

## **Angiogenin and Osteoprotegerin are type II muscle specific myokines protecting pancreatic beta-cells against proinflammatory cytokines**

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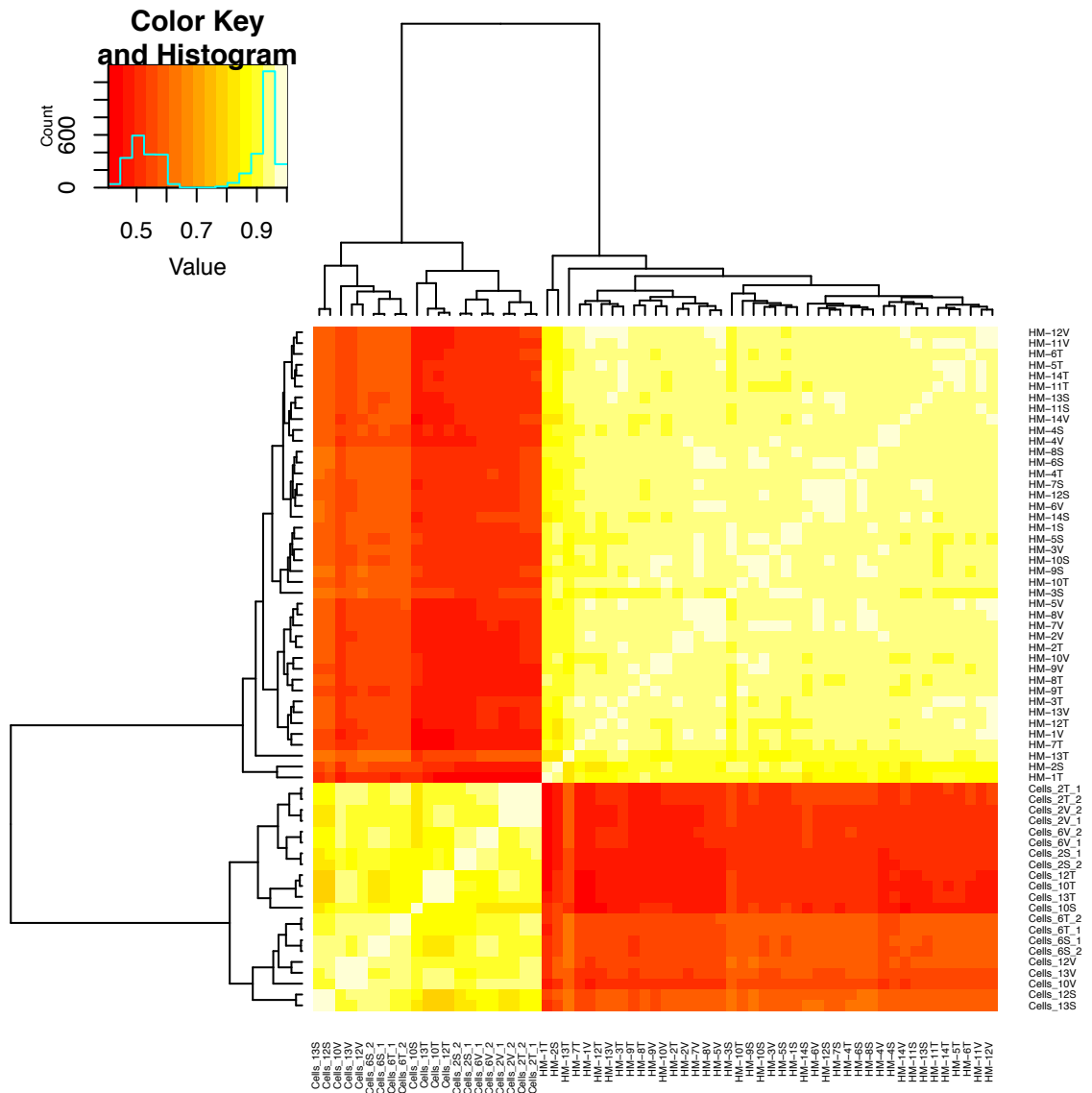
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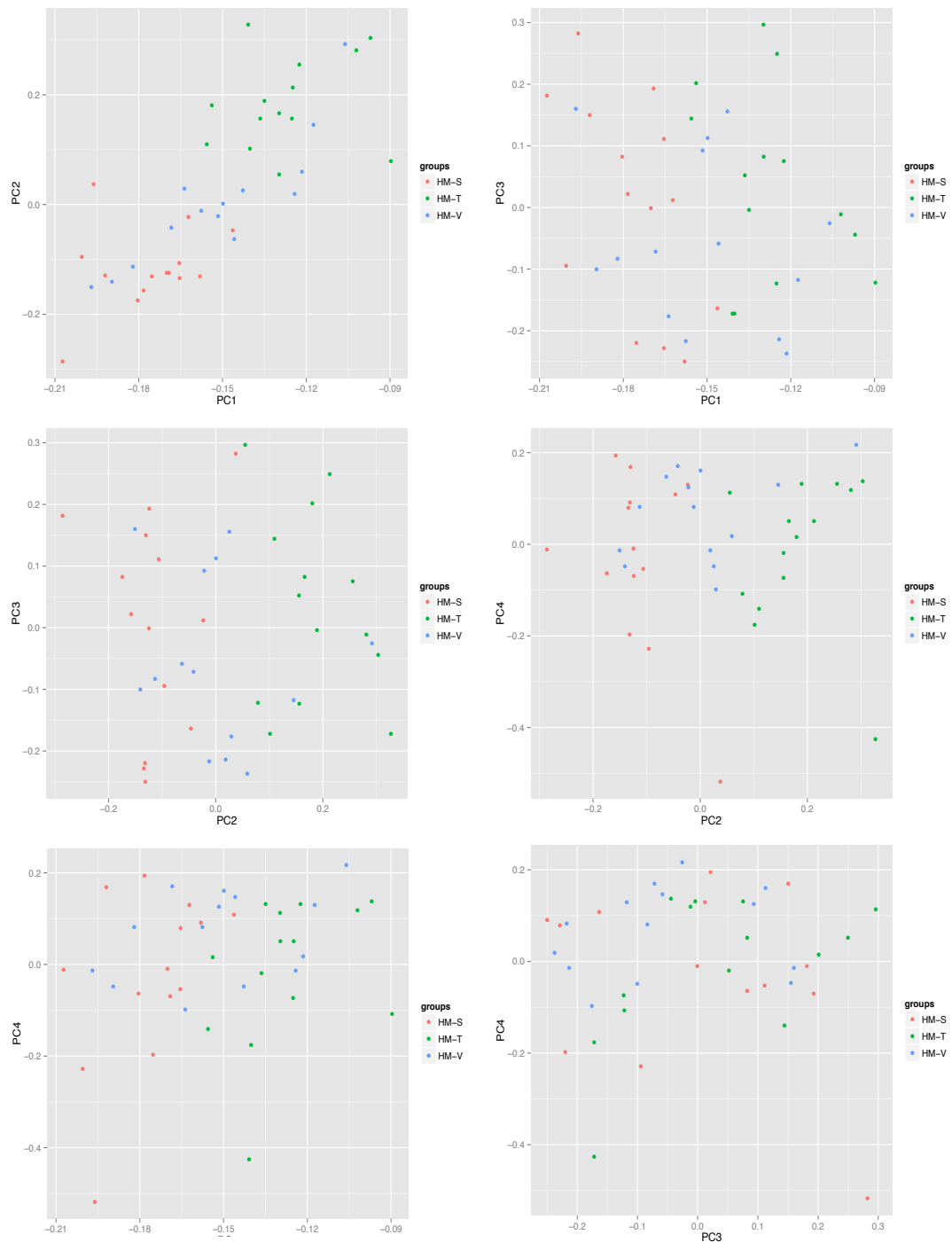
\* : Equally contribution

