Gene Onthology: Top Features in each gene cluster of Extended Data Fig.2c

Group	Term	Count	P-Value
1	Pyrimidine metabolism	16	3.80E-03
2	Cytokine-cytokine receptor interaction 1	14	2.40E-04
3	NOD-like receptor signaling pathway	8	2.90E-03
4	Wnt signaling pathway	19	5.10E-03
5	Cell cycle	17	4.60E-06
6	Adipocytokine signaling pathway	11	1.90E-02
7	Oxidative phosphorylation	46	1.30E-12
8	Cytokine-cytokine receptor interaction 2	25	9.00E-06

Pyrimidine metabolism		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
NT5C2	5'-nucleotidase, cytosolic II	12.6419	16.4211	17.2705	16.8707	18.2475	17.1893	15.8376	15.5199	14.6593	12.2511	12.3765	13.3335	7.0292	10.0318	10.5031	8.86951	8.73115	9.48871	8.89622	11.241	11.0268	16.3221	12.3774	11.7447
CTPS2	CTP synthase II	3.48581	3.47525	3.42129	3.29707	3.67362	3.21744	2.95099	2.78464	2.29042	2.76533	2.1948	2.64962	1.71616	1.82645	1.95155	2.35292	2.43154	2.0757	2.48257	2.78008	2.25775	1.44385	2.20327	1.86449
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	11.7124	15.2397	13.3863	14.1109	12.9968	13.5495	12.8653	12.3656	13.2062	9.94594	8.73271	9.78563	6.10954	7.78522	8.39281	6.25776	7.28066	8.91364	7.40816	9.39821	8.13135	10.0306	7.75566	8.4539
CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	53.3944	62.9207	57.0776	58.3637	58.8955	39.015	37.0437	34.9935	33.0545	31.7345	37.4826	31.5068	59.8391	63.0846	56.134	54.8581	35.3021	32.3318	20.5835	21.394	35.5255	23.5273	32.3769	34.3058
DPYD	dihydropyrimidine dehydrogenase	9.24558	15.2774	13.7416	17.0198	14.9325	13.1066	12.4318	11.7582	13.8281	10.8234	12.0298	11.9662	6.08713	8.98169	9.14547	7.61154	6.71439	6.75213	10.0081	10.4816	10.9432	5.50783	6.39992	6.97848
ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	1.1322	1.89475	2.09281	1.73042	1.89742	1.78863	1.35383	1.51063	1.21624	0.982204	1.3466	1.24289	1.2053	2.39529	1.91677	1.87104	1.68055	2.07017	1.0403	0.986541	0.952858	1.12304	1.15753	0.834183
ENTPD4	ectonucleoside triphosphate diphosphohydrolase 4	7.85402	19.8048	13.5365	13.4075	14.9169	14.2742	12.6927	14.7629	10.7827	9.75938	9.67057	9.23921	3.63486	9.07987	9.26341	7.79704	6.44028	7.4792	5.31343	5.73571	5.14899	7.82732	6.54493	6.6193
POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	1.5601	1.96157	1.53944	1.59573	2.08979	1.98344	1.91686	1.84689	2.12478	1.21125	1.82822	1.31464	0.633969	1.5869	1.3902	2.05514	1.34872	1.69006	0.848136	1.16667	1.18377	0.769392	0.656798	0.466345
POLR1E	polymerase (RNA) I polypeptide E, 53kDa	15.0191	14.1631	14.0228	15.0629	16.6333	16.5463	15.7491	15.0267	14.8824	15.6395	13.1787	14.8101	10.3803	11.9366	10.3274	8.00956	10.6826	10.8735	14.5299	10.5384	11.3064	7.83852	11.3358	11.5066
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	21.4151	32.0006	28.1935	31.9488	32.9975	30.2485	31.3984	34.9365	30.9911	31.8321	34.7259	31.7918	17.9445	29.7743	27.1848	29.49	24.9465	28.5229	22.15	28.557	25.702	21.9512	19.9295	18.6133
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	2.78105	3.27852	4.01807	3.70896	3.7934	3.42706	1.98974	3.34573	2.7957	2.12206	2.35738	1.95277	1.75647	2.6383	3.04608	2.18919	2.34925	2.40191	1.97539	2.32644	2.11019	2.07982	1.91345	1.60068
PRIM1	primase, DNA, polypeptide 1 (49kDa)	2.33034	3.95555	2.32504	4.33224	3.02551	2.52017	3.62062	2.57482	1.57986	1.40721	1.58698	1.26885	0.946969	1.8963	1.73411	1.48197	1.37583	1.32534	2.027	1.02129	1.44404	0	0.722894	0.975223
PRIM2	primase, DNA, polypeptide 2 (58kDa)	4.22121	4.77675	4.75156	4.87816	6.15704	5.76975	5.93382	5.95964	6.31975	3.65362	4.26847	2.97942	3.08763	2.64229	2.46368	2.77394	3.07371	2.84533	3.26376	4.24809	5.29378	1.16579	2.61892	2.74794
TXNRD1	thioredoxin reductase 1; hypothetical LOC100130902	61.5861	85.887	81.8782	94.14	99.138	83.6852	83.0661	90.1824	82.5285	83.8587	86.849	79.0816	43.831	64.3164	61.899	44.3836	42.4684	45.9745	26.964	33.2797	32.7665	117.859	58.2365	45.7088
TK2	thymidine kinase 2, mitochondrial	14.8637	16.1925	17.383	15.5761	15.0826	15.6409	15.016	14.3082	16.0971	11.7857	11.2554	10.5063	12.1425	11.3761	11.018	11.4457	12.0505	12.6915	12.4313	10.1925	9.27608	12.3362	12.7837	11.6089
UMPS	uridine monophosphate synthetase	4.55261	4.43344	5.4466	4.17123	5.19385	4.55856	4.53227	4.43843	4.39591	4.79456	4.80806	4.75248	4.2669	3.737	3.73166	3.51967	3.46005	3.2718	4.00076	4.5929	3.85235	4.19107	2.76913	2.64613

Cytokine-cytokine receptor interaction 1		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
BMP2	bone morphogenetic protein 2	0.132176	0.0623215	0.152164	0.0498088	0.190673	0.446698	0.440057	1.15617	0.672068	8.44059	11.0471	8.63624	28.1987	38.1622	38.0126	46.3364	44.0127	42.0969	14.5151	17.0402	15.8838	5.74934	29.2141	30.1463
CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	0	0.615272	0.751124	0.819566	0.313738	0.147001	3.98244	2.80353	3.04105	30.5346	32.9208	31.1836	15.3779	12.1502	13.7089	10.5807	7.12639	8.45225	9.93171	9.0549	9.96328	272.991	151.799	134.02
