

**S1 Table.** Raw data Stats

Sample ID	Total read bases (bp)	Total reads	GC (%)	AT (%)	Q20 (%)	Q30 (%)
IJF1	1,177,350,624	7,797,024	49.71	50.29	93.46	87.06
IJF2	1,152,255,934	7,630,834	54.38	45.62	93.85	86.68
IJF3	761,824,294	5,045,194	51.43	48.57	92.88	85.56
OJF1	494,050,558	3,271,858	52.0	48.0	92.38	84.91
OJF2	209,861,310	1,389,810	52.29	47.71	95.71	90.06
OJF3	400,444,752	2,651,952	53.03	46.97	95.3	89.31

**S2 Table.** Upregulated DEGs, Mean FPKM and edgeR statistics of inner and outer jaw fats

DEGs in two Jaw fats	Gene ID	Mean FPKM		edgeR		
		IJF	OJF	log2 FC	FDR	P value
<b>Outer jaw fat</b>						
MSTRG.24322	ALBU	5.823	5345.508	9.206	0.000	1.45E-13
MSTRG.47457	FETUB	0.000	1331.080	11.334	0.000	1.62E-11
MSTRG.18865	BHMT1	0.000	700.956	10.616	0.000	8.58E-10
MSTRG.51985	HEMO	0.000	285.017	10.313	0.000	3.87E-09
MSTRG.24275	VTDB	0.000	538.204	10.014	0.000	1.62E-08
MSTRG.66060	MLRS	4.201	1587.401	9.972	0.000	1.99E-08
MSTRG.60601	MYG	0.000	478.501	7.752	0.000	2.05E-08
MSTRG.36663	CO3	8.789	1823.189	7.310	0.000	4.42E-08
MSTRG.13093	FIBG	0.000	341.371	9.600	0.001	1.11E-07
MSTRG.6665	A1AT	1.656	626.012	7.937	0.001	1.78E-07
MSTRG.34120	APOH	0.000	349.494	9.445	0.001	2.19E-07
MSTRG.54800	GSTA2	0.000	147.901	9.316	0.002	3.77E-07
MSTRG.29415	ATTY	0.000	225.159	9.293	0.002	4.14E-07
MSTRG.53042	ALDOB	0.000	285.025	9.099	0.004	9.09E-07
MSTRG.19760	CO9	0.000	119.918	9.018	0.006	1.24E-06
MSTRG.38499	HEPC	0.000	257.177	8.933	0.007	1.73E-06
MSTRG.40379	FABPL	0.000	225.589	8.746	0.014	3.45E-06
MSTRG.13088	FIBA	0.000	185.310	8.713	0.014	3.90E-06
MSTRG.15202	28S rRNA	2139.990	36281.303	3.947	0.022	6.65E-06
MSTRG.58010	ARGH1	0.000	194.255	8.532	0.023	7.37E-06
MSTRG.36810	CP2E1	0.000	56.029	8.325	0.044	1.53E-05
<b>Inner jaw fat</b>						

MSTRG.14448	HBAZ	444.384	0.000	10.861	0.000	1.50E-08
MSTRG.5007	ENH1	259.219	0.000	9.543	0.014	3.96E-06
MSTRG.66992	APP	294.742	0.000	9.497	0.016	4.70E-06
MSTRG.55926	PXMP4	283.002	0.000	9.346	0.025	8.13E-06
MSTRG.18842	TSP4	193.170	0.000	9.117	0.050	1.79E-05

**S3 Table.** Upregulated DEGs of inner and outer jaw fats by Cuffdiff statistics

Name	Gene ID	Gene Name	Mean FPMK		Cuffdiff_q value
			Inner Jaw fat	Outer jaw Fat	
<b>Outer Jaw Fat</b>					
MSTRG.14337	TNNT1	Troponin T	0	69.9935913	0.020382
MSTRG.22223	TITIN	Titin	0	0	0.020382
MSTRG.24322	ALBU	Albumin	5.82328194	5345.50777	0.020382
MSTRG.30061	ZN37A	Zinc Finger Protein 37A	0.01295513	0.59409719	0.020382
MSTRG.31284	ORNT1	Mitochondrial Ornithine transporter 1	0	0	0.020382
MSTRG.47839	SLC2A2	Solute Carrier Family 2 Member 2	0	17.6323687	0.020382
MSTRG.51303	SLC1A2	Solute Carrier Family 1 Member 2	0	23.906817	0.020382
MSTRG.57284	S22A1	Solute carrier family 22 member 1	0	32.3267973	0.020382
MSTRG.59935	MYF6	Myogenic factor 6	0	17.8368643	0.020382
MSTRG.66621	LORF2	LINE-1 retrotransposable element ORF2 protein	0	37.8647587	0.020382
MSTRG.69146	HJURP	Holliday junction recognition protein	0	66.6651867	0.020382
MSTRG.43801	HNF4A	Hepatocyte nuclear factor 4, alpha	0	21.8277867	0.035669
MSTRG.48399	QGB1-102L23	<i>Pseudorca crassidens</i> genomic DNA, clone	0	13.6387	0.035669
<b>Inner Jaw Fat</b>					
MSTRG.7354	ZFP36L1	mRNA decay activator protein TISB Human	7.04334621	0.09702305	0.020382
MSTRG.9179	SINE Stec20	SINE flanking region Stec20	37.139266	0.72432567	0.020382

MSTRG.25499	43U ch13	Isolate 43U chromosome 13 sequence	39.6538683	0	0.047558
MSTRG.58852	DHX9	ATP-dependent RNA helicase A	3.94740411	0	0.047558

**S4 Table: Functional terms of Gene ontology enrichment analysis of OJF by Enricher.**

A: GO\_Biological\_Process

Term	P-value	Combin ed Score	Overl ap	Adjust ed P- value	Old P- valu e	Old Adjust ed P- value	Odds Ratio	Genes
regulation of peptide hormone secretion (GO:0090276)	0.00607205	87.3982713	Feb-73	1	0	0	17.1232877	HNF4A;SLC2A2
positive regulation of skeletal muscle fiber development (GO:0048743)	0.00956277	484.362251	6-Jan	1	0	0	104.166667	MYF6
negative regulation of muscle cell apoptotic process (GO:0010656)	0.00956277	484.362251	6-Jan	1	0	0	104.166667	APOH
negative regulation of myeloid cell apoptotic process (GO:0033033)	0.00956277	484.362251	6-Jan	1	0	0	104.166667	APOH
regulation of insulin secretion (GO:0050796)	0.01071262	57.8613875	Feb-98	1	0	0	12.755102	HNF4A;SLC2A2
amino acid import across plasma membrane (GO:0089718)	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	SLC1A2
fructose 1,6-bisphosphate metabolic process (GO:0030388)	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	ALDOB
regulation of skeletal muscle fiber development (GO:0048742)	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	MYF6
fructose metabolic process (GO:0006000)	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	ALDOB
regulation of protein secretion (GO:0050708)	0.01266811	51.0358303	2/107	1	0	0	11.682243	HNF4A;SLC2A2
regulation of smooth muscle cell apoptotic process (GO:0034391)	0.01273065	340.91743	8-Jan	1	0	0	78.125	APOH
phospholipid homeostasis (GO:0055091)	0.01273065	340.91743	8-Jan	1	0	0	78.125	HNF4A
positive regulation of lipoprotein lipase activity (GO:0051006)	0.01273065	340.91743	8-Jan	1	0	0	78.125	APOH
positive regulation of hemostasis (GO:1900048)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	APOH

