Supplemental Data

Data analysis of microarrays

Microarray data was processed using RMA normalization (Partek v6.4, Partek Inc. St. Louis, Missouri). Principle component analysis was used to ensure batch and technical variations were within limits. Differences across genotypes were compared using analysis of variance and unpaired *t*-test to look for differences between specific genotypes. This analysis demonstrated that 3212 genes were differentially expressed at a q value of 0.01. For detecting differentially expressed genes, the multiple-test correction of p-value was performed by using the positive false discovery rate (FDR) and genes were filtered by a given q-value threshold (1). For full details of this analysis, see: (2). Where multiple annotations of probes to the same gene occurred these were filtered by selecting genes with the highest mean expression across all genotypes.

VMus3D model

Construction of the VMus3D model

Construction of VMus3D has previously been described in detail (3). In brief, AC3D version 6 was used to build de-convoluted 3D models of the structural proteins and their arrangements within muscle (4). Data used for the construction of simplified structures was restricted to evidence from vertebrate due to muscle structural similarity and included where possible: protein-protein interaction data from public data repositories (HPRD and BIND), published experimental protein localization data, structural protein data, and previously published diagrammatic representations of the contractile apparatus (5-11).

Selection of gene lists using VMus3D

Gene lists were selected based on the patterns recognised using VMus3D as per the following criteria:

Equation 1: sham only and reciprocal:

Eq1(i): $p(cS \leq 0.05, dS \leq 0.05)$

DE(+cS, -dS) or DE(-cS, +dS)

(ii): $p(cM > 0.05, dM > 0.05)$

DE(+cS, -dS) or DE(-cS, +dS)

Equation 2: all significant and reciprocal:

Eq2: $p(cS \leq 0.05, dS \leq 0.05, cM \leq 0.05, dM \leq 0.05)$

DE(+cS, -dS) or DE(-cS, +dS)

DE(+cM, -dM) or DE(-cM, +dM)

Equation 3: sham or infarct significant:

Eq3: $p(cS \leq 0.05, dS \leq 0.05)$ or $p(cM \leq 0.05, dM \leq 0.05)$

where,

cS = caPI3K sham vs. Ntg sham

dS = dnPI3K sham vs. Ntg sham

cM = caPI3K MI vs. Ntg MI

dM = dnPI3K MI vs. Ntg MI

DE= differentially expressed

A Boolean descriptive index of direction of gene expression across the models was constructed (Supp table III). 183 significant genes were identified as significantly reciprocally differentially expressed in the sham models and 60 genes were identified across all models amongst 973 identified as differentially expressed in either sham (dnPI3K and caPI3K) or MI (dnPI3K and caPI3K) irrespective of direction of expression. Significant differential expression was relative to Ntg mice.

Gene set enrichment analysis

The resulting gene list generated from equation 3 was subject to gene set enrichment via DAVID (12). The gene list was uploaded using the functional annotation tool; identifier used was official gene symbol and list type selected as gene list using *Mus musculus* as background. All pathways listed in DAVID were selected for generating a functional annotation chart using an unadjusted p-value threshold of 0.05.

