

SUPPLEMENTARY MATERIAL

NAFLD and Vitamin D: Evidence for Intersection of MicroRNA Regulated Pathways

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Table of Contents

Supplementary Table 1 miRNAs dysregulated in liver from NAFLD patients and their functional/pathophysiological effects	2
Supplementary Table 2 miRNAs dysregulated in serum from NAFLD patients	4

Zhang et al. Supplementary Material

Supplementary Table 1 miRNAs dysregulated in liver from NAFLD patients and their functional/pathophysiological effects

miRNA	Summary	Functional/pathophysiological effects and/or genetic targets of dysregulated miRNA
miR-33	Up in NASH (n=22) or SS (n=18) vs. NL(n=22) [MO women]; up in NASH (n=12) vs. NL (n=9) [ModO women] ¹	Hepatic <i>SREBP2</i> and <i>ABCG1</i> mRNAs: up in NASH (n=22) vs. controls (n=22) [MO women]; hepatic <i>SREBP2</i> , <i>ABCG1</i> , <i>SREBP1c</i> , <i>CPT1a</i> and <i>ACCI</i> mRNAs: up in NASH (n=12) vs steatosis (n=9) and NL (n=9) of ModO women ¹
	Up (<i>miR-33a</i>) in NASH (n=38) vs. normal histology (n=10) [bariatric surgery patients] ²	Not investigated
	Down (<i>miR-33a-5p</i>) in NAFLD (n=58) vs. non-NAFLD (n=37), [postmortem samples, CSD and NCSD] ³	Not investigated
miR-141	Up (<i>miR-141</i>) in NASH fatty liver (n=20) vs. NASH non-fatty liver(n=15) and normal histology (n=10) [liver tissue bank] ⁴	Not investigated
	Up (<i>miR-141</i>) in steatosis (n=4) vs. non-steatosis (n=4) [liver tissue bank] ⁵	Not investigated
miR-155	Up (<i>miR-155</i>) in steatosis (n=4) vs. non-steatosis (n=4) [liver tissue bank] ⁵	Not investigated
	Down (<i>miR-155</i>) in NAFLD (n=11) vs. HCs (n=11) [biopsy consenting NAFLD and HCs] ⁶	Hepatic <i>SREBP1c</i> , <i>FAS</i> and <i>ACCI</i> mRNA: up in NAFLD (n=11) vs. HCs (n=11) Target: <i>LXRα</i> ⁶
miR-199	Up (<i>miR-199a-5p</i>) in steatosis (n=7) vs. HCs (n=7); [commercial liver tissue bank] ⁷	Hepatic <i>CAVI</i> and <i>PPARα</i> mRNA: down in steatosis (n=7) vs. HCs (n=7) Targets: <i>CAVI</i> ⁷

Zhang et al. Supplementary Material

Supplementary Table 1 miRNAs dysregulated in liver from NAFLD patients and their functional/pathophysiological effects

miRNA	Summary	Functional/pathophysiological effects and/or genetic targets of dysregulated miRNA
miR-199	Up (<i>miR-199a-5p</i>) in NAFLD (n=5) vs. HCs (n=6); liver steatosis score: up in NAFLD vs. HCs; [diagnosis and treatment of gallstone disease] ⁸	Hepatic <i>MST1</i> mRNA: down in NAFLD (n=5) vs. HCs (n=6) ⁸
miR-223	Up (<i>miR-223</i>) in NASH (n=10) vs. controls (n=14) [NIH liver tissue repository] ⁹	Hepatic <i>CXCL10</i> , <i>TAZ</i> , <i>SERPINB9</i> , <i>DOCK11</i> and <i>GOLM1</i> mRNA: up in NASH (n=10) vs. HCs (n=14); up in steatosis (n=10) vs. HCs; hepatic <i>GPC3</i> , <i>CXCL10</i> and <i>TAZ</i> mRNA: up in NASH vs. HCs Targets: <i>CXCL10</i> and <i>TAZ</i> ⁹
	Up (<i>miR-223</i>) in steatosis (n=4) vs. non-steatosis (n=4) [liver tissue bank] ⁵	Not investigated
miR-378	Up (<i>miR-378</i>) in NASH (n=24) vs. normal histology (n=19) [liver transplantation biopsies] ¹⁰	<i>Ppargc1β</i> mRNA: down in NASH (n=24) vs. HCs (n=19); LXRα targets miR-378 promoter ¹⁰
	Up (<i>miR-378</i>) in NASH (n=38) vs. normal histology (n=24) [liver transplantation biopsies] ¹¹	<i>Prkag2</i> mRNA and protein: down in NASH (n=38) vs. HCs (n=24) Target: <i>Prkag2</i> ¹¹
	Down (<i>miR-378i</i>) in NAFLD with severe fibrosis or cirrhosis (n=15) vs. NAFLD without fibrosis (n=15) [bariatric surgery patients] ¹²	Not investigated