muscle cell fate commitment (GO:0042693)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	MYF6
negative regulation of fibrinolysis (GO:0051918)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	APOH
positive regulation of triglyceride lipase activity (GO:0061365)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	APOH
vacuolar proton-transporting V-type ATPase complex assembly (GO:0070072)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	ALDOB
proton-transporting V-type ATPase complex assembly (GO:0070070)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	ALDOB
acidic amino acid transport (GO:0015800)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	SLC1A2
positive regulation of coagulation (GO:0050820)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	APOH
ornithine metabolic process (GO:0006591)	0.0143109	294.912064	9-Jan	1	0	0	69.4444444	HNF4A
L-glutamate transport (GO:0015813)	0.01588871	258.884172	10-Jan	1	0	0	62.5	SLC1A2
positive regulation of myoblast fusion (GO:1901741)	0.01746406	229.97784	11-Jan	1	0	0	56.8181818	MYF6
positive regulation of skeletal muscle tissue development (GO:0048643)	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	MYF6
skeletal muscle cell differentiation (GO:0035914)	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	MYF6
regulation of myoblast fusion (GO:1901739)	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	MYF6
regulation of cholesterol homeostasis (GO:2000188)	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	HNF4A
plasminogen activation (GO:0031639)	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	APOH
intestinal absorption (GO:0050892)	0.02060746	186.639534	13-Jan	1	0	0	48.0769231	SLC2A2
regulation of fibrinolysis (GO:0051917)	0.02060746	186.639534	13-Jan	1	0	0	48.0769231	APOH
negative regulation of hemostasis (GO:1900047)	0.02060746	186.639534	13-Jan	1	0	0	48.0769231	APOH
monosaccharide transport (GO:0015749)	0.0221755	170.034255	14-Jan	1	0	0	44.6428571	SLC2A2
positive regulation of myoblast differentiation (GO:0045663)	0.0221755	170.034255	14-Jan	1	0	0	44.6428571	MYF6
positive regulation of syncytium formation by plasma membrane fusion (GO:0060143)	0.02374111	155.856137	15-Jan	1	0	0	41.6666667	MYF6

L-alpha-amino acid transmembrane transport (GO:1902475)	0.02374 111	155.856 137	15-Jan	1	0	0	41.6666 667	SLC1A2
negative regulation of coagulation (GO:0050819)	0.02374 111	155.856 137	15-Jan	1	0	0	41.6666 667	APOH
hexose transport (GO:0008645)	0.02530 429	143.624 275	16-Jan	1	0	0	39.0625	SLC2A2
positive regulation of myotube differentiation (GO:0010831)	0.02530 429	143.624 275	16-Jan	1	0	0	39.0625	MYF6
glyceraldehyde-3-phosphate metabolic process (GO:0019682)	0.02842 338	123.629 975	18-Jan	1	0	0	34.7222 222	ALDOB
skeletal muscle contraction (GO:0003009)	0.02842 338	123.629 975	18-Jan	1	0	0	34.7222 222	TNNT1
anion homeostasis (GO:0055081)	0.02842 338	123.629 975	18-Jan	1	0	0	34.7222 222	HNF4A
positive regulation of blood coagulation (GO:0030194)	0.02997 93	115.370 009	19-Jan	1	0	0	32.8947 368	APOH
regulation of lipoprotein lipase activity (GO:0051004)	0.03153 28	108.022 719	20-Jan	1	0	0	31.25	APOH
acylglycerol homeostasis (GO:0055090)	0.03463 258	95.5386 476	22-Jan	1	0	0	28.4090 909	HNF4A
glutathione derivative metabolic process (GO:1901685)	0.03463 258	95.5386 476	22-Jan	1	0	0	28.4090 909	GSTA2
glutathione derivative biosynthetic process (GO:1901687)	0.03463 258	95.5386 476	22-Jan	1	0	0	28.4090 909	GSTA2
protein homotrimerization (GO:0070207)	0.03463 258	95.5386 476	22-Jan	1	0	0	28.4090 909	SLC1A2
glycolytic process (GO:0006096)	0.03617 887	90.1978 306	23-Jan	1	0	0	27.1739 13	ALDOB
ATP generation from ADP (GO:0006757)	0.03772 275	85.3513 521	24-Jan	1	0	0	26.0416 667	ALDOB
glycolytic process through glucose-6-phosphate (GO:0061620)	0.03926 424	80.9360 282	25-Jan	1	0	0	25	ALDOB
canonical glycolysis (GO:0061621)	0.03926 424	80.9360 282	25-Jan	1	0	0	25	ALDOB
negative regulation of wound healing (GO:0061045)	0.03926 424	80.9360 282	25-Jan	1	0	0	25	APOH
glucose catabolic process to pyruvate (GO:0061718)	0.03926 424	80.9360 282	25-Jan	1	0	0	25	ALDOB
L-amino acid transport (GO:0015807)	0.03926 424	80.9360 282	25-Jan	1	0	0	25	SLC1A2
positive regulation of wound healing (GO:0090303)	0.04080 334	76.8988 328	26-Jan	1	0	0	24.0384 615	APOH
regulation of muscle contraction (GO:0006937)	0.04080 334	76.8988 328	26-Jan	1	0	0	24.0384 615	TNNT1
response to hexose (GO:0009746)	0.04234 004	73.1949 531	27-Jan	1	0	0	23.1481 481	HNF4A

triglyceride homeostasis (GO:0070328)	0.04387 437	69.7862 728	28-Jan	1	0	0	22.3214 286	HNF4A
striated muscle tissue development (GO:0014706)	0.04540 631	66.6401 772	29-Jan	1	0	0	21.5517 241	MYF6
dicarboxylic acid transport (GO:0006835)	0.04540 631	66.6401 772	29-Jan	1	0	0	21.5517 241	SLC1A2
skeletal muscle organ development (GO:0060538)	0.04540 631	66.6401 772	29-Jan	1	0	0	21.5517 241	MYF6
regulation of myoblast differentiation (GO:0045661)	0.04540 631	66.6401 772	29-Jan	1	0	0	21.5517 241	MYF6
regulation of blood coagulation (GO:0030193)	0.04693 587	63.7286 045	30-Jan	1	0	0	20.8333 333	APOH
negative regulation of endothelial cell proliferation (GO:0001937)	0.04693 587	63.7286 045	30-Jan	1	0	0	20.8333 333	APOH
CENP-A containing nucleosome assembly (GO:0034080)	0.04693 587	63.7286 045	30-Jan	1	0	0	20.8333 333	HJURP
CENP-A containing chromatin organization (GO:0061641)	0.04693 587	63.7286 045	30-Jan	1	0	0	20.8333 333	HJURP
sarcomere organization (GO:0045214)	0.04846 306	61.0272 857	31-Jan	1	0	0	20.1612 903	TNNT1
alpha-amino acid metabolic process (GO:1901605)	0.04846 306	61.0272 857	31-Jan	1	0	0	20.1612 903	HNF4A
protein trimerization (GO:0070206)	0.04998 788	58.5151 305	Jan-32	1	0	0	19.5312 5	SLC1A2
chromatin remodeling at centromere (GO:0031055)	0.04998 788	58.5151 305	Jan-32	1	0	0	19.5312 5	HJURP