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Supplementary Table I

Transcriptomics data of structural components highlighted from VMus3D analysis

Probeset ID	Gene Title	Gene Symbol	p-value (GenotypeX Treatment)	Mean(Ntg MI)	StdErr(Ntg MI)	Mean(Ntg Sham)	StdErr(Ntg Sham)
1426043_a_at	calpain 3	Capn3	4.28E-08	5.51415	0.0647418	5.5248	0.241134
1426778_at	dystroglycan 1	Dag1	0.000334167	10.8459	0.0621043	10.7952	0.0902402
1456131_x_at	dystroglycan 1	Dag1	0.00212354	9.07871	0.0982226	8.99774	0.081506
1426779_x_at	dystroglycan 1	Dag1	0.0027238	9.50981	0.0721527	9.39697	0.0672233
1447812_x_at	filamin C, gamma (actin binding protein 280)	Flnc	0.00566103	9.60395	0.130057	9.43989	0.104706
1449073_at	filamin C, gamma (actin binding protein 280)	Flnc	0.0123629	9.166	0.134049	8.8799	0.158383
1428183_at	ankyrin repeat domain 23	Ankrd23	7.70E-05	12.2842	0.114426	11.9257	0.274857
1434369_a_at	crystallin, alpha B	Cryab	9.39E-05	13.8655	0.0276797	13.868	0.0354249
1416455_a_at	crystallin, alpha B	Cryab	0.000212472	14.0607	0.0247307	13.9853	0.0796876
1423238_at	integrin beta 1 binding protein 2	Itgb1bp2	2.29E-06	11.2488	0.0801044	11.2098	0.0296426
1416752_at	LIM domain binding 3	Ldb3	0.000135416	12.1496	0.0530017	12.1842	0.0758853
1450828_at	synaptopodin 2	Synpo2	1.61E-06	8.3419	0.0680548	8.33541	0.180341
1452879_at	synaptopodin 2	Synpo2	1.85E-06	9.62731	0.0760364	9.48847	0.211305
1428295_at	synaptopodin 2-like	Synpo2l	2.56E-06	8.44492	0.158753	7.3885	0.190618
1447657_s_at	synaptopodin 2-like	Synpo2l	1.72E-05	11.8887	0.0817434	11.3438	0.236248
1447658_x_at	synaptopodin 2-like	Synpo2l	1.74E-05	11.6761	0.0813851	11.2043	0.150146
1451691_at	endothelin receptor type A	Ednra	2.63E-07	8.41884	0.0465864	8.31592	0.139176
1433525_at	endothelin receptor type A	Ednra	2.92E-07	8.53663	0.0250542	8.44326	0.130773
1460513_a_at	endothelin receptor type A	Ednra	0.000135476	7.15355	0.138155	7.24928	0.0903131
1440093_at	endothelin receptor type A	Ednra	0.00657795	5.48236	0.0833596	5.53833	0.104976
1452982_at	insulin-like growth factor I receptor	Igf1r	9.21E-09	8.00033	0.0855573	7.76825	0.0362324
1428967_at	insulin-like growth factor I receptor	Igf1r	0.000141843	5.58115	0.101729	5.44581	0.0507945
1426565_at	insulin-like growth factor I receptor	Igf1r	0.00134888	6.05605	0.0644206	6.05635	0.107263
1416657_at	thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	Akt1 /// LOC100047666	5.68E-08	8.41809	0.0374833	8.50504	0.0467761
1425711_a_at	thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	Akt1 /// LOC100047666	3.95E-05	8.24249	0.0457736	8.33733	0.0431031
1423104_at	insulin receptor substrate 1	Irs1	1.02E-09	10.2621	0.0781668	9.832	0.0836127
1448595_a_at	brain expressed gene 1	Bex1	6.81E-08	9.25782	0.142267	8.72464	0.710716
1460585_x_at	phosphatidylserine decarboxylase	Pisd	1.29E-07	9.54206	0.0288596	9.76653	0.0394972
1436944_x_at	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase pseudogene /// p	4933439C20Rik /// LOC236604 /// Pisd	0.0134103	8.50912	0.129309	8.34837	0.155516
1435425_at	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	4933439C20Rik /// Pisd	0.0380703	6.15373	0.0224015	6.02385	0.0777252
1435426_s_at	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	4933439C20Rik /// Pisd	0.64048	4.39328	0.116822	4.41508	0.173436
1456114_at	CDP-diacylglycerol synthase 1	Cds1	9.36E-06	5.75564	0.0619083	5.68678	0.0937261
1428680_at	CDP-diacylglycerol synthase 1	Cds1	0.000663067	5.30693	0.15611	5.10555	0.146384
1429862_at	phospholipase A2, group IVE	Pla2g4e	7.61E-06	5.82775	0.0458212	5.87353	0.0323166
1417814_at	phospholipase A2, group V	Pla2g5	1.65E-10	7.29717	0.044195	7.30125	0.0808955
1451041_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	0.001769	9.1754	0.0771948	8.96659	0.120979
1423592_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	0.0230171	8.84718	0.0581	8.54993	0.119985
1437670_x_at	CD151 antigen	Cd151	4.81E-05	11.3713	0.0337425	11.2194	0.106448
1456085_x_at	CD151 antigen	Cd151	8.36E-05	12.4217	0.0263093	12.2495	0.0897386
1424093_x_at	CD151 antigen	Cd151	0.000407447	10.6084	0.0188943	10.4973	0.106957
1451232_at	CD151 antigen	Cd151	0.00115452	10.5515	0.0258109	10.3678	0.138166

