

Table 12. Canonical signaling and metabolic pathways enriched among the differentially expressed progenitor-specific mGEP transcripts after infection with Kx1 or Kx2.

Top seven statistically significant canonical signaling and metabolic pathways enriched among differentially expressed mGEP transcripts after infection with Kx1.			
Canonical Pathway	p-value	Gene symbols	Affymetrix probe set ID's
PPAR Signaling	9.21E-03*	Map3k14, Ikbke, Cited2, Map3k7ip1, Ppargc1a	1434364_at, 1417813_at, 1421267_a_at, 1426898_at, 1434100_x_at
TGF-β Signaling	3.3E-02*	Pias4, Smad7, Tgfb2, Map3k7ip1	1418861_at, 1423389_at, 1450922_a_at, 1426898_at
N-Glycan Biosynthesis	3.45E-02*	Fut8, Alg12, Mgat2	1460319_at, 1424818_at, 1426350_at
p38 MAPK Signaling	3.66E-02*	Tgfb2, Eef2k, Map3k5, Map3k7ip1	1450922_a_at, 1437829_s_at, 1421340_at, 1426898_at
Lysine Degradation	7.78E-02*	Aldh2, Dot1l	1434987_at, 1457268_at
Ephrin Receptor Signaling	8.42E-02*	Rgs3, Cfl2, Map4k4, Efnb3, Epha2	1425296_a_at, 1418066_at, 1448050_s_at, 1423085_at, 1421151_a_at
Death Receptor Signaling	8.92E-02*	Map3k14, Ikbke, Map3k5	1434364_at, 1417813_at, 1421340_at
Top seven statistically significant canonical signaling and metabolic pathways enriched among differentially expressed mGEP transcripts after infection with Kx2.			
Canonical Pathway	p-value	Gene symbols	Affymetrix probe set ID's
Xenobiotic Metabolism Signaling	1.7E-02*	Abcb1, Aldh1l2, Cyp3a7, Cat, Aldh3b1	1419758_at, 1436119_at, 1419523_at, 1416429_a_at, 1452301_at
Amyloid Processing	3.11E-02*	Prkar2b, Bace1	1430640_a_at, 1421824_at
Tryptophan Metabolism	5.21E-02*	Acat2, Cyp3a7, Cat	1435630_s_at, 1419523_at, 1416429_a_at
Aminophosphonate Metabolism	5.31E-02*	Chpt1	1426146_a_at
GM-CSF Signaling	5.87E-02*	Runx1, Jak2	1422864_at, 1421065_at
Synthesis and Degradation of Ketone Bodies	6.78E-02*	Acat2	1435630_s_at
Arginine and Proline Metabolism	8.96E-02*	Nos1, Odc1	1438483_at, 1427364_a_at

* indicates a p-value <0.1 in a right-tailed Fisher's Exact Test. Red indicates up-regulated genes upon infection and green indicates down-regulated transcripts. For fold changes see Tables 10 and 11.