SUPPLEMENTARY MATERIAL

PRENATAL STRESS IS ASSOCIATED WITH A SEX-SPECIFIC CAMKII MODULATION IN AGED MOUSE PREFRONTAL CORTEX

This supplementary document provides functional annotation and Gene Ontology (GO) enrichment analysis for biological processes, cellular components, and molecular functions associated with differentially expressed proteins in males datasets.

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Table S1: GO ONTOLOGY, BIOLOGICAL PROCESS, UP-REGULATED PROTEINS

ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:0045109	intermediate filament organization	6/13	78/28832	0,076923076923077	170,60355029585	31,856288947898 2	5,44495321529022E-13	5,44495321529022E-13	4,12670138421996E-11	Krt15/Krt79/Krt78/Krt1/Krt10/Krt77	6
GO:0045103	intermediate filament-based process	6/13	98/28832	0,061224489795918 4	135,78649921507 1	28,387259211685 7	2,22213726693678E-12	2,22213726693678E-12	5,61382046384029E-11	Krt15/Krt79/Krt78/Krt1/Krt10/Krt77	6
GO:0030216	keratinocyte differentiation	5/13	168/28832	0,029761904761904 8	66,007326007326	17,947775199551 7	7,84175277562658E-09	7,84175277562658E-09	1,48580578906609E-07	Krt79/Krt78/Krt1/Krt10/Krt77	5
GO:0043588	skin development	5/13	352/28832	0,014204545454545 5	31,503496503496 5	12,229622138190 2	3,13099516373291E-07	3,13099516373291E-07	3,38994965095894E-06	Krt79/Krt78/Krt1/Krt10/Krt77	5
GO:0008544	epidermis development	5/13	410/28832	0,012195121951219 5	27,046904315197	11,281914423009 4	6,64922260114997E-07	6,64922260114997E-07	6,29926351687892E-06	Krt79/Krt78/Krt1/Krt10/Krt77	5
GO:0051290	protein heterotetramerization	2/13	16/28832	0,125	277,230769230769	23,473468786519 5	2,24400935070096E-05	2,24400935070096E-05	0,00018896920848008 1	Krt1/Krt10	2
GO:0018149	peptide cross-linking	2/13	28/28832	0,071428571428571 4	158,417582417582	17,699782455390 7	7,04708594586984E-05	7,04708594586984E-05	0,00053409493484487 2	Krt1/Krt10	2
GO:0006893	Golgi to plasma membrane transport	2/13	65/28832	0,030769230769230 8	68,241420118343 2	11,526789026205 3	0,00038414420222803	0,00038414420222803	0,00242617390880861	Acsl3/Rab13	2
GO:0006633	fatty acid biosynthetic process	2/13	168/28832	0,011904761904761 9	26,402930402930 4	7,013456979145 26	0,00252379905795082	0,00252379905795082	0,01195483764292 49	Acsl3/Hacd3	2
GO:0015718	monocarboxylic acid transport	2/13	194/28832	0,010309278350515 5	22,864393338620 1	6,489765882549 74	0,00334594391172398	0,00334594391172398	0,01491690164979 11	Slc6a11/Acsl3	2
GO:0034379	very-low-density lipoprotein particle assembly	1/13	10/28832	0,1	221,784615384615	14,830945076346 5	0,00450044255258897	0,00450044255258897	0,01630942350614 02	Acsl3	1
GO:0046719	regulation by virus of viral protein levels in host cell	1/13	10/28832	0,1	221,784615384615	14,830945076346 5	0,00450044255258897	0,00450044255258897	0,01630942350614 02	Hacd3	1
GO:0150172	regulation of phosphatidylcholine metabolic process	1/13	10/28832	0,1	221,784615384615	14,830945076346 5	0,00450044255258897	0,00450044255258897	0,01630942350614 02	Acsl3	1
GO:0001867	complement activation,	1/13	11/28832	0,090909090909090 9	201,622377622378	14,134591728457 3	0,00494945699457172	0,00494945699457172	0,01630942350614 02	Krt1	1

	lectin pathway										
GO:0042996	regulation of Golgi to plasma membrane protein transport	1/13	11/28832	0,0909090909090909	201,62237762378	14,134591728457	0,00494945699457172	0,00494945699457172	0,0163094235061402	Acsl3	1
GO:0071073	positive regulation of phospholipid biosynthetic process	1/13	12/28832	0,0833333333333333	184,820512820513	13,526943742845	0,0053982844835232	0,0053982844835232	0,0170472141584943	Acsl3	1
GO:0070508	cholesterol import	1/13	14/28832	0,0714285714285714	158,417582417582	12,512595735568	0,0062953788773279	0,0062953788773279	0,0176712389831096	Stard5	1
GO:0048863	stem cell differentiation	2/13	304/28832	0,0065789473684210	14,591093117408	5,0596164113022	0,0080046361096058	0,0080046361096058	0,0178329716767229	Sema4b/Krt10	2
GO:0035336	long-chain fatty-acyl-CoA metabolic process	1/13	18/28832	0,0555555555555556	123,213675213675	11,015807973792	0,0080873273977923	0,0080873273977923	0,0178329716767229	Acsl3	1
GO:0072659	protein localization to plasma membrane	2/13	314/28832	0,0063694267515923	14,126408623223	4,9672187598420	0,0085191587976876	0,0085191587976876	0,0178329716767229	Acsl3/Rab13	2
GO:0044539	long-chain fatty acid import into cell	1/13	20/28832	0,05	110,892307692308	10,441374286306	0,0089821826435588	0,0089821826435588	0,0178329716767229	Acsl3	1
GO:0006656	phosphatidylcholine biosynthetic process	1/13	21/28832	0,0476190476190476	105,611721611722	10,185278445296	0,0094293307632874	0,0094293307632874	0,0178329716767229	Acsl3	1
GO:0060009	Sertoli cell development	1/13	26/28832	0,0384615384615385	85,301775147929	9,1336421281372	0,0116622791749951	0,0116622791749951	0,0194810886872096	Rab13	1
GO:0065005	protein-lipid complex assembly	1/13	26/28832	0,0384615384615385	85,301775147929	9,1336421281372	0,0116622791749951	0,0116622791749951	0,0194810886872096	Acsl3	1
GO:0015812	gamma-aminobutyric acid transport	1/13	27/28832	0,0370370370370370	82,142450142450	8,9589710937050	0,0121083109173657	0,0121083109173657	0,0194810886872096	Slc6a11	1
GO:0015849	organic acid transport	2/13	381/28832	0,0052493438320210	11,642237028063	4,4412858198989	0,0123380228352327	0,0123380228352327	0,0194810886872096	Slc6a11/Acsl3	2
GO:0045070	positive regulation of viral genome replication	1/13	29/28832	0,0344827586206897	76,477453580901	8,6369310422987	0,0129998170301678	0,0129998170301678	0,0197049858141491	Hacd3	1
GO:0045684	positive regulation of	1/13	29/28832	0,0344827586206897	76,477453580901	8,6369310422987	0,0129998170301678	0,0129998170301678	0,0197049858141491	Krt10	1

	epidermis development										
GO:0010737	protein kinase A signaling	1/13	30/28832	0,033333333333333	73,928205128205	8,4880299850056	0,0134452915424964	0,0134452915424964	0,019980619010521	Rab13	1
GO:0035767	endothelial cell chemotaxis	1/13	32/28832	0,03125	69,307692307692	8,2112719242554	0,0143356838833568	0,0143356838833568	0,0204998855216861	Rab13	1
GO:0006935	chemotaxis	2/13	475/28832	0,00421052631578947	9,3382995951417	3,8918512624812	0,0187349740078053	0,0187349740078053	0,0223733983054732	Sema4b/Rab13	2
GO:0030866	cortical actin cytoskeleton organization	1/13	43/28832	0,023255813953488	51,577817531305	7,0492530180873	0,0192195962453213	0,0192195962453213	0,0223733983054732	Rab13	1
GO:0061436	establishment of skin barrier	1/13	43/28832	0,023255813953488	51,577817531305	7,0492530180873	0,0192195962453213	0,0192195962453213	0,0223733983054732	Krt1	1
GO:0010876	lipid localization	2/13	485/28832	0,004123711340206	9,1457573354480	3,8424733256961	0,0194835010243496	0,0194835010243496	0,0223733983054732	Acsl3/Stard5	2
GO:0001504	neurotransmitter uptake	1/13	45/28832	0,022222222222222	49,285470085470	6,8847249182998	0,0201051767004472	0,0201051767004472	0,0224082464772786	Slc6a11	1
GO:0071827	plasma lipoprotein particle organization	1/13	45/28832	0,022222222222222	49,285470085470	6,8847249182998	0,0201051767004472	0,0201051767004472	0,0224082464772786	Acsl3	1
GO:0071526	semaphorin-plexin signaling pathway	1/13	54/28832	0,018518518518518	41,071225071225	6,2598117292345	0,0240811621201857	0,0240811621201857	0,0257056141238454	Sema4b	1
GO:1901568	fatty acid derivative metabolic process	1/13	54/28832	0,018518518518518	41,071225071225	6,2598117292345	0,0240811621201857	0,0240811621201857	0,0257056141238454	Acsl3	1
GO:0001755	neural crest cell migration	1/13	62/28832	0,016129032258064	35,771712158808	5,8212207048536	0,0276028641037889	0,0276028641037889	0,0278140855859498	Sema4b	1
GO:0090497	mesenchymal cell migration	1/13	64/28832	0,015625	34,653846153846	5,7244258302956	0,0284814547435 71	0,0284814547435 71	0,0278140855859498	Sema4b	1
GO:1903078	positive regulation of protein localization to plasma membrane	1/13	65/28832	0,015384615384615	34,120710059171	5,6776825441561	0,0289204752207793	0,0289204752207793	0,0278140855859498	Acsl3	1
GO:0072348	sulfur compound transport	1/13	66/28832	0,015151515151515	33,603729603729	5,6319862793714	0,0293593125 62947	0,0293593125 62947	0,0278140855859498	Slc6a11	1
GO:0097006	regulation of plasma lipoprotein	1/13	73/28832	0,013698630136986	30,381454162276 1	5,3383851244671 6	0,0324260520564292	0,0324260520564292	0,0296090773375131	Acsl3	1

