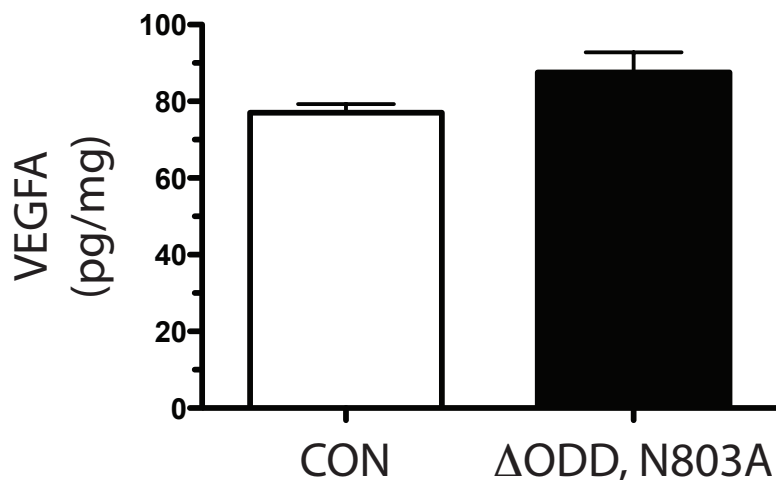
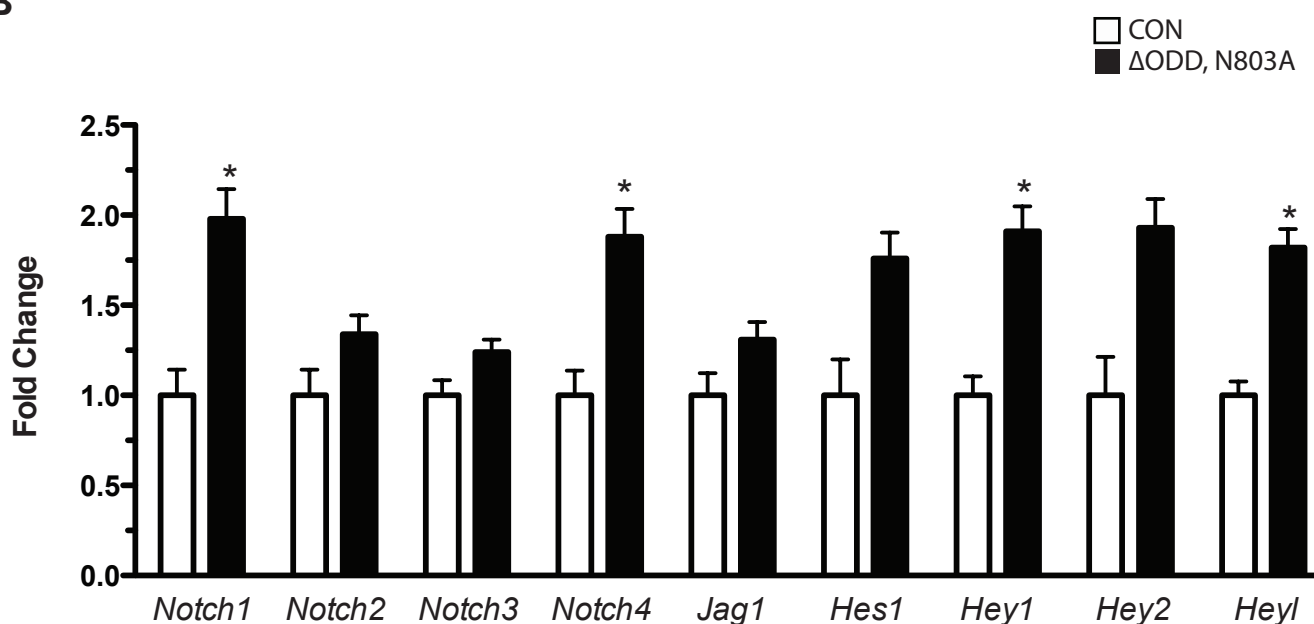