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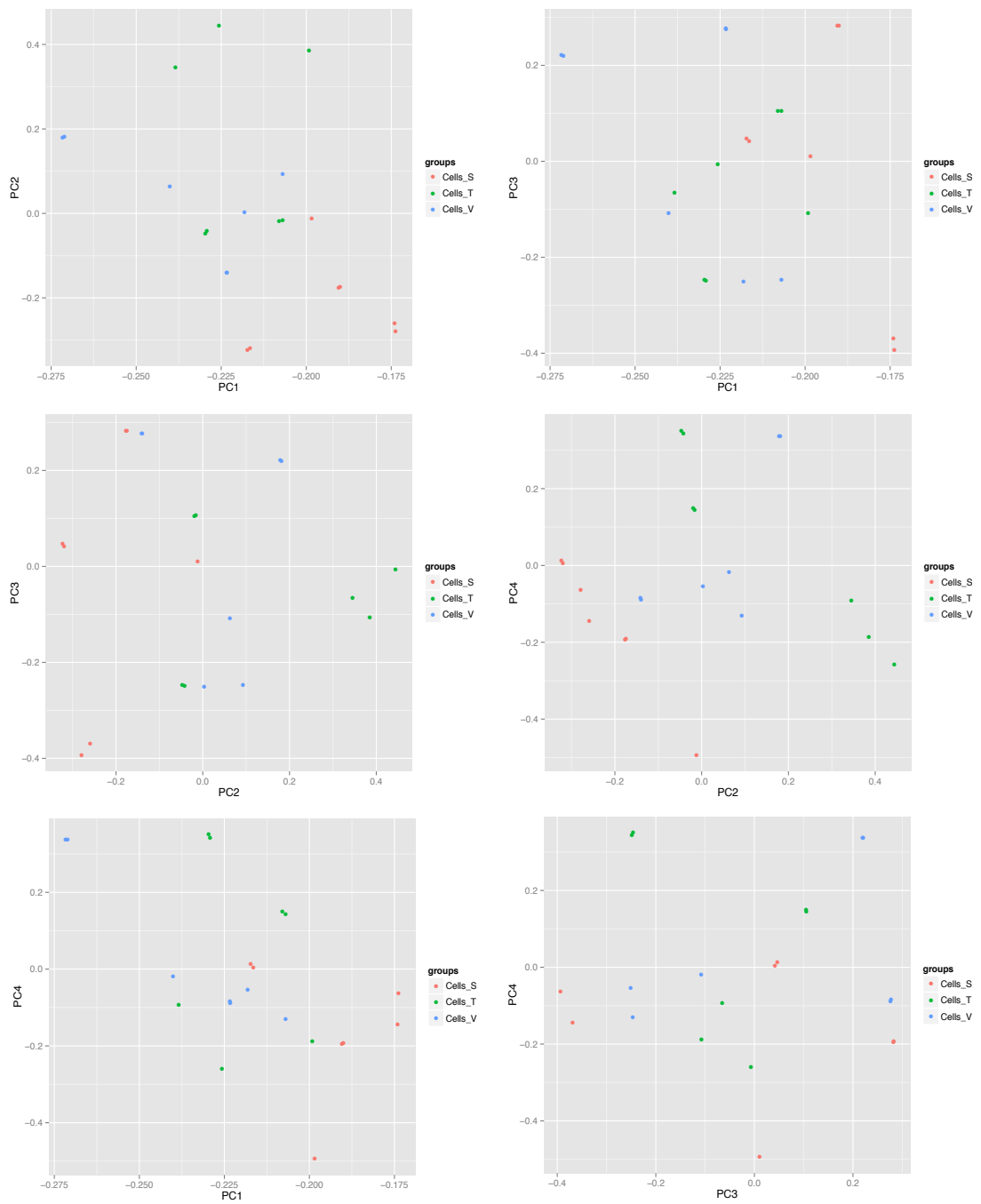
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**Figure S1:** Hierarchical clustering of the spearman correlation coefficients of RPKM values. Genes having a RPKM value  $\geq 1$  in at least 90% of the samples were taken into account. Myotubes are well segregated from biopsies but the type of tissue (soleus, triceps and vastus) doesn't cluster together.



**Figure S2:** principal component analysis of the RPKM values of all genes with a RPKM  $\geq 1$  in at least 90% of the samples. Only biopsies were kept. Principal component 2 (PC2 axis) separates the soleus (HM-S) from the triceps (HM-T) whereas the vastus (HM-V) is spread all over PC2 suggesting the heterogeneous nature of this tissue (mix of type I and type II fibers).



**Figure S3:** principal component analysis of the RPKM values of all genes with an RPKM  $\geq 1$  in at least 90% of the samples. Only myotubes were kept.

**Table S1:** GO terms and KEGG pathways of the the differentially expressed genes in Cells-S versus Cells-T/Biopsies-S versus Biopsies-T (A and D), Cells-T versus Cells –S (B and E) and Biopsies-S versus Biopsies-T (C and F).

