

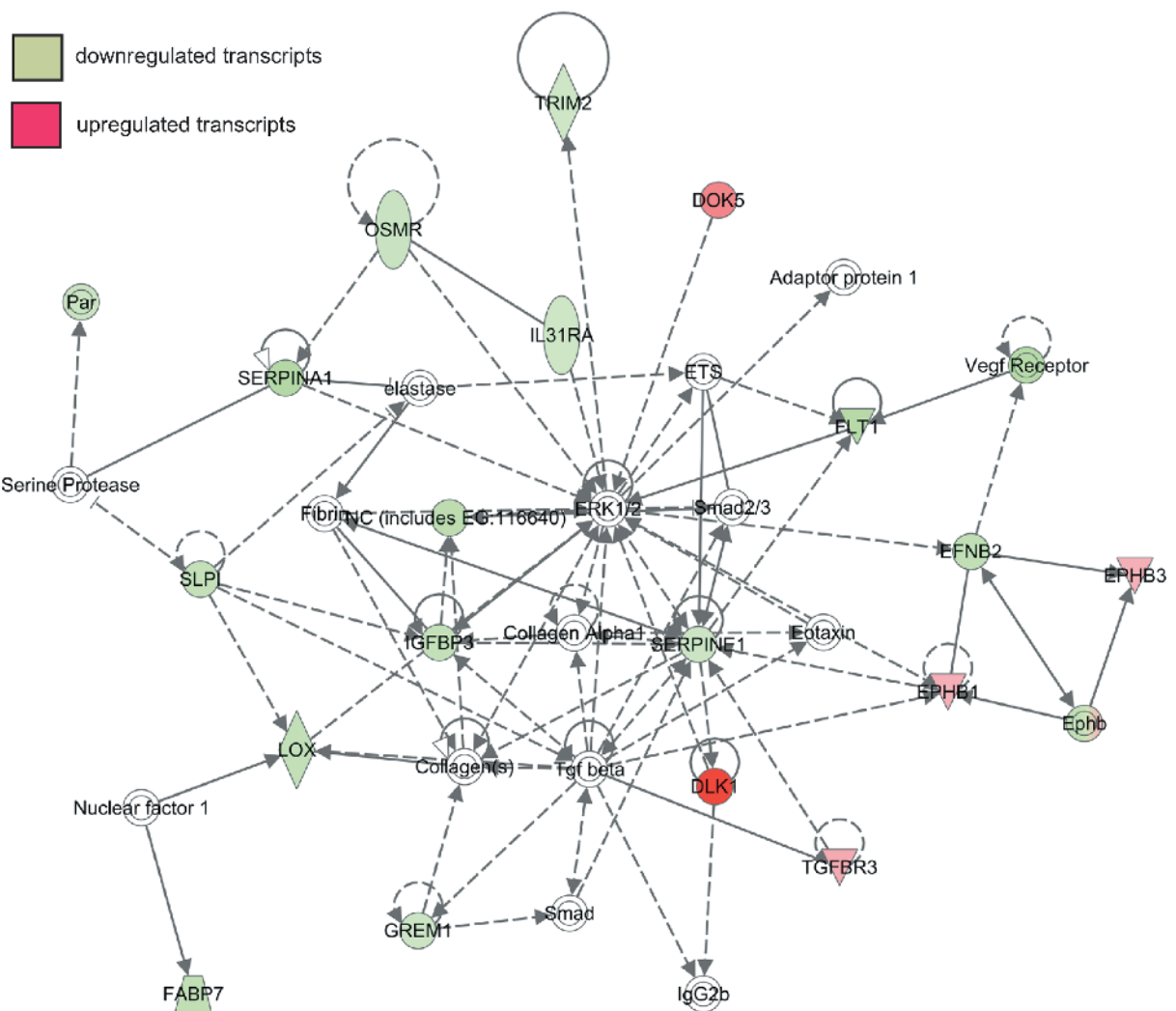
**Figure W1.** CD271 is enriched in tumor sphere culture and highly self-renewing MB subpopulations from multiple cell lines. (A, B) D283 parental adherent cultures grown in 10% FBS (left panels) do not express CD271 but exhibit high levels of CD133 expression by flow cytometry. Following culture as tumor spheres in BTPC conditions, D283 begin to exhibit a small but consistent significant subpopulation of CD271+ cells. CD133 expression is significantly decreased. Insets: live cell-only controls;  $N = 5$  independent experiments. (C, D) CD271 levels (C) are significantly higher in t-hENs relative to normal hENs. CD133 is unchanged t-hENs *versus* hENs (D);  $N = 3$  independent experiments.

**A****Diseases and Disorders**

Name	p-value	# Molecules
Cancer	6.24E-18 - 1.28E-04	114
Neurological Disease	3.71E-15 - 1.12E-04	82
Psychological Disorders	3.71E-15 - 2.15E-05	50
Connective Tissue Disorders	6.07E-15 - 9.81E-06	51
Inflammatory Disease	6.07E-15 - 4.41E-05	62