CXCL3	chemokine (C-X-C motif) ligand 3	0	0.389251	0.237599	2.79989	1.33978	2.65051	9.79165	9.50169	10.7564	35.7066	30.8576	33.5256	13.3352	13.468	12.7384	12.6002	9.68719	11.3467	39.9437	45.6778	43.8488	827.629	303.664	225.213
CXCL5	chemokine (C-X-C motif) ligand 5	0.259359	0.815257	0.59716	1.23799	0.561214	0.292173	0.935447	0.875626	0.439582	4.5419	5.37906	4.07964	4.53196	8.15794	7.72004	5.77284	5.20626	4.17934	2.72597	3.72571	3.84572	11.6396	8.6892	9.85895
CSF3	colony stimulating factor 3 (granulocyte)	0.153493	0.289763	0.176759	0.231532	0.221569	0	0.127698	0.282921	0	2.0528	1.71602	1.44145	14.8172	6.49294	7.56663	3.37928	5.57604	7.15803	14.5598	4.3542	8.27518	259.025	233.854	224.529
INHBA	inhibin, beta A	14.0465	72.5726	42.5902	89.1645	88.9	82.5726	192.577	235.442	217.784	551.399	684.546	655.3	326.199	1785.35	1675.71	1532.04	1474.35	1477.63	1118.01	1226.86	1254.26	1126.08	842.408	790.05
IL1A	interleukin 1, alpha	0	0.0674161	0.0823017	0.323283	0.10313	0	0.238016	0.263303	0.363504	0.971339	0.995845	1.1029	2.35315	1.77881	1.73681	2.45507	2.78573	2.23625	4.66385	3.55088	4.55662	9.92132	37.7897	39.1927
IL11	interleukin 11	7.43339	4.87262	5.11362	23.3659	26.0887	24.6927	140.416	152.496	147.151	54.1114	60.696	56.7624	231.081	152.442	168.446	233.825	198.935	228.652	294.311	445.025	347.875	253.673	129.328	130.122
IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	0.315509	0.446291	0.544832	0.475581	0.7965	0.426514	0.393912	0.290508	1.20319	1.28604	1.75798	3.00635	4.03867	1.99963	2.38238	2.40776	1.81619	0.897204	1.71524	3.11117	2.72319	8.82249	11.5981	11.2232
IL8	interleukin 8	0.130065	0.613261	0.74867	6.46975	5.15976	4.1319	18.1872	17.6045	14.2187	84.7071	90.9509	94.7796	49.1541	58.4966	51.0696	34.9882	35.9379	30.3287	38.1829	24.1308	33.3327	1474.99	1768.06	1842.89
NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	0	0.228303	0.139356	0.182465	0.0873117	0.0818197	0.100754	0.278646	0.0769372	0.274118	0.0562067	0.329554	2.73008	2.04585	2.54342	6.58193	5.84252	7.34353	63.1102	67.773	58.348	103.553	37.6824	31.0282
TGFB2	transforming growth factor, beta 2	1.16671	2.10336	2.09373	1.47415	1.41081	1.27566	1.54233	1.76937	1.43945	6.34088	8.04247	6.22991	8.40858	17.1571	15.2122	16.2034	11.8057	12.7182	11.6409	10.9657	14.6014	7.70422	14.8178	14.1244
TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	0.0808057	0.0761988	0.186093	0.304594	0.174889	0.109247	0.134536	0.148832	0.205483	0.429149	0.513306	0.440121	1.82903	2.27867	1.60727	2.31334	1.3986	1.94607	0.878903	1.29898	1.6254	0.669727	1.20364	0.743521
TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	0.336409	0.21149	0.193641	0.126771	0.121323	0.113691	0.793342	0.516252	0.712714	0.355503	0.728945	0.814094	0.751875	0.710696	1.0308	1.06969	0.744807	1.32866	2.13367	3.07153	1.71236	33.5628	28.4373	24.7544

NOD-like receptor signaling pathway		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
NLRC4	NLR family, CARD domain containing 4	0.128106	0.0603948	0.0737331	0.0482659	0.0461911	0.173182	0.106624	0.176937	0.0814164	0.116037	0.0594752	0.0581192	0.0780813	0.300727	0.0841091	0.427743	0.397107	0.303595	0.348244	0.608273	0.382769	0.663428	0.298066	0.193435
NLRP3	NLR family, pyrin domain containing 3	0.106765	0.0503364	0	0.0402288	0.0385025	0.0360778	0.0444283	0.0491489	0	0.0967093	0	0.045135	0.0650757	0.0751819	0.140205	0.203698	0.236387	0.202408	0.362728	0.861575	1.06747	2.87502	1.39086	1.68898
CCL5	chemokine (C-C motif) ligand 5	0.38192	0.180077	0.219838	0.575686	0.550945	0	0.476826	0.527485	0	0.172971	0.532004	0.866466	0.232798	0.0896494	0.376153	0.728642	1.1838	1.44807	2.9068	0.976379	1.26784	3.55984	18.4821	23.7746
CXCL2	chemokine (C-X-C motif) ligand 2	0.783887	1.10882	1.80486	31.1644	29.2597	22.6506	41.2677	37.7126	41.3525	26.2715	23.6586	26.6762	21.5017	15.5484	16.213	15.89	10.5867	14.4892	53.2694	58.1162	61.1524	1499.06	668.046	484.896
IL1B	interleukin 1, beta	0	0	0.173842	0.682855	0	0.408268	0.502748	0.695201	0	0.410342	1.40232	0.822213	0.736363	1.06338	1.09066	0.57619	0.668654	0.858822	4.43304	1.98538	2.50644	9.07063	39.4891	59.2447
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	17.771	14.731	14.0239	54.7623	60.5751	54.7306	95.4282	97.3852	102.747	71.0081	75.5945	72.7011	76.6995	64.1865	62.2944	65.0742	67.0134	69.1459	193.845	233.334	213.138	528.688	560.165	558.523
NOD2	nucleotide-binding oligomerization domain containing 2	0	0	0	0.0342461	0	0.0307127	0.0378202	0	0	0	0	0	0.0553943	0.10666	0.149176	0	0.0804812	0.215355	0.29643	0.298709	0.362019	1.60001	1.01488	1.52125
TNF	tumor necrosis factor (TNF superfamily, member 2)	0	0	0	0	0	0	0.221865	0.368155	0	1.32796	1.73278	0.967592	1.6248	1.50169	0.962624	1.14424	1.53442	1.13701	3.04317	1.84967	1.32732	22.9132	11.2871	10.1791