	particle levels										
GO:0071277	cellular response to calcium ion	1/13	86/28832	0,0116279069767442	25,788908765653	4,8896750649517	0,0380977087161148	0,0380977087161148	0,0339694740255142	Krt10	1
GO:0032456	endocytic recycling	1/13	91/28832	0,010989010989011	24,371935756551	4,7427094376632	0,0402709316401344	0,0402709316401344	0,0350817553307886	Rab13	1
GO:0070830	bicellular tight junction assembly	1/13	94/28832	0,0106382978723404	23,594108019639	4,6600752860516	0,0415726889730019	0,0415726889730019	0,0358042297375136	Rab13	1
GO:0035383	thioester metabolic process	1/13	100/28832	0,01	22,178461538461 5	4,505817063873	0,0441713154308053	0,0441713154308053	0,0359290593965699	Acsl3	1
GO:0030148	sphingolipid biosynthetic process	1/13	102/28832	0,00980392156862745	21,743589743589 7	4,4573656628173 9	0,0450360779241726	0,0450360779241726	0,0359290593965699	Hacd3	1
GO:0120193	tight junction organization	1/13	108/28832	0,00925925925925926	20,535612535612 5	4,3199480820704 4	0,0476260341736683	0,0476260341736683	0,0372118769452427	Rab13	1
GO:0003333	amino acid transmembrane transport	1/13	112/28832	0,00892857142857143	19,802197802197 8	4,2343571534208 1	0,0493490678394687	0,0493490678394687	0,0381646926363238	Slc6a11	1

Table S2:GO ONTOLOGY, CELLULAR COMPONENT, UP-REGULATED PROTEINS

ID	Description	Gene Ratio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:0045095	keratin filament	2/10	53/28779	0,0377358490566038	108,6	14,6177506388115	0,000148337104689102	0,000148337104689102	0,0021860204901 5518	Krt79/Krt10	2
GO:0031414	N-terminal protein acetyltransferase complex	1/10	11/28779	0,0909090909090909	261,627272727273	16,1186731190641	0,0038162596681 4969	0,0038162596681 4969	0,0112479232324412	Naa38	1
GO:0061700	GATOR2 complex	1/10	11/28779	0,0909090909090909	261,627272727273	16,1186731190641	0,0038162596681 4969	0,0038162596681 4969	0,0112479232324412	Wdr24	1
GO:0051233	spindle midzone	1/10	40/28779	0,025	71,9475	8,37142107629933	0,0138145594740383	0,0138145594740383	0,0290832831032386	Cenpv	1
GO:0001533	cornified envelope	1/10	67/28779	0,0149253731343284	42,9537313432836	6,40979577492117	0,0230420386581873	0,0230420386581873	0,0424458606861345	Krt10	1

Table S3: GO ONTOLOGY, MOLECULAR FUNCTION, UP-REGULATED PROTEINS

ID	Description	Gene Ratio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:0030280	structural	2/10	38/28366	0,0526315789473684	149,294736842105	17,1782330054958	7,8104619359143E-05	7,8104619359143E-05	0,0010688000 5438828	Krt79/Krt10	2

	constituent of skin epidermis										
GO:0016846	carbon-sulfur lyase activity	1/10	12/28366	0,0833333333333333	236,38333333333333	15,3153904916456	0,00422304109720162	0,00422304109720162	0,0288944917176953	Cenpv	1
GO:0005246	calcium channel regulator activity	1/10	46/28366	0,0217391304347826	61,6652173913044	7,732874460193	0,0161013033953933	0,0161013033953933	0,0734445418035483	Nrxn2	1

Table S4: GO ONTOLOGY, BIOLOGICAL PROCESS, DOWN-REGULATED PROTEINS

ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:1905475	regulation of protein localization to membrane	5/20	230/28832	0,0217391304347826	31,339130434782 6	12,171020496097 1	4,34900689434113E-07	4,34900689434113E-07	0,000115363130249891	Camk2b/Camk2a/Camk2g/Cd81/Iqsec2	5
GO:1990778	protein localization to cell periphery	5/20	408/28832	0,0122549019607843	17,666666666666 67	8,932939275684 47	7,20553730271096E-06	7,20553730271096E-06	0,000637121193081811	Camk2b/Camk2a/Camk2g/Cd81/Iqsec2	5
GO:0048168	regulation of neuronal synaptic plasticity	3/20	79/28832	0,0379746835443038	54,744303797468 4	12,602669660018 9	2,18242061170185E-05	2,18242061170185E-05	0,00144728945828649	Camk2b/Camk2a/Camk2g	3
GO:0002863	positive regulation of inflammatory response to antigenic stimulus	2/20	22/28832	0,0909090909090909	131,054545454545 5	16,077680524363	0,00010472392005861 2	0,00010472392005861 2	0,00307042891190253	Ighg1/Cd81	2
GO:0032011	ARF protein signal transduction	2/20	23/28832	0,0869565217391304	125,356521739 13	15,719058866325	0,00011464991073262 8	0,00011464991073262 8	0,00307042891190253	Iqsec2/Iqsec1	2
GO:0032012	regulation of ARF protein signal transduction	2/20	23/28832	0,0869565217391304	125,356521739 13	15,719058866325	0,00011464991073262 8	0,00011464991073262 8	0,00307042891190253	Iqsec2/Iqsec1	2
GO:0060996	dendritic spine development	3/20	139/28832	0,0215827338129496	31,113669064748 2	9,376510454673 22	0,00011771073761337 4	0,00011771073761337 4	0,00307042891190253	Camk2b/Camk2a/Iqsec1	3

GO:0098696	regulation of neurotransmitter receptor localization to postsynaptic specialization membrane	2/20	25/28832	0,08	115,328	15,067171863537	0,000135835425336251	0,000135835425336251	0,003070428911902 53	Camk2a/Iqsec2	2
GO:1902414	protein localization to cell junction	3/20	147/28832	0,020408163265306 1	29,420408163265 3	9,101640946908	0,000138900355538448	0,000138900355538448	0,003070428911902 53	Camk2a/Iqsec2/Jak1	3
GO:0099072	regulation of postsynaptic membrane neurotransmitter receptor levels	3/20	166/28832	0,018072289156626 5	26,053012048192 8	8,528812971147	0,000198816338713505	0,000198816338713505	0,003767046417729 57	Camk2a/Iqsec2/Iqsec1	3
GO:1902473	regulation of protein localization to synapse	2/20	34/28832	0,058823529411764 7	84,8	12,881322732104 9	0,000253062943370251	0,000253062943370251	0,004475218366968 66	Camk2a/Iqsec2	2
GO:0046777	protein autophosphorylation	3/20	200/28832	0,015	21,624	7,711168674035 05	0,000343585774259484	0,000343585774259484	0,005361214558104 64	Camk2b/Camk2a/Camk2g	3
GO:0001764	neuron migration	3/20	219/28832	0,013698630136986 3	19,747945205479 4	7,337568748759 03	0,000447918303764343	0,000447918303764343	0,006253485459757 04	Camk2b/Camk2a/Fbxo41	3
GO:0000082	G1/S transition of mitotic cell cycle	3/20	223/28832	0,013452914798206 3	19,393721973094 2	7,264886910336 09	0,000472194050621357	0,000472194050621357	0,006262784250346 42	Camk2b/Camk2a/Camk2g	3
GO:0044843	cell cycle G1/S phase transition	3/20	253/28832	0,011857707509881 4	17,094071146245 1	6,774243621131 15	0,000681561372956708	0,000681561372956708	0,007860570525633 43	Camk2b/Camk2a/Camk2g	3
GO:0002455	humoral immune response mediated by circulating immunoglobulin	2/20	59/28832	0,033898305084745 8	48,867796610169 5	9,696946909022 91	0,000763837174220464	0,000763837174220464	0,008442410872963 02	Ighg1/Cd81	2
GO:0031503	protein-containing complex localization	3/20	273/28832	0,010989010989011	15,841758241758 2	6,491623536458 8	0,000849515257940132	0,000849515257940132	0,008667119230806 2	Camk2a/Iqsec2/Iqsec1	3