## B: GO\_Cellular\_Component

Term	P-value	Combine d Score	Overl ap	Adjust ed P- value	Old P- value	Old Adjust ed P- value	Odds Ratio	Genes
platelet dense granule lumen (GO:0031089)	0.022175 5	170.0342 55	14-Jan	1	0	0	44.64285 71	APOH
very-low-density lipoprotein particle (GO:0034361)	0.023741 11	155.8561 37	15-Jan	1	0	0	41.66666 67	APOH
condensed chromosome kinetochore (GO:0000777)	0.029979 3	115.3700 09	19-Jan	1	0	0	32.89473 68	HJUR P
platelet dense granule (GO:0042827)	0.033083 89	101.4496 64	21-Jan	1	0	0	29.76190 48	APOH

centriolar satellite (GO:0034451)	0.039264 24	80.93602 82	25-Jan	1	0	0	25	ALDO B
condensed chromosome, centromeric region (GO:0000779)	0.040803 34	76.89883 28	26-Jan	1	0	0	24.03846 15	HJUR P

### C: GO\_Molecular\_Function

Term	P-value	Combin ed Score	Overl ap	Adjus ted P- value	Old P- val ue	Old Adjus ted P- value	Odds Ratio	Combin ed Score	Genes
aldehyde-lyase activity (GO:0016832)	0.01114 794	401.473 281	7-Jan	1	0	0	89.2857 143	401.473 281	ALD OB
lipase activator activity (GO:0060229)	0.01114 794	401.473 281	7-Jan	1	0	0	89.2857 143	401.473 281	APO H
high-affinity glutamate transmembrane transporter activity (GO:0005314)	0.01114 794	401.473 281	7-Jan	1	0	0	89.2857 143	401.473 281	SLC1 A2
D-glucose transmembrane transporter activity (GO:0055056)	0.01431 09	294.912 064	9-Jan	1	0	0	69.4444 444	294.912 064	SLC2 A2
metalloendopeptidase inhibitor activity (GO:0008191)	0.01903 698	206.321 452	12- Jan	1	0	0	52.0833 333	206.321 452	FETU B
sodium:amino acid symporter activity (GO:0005283)	0.01903 698	206.321 452	12- Jan	1	0	0	52.0833 333	206.321 452	SLC1 A2
acidic amino acid transmembrane transporter activity (GO:0015172)	0.02060 746	186.639 534	13- Jan	1	0	0	48.0769 231	186.639 534	SLC1 A2
hexose transmembrane transporter activity (GO:0015149)	0.02060 746	186.639 534	13- Jan	1	0	0	48.0769 231	186.639 534	SLC2 A2
tropomyosin binding (GO:0005523)	0.02217 55	170.034 255	14- Jan	1	0	0	44.6428 571	170.034 255	TNN T1
L-glutamate transmembrane transporter activity (GO:0005313)	0.02217 55	170.034 255	14- Jan	1	0	0	44.6428 571	170.034 255	SLC1 A2
glucose transmembrane transporter activity (GO:0005355)	0.03153 28	108.022 719	20- Jan	1	0	0	31.25	108.022 719	SLC2 A2
solute:sodium symporter activity (GO:0015370)	0.03463 258	95.5386 476	22- Jan	1	0	0	28.4090 909	95.5386 476	SLC1 A2
dicarboxylic acid transmembrane	0.04387 437	69.7862 728	28- Jan	1	0	0	22.3214 286	69.7862 728	SLC1 A2

transporter activity (GO:0005310)									
glutathione transferase activity (GO:0004364)	0.04693 587	63.7286 045	30- Jan	1	0	0	20.8333 333	63.7286 045	GST A2

#### D: Jensen\_compartments

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
protein-DNA-RNA complex	0.0079 7515	603.92 8165	5-Jan	1	0	0	125	HNF4A
ATP-sensitive potassium channel complex	0.0109 2266	57.031 7652	Feb-99	1	0	0	12.626 2626	HNF4A; SLC2A2
Cortical granule	0.0138 1693	47.788 6204	2/112	1	0	0	11.160 7143	GSTA2; FETUB
I(KACh) inward rectifier potassium channel complex	0.0174 6406	229.97 784	11-Jan	1	0	0	56.818 1818	HNF4A
Axolemma	0.0190 3698	206.32 1452	12-Jan	1	0	0	52.083 3333	SLC1A2
Chylomicron	0.0190 3698	206.32 1452	12-Jan	1	0	0	52.083 3333	APOH
Cell wall-bounded periplasmic space	0.0206 0746	186.63 9534	13-Jan	1	0	0	48.076 9231	TNNT1
Platelet dense granule lumen	0.0206 0746	186.63 9534	13-Jan	1	0	0	48.076 9231	APOH
Platelet dense granule	0.0299 793	115.37 0009	19-Jan	1	0	0	32.894 7368	APOH
triglyceride-rich lipoprotein particle	0.0299 793	115.37 0009	19-Jan	1	0	0	32.894 7368	APOH
very-low-density lipoprotein particle	0.0299 793	115.37 0009	19-Jan	1	0	0	32.894 7368	APOH
Striated muscle thin filament	0.0315 328	108.02 2719	20-Jan	1	0	0	31.25	TNNT1
CENP-A recruiting complex	0.0315 328	108.02 2719	20-Jan	1	0	0	31.25	HJURP
Pyruvate kinase complex	0.0328 0621	23.996 7512	2/178	1	0	0	7.0224 7191	SLC2A2 ;FETUB
Myofilament	0.0361 7887	90.197 8306	23-Jan	1	0	0	27.173 913	TNNT1
SPOTS complex	0.0361 7887	90.197 8306	23-Jan	1	0	0	27.173 913	SLC1A2
Sweet taste receptor complex	0.0377 2275	85.351 3521	24-Jan	1	0	0	26.041 6667	SLC2A2
Centriolar satellite	0.0392 6424	80.936 0282	25-Jan	1	0	0	25	ALDOB
Glutamate synthase complex	0.0392 6424	80.936 0282	25-Jan	1	0	0	25	SLC1A2



high-density lipoprotein particle	0.04080334	76.8988328	26-Jan	1	0	0	24.0384615	APOH
Ornithine carbamoyltransferase complex	0.04540631	66.6401772	29-Jan	1	0	0	21.5517241	ALDOB
skein-like inclusion	0.04540631	66.6401772	29-Jan	1	0	0	21.5517241	SLC1A2
Dendritic growth cone	0.04540631	66.6401772	29-Jan	1	0	0	21.5517241	SLC2A2