ABCG1, ATP binding cassette subfamily G member 1; ACC1, acetyl-CoA carboxylase; CAV, caveolin1; CPT1a, carnitine palmitoyltransferase 1a; CSD, cardiac sudden death; CXCL10, C-X-C motif chemokine 10; DOCK11, dedicator of cytokinesis 11; FAS, fatty acid synthase; GOLM1, Golgi membrane protein 1; GPC3, glypican-3; HCs, healthy controls; LXRα, liver X receptorα; MO, morbidly obese; ModO, moderately boese; MST1, mammalian sterile 20-like kinase 1; NAFLD, non-alcoholic fatty liver disease; NASH, non-alcoholic steatohepatitis; NCSD, non-cardiac sudden death; PPARα; Ppargc1β, peroxisome proliferator-activated receptor γ coactivator 1-beta; Prkag2, protein kinase AMP-activated non-catalytic subunit gamma 2; SREBP1c, sterol regulatory element-binding protein 1c; SREBP2, sterol regulatory element-binding protein 2; SERPINB9, Serpin family B member 9; TAZ, transcriptional coactivator with PDZ-binding motif.

Zhang et al. Supplementary Material

Supplementary Table 2 miRNAs dysregulated in serum from NAFLD patients

miRNA	Summary
miR-16	Up (<i>miR-16</i>) in NAFLD (n=34) vs. HCs (n=19), up in steatosis and NASH vs. HCs; discriminated steatosis from HCs (AUROC=0.962) ¹³
	Up (<i>miR-16</i>) in NASH (n=31) vs. HCs (n=37); positive correlation with hepatocellular ballooning and fibrosis ¹⁴
	Up (<i>miR-16-5p</i>) in fatty liver infiltration (n=10) vs. no fatty liver infiltration (n=12) [patients with obesity and T2DM] ¹⁵
	Down (<i>miR-16-5p</i>) in SAF \geq 2 (n=50) vs. SAF<2 (n=25); down in NAS \geq 5 (n=38) vs. NAS<5 (n=37); down in F>2 (n=29) vs. F \leq 2 (n=46); negative correlation with AST, APRI, FIB4, BARD and NAFLD fibrosis score (NAFL n=25, NASH n=50 and NL n=17) ¹⁶
miR-20	Up (<i>miR-20a-5p/miR-20b-5p</i>) in NAFLD (n=52) vs. Non-NAFLD (n=48) [adults with T2DM] ¹⁷
	Down (<i>miR-20a</i>) in NAFLD (n=92) vs. HCs (n=383), down in severe NAFLD (n=51) vs. mild NAFLD (n=41) and HCs; in multivariate logistic regression OR=4.09 for severe NAFLD ¹⁸
	Down (<i>miR-20a-5p</i>) in NAFLD (n=14) vs. HCs (n=13) ¹⁹
miR-22	Up (<i>mir-22-5p</i>) in NAFLD (n=32) and NAFLD+fibrate (n=11) vs. HCs (n=10) ²⁰
	Up (<i>miR-22-3p</i>) in SAF \geq 2 (n=50) vs. SAF<2 (n=25), up in NAS \geq 5 (n=38) vs. NAS<5 (n=37); positive correlation with AST, ALT, Ferritin and APRI (NAFL n=25, NASH n=50 and HC n=17) ¹⁶
miR-27	Up (<i>miR-27b-3p</i>) in NAFLD (n=103) vs. HCs (n=80); discriminated NAFLD from HCs (AUROC=0.693) ²¹
	Up (<i>miR-27b-3p</i>) in SAF \geq 2 (n=50) vs. SAF<2 (n=25), up in NAS \geq 5 (n=38) vs. NAS <5 (n=37), up in F>2 (n=29) vs. F \leq 2 (n=46); positive correlation with AST, ALT, Ferritin, APRI and FIB4 (NAFL n=25, NASH n=50 and NL n=17); discriminated NAS \geq 5 from NAS <5 (AUROC=0.73) ¹⁶
	Down (<i>miR-27a</i>) in NAFLD (n=92) vs. HCs (n=383), down in severe NAFLD (n=51) vs. mild NAFLD (n=41) and HCs; in multivariate logistic regression OR=4.09 for severe NAFLD ¹⁸