GO:190489	positive regulation of receptor signaling pathway via STAT	2/20	74/28832	0,027027027027027	38,962162162162	8,6148081059611	0,00119830634094243	0,00119830634094243	0,0117728342268028	Camk2a/Jak1	2
GO:000243	inflammatory response to antigenic stimulus	2/20	81/28832	0,0246913580246914	35,595061728395	8,2146353510641	0,00143326056356211	0,00143326056356211	0,0126730407725492	Ighg1/Cd81	2
GO:005196	positive regulation of synapse assembly	2/20	84/28832	0,0238095238095238	34,323809523809	8,0583962006633	0,00154016146880993	0,00154016146880993	0,0127671279651349	Iqsec2/Iqsec1	2
GO:005196	positive regulation of nervous system development	3/20	384/28832	0,0078125	11,2625	5,3339760396673	0,00225817366368415	0,00225817366368415	0,0179645881009692	Camk2b/Iqsec2/Iqsec1	3
GO:005080	regulation of synapse organization	3/20	393/28832	0,00763358778625954	11,004580152671	5,2613371232964	0,00241152734364537	0,00241152734364537	0,0182768388149965	Camk2b/Iqsec2/Iqsec1	3
GO:005080	regulation of synapse structure or activity	3/20	401/28832	0,00748129675810474	10,785037406483	5,1987239440476	0,00255316494317005	0,00255316494317005	0,0187851253875851	Camk2b/Iqsec2/Iqsec1	3
GO:007134	cellular response to type II interferon	2/20	117/28832	0,0170940170940171	24,642735042735	6,7514084607914	0,00295734266671977	0,00295734266671977	0,0206440540723928	Camk2a/Jak1	2
GO:190189	positive regulation of cell junction assembly	2/20	134/28832	0,0149253731343284	21,516417910447	6,2717143269598	0,00385612062638 54	0,00385612062638 54	0,0249484569409273	Iqsec2/Iqsec1	2
GO:000681	calcium ion transport	3/20	470/28832	0,006382978723404 25	9,201702127659 57	4,7232685929987 6	0,00399189522142246	0,00399189522142246	0,0252119698195103	Camk2b/Camk2a/Camk2g	3
GO:005085	T cell receptor signaling pathway	2/20	148/28832	0,0135135135135135	19,481081081081 1	5,9387702051825 7	0,00468005875439657	0,00468005875439657	0,0282147082800941	Lcp2/Cd81	2
GO:003162	receptor internalization	2/20	166/28832	0,0120481927710843	17,368674698795 2	5,5723984334905 8	0,00584821 39405687	0,00584821 39405687	0,0289485028828158	Cd81/Iqsec1	2
GO:000282	positive regulation of adaptive immune response based on somatic recombin	2/20	168/28832	0,0119047619047619	17,161904761904 8	5,5352460968766 3	0,00598545206130032	0,00598545206130032	0,0289485028828158	Ighg1/Cd81	2

	ation of immune receptors built from immunoglobulin superfamily domains										
GO:0008037	cell recognition	2/20	169/2883	0,011834319526627	17,060355029585	5,5169089924493	0,006054626416633005	0,006054626416633005	0,028948502828828158	Ighg1/Cd81	2
GO:0002708	positive regulation of lymphocyte mediated immunity	2/20	171/2883	0,011695906432748503	16,860818713450	5,4807013148359	0,006194072008178140	0,006194072008178140	0,028948502828828158	Ighg1/Cd81	2
GO:0014908	myotube differentiation involved in skeletal muscle regeneration	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Cd81	1
GO:0016068	type I hypersensitivity	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Ighg1	1
GO:0035723	interleukin-15-mediated signaling pathway	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Jak1	1
GO:0043490	malate-aspartate shuttle	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Got2	1
GO:0071352	cellular response to interleukin-2	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Jak1	1
GO:1904350	regulation of protein catabolic process in the vacuole	1/20	10/28832	0,1	144,16	11,929377466123	0,006916199878295730	0,006916199878295730	0,028948502828828158	Cd81	1
GO:0070672	response to interleukin-15	1/20	11/28832	0,090909090909090909	131,054545454545	11,366467205559	0,007605314998774150	0,007605314998774150	0,028948502828828158	Jak1	1
GO:0070863	positive regulation of protein exit from endoplasmic reticulum	1/20	11/28832	0,090909090909090909	131,054545454545	11,366467205559	0,007605314998774150	0,007605314998774150	0,028948502828828158	Cd81	1
GO:0072674	multinuclear osteoclas	1/20	11/28832	0,090909090909090909	131,054545454545	11,366467205559	0,007605314998774150	0,007605314998774150	0,028948502828828158	Cd81	1

	t differentiation										
GO:0009068	aspartate family amino acid catabolic process	1/20	12/28832	0,08333333333333333	120,13333333333333	10,875145497956	0,0082939758259496	0,0082939758259496	0,0289485028828158	Got2	1
GO:0070669	response to interleukin-2	1/20	12/28832	0,08333333333333333	120,13333333333333	10,875145497956	0,0082939758259496	0,0082939758259496	0,0289485028828158	Jak1	1
GO:2000434	regulation of protein neddylation	1/20	12/28832	0,08333333333333333	120,13333333333333	10,875145497956	0,0082939758259496	0,0082939758259496	0,0289485028828158	Dcun1d5	1
GO:2000551	regulation of T-helper 2 cell cytokine production	1/20	12/28832	0,08333333333333333	120,13333333333333	10,875145497956	0,0082939758259496	0,0082939758259496	0,0289485028828158	Cd81	1
GO:2000563	positive regulation of CD4-positive, alpha-beta T cell proliferation	1/20	12/28832	0,08333333333333333	120,13333333333333	10,875145497956	0,0082939758259496	0,0082939758259496	0,0289485028828158	Cd81	1
GO:0002291	T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	1/20	13/28832	0,07692307692307692	110,89230769230768	10,441374286308	0,0089821826435582	0,0089821826435582	0,0298629670116044	Cd81	1
GO:0006107	oxaloacetate metabolic process	1/20	13/28832	0,07692307692307692	110,89230769230768	10,441374286308	0,0089821826435582	0,0089821826435582	0,0298629670116044	Got2	1
GO:0051549	positive regulation of keratinocyte migration	1/20	13/28832	0,07692307692307692	110,89230769230768	10,441374286308	0,0089821826435582	0,0089821826435582	0,0298629670116044	Iqsec1	1
GO:0007343	egg activation	1/20	14/28832	0,07142857142857142	102,97142857142859	10,054691517036	0,0096699357351692	0,0096699357351692	0,0298629670116044	Camk2b	1
GO:0043650	dicarboxylic acid biosynthe	1/20	14/28832	0,07142857142857142	102,97142857142859	10,054691517036	0,0096699357351692	0,0096699357351692	0,0298629670116044	Got2	1