**A** Cells-S\_vs\_Cells-T/Biopsies-S\_vs\_Biopsies-T, 864 genes

GO terms	stats	adj_pvalue
organ_development	C=1538;O=167;E=112.45;R=1.49;rawP=1.54e-08	2.28E-05
system_development	C=2158;O=220;E=157.79;R=1.39;rawP=8.08e-09	2.28E-05
anatomical_structure_development	C=2485;O=244;E=181.70;R=1.34;rawP=2.67e-08	2.63E-05
developmental_process	C=2782;O=266;E=203.41;R=1.31;rawP=5.38e-08	3.98E-05
cell_migration	C=531;O=73;E=38.83;R=1.88;rawP=6.92e-08	4.09E-05
localization_of_cell	C=562;O=75;E=41.09;R=1.83;rawP=1.56e-07	6.59E-05
cell_motility	C=562;O=75;E=41.09;R=1.83;rawP=1.56e-07	6.59E-05
anatomical_structure_morphogenesis	C=1331;O=143;E=97.32;R=1.47;rawP=4.63e-07	1.00E-04
cellular_component_movement	C=754;O=92;E=55.13;R=1.67;rawP=3.84e-07	1.00E-04
multicellular_organismal_development	C=2475;O=238;E=180.96;R=1.32;rawP=2.99e-07	1.00E-04
locomotion	C=752;O=92;E=54.98;R=1.67;rawP=3.40e-07	1.00E-04
tissue_development	C=931;O=106;E=68.07;R=1.56;rawP=1.40e-06	3.00E-04
regulation_of_developmental_process	C=905;O=103;E=66.17;R=1.56;rawP=2.07e-06	5.00E-04
multicellular_organismal_process	C=3152;O=286;E=230.47;R=1.24;rawP=2.17e-06	5.00E-04
single-multicellular_organism_process	C=3142;O=284;E=229.73;R=1.24;rawP=3.51e-06	7.00E-04
skeletal_system_development	C=251;O=39;E=18.35;R=2.13;rawP=5.08e-06	9.00E-04
cell_differentiation	C=1568;O=157;E=114.65;R=1.37;rawP=8.45e-06	1.30E-03
immune_system_process	C=1012;O=110;E=73.99;R=1.49;rawP=7.90e-06	1.30E-03
cellular_developmental_process	C=1686;O=167;E=123.28;R=1.35;rawP=7.50e-06	1.30E-03
regulation_of_blood_vessel_endothelial_cell_migration	C=31;O=10;E=2.27;R=4.41;rawP=4.41e-05	6.50E-03
cell_fate_commitment	C=112;O=21;E=8.19;R=2.56;rawP=5.13e-05	7.20E-03
enzyme_linked_receptor_protein_signaling_pathway	C=628;O=72;E=45.92;R=1.57;rawP=6.67e-05	8.60E-03
single-organism_process	C=4462;O=374;E=326.25;R=1.15;rawP=6.95e-05	8.60E-03
actin_cytoskeleton_organization	C=310;O=42;E=22.67;R=1.85;rawP=6.68e-05	8.60E-03
biological_adhesion	C=533;O=62;E=38.97;R=1.59;rawP=0.0001	9.50E-03
skeletal_system_morphogenesis	C=118;O=21;E=8.63;R=2.43;rawP=0.0001	9.50E-03
blood_vessel_endothelial_cell_migration	C=48;O=12;E=3.51;R=3.42;rawP=0.0001	9.50E-03
regulation_of_cellular_response_to_growth_factor_stimulus	C=34;O=10;E=2.49;R=4.02;rawP=0.0001	9.50E-03
regionalization	C=174;O=27;E=12.72;R=2.12;rawP=0.0001	9.50E-03
cell_proliferation	C=990;O=103;E=72.39;R=1.42;rawP=9.87e-05	9.50E-03
cell_adhesion	C=532;O=62;E=38.90;R=1.59;rawP=0.0001	9.50E-03
negative_regulation_of_phosphorus_metabolic_process	C=188;O=28;E=13.75;R=2.04;rawP=0.0002	1.52E-02
metanephros_development	C=50;O=12;E=3.66;R=3.28;rawP=0.0002	1.52E-02
cell_surface_receptor_signaling_pathway	C=1364;O=133;E=99.73;R=1.33;rawP=0.0002	1.52E-02
organ_morphogenesis	C=487;O=57;E=35.61;R=1.60;rawP=0.0002	1.52E-02
connective_tissue_development	C=131;O=22;E=9.58;R=2.30;rawP=0.0002	1.52E-02
epithelium_development	C=357;O=45;E=26.10;R=1.72;rawP=0.0002	1.52E-02
negative_regulation_of_phosphate_metabolic_process	C=188;O=28;E=13.75;R=2.04;rawP=0.0002	1.52E-02
vasculature_development	C=368;O=46;E=26.91;R=1.71;rawP=0.0002	1.52E-02
peptide_cross-linking	C=14;O=6;E=1.02;R=5.86;rawP=0.0003	2.06E-02
growth_factor_binding	C=79;O=19;E=5.74;R=3.31;rawP=2.52e-06	1.40E-03
actin_binding	C=269;O=40;E=19.55;R=2.05;rawP=9.92e-06	2.80E-03
cytoskeletal_protein_binding	C=482;O=59;E=35.03;R=1.68;rawP=4.29e-05	8.10E-03
cell_adhesion_molecule_binding	C=35;O=10;E=2.54;R=3.93;rawP=0.0001	1.13E-02
calcium_ion_binding	C=350;O=45;E=25.44;R=1.77;rawP=0.0001	1.13E-02
extracellular_matrix_binding	C=30;O=9;E=2.18;R=4.13;rawP=0.0002	1.88E-02
glycosaminoglycan_binding	C=92;O=17;E=6.69;R=2.54;rawP=0.0003	2.42E-02
extracellular_region_part	C=482;O=70;E=35.37;R=1.98;rawP=1.79e-08	6.75E-06
cell_periphery	C=1999;O=205;E=146.68;R=1.40;rawP=4.59e-08	7.72E-06
plasma_membrane	C=1946;O=200;E=142.79;R=1.40;rawP=6.14e-08	7.72E-06
extracellular_region	C=815;O=100;E=59.80;R=1.67;rawP=1.14e-07	1.07E-05
plasma_membrane_part	C=889;O=102;E=65.23;R=1.56;rawP=2.15e-06	2.00E-04
extracellular_space	C=357;O=51;E=26.20;R=1.95;rawP=2.77e-06	2.00E-04
extracellular_matrix	C=226;O=37;E=16.58;R=2.23;rawP=2.85e-06	2.00E-04
stress_fiber	C=43;O=13;E=3.16;R=4.12;rawP=7.46e-06	4.00E-04
proteinaceous_extracellular_matrix	C=187;O=31;E=13.72;R=2.26;rawP=1.40e-05	5.00E-04
actin_filament_bundle	C=45;O=13;E=3.30;R=3.94;rawP=1.30e-05	5.00E-04
actomyosin	C=52;O=14;E=3.82;R=3.67;rawP=1.48e-05	5.00E-04
integral_to_plasma_membrane	C=496;O=62;E=36.39;R=1.70;rawP=2.00e-05	6.00E-04
intrinsic_to_plasma_membrane	C=519;O=64;E=38.08;R=1.68;rawP=2.26e-05	7.00E-04
cortical_cytoskeleton	C=37;O=11;E=2.71;R=4.05;rawP=4.49e-05	1.20E-03
adherens_junction	C=161;O=26;E=11.81;R=2.20;rawP=0.0001	2.50E-03
microvillus_membrane	C=9;O=5;E=0.66;R=7.57;rawP=0.0002	4.40E-03
microvillus	C=36;O=10;E=2.64;R=3.79;rawP=0.0002	4.40E-03
cell_cortex	C=134;O=22;E=9.83;R=2.24;rawP=0.0003	5.70E-03
anchoring_junction	C=170;O=26;E=12.47;R=2.08;rawP=0.0003	0.0057
cytoplasmic_vesicle_part	C=248;O=34;E=18.20;R=1.87;rawP=0.0003	0.0057
cell_cortex_part	C=61;O=13;E=4.48;R=2.90;rawP=0.0004	0.0072
Golgi_lumen	C=33;O=9;E=2.42;R=3.72;rawP=0.0005	0.0086
membrane	C=4169;O=348;E=305.90;R=1.14;rawP=0.0006	0.0094
cytoplasmic_membrane-bounded_vesicle_lumen	C=34;O=9;E=2.49;R=3.61;rawP=0.0006	0.0094
vesicle_lumen	C=35;O=9;E=2.57;R=3.50;rawP=0.0007	0.0106
neuronal_cell_body	C=156;O=23;E=11.45;R=2.01;rawP=0.0010	0.0145
lytic_vacuole	C=253;O=32;E=18.56;R=1.72;rawP=0.0017	0.0221
lysosome	C=253;O=32;E=18.56;R=1.72;rawP=0.0017	0.0221
cell_body	C=172;O=24;E=12.62;R=1.90;rawP=0.0017	0.0221
secretory_granule_lumen	C=33;O=8;E=2.42;R=3.30;rawP=0.0022	0.0266
cell_projection	C=717;O=73;E=52.61;R=1.39;rawP=0.0023	0.0266
platelet_alpha_granule	C=41;O=9;E=3.01;R=2.99;rawP=0.0024	0.0266
platelet_alpha_granule_lumen	C=33;O=8;E=2.42;R=3.30;rawP=0.0022	0.0266
cell_surface	C=248;O=31;E=18.20;R=1.70;rawP=0.0024	0.0266
cell-substrate_junction	C=119;O=18;E=8.73;R=2.06;rawP=0.0025	0.0269
lamellipodium	C=101;O=16;E=7.41;R=2.16;rawP=0.0027	0.0283
vesicle_membrane	C=220;O=28;E=16.14;R=1.73;rawP=0.0029	0.0295
apical_part_of_cell	C=141;O=20;E=10.35;R=1.93;rawP=0.0033	0.0327
cell-substrate_adherens_junction	C=114;O=17;E=8.36;R=2.03;rawP=0.0038	0.0367
cell_junction	C=427;O=46;E=31.33;R=1.47;rawP=0.0052	0.0461

