SUPPLEMENTARY MATERIAL

OBSTRUCTIVE SLEEP APNEA AND CPAP THERAPY ALTER DISTINCT TRANSCRIPTIONAL PROGRAMS IN SUBCUTANEOUS FAT TISSUE

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Supplementary Table S1. Demographics of Study Group 1 and Study Group 2.

Subject ID	Study Group	Description	Age	Sex	BMI
10-S-N	1	Normal Subject	66	F	31.3
12-S-N	1	Normal Subject	53	F	35.2
13-S-N	1	Normal Subject	61	F	41.7
18-S-N	1	Normal Subject	30	F	40.3
19-S-N	1	Normal Subject	56	M	42.5
21-S-N	1	Normal Subject	47	F	26.7
22-S-N	1	Normal Subject	60	F	33.6
25-S-N	1	Normal Subject	63	F	30.4
2-S-A	1	OSA Subject	34	F	50.9
3-S-A	1	OSA Subject	52	F	28.8
6-S-A	1	OSA Subject	64	F	32.4
7-S-A	1	OSA Subject	55	F	32.7
11-S-A	1	OSA Subject	58	M	35.5
14-S-A	1	OSA Subject	70	F	39.1
15-S-A	1	OSA Subject	62	F	20.6
16-S-A	1	OSA Subject	50	F	39.1
24-S-A	1	OSA Subject	48	M	50.3
26-S-A	1	OSA Subject	68	M	32
5001_before	2	OSA Subject before CPAP	69.0	M	32.2
5001_after	2	OSA Subject after CPAP	69.0	M	31.3
5002_before	2	OSA Subject before CPAP	33.9	M	37.5
5002_after	2	OSA Subject after CPAP	33.9	M	37.7
5003_before	2	OSA Subject before CPAP	53.9	M	32.2
5003_after	2	OSA Subject after CPAP	53.9	M	32.3
5004_before	2	OSA Subject before CPAP	51.4	F	43.1
5004_after	2	OSA Subject after CPAP	51.4	F	41.2
5006_before	2	OSA Subject before CPAP	34.0	F	59.4
5006_after	2	OSA Subject after CPAP	34.0	F	58.8
5009_before	2	OSA Subject before CPAP	67.2	M	39.8
5009_after	2	OSA Subject after CPAP	67.2	M	40.3
5011_before	2	OSA Subject before CPAP	51.8	F	37.8
5011_after	2	OSA Subject after CPAP	51.8	F	37.7
5012_before	2	OSA Subject before CPAP	57.5	F	36.4
5012_after	2	OSA Subject after CPAP	57.5	F	37.3
5015_before	2	OSA Subject before CPAP	54.1	M	61.0
5015_after	2	OSA Subject after CPAP	54.1	M	58.5
5016_before	2	OSA Subject before CPAP	47.9	F	41.2
5016_after	2	OSA Subject after CPAP	47.9	F	41.8
5017_before	2	OSA Subject before CPAP	59.1	M	30.3

5017_after	2	OSA Subject after CPAP	59.1	M	31.7
5018_before	2	OSA Subject before CPAP	56.6	F	39.1
5018_after	2	OSA Subject after CPAP	56.6	F	39.6
5020_before	2	OSA Subject before CPAP	46.9	M	62.5
5020_after	2	OSA Subject after CPAP	46.9	M	61.5
5021_before	2	OSA Subject before CPAP	42.1	M	37.5
5021_after	2	OSA Subject after CPAP	42.1	M	38.9
5022_before	2	OSA Subject before CPAP	67.9	F	49.2
5022_after	2	OSA Subject after CPAP	67.9	F	46.9
5025_before	2	OSA Subject before CPAP	43.0	F	29.3
5025_after	2	OSA Subject after CPAP	43.0	F	28.8
5026_before	2	OSA Subject before CPAP	31.7	F	54.1
5026_after	2	OSA Subject after CPAP	31.7	F	54.1
5028_before	2	OSA Subject before CPAP	34.9	M	40.2
5028_after	2	OSA Subject after CPAP	34.9	M	40.4
5030_before	2	OSA Subject before CPAP	33.7	F	53.8
5030_after	2	OSA Subject after CPAP	33.7	F	54.6
5031_before	2	OSA Subject before CPAP	50.9	M	37.4
5031_after	2	OSA Subject after CPAP	50.9	M	35.0
5032_before	2	OSA Subject before CPAP	53.8	M	37.8
5032_after	2	OSA Subject after CPAP	53.8	M	36.8
1038_before	2	OSA Subject before CPAP	52.8	M	43.5
1038_after	2	OSA Subject after CPAP	52.8	M	44.5
1046_before	2	OSA Subject before CPAP	46.0	F	44.0
1046_after	2	OSA Subject after CPAP	46.0	F	42.0
1089_before	2	OSA Subject before CPAP	45.9	M	42.3
1089_after	2	OSA Subject after CPAP	45.9	M	42.8

Supplementary Table S2. List of up-regulated gene sets (FDR < 0.05) in subcutaneous fat of OSA subjects (Study Group 1).

Gene Set Description	Number of Genes	FDR
HALLMARK_PROTEIN_SECRETION	96	>0.001
HALLMARK_MYC_TARGETS_V1	197	>0.001
KEGG_RNA_DEGRADATION	58	>0.001
KEGG_SPLICEOSOME	123	>0.001
HALLMARK_MTORC1_SIGNALING	197	>0.001
REACTOME_MRNA_PROCESSING	149	>0.001
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	131	>0.001
REACTOME_HIV_INFECTION	184	>0.001
REACTOME_HIV_LIFE_CYCLE	105	>0.001
REACTOME_RNA_POL_II_TRANSCRIPTION	94	>0.001
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	43	>0.001
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	234	>0.001
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	50	>0.001
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	133	>0.001
REACTOME_MRNA_SPLICING	104	>0.001
PID_FAK_PATHWAY	58	>0.001
PID_PDGFRB_PATHWAY	127	>0.001
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	63	>0.001
PID_ERBB1_DOWNSTREAM_PATHWAY	105	>0.001
PID_P53_REGULATION_PATHWAY	58	>0.001
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	92	>0.001
REACTOME_MRNA_3_END_PROCESSING	33	>0.001
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	198	>0.001
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	>0.001
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	334	>0.001
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	>0.001
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	>0.001
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	111	>0.001
HALLMARK_INTERFERON_GAMMA_RESPONSE	197	>0.001
PID_TGFBR_PATHWAY	55	>0.001
PID_FAS_PATHWAY	38	>0.001
BIOCARTA_D4GDI_PATHWAY	13	>0.001
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	118	>0.001
BIOCARTA_RAB_PATHWAY	12	>0.001
KEGG_COLORECTAL_CANCER	62	>0.001
REACTOME_DEADENYLATION_OF_MRNA	18	>0.001
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	56	>0.001
KEGG_PANCREATIC_CANCER	70	0.001
REACTOME_TCR_SIGNALING	50	0.001
REACTOME_INTERFERON_SIGNALING	147	0.001
BIOCARTA_ATRBRCA_PATHWAY	20	0.001
PID_ILK_PATHWAY	45	0.001
REACTOME_UNFOLDED_PROTEIN_RESPONSE	73	0.001
PID_RANBP2_PATHWAY	11	0.001
BIOCARTA_MET_PATHWAY	36	0.001
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	80	0.001
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	0.001
HALLMARK_ANDROGEN_RESPONSE	99	0.001
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	30	0.001
BIOCARTA_FAS_PATHWAY	30	0.001
PID_FOXO_PATHWAY	49	0.001
PID_TRAIL_PATHWAY	28	0.001
PID_FANCONI_PATHWAY	44	0.001
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGE	64	0.001
REACTOME_SIGNALING_BY_WNT	62	0.001