**S5 Table: Functional terms of Gene Ontology enrichment analysis of IJF by Enricher.**

A: GO\_Biological\_Process

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
positive regulation of binding (GO:0051099)	3.36E-04	564.312903	Feb-81	1	0	0	70.5467372	APP;DHX9
positive regulation of NF-kappaB transcription factor activity (GO:0051092)	8.36E-04	316.394438	2/128	1	0	0	44.6428571	APP;DHX9
positive regulation of nucleobase-containing compound transport (GO:0032241)	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	DHX9
positive regulation of microglial cell activation (GO:1903980)	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	APP
astrocyte activation (GO:0048143)	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	APP
neuron projection maintenance (GO:1990535)	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	APP
regulation of interferon-alpha secretion (GO:1902739)	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	DHX9
positive regulation of interferon-alpha	0.00209839	2936.46961	6-Jan	1	0	0	476.190476	DHX9

secretion (GO:1902741)								
positive regulation of RNA export from nucleus (GO:0046833)	0.002098 39	2936.469 61	6-Jan	1	0	0	476.1904 76	DHX9
neuron remodeling (GO:0016322)	0.002098 39	2936.469 61	6-Jan	1	0	0	476.1904 76	APP
regulation of translation (GO:0006417)	0.002288 69	163.1060 17	2/213	1	0	0	26.82763 25	APP;DHX9
positive regulation of sequence-specific DNA binding transcription factor activity (GO:0051091)	0.002331 19	161.0996 85	2/215	0.9913 393	0	0	26.57807 31	APP;DHX9
G-quadruplex DNA unwinding (GO:0044806)	0.002447 75	2454.116 18	7-Jan	0.9608 3738	0	0	408.1632 65	DHX9
protein localization to cytoplasmic stress granule (GO:1903608)	0.002447 75	2454.116 18	7-Jan	0.8922 0614	0	0	408.1632 65	DHX9
positive regulation of isomerase activity (GO:0010912)	0.002447 75	2454.116 18	7-Jan	0.8327 2573	0	0	408.1632 65	DHX9
regulation of microglial cell activation (GO:1903978)	0.002447 75	2454.116 18	7-Jan	0.7806 8037	0	0	408.1632 65	APP
regulation of interleukin-18 production (GO:0032661)	0.002447 75	2454.116 18	7-Jan	0.7347 5799	0	0	408.1632 65	DHX9
regulation of amyloid fibril formation (GO:1905906)	0.002797 02	2099.715 18	8-Jan	0.7929 5376	0	0	357.1428 57	APP
amyloid fibril formation (GO:1990000)	0.002797 02	2099.715 18	8-Jan	0.7512 1935	0	0	357.1428 57	APP
neuron projection organization (GO:0106027)	0.003146 17	1829.069 46	9-Jan	0.8027 4578	0	0	317.4603 17	APP
small RNA loading onto RISC (GO:0070922)	0.003146 17	1829.069 46	9-Jan	0.7645 1979	0	0	317.4603 17	DHX9
positive regulation of astrocyte differentiation (GO:0048711)	0.003146 17	1829.069 46	9-Jan	0.7297 6889	0	0	317.4603 17	APP
ionotropic glutamate receptor signaling pathway (GO:0035235)	0.003146 17	1829.069 46	9-Jan	0.6980 3981	0	0	317.4603 17	APP

positive regulation of cell activation (GO:0050867)	0.003146 17	1829.069 46	9-Jan	0.6689 5482	0	0	317.4603 17	APP
positive regulation of long-term synaptic potentiation (GO:1900273)	0.003146 17	1829.069 46	9-Jan	0.6421 9662	0	0	317.4603 17	APP
neuron maturation (GO:0042551)	0.003146 17	1829.069 46	9-Jan	0.6174 9675	0	0	317.4603 17	APP
positive regulation of amyloid-beta formation (GO:1902004)	0.003495 22	1616.102 21	10-Jan	0.6605 9739	0	0	285.7142 86	APP
pyroptosis (GO:0070269)	0.003495 22	1616.102 21	10-Jan	0.6370 0463	0	0	285.7142 86	DHX9
regulation of cytoplasmic translation (GO:2000765)	0.003495 22	1616.102 21	10-Jan	0.6150 3895	0	0	285.7142 86	DHX9
cellular copper ion homeostasis (GO:0006878)	0.003495 22	1616.102 21	10-Jan	0.5945 3765	0	0	285.7142 86	APP
astrocyte development (GO:0014002)	0.003495 22	1616.102 21	10-Jan	0.5753 5902	0	0	285.7142 86	APP
positive regulation of posttranscriptional gene silencing (GO:0060148)	0.003844 17	1444.466 76	11-Jan	0.6130 253	0	0	259.7402 6	DHX9
regulation of long-term neuronal synaptic plasticity (GO:0048169)	0.003844 17	1444.466 76	11-Jan	0.5944 4878	0	0	259.7402 6	APP
positive regulation of tumor necrosis factor secretion (GO:1904469)	0.003844 17	1444.466 76	11-Jan	0.5769 6499	0	0	259.7402 6	DHX9
positive regulation of amyloid precursor protein catabolic process (GO:1902993)	0.004193 02	1303.413 14	12-Jan	0.6113 416	0	0	238.0952 38	APP
alternative mRNA splicing, via spliceosome (GO:0000380)	0.004193 02	1303.413 14	12-Jan	0.5943 5989	0	0	238.0952 38	DHX9
cellular response to exogenous dsRNA (GO:0071360)	0.004541 75	1185.591 67	13-Jan	0.6263 9375	0	0	219.7802 2	DHX9
copper ion homeostasis (GO:0055070)	0.004541 75	1185.591 67	13-Jan	0.6099 097	0	0	219.7802 2	APP
regulation of NMDA receptor activity (GO:2000310)	0.004541 75	1185.591 67	13-Jan	0.5942 7099	0	0	219.7802 2	APP

RNA interference (GO:0016246)	0.004541 75	1185.591 67	13-Jan	0.5794 1422	0	0	219.7802 2	DHX9
regulation of defense response to virus (GO:0050688)	0.004890 39	1085.813 01	14-Jan	0.6086 7433	0	0	204.0816 33	DHX9
positive regulation of response to cytokine stimulus (GO:0060760)	0.004890 39	1085.813 01	14-Jan	0.5941 8209	0	0	204.0816 33	DHX9

## B: GO\_Cellular\_Component

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
micro-ribonucleoprotein complex (GO:0035068)	0.002447 75	2454.116 18	7-Jan	1	0	0	408.1632 65	DHX9
RISC-loading complex (GO:0070578)	0.003146 17	1829.069 46	9-Jan	0.70159 635	0	0	317.4603 17	DHX9
endoribonuclease complex (GO:1902555)	0.004541 75	1185.591 67	13-Jan	0.67520 737	0	0	219.7802 2	DHX9
endosome lumen (GO:0031904)	0.008370 98	569.4029 09	24-Jan	0.93336 416	0	0	119.0476 19	APP
polysomal ribosome (GO:0042788)	0.009760 29	472.3911 14	28-Jan	0.87061 809	0	0	102.0408 16	DHX9
endosomal part (GO:0044440)	0.010801 18	417.3363 72	31-Jan	0.80288 792	0	0	92.16589 86	APP
peroxisomal membrane (GO:0005778)	0.013918 23	305.3254 11	Jan-40	0.88679 011	0	0	71.42857 14	PXMP4
polysome (GO:0005844)	0.021845 81	173.4125 33	Jan-63	1	0	0	45.35147 39	DHX9
platelet alpha granule lumen (GO:0031093)	0.023218 92	160.4600 29	Jan-67	1	0	0	42.64392 32	APP
peroxisomal part (GO:0044439)	0.025960 2	139.0929 73	Jan-75	1	0	0	38.09523 81	PXMP4
ribosome (GO:0005840)	0.026302 4	136.7704 93	Jan-76	1	0	0	37.59398 5	DHX9
ribonucleoprotein granule (GO:0035770)	0.027670 15	128.1214 63	Jan-80	1	0	0	35.71428 57	DHX9
trans-Golgi network membrane (GO:0032588)	0.029377 53	118.5722 76	Jan-85	1	0	0	33.61344 54	APP
platelet alpha granule (GO:0031091)	0.031082 34	110.1941 47	Jan-90	0.99019 439	0	0	31.74603 17	APP

peroxisome (GO:0005777)	0.031763 54	107.1253 49	Jan-92	0.94443 588	0	0	31.05590 06	PXMP4
microbody (GO:0042579)	0.031763 54	107.1253 49	Jan-92	0.88540 864	0	0	31.05590 06	PXMP4
Golgi lumen (GO:0005796)	0.033804 69	98.75089 88	Jan-98	0.88687 59	0	0	29.15451 9	APP
membrane raft (GO:0045121)	0.040919 69	76.73814 98	1/119	1	0	0	24.00960 38	APP
axon (GO:0030424)	0.048325 29	61.39412 94	1/141	1	0	0	20.26342 45	APP