B

## Cells-S\_vs\_Cells-T, 2071 genes

GO terms	stats	adj_pvalue
multicellular_organismal_process	C=2814;O=616;E=485.36;R=1.27;rawP=2.19e-15	5.90E-12
single-multicellular_organism_process	C=2806;O=614;E=483.98;R=1.27;rawP=2.84e-15	5.90E-12
developmental_process	C=2516;O=557;E=433.96;R=1.28;rawP=1.67e-14	2.31E-11
multicellular_organismal_development	C=2232;O=500;E=384.97;R=1.30;rawP=1.18e-13	1.23E-10
anatomical_structure_morphogenesis	C=1189;O=297;E=205.08;R=1.45;rawP=1.78e-13	1.48E-10
single-organism_process	C=4040;O=820;E=696.82;R=1.18;rawP=7.17e-13	4.97E-10
system_development	C=1935;O=439;E=333.75;R=1.32;rawP=1.22e-12	7.25E-10
anatomical_structure_development	C=2243;O=496;E=386.87;R=1.28;rawP=1.87e-12	9.72E-10
cellular_developmental_process	C=1514;O=352;E=261.13;R=1.35;rawP=2.27e-11	1.05E-08
anatomical_structure_formation_involved_in_morphogenesis	C=928;O=235;E=160.06;R=1.47;rawP=2.68e-11	1.11E-08
cell_differentiation	C=1400;O=326;E=241.47;R=1.35;rawP=1.39e-10	5.25E-08
organ_morphogenesis	C=436;O=126;E=75.20;R=1.68;rawP=4.16e-10	1.44E-07
nervous_system_development	C=954;O=235;E=164.55;R=1.43;rawP=4.88e-10	1.56E-07
cell_development	C=820;O=207;E=141.43;R=1.46;rawP=7.01e-10	2.08E-07
organ_development	C=1380;O=318;E=238.02;R=1.34;rawP=9.31e-10	2.58E-07
regulation_of_developmental_process	C=810;O=203;E=139.71;R=1.45;rawP=2.04e-09	5.30E-07
response_to_wounding	C=570;O=152;E=98.31;R=1.55;rawP=3.48e-09	8.51E-07
cellular_component_morphogenesis	C=598;O=157;E=103.14;R=1.52;rawP=6.15e-09	1.40E-06
extracellular_matrix_organization	C=123;O=48;E=21.21;R=2.26;rawP=6.71e-09	1.40E-06
extracellular_structure_organization	C=123;O=48;E=21.21;R=2.26;rawP=6.71e-09	1.40E-06
cell_morphogenesis	C=567;O=150;E=97.80;R=1.53;rawP=8.01e-09	1.59E-06
cell_proliferation	C=913;O=221;E=157.47;R=1.40;rawP=9.25e-09	1.75E-06
tissue_development	C=833;O=204;E=143.68;R=1.42;rawP=1.43e-08	2.59E-06
regulation_of_cell_differentiation	C=562;O=146;E=96.93;R=1.51;rawP=4.59e-08	7.95E-06
regulation_of_cell_proliferation	C=688;O=172;E=118.67;R=1.45;rawP=5.05e-08	8.40E-06
positive_regulation_of_cell_differentiation	C=274;O=82;E=47.26;R=1.74;rawP=1.04e-07	1.66E-05
positive_regulation_of_developmental_process	C=373;O=104;E=64.33;R=1.62;rawP=1.16e-07	1.79E-05
locomotion	C=674;O=167;E=116.25;R=1.44;rawP=1.55e-07	2.30E-05
localization_of_cell	C=508;O=132;E=87.62;R=1.51;rawP=2.11e-07	2.74E-05
cell_motility	C=508;O=132;E=87.62;R=1.51;rawP=2.11e-07	2.74E-05
regulation_of_biological_quality	C=1342;O=298;E=231.47;R=1.29;rawP=1.99e-07	2.74E-05
cellular_component_movement	C=676;O=167;E=116.60;R=1.43;rawP=1.91e-07	2.74E-05
regulation_of_multicellular_organismal_development	C=600;O=151;E=103.49;R=1.46;rawP=2.34e-07	2.95E-05
regulation_of_localization	C=733;O=178;E=126.43;R=1.41;rawP=2.56e-07	2.97E-05
skeletal_system_development	C=227;O=70;E=39.15;R=1.79;rawP=2.57e-07	2.97E-05
positive_regulation_of_cell_proliferation	C=351;O=98;E=60.54;R=1.62;rawP=2.53e-07	2.97E-05
regulation_of_multicellular_organismal_process	C=914;O=214;E=157.65;R=1.36;rawP=2.81e-07	3.16E-05
cell_migration	C=478;O=125;E=82.45;R=1.52;rawP=3.12e-07	3.41E-05
cell_adhesion	C=484;O=126;E=83.48;R=1.51;rawP=3.64e-07	3.88E-05
biological_adhesion	C=485;O=126;E=83.65;R=1.51;rawP=4.11e-07	4.27E-05
transmembrane_signaling_receptor_activity	C=204;O=63;E=35.11;R=1.79;rawP=8.98e-07	3.00E-04
signal_transducer_activity	C=458;O=118;E=78.83;R=1.50;rawP=1.39e-06	3.00E-04
molecular_transducer_activity	C=458;O=118;E=78.83;R=1.50;rawP=1.39e-06	3.00E-04
receptor_activity	C=343;O=95;E=59.03;R=1.61;rawP=5.26e-07	3.00E-04
signaling_receptor_activity	C=248;O=69;E=42.68;R=1.62;rawP=1.63e-05	2.60E-03
G-protein_coupled_receptor_activity	C=69;O=26;E=11.88;R=2.19;rawP=3.84e-05	5.20E-03
receptor_binding	C=600;O=136;E=103.27;R=1.32;rawP=0.0002	2.31E-02
amino_acid_transmembrane_transporter_activity	C=35;O=15;E=6.02;R=2.49;rawP=0.0003	2.43E-02
protease_binding	C=35;O=15;E=6.02;R=2.49;rawP=0.0003	2.43E-02
3',5'-cyclic-nucleotide_phosphodiesterase_activity	C=10;O=7;E=1.72;R=4.07;rawP=0.0003	2.43E-02
lipid_binding	C=408;O=95;E=70.22;R=1.35;rawP=0.0008	4.98E-02
neutral_amino_acid_transmembrane_transporter_activity	C=14;O=8;E=2.41;R=3.32;rawP=0.0008	4.98E-02
cyclic-nucleotide_phosphodiesterase_activity	C=11;O=7;E=1.89;R=3.70;rawP=0.0008	4.98E-02
extracellular_region	C=707;O=218;E=121.89;R=1.79;rawP=1.46e-20	6.88E-18
extracellular_region_part	C=416;O=128;E=71.72;R=1.78;rawP=2.93e-12	6.90E-10
proteinaceous_extracellular_matrix	C=164;O=62;E=28.27;R=2.19;rawP=2.02e-10	3.17E-08
intrinsic_to_membrane	C=2210;O=477;E=381.01;R=1.25;rawP=7.28e-10	8.57E-08
cell_periphery	C=1771;O=391;E=305.32;R=1.28;rawP=2.94e-09	2.77E-07
extracellular_matrix	C=199;O=68;E=34.31;R=1.98;rawP=4.13e-09	3.24E-07
plasma_membrane	C=1722;O=380;E=296.88;R=1.28;rawP=5.80e-09	3.90E-07
integral_to_membrane	C=2176;O=464;E=375.15;R=1.24;rawP=8.90e-09	4.66E-07
extracellular_space	C=303;O=92;E=52.24;R=1.76;rawP=8.04e-09	4.66E-07
extracellular_matrix_part	C=92;O=38;E=15.86;R=2.40;rawP=4.25e-08	2.00E-06
plasma_membrane_part	C=759;O=185;E=130.85;R=1.41;rawP=1.19e-07	5.10E-06
membrane	C=3791;O=743;E=653.58;R=1.14;rawP=3.47e-07	1.36E-05
intrinsic_to_plasma_membrane	C=434;O=115;E=74.82;R=1.54;rawP=4.81e-07	1.74E-05
membrane_part	C=2697;O=546;E=464.97;R=1.17;rawP=6.98e-07	2.35E-05
integral_to_plasma_membrane	C=415;O=108;E=71.55;R=1.51;rawP=2.72e-06	8.54E-05
collagen	C=37;O=16;E=6.38;R=2.51;rawP=0.0002	0.0059
membrane_raft	C=120;O=36;E=20.69;R=1.74;rawP=0.0004	0.0111
endoplasmic_reticulum_lumen	C=106;O=32;E=18.27;R=1.75;rawP=0.0007	0.0183
cell_projection	C=660;O=144;E=113.79;R=1.27;rawP=0.0010	0.0248
cell_junction	C=379;O=88;E=65.34;R=1.35;rawP=0.0015	0.0336
basement_membrane	C=51;O=18;E=8.79;R=2.05;rawP=0.0015	0.0336
axon	C=137;O=37;E=23.62;R=1.57;rawP=0.0026	0.049
caecula	C=45;O=16;E=7.76;R=2.06;rawP=0.0024	0.049
Golgi_stack	C=87;O=26;E=15.00;R=1.73;rawP=0.0025	0.049
microfibril	C=7;O=5;E=1.21;R=4.14;rawP=0.0023	0.049