Wnt signaling pathway		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
CREBBP	CREB binding protein	5.01537	8.32549	7.40714	7.63632	6.36799	6.24342	7.17071	8.18337	7.95378	6.53496	6.74002	6.77721	3.64593	9.73326	9.81004	7.8871	10.3674	9.86617	10.2696	14.5601	13.472	20.1431	13.2496	12.3501
EP300	E1A binding protein p300	4.61026	9.63732	8.15724	8.84917	7.83002	6.76953	7.82574	9.28449	8.6029	7.96105	8.62589	7.83162	3.90378	12.2079	12.168	11.547	11.3032	13.4975	12.4699	15.1951	15.1537	19.569	18.8737	15.2066
SMAD2	SMAD family member 2	5.33535	6.22207	6.15416	6.33408	6.11677	5.4794	5.02624	4.90993	3.94186	4.08758	4.23439	4.1915	6.13801	7.57136	6.68264	7.70385	6.00481	7.01163	6.36804	6.651	7.82426	8.12275	9.62803	8.74572
SENP2	SUMO1/sentrin/SMT3 specific peptidase 2	7.42287	8.47346	7.12115	7.75366	8.82939	7.78988	6.0157	7.73397	7.44919	6.95952	6.34903	6.79522	7.69974	10.5461	11.2441	13.4784	10.8408	12.344	11.823	14.7437	13.0988	17.533	15.6943	13.352
CHD8	chromodomain helicase DNA binding protein 8	63.3557	41.2451	48.8712	49.4461	51.4965	58.9087	55.6774	48.8595	75.6294	76.9048	60.6271	83.7606	112.914	59.7887	61.4487	54.6073	65.2216	69.5043	42.3105	27.2493	30.1065	23.3148	24.542	34.6562
FZD6	frizzled homolog 6 (Drosophila)	9.87984	14.9236	12.0825	13.3753	13.8976	10.8052	7.98638	9.58046	8.78534	4.71218	7.34728	6.09769	6.00655	11.0059	10.4966	13.5722	9.74213	8.89259	11.1948	14.4365	15.1831	18.8572	14.272	15.2125
MAPK9	mitogen-activated protein kinase 9	9.52176	12.5405	9.80343	9.39699	9.6641	9.60846	8.74841	11.0762	8.00864	8.89085	9.73094	9.13892	11.5542	14.2084	13.1261	14.3871	12.5035	13.0354	10.991	11.1743	11.9975	10.6348	11.2363	9.69491
NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	3.23209	7.87944	6.19003	7.41151	7.1568	5.89721	5.57795	7.03753	6.33767	4.54731	6.08994	6.57892	2.63286	9.24351	10.1885	9.04727	8.46952	7.11847	7.72001	12.4391	11.9086	13.3184	13.6723	11.4815
NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	5.74183	7.674	6.78692	7.07874	7.41792	7.35491	6.73915	6.28034	6.21038	4.33379	3.98011	4.60132	6.54036	8.02565	7.46667	7.25382	6.77435	6.79983	8.92782	9.87744	9.27772	13.3395	11.2562	10.7496
PLCB4	phospholipase C, beta 4	0.698979	0.775446	0.516409	0.507047	0.431328	0.505259	0.435519	0.550705	0.522621	0.406316	0.449012	0.203463	0.41007	0.733313	0.687175	0.820148	0.62892	0.495995	0.731451	0.928276	0.7828	0.464498	0.591326	0.508348
PSEN1	presenilin 1	7.64578	8.32146	8.14663	8.65335	8.49187	8.55992	10.238	9.37292	9.4965	10.9275	11.3678	10.4733	11.1365	14.0194	14.1583	12.3647	13.886	13.7945	12.3619	15.0933	14.1602	13.3002	14.3433	14.1043
PRKX	protein kinase, X-linked	1.2234	1.65256	1.14195	1.246	1.04936	1.29624	1.04579	1.24823	0.75655	0.509149	0.859756	0.930178	0.685255	1.7696	1.58485	1.82939	1.87406	1.7238	2.193	2.05287	2.19527	2.12311	1.87703	1.41832
PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	6.50152	6.87734	9.31211	6.12262	6.97865	6.57422	5.26512	5.33404	5.67107	5.79016	4.26667	4.39177	7.63902	8.33963	9.73997	10.8171	7.86785	10.0403	9.91826	8.07375	10.4772	8.05496	10.0404	9.95594
PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	30.5346	28.2206	27.1082	31.1902	29.27	26.0866	28.5326	28.0936	26.8743	21.7829	24.5923	25.9587	28.6814	37.1865	34.2679	33.4757	33.7113	33.3567	38.6385	36.5131	40.9489	32.2279	28.0664	35.9669
PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	15.9992	21.8856	20.8207	20.9379	20.5614	15.4795	14.1414	13.232	13.4648	9.71765	11.4305	10.9744	17.9117	24.1139	23.8883	26.3858	17.9664	18.6782	22.1392	23.9885	32.0091	23.2193	26.4953	22.1277
SFRP4	secreted frizzled-related protein 4	6.46993	5.23906	6.88161	6.20127	5.32607	5.27625	5.26806	6.92854	4.46973	7.38924	7.64098	7.46683	9.25919	8.1548	7.20339	9.59311	8.15868	9.73245	9.94029	7.60241	9.15146	13.6926	10.9296	10.5949
SIAH1	seven in absentia homolog 1 (Drosophila)	10.2408	8.26171	9.0174	6.31877	7.50577	4.74907	9.84632	8.98188	6.32204	9.10999	9.55493	11.6221	10.3893	11.0205	13.9912	15.6058	10.6246	13.6671	14.4397	7.98298	9.52135	15.2709	16.1871	15.2538
TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	2.94195	4.26291	3.55205	3.13662	3.62289	3.9285	2.56812	3.69986	4.56059	3.89971	4.19801	3.84187	5.68594	4.9856	5.51236	5.33897	4.8295	5.10118	4.99316	3.66883	3.57302	4.16155	5.80961	4.87965
WNT5A	wingless-type MMTV integration site family, member 5A	18.8083	29.1918	24.3542	26.2698	23.9709	19.4074	19.9059	20.718	19.6092	20.0687	26.9846	21.5154	34.3305	66.0701	63.4924	64.1289	57.7022	54.2697	30.7688	29.6945	33.6587	22.374	46.8902	51.0897

Cell cycle		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
CDC45	CDC45 cell division cycle 45-like (S. cerevisiae)	3.5454	3.16452	2.50139	1.89616	2.77582	2.47354	2.57006	2.84303	3.48247	4.35067	3.82317	4.81774	3.78845	2.16718	1.57685	1.52724	1.51914	1.84283	0.405497	0.544821	0.49522	0.710604	0.744964	0.130052