PID_TELOMERASE_PATHWAY	68	0.001
HALLMARK_INTERFERON_ALPHA_RESPONSE	94	0.001
HALLMARK_MITOTIC_SPINDLE	198	0.001
REACTOME_CELL_CYCLE_CHECKPOINTS	111	0.001
REACTOME_DIABETES_PATHWAYS	122	0.001
KEGG_APOPTOSIS	86	0.001
KEGG_PROTEASOME	44	0.001
PID_NFAT_3PATHWAY	53	0.001
REACTOME_CELL_CYCLE_MITOTIC	303	0.001
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	0.001
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	0.001
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	79	0.002
PID_ATM_PATHWAY	34	0.002
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	61	0.002
REACTOME_NOD1_2_SIGNALING_PATHWAY	28	0.002
PID_ERBB1_INTERNALIZATION_PATHWAY	41	0.002
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_	20	0.002
REACTOME_METABOLISM_OF_NON_CODING_RNA	45	0.002
KEGG_PROTEIN_EXPORT	22	0.002
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	25	0.002
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.002
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	71	0.002
REACTOME_MITOTIC_M_M_G1_PHASES	164	0.002
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	0.003
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	60	0.003
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	47	0.003
HALLMARK_UV_RESPONSE_DN	142	0.003
REACTOME_MITOTIC_PROMETAPHASE	82	0.003
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	256	0.003
HALLMARK_PI3K_AKT_MTOR_SIGNALING	103	0.003
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLF	43	0.003
BIOCARTA_PROTEASOME_PATHWAY	28	0.003
PID_BARD1_PATHWAY	29	0.003
REACTOME_DOWNSTREAM_TCR_SIGNALING	33	0.003
ST_JNK_MAPK_PATHWAY	40	0.003
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	49	0.003
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	0.003
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	0.003
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	56	0.003
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	60	0.003
REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	25	0.003
REACTOME_PYRUVATE_METABOLISM	18	0.003
HALLMARK_E2F_TARGETS	199	0.003
BIOCARTA_CASPASE_PATHWAY	23	0.003
BIOCARTA_TFF_PATHWAY	21	0.003
BIOCARTA_CDC42RAC_PATHWAY	16	0.003
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.003
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	0.003
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.003
PID_CDC42_PATHWAY	70	0.003
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	30	0.003
REACTOME_MEMBRANE_TRAFFICKING	122	0.003
REACTOME_TRNA_AMINOACYLATION	42	0.003
REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS	14	0.003
BIOCARTA_RAS_PATHWAY	23	0.003
ST_INTEGRIN_SIGNALING_PATHWAY	81	0.004
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	25	0.004

REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.004
REACTOME_SIGNALING_BY_HIPPO	19	0.004
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	0.004
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.004
REACTOME_DNA_REPLICATION	184	0.004
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.004
BIOCARTA_FCER1_PATHWAY	38	0.004
PID_VEGFR1_PATHWAY	26	0.004
BIOCARTA_ACTINY_PATHWAY	20	0.005
PID_P38_ALPHA_BETA_PATHWAY	31	0.005
REACTOME_CALNEXIN_CALRETICULIN_CYCLE	11	0.005
REACTOME_PERK_REGULATED_GENE_EXPRESSION	26	0.005
BIOCARTA_TNFR1_PATHWAY	29	0.005
HALLMARK_ADIPOGENESIS	194	0.005
REACTOME_REGULATION_OF_APOPTOSIS	56	0.005
PID_TCPTP_PATHWAY	41	0.005
REACTOME_ER_PHAGOSOME_PATHWAY	58	0.005
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	0.005
KEGG_NON_HOMOLOGOUS_END_JOINING	13	0.005
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATE	16	0.006
REACTOME_APOPTOSIS	142	0.006
PID_TNF_PATHWAY	46	0.006
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.006
PID_ANGIOPOIETIN_RECEPTOR_PATHWAY	50	0.006
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	69	0.006
BIOCARTA_P38MAPK_PATHWAY	39	0.006
BIOCARTA_IGF1_PATHWAY	21	0.006
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	21	0.006
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.007
BIOCARTA_HIVNEF_PATHWAY	57	0.007
PID_IFNG_PATHWAY	40	0.007
PID_VEGFR1_2_PATHWAY	67	0.007
KEGG_N_GLYCAN_BIOSYNTHESIS	45	0.007
PID_ECADHERIN_NASCENT_AJ_PATHWAY	39	0.007
REACTOME_CELL_CYCLE	391	0.007
BIOCARTA_SALMONELLA_PATHWAY	13	0.007
PID_CXCR4_PATHWAY	101	0.007
REACTOME_METABOLISM_OF_RNA	251	0.007
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	36	0.007
REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	26	0.007
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	49	0.007
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.007
REACTOME_ERK_MAPK_TARGETS	21	0.007
PID_WNT_NONCANONICAL_PATHWAY	32	0.007
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	30	0.007
REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE	13	0.008
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	72	0.008
REACTOME_ACTIVATED_TLR4_SIGNALLING	89	0.008
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	26	0.008
REACTOME_PROTEIN_FOLDING	50	0.008
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	0.008
REACTOME_ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	16	0.008
REACTOME_TOLL_RECEPTOR_CASCADES	109	0.009
REACTOME_INTEGRATION_OF_PROVIRUS	8	0.009
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	53	0.009
BIOCARTA_PDGF_PATHWAY	32	0.009
REACTOME_TRANSCRIPTION	189	0.009

PID_HDAC_CLASSII_PATHWAY	34	0.009
PID_ERBB2_ERBB3_PATHWAY	44	0.009
PID_ERBB1_RECEPTOR_PROXIMAL_PATHWAY	35	0.009
BIOCARTA_AT1R_PATHWAY	32	0.009
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.009
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET	18	0.01
KEGG_BASAL_TRANSCRIPTION_FACTORS	32	0.01
KEGG_RENAL_CELL_CARCINOMA	70	0.01
REACTOME_TIE2_SIGNALING	17	0.011
BIOCARTA_INSULIN_PATHWAY	21	0.011
HALLMARK_COMPLEMENT	195	0.011
REACTOME_SYNTHESIS_OF_DNA	90	0.011
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	80	0.012
PID_IL6_7_PATHWAY	47	0.012
PID_LYMPH_ANGIOGENESIS_PATHWAY	24	0.012
PID_RAC1_PATHWAY	54	0.012
BIOCARTA_IL6_PATHWAY	22	0.012
REACTOME_REGULATION_OF_PYRUVATE_DEHYDROGENASE_PDH_COMPLEX	12	0.012
REACTOME_INTERFERON_GAMMA_SIGNALING	58	0.013
BIOCARTA_CHREBP2_PATHWAY	41	0.013
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	23	0.013
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.013
BIOCARTA_RARRXR_PATHWAY	15	0.013
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	0.013
BIOCARTA_TEL_PATHWAY	18	0.014
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	0.014
PID_ATF2_PATHWAY	56	0.014
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	55	0.014
PID_FCER1_PATHWAY	61	0.014
REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCRIPTION_FACTORS	10	0.015
PID_BCR_5PATHWAY	65	0.015
REACTOME_REGULATION_OF_AMPK_ACTIVITY_VIA_LKB1	13	0.015
REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6_ALPHA	11	0.015
REACTOME_DESTABILIZATION_OF_MRNA_BY_TRISTETRAPROLIN_TTP	17	0.015
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	62	0.016
BIOCARTA_NGF_PATHWAY	18	0.016
PID_IL12_STAT4_PATHWAY	33	0.016
BIOCARTA_EIF2_PATHWAY	11	0.016
REACTOME_MITOTIC_G1_G1_S_PHASES	130	0.017
HALLMARK_G2M_CHECKPOINT	199	0.017
REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	15	0.017
ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY	37	0.017
BIOCARTA_MAPK_PATHWAY	86	0.018
HALLMARK_APOPTOSIS	157	0.018
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	87	0.018
PID_IL1_PATHWAY	33	0.018
PID_S1P_S1P2_PATHWAY	24	0.018
PID_MTOR_4PATHWAY	69	0.018
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	106	0.018
BIOCARTA_TGFB_PATHWAY	19	0.018
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	0.018
BIOCARTA_EGF_PATHWAY	31	0.018
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	0.018
REACTOME_G1_S_TRANSITION	106	0.018
PID_CASPASE_PATHWAY	51	0.018
REACTOME_M_G1_TRANSITION	78	0.018
REACTOME_PD1_SIGNALING	17	0.019

REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	13	0.019
PID_MAPK_TRK_PATHWAY	34	0.019
BIOCARTA_GLEEVEC_PATHWAY	23	0.019
REACTOME_DARPP_32_EVENTS	24	0.019
PID_MYC_ACTIV_PATHWAY	76	0.019
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	0.019
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	84	0.02
PID_CXCR3_PATHWAY	43	0.02
REACTOME_MRNA_DECAY_BY_5_TO_3_EXORIBONUCLEASE	14	0.02
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	0.02
PID_HEDGEHOG_GLI_PATHWAY	48	0.02
PID_INSULIN_PATHWAY	43	0.02
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	0.02
PID_TCR_PATHWAY	66	0.02
REACTOME_SIGNALING_BY_ILS	105	0.02
PID_DNA_PK_PATHWAY	16	0.02
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_AC	74	0.02
REACTOME_PKB_MEDIATED_EVENTS	27	0.021
BIOCARTA_TCR_PATHWAY	44	0.022
REACTOME_DESTABILIZATION_OF_MRNA_BY_KSRP	17	0.022
BIOCARTA_BAD_PATHWAY	26	0.023
BIOCARTA_NFAT_PATHWAY	53	0.023
REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RB1_E2F1	12	0.023
KEGG_ENDOCYTOSIS	176	0.023
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	22	0.023
REACTOME_S_PHASE	106	0.023
KEGG_CELL_CYCLE	123	0.023
BIOCARTA_GPCR_PATHWAY	34	0.023
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	37	0.023
PID_AVB3_OPN_PATHWAY	31	0.023
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	67	0.024
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	0.024
REACTOME_MITOTIC_G2_G2_M_PHASES	77	0.024
REACTOME_ERKS_ARE_INACTIVATED	12	0.025
PID_ARF6_TRAFFICKING_PATHWAY	46	0.025
PID_EPHB_FWD_PATHWAY	40	0.025
BIOCARTA_CERAMIDE_PATHWAY	22	0.025
REACTOME_COPI_MEDIATED_TRANSPORT	9	0.025
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	0.025
KEGG_MTOR_SIGNALING_PATHWAY	50	0.025
ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS	45	0.025
BIOCARTA_RHO_PATHWAY	32	0.025
BIOCARTA_LEPTIN_PATHWAY	10	0.026
SIG_REGULATION_OF_THE_ACTIN_CYTOSKELETON_BY_RHO_GTPASES	35	0.026
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	21	0.026
REACTOME_DNA_REPAIR	101	0.027
KEGG_OOCYTE_MEIOSIS	110	0.027
REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	13	0.027
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	38	0.027
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_ATF6_ALPHA	9	0.027
REACTOME_METABOLISM_OF_MRNA	209	0.027
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	40	0.027
PID_MET_PATHWAY	80	0.028
BIOCARTA_MTOR_PATHWAY	23	0.028
PID_AR_PATHWAY	60	0.028
REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	15	0.029
KEGG_VIRAL_MYOCARDITIS	68	0.029

REACTOME_HORMONE_SENSITIVE_LIPASE_HSL_MEDIATED_TRIACYLGLYCEROL_HYDROLYSIS	12	0.029
PID_NFKAPPAB_CANONICAL_PATHWAY	23	0.029
REACTOME_DESTABILIZATION_OF_MRNA_BY_BRF1	17	0.029
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	25	0.029
BIOCARTA_EIF4_PATHWAY	24	0.029
REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	14	0.029
BIOCARTA_HDAC_PATHWAY	27	0.03
PID_TCR_JNK_PATHWAY	14	0.03
KEGG_LEISHMANIA_INFECTION	68	0.031
PID_HDAC_CLASSI_PATHWAY	66	0.031
REACTOME_SIGNALING_BY_ROBO_RECEPTOR	29	0.032
SIG_CHEMOTAXIS	45	0.032
REACTOME_RAP1_SIGNALLING	15	0.032
REACTOME_CD28_CO_STIMULATION	31	0.032
BIOCARTA_HCMV_PATHWAY	17	0.032
PID_SMAD2_3PATHWAY	17	0.033
BIOCARTA_ECM_PATHWAY	23	0.033
PID_PDGFRA_PATHWAY	22	0.033
REACTOME_INTRINSIC_PATHWAY_FOR_APOPTOSIS	29	0.033
KEGG_FOCAL_ADHESION	198	0.035
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	83	0.035
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	97	0.035
BIOCARTA_NDKDYNAMIN_PATHWAY	17	0.035
REACTOME_PI_METABOLISM	47	0.035
REACTOME_NGF_SIGNALLING_VIA_TRKA_FROM_THE_PLASMA_MEMBRANE	133	0.035
BIOCARTA_PML_PATHWAY	17	0.035
PID_CD40_PATHWAY	30	0.035
REACTOME_SIGNALING_BY_INSULIN_RECEPTOR	103	0.035
KEGG_MAPK_SIGNALING_PATHWAY	263	0.035
PID_IL2_1PATHWAY	55	0.036
PID_AR_TF_PATHWAY	53	0.036
REACTOME_IKK_COMPLEX_RECRUITMENT_MEDIATED_BY_RIP1	9	0.037
BIOCARTA_MEF2D_PATHWAY	18	0.038
HALLMARK_ALLOGRAFT_REJECTION	196	0.039
PID_PI3KCI_AKT_PATHWAY	35	0.038
HALLMARK_HEME_METABOLISM	195	0.039
PID_ERBB4_PATHWAY	38	0.039
ST_TUMOR_NECROSIS_FACTOR_PATHWAY	29	0.04
REACTOME_INSULIN_RECEPTOR_SIGNALLING_CASCADE	82	0.039
REACTOME_NFKB_ACTIVATION_THROUGH_FADD_RIP1_PATHWAY_MEDIATED_BY_CASPASE_8_AND1	12	0.039
REACTOME_EXTRINSIC_PATHWAY_FOR_APOPTOSIS	13	0.04
PID_ALK1_PATHWAY	26	0.041
ST_GRANULE_CELL_SURVIVAL_PATHWAY	27	0.043
BIOCARTA_HIF_PATHWAY	15	0.043
BIOCARTA_DNAFRAGMENT_PATHWAY	10	0.043
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	37	0.043
REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS	10	0.043
KEGG_ADHERENS_JUNCTION	73	0.043
REACTOME_RNA_POL_I_TRANSCRIPTION_TERMINATION	19	0.043
PID_P75_NTR_PATHWAY	69	0.043
BIOCARTA_AKAP95_PATHWAY	12	0.043
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	0.043
BIOCARTA_CREB_PATHWAY	27	0.043
REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY	12	0.044
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	25	0.044
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_LATE_ENDOSOME_MEMBRANE	10	0.045
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	0.045

BIOCARTA_GSK3_PATHWAY	27	0.045
PID_ATR_PATHWAY	39	0.045
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_EARLY_ENDOSOME_MEMBRANE	12	0.045
BIOCARTA_CTLA4_PATHWAY	19	0.045
BIOCARTA_MITOCHONDRIA_PATHWAY	21	0.046
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	0.047
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	33	0.047
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	20	0.047
KEGG_TGF_BETA_SIGNALING_PATHWAY	84	0.047
PID_NEPHRIN_NEPH1_PATHWAY	31	0.047
PID_CERAMIDE_PATHWAY	48	0.047
REACTOME_PEROXISOMAL_LIPID_METABOLISM	20	0.047
PID_IL8_CXCR2_PATHWAY	33	0.048
PID_REELIN_PATHWAY	29	0.048
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	42	0.048
BIOCARTA_AKAP13_PATHWAY	12	0.049
PID_ER_NONGENOMIC_PATHWAY	41	0.049
PID_THROMBIN_PAR4_PATHWAY	15	0.049
REACTOME_ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT	26	0.049
REACTOME_PI3K_CASCADE	66	0.049
PID_GMCSF_PATHWAY	37	0.049

Supplementary Table S3. List of down-regulated gene sets (FDR < 0.05) in subcutaneous fat of OSA subjects (Study Group 1).