## C

## Biopsies-S\_vs\_Biopsies-T, 3725 genes

GO terms	stats	adj_pvalue
cellular_respiration	C=136;O=103;E=48.48;R=2.12;rawP=7.28e-22	3.65E-18
respiratory_electron_transport_chain	C=96;O=78;E=34.22;R=2.28;rawP=3.60e-20	9.02E-17
energy_derivation_by_oxidation_of_organic_compounds	C=233;O=147;E=83.06;R=1.77;rawP=4.65e-18	7.76E-15
generation_of_precursor_metabolites_and_energy	C=311;O=182;E=110.87;R=1.64;rawP=4.06e-17	5.08E-14
oxidation-reduction_process	C=370;O=208;E=131.90;R=1.58;rawP=1.02e-16	9.60E-14
electron_transport_chain	C=118;O=86;E=42.07;R=2.04;rawP=1.15e-16	9.60E-14
mitochondrial_ATP_synthesis_coupled_electron_transport	C=47;O=37;E=16.76;R=2.21;rawP=1.74e-09	1.09E-06
ATP_synthesis_coupled_electron_transport	C=47;O=37;E=16.76;R=2.21;rawP=1.74e-09	1.09E-06
acetyl-CoA_metabolic_process	C=41;O=33;E=14.62;R=2.26;rawP=4.81e-09	2.44E-06
oxidative_phosphorylation	C=57;O=42;E=20.32;R=2.07;rawP=4.88e-09	2.44E-06
homophilic_cell_adhesion	C=37;O=30;E=13.19;R=2.27;rawP=1.80e-08	8.20E-06
mitochondrial_electron_transport_NADH_to_ubiquinone	C=36;O=29;E=12.83;R=2.26;rawP=4.13e-08	1.72E-05
aerobic_respiration	C=38;O=30;E=13.55;R=2.21;rawP=5.62e-08	2.17E-05
small_molecule_metabolic_process	C=1435;O=598;E=511.57;R=1.17;rawP=7.74e-08	2.77E-05
cofactor_catabolic_process	C=32;O=26;E=11.41;R=2.28;rawP=1.55e-07	5.18E-05
tricarboxylic_acid_cycle	C=24;O=21;E=8.56;R=2.45;rawP=2.18e-07	6.82E-05
muscle_system_process	C=182;O=98;E=64.88;R=1.51;rawP=2.93e-07	8.63E-05
catabolic_process	C=1301;O=542;E=463.80;R=1.17;rawP=4.22e-07	1.00E-04
striated_muscle_contraction	C=62;O=41;E=22.10;R=1.85;rawP=9.32e-07	2.00E-04
organic_substance_catabolic_process	C=1207;O=504;E=430.29;R=1.17;rawP=8.82e-07	2.00E-04
acetyl-CoA_catabolic_process	C=25;O=21;E=8.91;R=2.36;rawP=9.03e-07	2.00E-04
actin-myosin_filament_sliding	C=34;O=26;E=12.12;R=2.15;rawP=1.35e-06	2.00E-04
translational_termination	C=88;O=54;E=31.37;R=1.72;rawP=7.02e-07	2.00E-04
translational_elongation	C=104;O=61;E=37.08;R=1.65;rawP=1.25e-06	2.00E-04
organic_acid_catabolic_process	C=121;O=69;E=43.14;R=1.60;rawP=1.10e-06	2.00E-04
muscle_filament_sliding	C=34;O=26;E=12.12;R=2.15;rawP=1.35e-06	2.00E-04
carboxylic_acid_catabolic_process	C=121;O=69;E=43.14;R=1.60;rawP=1.10e-06	2.00E-04
muscle_contraction	C=156;O=85;E=55.61;R=1.53;rawP=9.29e-07	2.00E-04
coenzyme_catabolic_process	C=28;O=23;E=9.98;R=2.30;rawP=5.79e-07	2.00E-04
protein_complex_subunit_organization	C=567;O=255;E=202.13;R=1.26;rawP=1.19e-06	2.00E-04
skeletal_muscle_contraction	C=19;O=17;E=6.77;R=2.51;rawP=1.77e-06	3.00E-04
protein_complex_disassembly	C=122;O=69;E=43.49;R=1.59;rawP=1.65e-06	3.00E-04
cellular_protein_complex_disassembly	C=119;O=67;E=42.42;R=1.58;rawP=2.90e-06	4.00E-04
acyl-CoA_metabolic_process	C=64;O=41;E=22.82;R=1.80;rawP=3.21e-06	5.00E-04
thioester_metabolic_process	C=64;O=41;E=22.82;R=1.80;rawP=3.21e-06	5.00E-04
translational_initiation	C=140;O=76;E=49.91;R=1.52;rawP=4.19e-06	6.00E-04
cellular_catabolic_process	C=1145;O=473;E=408.18;R=1.16;rawP=8.92e-06	1.20E-03
single-organism_catabolic_process	C=149;O=79;E=53.12;R=1.49;rawP=8.92e-06	1.20E-03
small_molecule_catabolic_process	C=148;O=78;E=52.76;R=1.48;rawP=1.35e-05	1.70E-03
protein_targeting_to_membrane	C=133;O=71;E=47.41;R=1.50;rawP=1.85e-05	2.30E-03
oxidoreductase_activity	C=391;O=204;E=139.29;R=1.46;rawP=4.56e-12	5.34E-09
structural_constituent_of_ribosome	C=147;O=86;E=52.37;R=1.64;rawP=9.76e-09	5.71E-06
NADH_dehydrogenase_(quinone)_activity	C=37;O=29;E=13.18;R=2.20;rawP=1.24e-07	2.90E-05
NADH_dehydrogenase_activity	C=37;O=29;E=13.18;R=2.20;rawP=1.24e-07	2.90E-05
NADH_dehydrogenase_(ubiquinone)_activity	C=37;O=29;E=13.18;R=2.20;rawP=1.24e-07	2.90E-05
cofactor_binding	C=155;O=83;E=55.22;R=1.50;rawP=3.08e-06	5.00E-04
oxidoreductase_activity_acting_on_NADH_or_NADPH_quinone	C=46;O=32;E=16.39;R=1.95;rawP=2.75e-06	5.00E-04
inorganic_cation_transmembrane_transporter_activity	C=171;O=90;E=60.92;R=1.48;rawP=3.13e-06	5.00E-04
ion_transmembrane_transporter_activity	C=284;O=137;E=101.17;R=1.35;rawP=5.78e-06	8.00E-04
hydrogen_ion_transmembrane_transporter_activity	C=70;O=43;E=24.94;R=1.72;rawP=8.97e-06	1.00E-03
structural_molecule_activity	C=357;O=165;E=127.18;R=1.30;rawP=1.56e-05	1.70E-03
transmembrane_transporter_activity	C=339;O=156;E=120.77;R=1.29;rawP=3.55e-05	2.80E-03
acyl-CoA_dehydrogenase_activity	C=13;O=12;E=4.63;R=2.59;rawP=3.59e-05	2.80E-03
coenzyme_binding	C=114;O=62;E=40.61;R=1.53;rawP=2.87e-05	0.0028
substrate-specific_transmembrane_transporter_activity	C=319;O=148;E=113.64;R=1.30;rawP=3.38e-05	0.0028
monovalent_inorganic_cation_transmembrane_transporter_activity	C=115;O=62;E=40.97;R=1.51;rawP=4.09e-05	0.003
cation_transmembrane_transporter_activity	C=211;O=103;E=75.17;R=1.37;rawP=4.53e-05	0.0031
oxidoreductase_activity_acting_on_the_CH-CH_group_of_donor	C=41;O=27;E=14.61;R=1.85;rawP=7.62e-05	0.005
oxidoreductase_activity_acting_on_NADH_or_NADPH	C=65;O=38;E=23.16;R=1.64;rawP=0.0001	0.0062
NAD_binding	C=37;O=24;E=13.18;R=1.82;rawP=0.0003	0.0175
flavin_adenine_dinucleotide_binding	C=42;O=26;E=14.96;R=1.74;rawP=0.0005	0.0279
mitochondrial_part	C=586;O=322;E=207.58;R=1.55;rawP=9.02e-24	5.88E-21
mitochondrial_inner_membrane	C=278;O=178;E=98.47;R=1.81;rawP=5.23e-23	1.70E-20
organelle_inner_membrane	C=300;O=182;E=106.27;R=1.71;rawP=1.06e-19	1.73E-17
mitochondrial_membrane	C=388;O=223;E=137.44;R=1.62;rawP=9.37e-20	1.73E-17
mitochondrial_envelope	C=406;O=230;E=143.82;R=1.60;rawP=2.85e-19	3.72E-17
mitochondrion	C=1156;O=543;E=409.48;R=1.33;rawP=1.44e-18	1.56E-16
mitochondrial_membrane_part	C=121;O=84;E=42.86;R=1.96;rawP=1.88e-14	1.75E-12
mitochondrial_matrix	C=237;O=136;E=83.95;R=1.62;rawP=2.20e-12	1.79E-10
respiratory_chain	C=65;O=50;E=23.02;R=2.17;rawP=8.33e-12	6.03E-10
organelle_envelope	C=600;O=290;E=212.53;R=1.36;rawP=9.80e-12	6.39E-10
mitochondrial_respiratory_chain	C=60;O=47;E=21.25;R=2.21;rawP=1.12e-11	6.64E-10
envelope	C=601;O=290;E=212.89;R=1.36;rawP=1.25e-11	6.79E-10
mitochondrial_respiratory_chain_complex_I	C=39;O=32;E=13.81;R=2.32;rawP=2.81e-09	1.22E-07
respiratory_chain_complex_I	C=39;O=32;E=13.81;R=2.32;rawP=2.81e-09	1.22E-07
NADH_dehydrogenase_complex	C=39;O=32;E=13.81;R=2.32;rawP=2.81e-09	1.22E-07
ribosomal_subunit	C=128;O=76;E=45.34;R=1.68;rawP=2.27e-08	9.25E-07
ribosome	C=189;O=103;E=66.95;R=1.54;rawP=4.64e-08	1.78E-06
cytosolic_ribosome	C=86;O=53;E=30.46;R=1.74;rawP=5.90e-07	2.14E-05
cytosolic_part	C=158;O=84;E=55.97;R=1.50;rawP=3.09e-06	0.0001
contractile_fiber_part	C=120;O=67;E=42.51;R=1.58;rawP=3.39e-06	0.0001
cytoplasmic_part	C=4185;O=1573;E=1482.43;R=1.06;rawP=1.12e-05	0.0003
contractile_fiber	C=133;O=71;E=47.11;R=1.51;rawP=1.47e-05	0.0004
myofibril	C=124;O=67;E=43.92;R=1.53;rawP=1.51e-05	0.0004
striated_muscle_thin_filament	C=13;O=12;E=4.60;R=2.61;rawP=3.37e-05	0.0009
sarcomere	C=105;O=57;E=37.19;R=1.53;rawP=5.37e-05	0.0013
small_ribosomal_subunit	C=59;O=36;E=20.90;R=1.72;rawP=5.15e-05	0.0013
cytosolic_large_ribosomal_subunit	C=49;O=31;E=17.36;R=1.79;rawP=6.36e-05	0.0015
cytoplasm	C=5398;O=1988;E=1912.10;R=1.04;rawP=6.94e-05	0.0016
mitochondrial_proton-transporting_ATP_synthase_complex	C=19;O=15;E=6.73;R=2.23;rawP=0.0001	0.0022
large_ribosomal_subunit	C=70;O=40;E=24.80;R=1.61;rawP=0.0002	0.0042
sarcoplasm	C=49;O=30;E=17.36;R=1.73;rawP=0.0002	0.0042
proton-transporting_ATP_synthase_complex	C=20;O=15;E=7.08;R=2.12;rawP=0.0004	0.0082
membrane_part	C=2301;O=878;E=815.07;R=1.08;rawP=0.0006	0.0115
sarcoplasmic_reticulum	C=45;O=27;E=15.94;R=1.69;rawP=0.0006	0.0115
troponin_complex	C=7;O=7;E=2.48;R=2.82;rawP=0.0007	0.013
cytosolic_small_ribosomal_subunit	C=35;O=22;E=12.40;R=1.77;rawP=0.0008	0.0141
membrane	C=3251;O=1218;E=1151.58;R=1.06;rawP=0.0008	0.0141
ion_channel_complex	C=46;O=27;E=16.29;R=1.66;rawP=0.0010	0.0172
T-tubule	C=18;O=13;E=6.38;R=2.04;rawP=0.0016	0.0254
mitochondrial_nucleoid	C=32;O=20;E=11.34;R=1.76;rawP=0.0016	0.0254