Zhang et al. Supplementary Material

Supplementary Table 2 miRNAs dysregulated in serum from NAFLD patients

miRNA	Summary
miR-29	Up (<i>miR-29a-3p</i>) in NAFLD (n=32) and NAFLD+fibrate (n=11) vs. HCs (n=10) ²⁰
	Up (<i>miR-29b-3p</i> but no change in <i>miR-29a-3p</i> or <i>miR-29b-3p</i>) in multivariate logistic regression OR=1.49 for NAFLD [non-T2D NAFLD (n=73) and non-T2D non-NAFLD (n=68)]; positive correlation with intrahepatic lipid content [N=99] ²²
	Down (<i>miR-29a</i>) in NAFLD (n=58) vs. HCs (n=34); discriminated NAFLD from HCs (AUROC=0.679) ²³
miR-99	Down (<i>miR-99a</i>) in NAFLD (n=20) vs. HCs (n=20); negative correlation with GGT; discriminated NAFLD from HCs (AUROC=0.76) ²⁴
	Down (<i>miR-99a</i>) in NAFLD (n=210) vs. Controls (n=90), down in NASH (n=86) vs. steatosis (n=124); negative correlation with ALT, activity, inflammation, ballooning and fibrosis; discriminated NAFLD from HCs (AUROC=0.73) and NASH vs. steatosis (AUROC=0.91) ²⁵
miR-125	Up (<i>miR-125b-5p</i>) in NAFLD (n=29) vs. HCs (n=24); ALT: up in NAFLD vs. HCs; serum TNFAIP3 mRNA: down in NAFLD vs. HCs ²⁶
	Down (<i>miR-125b-5p</i>) in NAFLD (n=34) vs HCs (n=20); serum ITGA8 mRNA: up in NAFLD vs. HCs ²⁷
miR-181	Up (<i>miR-181b-3p</i>) in NAFLD (n=25) vs. HCs (n=21) ²⁸
	Up (<i>miR-181a-5p</i>) in NAFLD (n=30) vs. HCs (n=30) ²⁹
	Down (<i>miR-181d</i>) in NAFLD (n=20) vs. HCs (n=20); negative correlation with GGT; discriminated NAFLD from HCs (AUROC=0.86) ²⁴
miR-192	Up (<i>miR-192-5p</i>) in NAFLD (n=103) vs. HCs (n=80); discriminated NAFLD from HCs (AUROC=0.652) ²¹
	Up (<i>miR-192</i>) in NASH (n=87) vs. NAFL (n=50) and HCs (n=61); positive correlation with ALT, steatosis and serum CK18-Asp396 ³⁰
	Up (<i>miR-192</i>) in NASH (n=47) vs. steatosis (n=30) and HCs (n=19); positive correlation with AST, GGT; discriminated histological severity (AUROC range 0.676-0.709) ³¹