Gene Set Description	Number of Genes	FDR
REACTOME_OLFACTORY_SIGNALING_PATHWAY	315	>0.001
KEGG_OLFACTORY_TRANSDUCTION	376	>0.001
REACTOME_BETA_DEFENSINS	34	>0.001
REACTOME_DEFENSINS	41	>0.001
PID_CONE_PATHWAY	23	0.001
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	265	0.009
HALLMARK_KRAS_SIGNALING_DN	192	0.008
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	60	0.008
KEGG_RETINOL_METABOLISM	53	0.008
PID_RHODOPSIN_PATHWAY	24	0.016
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	41	0.016
REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHEROMONE_RECEPTORS	13	0.015
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	37	0.015
REACTOME_GPCR_LIGAND_BINDING	375	0.02
REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	11	0.021
REACTOME_TIGHT_JUNCTION_INTERACTIONS	28	0.024
BIOCARTA_CYTOKINE_PATHWAY	19	0.031
REACTOME_COMMON_PATHWAY	14	0.03
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	0.035
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	280	0.038
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	62	0.042
REACTOME_PEPTIDE_CHAIN_ELONGATION	86	0.048

Supplementary Table S4. List of Adipogenesis-associated genes up-regulated in subcutaneous fat of OSA subjects (Study Group 1).

Gene Symbol	Gene Name
MAP4K3	mitogen-activated protein kinase kinase kinase kinase 3(MAP4K3)
ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2(ENPP2)
CMPK1	cytidine/uridine monophosphate kinase 1(CMPK1)
TOB1	transducer of ERBB2, 1(TOB1)
ATL2	atlastin GTPase 2(ATL2)
NKIRAS1	NFKB inhibitor interacting Ras like 1(NKIRAS1)
NDUFA5	NADH:ubiquinone oxidoreductase subunit A5(NDUFA5)
RIOK3	RIO kinase 3(RIOK3)
IFNGR1	interferon gamma receptor 1(IFNGR1)
CHUK	conserved helix-loop-helix ubiquitous kinase(CHUK)
PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)(PDCD4)
DBT	dihydrolipoamide branched chain transacylase E2(DBT)
TANK	TRAF family member associated NFKB activator(TANK)
DNAJC15	DnaJ heat shock protein family (Hsp40) member C15(DNAJC15)
NMT1	N-myristoyltransferase 1(NMT1)
HIBCH	3-hydroxyisobutyryl-CoA hydrolase(HIBCH)
HSPB8	heat shock protein family B (small) member 8(HSPB8)
CD36	CD36 molecule(CD36)
DHRS7	dehydrogenase/reductase 7(DHRS7)
IDH3A	isocitrate dehydrogenase 3 (NAD(+)) alpha(IDH3A)
SORBS1	sorbin and SH3 domain containing 1(SORBS1)
SPARCL1	SPARC like 1(SPARCL1)
ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain(ACADM)
MTCH2	mitochondrial carrier 2(MTCH2)
PRDX3	peroxiredoxin 3(PRDX3)
PTCD3	pentatricopeptide repeat domain 3(PTCD3)
GBE1	1,4-alpha-glucan branching enzyme 1(GBE1)
ME1	malic enzyme 1(ME1)
ANGPT1	angiopoietin 1(ANGPT1)
UCP2	uncoupling protein 2(UCP2)
RETSAT	retinol saturase(RETSAT)
DRAM2	DNA damage regulated autophagy modulator 2(DRAM2)
DLD	dihydrolipoamide dehydrogenase(DLD)
G3BP2	G3BP stress granule assembly factor 2(G3BP2)
RNF11	ring finger protein 11(RNF11)
AIFM1	apoptosis inducing factor, mitochondria associated 1(AIFM1)
MYLK	myosin light chain kinase(MYLK)
SOD1	superoxide dismutase 1, soluble(SOD1)
PLIN2	perilipin 2(PLIN2)
PPM1B	protein phosphatase, Mg2+/Mn2+ dependent 1B(PPM1B)
LEP	leptin(LEP)
PQLC3	PQ loop repeat containing 3(PQLC3)
CCNG2	cyclin G2(CCNG2)
ITIH5	inter-alpha-trypsin inhibitor heavy chain family member 5(ITIH5)
LIFR	leukemia inhibitory factor receptor alpha(LIFR)

UBQLN1	ubiquilin 1(UBQLN1)
EPHX2	epoxide hydrolase 2(EPHX2)
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial(GPAM)
UBC	ubiquitin C(UBC)
SAMM50	SAMM50 sorting and assembly machinery component(SAMM50)
ATP1B3	ATPase Na+/K+ transporting subunit beta 3(ATP1B3)
SDHB	succinate dehydrogenase complex iron sulfur subunit B(SDHB)
BCL2L13	BCL2 like 13(BCL2L13)
ACADL	acyl-CoA dehydrogenase, long chain(ACADL)
LAMA4	laminin subunit alpha 4(LAMA4)
GPD2	glycerol-3-phosphate dehydrogenase 2(GPD2)
SCP2	sterol carrier protein 2(SCP2)
TALDO1	transaldolase 1(TALDO1)
SSPN	sarcospan(SSPN)
FABP4	fatty acid binding protein 4(FABP4)
ADIPOQ	adiponectin, C1Q and collagen domain containing(ADIPOQ)
QDPR	quinoid dihydropteridine reductase(QDPR)
ACOX1	acyl-CoA oxidase 1(ACOX1)
OMD	osteomodulin(OMD)
GHITM	growth hormone inducible transmembrane protein(GHITM)
REEP5	receptor accessory protein 5(REEP5)
DECR1	2,4-dienoyl-CoA reductase 1, mitochondrial(DECR1)
CD151	CD151 molecule (Raph blood group)(CD151)
CYP4B1	cytochrome P450 family 4 subfamily B member 1(CYP4B1)
PHYH	phytanoyl-CoA 2-hydroxylase(PHYH)
PPP1R15B	protein phosphatase 1 regulatory subunit 15B(PPP1R15B)

Supplementary Table S5. List of interferon-gamma network genes up-regulated in subcutaneous fat of OSA subjects (Study Group 1). Highly connected nodes (e.g., hubs) are in bold.