**D Cells-S\_vs\_Cells-T/Biopsies-S\_vs\_Biopsies-T, 864 genes**

KEGG pathway	stats	adj_pvalue
Regulation_of_actin_cytoskeleton	C=154;O=26;E=10.55;R=2.46;rawP=1.56e-05	2.20E-03
Focal_adhesion	C=158;O=24;E=10.82;R=2.22;rawP=0.0002	1.06E-02
Pathogenic_Escherichia_coli_infection	C=40;O=10;E=2.74;R=3.65;rawP=0.0003	1.06E-02
Leukocyte_transendothelial_migration	C=71;O=14;E=4.86;R=2.88;rawP=0.0003	1.06E-02

**E Cells-S\_vs\_Cells-T, 2071 genes**

KEGG pathway	stats	adj_pvalue
Protein_digestion_and_absorption	C=32;O=17;E=5.37;R=3.17;rawP=2.71e-06	5.00E-04
Cytokine-cytokine_receptor_interaction	C=68;O=25;E=11.40;R=2.19;rawP=5.65e-05	5.50E-03
ECM-receptor_interaction	C=51;O=19;E=8.55;R=2.22;rawP=0.0004	0.0241
Focal_adhesion	C=143;O=40;E=23.98;R=1.67;rawP=0.0005	0.0241
Nitrogen_metabolism	C=9;O=6;E=1.51;R=3.98;rawP=0.0012	0.0386
Gap_junction	C=55;O=19;E=9.22;R=2.06;rawP=0.0010	0.0386
Amoebiasis	C=57;O=19;E=9.56;R=1.99;rawP=0.0017	0.041
Pathways_in_cancer	C=219;O=54;E=36.73;R=1.47;rawP=0.0017	0.041