### C: GO\_Molecular\_Function

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
ATP-dependent 3'-5' DNA helicase activity (GO:0043140)	0.002447 75	2454.1161 8	7-Jan	1	0	0	408.1632 65	DHX9
sequence-specific mRNA binding (GO:1990825)	0.002797 02	2099.7151 8	8-Jan	1	0	0	357.1428 57	DHX9
nucleoside-triphosphate diphosphatase activity (GO:0047429)	0.003146 17	1829.0694 6	9-Jan	1	0	0	317.4603 17	DHX9
siRNA binding (GO:0035197)	0.003146 17	1829.0694 6	9-Jan	0.90531 099	0	0	317.4603 17	DHX9
DNA replication origin binding (GO:0003688)	0.004193 02	1303.4131 4	12-Jan	0.96523 208	0	0	238.0952 38	DHX9
3'-5' DNA helicase activity (GO:0043138)	0.004541 75	1185.5916 7	13-Jan	0.87125 973	0	0	219.7802 2	DHX9
RNA stem-loop binding (GO:0035613)	0.004541 75	1185.5916 7	13-Jan	0.74679 406	0	0	219.7802 2	DHX9
RNA polymerase binding (GO:0070063)	0.006631 99	754.26323 5	19-Jan	0.95417 743	0	0	150.3759 4	DHX9
RNA polymerase II core binding (GO:0000993)	0.009065 84	516.83970 3	26-Jan	1	0	0	109.8901 1	DHX9
basal RNA polymerase II transcription machinery binding (GO:0001099)	0.009413 12	493.71965 7	27-Jan	1	0	0	105.8201 06	DHX9
ATP-dependent DNA helicase	0.009760 29	472.39111 4	28-Jan	1	0	0	102.0408 16	DHX9

activity (GO:0004003)								
RNA polymerase core enzyme binding (GO:0043175)	0.011841 14	372.78787 9	Jan-34	1	0	0	84.03361 34	DHX9
helicase activity (GO:0004386)	0.011841 14	372.78787 9	Jan-34	1	0	0	84.03361 34	DHX9
RNA polymerase II transcription coactivator activity (GO:0001105)	0.013572 31	314.99807 6	Jan-39	1	0	0	73.26007 33	DHX9
DNA helicase activity (GO:0003678)	0.013918 23	305.32541 1	Jan-40	1	0	0	71.42857 14	DHX9
pyrophosphatase activity (GO:0016462)	0.014264 05	296.16815 1	Jan-41	1	0	0	69.68641 11	DHX9
single-stranded RNA binding (GO:0003727)	0.015646 28	263.96964 1	Jan-45	1	0	0	63.49206 35	DHX9
transcriptional activator activity, RNA polymerase II transcription factor binding (GO:0001190)	0.017371 74	231.59488 3	Jan-50	1	0	0	57.14285 71	DHX9
serine-type endopeptidase inhibitor activity (GO:0004867)	0.019438 87	201.04493 3	Jan-56	1	0	0	51.02040 82	APP
double-stranded RNA binding (GO:0003725)	0.020471 03	188.31691 9	Jan-59	1	0	0	48.42615 01	DHX9
ATP-dependent RNA helicase activity (GO:0004004)	0.023218 92	160.46002 9	Jan-67	1	0	0	42.64392 32	DHX9
RNA helicase activity (GO:0003724)	0.023218 92	160.46002 9	Jan-67	1	0	0	42.64392 32	DHX9
RNA-dependent ATPase activity (GO:0008186)	0.023561 94	157.48413 4	Jan-68	1	0	0	42.01680 67	DHX9
DNA-dependent ATPase activity (GO:0008094)	0.024933	146.49060 2	Jan-72	1	0	0	39.68253 97	DHX9
RNA polymerase II transcription cofactor activity (GO:0001104)	0.029036 26	120.38128 9	Jan-84	1	0	0	34.01360 54	DHX9
ATP-dependent helicase activity (GO:0008026)	0.029377 53	118.57227 6	Jan-85	1	0	0	33.61344 54	DHX9
single-stranded DNA binding (GO:0003697)	0.030059 76	115.09254 1	Jan-87	1	0	0	32.84072 25	DHX9

core promoter binding (GO:0001047)	0.03346475	100.066645	Jan-97	1	0	0	29.455081	DHX9
double-stranded DNA binding (GO:0003690)	0.03414452	97.4647388	Jan-99	1	0	0	28.8600289	DHX9
DNA binding (GO:0003677)	0.03601014	21.2699066	2/893	1	0	0	6.39897616	APP;DHX9
endopeptidase inhibitor activity (GO:0004866)	0.03821453	84.029333	1/111	1	0	0	25.7400257	APP
sequence-specific double-stranded DNA binding (GO:1990837)	0.03855303	83.0540977	1/112	1	0	0	25.5102041	DHX9
RNA polymerase II transcription factor binding (GO:0001085)	0.04159496	75.083265	1/121	1	0	0	23.6127509	DHX9

#### D: Jensen\_compartments

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
CRD-mediated mRNA stability complex	0.00174892	3627.86218	5-Jan	1	0	0	571.428571	DHX9
Nuclear envelope lumen	0.00244775	2454.11618	7-Jan	1	0	0	408.163265	APP
Ciliary rootlet	0.00244775	2454.11618	7-Jan	1	0	0	408.163265	APP
Astrocyte projection	0.00279702	2099.71518	8-Jan	1	0	0	357.142857	APP
Plastid acetyl-CoA carboxylase complex	0.00314617	1829.06946	9-Jan	1	0	0	317.460317	APP
Glial cell projection	0.00489039	1085.81301	14-Jan	1	0	0	204.081633	APP
Acetolactate synthase complex	0.00558734	926.294937	16-Jan	1	0	0	178.571429	APP
Polar tube	0.00628388	804.725081	18-Jan	1	0	0	158.730159	APP
Noc4p-Nop14p complex	0.00628388	804.725081	18-Jan	1	0	0	158.730159	DHX9
Endosome lumen	0.00802339	599.427861	23-Jan	1	0	0	124.223602	APP
Spindle midzone	0.00941312	493.719657	27-Jan	1	0	0	105.820106	APP
Cortical Lewy body	0.01045432	434.356157	30-Jan	1	0	0	95.2380952	APP
Dendritic shaft	0.01045432	434.356157	30-Jan	1	0	0	95.2380952	APP