	tic process										
GO:0016081	synaptic vesicle docking	1/20	15/28832	0,0666666666666667	96,106666666666667	9,70711902328293	0,0103572353841834	0,0103572353841834	0,0298629670116044	Camk2a	1
GO:0043649	dicarboxylic acid catabolic process	1/20	15/28832	0,0666666666666667	96,106666666666667	9,70711902328293	0,0103572353841834	0,0103572353841834	0,0298629670116044	Got2	1
GO:0055119	relaxation of cardiac muscle	1/20	15/28832	0,0666666666666667	96,106666666666667	9,70711902328293	0,0103572353841834	0,0103572353841834	0,0298629670116044	Camk2g	1
GO:0090713	immunological memory process	1/20	16/28832	0,0625	90,1	9,3924522416639 2	0,0110440818738359	0,0110440818738359	0,0302968820942306	Cd81	1
GO:0034112	positive regulation of homotypic cell-cell adhesion	1/20	17/28832	0,0588235294117647	84,8	9,1057833936142 8	0,0117304754871936	0,0117304754871936	0,0302968820942306	Jak1	1
GO:1901077	regulation of relaxation of muscle	1/20	17/28832	0,0588235294117647	84,8	9,1057833936142 8	0,0117304754871936	0,0117304754871936	0,0302968820942306	Camk2g	1
GO:0001771	immunological synapse formation	1/20	18/28832	0,0555555555555556	80,088888888888889	8,8431725407007 9	0,0124164106507158	0,0124164106507158	0,0302968820942306	Cd81	1
GO:0002830	positive regulation of type 2 immune response	1/20	18/28832	0,0555555555555556	80,088888888888889	8,8431725407007 9	0,0124164106507158	0,0124164106507158	0,0302968820942306	Cd81	1
GO:0006116	NADH oxidation	1/20	18/28832	0,0555555555555556	80,088888888888889	8,8431725407007 9	0,0124164106507158	0,0124164106507158	0,0302968820942306	Got2	1
GO:0035745	T-helper 2 cell cytokine production	1/20	18/28832	0,0555555555555556	80,088888888888889	8,8431725407007 9	0,0124164106507158	0,0124164106507158	0,0302968820942306	Cd81	1
GO:0090110	COPII-coated vesicle cargo loading	1/20	18/28832	0,0555555555555556	80,088888888888889	8,8431725407007 9	0,0124164106507158	0,0124164106507158	0,0302968820942306	Sec24d	1
GO:0060396	growth hormone receptor signaling pathway	1/20	20/28832	0,05	72,08	8,3778747194013 8	0,0137869418976698	0,0137869418976698	0,0318995460728935	Jak1	1
GO:0045836	positive regulation of meiotic nuclear division	1/20	21/28832	0,0476190476190476	68,647619047619	8,1703590944258 8	0,0144715268331845	0,0144715268331845	0,0322585118262937	Camk2b	1

GO:0051546	keratinocyte migration	1/20	21/28832	0,0476190476190476	68,647619047619	8,1703590944258	0,0144715268331845	0,0144715268331845	0,0322585118262937	Iqsec1	1
GO:0098761	cellular response to interleukin-7	1/20	21/28832	0,0476190476190476	68,647619047619	8,1703590944258	0,0144715268331845	0,0144715268331845	0,0322585118262937	Jak1	1
GO:0009067	aspartate family amino acid biosynthetic process	1/20	22/28832	0,0454545454545455	65,527272727272727	7,9770289642058 3	0,0151556603052379	0,0151556603052379	0,0325704964028247	Got2	1
GO:0098760	response to interleukin-7	1/20	22/28832	0,0454545454545455	65,527272727272727	7,9770289642058 3	0,0151556603052379	0,0151556603052379	0,0325704964028247	Jak1	1
GO:0007039	protein catabolic process in the vacuole	1/20	23/28832	0,0434782608695652	62,678260869565 2	7,7963278469228	0,0158393425958975	0,0158393425958975	0,0325704964028247	Cd81	1
GO:0045116	protein neddylation	1/20	23/28832	0,0434782608695652	62,678260869565 2	7,7963278469228	0,0158393425958975	0,0158393425958975	0,0325704964028247	Dcun1d5	1
GO:0006898	receptor-mediated endocytosis	2/20	287/28832	0,00696864111491258	10,045993031358 9	4,0577970434326	0,0166699627376844	0,0166699627376844	0,0340148227521982	Cd81/Iqsec1	2
GO:0002440	production of molecular mediator of immune response	2/20	297/28832	0,00673400673400673	9,707744107744 11	3,9742308670106 5	0,0177803847180139	0,0177803847180139	0,0340438669447028	Ighg1/Cd81	2
GO:0098877	neurotransmitter receptor transport to plasma membrane	1/20	26/28832	0,0384615384615385	55,446153846153 8	7,3176317368974 4	0,0178876851976802	0,0178876851976802	0,0340438669447028	Camk2a	1
GO:0010666	positive regulation of cardiac muscle cell apoptotic process	1/20	27/28832	0,0370370 37037037	53,392592592926	7,1758934199206 2	0,0185695655801024	0,0185695655801024	0,0340438669447028	Camk2a	1
GO:0035739	CD4-positive, alpha-beta T cell proliferation	1/20	27/28832	0,0370370 37037037	53,392592592926	7,1758934199206 2	0,0185695655801024	0,0185695655801024	0,0340438669447028	Cd81	1
GO:1903672	positive regulation of sprouting	1/20	27/28832	0,0370370 37037037	53,392592592926	7,1758934199206 2	0,0185695655801024	0,0185695655801024	0,0340438669447028	Jak1	1

	angiogenesis										
GO:0035459	vesicle cargo loading	1/20	28/28832	0,0357142857142857	51,485714285714 3	7,0417283553988 1	0,0192509961889689	0,0192509961889689	0,0340438669447028	Sec24d	1
GO:0006959	humoral immune response	2/20	322/28832	0,0062111801242236	8,9540372670807 4	3,7815957088524 5	0,0206905443877849	0,0206905443877849	0,0347369566004116	Ighg1/Cd81	2
GO:0042113	B cell activation	2/20	326/28832	0,0061349693251533 7	8,8441717791411	3,7527177650548 5	0,0211736223065562	0,0211736223065562	0,0348692241692256	Ighg1/Cd81	2
GO:0021542	dentate gyrus development	1/20	31/28832	0,0322580645161 29	46,503225806451 6	6,6784764186455 6	0,0212925921841003	0,0212925921841003	0,0348692241692256	Fbxo41	1
GO:0051446	positive regulation of meiotic cell cycle	1/20	32/28832	0,03125	45,05	6,5687510963912 4	0,0219722265077803	0,0219722265077803	0,0353237708450439	Camk2b	1
GO:0061003	positive regulation of dendritic spine morphogenesis	1/20	32/28832	0,03125	45,05	6,5687510963912 4	0,0219722265077803	0,0219722265077803	0,0353237708450439	Camk2b	1
GO:0031295	T cell costimulation	1/20	33/28832	0,0303030303030303	43,684848484848 5	6,4639822921744 7	0,0226514124615947	0,0226514124615947	0,0355537585818865	Cd81	1
GO:0060416	response to growth hormone	1/20	33/28832	0,0303030303030303	43,684848484848 5	6,4639822921744 7	0,0226514124615947	0,0226514124615947	0,0355537585818865	Jak1	1
GO:0150146	cell junction disassembly	1/20	33/28832	0,0303030303030303	43,684848484848 5	6,4639822921744 7	0,0226514124615947	0,0226514124615947	0,0355537585818865	Iqsec1	1
GO:0006910	phagocytosis, recognition	1/20	34/28832	0,0294117647058824	42,4	6,3638038318513 4	0,0233301503257834	0,0233301503257834	0,0359805350928714	Ighg1	1
GO:0006536	glutamate metabolic process	1/20	35/28832	0,0285714285714286	41,188571428571 4	6,2678863838323 3	0,0240084403804219	0,0240084403804219	0,0359805350928714	Got2	1
GO:0007271	synaptic transmission, cholinergic	1/20	35/28832	0,0285714285714286	41,188571428571 4	6,2678863838323 3	0,0240084403804219	0,0240084403804219	0,0359805350928714	Camk2b	1
GO:0150117	positive regulation of cell-substrate junction organization	1/20	35/28832	0,0285714285714286	41,188571428571 4	6,2678863838323 3	0,0240084403804219	0,0240084403804219	0,0359805350928714	Iqsec1	1
GO:0030100	regulation of endocytosis	2/20	352/28832	0,0056818181818181 8	8,1909090909090 9	3,5763769357476	0,0244279350828791	0,0244279350828791	0,0362001743068835	Ighg1/Iqsec1	2

GO:0099637	neurotransmitter receptor transport	1/20	37/28832	0,027027027027027	38,962162162162	6,0876742928368 7	0,0253636781805244	0,0253636781805244	0,0365654857064769	Camk2a	1
GO:0071404	cellular response to low-density lipoprotein particle stimulus	1/20	38/28832	0,0263157894736842	37,936842105263 2	6,0028668301223 4	0,0260406264853132	0,0260406264853132	0,0369118217160022	Cd81	1
GO:0006904	vesicle docking involved in exocytosis	1/20	39/28832	0,0256410256410256	36,964102564102 6	5,9212884829361 6	0,0267171280992016	0,0267171280992016	0,0369118217160022	Camk2a	1
GO:0099149	regulation of postsynaptic neurotransmitter receptor internalization	1/20	39/28832	0,0256410256410256	36,964102564102 6	5,9212884829361 6	0,0267171280992016	0,0267171280992016	0,0369118217160022	Iqsec1	1
GO:0070670	response to interleukin-4	1/20	40/28832	0,025	36,04	5,8427368167959 4	0,0273931833014388	0,0273931833014388	0,0374556819965414	Jak1	1
GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	1/20	41/28832	0,024390243902439	35,160975609756 1	5,7670267614 01	0,0280687923711097	0,0280687923711097	0,0377950076276765	Camk2a	1
GO:0070741	response to interleukin-6	1/20	42/28832	0,0238095238095238	34,323809523809 5	5,6939887402750 3	0,0287439555871353	0,0287439555871353	0,0383151378363295	Jak1	1
GO:0019674	NAD metabolic process	1/20	44/28832	0,0227272727272727	32,763636363636 4	5,5553183899968 6	0,0300929455731036	0,0300929455731036	0,039236977585102	Got2	1
GO:0006734	NADH metabolic process	1/20	45/28832	0,0222222222222222	32,035555555555 6	5,4894107030469 5	0,0307667729000641	0,0307667729000641	0,039236977585102	Got2	1
GO:0032527	protein exit from endoplasmic reticulum	1/20	45/28832	0,0222222222222222	32,035555555555 6	5,4894107030469 5	0,0307667729000641	0,0307667729000641	0,039236977585102	Cd81	1
GO:0035987	endodermal cell differentiation	1/20	45/28832	0,0222222222222222	32,035555555555 6	5,4894107030469 5	0,0307667729000641	0,0307667729000641	0,039236977585102	Col4a2	1