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	18.7215	13.7645	16.6211	14.9469	14.9912	9.75869	11.6209	11.2485	7.66377	9.91605	13.4076	10.6544	7.73672	10.5023	8.75063	9.68614	5.62026	3.60934	2.9326	2.54953	4.5295	0	3.10066	2.82184
TTK	TTK protein kinase	2.8452	3.53377	4.46687	5.70084	4.30021	3.09096	2.83003	2.2292	2.11689	0.754078	1.28867	1.2595	0.507366	1.14005	1.04799	1.72093	0.983301	0.591787	0.527939	0.557345	0.967545	0.14351	0.193434	0.362762
ANAPC7	anaphase promoting complex subunit 7	18.5391	17.6036	18.9145	18.9094	18.643	21.0458	22.5843	17.4628	20.7899	16.3984	15.0645	15.5457	10.4738	9.16746	10.1875	8.69439	9.31416	8.54147	6.36756	6.92449	7.09758	8.51779	7.79384	5.59306
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	6.25576	7.12359	7.74531	7.25011	6.68313	8.25725	6.4349	5.86873	7.05183	3.52816	3.94601	4.60587	2.80593	2.99228	3.17752	2.13929	2.87458	2.68518	1.47586	1.50876	2.03751	0.366725	1.15337	0.740934
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	4.72905	6.53549	5.88891	6.71569	7.06185	7.62144	5.43975	5.52033	4.75446	3.1388	3.77986	5.28913	1.04954	2.00619	2.01675	1.72992	1.16254	1.2513	0.615611	0.639649	0.693855	0.22786	0.409504	0.287731
CDK1	cell division cycle 2, G1 to S and G2 to M	14.4292	15.3872	10.8318	12.958	16.3033	10.1463	9.21666	8.02944	7.42266	7.54852	6.81589	8.02746	4.59259	3.89687	4.65774	3.15802	3.35399	2.72527	1.01639	1.41753	1.44009	0.525768	0.236219	0.663918
CDC20	cell division cycle 20 homolog (S. cerevisiae)	27.096	22.1699	23.0893	24.8262	22.7054	23.2523	23.7689	26.4165	29.2093	18.8888	17.5152	19.4062	10.5251	9.29108	9.33167	7.72888	7.0577	11.0794	10.1092	11.3511	10.6705	11.8301	4.57354	4.44682
CDC25C	cell division cycle 25 homolog C (S. pombe)	2.76539	1.95536	1.05722	2.00556	2.57779	2.64727	2.29311	1.80292	2.46443	0.739409	1.61417	1.29638	1.26682	0.910173	1.28543	0.778688	1.02118	1.09415	0.125367	0.505348	0.362671	0.634057	0.107303	0
CCNA2	cyclin A2	14.7935	18.7461	16.5649	17.1375	17.886	15.541	13.6298	10.964	8.9062	6.24127	7.63915	6.55136	2.40487	3.35841	2.73037	2.2917	3.0083	2.64905	0.76935	1.1587	1.46633	1.08867	0.349381	0.317794
CCNB1	cyclin B1	35.3428	29.333	31.6458	31.6216	34.2132	36.2521	36.9862	31.0198	34.4172	28.7371	26.7751	29.7285	12.4723	9.16941	8.61746	8.37925	8.96887	8.13038	4.38211	3.84966	4.52836	2.35458	3.07752	1.51366
CCNB2	cyclin B2	17.5746	16.299	15.8848	14.0118	17.3906	15.3149	15.8368	13.9085	15.6934	10.5249	13.4881	11.3354	5.48907	5.72775	3.71933	3.74089	4.63062	2.89119	2.68468	2.44009	2.31437	2.40677	0.675843	1.21567
MCM3	minichromosome maintenance complex component 3	16.3425	13.8952	13.4164	13.6798	16.2803	16.207	14.773	15.5408	16.1764	13.6502	12.3775	12.5208	8.90003	9.46452	10.4226	8.36971	7.47369	7.93589	5.68023	5.23467	5.24725	3.607	4.61249	5.39563
MCM5	minichromosome maintenance complex component 5	17.8033	13.4152	13.9829	13.4806	12.7212	17.0943	14.8875	15.9329	17.5547	17.5579	14.6016	16.9867	11.6633	5.74128	7.70205	5.79323	6.55712	8.12234	5.42727	4.92209	4.63968	1.72318	2.32265	1.39261
PLK1	polo-like kinase 1 (Drosophila)	17.4631	13.5672	13.9356	14.8066	12.8105	17.7723	17.2604	19.4596	18.919	16.8965	14.0056	17.1981	10.1607	5.17053	5.79827	4.16459	5.18438	5.92524	4.74684	4.71085	4.15022	5.34351	2.77016	3.42567
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1	5.65004	4.43682	3.7595	4.49901	3.80121	5.53206	4.72121	4.47426	4.7092	4.22824	3.89716	5.69989	3.48895	1.54697	2.04065	1.98212	2.40629	2.38835	0.854822	0.693945	1.3995	0.228789	0.446537	0.652909
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	113.285	116.608	114.911	126.82	131.75	122.444	125.989	113.404	111.205	119.104	122.456	122.56	85.1655	90.7374	88.9639	84.9442	71.0789	71.9285	36.6211	33.4197	35.7769	38.441	29.7873	32.6063

Adipocytokine signaling pathway		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
ACACB	acetyl-Coenzyme A carboxylase beta	0.322263	0.547013	0.296797	0.38861	0.371909	0.348515	0.339757	0.415417	0.382338	0.272444	0.199513	0.194966	0.104765	0.201722	0.183385	0.327907	0.342475	0.325834	0.770863	0.831712	0.527769	0.97901	0.659795	0.4945
ACSL1	acyl-CoA synthetase long-chain family member 1	10.8619	14.3705	13.251	14.0919	13.876	12.8571	13.6285	11.5437	11.1282	10.3771	9.63523	9.70987	7.24669	9.41213	10.1834	9.38193	8.37499	8.96407	19.272	19.3807	22.5316	23.8415	29.6211	28.212
ADIPOR1	adiponectin receptor 1	40.3946	37.2316	39.8726	38.2282	36.7077	43.4761	48.3403	43.1405	47.6205	49.5736	41.6347	45.3591	49.8556	52.3026	47.4233	45.7537	50.4356	53.0259	63.4589	62.0469	59.0362	67.7659	60.7996	63.4921
MAPK8	mitogen-activated protein kinase 8	5.31826	9.61392	5.40244	9.49443	10.4746	9.91261	10.7617	9.68512	12.7538	14.7437	15.2654	14.1862	6.48346	15.4344	12.718	14.6048	13.7015	17.4315	15.2616	22.4087	14.1329	19.4417	15.9637	15.512