**F Biopsies-S\_vs\_Biopsies-T, 3725 genes**

KEGG pathway	stats	adj_pvalue
Oxidative_phosphorylation	C=104;O=76;E=36.63;R=2.08;rawP=2.89e-15	6.10E-13
Alzheimer's_disease	C=131;O=89;E=46.13;R=1.93;rawP=1.73e-14	1.83E-12
Parkinson's_disease	C=102;O=73;E=35.92;R=2.03;rawP=6.18e-14	4.35E-12
Huntington's_disease	C=139;O=84;E=48.95;R=1.72;rawP=9.38e-10	4.95E-08
Cardiac_muscle_contraction	C=48;O=36;E=16.90;R=2.13;rawP=2.04e-08	8.61E-07
Valine,_leucine_and_isoleucine_degradation	C=37;O=29;E=13.03;R=2.23;rawP=9.44e-08	2.85E-06
Ribosome	C=85;O=54;E=29.93;R=1.80;rawP=8.84e-08	2.85E-06
Metabolic_pathways	C=645;O=287;E=227.15;R=1.26;rawP=2.85e-07	7.52E-06
Citrate_cycle_(TCA_cycle)	C=26;O=21;E=9.16;R=2.29;rawP=2.50e-06	5.86E-05
Calcium_signaling_pathway	C=66;O=41;E=23.24;R=1.76;rawP=7.18e-06	0.0002
Propanoate_metabolism	C=25;O=19;E=8.80;R=2.16;rawP=3.71e-05	0.0007
Fatty_acid_metabolism	C=31;O=22;E=10.92;R=2.02;rawP=5.29e-05	0.0009
Glycolysis/_Gluconeogenesis	C=37;O=25;E=13.03;R=1.92;rawP=6.03e-05	0.001
Pyruvate_metabolism	C=30;O=19;E=10.57;R=1.80;rawP=0.0015	0.0226
Tight_junction	C=80;O=41;E=28.17;R=1.46;rawP=0.0023	0.0324



**Table S2:** Cytokine assay of the CM of SKMC-S and SKMC-T cells in control conditions of after 24h TNF-alpha treatment.

Cytokine	C-SKMC-S-CM		C-SKMC-T-CM		TNF-SKMC-S-CM		TNF-SKMC-T-CM	
	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)
<i>Angiogenin</i>	1.00	0.22	4.92	1.54	1.30	0.28	3.17	1.05
<i>Acrp30</i>	1.00	0.31	1.06	0.16	1.02	0.12	1.20	0.13
<i>AgRP</i>	1.00	0.25	1.04	0.21	1.01	0.21	1.15	0.13
<i>ANGPT2</i>	1.00	0.23	1.00	0.18	1.06	0.17	1.21	0.07
<i>AREG</i>	1.00	0.22	0.97	0.22	0.98	0.22	0.99	0.18
<i>Axl</i>	1.00	0.23	1.03	0.17	0.98	0.19	1.10	0.11
<i>b-NGF</i>	1.00	0.17	1.03	0.17	1.05	0.35	1.13	0.12
<i>BDNF</i>	1.00	0.18	0.84	0.07	0.96	0.07	0.99	0.06
<i>bFGF</i>	1.00	0.26	1.00	0.15	1.02	0.20	1.15	0.09
<i>BLC</i>	1.00	0.15	0.90	0.07	1.04	0.07	1.08	0.12
<i>BMP-4</i>	1.00	0.12	0.97	0.05	1.09	0.09	1.19	0.11
<i>BMP-6</i>	1.00	0.16	0.89	0.14	1.13	0.08	1.16	0.06
<i>BTC</i>	1.00	0.27	1.03	0.21	0.98	0.14	1.21	0.12
<i>CCL11</i>	1.00	0.17	1.04	0.27	1.19	0.29	2.11	0.70
<i>CCL24</i>	1.00	0.12	0.89	0.09	1.05	0.06	1.17	0.10
<i>CCL26</i>	1.00	0.13	0.98	0.10	1.14	0.08	1.21	0.10
<i>CCL28</i>	1.00	0.21	1.09	0.23	1.05	0.25	1.12	0.10
<i>CKB 8-1</i>	1.00	0.15	0.94	0.06	1.06	0.07	1.23	0.11
<i>CNTF</i>	1.00	0.14	0.92	0.08	1.11	0.08	1.17	0.10
<i>CSF2</i>	1.00	0.19	1.09	0.27	1.55	0.27	1.54	0.41
<i>CSF3</i>	1.00	0.28	1.00	0.22	1.06	0.30	1.18	0.23
<i>CTACK</i>	1.00	0.22	0.95	0.22	0.92	0.21	1.21	0.13
<i>CX3CL1</i>	1.00	0.17	0.93	0.08	1.05	0.06	1.18	0.10
<i>Dtk</i>	1.00	0.21	0.95	0.21	0.93	0.14	1.16	0.06
<i>EGF</i>	1.00	0.16	0.92	0.05	1.06	0.06	1.18	0.09
<i>EGFR</i>	1.00	0.22	1.05	0.15	0.95	0.13	1.17	0.11
<i>ENA-78</i>	1.00	0.23	1.13	0.32	1.17	0.41	2.63	1.01
<i>Fas</i>	1.00	0.38	1.09	0.35	1.23	0.48	1.12	0.31
<i>FGF4</i>	1.00	0.25	0.97	0.19	0.95	0.25	1.12	0.12
<i>FGF6</i>	1.00	0.14	0.98	0.10	1.10	0.07	1.13	0.13
<i>FGF7</i>	1.00	0.15	0.89	0.08	1.00	0.08	1.13	0.09
<i>FGF9</i>	1.00	0.19	0.93	0.22	1.01	0.20	1.04	0.10
<i>Fit-3L</i>	1.00	0.15	0.96	0.10	1.06	0.06	1.20	0.12
<i>GCP-2</i>	1.00	0.16	0.99	0.05	1.10	0.08	1.12	0.11
<i>GDNF</i>	1.00	0.17	0.95	0.07	1.16	0.10	1.24	0.10
<i>GITR</i>	1.00	0.18	0.87	0.14	0.87	0.21	1.04	0.11
<i>GITRL</i>	1.00	0.21	0.99	0.18	0.93	0.08	1.06	0.09
<i>GRO</i>	1.00	0.20	1.71	0.79	9.12	5.16	19.09	10.13
<i>GRO-α</i>	1.00	0.24	1.06	0.25	1.10	0.35	1.22	0.23
<i>HCC-4</i>	1.00	0.16	0.96	0.17	0.97	0.20	1.12	0.12
<i>HGF</i>	1.00	0.24	1.26	0.28	0.97	0.13	1.11	0.16
<i>I-309</i>	1.00	0.15	0.94	0.07	1.04	0.06	1.13	0.05
<i>I-TAC</i>	1.00	0.24	0.94	0.23	1.35	0.46	1.13	0.17
<i>ICAM1</i>	1.00	0.26	1.04	0.18	0.98	0.19	1.17	0.09
<i>ICAM3</i>	1.00	0.20	0.94	0.13	0.86	0.13	1.01	0.08
<i>IFN-γ</i>	1.00	0.20	0.94	0.31	1.14	0.27	1.21	0.33
<i>IGF-1</i>	1.00	0.15	0.91	0.09	1.04	0.10	1.21	0.08
<i>IGFBP1</i>	1.00	0.16	0.92	0.04	1.01	0.04	1.16	0.12
<i>IGFBP2</i>	1.00	0.19	0.91	0.07	1.12	0.16	1.13	0.08
<i>IGFBP4</i>	1.00	0.16	0.99	0.08	1.12	0.09	1.22	0.09
<i>IGFBP6</i>	1.00	0.22	2.00	0.60	1.23	0.40	1.77	0.56
<i>IGFBP3</i>	1.00	0.21	1.02	0.13	0.90	0.16	1.11	0.12
<i>IL-1 R1</i>	1.00	0.25	0.93	0.22	1.05	0.12	1.11	0.11
<i>IL-10</i>	1.00	0.14	0.93	0.11	1.11	0.08	1.21	0.10
<i>IL-11</i>	1.00	0.27	0.83	0.20	0.90	0.13	0.92	0.13