Gene Title	Mean(caPI3K MI)	StdErr(caPI3K MI)	Mean(caPI3K Sham)	StdErr(caPI3K Sham)	Mean(dnPI3K MI)	StdErr(dnPI3K MI)	Mean(dnPI3K Sham)	StdErr(dnPI3K Sham)
calpain 3	5.90039	0.154975	6.27228	0.156392	4.31838	0.0785752	4.38538	0.111122
dystroglycan 1	10.8636	0.0326845	11.0161	0.0244785	10.7537	0.0344861	10.5714	0.0260224
dystroglycan 1	9.08977	0.0457583	9.28701	0.0371078	8.86798	0.0758096	8.835	0.0488653
dystroglycan 1	9.49399	0.0342556	9.59743	0.0487006	9.32493	0.0592789	9.19277	0.0768127
filamin C, gamma (actin binding protein 280)	9.5739	0.0503767	9.73098	0.0638876	9.46736	0.122064	9.11437	0.0765404
filamin C, gamma (actin binding protein 280)	9.02814	0.0767191	9.21142	0.0556744	9.01783	0.101555	8.62634	0.0702658
ankyrin repeat domain 23	12.5057	0.0634164	12.5392	0.0619205	12.1349	0.130628	11.3132	0.0731619
crystallin, alpha B	14.016	0.0255856	14.0072	0.0202924	13.8547	0.0519824	13.7431	0.0228331
crystallin, alpha B	14.2079	0.0347028	14.2174	0.0234616	13.9739	0.0642016	13.808	0.0589953
integrin beta 1 binding protein 2	11.1671	0.0545525	11.3797	0.0256988	10.7693	0.0256103	11.0427	0.0596402
LIM domain binding 3	12.1535	0.0430578	12.3731	0.0449605	11.9322	0.0591673	11.9076	0.0535927
synaptopodin 2	8.54506	0.061612	8.85594	0.109851	7.86964	0.0344443	7.59211	0.118143
synaptopodin 2	9.73295	0.0594261	10.0289	0.0842387	9.08943	0.0652608	8.76629	0.0633889
synaptopodin 2-like	8.17318	0.147026	7.73945	0.146579	9.02553	0.221597	7.18905	0.106171
synaptopodin 2-like	11.8367	0.0544752	11.6068	0.0449332	12.0945	0.133528	10.8547	0.078513
synaptopodin 2-like	11.6195	0.0372828	11.4256	0.0564858	11.9868	0.137697	10.985	0.0745224
endothelin receptor type A	7.90806	0.0821815	8.01335	0.0611877	8.76515	0.141953	9.12006	0.0361452
endothelin receptor type A	8.0414	0.0597314	8.07011	0.0737053	8.85911	0.129568	9.17639	0.0861077
endothelin receptor type A	6.89479	0.0638794	7.0288	0.0645823	7.50467	0.183027	7.81065	0.0327946
endothelin receptor type A	5.42628	0.13	5.16744	0.100471	5.72153	0.165928	6.09618	0.231786
insulin-like growth factor I receptor	7.73208	0.0249535	7.55836	0.020818	8.55173	0.110356	8.39966	0.0655084
insulin-like growth factor I receptor	5.39923	0.0660306	5.13376	0.0574057	5.99898	0.171336	5.90485	0.13018
insulin-like growth factor I receptor	6.09811	0.0523289	5.91665	0.118937	6.60526	0.161164	6.52609	0.128079
thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	8.26244	0.0215843	8.19428	0.0447394	8.56832	0.011011	8.7142	0.0412696
thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	8.0403	0.106182	8.01213	0.0433489	8.30153	0.0401193	8.53888	0.0362117
insulin receptor substrate 1	9.69582	0.0756093	9.36007	0.0736976	10.8603	0.144029	10.8722	0.0718236
brain expressed gene 1	7.48161	0.132241	6.84461	0.376696	11.1785	0.370007	11.7645	0.0512192
phosphatidylserine decarboxylase	9.82328	0.0163945	9.89878	0.016656	9.34992	0.0470535	9.6082	0.0671671
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase pseudogene /// p	8.69649	0.0550043	8.43782	0.0644839	8.76807	0.0716533	8.23787	0.095918
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	6.07043	0.0678648	6.27462	0.0300251	5.89214	0.126249	6.09039	0.0682769
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	4.31641	0.0604491	4.16094	0.0568821	4.34412	0.119071	4.28823	0.086738
CDP-diacylglycerol synthase 1	5.89724	0.0842263	6.20452	0.114794	5.54305	0.0513161	5.21855	0.101993
CDP-diacylglycerol synthase 1	5.28577	0.159275	5.64221	0.147127	4.62976	0.2426	4.50397	0.0547029
phospholipase A2, group IVE	5.88706	0.0323284	6.10066	0.0360656	5.50309	0.0844635	5.50406	0.0993139
phospholipase A2, group V	7.69497	0.0799816	8.09725	0.068896	5.15422	0.24367	5.69737	0.248268
Rho-associated coiled-coil containing protein kinase 2	9.10078	0.0583812	9.22938	0.0386874	9.04613	0.0300576	8.71661	0.0808753
Rho-associated coiled-coil containing protein kinase 2	8.71848	0.0649425	8.70939	0.066943	8.66298	0.0557699	8.45294	0.0606851
CD151 antigen	11.4739	0.0237709	11.4234	0.0282717	11.2239	0.0518427	10.9719	0.036779
CD151 antigen	12.4637	0.0421009	12.4753	0.0232763	12.3007	0.0584263	12.0646	0.00463218
CD151 antigen	10.6014	0.0355254	10.6827	0.0337135	10.4056	0.0580436	10.2609	0.0248515
CD151 antigen	10.5315	0.034843	10.6185	0.0470119	10.3433	0.0461168	10.1673	0.0144076