Gene Symbol	Gene Name	Location	Family
APOL6	apolipoprotein L6	Extracellular Space	transporter
ARL4A	ADP ribosylation factor like GTPase 4A	Nucleus	enzyme
BANK1	B cell scaffold protein with ankyrin repeats 1	Extracellular Space	other
BTG1	BTG anti-proliferation factor 1	Nucleus	transcription regulator
C1S	complement C1s	Extracellular Space	peptidase
CAMK2D	calcium/calmodulin dependent protein kinase II delta	Cytoplasm	kinase
CASP1	caspase 1	Cytoplasm	peptidase
CASP3	**caspase 3**	**Cytoplasm**	**peptidase**
CASP4	caspase 4	Cytoplasm	peptidase
CASP8	**caspase 8**	**Nucleus**	**peptidase**
CCL2	C-C motif chemokine ligand 2	Extracellular Space	cytokine
CCL5	C-C motif chemokine ligand 5	Extracellular Space	cytokine
CD44	CD44 molecule (Indian blood group)	Plasma Membrane	other
CD69	CD69 molecule	Plasma Membrane	transmembrane receptor
CFH	complement factor H	Extracellular Space	other
CXCL10	C-X-C motif chemokine ligand 10	Extracellular Space	cytokine
CXCL11	C-X-C motif chemokine ligand 11	Extracellular Space	cytokine
CXCL9	C-X-C motif chemokine ligand 9	Extracellular Space	cytokine
DDX58	DExD/H-box helicase 58	Cytoplasm	enzyme
DDX60	DExD/H-box helicase 60	Cytoplasm	enzyme
EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2	Cytoplasm	kinase
FAS	**Fas cell surface death receptor**	**Plasma Membrane**	**transmembrane receptor**
FCGR1A	Fc fragment of IgG receptor Ia	Plasma Membrane	transmembrane receptor
FGL2	fibrinogen like 2	Extracellular Space	peptidase
GBP1	guanylate binding protein 1	Cytoplasm	enzyme
GBP2	guanylate binding protein 2	Cytoplasm	enzyme
GBP4	guanylate binding protein 4	Cytoplasm	enzyme
GBP5	guanylate binding protein 5	Plasma Membrane	enzyme
GBP7	guanylate binding protein 7	Cytoplasm	enzyme
GCH1	GTP cyclohydrolase 1	Cytoplasm	enzyme
GZMA	granzyme A	Cytoplasm	peptidase
HIF1A	hypoxia inducible factor 1 subunit alpha	Nucleus	transcription regulator
HLA-B	major histocompatibility complex, class I, B	Plasma Membrane	transmembrane receptor
HLA-C	major histocompatibility complex, class I, C	Plasma Membrane	other
HLA-DMA	major histocompatibility complex, class II, DM alpha	Plasma Membrane	transmembrane receptor
HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	Plasma Membrane	transmembrane receptor
HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	Plasma Membrane	transmembrane receptor
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	Plasma Membrane	transmembrane receptor
HLA-DRB5	major histocompatibility complex, class II, DR beta 5	Plasma Membrane	transmembrane receptor
HLA-G	major histocompatibility complex, class I, G	Plasma Membrane	other
IDO1	indoleamine 2,3-dioxygenase 1	Cytoplasm	enzyme
IFI44	interferon induced protein 44	Cytoplasm	other
IFI44L	interferon induced protein 44 like	Nucleus	other
IFIH1	interferon induced with helicase C domain 1	Nucleus	enzyme
IFIT1	interferon induced protein with tetratricopeptide repeats 1	Cytoplasm	other
IFIT2	interferon induced protein with tetratricopeptide repeats 2	Cytoplasm	other
IFIT3	interferon induced protein with tetratricopeptide repeats 3	Cytoplasm	other
IFNAR2	interferon alpha and beta receptor subunit 2	Plasma Membrane	transmembrane receptor
IFNG	**interferon gamma**	**Extracellular Space**	**cytokine**
IFNGR1	interferon gamma receptor 1	Plasma Membrane	transmembrane receptor
IRF4	interferon regulatory factor 4	Nucleus	transcription regulator
IRF8	interferon regulatory factor 8	Nucleus	transcription regulator

JAK1	Janus kinase 1	Cytoplasm	kinase
JAK2	Janus kinase 2	Cytoplasm	kinase
LATS2	large tumor suppressor kinase 2	Nucleus	kinase
LCP2	lymphocyte cytosolic protein 2	Cytoplasm	other
MX2	MX dynamin like GTPase 2	Nucleus	enzyme
NAMPT	nicotinamide phosphoribosyltransferase	Extracellular Space	cytokine
NCOA3	nuclear receptor coactivator 3	Nucleus	transcription regulator
NFKB1	nuclear factor kappa B subunit 1	Nucleus	transcription regulator
NMI	N-myc and STAT interactor	Cytoplasm	transcription regulator
NUP93	nucleoporin 93	Nucleus	other
OAS2	2'-5'-oligoadenylate synthetase 2	Cytoplasm	enzyme
PARP12	poly(ADP-ribose) polymerase family member 12	Nucleus	other
PIAS1	protein inhibitor of activated STAT 1	Nucleus	transcription regulator
PLA2G4A	phospholipase A2 group IVA	Cytoplasm	enzyme
PLSCR1	phospholipid scramblase 1	Plasma Membrane	enzyme
PML	promyelocytic leukemia	Nucleus	transcription regulator
PNP	purine nucleoside phosphorylase	Nucleus	enzyme
PNPT1	polyribonucleotide nucleotidyltransferase 1	Cytoplasm	enzyme
PSMA2	proteasome subunit alpha 2	Cytoplasm	peptidase
PSMA3	proteasome subunit alpha 3	Cytoplasm	peptidase
PSMB2	proteasome subunit beta 2	Cytoplasm	peptidase
RIPK1	receptor interacting serine/threonine kinase 1	Plasma Membrane	kinase
RIPK2	receptor interacting serine/threonine kinase 2	Plasma Membrane	kinase
SAMD9L	sterile alpha motif domain containing 9 like	Extracellular Space	other
SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase	Nucleus	enzyme
SELP	selectin P	Plasma Membrane	transmembrane receptor
SERPING1	serpin family G member 1	Extracellular Space	other
SOD2	superoxide dismutase 2	Cytoplasm	enzyme
SP100	SP100 nuclear antigen	Nucleus	transcription regulator
SP110	SP110 nuclear body protein	Nucleus	transcription regulator
SPPL2A	signal peptide peptidase like 2A	Plasma Membrane	peptidase
SRI	sorcin	Cytoplasm	transporter
SSPN	sarcospan	Plasma Membrane	other
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	Cytoplasm	enzyme
STAT1	**signal transducer and activator of transcription 1**	**Nucleus**	**transcription regulator**
STAT2	signal transducer and activator of transcription 2	Nucleus	transcription regulator
STAT3	**signal transducer and activator of transcription 3**	**Nucleus**	**transcription regulator**
STAT4	signal transducer and activator of transcription 4	Nucleus	transcription regulator
SUMO1	small ubiquitin-like modifier 1	Nucleus	enzyme
TNFSF10	**TNF superfamily member 10**	**Extracellular Space**	**cytokine**
TRAFD1	TRAF-type zinc finger domain containing 1	Other	other
TRIM21	tripartite motif containing 21	Nucleus	enzyme
TRIM25	tripartite motif containing 25	Cytoplasm	transcription regulator
VCAM1	vascular cell adhesion molecule 1	Plasma Membrane	transmembrane receptor
WARS	tryptophanyl-tRNA synthetase	Cytoplasm	enzyme
XAF1	XIAP associated factor 1	Nucleus	other

Supplementary Table S6. List of up-regulated gene sets (FDR < 0.05) in visceral fat of OSA subjects (Study Group 1).

Gene Set Description	Number of Genes	FDR
HALLMARK_PROTEIN_SECRETION	96	>0.001
HALLMARK_MYC_TARGETS_V1	197	>0.001
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	131	>0.001
HALLMARK_INTERFERON_GAMMA_RESPONSE	197	>0.001
REACTOME_MRNA_PROCESSING	149	>0.001
REACTOME_HIV_INFECTION	184	>0.001
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	50	>0.001
REACTOME_HIV_LIFE_CYCLE	105	>0.001
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	133	>0.001
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	111	>0.001
REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	77	>0.001
REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION	79	>0.001
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	118	>0.001
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	>0.001
HALLMARK_MTORC1_SIGNALING	197	>0.001
REACTOME_MRNA_SPLICING	104	>0.001
REACTOME_SIGNALING_BY_WNT	62	>0.001
HALLMARK_INTERFERON_ALPHA_RESPONSE	94	>0.001
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	65	>0.001
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	71	>0.001
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_	18	>0.001
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	234	>0.001
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	92	>0.001
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	>0.001
REACTOME_RNA_POL_II_TRANSCRIPTION	94	>0.001
REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	30	>0.001
REACTOME_TRNA_AMINOACYLATION	42	>0.001
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	>0.001
KEGG_RNA_DEGRADATION	58	>0.001
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	197	>0.001
REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_APC_C_CDH1_TARGETED_	64	>0.001
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	56	>0.001
REACTOME_TRANSCRIPTION	189	>0.001
KEGG_N_GLYCAN_BIOSYNTHESIS	45	>0.001
PID_ALK1_PATHWAY	26	>0.001
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	334	>0.001
PID_RANBP2_PATHWAY	11	>0.001
KEGG_PROTEASOME	44	>0.001
REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	20	>0.001
PID_TRAIL_PATHWAY	28	>0.001
REACTOME_MRNA_3_END_PROCESSING	33	>0.001
PID_CDC42_PATHWAY	70	>0.001
KEGG_SPLICEOSOME	123	>0.001
REACTOME_UNFOLDED_PROTEIN_RESPONSE	73	>0.001
HALLMARK_UV_RESPONSE_DN	142	>0.001
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	17	>0.001
REACTOME_MEMBRANE_TRAFFICKING	122	>0.001
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	63	>0.001
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	16	>0.001
PID_P53_REGULATION_PATHWAY	58	>0.001
REACTOME_METABOLISM_OF_NON_CODING_RNA	45	>0.001

REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	25	>0.001
BIOCARTA_ARAP_PATHWAY	17	>0.001
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1	47	>0.001
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	>0.001
REACTOME_CELL_CYCLE_CHECKPOINTS	111	>0.001
BIOCARTA_FCER1_PATHWAY	38	>0.001
HALLMARK_E2F_TARGETS	199	>0.001
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	198	>0.001
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	0.002
REACTOME_CELL_CYCLE_MITOTIC	303	0.002
BIOCARTA_RAB_PATHWAY	12	0.002
REACTOME_INTERFERON_GAMMA_SIGNALING	58	0.002
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.002
PID_RAC1_PATHWAY	54	0.002
PID_LYMPH_ANGIOGENESIS_PATHWAY	24	0.002
PID_TGFBR_PATHWAY	55	0.002
REACTOME_TCR_SIGNALING	50	0.002
BIOCARTA_ACTINY_PATHWAY	20	0.002
REACTOME_TRANS_GOLGI_NETWORK_VESICLE_BUDDING	56	0.002
REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	25	0.002
REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	13	0.002
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS	80	0.003
PID_BARD1_PATHWAY	29	0.003
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.003
REACTOME_CS_DS_DEGRADATION	12	0.003
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE	53	0.003
REACTOME_ER_PHAGOSOME_PATHWAY	58	0.003
REACTOME_G1_S_TRANSITION	106	0.003
ST_FAS_SIGNALING_PATHWAY	63	0.003
BIOCARTA_SALMONELLA_PATHWAY	13	0.003
KEGG_LYSOSOME	118	0.003
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_EARLY_ENDOSOME_MEMBRANE	12	0.003
BIOCARTA_PROTEASOME_PATHWAY	28	0.003
PID_FAS_PATHWAY	38	0.003
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.003
REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS	14	0.003
REACTOME_COPI_MEDIATED_TRANSPORT	9	0.004
REACTOME_DIABETES_PATHWAYS	122	0.004
REACTOME_INTERFERON_SIGNALING	147	0.004
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	21	0.004
HALLMARK_PI3K_AKT_MTOR_SIGNALING	103	0.004
REACTOME_GOLGI_ASSOCIATED_VESICLE_BIOGENESIS	49	0.004
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	0.004
REACTOME_INTEGRATION_OF_PROVIRUS	8	0.004
HALLMARK_MITOTIC_SPINDLE	198	0.004
PID_ERBB1_DOWNSTREAM_PATHWAY	105	0.004
KEGG_TGF_BETA_SIGNALING_PATHWAY	84	0.004
REACTOME_CELL_CYCLE	391	0.004
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.004
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	0.004
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	19	0.004
REACTOME_MITOTIC_G1_G1_S_PHASES	130	0.004
REACTOME_MITOTIC_M_M_G1_PHASES	164	0.004
REACTOME_TOLL_RECEPTOR_CASCADES	109	0.004

REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	26	0.005
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.005
REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIGOSACCHAF	27	0.005
REACTOME_METABOLISM_OF_RNA	251	0.005
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	87	0.005
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.006
PID_FAK_PATHWAY	58	0.006
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	36	0.006
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.007
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.007
REACTOME_SIGNALING_BY_BMP	22	0.007
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	30	0.007
PID_PDGFRB_PATHWAY	127	0.007
PID_IL8_CXCR2_PATHWAY	33	0.007
REACTOME_PERK_REGULATED_GENE_EXPRESSION	26	0.007
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	49	0.007
REACTOME_REGULATION_OF_APOPTOSIS	56	0.007
BIOCARTA_FAS_PATHWAY	30	0.007
KEGG_PROTEIN_EXPORT	22	0.008
REACTOME_MAP_KINASE_ACTIVATION_IN_TLR_CASCADE	49	0.008
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_XBP1S	42	0.008
PID_CXCR4_PATHWAY	101	0.008
BIOCARTA_RHO_PATHWAY	32	0.008
PID_ANGIOPOIETIN_RECEPTOR_PATHWAY	50	0.008
REACTOME_APOPTOSIS	142	0.008
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	0.008
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	0.008
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	60	0.008
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	25	0.008
REACTOME_ACTIVATED_TLR4_SIGNALLING	89	0.009
BIOCARTA_TCR_PATHWAY	44	0.009
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	25	0.009
REACTOME_PROTEIN_FOLDING	50	0.009
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	0.010
BIOCARTA_CDC42RAC_PATHWAY	16	0.010
PID_FANCONI_PATHWAY	44	0.010
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.010
REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6_ALPHA	11	0.011
REACTOME_PD1_SIGNALING	17	0.011
REACTOME_DOWNSTREAM_TCR_SIGNALING	33	0.011
REACTOME_METAL_ION_SLC_TRANSPORTERS	22	0.011
REACTOME_CALNEXIN_CALRETICULIN_CYCLE	11	0.011
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	43	0.012
HALLMARK_COMPLEMENT	195	0.012
PID_DNA_PK_PATHWAY	16	0.012
KEGG_LEISHMANIA_INFECTION	68	0.012
REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	69	0.012
REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE	13	0.012
REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	55	0.012
HALLMARK_ANDROGEN_RESPONSE	99	0.012
REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	16	0.012
BIOCARTA_MAPK_PATHWAY	86	0.012
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	121	0.012
KEGG_CELL_CYCLE	123	0.013

