Electronic Supplementary Material (ESI) for Molecular BioSystems.
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Table S1 Enriched biological process terms of gene ontology

Comparison	Regulation	Number of regulated genes	Functional Cluster		Gene ontology class	Number of regulated genes in GO class	Enrichment P-value	Regulated genes in Functional Cluster
			ID	Enrichment score				
B19A6-S-14 vs. B19A6-S-41	Up	2	---	---	---	---	---	---
	Down	11	---	---	---	---	---	---
B19A6-U-13 VS B19A6-U-39	Up	12	---	---	---	---	---	---
	Down	104	1	1.79	sterol metabolic process	5	0.0012	Abca1, Nsdhl, Aldh1a1, Cat, Ppap2a, Hmgcs1, Sc5d
					cholesterol metabolic process	4	0.0090	
					sterol biosynthetic process	3	0.0140	
					steroid metabolic process	5	0.0170	
					steroid biosynthetic process	3	0.0700	
					lipid biosynthetic process	5	0.0970	
			2	1.33	macromolecule catabolic process	10	0.0180	Cd36, Edem3, Ranbp2, Adam10, Cast, C3, Mmp19, Metap2, Pja2, Pias2, Ubr2, Ubr3, Usp32
					protein catabolic process	9	0.0200	
					cellular macromolecule catabolic process	9	0.0320	
					proteolysis involved in cellular protein catabolic process	8	0.0440	
					cellular protein catabolic process	8	0.0460	
					ubiquitin-dependent protein catabolic process	4	0.0550	
					modification-dependent macromolecule catabolic process	7	0.0900	
					modification-dependent protein catabolic process	7	0.0900	
					proteolysis	11	0.0980	
			3	1.32	glycosaminoglycan metabolic process	3	0.0250	Chst12, Dcn, Gns
					aminoglycan metabolic process	3	0.0400	
					polysaccharide metabolic process	3	0.1100	
			4	1.2	mRNA transport	3	0.0550	G3bp2, Ranbp2, Nxf7
					establishment of RNA localization	3	0.0620	
					RNA transport	3	0.0620	
					nucleic acid transport	3	0.0620	
					RNA localization	3	0.0630	
					nucleobase, nucleoside, nucleotide and nucleic acid transport	3	0.0750	

Table S2. Enriched KEGG pathways

Comparison	**Regulation**	**Number of regulated genes**	**KEGG pathway**	**Number of regulated genes in pathway**	**Enrichment P-value**
B19A6-S-14 vs. B19A6-S-41	Up	2	---	---	---
	Down	11	---	---	---
B19A6-U-13 vs. B19A6-U-39	Up	12	---	---	---
	Down	104	Fatty acid metabolism	5	0.00034
			Steroid biosynthesis	3	0.0021
			Drug metabolism - cytochrome P450	4	0.0026
			Fat digestion and absorption	3	0.0037
			Valine, leucine and isoleucine degradation	4	0.0050
			Tryptophan metabolism	3	0.0052

Figure S1

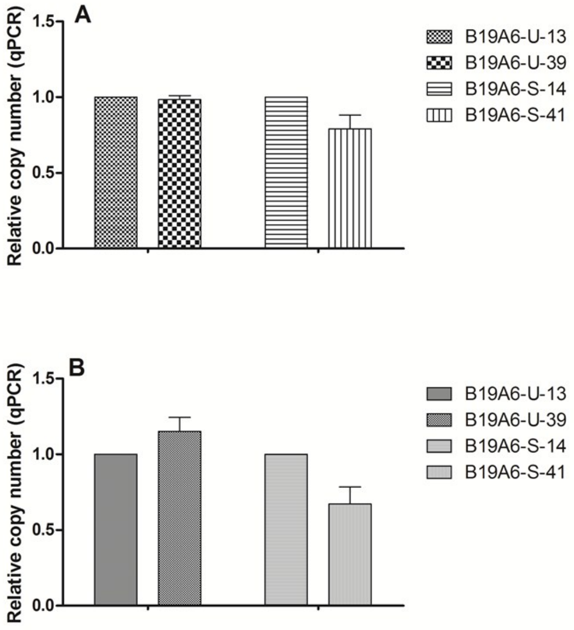

Fig. S1 Relative gene copy number of the unstable cell line (B19A6-U-13 and B19A6-U-39) and the stable cell line (B19A6-S-14 and B19A6-S-41). GAPDH was used for normalization (a). β-actin was used for normalization (b)

Figure S2

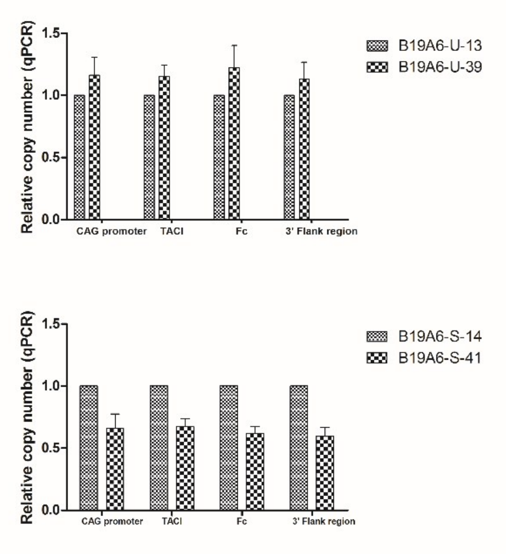

Fig. S2 Changes in of gene copy number of the CAG promoter, TACI, Fc and downstream flanking sequence of Fc in high generation cells relative to low generation cells. β - actin was used for normalization.