GO:0046677	response to antibiotic	1/20	45/28832	0,0222222222222222	32,035555555555556	5,4894107030469 5	0,0307667729000641	0,0307667729000641	0,039236977585102	Jak1	1
GO:0071402	cellular response to lipoprotein particle stimulus	1/20	46/28832	0,0217391304347826	31,339130434782 6	5,4256219851225 5	0,0314401554874121	0,0314401554874121	0,0397138806156784	Cd81	1
GO:0070269	pyroptotic inflammatory response	1/20	48/28832	0,0208333333333333	30,033333333333 3	5,3039582125944 1	0,0327855875554984	0,0327855875554984	0,0403412663787966	Gsdmc3	1
GO:0042742	defense response to bacterium	2/20	415/28832	0,0048192771084337 4	6,9474698795180 7	3,2153283799594 1	0,0330990515434992	0,0330990515434992	0,0403412663787966	Ighg1/Gsdmc3	2
GO:0170034	L-amino acid biosynthetic process	1/20	49/28832	0,0204081632653061	29,420408163265 3	5,2458814250044 9	0,0334576375919384	0,0334576375919384	0,0403412663787966	Got2	1
GO:1905521	regulation of macrophage migration	1/20	49/28832	0,0204081632653061	29,420408163265 3	5,2458814250044 9	0,0334576375919384	0,0334576375919384	0,0403412663787966	Cd81	1
GO:0030890	positive regulation of B cell proliferation	1/20	50/28832	0,02	28,832	5,1895187009610 7	0,0341292440001716	0,0341292440001716	0,0409556975008257	Cd81	1
GO:0021700	developmental maturation	2/20	423/28832	0,0047281323877068 6	6,8160756501182	3,1749025884386 1	0,0342760182655 72	0,0342760182655 72	0,0409556975008257	Camk2b/Fbxo41	2
GO:0140239	postsynaptic endocytosis	1/20	51/28832	0,0196078431372549	28,266666666666 7	5,1347859605142 5	0,0348004070576373	0,0348004070576373	0,0412110083577284	Iqsec1	1
GO:0007520	myoblast fusion	1/20	52/28832	0,0192307692307692	27,723076923076 9	5,0816048001737 8	0,0354711270 41615	0,0354711270 41615	0,0414501461371991	Cd81	1
GO:0042092	type 2 immune response	1/20	52/28832	0,0192307692307692	27,723076923076 9	5,0816048001737 8	0,0354711270 41615	0,0354711270 41615	0,0414501461371991	Cd81	1
GO:0170038	proteinogenic amino acid biosynthetic process	1/20	53/28832	0,0188679245283019	27,2	5,0299020091186 2	0,0361414042292166	0,0361414042292166	0,0418645546576079	Got2	1
GO:0061462	protein localization to lysosome	1/20	54/28832	0,0185185185185185	26,696296296296 3	4,9796091348831	0,0368112388973915	0,0368112388973915	0,0421121123739893	Cd81	1
GO:0002891	positive regulation of immunogl	1/20	55/28832	0,0181818181818182	26,210909090909 1	4,9306620926476	0,0374806313229267	0,0374806313229267	0,0423073643600337	Ighg1	1

	obulin mediated immune response										
GO:0046686	response to cadmium ion	1/20	56/28832	0,0178571428571429	25,742857142857 1	4,8830008130518	0,0381495817824445	0,0381495817824445	0,0425196577141797	Camk2b	1
GO:0043403	skeletal muscle tissue regeneration	1/20	57/28832	0,0175438596491228	25,291228070175 4	4,8365689241196 7	0,0388180905524037	0,0388180905524037	0,0427261795990641	Cd81	1
GO:0002449	lymphocyte mediated immunity	2/20	477/28832	0,0041928721174004 2	6,044444444444 5	2,9269537158750 5	0,0426405169403511	0,0426405169403511	0,0456087023300869	Ighg1/Cd81	2
GO:0006911	phagocytosis, engulfment	1/20	63/28832	0,0158730158730159	22,882539682539 7	4,5810366272027 5	0,0428198831525786	0,0428198831525786	0,045616616167617	Ighg1	1
GO:0002931	response to ischemia	1/20	65/28832	0,0153846153846154	22,178461538461 5	4,5036221667375 8	0,0441502930092187	0,0441502930092187	0,0460485132514959	Camk2a	1
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2/20	487/28832	0,0041067761806981 5	5,920328542094 46	2,8852171193018 3	0,0442668743459 32	0,0442668743459 32	0,0460485132514959	Ighg1/Cd81	2
GO:0010770	positive regulation of cell morphogenesis	1/20	67/28832	0,0149253731343284	21,516417910447 8	4,4296039407952 2	0,0454789460306366	0,0454789460306366	0,0465787213969536	Camk2b	1
GO:0051785	positive regulation of nuclear division	1/20	69/28832	0,0144927536231884	20,892753623188 4	4,3587354070692 4	0,0468058444148218	0,0468058444148218	0,0466358532110588	Camk2b	1
GO:1905517	macrophage migration	1/20	69/28832	0,0144927536231884	20,892753623188 4	4,3587354070692 4	0,0468058444148218	0,0468058444148218	0,0466358532110588	Cd81	1
GO:0007260	tyrosine phosphorylation of STAT protein	1/20	70/28832	0,0142857142857143	20,594285714285 7	4,3244119947679 5	0,0474686363041135	0,0474686363041135	0,0466358532110588	Jak1	1
GO:0035458	cellular response to interferon-beta	1/20	70/28832	0,0142857142857143	20,594285714285 7	4,3244119947679 5	0,0474686363041135	0,0474686363041135	0,0466358532110588	Camk2a	1

GO:0140253	cell-cell fusion	1/20	70/28832	0,0142857142857143	20,594285714285 7	4,3244119947679 5	0,0474686363041135	0,0474686363041135	0,0466358532110588	Cd81	1
GO:0042551	neuron maturation	1/20	72/28832	0,0138888888888889	20,022222222222 2	4,2578583187865	0,0487929068848	0,0487929068848	0,0470653111031426	Fbxo41	1
GO:0099024	plasma membrane invagination	1/20	72/28832	0,0138888888888889	20,022222222222 2	4,2578583187865	0,0487929068848	0,0487929068848	0,0470653111031426	Ighg1	1
GO:0170040	proteinogenic amino acid catabolic process	1/20	73/28832	0,0136986301369863	19,747945205479 4	4,2255803377322 6	0,0494543860504706	0,0494543860504706	0,0475305312155553	Got2	1

Table S5: GO ONTOLOGY, MOLECULAR FUNCTION, DOWN-REGULATED PROTEINS

ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:0004683	calcium/calmodulin-dependent protein kinase activity	3/19	24/28366	0,125	186,618421052632	23,5519076989851	5,11066873623269E-07	5,11066873623269E-07	1,7752849294282E-05	Camk2b/Camk2a/Camk2g	3
GO:0005516	calmodulin binding	3/19	198/28366	0,0151515151515152	22,6204146730463	7,9037510225188 3	0,0002989000332243473	0,0002989000332243473	0,0051914268231 7612	Camk2b/Camk2a/Camk2g	3
GO:1990459	transferrin receptor binding	1/19	12/28366	0,0833333333333333	124,412280701754	11,0702257257515	0,0080097940621 7994	0,0080097940621 7994	0,0410280556415897	Cd81	1
GO:0005085	guanyl-nucleotide exchange factor activity	2/19	206/28366	0,0097087378640 7767	14,4946346448646	5,0326074762 1466	0,0082740061657 1791	0,0082740061657 1791	0,0410280556415897	Iqsec2/Iqsec1	2
GO:0032794	GTPase activating protein binding	1/19	20/28366	0,05	74,6473684210526	8,52984191108014	0,0133158487989004	0,0133158487989004	0,0410280556415897	Camk2a	1
GO:0034987	immunoglobulin receptor binding	1/19	21/28366	0,0476190476190476	71,0927318295739	8,3187686 4098233	0,0139772119144305	0,0139772119144305	0,0410280556415897	Ighg1	1
GO:0008483	transaminase activity	1/19	26/28366	0,0384615384615385	57,421052631579	7,4514806498521	0,0172777327204832	0,0172777327204832	0,0410280556415897	Got2	1
GO:0099186	structural constituent of postsynapse	1/19	28/28366	0,0357142857142857	53,3195488721804	7,1708898 3995431	0,0185950081789416	0,0185950081789416	0,0410280556415897	Camk2b	1
GO:0051427	hormone receptor binding	1/19	29/28366	0,0344827586206897	51,480943738657	7,0414835 9567526	0,0192530184423546	0,0192530184423546	0,0410280556415897	Jak1	1