Gene Title	p-value(Ntg MI vs. Ntg Sham)	Ratio(Ntg MI vs. Ntg Sham)	Fold-Change(Ntg MI vs. Ntg Sham)	Fold-Change(Ntg MI vs. Ntg Sham) (Description)	p-value(caPI3K MI vs. Ntg Sham)	Ratio(caPI3K MI vs. Ntg Sham)
calpain 3	0.959677	0.992649	-1.00741	Ntg MI down vs Ntg Sham	0.087194	1.29738
dystroglycan 1	0.490306	1.03575	1.03575	Ntg MI up vs Ntg Sham	0.354942	1.0485
dystroglycan 1	0.412107	1.05773	1.05773	Ntg MI up vs Ntg Sham	0.352568	1.06587
dystroglycan 1	0.210798	1.08135	1.08135	Ntg MI up vs Ntg Sham	0.279246	1.06956
filamin C, gamma (actin binding protein 280)	0.242365	1.12043	1.12043	Ntg MI up vs Ntg Sham	0.336517	1.09734
filamin C, gamma (actin binding protein 280)	0.0721608	1.21934	1.21934	Ntg MI up vs Ntg Sham	0.335405	1.10821
ankyrin repeat domain 23	0.0885124	1.28211	1.28211	Ntg MI up vs Ntg Sham	0.00927118	1.4949
crystallin, alpha B	0.957131	0.998269	-1.00173	Ntg MI down vs Ntg Sham	0.00467274	1.10805
crystallin, alpha B	0.320327	1.05363	1.05363	Ntg MI up vs Ntg Sham	0.00739846	1.16679
integrin beta 1 binding protein 2	0.589347	1.02744	1.02744	Ntg MI up vs Ntg Sham	0.555802	0.97087
LIM domain binding 3	0.667835	0.976336	-1.02424	Ntg MI down vs Ntg Sham	0.702823	0.978945
synaptopodin 2	0.966171	1.0045	1.0045	Ntg MI up vs Ntg Sham	0.181228	1.15641
synaptopodin 2	0.373208	1.10101	1.10101	Ntg MI up vs Ntg Sham	0.125202	1.18467
synaptopodin 2-like	0.000274371	2.07975	2.07975	Ntg MI up vs Ntg Sham	0.00359905	1.7227
synaptopodin 2-like	0.00590818	1.45892	1.45892	Ntg MI up vs Ntg Sham	0.011274	1.40727
synaptopodin 2-like	0.00329024	1.38693	1.38693	Ntg MI up vs Ntg Sham	0.00802831	1.33355
endothelin receptor type A	0.450897	1.07394	1.07394	Ntg MI up vs Ntg Sham	0.0068272	0.753738
endothelin receptor type A	0.482843	1.06686	1.06686	Ntg MI up vs Ntg Sham	0.00639592	0.756878
endothelin receptor type A	0.538932	0.9358	-1.0686	Ntg MI down vs Ntg Sham	0.0323256	0.78215
endothelin receptor type A	0.788097	0.961954	-1.03955	Ntg MI down vs Ntg Sham	0.591619	0.925279
insulin-like growth factor I receptor	0.0230004	1.17452	1.17452	Ntg MI up vs Ntg Sham	0.70306	0.975242
