989	0.977	-	-	-	-	-	-	-	-
p-value	0.001	0.001	-	-	-	-	-	-	-	-
<i>EEF1A1</i>	0.682	0.805	0.721	-	-	-	-	-	-	-
p-value	0.014	0.002	0.008	-	-	-	-	-	-	-
<i>RPS15</i>	0.870	0.925	0.911	0.759	-	-	-	-	-	-
p-value	0.001	0.001	0.001	0.004	-	-	-	-	-	-
<i>RPS23</i>	0.951	0.984	0.979	0.769	0.922	-	-	-	-	-

p-value	0.001	0.001	0.001	0.003	0.001	-	-	-	-	-
<i>B2M</i>	0.950	0.998	0.981	0.813	0.925	0.987	-	-	-	-
p-value	0.001	0.001	0.001	0.001	0.001	0.001	-	-	-	-
<i>UXT</i>	0.878	0.819	0.881	0.356	0.751	0.834	0.820	-	-	-
p-value	0.001	0.001	0.001	0.256	0.005	0.001	0.001	-	-	-
<i>HPRT</i>	0.959	0.975	0.985	0.707	0.947	0.978	0.977	0.894	-	-
p-value	0.001	0.001	0.001	0.010	0.001	0.001	0.001	0.001	-	-
<i>RPL4</i>	0.979	0.983	0.997	0.748	0.924	0.983	0.987	0.861	0.985	-
p-value	0.001	0.001	0.001	0.005	0.001	0.001	0.001	0.001	0.001	-

BestKeeper vs.	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
coeff. of corr. [r]	0.961	0.993	0.986	0.807	0.947	0.988	0.996	0.825	0.985	0.991
p-value	0.001	0.001	0.001	0.002	0.001	0.001	0.001	0.001	0.001	0.001

Table S5 Combined (LAY-Fb and SAC-Fb) analysis of parameters based quantitative cycling points (CP) for 10 candidate RGs

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
n	24	24	24	24	24	24	24	24	24	24
geo Mean [CP]	21.35	20.32	22.50	18.16	25.04	20.42	19.02	27.35	25.16	22.34
AR Mean [CP]	21.38	20.35	22.53	18.23	25.09	20.45	19.06	27.38	25.19	22.37
min [CP]	19.99	18.90	21.09	15.91	23.23	19.13	17.38	25.44	23.47	20.92
max [CP]	23.32	22.46	24.79	21.59	28.96	22.47	21.17	29.48	27.41	24.36
std dev [+/- CP]	1.01	1.00	1.09	1.32	1.41	1.01	1.03	1.03	1.11	0.98
CV [% CP]	4.74	4.92	4.85	7.24	5.62	4.96	5.40	3.77	4.42	4.37
min [x-fold]	-2.56	-2.68	-2.66	-4.78	-3.50	-2.45	-3.13	-3.76	-3.21	-2.67
max [x-fold]	3.91	4.41	4.88	10.72	15.13	4.15	4.42	4.38	4.78	4.06
std dev [+/- x-fold]	2.02	2.00	2.13	2.50	2.66	2.02	2.04	2.05	2.16	1.97

Table S6 Combined (LAY-Fb and SAC-Fb) analysis of repeated pair-wise correlation amongst genes with BestKeeper index

	<i>GAPDH</i>	<i>ACTB</i>	<i>RPS9</i>	<i>EEF1A1</i>	<i>RPS15</i>	<i>RPS23</i>	<i>B2M</i>	<i>UXT</i>	<i>HPRT1</i>	<i>RPL4</i>
<i>ACTB</i>	0.960	-	-	-	-	-	-	-	-	-
p-value	0.001	-	-	-	-	-	-	-	-	-
<i>RPS9</i>	0.977	0.975	-	-	-	-	-	-	-	-
p-value	-	0.001	-	-	-	-	-	-	-	-
<i>EEF1A1</i>	0.697	0.812	0.731	-	-	-	-	-	-	-
p-value	0.001	0.001	0.001	-	-	-	-	-	-	-
<i>RPS15</i>	0.869	0.923	0.912	0.779	-	-	-	-	-	-

p-value	0.001	0.001	0.001	0.001	-	-	-	-	-	-
<i>RPS23</i>	0.967	0.979	0.980	0.759	0.907	-	-	-	-	-
p-value	0.001	0.001	-	0.001	0.001	-	-	-	-	-
<i>B2M</i>	0.962	0.998	0.971	0.819	0.918	0.978	-	-	-	-
p-value	0.001	-	0.001	0.001	0.001	-	-	-	-	-
<i>UXT</i>	0.888	0.826	0.888	0.369	0.736	0.860	0.819	-	-	-
p-value	0.001	0.001	0.001	0.076	0.001	0.001	0.001	-	-	-
<i>HPRT</i>	0.968	0.974	0.970	0.758	0.913	0.981	0.975	0.854	-	-
p-value	0.001	0.001	0.001	0.001	0.001	-	0.001	0.001	-	-
<i>RPL4</i>	0.982	0.977	0.982	0.750	0.894	0.983	0.976	0.866	0.985	-
p-value	-	0.001	-	0.001	0.001	-	0.001	0.001	0.001	-

<i>BestKeeper</i> vs. <i>GAPDH</i> <i>ACTB</i> <i>RPS9</i> <i>EEF1A1</i> <i>RPS15</i> <i>RPS23</i> <i>B2M</i> <i>UXT</i> <i>HPRT1</i> <i>RPL4</i>										
coeff. of corr. [r]	0.969	0.994	0.984	0.816	0.938	0.987	0.994	0.829	0.985	0.986
p-value	0.001	0.001		0.001	0.001			0.001	0.001	