PID_FCER1_PATHWAY	61	0.013
REACTOME_PI_METABOLISM	47	0.013
REACTOME_TRANSLOCATION_OF_ZAP_70_TO_IMMUNOLOGICAL_SYNAPSE	13	0.013
HALLMARK_TGF_BETA_SIGNALING	54	0.014
BIOCARTA_EIF2_PATHWAY	11	0.014
REACTOME_ACTIVATION_OF_THE_AP1_FAMILY_OF_TRANSCRIPTION_FACTORS	10	0.014
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	89	0.014
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	23	0.014
REACTOME_M_G1_TRANSITION	78	0.015
REACTOME_DNA_REPLICATION	184	0.015
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	62	0.015
PID_SYNDECAN_4_PATHWAY	31	0.015
PID_P38_ALPHA_BETA_PATHWAY	31	0.015
HALLMARK_APICAL_JUNCTION	198	0.015
BIOCARTA_NDKDYNAMIN_PATHWAY	17	0.015
REACTOME_MITOTIC_G2_G2_M_PHASES	77	0.015
REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	80	0.015
BIOCARTA_MEF2D_PATHWAY	18	0.016
REACTOME_PECAM1_INTERACTIONS	9	0.016
REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	109	0.016
PID_HEDGEHOG_GLI_PATHWAY	48	0.016
REACTOME_SMOOTH_MUSCLE_CONTRACTION	23	0.016
REACTOME_MITOTIC_PROMETAPHASE	82	0.016
BIOCARTA_RAC1_PATHWAY	23	0.016
PID_NFAT_3PATHWAY	53	0.016
PID_ALK2_PATHWAY	11	0.017
REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	72	0.018
PID_ATM_PATHWAY	34	0.018
BIOCARTA_PDGF_PATHWAY	32	0.019
REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	24	0.019
PID_WNT_CANONICAL_PATHWAY	20	0.019
REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVAT	74	0.019
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_ATF6_ALPHA	9	0.020
PID_AVB3_OPN_PATHWAY	31	0.021
REACTOME_DARPP_32_EVENTS	24	0.021
PID_NFKAPPAB_CANONICAL_PATHWAY	23	0.021
PID_TCR_PATHWAY	66	0.021
BIOCARTA_HCMV_PATHWAY	17	0.021
REACTOME_REGULATION_OF_IFNG_SIGNALING	13	0.022
REACTOME_METABOLISM_OF_MRNA	209	0.022
HALLMARK_KRAS_SIGNALING_UP	193	0.022
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	92	0.022
BIOCARTA_CERAMIDE_PATHWAY	22	0.022
REACTOME_DEADENYLATION_OF_MRNA	18	0.022
PID_SMAD2_3PATHWAY	17	0.022
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	37	0.023
REACTOME_RNA_POL_I_TRANSCRIPTION_INITIATION	22	0.023
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_LATE_ENDOSOME_MEMBRANE	10	0.023
REACTOME_APOBEC3G_MEDIATED_RESISTANCE_TO_HIV1_INFECTION	5	0.023
BIOCARTA_HIVNEF_PATHWAY	57	0.024
PID_AVB3_INTEGRIN_PATHWAY	74	0.024
BIOCARTA_TGFB_PATHWAY	19	0.024
BIOCARTA_STRESS_PATHWAY	25	0.025
BIOCARTA_ATRBRCA_PATHWAY	20	0.025

KEGG_COLORECTAL_CANCER	62	0.025
PID_AR_PATHWAY	60	0.026
PID_CDC42_REG_PATHWAY	29	0.026
BIOCARTA_EPHA4_PATHWAY	9	0.026
BIOCARTA_TNFR1_PATHWAY	29	0.027
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	256	0.027
REACTOME_RNA_POL_II_TRANSCRIPTION_PRE_INITIATION_AND_PROMOTER_OPENING	37	0.027
REACTOME_RNA_POL_I_TRANSCRIPTION	77	0.027
PID_VEGFR1_2_PATHWAY	67	0.028
REACTOME_PHOSPHORYLATION_OF_CD3_AND_TCR_ZETA_CHAINS	15	0.028
ST_JNK_MAPK_PATHWAY	40	0.028
KEGG_NON_HOMOLOGOUS_END_JOINING	13	0.030
REACTOME_METABOLISM_OF_PROTEINS	415	0.030
REACTOME_IKK_COMPLEX_RECRUITMENT_MEDIATED_BY_RIP1	9	0.030
REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC	20	0.030
REACTOME_TIE2_SIGNALING	17	0.031
REACTOME_KERATAN_SULFATE_DEGRADATION	11	0.031
HALLMARK_G2M_CHECKPOINT	199	0.033
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	17	0.033
BIOCARTA_TCRA_PATHWAY	11	0.033
REACTOME_ERK_MAPK_TARGETS	21	0.035
KEGG_APOPTOSIS	86	0.036
REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	21	0.036
REACTOME_SYNTHESIS_OF_DNA	90	0.036
REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING	18	0.036
PID_TOLL_ENDOGENOUS_PATHWAY	25	0.036
REACTOME_SIGNALING_BY_NOTCH1	67	0.037
PID_MAPK_TRK_PATHWAY	34	0.038
PID_INTEGRIN5_PATHWAY	17	0.039
REACTOME_SEMA3A_PAK_DEPENDENT_AXON_REPULSION	14	0.039
BIOCARTA_THELPER_PATHWAY	12	0.039
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	24	0.039
KEGG_OTHER_GLYCAN_DEGRADATION	16	0.039
PID_NFKAPPAB_ATYPICAL_PATHWAY	17	0.039
REACTOME_S_PHASE	106	0.039
PID_MYC_PATHWAY	24	0.039
REACTOME_COLLAGEN_FORMATION	54	0.040
REACTOME_NOD1_2_SIGNALING_PATHWAY	28	0.040
BIOCARTA_MET_PATHWAY	36	0.041
REACTOME_DNA_REPAIR	101	0.041
BIOCARTA_41BB_PATHWAY	16	0.041
BIOCARTA_RNA_PATHWAY	10	0.042
KEGG_ENDOCYTOSIS	176	0.042
REACTOME_RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2_	79	0.042
REACTOME_REGULATION_OF_KIT_SIGNALING	16	0.043
PID_EPHB_FWD_PATHWAY	40	0.044
PID_RHOA_PATHWAY	45	0.044
REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS	14	0.044
BIOCARTA_D4GDI_PATHWAY	13	0.044
REACTOME_MRNA_CAPPING	27	0.044
PID_INTEGRIN1_PATHWAY	65	0.044
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	33	0.045
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUI	16	0.045
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	0.045

REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	177	0.045
BIOCARTA_BCR_PATHWAY	34	0.045
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	60	0.045
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIG	43	0.045
BIOCARTA_LEPTIN_PATHWAY	10	0.045
PID_ARF_3PATHWAY	19	0.045
PID_ERBB2_ERBB3_PATHWAY	44	0.045
PID_ILK_PATHWAY	45	0.046
BIOCARTA_RANKL_PATHWAY	14	0.046
REACTOME_RNA_POL_III_TRANSCRIPTION	33	0.047
REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEINS	26	0.048
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	44	0.048
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	44	0.048
KEGG_BASAL_TRANSCRIPTION_FACTORS	32	0.048
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	22	0.049
REACTOME_DOUBLE_STRAND_BREAK_REPAIR	22	0.049
REACTOME_MYOGENESIS	26	0.049
PID_INTEGRIN3_PATHWAY	42	0.050

Supplementary Table S7. List of down-regulated gene sets (FDR < 0.05) in visceral fat of OSA subjects (Study Group 1).

Gene Set Description	Number of Genes	FDR
REACTOME_OLFACTORY_SIGNALING_PATHWAY	315	>0.001
KEGG_OLFACTORY_TRANSDUCTION	376	>0.001
REACTOME_BETA_DEFENSINS	34	>0.001
REACTOME_DEFENSINS	41	>0.001
KEGG_RETINOL_METABOLISM	53	>0.001
REACTOME_XENOBIOTICS	15	>0.001
KEGG_STEROID_HORMONE_BIOSYNTHESIS	45	>0.001
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	60	0.001
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	62	0.003
KEGG_LINOLEIC_ACID_METABOLISM	27	0.005
REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	21	0.007
PID_CONE_PATHWAY	23	0.008
REACTOME_GABA_A_RECEPTOR_ACTIVATION	12	0.009
BIOCARTA_CYTOKINE_PATHWAY	19	0.014
REACTOME_REGULATION_OF_IFNA_SIGNALING	21	0.014
REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS	11	0.015
REACTOME_HORMONE_LIGAND_BINDING_RECEPTORS	10	0.016
REACTOME_CYTOCHROME_P450_ARRANGED_BY_SUBSTRATE_TYPE	50	0.017
REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT	13	0.019
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	280	0.019
KEGG_PPAR_SIGNALING_PATHWAY	68	0.021
KEGG_STARCH_AND_SUCROSE_METABOLISM	41	0.024
REACTOME_STRIATED_MUSCLE_CONTRACTION	27	0.028
PID_RHODOPSIN_PATHWAY	24	0.029
REACTOME_BIOLOGICAL_OXIDATIONS	126	0.029
HALLMARK_KRAS_SIGNALING_DN	192	0.029
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	265	0.040
NABA_SECRETED_FACTORS	328	0.041
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	247	0.041
REACTOME_POTASSIUM_CHANNELS	97	0.044
REACTOME_INTERACTION_BETWEEN_L1_AND_ANKYRINS	21	0.045
REACTOME_BILE_ACID_AND_BILE_SALT_METABOLISM	27	0.046

Supplementary Table S8. List of up-regulated gene sets (FDR < 0.05) in subcutaneous fat of OSA subjects after CPAP therapy (Study Group 2).