insulin-like growth factor I receptor	0.376695	1.09835	1.09835	Ntg MI up vs Ntg Sham	0.758686	0.968232
insulin-like growth factor I receptor	0.99848	0.999788	-1.00021	Ntg MI down vs Ntg Sham	0.794571	1.02937
thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	0.107108	0.941511	-1.06212	Ntg MI down vs Ntg Sham	0.000166308	0.845218
thymoma viral proto-oncogene 1 /// similar to serine/threonine protein kinase	0.260921	0.936378	-1.06795	Ntg MI down vs Ntg Sham	0.00189212	0.813923
insulin receptor substrate 1	0.00375532	1.34732	1.34732	Ntg MI up vs Ntg Sham	0.306146	0.909922
brain expressed gene 1	0.322551	1.44711	1.44711	Ntg MI up vs Ntg Sham	0.029081	0.422484
phosphatidylserine decarboxylase	0.000928897	0.855912	-1.16834	Ntg MI down vs Ntg Sham	0.330658	1.04012
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase pseudogene /// p	0.279759	1.11787	1.11787	Ntg MI up vs Ntg Sham	0.0266871	1.2729
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	0.229136	1.0942	1.0942	Ntg MI up vs Ntg Sham	0.6606	1.03281
RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	0.889909	0.985005	-1.01522	Ntg MI down vs Ntg Sham	0.533104	0.933895
CDP-diacylglycerol synthase 1	0.584702	1.04889	1.04889	Ntg MI up vs Ntg Sham	0.106153	1.15706
CDP-diacylglycerol synthase 1	0.386822	1.1498	1.1498	Ntg MI up vs Ntg Sham	0.437703	1.13305
phospholipase A2, group IVE	0.603403	0.968764	-1.03224	Ntg MI down vs Ntg Sham	0.877578	1.00942
phospholipase A2, group V	0.985184	0.997178	-1.00283	Ntg MI down vs Ntg Sham	0.0856921	1.31378
Rho-associated coiled-coil containing protein kinase 2	0.0616913	1.15573	1.15573	Ntg MI up vs Ntg Sham	0.216605	1.09748
Rho-associated coiled-coil containing protein kinase 2	0.0112703	1.2288	1.2288	Ntg MI up vs Ntg Sham	0.126863	1.12392
CD151 antigen	0.0647216	1.11101	1.11101	Ntg MI up vs Ntg Sham	0.00400402	1.19294
CD151 antigen	0.0234334	1.12672	1.12672	Ntg MI up vs Ntg Sham	0.00644296	1.16002
CD151 antigen	0.170669	1.08005	1.08005	Ntg MI up vs Ntg Sham	0.197818	1.07482
CD151 antigen	0.0617712	1.13579	1.13579	Ntg MI up vs Ntg Sham	0.0929831	1.12008