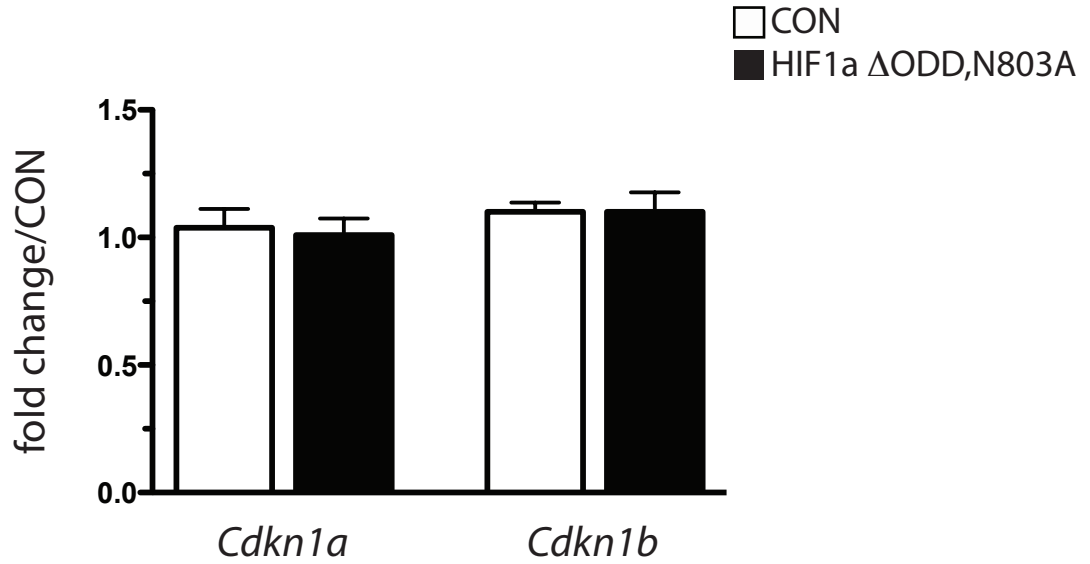
Table I. Taqman primer probe sets

<i>Aldoc</i>	(Mm01298110_g1)
<i>Arnt</i>	(Mm00507836_m1)
<i>Bhlhe40</i>	(Mm00478593_m1)
<i>Car4</i>	(Mm00483021_m1)
<i>Car9</i>	(Mm00519870_m1)
<i>Ccl21a</i>	(Mm03646971_gH)
<i>Cdkn1a</i>	(Mm00432448_m1)
<i>Cdkn1b</i>	(Mm00438168_m1)
<i>Cox4i2</i>	(Mm00438289_g1)
<i>Epas1</i>	(Mm00438717_m1)
<i>Foxc2</i>	(Mm00546194_s1)
<i>Hey1</i>	(Mm00468865_m1)
<i>Hey2</i>	(Mm00469280_m1)
<i>Heyl</i>	(Mm00516555_m1)
<i>HIF1a</i>	(Mm00468875_m1)
<i>Hif3a(Nepas)</i>	(Mm00469373_m1)
<i>Hk2</i>	(Mm00443385_m1)
<i>Ldha</i>	(Mm00495282_g1)
<i>Lpcat1</i>	(Mm00628177_m1)
<i>Notch1</i>	(Mm00435245_m1)
<i>Notch3</i>	(Mm03053620_s1)
<i>Notch4</i>	(Mm00440536_g1)
<i>Pdk1</i>	(Mm00554306_m1)
<i>Pdpm</i>	(Mm00494716_m1)
<i>Pgk1</i>	(Mm00435617_m1)
<i>Prox1</i>	(Mm00435969_m1)
<i>Serpine1</i>	(Mm00435860_m1)
<i>Sftpb</i>	(Mm00455681_m1)
<i>Sftpc</i>	(Mm00488144_m1)
<i>Slc2a1</i>	(Mm01192270_m1)
<i>Slc2a3</i>	(Mm03053806_s1)
<i>Sox17</i>	(Mm00488369_s1)
<i>Sox18</i>	(Mm00656049_gH)
<i>Vegfa</i> all isoforms	(Mm00437304_m1)
<i>Vegfa120</i>	(custom ordered – probe spans exon 5/8 junction)
<i>Vegfa164</i>	(custom ordered – probe spans exon 5/7 junction)
<i>Vegfa188</i>	(custom ordered – probe spans exon 6/7 junction)
<i>Vegfc</i>	(Mm01202432_m1)

**A****B**

Supplementary Figure 1 – Analysis of VEGFA protein levels and Notch signaling components in HIF1a  $\Delta$ ODD,N803A lungs. A) VEGFA protein levels were not increased in E15.5 HIF1a  $\Delta$ ODD,N803A whole lung homogenates compared to CON animals. n=4-6 samples per genotype. \* $p < 0.05$  vs. CON. B) qPCR analyses demonstrates increased expression of distinct Notch signaling pathway genes in HIF1a  $\Delta$ ODD,N803A lungs. n=5 samples per genotype. \* $p < 0.05$  vs. CON.

A



Supplementary Figure 2 – Analysis of Cdkn1a and Cdkn1b mRNA levels in HIF1a  $\Delta$ ODD,N803A lungs. A) qPCR analyses demonstrates similar levels of Cdkn1a and Cdkn1b mRNA in HIF1a  $\Delta$ ODD,N803A and littermate control lungs at E14.5. n=4-6 samples per genotype.