Gene Set Description	Number of Genes	FDR
HALLMARK_MYC_TARGETS_V2	56	>0.001
HALLMARK_TNFA_SIGNALING_VIA_NFKB	197	>0.001
REACTOME_CHOLESTEROL_BIOSYNTHESIS	21	>0.001
KEGG_STEROID_BIOSYNTHESIS	16	>0.001
HALLMARK_MYC_TARGETS_V1	197	>0.001
REACTOME_MRNA_SPLICING	104	>0.001
REACTOME_MRNA_PROCESSING	149	>0.001
PID_AP1_PATHWAY	68	>0.001
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	131	0.001
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	40	0.002
REACTOME_RNA_POL_II_TRANSCRIPTION	94	0.003
BIOCARTA_CARDIACEGF_PATHWAY	18	0.004
KEGG_SPLICEOSOME	123	0.004
REACTOME_TRNA_AMINOACYLATION	42	0.006
HALLMARK_E2F_TARGETS	199	0.006
KEGG_STEROID_HORMONE_BIOSYNTHESIS	45	0.007
PID_P38_ALPHA_BETA_DOWNSTREAM_PATHWAY	38	0.007
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	15	0.01
REACTOME_UNFOLDED_PROTEIN_RESPONSE	73	0.011
REACTOME_CLEAVAGE_OF_GROWING_TRANSCRIPT_IN_THE_TERMINATION_REGION_	42	0.012
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	0.011
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX	54	0.012
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0	50	0.013
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX	63	0.013
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	33	0.014
PID_S1P_S1P2_PATHWAY	24	0.014
REACTOME_FORMATION_OF_RNA_POL_II_ELONGATION_COMPLEX_	37	0.013
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN	65	0.015
REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA	23	0.016
PID_NFAT_TFPATHWAY	45	0.016
REACTOME_MITOTIC_G1_G1_S_PHASES	130	0.015
PID_ATF2_PATHWAY	56	0.016
PID_MYC_ACTIV_PATHWAY	76	0.016
REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6	46	0.016
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	0.018
REACTOME_PERK_REGULATED_GENE_EXPRESSION	26	0.018
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	45	0.018
BIOCARTA_CCR5_PATHWAY	17	0.02
REACTOME_MITOTIC_M_M_G1_PHASES	164	0.02
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC	48	0.02
BIOCARTA_CDMAC_PATHWAY	16	0.023
REACTOME_SIGNALING_BY_WNT	62	0.024
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	111	0.024
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1	49	0.026
REACTOME_ACTIVATION_OF_CHAPERONE_GENES_BY_ATF6_ALPHA	9	0.027
REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS	61	0.026
REACTOME_ELONGATION_ARREST_AND_RECOVERY	27	0.026
KEGG_PROTEASOME	44	0.026
BIOCARTA_RANMS_PATHWAY	10	0.027
REACTOME_DNA_REPLICATION	184	0.027
REACTOME_HIV_INFECTION	184	0.031
PID_CIRCADIAN_PATHWAY	16	0.032

REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	118	0.032
REACTOME_G0_AND_EARLY_G1	23	0.034
REACTOME_METABOLISM_OF_RNA	251	0.035
REACTOME_CELL_CYCLE_MITOTIC	303	0.034
REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	34	0.034
REACTOME_METABOLISM_OF_NUCLEOTIDES	68	0.036
REACTOME_G1_S_TRANSITION	106	0.036
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT	48	0.036
REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC_ORIGIN_COMPLEX	11	0.036
HALLMARK_CHOLESTEROL_HOMEOSTASIS	73	0.037
REACTOME_ACTIVATION_OF_CHAPERONES_BY_ATF6_ALPHA	11	0.036
KEGG_CIRCADIAN_RHYTHM_MAMMAL	13	0.036
REACTOME_MRNA_3_END_PROCESSING	33	0.036
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21	53	0.036
PID_REG_GR_PATHWAY	79	0.036
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	17	0.037
REACTOME_M_G1_TRANSITION	78	0.037
BIOCARTA_DREAM_PATHWAY	14	0.038
PID_IL6_7_PATHWAY	47	0.037
REACTOME_SLBP_DEPENDENT_PROCESSING_OF_REPLICATION_DEPENDENT_HISTONE_PRE_MRNAS	11	0.037
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_	62	0.037
REACTOME_P2Y_RECEPTORS	11	0.037
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	52	0.037
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	30	0.037
KEGG_TAURINE_AND_HYPOTAURINE_METABOLISM	10	0.037
BIOCARTA_PROTEASOME_PATHWAY	28	0.039
REACTOME_MITOTIC_PROMETAPHASE	82	0.039
PID_TCR_CALCIUM_PATHWAY	27	0.041
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	0.042
REACTOME_ACTIVATION_OF_GENES_BY_ATF4	23	0.045
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G	49	0.047
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	50	0.047
REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	92	0.048
REACTOME_DEFENSINS	41	0.048
PID_AVB3_OPN_PATHWAY	31	0.049
REACTOME_S_PHASE	106	0.049

Supplementary Table S9. Cholesterol biosynthesis steps mediated by up-regulated genes in subcutaneous fat after CPAP therapy in OSA subjects (Study Group 2).

1. ACAT2: condenses 2 Ac-CoA to form ACA-CoA
2. HMGCS1: condenses Ac-CoA and ACA-CoA to form bHMG-CoA
3. HMGCR: reduction of HMG-CoA produces mevalonate
4. MVK: mevalonate is phosphorylated to mevalonate-5-phosphate
5. MVD: decarboxylates MVA5PP to IPPP
6. IDL1/IDL2: isopentenyl pyrophosphate rearranges to dimethylallyl pyrophosphate
7. FDPS: addition of isopentenyl pyrophosphate to DMAPP
8. FDPS: another isopentenyl pyrophosphate is added to geranyl pyrophosphate
9. FDFT: two FPP molecules dimerize to form presqualene diphosphate
10. FDFT: reduction of presqualene diphosphate to form squalene
11. SQLE: squalene is oxidized to its epoxide
12. LSS: squalene 2,3-epoxide cyclizes, forming lanosterol
13. CYP51A1: demethylates LNSOL
14. TM7SF2: 4,4-dimethylcholesta-8(9),14,24-trien-3beta-ol is reduced to 4,4-dimethylcholesta-8(9),24-dien-3beta-ol
15. MSMO1: 4,4-dimethylcholesta-8(9),24-dien-3beta-ol is oxidized to 4-methyl,4-carboxycholesta-8(9),24-dien-3beta-ol
16. NSDHL: 4-methyl,4-carboxycholesta-8(9),24-dien-3beta-ol is decarboxylated and oxidized to form 4-methylcholesta-8(9),
17. HSD17B7: 4-methylcholesta-8(9),24-dien-3-one is reduced to 4-methylcholesta-8(9),24-dien-3beta-ol
18. MSMO1: 4-methylcholesta-8(9),24-dien-3beta-ol is oxidized to 4-carboxycholesta-8(9),24-dien-3beta-ol
19. NSDHL : 4-carboxycholesta-8(9),24-dien-3beta-ol is decarboxylated and oxidized to form cholesta-8(9),24-dien-3-one (zy
20. HSD17B7: zymosterone (cholesta-8(9),24-dien-3-one) is reduced to zymosterol (cholesta-8(9),24-dien-3beta-ol)
21. EBP: zymosterol is isomerized to cholesta-7,24-dien-3beta-ol
22. DHCR7: cholesta-5,7,24-trien-3beta-ol is reduced to desmosterol
23. EBP: isomerizes ZYMSTNL to LTHSOL
24. DHCR7: reduces 7-dehydroCHOL to CHOLESTEROL