NELFE-Dependent MYC Signature Identifies a Unique Cancer Subtype in Hepatocellular Carcinoma

Hien Dang^{1,4*}, Yotsawat Pomyen^{1,3}, Sean P. Martin¹, Dana A. Dominguez¹, Sun Young Yim², Ju-Seog Lee², Anuradha Budhu¹, Ashesh A. Shah⁵, Adam S. Bodzin⁵, and Xin Wei Wang^{1*}

¹Laboratory of Human Carcinogenesis, Center for Cancer Research, National Cancer Institute, Bethesda, Maryland, United States
²Department of Systems Biology, Division of Cancer Medicine, UT MDACC, Houston, TX, United States
³Translational Research Unit, Chulabhorn Research Institute, Bangkok, 10210, Thailand
⁴Department of Surgery, Division of Surgical Research, Thomas Jefferson University, Philadelphia, PA, United States
⁵Department of Surgery, Division of Transplantation, Thomas Jefferson University, Philadelphia, PA, United States

*Co-corresponding authors Xin Wei Wang: xw3u@nih.gov Hien Dang: hien.dang@jefferson.edu

KOREAN **TCGA-LIHC** LEC Cohort LCI Non-NDMTs NDMTs p value^a Non-NDMTs NDMTs p value^a Non-NDMTs NDMTs p value^a **Clinical variable** Non-NDMTs NDMTs p value^a (115)(43) (121)(120)(273) (91) (107)(32) Demographics 0.009 Sex 0.348 0.489 0.518 106 (87%) 102 (85%) 190 (70%) 48 (53%) 77 (72%) 25 (78%) 96 (83%) 34 (79%) Male 18 (15%) 75 (27%) 37 (41%) 30 (28%) 9 (21%) Female 13 (11%) 7 (22%) 19 (17%) No. (%) missing data 2 (2%) 0 (0%) 8 (3%) 6 (6%) 0 (0%) 0 (0%) 0 (0%) 0 (0%) 0.841 0.008 Age 0.758 0.862 ≥50 yr 53 (44%) 55 (46%) 219 (80%) 69 (76%) 77 (72%) 15 (47%) 84 (73%) 32 (74%) <50 yr 66 (54%) 65 (54%) 46 (17%) 13 (14%) 30 (28%) 17 (53%) 31 (27%) 11 (26%) 3 (2%) 0 (0%) 9 (10%) 0 (0%) 0 (0%) 0 (0%) 0 (0%) No. (%) missing data 8 (3%) Risk factors 0.03 Cirrhosis 0.092 0.653 0.134 115 (96%) 40 (35%) 2 (5%) Yes 105 (87%) 99 (36% 9 (25%) 52 (49%) 17 (53%) No 14 (11%) 5 (À%) 66 (24%) 27 (75%) 55 (51%) 15 (47%) 46 40%) 0 (0%) No. (%) missing data 2 (2%) 0 (0%) 108 (40%) 0 (0%) 0 (0%) 0 (0%) 29 (25%) 41 (0%) BMI 0.824 0.340 N/A N/A 4 (3%) Under weight, BMI <18.5 6 (5%) 18 (7%) 2 (2%) Overweight/Obesity, BMI >24 49 (40%) 38 (32%) 140 (51%) 32 (35%) No. (%) missing data 66 (55%) 48 (65%) 115 (42%) 57 (63%) **HBV** status 0.008 N/A N/A N/A CC 93 (77%) 76 (63%) 40 (33%) AVR-CC 22 (18%) No. (%) missing data 6 (5%) 4 (4%) Liver function factors AFP 0.011 p<0.001 0.200 0.169 Normal, ≤400 ng/ml 72 (60%) 53 (44%) 169 (62%) 32 (35%) 60 (56%) 13 (40%) 89 (77%) 29 (67%) 40 (37%) 15 (47%) Abnormal. >400 ng/ml 45 (37%) 65 (54%) 40 (15%) 23 (25%) 25 (22%) 14 (33%) 36 (40%) 0 (0%) No. (%) missing data 4 (3%) 2 (2%) 64 (23%) 7 (7%) 4 (13%) 1 (1%) ALT 0.165 N/A N/A 0.020 ALT < 50 75 (62%) 65 (54%) 89 (77%) 22 (51%) 44 (36%) 55 (46%) 26 (23%) 16 (37%) ALT > 50 No. (%) missing data 2 (2%) 0 (0%) 0 (0%) 5 (12%) Tumor features 0.442 **Histological grade** 0.071 N/A 0.040 6 (5%) 5 (4%) 42 (15%) 7 (8%) 2 (2%) 0 (0%) Т II-IV 52 (43%) 51 (43%) 207 (76%) 74 (81%) 101 (94%) 30 (94%) No. (%) missing data 63 (52%) 64 (53%) 24 (9%) 10 (11%) 4 (4%) 2 (6%) p<0.001 TNM staging 0.034 0.503 0.003 82 (71%) 19 (44%) 58 (48%) 36 (30%) 147 (54%) 27 (32%) Т 4 (4%) 0 (0%) 44 (37%) 40 (33%) 115 (42%) 11 (4%) 57 (68%) 49 (54%) 37 (31%) 26 (21%) 33 (29%) 23 (54%) ||+||| 62 (58%) 7 (22%) 41 (38%) 0 (0%) 1 (2%) No. (%) missing data 25 (78%) Microvascular invasion 0.019 0.021 0.110 < 0.001 83 (68%) 66 (55%) 160 (59%) 98 (85%) 34 (37%) 21 (20%) 1 (3%) 23 (53%) No 36 (30%) 2 (2%) 54 (45%) 73 (27%) 40 (15%) 30 (33%) 43 (40%) 10 (31%) Yes 16 (14%) 20 (47%) 0 (0%) 27 (30%) 0 (0%) No. (%) missing data 43 (40%) 21 (66%) 1 (1%) Child-Pugh class 0.727 0.659 N/A 0.878 39 (32%) 40 (33%) 39 (43%) 85 (74%) 166 (61%) 2 (5%) А В 18 (15%) 16 (14%)́ 3 (3%) 1 (1%) 0 (0%) 17 (6%) No. (%) missing data 64 (53%) 64 (53%) 90 (33%) 49 (54%) 29 (25%) 41 (95%) Tumor size 0.039 0.325 0.517 N/A >3 cm 39 (32%) 35 (26%) 83 (76%) 30 (94%) 33 (29%) 9 (21%) 79 (65%) 3 (3%) 85 (71%) 0 (0%) 24 (22%) 0 (0%) 2 (6%) 0 (0%) 82 (71%) 0 (0%) 34 (79%) 0 (0%) ≤3 cm No. (%) missing data Multinodular tumor 0.093 0.748 N/A N/A 68 (59%) 1 (2%) No 98 (82%) 88 (73%) 32 (27%) Yes 21 (18%) 7 (6%) 0 (0%) No. (%) missing data 42 (98%) 0 (0%) 40 (35%) 3 (3%) BCLC staging 0.008 0.371 NA 0.658 0&A 93 (76%) 77 (64%) 99 (37%) 0 (0%) 56 (49%) 1 (2%) 18 (15%) 35 (29%) 102`(37%) 30 (33%) 30 (26%) 1 (2%) B&C No. (%) missing data 8 (7%) 72 (26%) 10 (9%) 61 (67%) 29 (25%) 41 (96%) NA N/A **Recurrent Metastasis** 0.827 N/A No 76 (63%) 75 (63%) Yes 43 (35%) 45 (37%) 2 (2%) 0 (0%) No. (%) missing data