GO:0097602	cullin family protein binding	1/19	29/28366	0,0344827586206897	51,480943738657	7,04148359567526	0,0192530184423546	0,0192530184423546	0,0410280556415897	Dcun1d5	1
GO:0043274	phospholipase binding	1/19	30/28366	0,0333333333333333	49,7649122807018	6,91852389679125	0,0199106107298090	0,0199106107298090	0,0410280556415897	Camk2b	1
GO:0031624	ubiquitin conjugating enzyme binding	1/19	37/28366	0,0270270270027027	40,3499288762447	6,20074446282152	0,0245020744613202	0,0245020744613202	0,0410280556415897	Dcun1d5	1
GO:0030159	signaling receptor complex adaptor activity	1/19	39/28366	0,0256410256410256	38,280701754386	6,03157501483873	0,0258101737277906	0,0258101737277906	0,0410280556415897	Gnb4	1
GO:0070273	phosphatidylinositol-4-phosphate binding	1/19	39/28366	0,0256410256410256	38,280701754386	6,03157501483873	0,0258101737277906	0,0258101737277906	0,0410280556415897	Gsdmc3	1
GO:0022829	wide pore channel activity	1/19	41/28366	0,0243902439024390	36,413350449294	5,87473970502947	0,0271166110953124	0,0271166110953124	0,0410280556415897	Gsdmc3	1
GO:0004715	non-membrane spanning protein tyrosine kinase activity	1/19	44/28366	0,0227272727272727	33,9306220095694	5,65951161481943	0,0290731554478316	0,0290731554478316	0,0410280556415897	Jak1	1
GO:0001618	virus receptor activity	1/19	45/28366	0,0222222222222222	33,1766081871345	5,59251129138675	0,0297245081081835	0,0297245081081835	0,0410280556415897	Cd81	1
GO:0030020	extracellular matrix structural constituent conferring tensile strength	1/19	46/28366	0,0217391304347826	32,4553775743707	5,52766654561637	0,0303754467878187	0,0303754467878187	0,0410280556415897	Col4a2	1
GO:0015485	cholesterol binding	1/19	50/28366	0,02	29,8589473684211	5,28766800025269	0,0329750666671909	0,0329750666671909	0,0410280556415897	Cd81	1
GO:0030170	pyridoxal phosphate binding	1/19	54/28366	0,0185185185185185	27,6471734892788	5,07431469100722	0,0355680827102656	0,0355680827102656	0,0419335103055045	Got2	1
GO:0042287	MHC protein binding	1/19	61/28366	0,0163934426229508	24,4745470232959	4,75165828791226	0,0400900107946258	0,0400900107946258	0,0449104789873656	Cd81	1
GO:0048020	CCR chemokine receptor binding	1/19	65/28366	0,0153846153846154	22,9684210526316	4,59059811478281	0,0426649550379973	0,0426649550379973	0,0449104789873656	Jak1	1
GO:0016597	amino acid binding	1/19	70/28366	0,0142857142857143	21,3278195488722	4,40851107319475	0,0458744249037821	0,0458744249037821	0,0461653569134246	Got2	1
GO:0001786	phosphatidylserine binding	1/19	71/28366	0,0140845070422535	21,0274277242402	4,37435616522251	0,0465150944465799	0,0465150944465799	0,0461653569134246	Gsdmc3	1

GO:0005200	structural constituent of cytoskeleton	1/19	74/28366	0,0135135135135135	20,1749644381223	4,27595617017772	0,048434658741133	0,048434658741133	0,0467351970309178	Camk2b	1

Table S6: GO ONTOLOGY, CELLULAR COMPONENT, DOWN-REGULATED PROTEINS

ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
GO:0014069	postsynaptic density	5/20	464/28779	0,0107758620689655	15,505926724137	8,3071986939700	1,35350079214177E-05	1,35350079214177E-05	0,000381382978127189	Camk2b/Camk2a/Camk2g/Iqsec2/Iqsec1	5
GO:0032279	asymmetric synapse	5/20	488/28779	0,0102459016393443	14,743340163934	8,0748872902265	1,72530394867062E-05	1,72530394867062E-05	0,000381382978127189	Camk2b/Camk2a/Camk2g/Iqsec2/Iqsec1	5
GO:0098685	Schaffer collateral - CA1 synapse	3/20	151/28779	0,0198675496688742	28,588410596026 5	8,9635090615926 2	0,00015118069933712	0,00015118069933712	0,0022279260954944	Camk2a/Iqsec2/Iqsec1	3
GO:0033017	sarcoplasmic reticulum membrane	2/20	40/28779	0,05	71,9475	11,841035351762 7	0,00035225889519305 7	0,00035225889519305 7	0,0038933877889759	Camk2b/Camk2g	2
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	2/20	51/28779	0,0392156862745098	56,429411764705 9	10,447949704623	0,00057317505426529 7	0,00057317505426529 7	0,0045607781091305 1	Jak1/Gnb4	2
GO:0016529	sarcoplasmic reticulum	2/20	82/28779	0,024390243902439	35,096341463414 6	8,1537026702420 4	0,0014738054795595	0,0014738054795595	0,0081447144923025 1	Camk2b/Camk2g	2
GO:0016528	sarcoplasm	2/20	110/28779	0,0181818181818182	26,162727272727 3	6,9727836838882 9	0,0026296696001801 2	0,0026296696001801 2	0,0129176752289 55	Camk2b/Camk2g	2
GO:0019897	extrinsic component of plasma membrane	2/20	129/28779	0,0155038759689922	22,309302325581 4	6,3967618825022	0,0035929467534528 9	0,0035929467534528 9	0,0151038536728307	Jak1/Gnb4	2
GO:0019814	immunoglobulin complex	2/20	132/28779	0,0151515151515152	21,802272727272 7	6,3170830856512 3	0,0037579826400257 3	0,0037579826400257 3	0,0151038536728307	Igkv10-96/Ighg1	2

GO:0097197	tetraspanin-enriched microdomain	1/20	10/28779	0,1	143,895	11,918265647043	0,00692889906534633	0,00692889906534633	0,0235638672667648	Cd81	1
GO:0019898	extrinsic component of membrane	2/20	192/28779	0,010416666666666667	14,9890625	5,1287714412594	0,00777360345409077	0,00777360345409077	0,0245482214339709	Jak1/Gnb4	2
GO:0043209	myelin sheath	2/20	211/28779	0,009478672985781	13,639336492891	4,8594150756834	0,00931893797058614	0,00931893797058614	0,0247301384923388	Got2/Gnb4	2
GO:0030127	COPII vesicle coat	1/20	15/28779	0,0666666666666667	95,93	9,6980156790718	0,0103762213978039	0,0103762213978039	0,0247301384923388	Sec24d	1
GO:0043204	perikaryon	2/20	226/28779	0,008849557522123809	12,7340707964602	4,6701998185444	0,0106280714234932	0,0106280714234932	0,0247301384923388	Camk2b/Got2	2
GO:0098684	photoreceptor ribbon synapse	1/20	18/28779	0,05555555555555556	79,941666666666667	8,8348456051130	0,0124391546442172	0,0124391546442172	0,0274970786872169	Iqsec2	1
GO:0098644	complex of collagen trimers	1/20	19/28779	0,052631578947368405	75,734210526315788	8,5933049190498	0,0131258907419574	0,0131258907419574	0,0276334541935944	Col4a2	1
GO:0098831	presynaptic active zone cytoplasmic component	1/20	22/28779	0,045454545454545455	65,406818181818182	7,9694767502326	0,0151833780597445	0,0151833780597445	0,0305019975757587	Iqsec2	1
GO:0042571	immunoglobulin complex, circulating	1/20	23/28779	0,043478260869565217	62,563034782609	7,7889366914384	0,0158683011198276	0,0158683011198276	0,0305019975757587	Ighg1	1
GO:0000314	organellar small ribosomal subunit	1/20	33/28779	0,030303030303030303	43,604545454545455	6,4577705049463	0,0226926881379409	0,0226926881379409	0,0355522400753443	Mrps25	1
GO:0005763	mitochondrial small ribosomal subunit	1/20	33/28779	0,030303030303030303	43,604545454545455	6,4577705049463	0,0226926881379409	0,0226926881379409	0,0355522400753443	Mrps25	1
GO:0032839	dendrite cytoplasm	1/20	37/28779	0,027027027027027027	38,890540540545	6,0817922655810	0,0254098348402971	0,0254098348402971	0,0362381345769942	Camk2a	1