Smooth endoplasmic reticulum	0.01114794	401.473281	Jan-32	1	0	0	89.2857143	APP
RNA nuclear export complex	0.01288015	336.067014	Jan-37	1	0	0	77.2200772	DHX9
Mitochondrial inner membrane protein insertion complex	0.01391823	305.325411	Jan-40	1	0	0	71.4285714	PXMP4
Mitosome	0.01426405	296.168151	Jan-41	1	0	0	69.6864111	DHX9
Thylakoid lumen	0.01702686	237.490573	Jan-49	1	0	0	58.3090379	APP
Cell septum	0.01737174	231.594883	Jan-50	1	0	0	57.1428571	DHX9
Cytochrome b6f complex	0.0180612	220.548867	Jan-52	1	0	0	54.9450549	DHX9
Neuromuscular junction	0.01875024	210.399402	Jan-54	1	0	0	52.9100529	APP
Platelet alpha granule lumen	0.01875024	210.399402	Jan-54	1	0	0	52.9100529	APP
Perinucleolar compartment	0.01909461	205.628539	Jan-55	1	0	0	51.9480519	DHX9
Main axon	0.01909461	205.628539	Jan-55	1	0	0	51.9480519	APP
Microbody membrane	0.01943887	201.044933	Jan-56	1	0	0	51.0204082	PXMP4
CIA complex	0.01978303	196.638142	Jan-57	1	0	0	50.1253133	APP
Peroxisomal membrane	0.01978303	196.638142	Jan-57	1	0	0	50.1253133	PXMP4
NSL complex	0.02047103	188.316919	Jan-59	1	0	0	48.4261501	APP
Pick body	0.02081488	184.385099	Jan-60	1	0	0	47.6190476	APP
Microprocessor complex	0.02081488	184.385099	Jan-60	1	0	0	47.6190476	DHX9
Rough endoplasmic reticulum	0.02150227	176.939948	Jan-62	1	0	0	46.0829493	APP
Terminal bouton	0.02150227	176.939948	Jan-62	1	0	0	46.0829493	APP
Ribonuclease III complex	0.02150227	176.939948	Jan-62	1	0	0	46.0829493	DHX9
Nitrogenase complex	0.02184581	173.412533	Jan-63	1	0	0	45.3514739	DHX9
[Ni-Fe] hydrogenase complex	0.02253257	166.716194	Jan-65	1	0	0	43.956044	DHX9
clathrin-coated pit	0.02253257	166.716194	Jan-65	1	0	0	43.956044	APP
Mitochondrial pyruvate dehydrogenase complex	0.02253257	166.716194	Jan-65	1	0	0	43.956044	DHX9
Dense fibrillar component	0.0228758	163.535747	Jan-66	1	0	0	43.2900433	DHX9
ER to Golgi transport vesicle	0.02493302	146.490602	Jan-72	1	0	0	39.6825397	APP



Platelet alpha granule	0.024933	146.490602	Jan-72	1	0	0	39.6825397	APP
Dosage compensation complex	0.0256179	141.485088	Jan-74	1	0	0	38.6100386	DHX9
5-lipoxygenase complex	0.02664449	134.514761	Jan-77	1	0	0	37.1057514	APP
IHF-DNA complex	0.02698648	132.323048	Jan-78	1	0	0	36.6300366	DHX9
Mycolate outer membrane	0.02698648	132.323048	Jan-78	1	0	0	36.6300366	DHX9
trans-Golgi network membrane	0.02869489	122.238772	Jan-83	1	0	0	34.4234079	APP
Organelle envelope lumen	0.02903626	120.381289	Jan-84	1	0	0	34.0136054	APP
Secretory granule lumen	0.02937753	118.572276	Jan-85	1	0	0	33.6134454	APP
CVT complex	0.03005976	115.092541	Jan-87	1	0	0	32.8407225	APP
Filopodium	0.03108234	110.194147	Jan-90	1	0	0	31.7460317	APP
Microbody part	0.03142299	108.64099	Jan-91	1	0	0	31.3971743	PXMP4
Peroxisomal part	0.03176354	107.125349	Jan-92	1	0	0	31.0559006	PXMP4
Glycosome	0.03550282	92.5975869	1/103	1	0	0	27.739251	PXMP4
Cytoplasmic membrane-bounded vesicle lumen	0.03584215	91.4459019	1/104	1	0	0	27.4725275	APP
Dendritic spine	0.03584215	91.4459019	1/104	1	0	0	27.4725275	APP
Vesicle lumen	0.03618136	90.3186696	1/105	1	0	0	27.2108844	APP
Neuron spine	0.03652048	89.2151507	1/106	1	0	0	26.9541779	APP
L-type voltage-gated calcium channel complex	0.03787592	85.0244079	1/110	1	0	0	25.974026	APP
Dendritic lamellar body	0.03821453	84.029333	1/111	1	0	0	25.7400257	APP
Axon terminus	0.03821453	84.029333	1/111	1	0	0	25.7400257	APP
Vacuolar lumen	0.03889143	82.0981389	1/113	1	0	0	25.2844501	APP
Cell outer membrane	0.03990602	79.3405946	1/116	1	0	0	24.6305419	DHX9
acetyl-CoA carboxylase complex	0.04193244	74.2785823	1/122	1	0	0	23.4192037	APP
Golgi trans cisterna	0.04193244	74.2785823	1/122	1	0	0	23.4192037	APP
Neuron projection terminus	0.04226982	73.4885445	1/123	1	0	0	23.2288037	APP
Microbody	0.04361833	70.467443	1/127	1	0	0	22.4971879	PXMP4

Peroxisome	0.0439552	69.7451861	1/128	1	0	0	22.3214286	PXMP4
Kinetoplast	0.04429197	69.0354789	1/129	1	0	0	22.1483942	DHX9
Neurofibrillary tangle	0.04462864	68.3380109	1/130	1	0	0	21.978022	APP
Growth cone	0.04530167	66.9786009	1/132	1	0	0	21.6450216	APP
Formate dehydrogenase complex	0.04563803	66.3160864	1/133	1	0	0	21.4822771	DHX9
Site of polarized growth	0.04698247	63.774362	1/137	1	0	0	20.8550574	APP
Photosystem I	0.04765408	62.5649939	1/139	1	0	0	20.5549846	DHX9

**S6 Table: Functional terms of pathways enrichment analysis of OJF by Enricher.**

A: KEGG 2019 human

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
Maturity onset diabetes of the young	7.87E-04	343.624608	26-Feb	0.24236945	0	0	48.0769231	HNF4A;SLC2A2
Pentose phosphate pathway	0.04693587	63.7286045	30-Jan	1	0	0	20.8333333	ALDOB

B: MGI-Mammalian

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
MP:0030589 increased pancreatic alpha cell mass	0.00797515	603.928165	5-Jan	1	0	0	125	SLC2A2
MP:0004677 truncated ribs	0.00797515	603.928165	5-Jan	1	0	0	125	MYF6
MP:0003696 abnormal zona pellucida morphology	0.00956277	484.362251	6-Jan	1	0	0	104.166667	FETUB
MP:0003895 increased ectoderm apoptosis	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	HNF4A
MP:0004036 abnormal muscle relaxation	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	TNNT1
MP:0012131 small visceral yolk sac	0.01114794	401.473281	7-Jan	1	0	0	89.2857143	HNF4A