Zhang et al. Supplementary Material

Supplementary Table 2 miRNAs dysregulated in serum from NAFLD patients

miRNA	Summary
miR-192	Up (<i>miR-192</i>) in NASH (n=31) vs. NAFL (n=17) and HCs (n=37), up in NAFL (n=17) vs HCs (n=37); positive correlation with histological severity but not fibrosis ¹⁴
	Up (<i>miR-192</i>) in circulating exosomes in advanced stage NAFLD (n=3) vs. early stage NAFLD (n=3) ³²
	Up (<i>miR-192-5p</i>) in SAF \geq 2 (n=50) vs. SAF>2 (n=25), up in NAS \geq 5 (n=38) vs. NAS<5 (n=37); positive correlation with AST, ALT, Ferritin, APRI and BARD (NAFL n=25, NASH n=50 and NL n=17) ¹⁶
	Up (<i>miR-192-5p</i>) in NASH (n=31) vs. HCs (n=37), up in NAFL (n=17) vs. HCs, positive correlation with ALT, AST, steatosis, activity, ballooning and inflammation ³³
	Up (<i>miR-192-5p</i>) with increasing fibrosis severity (n=132 NAFLD patients); in multivariate analyses, positive correlation with steatosis, fibrosis, and the PNPLA3 I148M and TM6SF2 E167K variants ³⁴
	Down (<i>miR-192-5p</i>) in NASH (n=60) vs. HCs (n=60); discriminated NAFLD vs. HCs (AUROC=0.791) ³⁵
miR-197	Down (<i>miR-197</i>) in NAFLD (n=20) vs. HCs (n=20); negative correlation with inflammation; discriminated NAFLD from HCs (AUROC=0.77) ²⁴
	Down (<i>miR-197-3p</i>) in SAF \geq 2 (n=50) vs. SAF<2 (n=25) ¹⁶
miR-375	Up (<i>miR-375</i>) in NASH (n=47) vs. steatosis (n=30) and HCs (n=19); discriminated NAS>5 from NAS<5 (AUROC=0.72) ³¹
	Up (<i>miR-375-3p</i>) in fatty liver infiltration (n=10) vs. no fatty liver infiltration (n=12) [patients with obesity and T2DM] ¹⁵
miR-379	Up (<i>miR-379</i>) in Steatosis (n=10) vs. HCs, Down in NASH (n=10) vs. HCs; discriminate steatosis and NASH from HCs (AUROC=0.92) ³⁶
	Up (<i>miR-379</i>) in NAFLD (n=79) vs. HCs (n=10); discriminated: NAFLD from HC (AUROC= 0.72) ³⁷
miR-451	Up (<i>miR-451</i>) in NAFLD (n=48) vs. HCs (n=90) [adult males] ³⁸
	Down (<i>miR-451</i>) in NAFLD (n=20) vs. HCs (n=20); serum MIF mRNA: up in NAFLD vs. HCs ³⁹

Zhang et al. Supplementary Material

ALT, alanine aminotransferase; APOE, apolipoprotein E; APTI, AST to platelet ratio index; AST, aspartate transaminase; AUROC, the area under the receiver operating characteristic; CK18, cytokeratin-18; eLP-IR, enhanced lipo-protein insulin-resistance index; F, fibrosis%; FIB4, fibrosis 4; FPG, fasting plasma glucose; GGT, gamma-glutamyl transpeptidase; HC, healthy control; γ -GT, γ -glutamyl transpeptidase; NAFL, non-alcoholic fatty liver; NAFLD, non-alcoholic fatty liver disease; NAS, NAFLD activity score; NASH, non-alcoholic steatohepatitis; NNL, near normal liver; NS, not specified; PNPLA3, patatin-like phospholipase domain containing protein 3; SIRT1, sirtuin 1; SAF, steatosis, activity, fibrosis score; T2DM, type 2 diabetes mellitus; TG, triglyceride

