**Figure S1.** Validation the IHC protocol for LDHB using FFPE MDAMB231 cells with stable knockdown of LDHA or LDHB. Reduced staining for LDHB was detected only in the LDHB knockdown line. Control cells were infected with a non-silencing shRNA.
**Figure S2.** LDHB, when present, substantially contributed to the total LDH activity in cell lines. **A**, non-denatured electrophoresis, 10 μg/well. LDH activity was determined for each LDH tetramer after separation by non-denatured electrophoresis (10 μg/well). The HCC70 cell line expressed a faster migrating LDHA, presumably caused by a missense mutation in *LDHA* p.K261N (http://www.broadinstitute.org) **B**, quantification of LDH activity using ImageJ and the gel from **A**. LDH5 = LDHAx4; LDH4 = LDHAx3,LDHB; LDH3 = LDHAx2,LDHBx2; LDH2 = LDHA,LDHBx3; LDH1 = LDHBx4
**Figure S3.** A, verification of LDHA or LDHB knockdown by LDH activity in stable isogenic cell lines, MDAMB231 and HCC1937. Non-denatured electrophoresis, 10 μg/well. NS = non-silencing shRNA control. B, LDHA or LDHB knockdown in MDAMB231 and HCC1937 breast cancer cell lines increased ATP-synthase derived oxygen consumption (OCR\textsubscript{ATP}) but did not alter ECAR values with the exception of the LDHB knockdown in HCC1937 cells. *, \( P < 0.05 \); ***, \( P < 0.001 \)
Figure S4. LDHB association with PAM50 intrinsic subtype in primary breast cancers. A, LDHB mRNA expression separated by intrinsic subtype: Perou [GSE10893] (8). The basal-like group had significantly higher expression of LDHB as compared to the HER2 or luminal A/B groups, *P < .001. LDHB in tumors with normal-like gene expression (not shown) was intermediate between luminal A/B and the basal-like groups, *P < .001. B, LDHB mRNA expression separated by intrinsic subtype: Pawitan [GSE1456] (9). The ability of LDHB to predict PAM50 subtype within Perou and Pawitan clinical groups was not determined because clinical ER/PR/HER2 status was not available for these cohorts. LDHB mRNA expression separated by subtype for HER2-negative disease by IHC/FISH: C, MAQC; D, MDACCSS; and E, XeNA. PAM50 HER2 group was not plotted for MAQC (N = 1). *, *P < .05; **, *P < .01; ***, *P < .001.
Figure S5. High LDHB was associated with triple-negative breast cancer. LDHB mRNA expression of HER2 (by IHC/FISH)-negative disease separated by clinical classification: A, MAQC; B, MDACCSS; and C, XeNA. ***, P < .001
Figure S6. LDHB mRNA expression within PAM50 intrinsic subtypes for HR-positive/HER2-negative breast cancers. Dotted line represents the threshold (0.60) used to split LDHB high/low expression for prediction of basal-like phenotype and response to neoadjuvant chemotherapy. Claudin low subtyping information was available for the TCGA cohort only.
Figure S7. LDHB mRNA expression within PAM50 intrinsic subtypes for triple-negative breast cancers. A, ER-negative/HER2-negative breast cancer cell lines. B, primary breast cancers. Dotted line represents the threshold (0.60) used to split LDHB high/low expression for prediction of basal-like phenotype.
Figure S8. *LDHB* mRNA expression was highly associated with cell cycle proliferation marker, *CCNB1*, for basal-like cancers within the triple-negative group. A, MAQC; B, MDACCSS; C, XeNA; D, TCGA
Figure S9. Association between mRNA expression and copy number for LDHB for the breast invasive carcinoma cohort separated by (A) basal and (B) luminal A/B subtypes for TCGA “manuscript samples” within the cBio Cancer Genomics Portal (web site http://www.cbioportal.org). Association between mRNA expression and DNA methylation for LDHB in (C) basal and (D) luminal A/B subtypes.