MP:0011854 cerebral edema	0.01273065	340.91743	8-Jan	1	0	0	78.125	SLC1A2
MP:0009109 decreased pancreas weight	0.01273065	340.91743	8-Jan	1	0	0	78.125	SLC2A2
MP:0011964 increased total retina thickness	0.0143109	294.912064	9-Jan	1	0	0	69.444444	HNF4A
MP:0009401 increased skeletal muscle fiber diameter	0.01588871	258.884172	10-Jan	1	0	0	62.5	TNNT1
MP:0004119 hypokalemia	0.01746406	229.97784	11-Jan	1	0	0	56.8181818	HNF4A
MP:0002280 abnormal intercostal muscle morphology	0.02060746	186.639534	13-Jan	1	0	0	48.0769231	MYF6
MP:0000737 abnormal myotome development	0.02060746	186.639534	13-Jan	1	0	0	48.0769231	MYF6
MP:0002118 abnormal lipid homeostasis	0.02131855	34.115049	2/141	1	0	0	8.86524823	HNF4A;SLC2A2
MP:0008997 increased blood osmolality	0.0221755	170.034255	14-Jan	1	0	0	44.6428571	SLC2A2
MP:0009593 absent chorion	0.02374111	155.856137	15-Jan	1	0	0	41.6666667	HNF4A
MP:0005291 abnormal glucose tolerance	0.02686504	132.975343	17-Jan	1	0	0	36.7647059	SLC2A2
MP:0002823 abnormal rib development	0.02842338	123.629975	18-Jan	1	0	0	34.7222222	MYF6
MP:0002712 increased circulating glucagon level	0.0299793	115.370009	19-Jan	1	0	0	32.8947368	SLC2A2
MP:0005030 absent amnion	0.0315328	108.022719	20-Jan	1	0	0	31.25	HNF4A
MP:0003087 absent allantois	0.0315328	108.022719	20-Jan	1	0	0	31.25	HNF4A
MP:0009413 skeletal muscle fiber atrophy	0.03772275	85.3513521	24-Jan	1	0	0	26.0416667	TNNT1
MP:0002230 abnormal primitive streak formation	0.03926424	80.9360282	25-Jan	1	0	0	25	HNF4A
MP:0008263 abnormal hippocampus CA1 region morphology	0.03926424	80.9360282	25-Jan	1	0	0	25	SLC1A2
MP:0005620 abnormal muscle contractility	0.04234004	73.1949531	27-Jan	1	0	0	23.1481481	TNNT1
MP:0009114 decreased pancreatic beta cell mass	0.04234004	73.1949531	27-Jan	1	0	0	23.1481481	SLC2A2
MP:0002628 hepatic steatosis	0.0427788	19.1244698	2/206	1	0	0	6.06796117	HNF4A;ALDOB
MP:0004672 short ribs	0.04693587	63.7286045	30-Jan	1	0	0	20.8333333	MYF6
MP:0000153 rib bifurcation	0.04998788	58.5151305	Jan-32	1	0	0	19.53125	MYF6

C; BioPlanet 2019

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
HNF3B pathway	5.04E-05	412.284282	Mar-45	0.07615703	0	0	41.6666667	HNF4A;SLC2A2;ALDOB
Gene expression regulation in pancreatic beta cells	4.63E-04	479.887741	20-Feb	0.34941809	0	0	62.5	HNF4A;SLC2A2
Maturity onset diabetes of the young	7.27E-04	361.321825	25-Feb	0.36597734	0	0	50	HNF4A;SLC2A2
Pancreatic beta-cell development regulation	0.00119378	262.915155	Feb-32	0.45065311	0	0	39.0625	HNF4A;SLC2A2
Glycolysis and gluconeogenesis	0.00639896	84.1936597	Feb-75	1	0	0	16.6666667	SLC2A2;ALDOB
Facilitative sodium-independent glucose transporters	0.01903698	206.321452	12-Jan	1	0	0	52.0833333	SLC2A2
Developmental biology	0.02907462	15.7941503	3/420	1	0	0	4.46428571	HNF4A;MYF6;SLC2A2
Oxidative stress-induced gene expression via Nrf2	0.03308389	101.449664	21-Jan	1	0	0	29.7619048	GSTA2
Glutathione conjugation	0.03926424	80.9360282	25-Jan	1	0	0	25	GSTA2
Pentose phosphate pathway	0.04234004	73.1949531	27-Jan	1	0	0	23.1481481	ALDOB
Glycolysis	0.04234004	73.1949531	27-Jan	1	0	0	23.1481481	ALDOB
CDO in myogenesis	0.04540631	66.6401772	29-Jan	1	0	0	21.5517241	MYF6
Gluconeogenesis	0.04846306	61.0272857	31-Jan	1	0	0	20.1612903	ALDOB

D; WikiPathways 2019

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
Glycolysis and Gluconeogenesis WP534	0.00235207	168.123926	Feb-45	1	0	0	27.7777778	SLC2A2;ALDOB
NRF2 pathway WP2884	0.02275027	32.3902243	2/146	1	0	0	8.56164384	GSTA2;SLC2A2
Phytochemical activity on NRF2 transcriptional activation WP3	0.02374111	155.856137	15-Jan	1	0	0	41.6666667	GSTA2
Cori Cycle WP1946	0.02530429	143.624275	16-Jan	1	0	0	39.0625	SLC2A2

Type II diabetes mellitus WP1584	0.03463 258	95.5386 476	22- Jan	1	0	0	28.4090 909	SLC2A2
NRF2-ARE regulation WP4357	0.03617 887	90.1978 306	23- Jan	1	0	0	27.1739 13	GSTA2
Constitutive Androstane Receptor Pathway WP2875	0.04998 788	58.5151 305	Jan- 32	1	0	0	19.5312 5	GSTA2

**S7 Table: Functional terms of pathways enrichment analysis of IJF by Enricher.**

A: KEGG 2019 human

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
Peroxisome	0.02869 489	122.2387 72	Jan- 83	1	0	0	34.4234 079	PXMP4
Serotonergic synapse	0.03889 143	82.09813 89	1/113	1	0	0	25.2844 501	APP

B: MGI-Mammalian

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
MP:0020408 altered susceptibility to induced thrombosis	0.001748 92	3627.862 18	5-Jan	1	0	0	571.428 571	APP
MP:0003895 increased ectoderm apoptosis	0.002447 75	2454.116 18	7-Jan	1	0	0	408.163 265	DHX9
MP:0008222 decreased hippocampal commissure size	0.002447 75	2454.116 18	7-Jan	1	0	0	408.163 265	APP
MP:0011187 abnormal parietal endoderm morphology	0.003146 17	1829.069 46	9-Jan	1	0	0	317.460 317	DHX9
MP:0002798 abnormal active avoidance behavior	0.003844 17	1444.466 76	11- Jan	1	0	0	259.740 26	APP
MP:0008226 decreased anterior commissure size	0.003844 17	1444.466 76	11- Jan	1	0	0	259.740 26	APP
MP:0002065 abnormal fear/anxiety-related behavior	0.004193 02	1303.413 14	12- Jan	1	0	0	238.095 238	APP
MP:0000604 amyloidosis	0.004541 75	1185.591 67	13- Jan	1	0	0	219.780 22	APP