Fold-Change(caPI3K MI vs. Ntg Sham)	Fold-Change(caPI3K MI vs. Ntg Sham) (Description)	p-value(caPI3K Shar	Ratio(caPI3K Sham vs. Ntg Sham)	Fold-Change(caPI3K Sham vs. Ntg Sham)	Fold-Change(caPI3K Sham vs. Ntg Sham) (Description)	p-value(dnPI3K MI vs. Ntg Sham)	Ratio(dnPI3K MI vs. Ntg Sham)
1.29738	caPI3K MI up vs Ntg Sham	0.0020471	1.67886	1.67886	caPI3K Sham up vs Ntg Sham	1.67E-05	0.433343
1.0485	caPI3K MI up vs Ntg Sham	0.00660576	1.16544	1.16544	caPI3K Sham up vs Ntg Sham	0.570581	0.971594
1.06587	caPI3K MI up vs Ntg Sham	0.00769053	1.22202	1.22202	caPI3K Sham up vs Ntg Sham	0.195128	0.913983
1.06956	caPI3K MI up vs Ntg Sham	0.0332756	1.14906	1.14906	caPI3K Sham up vs Ntg Sham	0.418278	0.951294
1.09734	caPI3K MI up vs Ntg Sham	0.0458601	1.22356	1.22356	caPI3K Sham up vs Ntg Sham	0.841853	1.01923
1.10821	caPI3K MI up vs Ntg Sham	0.0400155	1.25833	1.25833	caPI3K Sham up vs Ntg Sham	0.369281	1.10032
1.4949	caPI3K MI up vs Ntg Sham	0.00643256	1.52999	1.52999	caPI3K Sham up vs Ntg Sham	0.307209	1.15607
1.10805	caPI3K MI up vs Ntg Sham	0.00710559	1.10133	1.10133	caPI3K Sham up vs Ntg Sham	0.774734	0.990806
1.16679	caPI3K MI up vs Ntg Sham	0.00559181	1.17446	1.17446	caPI3K Sham up vs Ntg Sham	0.878618	0.992112
-1.03	caPI3K MI down vs Ntg Sham	0.0279645	1.12494	1.12494	caPI3K Sham up vs Ntg Sham	7.50E-06	0.736866
-1.02151	caPI3K MI down vs Ntg Sham	0.0282896	1.13987	1.13987	caPI3K Sham up vs Ntg Sham	0.00516662	0.839746
1.15641	caPI3K MI up vs Ntg Sham	0.00283603	1.43448	1.43448	caPI3K Sham up vs Ntg Sham	0.0063156	0.724084
1.18467	caPI3K MI up vs Ntg Sham	0.00226408	1.45439	1.45439	caPI3K Sham up vs Ntg Sham	0.0171772	0.75836
1.7227	caPI3K MI up vs Ntg Sham	0.151895	1.27539	1.27539	caPI3K Sham up vs Ntg Sham	1.61E-06	3.11024
1.40727	caPI3K MI up vs Ntg Sham	0.149345	1.19999	1.19999	caPI3K Sham up vs Ntg Sham	0.000431716	1.68267
1.33355	caPI3K MI up vs Ntg Sham	0.129576	1.16584	1.16584	caPI3K Sham up vs Ntg Sham	2.50E-05	1.72023
-1.32672	caPI3K MI down vs Ntg Sham	0.0360276	0.810805	-1.23334	caPI3K Sham down vs Ntg Sham	0.00345525	1.36531
-1.32122	caPI3K MI down vs Ntg Sham	0.0103192	0.772093	-1.29518	caPI3K Sham down vs Ntg Sham	0.00505566	1.33408
-1.27853	caPI3K MI down vs Ntg Sham	0.166294	0.858281	-1.16512	caPI3K Sham down vs Ntg Sham	0.111991	1.19366