GO:0051233	spindle midzone	1/20	40/28779	0,025	35,97375	5,8370683975293	0,0274429835863802	0,0274429835863802	0,036725581954088	Camk2b	1
GO:1905360	GTPase complex	1/20	41/28779	0,024390243902439	35,096341463414	5,7614241857103	0,028119803946458	0,028119803946458	0,036725581954088	Gnb4	1
GO:0005759	mitochondrial matrix	2/20	380/28779	0,00526315789473684	7,5734210526315	3,4016540017904	0,0282437213599296	0,0282437213599296	0,036725581954088	Got2/Mrps25	2
GO:0099524	postsynaptic cytosol	1/20	47/28779	0,021276595744680	30,615957446808	5,3585858018809	0,0321713388993858	0,0321713388993858	0,0395086618062633	Camk2a	1
GO:0030133	transport vesicle	2/20	438/28779	0,004566210045662	6,5705479452054	3,0980312791770	0,0366495231606797	0,0366495231606797	0,0405073677039092	Sec24d/Iqsec1	2
GO:0030134	COPII-coated ER to Golgi transport vesicle	1/20	60/28779	0,016666666666667	23,9825	4,6994458388665	0,0408946889296372	0,0408946889296372	0,0440969688807311	Sec24d	1

Table S7: KEGG PATHWAYS – DOWN REGULATED PROTEINS

category	subcategory	ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
Organismal Systems	Environmental adaptation	mmu04713	Circadian entrainment	4/13	100/11159	0,04	34,335384615384 6	11,435439921356 7	4,080294146731 77E-06	0,000350919963 398623	0,000206423507 881543	Camk2b/Camk2a/Camk2g/Gnb4	4
Organismal Systems	Nervous system	mmu04725	Cholinergic synapse	4/13	114/11159	0,035087	30,118758434 5479	10,672047 6208	6,880783596 05143E-06	0,000350919963 398623	0,000206423507 881543	Camk2b/Camk2a/Camk2g/Gnb4	4
Organismal Systems	Nervous system	mmu04728	Dopaminergic synapse	4/13	137/11159	0,029197	25,062324536 7771	9,6777187 2495462	1,426675260 25986E-05	0,000485069 588488 352	0,000285335 052051 972	Camk2b/Camk2a/Camk2g/Gnb4	4
Cellular Processes	Cell growth and death	mmu04217	Necroptosis	4/13	177/11159	0,022598	19,398522381 5732	8,4262471 6955375	3,912034477 41064E-05	0,000852374 080852 771	0,000501396 518148 689	Camk2b/Camk2a/Camk2g/Jak1	4
Human Diseases	Infectious disease: bacterial	mmu05152	Tuberculosis	4/13	180/11159	0,022222	19,075213675 2137	8,3491763 7071561	4,178304317 90574E-05	0,000852374 080852 771	0,000501396 518148 689	Camk2b/Camk2a/Camk2g/Jak1	4
Organismal Systems	Nervous system	mmu04720	Long-term potentiation	3/13	67/11159	0,044776	38,435132032 147	10,495839366 6853	5,668016149 24575E-05	0,000900599659 323451	0,000529764505 484383	Camk2b/Camk2a/Camk2g	3
Human Diseases	Substance dependence	mmu05031	Amphetamine addiction	3/13	69/11159	0,043478	37,321070234 1137	10,335291843 4236	6,190798348 06145E-05	0,000900599659 323451	0,000529764505 484383	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Digestive system	mmu04971	Gastric acid secretion	3/13	75/11159	0,04	34,335384615384 6	9,8922066151 1955	7,946467582 26575E-05	0,000900599659 323451	0,000529764505 484383	Camk2b/Camk2a/Camk2g	3
Human Diseases	Cancer: specific types	mmu05214	Glioma	3/13	75/11159	0,04	34,335384615384 6	9,8922066151 1955	7,946467582 26575E-05	0,000900599659 323451	0,000529764505 484383	Camk2b/Camk2a/Camk2g	3
Environmental Information Processing	Signal transduction	mmu04012	ErbB signaling pathway	3/13	84/11159	0,035714	30,656593406 5934	9,3173921391 4455	0,000111453 990586 956	0,001108519026 4889	0,000652070015 581707	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Endocrine system	mmu04911	Insulin secretion	3/13	86/11159	0,034883	29,943649373 8819	9,2018510580 4292	0,000119546 169523 313	0,001108519026 4889	0,000652070015 581707	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Endocrine system	mmu04912	GnRH signaling pathway	3/13	90/11159	0,033333	28,612820512 8205	8,9822092101 0913	0,000136862 137883 398	0,001163328172 00888	0,000684310689 416991	Camk2b/Camk2a/Camk2g	3

Organismal Systems	Endocrine system	mmu04916	Melanogenesis	3/13	100/11159	0,03	25,751538461538 5	8,490819419177 89	0,000187112024792687	0,001429054478036 07	0,000840620281197691	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Endocrine system	mmu04922	Glucagon signaling pathway	3/13	104/11159	0,028846153846153 8	24,761094674556 2	8,313981930021 54	0,000210155070299423	0,001429054478036 07	0,000840620281197691	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Endocrine system	mmu04925	Aldosterone synthesis and secretion	3/13	104/11159	0,028846153846153 8	24,761094674556 2	8,313981930021 54	0,000210155070299423	0,001429054478036 07	0,000840620281197691	Camk2b/Camk2a/Camk2g	3
Environmental Information Processing	Signal transduction	mmu04066	HIF-1 signaling pathway	3/13	117/11159	0,025641025641025 6	22,009861932938 9	7,801849946387 01	0,000297579702609858	0,001897070604137 85	0,001115923884786 97	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Nervous system	mmu04722	Neurotrophin signaling pathway	3/13	121/11159	0,024793388429752 1	21,282263191354 1	7,660713835094 47	0,000328551453889923	0,001953807853319 33	0,001149298737246 66	Camk2b/Camk2a/Camk2g	3
Cellular Processes	Cell growth and death	mmu04114	Oocyte meiosis	3/13	123/11159	0,024390243902439	20,936210131332 1	7,592672152730 05	0,000344789621173999	0,001953807853319 33	0,001149298737246 66	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Sensory system	mmu04750	Inflammatory mediator regulation of TRP channels	3/13	130/11159	0,023076923076923 1	19,808875739645	7,366679582831 68	0,000405691461866629	0,002177922584757 69	0,001281130932210 41	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Endocrine system	mmu04921	Oxytocin signaling pathway	3/13	154/11159	0,019480519480519 5	16,721778221778 2	6,709224712003 07	0,000665999206717696	0,003358840937899 43	0,001975788786999 66	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Circulatory system	mmu04261	Adrenergic signaling in cardiomyocytes	3/13	156/11159	0,019230769230769 2	16,507396449704 1	6,661176908765 12	0,000691526075449882	0,003358840937899 43	0,001975788786999 66	Camk2b/Camk2a/Camk2g	3
Human Diseases	Endocrine and metabolic disease	mmu04934	Cushing syndrome	3/13	162/11159	0,018518518518518 5	15,896011396011 4	6,522224236965 91	0,000771850083114 04	0,003484814328451 64	0,002049890781442 14	Camk2b/Camk2a/Camk2g	3
Cellular	Transport and	mmu04148	Efferocytosis	3/13	163/11159	0,018404907975460 1	15,798489853704 6	6,499787689937 96	0,000785791466219488	0,003484814328451 64	0,002049890781442 14	Camk2b/Camk2a/Camk2g	3