Supplemental Table 1. Demographic, clinical and laboratory characteristics of HCC patients in the LCI, TCGA-LIHC,

Abbreviations: NA: Not available, HBV-hepatitis B virus, AVR-CC, active viral replication chronic carrier, CC, chronic carrier, HCV-hepatitis C virus, AFP-alpha-fetoprotein, ALT-alminotransferase, BCLC-Barcelona-Clinic liver cancer, and BMI-body mass index

^aChi-squared test

and LEC cohorts.



Gene Id	Weights (w _i)
CAD	0.061746
CALM2	0.042413
DPAGT1	0.020167
ENOPH1	0.048531
GNS	0.031138
ID3	-0.019005
IER2	0.049337
MFAP1	0.022254
MT2A	-0.152551
NCBP2	0.092179
PA2G4	0.03582
PLXNC1	-0.015257
PPA1	0.011134
PPIA	0.0353
PRKAB2	-0.032401
PTDSS1	0.040496
SERPINE1	0.608612
SRD5A1	-0.19421
SREBF2	0.097164
SYNGR2	0.078953

Supplementary Figure S1. NELFE dependent MYC target (NDMTs) genes. (A) Gene expression of 20-NDMTs in the LCI cohort. (B) Regression coefficient (Weight) of each gene in the 20-NDMT signature used to calculate the index for each patient.



Supplementary Figure S2. NDMT performance in HCC cohorts. ROC curves for the (A) TCGA-LIHC and (B) LEC cohorts comparing the NDMT gene signature with Non-NDMTs. Forest plot represents AUC (±95% Confidence Interval). (C) Kaplan-Meier curve survival analyses of the LCI cohort stratified by AFP and BCLC staging with NDMTs or Non-NDMTs. P value is from Mantel-Cox log rank analyses. (D) Time-dependent ROC curve analyses of the TCGA-LIHC cohort at two years of Bacrecelon-Clinic Liver Cancer (BCLC), alpha-feto protein (AFP), BCLC +NDMTs, or AFP+NDMTs with associated area under the curve values (AUC).



Alterations Amplification Deep deletion Mutation **Supplementary Figure S3. Genomic alterations of NDMTs.** (A) Heatmap of NELFE/ MYC target genes differentially expressed between NDMTs and Non-NDMTs (p<0.001) in TCGA-LIHC cohort. Student's t-test was performed to identify DEGs following enrichment analysis for NELFE/MYC target genes. (B) TP53 mutation and MYC gene copy number alteration analyses in the LCI cohort. Mutation and gene copy number alterations of most frequently altered genes in NDMTs (C) and Non-NDMTs (D) TCGA-LIHC cohort.



Supplementary Figure S4. The NDMT subtype in other tumor types. The NDMT gene signature identifies NDMTs in Burkitt's lymphoma (LYM) but not in prostate adenocarcinoma (PRAD). (B) Kaplan-Meier curve of TCGA breast cancer (BRCA) cohort.