-1.08076	caPI3K MI down vs Ntg Sham	0.0873173	0.773305	-1.29315	caPI3K Sham down vs Ntg Sham	0.383553	1.1354
-1.02539	caPI3K MI down vs Ntg Sham	0.0373653	0.864603	-1.1566	caPI3K Sham down vs Ntg Sham	1.24E-07	1.72128
-1.03281	caPI3K MI down vs Ntg Sham	0.0510981	0.805498	-1.24147	caPI3K Sham down vs Ntg Sham	0.00162164	1.46731
1.02937	caPI3K MI up vs Ntg Sham	0.388321	0.907705	-1.10168	caPI3K Sham down vs Ntg Sham	0.00271171	1.46297
-1.18313	caPI3K MI down vs Ntg Sham	9.94E-06	0.806218	-1.24036	caPI3K Sham down vs Ntg Sham	0.233007	1.04483
-1.22862	caPI3K MI down vs Ntg Sham	0.000877869	0.798188	-1.25284	caPI3K Sham down vs Ntg Sham	0.666508	0.975492
-1.099	caPI3K MI down vs Ntg Sham	0.00183141	0.720996	-1.38697	caPI3K Sham down vs Ntg Sham	2.66E-07	2.03969
-2.36696	caPI3K MI down vs Ntg Sham	0.00210888	0.271678	-3.68083	caPI3K Sham down vs Ntg Sham	0.000185885	5.47878
1.04012	caPI3K MI up vs Ntg Sham	0.0316342	1.09601	1.09601	caPI3K Sham up vs Ntg Sham	8.17E-07	0.749183
1.2729	caPI3K MI up vs Ntg Sham	0.54296	1.06396	1.06396	caPI3K Sham up vs Ntg Sham	0.0093501	1.33765
1.03281	caPI3K MI up vs Ntg Sham	0.027219	1.18984	1.18984	caPI3K Sham up vs Ntg Sham	0.222879	0.912749
-1.07078	caPI3K MI down vs Ntg Sham	0.119025	0.838487	-1.19262	caPI3K Sham down vs Ntg Sham	0.653136	0.952008
1.15706	caPI3K MI up vs Ntg Sham	0.000557073	1.43171	1.43171	caPI3K Sham up vs Ntg Sham	0.260518	0.905171
1.13305	caPI3K MI up vs Ntg Sham	0.0295517	1.45061	1.45061	caPI3K Sham up vs Ntg Sham	0.0505336	0.719072
1.00942	caPI3K MI up vs Ntg Sham	0.0172297	1.1705	1.1705	caPI3K Sham up vs Ntg Sham	0.000451922	0.773545
1.31378	caPI3K MI up vs Ntg Sham	0.00172781	1.73628	1.73628	caPI3K Sham up vs Ntg Sham	1.02E-08	0.225778
1.09748	caPI3K MI up vs Ntg Sham	0.0219503	1.1998	1.1998	caPI3K Sham up vs Ntg Sham	0.457635	1.05668
1.12392	caPI3K MI up vs Ntg Sham	0.147305	1.11687	1.11687	caPI3K Sham up vs Ntg Sham	0.297191	1.08151
1.19294	caPI3K MI up vs Ntg Sham	0.0165252	1.15191	1.15191	caPI3K Sham up vs Ntg Sham	0.954406	1.00311
1.16002	caPI3K MI up vs Ntg Sham	0.00446375	1.16941	1.16941	caPI3K Sham up vs Ntg Sham	0.47129	1.03609
1.07482	caPI3K MI up vs Ntg Sham	0.0284879	1.13713	1.13713	caPI3K Sham up vs Ntg Sham	0.253802	0.938368
1.12008	caPI3K MI up vs Ntg Sham	0.0141209	1.1897	1.1897	caPI3K Sham up vs Ntg Sham	0.793106	0.983127

