#### SUPPLEMENTARY FIGURES AND TABLES



**Supplementary Figure S1: The subgroup specific expression of PDGFRa and PDGFRb in primary MB.** Boxplot showing PDGFRa and PDGFRb expression in three independent, non-overlapping gene expression profiling studies derived from Toronto (a/b), Amsterdam (c/d), and Memphis (e/f).



Supplementary Figure S2: The effect of PDGFR siRNA on Daoy cell invasion. A multi-well chamber-based assay was used to access the ability of cells to migrate through a membrane coated with matrigel. In the presence of control or PDGFR siRNAs,  $2.5 \times 10^4$  Daoy cells were seeded in the upper chamber. 24 h later, cells that invaded or migrated to the lower chamber were labeled with Calcein AM. The labeled cells were measured for fluorescence with a fluorescence plate reader and set at an excitation wavelength of 485 nm and an emission wavelength of 520 nm. \*\*p < 0.05 (paired *T* test, sample vs. control)



Supplementary Figure S3: The representative figures of co-targeting PDGFR and c-MYC on MB cell migration. Daoy cells were treated with siRNAs for PDGFR $\beta$  and c-MYC and the specific inhibitors of PDGFR $\beta$  and c-MYC for 36 h. Treated cells were then detached and re-distributed in equal amounts in a 48-well plate before a linear wound was made. The images were captured immediately after that an artificial wound was made at 0th h and also at 24th h. The experiments were repeated for 3 times. The data are representative images for each condition.



Supplementary Figure S4: The representative figures of miR-1280 inhibitors and JAG2 siRNA on MB cell migration. PDGFR $\beta^{\text{KD}}$  Daoy cells were treated with either inhibitor of miR-1280, or JAG2 siRNA for 36 h and then detached and re-distributed in equal amounts in a 48-well plate before a linear wound was made. The images were captured immediately after that an artificial wound was made at 0th h and also at 24th h. The experiments were repeated for 3 times. The data are representative images for each condition.

# Supplementary Table S1: The *p* values of subgroup comparisons for the Heidelberg dataset in Figure 1 PDGFRα – Boston cohort

Comparison	Posthoc test ( <i>p</i> -value)
NCB vs WNT	0.06
NCB vs SHH	0.01
NCB vs Group 3	1.60e-09
NCB vs Group 4	3.70e-04
WNT vs SHH	0.83
WNT vs Group 3	1.70e-12
WNT vs Group 4	1.20e-08
SHH vs Group 3	1.90e-24
SHH vs Group 4	8.80e-19
Group 3 vs Group 4	0.02

## **PDGFRβ** – Boston cohort

Comparison	Posthoc test (p-value)
NCB vs WNT	0.10
NCB vs SHH	1.4e-03
NCB vs Group 3	0.13
NCB vs Group 4	0.24
WNT vs SHH	0.17
WNT vs Group 3	0.70
WNT vs Group 4	0.41
SHH vs Group 3	8.2e-03
SHH vs Group 4	4.3e-04
Group 3 vs Group 4	0.51

## PDGFRα – Heidelberg cohort

Comparison	Posthoc test (p-value)
WNT vs SHH	0.85
WNT vs Group 3	3.7e-03
WNT vs Group 4	7.2e-04
SHH vs Group 3	1.6e-03
SHH vs Group 4	1.9e-04
Group 3 vs Group 4	0.33

### **PDGFRβ** – Heidelberg cohort

Comparison	Posthoc test (p-value)
WNT vs SHH	2.6e-06
WNT vs Group 3	0.48
WNT vs Group 4	0.31
SHH vs Group 3	6.5e-04
SHH vs Group 4	2.6e-05
Group 3 vs Group 4	0.98

Supplementary Table S2: Pathway analysis of genes co-expressed with PDGFRα in MB tumors (\*indicates genes in the pathways that are specific for PDGFRα.)

Supplementary Table S3: Pathway analysis of genes co-expressed with PDGFRβ in MB tumors (\*indicates genes in the pathways that are specific for PDGFRβ.)

Supplementary Table S4: Pathway analysis of genes co-expressed with c-MYC in MB tumors