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	9.18129	10.3612	9.29184	10.9278	11.9365	11.661	14.8207	18.8454	13.4566	21.1708	24.501	22.0321	13.4553	15.7725	16.6956	14.3099	13.3635	13.8311	18.4311	23.9887	19.2092	78.1	57.8295	52.3445
NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	20.3488	13.1083	15.9575	14.5799	14.5581	15.0158	18.1892	18.4334	21.3385	29.8408	25.2957	26.136	23.6388	16.9518	19.5282	18.4742	18.242	22.0748	22.4145	27.6481	20.6687	68.3554	36.3966	37.4263
PRKCQ	protein kinase C, theta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.146854	0.0493217	0.0448303	0.13988	0	0
PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	6.24825	5.6202	6.52915	6.23055	8.59751	7.154	6.24073	6.81525	5.25428	4.98191	5.09464	4.79785	3.39844	4.74106	5.30182	4.21808	4.01181	3.82694	4.69942	4.9341	4.34583	14.0276	10.4389	12.2016
RXRA	retinoid X receptor, alpha	7.13008	8.79254	8.41878	8.51532	8.14937	9.83634	8.49102	9.12379	8.7381	7.05455	7.60605	6.53679	6.46346	6.28269	6.31417	8.5455	6.9944	7.55569	9.58122	8.70673	7.9869	14.087	11.0591	10.8643
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	23.0907	32.3664	30.2766	31.656	33.0527	29.9697	34.5428	33.5753	34.9699	31.1111	29.9825	27.1095	22.4709	33.0238	32.2651	33.6828	36.1992	36.5726	65.1641	71.5562	65.3248	81.6954	61.7061	58.0368
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	35.9456	28.6344	35.1459	34.6372	33.7406	39.606	43.102	40.3515	40.3722	55.8267	50.2999	57.1223	55.0275	39.8765	48.2276	44.3098	49.0583	45.8967	53.8955	49.9937	42.1186	80.5741	75.5343	80.4518

Oxidative phosphorylation		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
ATP5F1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	54.8922	46.6261	52.1876	49.5054	53.2353	52.4574	49.4531	51.5836	51.8752	61.9186	58.0396	51.6794	55.515	40.5854	35.3672	42.3608	41.3297	34.8827	33.4183	32.6615	33.0322	20.4402	28.125	29.36
ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	137.071	89.552	92.5183	95.3381	80.4192	108.969	107.527	103.713	147.248	136.235	135.31	159.845	156.815	56.8124	66.9229	60.5194	74.7217	80.9623	45.8396	43.6721	34.025	27.6433	37.7568	31.7588
ATP5G3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	57.6853	48.1934	54.1932	50.896	55.827	55.5659	67.1195	56.5582	67.9206	76.5619	67.4216	73.752	59.6709	36.3308	42.4222	41.9268	41.9109	43.2841	29.8384	26.8711	26.2706	22.8366	24.4838	28.24
ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	302.111	164.896	194.86	181.669	184.178	220.717	236.986	214.783	259.247	342.307	264.047	316.875	322.455	156.636	149.221	154.002	177.16	171.225	94.9423	113.715	96.8198	64.1984	58.7523	72.0959
ATP5J	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	127.426	102.366	95.7638	93.2318	85.6797	98.8829	100.082	99.8836	97.8995	113.225	110.778	113.173	160.9	72.3319	79.7074	74.0859	74.077	84.3987	54.0644	61.7329	53.1361	52.4627	56.4954	62.687
ATP5L	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	78.8186	53.1832	50.5755	48.3546	58.9653	56.1888	62.5519	61.1391	58.536	75.1428	62.9442	73.0917	82.4206	54.33	45.5238	43.9273	49.077	39.2357	30.9414	32.25	24.2756	22.1487	18.9396	23.0965
ATP5A1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	191.637	160.854	183.048	185.423	200.409	203.133	213.926	204.262	215.21	236.686	213.857	232.191	203.997	140.818	146.648	150.13	148.192	154.995	122.049	125.692	107.18	79.3399	107.695	110.175
ATP5B	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	328.243	262.381	281.8	301.137	335.168	368.727	388.356	378.86	406.655	494.78	417.928	478.74	358.358	284.611	280.017	271.664	301.763	300.191	225.632	237.584	202.358	189.64	167.749	183.105
ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	143.827	114.372	119.387	134.01	140.373	128.368	151.4	138.716	154.768	190.731	166.667	180.8	184.781	112.268	110.558	112.181	113.058	105.37	74.6015	95.8065	90.6417	67.6039	70.5307	82.2712
ATP6V1F	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F	139.825	97.521	94.4358	109.036	101.661	131.054	144.002	125.312	162.099	208.387	167.022	217.911	210.64	94.5829	111.15	89.9885	126.141	122.996	88.7856	81.4336	66.098	71.0539	71.1352	88.5533
ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	47.8761	36.5316	41.0916	42.1427	42.001	45.123	42.0795	38.4739	44.1338	49.435	44.9126	44.7734	48.2667	37.5176	33.2752	35.9084	31.071	30.3697	22.9148	18.1524	22.4042	24.2238	27.3224	32.5006
ATP6V0D1	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	66.1945	47.2245	53.2052	59.7262	58.3122	65.6271	84.251	74.4389	89.8999	102.666	97.711	98.1432	78.9113	52.5855	51.6837	51.7096	60.1551	56.6851	42.72	43.6807	35.1942	80.0034	42.2664	46.6804
NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	244.027	151.183	163.331	154.511	145.313	157.749	149.381	158.72	180.347	208.188	161.398	202.138	274.143	154.193	135.542	156.316	133.184	140.535	93.3274	86.0133	63.5823	74.9369	51.4933	78.6702
NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa	13.1283	10.7839	11.4541	11.5747	11.8812	12.5849	14.5351	13.0003	14.6415	15.7807	15.4504	18.6574	15.8537	11.8421	11.8458	10.6331	13.1986	11.7007	10.5037	9.55916	8.05847	6.15688	8.2219	7.3427
NDUFA4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	59.4319	45.0341	41.1727	41.304	46.5849	47.2096	52.006	49.3955	60.7053	63.7423	56.2659	64.4338	81.5579	33.6791	40.7496	36.8255	41.6405	39.1851	33.5106	33.3456	28.4242	23.0952	21.8299	26.9626
NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	60.141	43.3357	45.3137	43.369	39.0552	43.4861	52.718	48.9363	53.8442	63.1625	50.0978	59.4725	75.7533	38.5523	37.1271	35.2604	38.7512	38.8253	31.7176	30.356	25.3372	21.9344	19.7099	26.9661
NDUFA7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa	43.2381	27.0188	21.5899	34.5505	29.6839	44.7181	45.5275	36.9339	52.9759	51.4334	38.2179	52.4747	61.6024	27.8803	28.7322	36.2763	33.6781	33.578	30.0198	23.2111	21.7897	9.71127	15.5137	13.6255
NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa	27.801	17.9583	25.2841	25.353	24.7647	25.5558	28.4617	28.1578	33.0424	32.6107	26.9791	35.1944	31.0112	16.7714	16.0636	16.4423	17.4806	17.9195	13.7536	14.7223	12.8283	14.6841	9.44342	11.3436
NDUFB1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	153.1	85.9162	89.7483	81.4084	77.9098	69.8348	96.9407	88.2135	99.0983	139.528	109.903	110.808	138.552	72.3165	55.5049	80.6386	84.8449	61.4321	33.7013	38.4197	35.5456	23.3461	36.7125	40.2899
NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	122.572	78.9462	74.7042	92.3793	74.2522	98.0098	100.687	108.065	116.602	134.609	106.387	116.685	111.826	72.9637	60.7551	66.104	70.238	74.7987	68.3776	71.9752	58.508	82.969	70.0816	75.0149
NDUFB2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	192.969	138.55	169.172	155.241	132.717	206.571	209.198	188.435	211.221	283.579	210.413	277.933	295.526	98.5685	144.261	137.559	162.268	168.54	144.792	119.356	94.6982	76.6661	54.2668	97.6817
NDUFB3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa	62.2488	49.9296	52.7171	46.6456	49.5438	45.9437	46.4518	43.4812	50.4783	50.2278	48.505	50.3214	57.5696	37.7893	33.1209	29.6902	37.7021	38.9976	21.3938	19.3371	16.8641	12.5973	12.9844	20.5859
NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	60.141	43.3357	45.3137	43.369	39.0552	43.4861	52.718	48.9363	53.8442	63.1625	50.0978	59.4725	75.7533	38.5523	37.1271	35.2604	38.7512	38.8253	31.7176	30.356	25.3372	21.9344	19.7099	26.9661
NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	27.801	17.9583	25.2841	25.353	24.7647	25.5558	28.4617	28.1578	33.0424	32.6107	26.9791	35.1944	31.0112	16.7714	16.0636	16.4423	17.4806	17.9195	13.7536	14.7223	12.8283	14.6841	9.44342	11.3436
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa	96.5001	60.3984	62.4284	66.2933	65.2922	62.9168	67.5257	61.7256	65.1329	88.1829	72.5641	86.7973	85.8896	49.3127	58.5958	59.4681	67.3095	62.3301	48.7475	50.5257	43.9414	43.3372	43.3134	41.9925
NDUFC2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	43.455	29.2798	28.6278	33.9223	26.5718	34.9412	34.4305	34.0948	29.8035	37.9164	36.626	36.337	43.141	21.1013	24.9425	25.695	21.5322	21.0934	13.8131	11.1031	11.5909	10.9071	9.94959	13.2083
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	14.5988	18.8659	16.1086	21.1361	22.8938	18.4732	21.559	17.9849	20.0786	22.0772	20.4666	21.661	12.6501	17.716	17.1217	16.1317	15.0148	13.6023	10.9651	10.8728	10.0911	9.87621	7.86864	8.59654
NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)	34.4807	27.1315	30.6777	31.4257	30.8014	33.565	38.4735	33.2237	38.8197	37.6988	33.3747	37.3573	18.468	21.6452	22.0926	22.2272	24.4831	25.1961	22.1057	27.0598	21.6968	10.3355	20.9048	20.9777
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	168.303	101.989	125.84	101.128	99.2845	112.585	133.344	121.417	128.658	171.308	134.81	161.13	155.822	81.7278	73.6717	83.3081	76.3171	83.3297	52.194	53.6513	31.8713	57.5023	39.2914	52.0381
NDUFS7	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	62.9462	26.488	29.6094	38.2587	38.8114	51.0096	50.1386	58.8931	60.226	64.0667	61.2833	68.1786	58.997	26.8502	31.1089	31.3141	29.6707	34.324	38.6357	27.9327	21.1206	21.0292	21.1012	36.1144
COX8A	cytochrome c oxidase subunit 8A (ubiquitous)	451.957	267.772	320.828	302.394	299.853	348.233	374.533	360.334	414.551	521.572	405.637	463.952	501.984	210.323	263.878	224.992	297.564	297.261	212.035	203.078	150.909	124.182	116.494	149.574
COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	178.381	108.123	110.224	119.769	120.926	127.551	133.119	140.564	157.563	188.206	162.701	188.196	195.184	99.3844	100.691	106.113	111.749	103.793	96.7593	96.1565	78.0755	52.6655	67.6594	86.039