Cytokine	C-SKMC-S-CM		C-SKMC-T-CM		TNF-SKMC-S-CM		TNF-SKMC-T-CM	
	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)	Protein level (fold C-SKMC-S-CM)	ESM (±)
<i>IL-12 p40</i>	1.00	0.17	1.05	0.16	0.96	0.18	1.01	0.13
<i>IL-12 p70</i>	1.00	0.21	1.00	0.14	0.91	0.18	1.04	0.15
<i>IL-13</i>	1.00	0.06	0.98	0.17	1.12	0.09	1.25	0.17
<i>IL-15</i>	1.00	0.14	0.86	0.10	1.05	0.08	1.18	0.11
<i>IL-16</i>	1.00	0.17	0.89	0.09	1.02	0.06	1.14	0.07
<i>IL-17</i>	1.00	0.22	1.04	0.13	1.04	0.20	1.11	0.12
<i>IL-1a</i>	1.00	0.12	0.97	0.16	1.22	0.08	1.21	0.11
<i>IL-1b</i>	1.00	0.12	0.84	0.09	1.12	0.07	1.09	0.12
<i>IL-1ra</i>	1.00	0.16	0.88	0.10	1.10	0.09	1.17	0.10
<i>IL-2</i>	1.00	0.13	0.84	0.09	1.12	0.07	1.14	0.14
<i>IL-2 Ra</i>	1.00	0.22	0.99	0.19	0.99	0.21	1.20	0.10
<i>IL-3</i>	1.00	0.16	0.99	0.11	1.23	0.04	1.30	0.11
<i>IL-4</i>	1.00	0.15	0.90	0.10	1.07	0.06	1.16	0.07
<i>IL-5</i>	1.00	0.18	0.83	0.11	1.00	0.09	1.10	0.07
<i>IL-6</i>	1.00	0.08	4.92	3.49	14.56	7.47	20.38	9.55
<i>IL-7</i>	1.00	0.16	1.03	0.13	1.03	0.08	1.26	0.10
<i>IL-8</i>	1.00	0.21	1.18	0.35	2.13	1.24	3.29	1.51
<i>IL1R4</i>	1.00	0.24	1.08	0.25	1.17	0.33	1.27	0.39
<i>Leptin</i>	1.00	0.15	0.85	0.05	1.00	0.18	1.25	0.19
<i>LIGHT</i>	1.00	0.15	1.02	0.20	1.08	0.08	1.16	0.09
<i>M-CSF</i>	1.00	0.13	0.93	0.06	1.06	0.07	1.10	0.07
<i>MCP1</i>	1.00	0.34	1.19	0.54	3.12	0.63	3.00	0.48
<i>MCP2</i>	1.00	0.15	1.03	0.24	1.66	0.39	2.35	0.80
<i>MCP3</i>	1.00	0.18	1.05	0.29	7.96	3.85	9.81	4.32
<i>MCP4</i>	1.00	0.16	0.96	0.08	1.05	0.06	1.12	0.09
<i>MDC</i>	1.00	0.19	0.88	0.07	1.00	0.06	1.12	0.09
<i>MIF</i>	1.00	0.30	1.76	0.61	0.96	0.33	1.23	0.38
<i>MIG</i>	1.00	0.15	0.85	0.12	1.31	0.03	1.17	0.10
<i>MIP-1a</i>	1.00	0.21	1.07	0.14	0.90	0.15	1.21	0.07
<i>MIP-1b</i>	1.00	0.23	1.02	0.14	0.82	0.15	1.09	0.11
<i>MIP-1d</i>	1.00	0.14	0.98	0.07	1.10	0.08	1.14	0.08
<i>MIP-3a</i>	1.00	0.17	1.11	0.27	1.31	0.26	2.49	0.81
<i>MIP-3b</i>	1.00	0.18	0.97	0.16	0.89	0.11	1.00	0.17
<i>MSP-a</i>	1.00	0.21	0.97	0.18	0.92	0.21	1.02	0.14
<i>NAP-2</i>	1.00	0.12	1.00	0.04	1.07	0.07	1.42	0.21
<i>NT-3</i>	1.00	0.17	0.93	0.06	1.03	0.07	1.12	0.08
<i>NT-4</i>	1.00	0.31	0.92	0.16	0.87	0.15	0.90	0.10
<i>OPG</i>	1.00	0.39	2.31	0.54	1.45	0.22	5.44	1.38
<i>OSM</i>	1.00	0.16	0.81	0.08	0.81	0.15	0.78	0.10
<i>PARC</i>	1.00	0.15	0.95	0.06	1.06	0.08	1.16	0.07
<i>PDGF-BB</i>	1.00	0.14	0.86	0.09	1.01	0.06	1.12	0.09
<i>PLGF</i>	1.00	0.20	1.01	0.14	0.93	0.18	1.06	0.18
<i>RANTES</i>	1.00	0.18	1.03	0.28	24.27	3.43	27.75	2.13
<i>SCF</i>	1.00	0.20	0.91	0.08	0.97	0.06	1.10	0.08
<i>SDF-1</i>	1.00	0.15	0.85	0.10	1.03	0.06	1.14	0.08
<i>sgp130</i>	1.00	0.22	0.99	0.16	0.94	0.20	1.08	0.11
<i>siGF-1R</i>	1.00	0.17	0.98	0.13	0.81	0.11	1.01	0.13
<i>siL-6R</i>	1.00	0.22	0.94	0.20	1.00	0.18	1.12	0.09
<i>sTNFR1</i>	1.00	0.23	0.98	0.19	0.90	0.19	1.08	0.09
<i>sTNFR2</i>	1.00	0.24	1.06	0.12	0.88	0.19	1.07	0.13
<i>TARC</i>	1.00	0.15	0.96	0.06	1.02	0.08	1.17	0.12
<i>TECK</i>	1.00	0.21	1.01	0.24	0.91	0.16	1.15	0.10
<i>TGF-b1</i>	1.00	0.12	0.95	0.12	1.10	0.05	1.19	0.12
<i>TGF-b3</i>	1.00	0.13	1.00	0.04	1.07	0.08	1.20	0.08
<i>THPO</i>	1.00	0.23	1.00	0.14	0.89	0.22	1.07	0.12
<i>TIMP1</i>	1.00	0.40	1.36	0.56	1.30	0.63	1.49	0.76
<i>TIMP2</i>	1.00	0.38	1.31	0.38	1.17	0.41	1.18	0.34
<i>TNF-a</i>	1.00	0.12	1.17	0.23	10.35	4.21	10.19	4.01
<i>TRAIL R3</i>	1.00	0.24	1.00	0.17	0.87	0.12	1.09	0.11
<i>TRAIL R4</i>	1.00	0.31	1.03	0.20	0.95	0.22	1.03	0.19
<i>uPAR</i>	1.00	0.23	1.00	0.22	1.07	0.16	1.14	0.17
<i>VEGF-A</i>	1.00	0.24	0.82	0.17	0.88	0.13	0.95	0.07
<i>VEGF-D</i>	1.00	0.20	0.96	0.17	0.93	0.16	0.96	0.16
<i>XCL1</i>	1.00	0.18	0.93	0.17	0.88	0.13	1.11	0.11

**Table S3:** Muscle biopsies donors informations.

	MEAN	SEM
Age	22.79	0.38
Height	182.79	1.71
Weight	75.96	1.89
BMI	22.71	0.39
P	51.36	1.84
S-BP (mmHg)	135.71	1.87
D-BP (mmHg)	78.43	1.62
Hb	9.10	0.16
Hct	0.43	0.01
Leuco	5.67	0.36
Trombo	214.21	10.42
Crp	1.43	0.43
Na	142.50	0.57
K	3.91	0.05
TG	0.89	0.11
Total chol	4.15	0.21
HDL	1.44	0.06
LDL	2.34	0.18
Creatinin	82.64	2.68
Carbamid	5.24	0.43
ALAT	18.18	1.51
Bilirubin	13.36	1.91
Alcalic phos	61.43	4.52
F II+VII+X	0.66	0.02
HbA1c	5.11	0.05
TSH	2.13	0.22