

Control	YAP IP	YAP IP + Oleic Acid	Uniprot Accession No	Protein name	Gene name
			P13647	Keratin, type II cytoskeletal 5	KRT5
			P46937	Transcriptional coactivator YAP1	YAP1
			P02533	Keratin, type I cytoskeletal 14	KRT14
			Q13123	Protein Red	IK
			P15311	Ezrin	EZR
			P14923	Junction plakoglobin	JUP
			P23588	Eukaryotic translation initiation factor 4B	EIF4B
			Q86YZ3	Hornerin	HRNR
			P35241	Radixin	RDX
			P33993	DNA replication licensing factor MCM7	MCM7
			P40227	T-complex protein 1 subunit zeta	CCT6A
			Q15061	WD repeat-containing protein 43	WDR43
			O95429	BAG family molecular chaperone regulator	BAG4
			P54886	Delta-1-pyrroline-5-carboxylate synthase	ALDH18A1
			Q9BZZ5	Apoptosis inhibitor 5	API5
			O95453	Poly(A)-specific ribonuclease PARN	PARN
			P43243	Matrin-3	MATR3
			P16401	Histone H1.5	H1-5
			P48444	Coatomer subunit delta	ARCN1
			Q9H8H0	Nucleolar protein 11	NOL11
			P16403	Histone H1.2	H1-2
			Q9Y3X0	Coiled-coil domain-containing protein 9	CCDC9
			Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1
			Q9Y5Q8	General transcription factor 3C polypeptide 5	GTF3C5
			Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	HNRNPPL
			Q9UBD5	Origin recognition complex subunit 3	ORC3
			Q86XZ4	Spermatogenesis-associated serine-rich protein 2	SPATS2
			Q8WVY3	U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31
			P07477	Serine protease 1	PRSS1
			P50990	T-complex protein 1 subunit theta	CCT8
			Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18
			Q99829	Copine-1	CPNE1
			Q06330	Recombining binding protein suppressor of hairless	RBPJ
			P42166	Lamina-associated polypeptide 2, isoform alpha	TMPO
			Q9P2K5	Myelin expression factor 2	MYEF2
			Q9Y2J4	Angiomotin-like protein 2	AMOTL2
			P06748	Nucleophosmin	NPM1

	NEGATIVE
	POSITIVE

Figure S1. Mass spectrometry-based analysis of YAP-interacting proteins regulated by lipid metabolism. Heatmap displaying changes in YAP-associated protein interactions identified by mass spectrometry following OA treatment. Each row represents a YAP-binding protein, with red indicating increased association (positive enrichment) and blue indicating decreased association

(negative enrichment) relative to control conditions. Association is measured relative to binding to unique peptides when compared to control. The data highlight dynamic modulation of the YAP interactome in response to lipid metabolic cues.