References

- [1] Auguet T, Aragonès G, Berlanga A, et al. miR33a/miR33b* and miR122 as Possible Contributors to Hepatic Lipid Metabolism in Obese Women with Nonalcoholic Fatty Liver Disease. *Int J Mol Sci.* 2016;17(10).
- [2] Vega-Badillo J, Gutiérrez-Vidal R, Hernández-Pérez HA, et al. Hepatic miR-33a/miR-144 and their target gene ABCA1 are associated with steatohepatitis in morbidly obese subjects. *Liv Int.* 2016;36(9):1383-91.
- [3] Braza-Boïls A, Mari-Alexandre J, Molina P, et al. Deregulated hepatic microRNAs underlie the association between non-alcoholic fatty liver disease and coronary artery disease. *Liver Int.* 2016;36(8):1221-9.
- [4] Tran M, Lee S-M, Shin D-J, et al. Loss of miR-141/200c ameliorates hepatic steatosis and inflammation by reprogramming multiple signaling pathways in NASH. *JCI Insight.* 2017;2(21).
- [5] Wang JM, Qiu Y, Yang Z, et al. IRE1 α prevents hepatic steatosis by processing and promoting the degradation of select microRNAs. *Sci Signal.* 2018;11(530).
- [6] Wang L, Zhang N, Wang Z, et al. Decreased MiR-155 Level in the Peripheral Blood of Non-Alcoholic Fatty Liver Disease Patients may Serve as a Biomarker and may Influence LXR Activity. *Cell Physiol Biochem.* 2016;39(6):2239-48.
- [7] Li B, Zhang Z, Zhang H, et al. Aberrant miR199a-5p/caveolin1/PPAR α axis in hepatic steatosis. *J Mol Endocrinol.* 2014;53(3):393-403.
- [8] Li Y, Luan Y, Li J, et al. Exosomal miR-199a-5p promotes hepatic lipid accumulation by modulating MST1 expression and fatty acid metabolism. *Hepatol Int.* 2020;14(6):1057-74.
- [9] He Y, Hwang S, Cai Y, et al. MicroRNA-223 Ameliorates Nonalcoholic Steatohepatitis and Cancer by Targeting Multiple Inflammatory and Oncogenic Genes in Hepatocytes. *Hepatology.* 2019;70(4):1150-67.
- [10] Zhang T, Duan J, Zhang L, et al. LXR α Promotes Hepatosteatosis in Part Through Activation of MicroRNA-378 Transcription and Inhibition of Ppargc1 β Expression. *Hepatology.* 2019;69(4):1488-503.
- [11] Zhang T, Hu J, Wang X, et al. MicroRNA-378 promotes hepatic inflammation and fibrosis via modulation of the NF- κ B-TNF α pathway. *J Hepatol.* 2019;70(1):87-96.
- [12] Leti F, Malenica I, Doshi M, et al. High-throughput sequencing reveals altered expression of hepatic microRNAs in nonalcoholic fatty liver disease-related fibrosis. *Transl Res.* 2015;166(3):304-14.
- [13] Cermelli S, Ruggieri A, Marrero JA, et al. Circulating MicroRNAs in Patients with Chronic Hepatitis C and Non-Alcoholic Fatty Liver Disease. *PLoS One.* 2011;6(8):e23937.
- [14] Liu XL, Pan Q, Zhang RN, et al. Disease-specific miR-34a as diagnostic marker of non-alcoholic steatohepatitis in a Chinese population. *World J Gastroenterol.* 2016;22(44):9844-52.
- [15] Pillai SS, Lakhani HV, Zehra M, et al. Predicting Nonalcoholic Fatty Liver Disease through a Panel of Plasma Biomarkers and MicroRNAs in Female West Virginia Population. *Int J Mol Sci.* 2020;21(18).
- [16] López-Riera M, Conde I, Quintas G, et al. Non-invasive prediction of NAFLD severity: a comprehensive, independent validation of previously postulated serum microRNA biomarkers. *Sci Rep.* 2018;8(1):10606.
- [17] Ye D, Zhang T, Lou G, et al. Plasma miR-17, miR-20a, miR-20b and miR-122 as potential biomarkers for diagnosis of NAFLD in type 2 diabetes mellitus patients. *Life Sci.* 2018;208:201-7.

