Suppl. Table 4. Signal transduction pathways that are significantly differentially regulated ($p < 0.05$, corrected for multiple testing) between UKF-NB-4^{HiGCV} and UKF-NB-4 cells but not between UKF-NB-4^{Hi} and UKF-NB-4 cells as identified by PANTHER pathway analysis (www.pantherdb.org).

Pathway (number of genes annotated in the pathway)	UKF-NB-4^{HiGCV} vs. UKF-NB-4 (rank[1]/p-value/ genes affected[2])	UKF-NB-4^{Hi} vs. UKF-NB-4 (rank[1]/p-value/ genes affected[2])
Axon guidance mediated by semaphorins (46)	10/ 3.62×10^{-3}/ 33	19/ 8.72×10^{-2}/ 29
Metabotropic glutamate receptor group II pathway (54)	14/ 1.52×10^{-2}/ 35	18/ 6.48×10^{-2}/ 33
FAS signaling pathway (36)	15/ 2.27×10^{-2}/ 26	21/ 1.20×10^{-1}/ 24
Muscarinic acetylcholine receptor 1 and 3 signaling pathway (62)	17/ 4.77×10^{-2}/ 37	32/ 5.73×10^{-1}/ 33

[1] Pathways were ranked by their p-values with the lowest p-value being rank 1

[2] Pathway genes differentially expressed between the data sets ($FDR < 0.05$). In total, 25,431 genes were annotated in the PANTHER reference list. 8,832 genes were differentially expressed between UKF-NB-4^{Hi} and UKF-NB-4, 8,873 between UKF-NB-4^{HiGCV} and UKF-NB-4.