**Molecular and Cellular Functions**

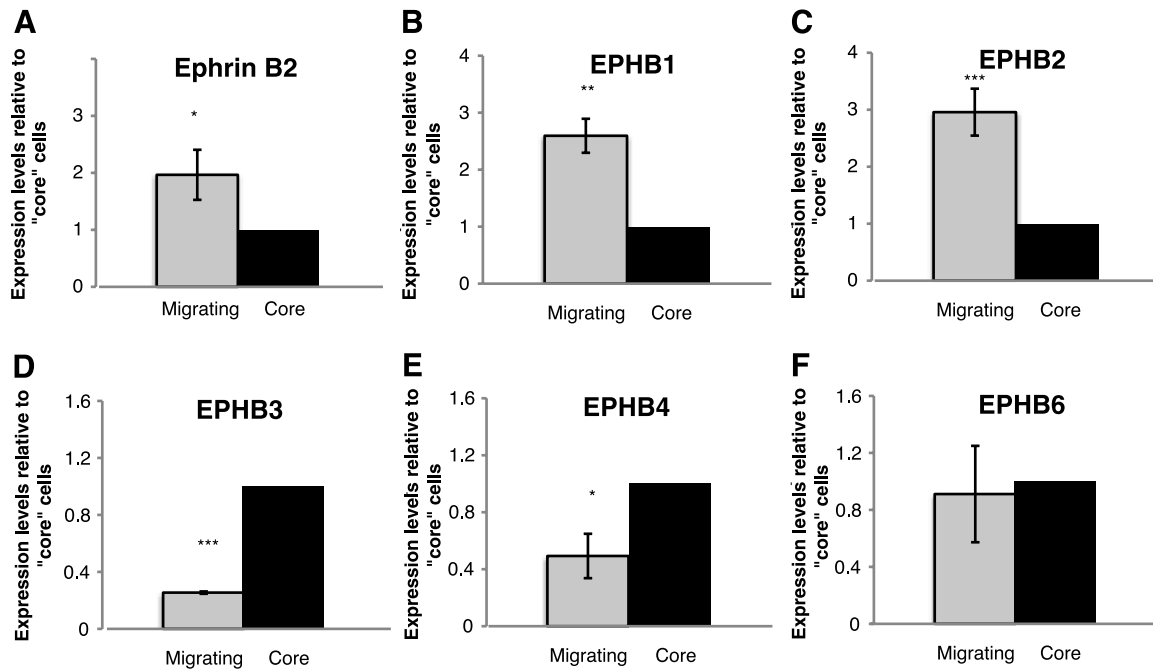
Name	p-value	# Molecules
Cellular Movement	1.17E-22 - 1.15E-04	84
Cell-To-Cell Signaling and Interaction	3.95E-15 - 1.20E-04	72
Cellular Growth and Proliferation	1.95E-13 - 8.68E-05	97
Cell Death and Survival	1.95E-10 - 1.28E-04	81
Cellular Development	2.39E-10 - 1.28E-04	97

**B**

**Figure W2.** Top diseases, molecular/cellular functions, and networks dysregulated in higher *versus* lower self-renewing MB tumor spheres. (A) Top diseases (upper panel) and molecular and cellular functions (lower panel) dysregulated in higher self-renewing *versus* lower self-renewing tumor spheres. (B) Top dysregulated cellular network consisting of molecules associated with cellular movement. Note the presence of EPHB receptors and ephrin B2 ligand. Shaded green areas denote transcripts that are significantly downregulated and red areas denote significantly upregulated transcripts in higher self-renewing *versus* lower self-renewing tumor spheres.

**Table W4.** Primer Sequences Used for qPCR Reactions.

Gene	Forward Sequence	Reverse Sequence	Product (bp)
<i>Ephrin B2</i>	5'-GTT CGA CAA CAA GTC CCT TTG-3'	5'-CTG AAG CAA TCC CTG CAA ATA-3'	123
<i>EPHB1</i>	5'-GGA AAC GGG CTT ATA GCA AAG-3'	5'-TCG TAA GTG AAG GGG TCA ATG-3'	110
<i>EPHB2</i>	5'-GAC TCC ACT ACA GCG ACT GCT-3'	5'-TCT CAT CGT AGC CAC TCA CCT-3'	82
<i>EPHB3</i>	5'-TTG TCA ATA CCC TGG ACA AGC-3'	5'-AAT CAC CAA CTG TCG TGA AGG-3'	135
<i>EPHB4</i>	5'-AAT GTC ACC ACT GAC CGA GAG-3'	5'-ATT TGA CCT CGT AGT CCA GCA-3'	136
<i>EPHB6</i>	5'-AAT AGC CAC TTG GTG TGC AAG-3'	5'-CAT GAG TAT CCC AAA GCT CCA-3'	144
<i>Otx2</i>	5'-GAG GTG GCA CTG AAA ATC AAC-3'	5'-TCT TCT TTT TGG CAG GTC TCA-3'	136
<i>Sox1</i>	5'-TGG ATG AAG GAC AAA GAC CAG-3'	5'-GTT TTG GTT CAG CGA TTG TGT-3'	116
<i>βIII tubulin</i>	5'-GGC CTT TGG ACA TCT CTT CA-3'	5'-TCG CAG TTT TCA CAC TCC TTC-3'	147



**Figure W3.** The Eph-ephrin signaling pathway is dysregulated in migrating *versus* core MB cells. (A–F) qPCR analysis of the ephrin B2 ligand and EPHB1, B2, B3, B4, and B6 receptors in "core" *versus* "migrating" Daoy MB cells. Note the up-regulation of ephrin B2, EPHB1, and EPHB2 and significant down-regulation of EPHB3 and EPHB4 in "migrating" *versus* "core" cells. Error bars, SEM; \* $P < .05$ , \*\* $P < .01$ , \*\*\* $P < .001$ .