COX7A2L	cytochrome c oxidase subunit VIIa polypeptide 2 like	139.74	109.847	131.622	114.73	132.939	103.184	129.213	114.987	127.818	139.642	119.371	146.937	129.407	108.361	89.3495	93.2485	80.2774	81.2298	51.504	50.6417	49.0333	35.2328	51.8979	59.0201
COX7B	cytochrome c oxidase subunit VIIb	246.185	170.547	154.089	144.111	166.65	165.861	169.761	165.056	170.142	220.828	185.707	195.211	297.209	184.023	143.335	155.04	152.403	142.732	110.015	96.0206	90.9816	52.8078	91.1977	110.027
COX6A1	cytochrome c oxidase subunit VIa polypeptide 1	135.973	96.8556	104.805	114.794	101.443	116.362	143.29	138.095	169.876	198.225	139.82	182.707	185.684	83.5607	100.775	102.43	122.485	133.866	93.2736	85.2521	87.5645	65.2734	68.9727	95.2459
COX5A	cytochrome c oxidase subunit Va	104.278	62.4868	69.0571	76.7513	83.5149	90.0481	87.9547	90.2345	86.0046	130.467	100.076	100.011	100.339	60.9071	58.622	71.527	73.5079	69.422	64.4634	56.2976	46.5413	75.8499	52.9034	55.0962
CYC1	cytochrome c-1	76.4766	44.7755	60.0385	66.7314	61.337	86.6786	85.3576	73.1041	84.3509	111.752	91.2596	118.141	94.8928	47.0487	54.1754	48.4493	66.0042	68.9866	58.3967	60.9776	49.6123	54.0114	40.5658	54.5626
NDUFB4	hypothetical gene supported by AF044957; NM_004547; NADH dehydrogenase (ubiquinone) 1 beta sub	131.455	107.754	105.244	109.673	116.599	119.451	141.062	138.898	162.609	163.628	136.043	167.52	137.642	103.459	102.723	85.0032	119.816	107.916	118.369	103.818	90.1835	82.9183	88.6777	94.5573
PPA2	pyrophosphatase (inorganic) 2	18.8399	16.3393	16.7014	18.8448	20.6835	17.1592	19.6919	16.3992	16.8955	16.7347	18.7615	18.3339	20.4884	13.1038	12.0435	12.679	14.1471	10.2943	9.82709	8.93179	10.9425	9.08514	7.29795	8.85098
NDUFS5	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NAD	280.823	187.664	201.922	194.824	219.825	230.13	214.785	226.591	232.107	275.12	221.608	292.053	357.904	191.959	177.609	174.559	147.613	158.815	113.392	97.3055	93.1365	61.9269	62.1474	78.7187
SDHD	similar to succinate dehydrogenase complex, subunit D, integral membrane protein; succinate dehydrog	57.4345	42.09	51.1896	50.1416	51.1454	36.3162	41.2156	40.1665	39.6086	38.5984	43.0133	34.6963	45.9943	43.8059	42.0245	45.6298	38.0361	26.9813	26.0046	17.8387	25.1607	13.9548	23.5118	26.4322
SDHC	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	20.0913	20.8623	21.6188	22.1197	22.5534	21.0696	24.3662	20.5571	23.8405	26.3441	24.1587	24.5775	18.4959	14.2968	18.4623	16.5752	15.8604	18.5561	11.0077	14.8172	11.1601	8.53117	10.6919	12.1667
UQCRC2	ubiquinol-cytochrome c reductase core protein II	67.2087	64.3803	68.0447	59.4627	75.7805	73.4377	69.5379	69.8325	67.3671	86.1427	76.2281	85.7005	80.1526	63.541	59.3913	50.3011	65.0485	65.2173	54.4453	50.8375	48.1493	33.8396	48.084	51.2774
UQCRHL	ubiquinol-cytochrome c reductase hinge protein-like; ubiquinol-cytochrome c reductase hinge protein	53.6507	30.9179	39.1171	36.3916	43.857	45.9334	52.0977	49.3994	51.5278	51.8363	54.8049	57.3426	63.9518	61.5687	33.27	48.3352	36.9545	38.4237	30.4631	33.0921	33.6414	19.756	22.7454	21.2049
UQCR11	ubiquinol-cytochrome c reductase, 6.4kDa subunit	54.8189	36.5287	42.6034	40.0122	44.0303	52.7155	50.9531	52.3857	51.2185	72.3674	63.4336	70.1484	83.0625	29.3078	36.6753	39.2608	47.7818	48.1921	35.1606	31.3257	24.5701	24.3571	19.7949	23.8819
UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide-like 1; ubiquinol-cytochrome c reduct	73.6911	48.4991	60.7541	55.9729	67.2707	59.9262	74.7525	63.0809	59.2775	83.9578	70.3934	68.0925	75.5655	45.767	53.0477	50.3417	45.5466	42.3836	24.4126	19.3437	21.0228	19.8746	16.609	21.0813

Cytokine-cytokine receptor interaction		**FPKM**																							
Genes	**Description**	0hr_1	0hr_2	0hr_3	1hr_1	1hr_2	1hr_3	2hr_1	2hr_2	2hr_3	4hr_1	4hr_2	4hr_3	8hr_1	8hr_2	8hr_3	12hr_1	12hr_2	12hr_3	24hr_1	24hr_2	24hr_3	48hr_1	48hr_2	48hr_3
RELT	RELT tumor necrosis factor receptor	3.60787	3.17542	3.04587	4.21469	4.33716	4.43014	9.25913	12.0699	12.3063	19.9894	19.9353	21.5	17.5182	10.7332	13.0686	10.9559	12.9375	16.0734	13.4029	11.771	9.77981	13.327	7.44267	8.36516
CCL2	chemokine (C-C motif) ligand 2	38.8522	18.8325	19.6467	20.7983	23.833	17.6708	42.3112	35.7735	39.6945	107.221	89.0199	101.819	67.7268	47.3894	41.9609	26.3243	38.9094	43.7112	36.7163	24.9309	29.1702	84.9876	46.6323	41.0279
CCL28	chemokine (C-C motif) ligand 28	0	0	0	0	0	0.217375	0	0.296118	0.817615	0	0.597311	0.291849	0	2.11374	1.68931	2.14748	1.99367	1.82906	1.04902	0.93963	0.640565	1.33228	1.79575	2.01881
CCL3	chemokine (C-C motif) ligand 3	0	0	0	0.250688	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.242957	0	1.37793	8.66733	9.04792
CCL7	chemokine (C-C motif) ligand 7	0.655143	1.23561	0	0.246881	1.18136	0.22141	0.272648	0.904843	1.66558	10.0882	6.38817	10.4043	6.78878	5.99756	5.80724	6.87448	4.64155	3.72602	1.42465	0.957069	0.869938	2.03551	1.52423	6.16882
CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	0.671004	0.506209	0.463485	0.404574	0.29039	0.272124	0.670197	0.988533	0.852952	11.9127	12.8364	10.9606	9.16179	9.00939	7.75422	9.34522	4.39738	4.83388	0.875488	1.17629	0.890999	0.833914	4.62096	6.03737
CSF1R	colony stimulating factor 1 receptor	0.565471	0.58172	0.177541	0.387437	0.482022	0.208478	0.556234	0.615329	0.522766	1.11753	0.763817	0.83971	2.00542	1.32735	1.14762	0.980752	1.68444	1.51056	1.67681	1.72724	0.989779	1.38422	1.29169	1.237
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	3.05272	11.0779	8.2653	11.2437	10.9944	9.2068	9.74778	11.3475	11.6348	13.3336	12.4821	12.0995	5.13984	32.312	35.3341	26.9841	38.6143	33.8158	35.3009	35.5861	35.7584	19.705	36.7947	40.1119
HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	1.42643	3.16728	1.36307	1.35448	2.3425	1.33246	0.756314	2.13839	1.14889	2.7082	3.19878	3.30764	3.88267	6.86724	7.28488	6.49443	5.80259	6.92031	6.59061	4.18415	6.86535	6.38929	4.92232	4.75209
IFNGR1	interferon gamma receptor 1	20.2523	17.3706	18.98	18.5618	21.2142	17.6785	20.499	20.8028	20.4399	28.2081	28.7308	26.6906	34.9872	42.9523	43.0337	38.9294	38.8451	37.0434	40.8312	38.2831	38.6492	47.4297	47.45	41.7381
IFNE	interferon, epsilon	1.07715	1.30598	0.531445	0.463896	0.55495	0.104008	0.128078	0.141685	0	0.696912	1.28609	1.25678	1.68833	3.61204	2.82902	4.84399	4.22451	2.9172	0	0.112397	0.102165	0	0	0
IL1R1	interleukin 1 receptor, type I	12.9853	20.7077	17.8531	20.4149	21.715	20.4609	24.8861	26.4638	27.9662	37.159	43.6266	42.0694	23.7959	42.2848	41.4902	34.7938	34.8289	34.1819	37.9047	55.8215	52.7713	43.0003	29.7494	26.8249
IL15RA	interleukin 15 receptor, alpha	1.35331	1.02091	1.17134	1.999	1.46777	1.08069	2.05668	1.869	1.66289	4.21311	3.23955	3.6611	6.20196	4.72209	6.01263	4.906	5.02025	6.36544	5.89016	5.43113	4.91393	13.2471	7.37816	7.18609
IL21R	interleukin 21 receptor	1.18145	1.15395	1.30439	0.957014	0.614144	1.03684	1.31493	1.96124	2.02435	1.92937	2.06276	2.22383	3.41076	2.06176	2.26986	2.841	3.80617	3.05933	6.36997	8.27678	6.56182	4.22394	2.21299	2.42125
IL4R	interleukin 4 receptor	9.15761	7.84099	7.43792	7.70362	7.13203	8.734	11.911	12.2414	11.2123	26.7168	24.3436	25.4573	23.3553	22.1966	21.8558	24.4332	21.7427	25.0826	27.4486	36.6283	26.9351	55.2756	33.8279	31.4465
IL6	interleukin 6 (interferon, beta 2)	24.7757	15.6385	17.7114	59.03	67.8782	67.1198	192.579	194.458	204.964	219.349	239.171	226.648	249.182	185.914	176.714	133.036	116.784	121.4	174.012	105.224	116.87	230.931	262.923	276.141
IL6R	interleukin 6 receptor	0.242331	0.0652773	0.119552	0.208727	0.224728	0.259107	1.67134	2.06929	1.76035	1.88142	1.89958	1.88508	0.633083	1.42515	1.0684	1.68431	1.80896	1.78198	2.14913	1.90644	1.65631	2.65332	2.09426	1.9167
LIF	leukemia inhibitory factor (cholinergic differentiation factor)	3.66641	3.65502	3.55758	7.57926	9.93584	9.9835	57.8945	57.3417	62.3187	51.0013	62.843	53.3304	123.364	128.775	130.926	80.7913	107.846	108.133	92.3145	29.4585	52.6839	55.6552	98.9986	104.5
TGFB1	transforming growth factor, beta 1	42.2931	24.9612	36.2073	40.488	34.8732	40.2059	50.9735	47.7553	51.5263	73.3442	65.5799	65.1489	68.706	54.2464	65.3516	79.9429	92.7284	87.5851	132.325	99.3825	89.6214	66.1568	79.5363	91.8682
TGFB3	transforming growth factor, beta 3	36.2061	34.0193	35.6623	32.4594	34.647	33.7928	38.7844	38.9936	37.7162	74.4703	78.1092	70.3982	97.4397	102.936	99.5115	108.725	114.597	114.728	176.936	148.269	159.894	44.2655	40.932	38.1532
TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	1.09707	0.841465	0.770406	0.643086	0.175831	0.782181	0.913124	1.01014	0.619794	1.5458	1.91155	0.995574	2.9721	2.14111	2.88441	1.59594	2.66702	1.38654	3.4472	1.42375	2.58929	1.15512	4.08024	4.71878
TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1.51511	2.85751	1.88958	1.71284	3.36953	2.30418	1.78651	4.06889	3.37039	5.14641	4.4555	6.30178	4.3098	8.23912	7.62693	7.106	8.38609	8.01852	5.90301	13.9257	8.63418	21.7063	11.515	8.58616
TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	21.9441	27.1758	26.3923	28.2892	29.2015	28.0163	33.7672	37.3403	37.3197	70.8651	76.366	71.0711	68.5379	99.2079	99.0931	75.4447	88.3158	95.3412	64.3226	63.5267	64.6735	85.7778	81.43	83.9794
TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	21.2879	23.6594	22.2853	24.9918	25.4785	24.1131	27.6488	30.1555	25.0531	38.0882	39.375	36.0894	74.2911	78.7711	82.9442	73.2501	82.454	87.7547	112.996	107.35	101.266	153.481	108.743	105.118
VEGFA	vascular endothelial growth factor A	36.6243	42.176	38.5746	50.1084	53.5906	50.3309	163.354	172.89	183.135	232.71	270.912	236.62	273.716	439.036	413.679	335.783	332.703	349.737	421.1	279.778	318.985	313.588	419.04	389.643

Supplementary Table.1 Differentially expressed genes during hADSC self organization