Type of file: table
Label: Table S1cmbPCMR
Filename: 2011-1015-LIBPB-405 TableS1cmbPCMR.doc

Taqman Expression Assays Used

Gene Name	Assay ID
Human	
ABCB5	Hs00698751_m1
ACTB	4333762F
AXIN2	Hs01063168_m1
BCL2	Hs00153350_m1
BMP2	Hs00154192_m1
BMP4	Hs00370078_m1
BMPR1A	Hs01034913_g1
BMPR1B	Hs00176144_m1
BMPR2	Hs00176148_m1
CDH1	Hs01013953_m1
CDH2	Hs00983062_m1
CDH5	Hs00174344_m1
CDH6	Hs00191832_m1
CDH7	Hs00189053_m1
CD133	Hs01009250_m1
CXCR4	Hs00237052_m1
EDN1	Hs01115919_m1
EDN2	Hs00266516_m1
EDN3	Hs00171177_m1
EDNRA	Hs03988672_m1
EDNRB	Hs00240747_m1
EFNB2	Hs00187950_m1
EPHA2	Hs00171656_m1
EPHA4	Hs00953178_m1
EPHB2	Hs01031827_m1
EPHB4	Hs00174752_m1
ERBB2	Hs01001599_m1
ERBB3	Hs00951455_m1
ERBB4	Hs00171783_m1
FGF2	Hs00266645_m1
FGFR1	Hs00241111_m1
FOXD3	Hs00255287_s1
GAPDH	4333764F
GLI1	Hs00171790_m1
GJA1	Hs00748445_s1
KDR	Hs00911700_m1
KIT	Hs00174029_m1
KITLG	Hs00241497_m1
KLF4	Hs00358836_m1
LRP5	Hs00182031_m1
LRP6	Hs00233935_m1
MLANA	Hs00194133_m1
MITF	Hs01117294_m1
MMP2	Hs00234422_m1
MSX1	Hs00427183_m1

MYB	Hs00193527_m1
MYC	Hs00153408_m1
NANOG	Hs02387400_g1
NEDD9	Hs00610590_m1
NES	Hs00707120_s1
NOTCH4	Hs00965897_m1
NRP1	Hs00826121_m1
NRP2	Hs00187290_m1
OCT4	Hs00742896_s1
PAX3	Hs00240950_m1
PLXNA1	Hs00413698_m1
PLXNA2	Hs00257877_m1
PLXNA4	Hs00326001_m1
RHOA	Hs01051295_m1
ROBO1	Hs00268049_m1
ROBO2	Hs00326067_m1
RPLP0	4333761F
SIP1	Hs00186207_m1
SHH	Hs00179843_m1
SNAI2	Hs00161904_m1
SNAI1	Hs00195591_m1
SOX2	Hs01053049_s1
SOX9	Hs00165814_m1
SOX10	Hs00366918_m1
TUBB3	Hs00964965_m1
TWIST1	Hs00361186_m1
WNT3A	Hs01055707_m1
ZEB1	Hs00611018_m1
Chick	
18S	4352930E
AQP1	Gg03358589_m1
CFC1B	Gg03338500_m1
CXCR4	AI5IOS0
EPHA2	AIMSF5V
GAPDH	Gg03346982_m1
KRT15	Gg03345598_m1
KRT19	Gg03348102_m1
MITF	Gg03348224_m1
NEDD9	Gg03310488_m1
NRP1	Gg03371276_m1
NRP2	Gg03364413_m1
RHOA	Gg03338538_m1
RHOB	Gg03339342_s1
SNAI2	Gg03333502_m1

Type of file: table
Label: Table S2cmbPCMR
Filename: 2011-1015-LIBPB-405 TableS2_resultsSummary_PCMR_cmb.doc

Table S2. A Summary of the Gene Expression Comparisons Performed

Comparison	Rationale	Summary of Findings	Figures
transplanted cells to cultured cells	evaluate effects of embryonic neural crest microenvironment on transplanted cells	c8161 cells showed an induction rate of 40%; c81-61 induction rate was significantly lower (8%); primary melanocytes showed no gene induction	**Fig. 2**
migrating cells to non-migrating cells (c8161)	compare/contrast the neural crest migration program with melanoma migration to identify genes that may promote or inhibit melanoma migration	some genes implicated in neural crest migration are down-regulated, suggesting that migrating melanoma cells do nor precisely replicate the neural crest program	**Fig. 3B**
migrating lead cells to trailing cells (c8161)	determine effects of changing micro-environments on migrating melanoma cells	down-regulation of EMT and early migration markers (*MYB, NEDD9*) and the down-regulation of pluripotency markers (*SOX2*, *NANOG*, and *NES*) suggest dynamic gene regulation in response to changing micro-environmental cues	**Fig. 3B**
c8161 to host chick neural crest	directly compare/contrast gene expression in migrating c8161 cells compared to the chick neural crest cells	some genes follow similar expression patterns while others do not, suggesting absolute adherence to the neural crest program is not a requirement for c8161 migration	**Fig. 4**
c8161 (aggressive melanoma) to primary melanocytes	evaluate which aspects of the neural crest program are up-regulated in c8161 melanoma cells	c8161 cells aberrantly re-express neural crest-related genes associated with EMT and migration, while silencing genes associated with melanocyte differentiation	**Fig. 5A,B**
c8161 (aggressive melanoma) to c81-61 (poorly aggressive melanoma)	evaluate which aspects of the neural crest program are up-regulated in c8161 melanoma cells	14 genes displayed moderate expression changes in c81-61 cells compared to the overall significant changes observed in c8161 cells, suggesting their possible use as prognostic indicators	**Fig. 5C**