

Supplemental Tables

Supplemental Table 1. Examples of hypoxia-inducible genes, whose expression levels are reversed by propranolol

| Illumina ID | Gene Symbol | Gene Name |
|--------------|--------------|---|
| ILMN_2135798 | NR2C2AP | nuclear receptor 2C2-associated protein |
| ILMN_1733863 | Fam100a | family with sequence similarity 100, member A |
| ILMN_2325168 | ARRB1 | arrestin, beta 1 |
| ILMN_1705753 | C3orf26 | chromosome 3 open reading frame 26 |
| ILMN_1704571 | FAM53B | family with sequence similarity 53, member B |
| ILMN_1686664 | MT2A | metallothionein 2A |
| ILMN_1776147 | C21orf59 | chromosome 21 open reading frame 59 |
| ILMN_1660554 | VWA1 | von Willebrand factor A domain containing 1 |
| ILMN_2409642 | Tro | trophinin |
| ILMN_1775823 | POFUT2 | protein O-fucosyltransferase 2 |
| ILMN_1766264 | PI16 | peptidase inhibitor 16 |
| ILMN_2205350 | LOC100131149 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4; similar to HSPC125 |
| ILMN_2205350 | Ndufa4 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4; similar to HSPC125 |
| ILMN_1698020 | DLC1 | deleted in liver cancer 1 |
| ILMN_1803772 | POLD4 | polymerase (DNA-directed), delta 4 |
| ILMN_1702363 | Sulf1 | sulfatase 1 |
| ILMN_2391150 | FILIP1L | filamin A interacting protein 1-like |
| ILMN_2126832 | Sec24a | SEC24 family, member A (S. cerevisiae) |
| ILMN_1767542 | THAP10 | THAP domain containing 10 |
| ILMN_2133799 | Acat2 | acetyl-Coenzyme A acetyltransferase 2 |
| ILMN_1682015 | GAL | galanin prepropeptide |
| ILMN_1776157 | SEPT4 | septin 4 |
| ILMN_1705814 | KRT80 | keratin 80 |
| ILMN_1743402 | Six4 | SIX homeobox 4 |
| ILMN_1844593 | MST131 | MSTP131 |
| ILMN_2104356 | COL1A2 | collagen, type I, alpha 2 |
| ILMN_1675612 | BLCAP | bladder cancer associated protein |
| ILMN_1779257 | CD40 | CD40 molecule, TNF receptor superfamily member 5 |
| ILMN_1755711 | C17orf68 | chromosome 17 open reading frame 68 |

Supplemental Table 2. KEGG pathway analysis of transcripts reversed by propranolol under hypoxia

| KEGG Pathway Term | Count | $-\log(P\text{-Value})$ | $P\text{-Value}$ | Genes |
|-------------------------------------|-------|-------------------------|------------------|--|
| Focal adhesion | 16 | 3.791795423 | 1.62E-04 | <i>ACTB, COL4A2, COL3A1, MYLK2, CAPN2, BIRC2, MYL9, ACTG1, CCND1, LAMA3, ITGA6, CCND2, ITGAV, COL1A2, PDGFC, THBS1</i> |
| ECM-receptor interaction | 8 | 2.270517195 | 0.005363926 | <i>COL4A2, LAMA3, ITGA6, ITGAV, COL3A1, COL1A2, THBS1, SDC2</i> |
| Small cell lung cancer | 8 | 2.270517195 | 0.005363926 | <i>CCND1, COL4A2, LAMA3, ITGA6, ITGAV, RARB, BIRC2, MYC</i> |
| Glycolysis / Gluconeogenesis | 6 | 1.745700858 | 0.017959703 | <i>TPI1, LDHA, LOC100133042, PFKP, BPGM, GAPDH, GAPDHL6, ALDH3A2, TPI1P1</i> |
| NOD-like receptor signaling pathway | 6 | 1.689516197 | 0.020440137 | <i>IL8, MAPK14, CXCL2, RIPK2, TNFAIP3, BIRC2</i> |
| p53 signaling pathway | 6 | 1.534734574 | 0.029192106 | <i>CCND1, CCND2, GADD45G, GADD45B, THBS1, IGFBP3</i> |
| Dilated cardiomyopathy | 7 | 1.528905604 | 0.029586555 | <i>ACTG1, ACTB, ADCY4, ITGA6, ITGAV, TPM1, TGFB2</i> |
| Glutathione metabolism | 5 | 1.420342093 | 0.037989004 | <i>ODC1, G6PD, GGCT, IDH1, MGST1</i> |
| Arginine and proline metabolism | 5 | 1.34116415 | 0.045586458 | <i>ODC1, ASS1, NAGS, AMD1, ALDH3A2</i> |
| Hypertrophic cardiomyopathy (HCM) | 6 | 1.18386797 | 0.065483522 | <i>ACTG1, ACTB, ITGA6, ITGAV, TPM1, TGFB2</i> |
| Vascular smooth muscle contraction | 7 | 1.180002862 | 0.066068909 | <i>KCNMA1, ADCY4, CALD1, MYLK2, PLCB1, ITPR3, MYL9</i> |
| hsa05219:Bladder cancer | 4 | 1.040051898 | 0.091190186 | <i>CCND1, IL8, THBS1, MYC</i> |
| Regulation of actin cytoskeleton | 10 | 1.008811446 | 0.097991534 | <i>ACTG1, ACTB, ITGA6, ITGAV, SSH2, MYLK2, RRAS, PDGFC, MYH9, MYL9</i> |
| Cell cycle | 7 | 1.001445768 | 0.099667653 | <i>CCND1, CCND2, GADD45G, PCNA, GADD45B, MYC, TGFB2</i> |

Supplemental Table 3. Percent phosphorylation of β_2 AR sites at 21% or 2% oxygen, or with isoproterenol (ISO)

| Site | Peptide | % Phosphorylated | | | Fold change | |
|----------------|------------------------------|--------------------|-------------------|-------------|-------------------|----------|
| | | 21% O ₂ | 2% O ₂ | ISO | 2% O ₂ | ISO |
| S246 | FHVQNLpSQVEQDGR | 8±2.3 | 4.0±1.6 | 4.6±1.7 | ↓ 2.0 | ↓ 1.7 |
| S262 | RSpSKFCLK | 99±0 | 98±0.6 | 98±1.4 | NC | NC |
| S261+S262 | RpSpSKFCLK | 0.45±0.29 | 0.53±0.19 | 1.6±0.42 | NC | ↑ 4.9 |
| S346 | RRSpSLKAYGNGYSSNGNTGEQSGYHV | 1.02±0.78 | 1.53±1.72 | 0.65±0.92 | NC | NC |
| S355,S356 | AYGNGYpSpSNGNTGEQSGYHVEQEK | 0.098±0.00 | 0.16±0.04 | 15±0.6 | ↑ 1.6 | ↑ 153 |
| S355,S356,T360 | AYGNGYpSpSNGNpTGEQSGYHVEQEK | 0 | 0 | 0.39±0.25 | NI | ISO only |
| S355,S356,S364 | AYGNGYpSpSNGNTGEQpSGYHVEQEK | 0 | 0 | 0.079±0.006 | NI | ISO only |
| S396 | LLCEDLPGTEDFVGHQGTVPpSDNIDSQ | 0.045±0.06 | 0.3±0.2 | 0.3 | ↑ 6.7 | ↑ 6.7 |

NC, no change; NI, not identified

[¶] Identified in two of three independent experiments.

Data are mean±S.D.