MP:0003329 amyloid beta deposits	0.005238 92	1000.312 48	15- Jan	1	0	0	190.476 19	APP
MP:0005032 abnormal ectoplacental cone morphology	0.006283 88	804.7250 81	18- Jan	1	0	0	158.730 159	DHX9
MP:0008817 hematoma	0.006631 99	754.2632 35	19- Jan	1	0	0	150.375 94	APP
MP:0005030 absent amnion	0.00698	709.2438 5	20- Jan	1	0	0	142.857 143	DHX9
MP:0004510 myositis	0.007327 9	668.8525 9	21- Jan	1	0	0	136.054 422	APP
MP:0005635 decreased circulating bilirubin level	0.008370 98	569.4029 09	24- Jan	1	0	0	119.047 619	APP
MP:0002230 abnormal primitive streak formation	0.008718 46	541.9785 4	25- Jan	1	0	0	114.285 714	DHX9
MP:0001916 intracerebral hemorrhage	0.008718 46	541.9785 4	25- Jan	1	0	0	114.285 714	APP
MP:0002199 abnormal brain commissure morphology	0.009760 29	472.3911 14	28- Jan	1	0	0	102.040 816	APP
MP:0004000 impaired passive avoidance behavior	0.010107 36	452.6592 51	29- Jan	1	0	0	98.5221 675	APP
MP:0000749 muscle degeneration	0.010107 36	452.6592 51	29- Jan	1	0	0	98.5221 675	APP
MP:0002207 abnormal long term potentiation	0.011494 59	386.6561 82	Jan- 33	1	0	0	86.5800 866	APP
MP:0002572 abnormal emotion/affect behavior	0.011494 59	386.6561 82	Jan- 33	1	0	0	86.5800 866	APP
MP:0002801 abnormal long term object recognition memory	0.011494 59	386.6561 82	Jan- 33	1	0	0	86.5800 866	APP
MP:0002196 absent corpus callosum	0.011841 14	372.7878 79	Jan- 34	1	0	0	84.0336 134	APP
MP:0020467 abnormal circadian behavior	0.011841 14	372.7878 79	Jan- 34	1	0	0	84.0336 134	APP
MP:0009403 increased variability of skeletal muscle fiber size	0.012880 15	336.0670 14	Jan- 37	1	0	0	77.2200 772	APP
MP:0008414 abnormal spatial reference memory	0.012880 15	336.0670 14	Jan- 37	1	0	0	77.2200 772	APP
MP:0000787 abnormal telencephalon morphology	0.013572 31	314.9980 76	Jan- 39	1	0	0	73.2600 733	APP
MP:0000781 decreased corpus callosum size	0.013572 31	314.9980 76	Jan- 39	1	0	0	73.2600 733	APP
MP:0001675 abnormal ectoderm development	0.016336 78	250.1116 34	Jan- 47	1	0	0	60.7902 736	DHX9

MP:0011186 abnormal visceral endoderm morphology	0.01633678	250.111634	Jan-47	1	0	0	60.7902736	DHX9
MP:0008918 microgliosis	0.01633678	250.111634	Jan-47	1	0	0	60.7902736	APP
MP:0001695 abnormal gastrulation	0.01771652	225.952809	Jan-51	1	0	0	56.022409	DHX9
MP:0009538 abnormal synapse morphology	0.01909461	205.628539	Jan-55	1	0	0	51.9480519	APP
MP:0001454 abnormal cued conditioning behavior	0.01909461	205.628539	Jan-55	1	0	0	51.9480519	APP
MP:0002063 abnormal learning/memory/conditioning	0.01943887	201.044933	Jan-56	1	0	0	51.0204082	APP
MP:0002797 increased thigmotaxis	0.01943887	201.044933	Jan-56	1	0	0	51.0204082	APP
MP:0001683 absent mesoderm	0.0228758	163.535747	Jan-66	1	0	0	43.2900433	DHX9
MP:0009404 centrally nucleated skeletal muscle fibers	0.0252755	143.949888	Jan-73	1	0	0	39.1389432	APP
MP:0002175 decreased brain weight	0.0252755	143.949888	Jan-73	1	0	0	39.1389432	APP
MP:0002183 gliosis	0.0256179	141.485088	Jan-74	1	0	0	38.6100386	APP
MP:0003354 astrocytosis	0.0297187	116.809931	Jan-86	1	0	0	33.2225914	APP
MP:0001522 impaired swimming	0.03074158	111.786169	Jan-89	1	0	0	32.1027287	APP
MP:0003313 abnormal locomotor activation	0.03244433	104.201506	Jan-94	1	0	0	30.3951368	APP
MP:0013504 increased embryonic tissue cell apoptosis	0.03244433	104.201506	Jan-94	1	0	0	30.3951368	DHX9
MP:0001417 decreased exploration in new environment	0.0351634	93.7744944	1/102	1	0	0	28.0112045	APP
MP:0002882 abnormal neuron morphology	0.03618136	90.3186696	1/105	1	0	0	27.2108844	APP
MP:0001473 reduced long-term potentiation	0.0426071	72.7127723	1/124	1	0	0	23.0414747	APP
MP:0001392 abnormal locomotor behavior	0.04496521	67.6524819	1/131	1	0	0	21.8102508	APP

### C: BioPlanet 2019

Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
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Formyl peptide interaction with formyl peptide receptors	0.00279702	2099.71518	8-Jan	1	0	0	357.142857	APP
Deregulation of CDK5 in Alzheimer's disease	0.00349522	1616.10221	10-Jan	1	0	0	285.714286	APP
Advanced glycosylation endproduct receptor signaling	0.00454175	1185.59167	13-Jan	1	0	0	219.78022	APP
Platelet amyloid precursor protein pathway	0.00489039	1085.81301	14-Jan	1	0	0	204.081633	APP
Inflammasomes	0.00593566	861.643146	17-Jan	1	0	0	168.067227	APP
Cytosolic sensors of pathogen-associated DNA	0.0073279	668.85259	21-Jan	1	0	0	136.054422	APP
TRAF6 mediated NF-kB activation	0.0076757	632.428088	22-Jan	1	0	0	129.87013	APP
TAK1 activates NF-kappaB by phosphorylation and activation of IKK complex	0.00837098	569.402909	24-Jan	1	0	0	119.047619	APP
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	0.01633678	250.111634	Jan-47	1	0	0	60.7902736	APP
Amyloids	0.01771652	225.952809	Jan-51	1	0	0	56.022409	APP
Caspase cascade in apoptosis	0.02047103	188.316919	Jan-59	1	0	0	48.4261501	APP
Messenger RNA splicing: major pathway	0.02356194	157.484134	Jan-68	1	0	0	42.0168067	DHX9
RIG-I/MDA5-mediated induction of interferon-alpha/beta pathways	0.0263024	136.770493	Jan-76	1	0	0	37.593985	APP
Peroxisome	0.02698648	132.323048	Jan-78	1	0	0	36.6300366	PXMP4
Response to elevated platelet cytosolic calcium	0.02869489	122.238772	Jan-83	1	0	0	34.4234079	APP
p75 neurotrophin receptor-mediated signaling	0.0426071	72.7127723	1/124	1	0	0	23.0414747	APP
Capped intron-containing pre-mRNA processing	0.04731833	63.1647526	1/138	1	0	0	20.7039337	DHX9



Term	P-value	Combined Score	Overlap	Adjusted P-value	Old P-value	Old Adjusted P-value	Odds Ratio	Genes
Copper homeostasis WP3286	0.0180612	220.548867	Jan-52	1	0	0	54.9450549	APP
Apoptosis-related network due to altered Notch3 in ovarian cancer WP2864	0.01840577	215.368787	Jan-53	1	0	0	53.9083558	APP
Alzheimers Disease WP2059	0.02869489	122.238772	Jan-83	1	0	0	34.4234079	APP
mRNA Processing WP411	0.04328135	71.2025701	1/126	1	0	0	22.675737	DHX9
TGF-beta Signaling Pathway WP366	0.04530167	66.9786009	1/132	1	0	0	21.6450216	APP
Endoderm Differentiation WP2853	0.04832529	61.3941294	1/141	1	0	0	20.2634245	APP