Zhang et al. Supplementary Material

- [18] Ando Y, Yamazaki M, Yamada H, et al. Association of circulating miR-20a, miR-27a, and miR-126 with non-alcoholic fatty liver disease in general population. *Sci Rep*. 2019;9(1):18856.
- [19] Wang X, Ma Y, Yang LY, et al. MicroRNA-20a-5p Ameliorates Non-alcoholic Fatty Liver Disease via Inhibiting the Expression of CD36. *Front Cell Dev Biol*. 2020;8:596329.
- [20] López-Riera M, Conde I, Tolosa L, et al. New microRNA Biomarkers for Drug-Induced Steatosis and Their Potential to Predict the Contribution of Drugs to Non-alcoholic Fatty Liver Disease. *Front Pharmacol*. 2017;8:3.
- [21] Tan Y, Ge G, Pan T, et al. A Pilot Study of Serum MicroRNAs Panel as Potential Biomarkers for Diagnosis of Nonalcoholic Fatty Liver Disease. *PLoS One*. 2014;9(8):e105192.
- [22] He Z, Yang JJ, Zhang R, et al. Circulating miR-29b positively correlates with non-alcoholic fatty liver disease in a Chinese population. *J Dig Dis*. 2019;20(4):189-95.
- [23] Jampoka K, Muangpaisarn P, Khongnomnan K, et al. Serum miR-29a and miR-122 as Potential Biomarkers for Non-Alcoholic Fatty Liver Disease (NAFLD). *MicroRNA*. 2018;7(3):215-22.
- [24] Celikbilek M, Baskol M, Taheri S, et al. Circulating microRNAs in patients with non-alcoholic fatty liver disease. *World J Hepatol*. 2014;6(8):613-20.
- [25] Hendy OM, Rabie H, El Fouly A, et al. The Circulating Micro-RNAs (-122, -34a and -99a) as Predictive Biomarkers for Non-Alcoholic Fatty Liver Diseases. *Diabetes Metab Syndr Obes*. 2019;12:2715-23.
- [26] Zhang Q, Yu K, Cao Y, et al. miR-125b promotes the NF- κ B-mediated inflammatory response in NAFLD via directly targeting TNFAIP3. *Life Sci*. 2021;270:119071.
- [27] Cai Q, Chen F, Xu F, et al. Epigenetic silencing of microRNA-125b-5p promotes liver fibrosis in nonalcoholic fatty liver disease via integrin α 8-mediated activation of RhoA signaling pathway. *Metabolism*. 2020;104:154140.
- [28] Wang Y, Zhu K, Yu W, et al. MiR-181b regulates steatosis in nonalcoholic fatty liver disease via targeting SIRT1. *Biochem Biophys Res Commun*. 2017;493(1):227-32.
- [29] Huang R, Duan X, Liu X, et al. Upregulation of miR-181a impairs lipid metabolism by targeting PPAR α expression in nonalcoholic fatty liver disease. *Biochem Biophys Res Commun*. 2019;508(4):1252-8.
- [30] Becker PP, Rau M, Schmitt J, et al. Performance of Serum microRNAs -122, -192 and -21 as Biomarkers in Patients with Non-Alcoholic Steatohepatitis. *PLoS One*. 2015;10(11):e0142661.
- [31] Pirola CJ, Fernández Gianotti T, Castaño GO, et al. Circulating microRNA signature in non-alcoholic fatty liver disease: from serum non-coding RNAs to liver histology and disease pathogenesis. *Gut*. 2015;64(5):800-12.
- [32] Lee YS, Kim SY, Ko E, et al. Exosomes derived from palmitic acid-treated hepatocytes induce fibrotic activation of hepatic stellate cells. *Sci Rep*. 2017;7(1):3710.
- [33] Liu XL, Pan Q, Cao HX, et al. Lipotoxic Hepatocyte-Derived Exosomal MicroRNA 192-5p Activates Macrophages Through Rictor/Akt/Forkhead Box Transcription Factor O1 Signaling in Nonalcoholic Fatty Liver Disease. *Hepatology*. 2020;72(2):454-69.
- [34] Ezaz G, Trivedi HD, Connelly MA, et al. Differential Associations of Circulating MicroRNAs With Pathogenic Factors in NAFLD. *Hepatol Commun*. 2020;4(5):670-80.
- [35] Hu Y, Yu Y. Dysregulation of miR-192-5p in acute pancreatitis patients with nonalcoholic fatty liver and its functional role in acute pancreatitis progression. *Biosci Rep*. 2020;40(5).

Zhang et al. Supplementary Material

- [36] Okamoto K, Koda M, Okamoto T, et al. A Series of microRNA in the Chromosome 14q32.2 Maternally Imprinted Region Related to Progression of Non-Alcoholic Fatty Liver Disease in a Mouse Model. *PLoS One*. 2016;11(5):e0154676.
- [37] Okamoto K, Koda M, Okamoto T, et al. Serum miR-379 expression is related to the development and progression of hypercholesterolemia in non-alcoholic fatty liver disease. *PLoS One*. 2020;15(2):e0219412.
- [38] Yamada H, Suzuki K, Ichino N, et al. Associations between circulating microRNAs (miR-21, miR-34a, miR-122 and miR-451) and non-alcoholic fatty liver. *Clin Chim Acta*. 2013;424:99-103.
- [39] Tang H, Tan X, Zhu L, et al. Swimming prevents nonalcoholic fatty liver disease by reducing migration inhibitory factor through Akt suppression and autophagy activation. *Am J Transl Res*. 2019;11(7):4315-25.