Processes	catabolism												
Environmental Information Processing	Signal transduction	mmu04310	Wnt signaling pathway	3/13	179/11159	0,01675977653631328	14,386334336055	6,16584138604782	0,001031173692440 17	0,004344732156042 74	0,002555724797672 2	Camk2b/Camk2a/Camk2g	3
Organismal Systems	Development and regeneration	mmu04360	Axon guidance	3/13	181/11159	0,01657458563535 91	14,2273693157671	6,12712145190094	0,001064885332363 42	0,004344732156042 74	0,002555724797672 2	Camk2b/Camk2a/Camk2g	3
Human Diseases	Cancer: overview	mmu05205	Proteoglycans in cancer	3/13	204/11159	0,01470588235294 12	12,6233031674208	5,72194651027855	0,001503924923380 35	0,005900013160953 7	0,003470595977031 59	Camk2b/Camk2a/Camk2g	3
Human Diseases	Cardiovascular disease	mmu05415	Diabetic cardiomyopathy	3/13	216/11159	0,01388888888888 89	11,9220085470085	5,53562323247155	0,001772275585077 27	0,006542228375867 86	0,003848369632863 45	Camk2b/Camk2a/Camk2g	3
Human Diseases	Cardiovascular disease	mmu05417	Lipid and atherosclerosis	3/13	217/11159	0,01382488479262 67	11,8670684154555	5,52076483687497	0,001795905828669 61	0,006542228375867 86	0,003848369632863 45	Camk2b/Camk2a/Camk2g	3
Environmental Information Processing	Signal transduction	mmu04024	cAMP signaling pathway	3/13	224/11159	0,01339285714285 71	11,4962225274725	5,41942212837871	0,001966897315209 08	0,006918052625907 81	0,004069442721122 24	Camk2b/Camk2a/Camk2g	3
Environmental Information Processing	Signal transduction	mmu04020	Calcium signaling pathway	3/13	255/11159	0,01176470588235 29	10,0986425339367	5,01948437889365	0,002846177321398 53	0,009677002892755 01	0,005692354642797 06	Camk2b/Camk2a/Camk2g	3
Human Diseases	Neurodegenerative disease	mmu05012	Parkinson disease	3/13	274/11159	0,01094890510948 91	9,39837170129141	4,80686020625842	0,003488701930394 7	0,011478954738718	0,006752326316892 97	Camk2b/Camk2a/Camk2g	3
Environmental Information Processing	Signal transduction	mmu04151	PI3K-Akt signaling pathway	3/13	368/11159	0,00815217391304348	6,99770066889632	3,99561086814543	0,007952545756464 63	0,025348739598731	0,014911023293371 2	Col4a2/Jak1/Gnb4	3
Organismal Systems	Endocrine system	mmu04926	Relaxin signaling pathway	2/13	131/11159	0,01526717557251 91	13,1051086318262	4,75949961051388	0,009801667062819	0,029837803543041 5	0,017551649142965 6	Col4a2/Gnb4	2

Organismal Systems	Development and regeneration	mmu04380	Osteoclast differentiation	2/13	132/11159	0,01515151515151552	13,0058275058275	4,73866178818389	0,009945934514347 17	0,029837803543041 5	0,017551649142965 6	Lcp2/Jak1	2
Human Diseases	Infectious disease: viral	mmu05160	Hepatitis C	2/13	164/11159	0,012195121951219595	10,468105065666	4,17150444865479	0,015056253511950 8	0,043878224520542 2	0,025810720306201 3	Cd81/Jak1	2
Human Diseases	Neurodegenerative disease	mmu05022	Pathways of neurodegeneration - multiple diseases	3/13	481/11159	0,006237006237006624	5,35375019990405	3,33346901502498	0,016477635394474 6	0,046686633617678	0,027462725657457 7	Camk2b/Camk2a/Camk2g	3

Table S8: REACTOME – DOWN REGULATED PROTEINS

ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue	geneID	Count
R-MMU-877300	Interferon gamma signaling	3/13	19/8731	0,157894736842105	106,044534412955	17,6995283357719	2,46503552837761E-06	0,000162812663546499	8,36342945375702E-05	Camk2b/Camk2a/Camk2g	3
R-MMU-3371571	HSF1-dependent transactivation	3/13	22/8731	0,136363636363636	91,5839160839161	16,4266367232736	3,90750392511599E-06	0,000162812663546499	8,36342945375702E-05	Camk2b/Camk2a/Camk2g	3
R-MMU-438066	Unblocking of NMDA receptors, glutamate binding and activation	3/13	22/8731	0,136363636363636	91,5839160839161	16,4266367232736	3,90750392511599E-06	0,000162812663546499	8,36342945375702E-05	Camk2b/Camk2a/Camk2g	3
R-MMU-399719	Trafficking of AMPA receptors	3/13	28/8731	0,107142857142857	71,9587912087912	14,5218216348346	8,26953034377845E-06	0,000206738258594461	0,000106198179151681	Camk2b/Camk2a/Camk2g	3
R-MMU-399721	Glutamate binding, activation of AMPA receptors and synaptic plasticity	3/13	28/8731	0,107142857142857	71,9587912087912	14,5218216348346	8,26953034377845E-06	0,000206738258594461	0,000106198179151681	Camk2b/Camk2a/Camk2g	3
R-MMU-567	RAF activation	3/13	34/8731	0,088235294117647 1	59,2601809954751	13,143072956645	1,50274859960 76E-05	0,000293253109618791	0,000150639492098916	Camk2b/Camk2a/Camk2g	3

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R-MMU-442755	Activation of NMDA receptors and postsynaptic events	3/13	35/8731	0,0857142857142857	57,567032967033	12,9481589523233	1,64221741386523E-05	0,000293253109618791	0,000150639492098916	Camk2b/Camk2a/Camk2g	3
R-MMU-112314	Neurotransmitter receptors and postsynaptic signal transmission	4/13	136/8731	0,0294117647058824	19,7533936651584	8,51131668085577	3,61138068560437E-05	0,000564278232125682	0,000289860818186666	Camk2b/Camk2a/Camk2g/Gnb4	4
R-MMU-5578775	Ion homeostasis	3/13	52/8731	0,0576923076923077	38,7470414201184	10,5419295842158	5,46459138280394E-05	0,000758971025389436	0,000389871431989521	Camk2b/Camk2a/Camk2g	3
R-MMU-936837	Ion transport by P-type ATPases	3/13	54/8731	0,0555555555555556	37,3119658119658	10,3355170486539	6,12264654834719E-05	0,000765330818543398	0,000393138357314925	Camk2b/Camk2a/Camk2g	3
R-MMU-112315	Transmission across Chemical Synapses	4/13	199/8731	0,0201005025125628	13,4998067259374	6,88770881218963	0,000159323103766939	0,0018104898155334	0,000930020031558207	Camk2b/Camk2a/Camk2g/Gnb4	4
R-MMU-3371556	Cellular response to heat stress	3/13	80/8731	0,0375	25,1855769230769	8,39148175523711	0,000198312460620927	0,002065754798134 65	0,001061145622620 75	Camk2b/Camk2a/Camk2g	3
R-MMU-5576891	Cardiac conduction	3/13	98/8731	0,0306122448979592	20,5596546310832	7,51906285251047	0,000361466301730407	0,003475637516638 53	0,001785380113810 11	Camk2b/Camk2a/Camk2g	3
R-MMU-913531	Interferon Signaling	3/13	134/8731	0,0223880597014925	15,0361653272101	6,32263012802695	0,000903313154619304	0,008065296023386 64	0,004143015220434 4	Camk2b/Camk2a/Camk2g	3
R-MMU-112316	Neuronal System	4/13	320/8731	0,0125	8,39519230769231	5,20440410074897	0,000973697286276639	0,008114144052305 33	0,004168107681605 26	Camk2b/Camk2a/Camk2g/Gnb4	4
R-MMU-	Muscle contraction	3/13	152/8731	0,0197368421052632	13,2555668016194	5,88582339984986	0,001301573186839 49	0,010168540522183 5	0,005223418710342 7	Camk2b/Camk2a/Camk2g	3

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R-MMU-983712	Ion channel transport	3/13	168/8731	0,0178571428571429	11,9931318681319	5,55563201727834	0,00173654655927658	0,0127687247005631	0,00655909226723664	Camk2b/Camk2a/Camk2g	3
R-MMU-4086398	Ca2+ pathway	2/13	46/8731	0,0434782608695652	29,2006688963211	7,40497812067182	0,00204142377986632	0,0141765540268495	0,00728227196326584	Camk2a/Gnb4	2
R-MMU-5673001	RAF/MAP kinase cascade	3/13	252/8731	0,0119047619047619	7,9954212454125	4,3512315026368	0,00548273399908473	0,0360706183608375	0,0185289071158828	Camk2b/Camk2a/Camk2g	3
R-MMU-5684996	MAPK1/MAPK3 signaling	3/13	258/8731	0,0116279069767442	7,8094812164579	4,2872187329727	0,00585487657253506	0,0365929785783442	0,0187972353118231	Camk2b/Camk2a/Camk2g	3
R-MMU-5683057	MAPK family signaling cascades	3/13	281/8731	0,0106761565836299	7,1702710101286	4,0597511232319	0,00742223059068206	0,0441799439921551	0,0226945396507	Camk2b/Camk2a/Camk2g	3