Fold-Change(dnPI3K MI vs. Ntg Sham)	Fold-Change(dnPI3K MI vs. Ntg Sham) (Description)	p-value(dnPI3K Sham vs. Ntg Sham)	Ratio(dnPI3K Sham vs. Ntg Sham)	Fold-Change (dnPI3K Sham vs. Ntg Sham)	Fold-Change(dnPI3K Sham vs. Ntg Sham) (Description)	F(GenotypeX Treatment)	F(Error)	Entrez Gene
-2.30764	dnPI3K MI down vs Ntg Sham	3.27E-05	0.453944	-2.20291	dnPI3K Sham down vs Ntg Sham	29.6911	1	12335
-1.02924	dnPI3K MI down vs Ntg Sham	0.00603025	0.856262	-1.16787	dnPI3K Sham down vs Ntg Sham	8.26158	1	13138
-1.09411	dnPI3K MI down vs Ntg Sham	0.108717	0.893322	-1.11942	dnPI3K Sham down vs Ntg Sham	5.90263	1	13138
-1.0512	dnPI3K MI down vs Ntg Sham	0.0304881	0.868022	-1.15205	dnPI3K Sham down vs Ntg Sham	5.61878	1	13138
1.01923	dnPI3K MI up vs Ntg Sham	0.0275093	0.798012	-1.25311	dnPI3K Sham down vs Ntg Sham	4.82554	1	68794
1.10032	dnPI3K MI up vs Ntg Sham	0.107678	0.838821	-1.19215	dnPI3K Sham down vs Ntg Sham	4.04068	1	68794
1.15607	dnPI3K MI up vs Ntg Sham	0.00650534	0.654062	-1.52891	dnPI3K Sham down vs Ntg Sham	10.499	1	78321
-1.00928	dnPI3K MI down vs Ntg Sham	0.0139476	0.917068	-1.09043	dnPI3K Sham down vs Ntg Sham	10.1739	1	12955
-1.00795	dnPI3K MI down vs Ntg Sham	0.0271673	0.884326	-1.1308	dnPI3K Sham down vs Ntg Sham	8.91396	1	12955
-1.3571	dnPI3K MI down vs Ntg Sham	0.0302669	0.890631	-1.1228	dnPI3K Sham down vs Ntg Sham	17.5673	1	26549
-1.19084	dnPI3K MI down vs Ntg Sham	0.00260277	0.825563	-1.21129	dnPI3K Sham down vs Ntg Sham	9.59542	1	24131
-1.38105	dnPI3K MI down vs Ntg Sham	0.000107764	0.59737	-1.674	dnPI3K Sham down vs Ntg Sham	18.4359	1	118449
-1.31863	dnPI3K MI down vs Ntg Sham	0.000159806	0.606178	-1.64968	dnPI3K Sham down vs Ntg Sham	18.0924	1	118449
3.11024	dnPI3K MI up vs Ntg Sham	0.40626	0.870881	-1.14826	dnPI3K Sham down vs Ntg Sham	17.2989	1	68760
1.68267	dnPI3K MI up vs Ntg Sham	0.0118235	0.712506	-1.4035	dnPI3K Sham down vs Ntg Sham	13.1824	1	68760
1.72023	dnPI3K MI up vs Ntg Sham	0.133106	0.859027	-1.16411	dnPI3K Sham down vs Ntg Sham	13.1568	1	68760
1.36531	dnPI3K MI up vs Ntg Sham	1.08E-05	1.7461	1.7461	dnPI3K Sham up vs Ntg Sham	23.4956	1	13617
1.33408	dnPI3K MI up vs Ntg Sham	2.44E-05	1.66224	1.66224	dnPI3K Sham up vs Ntg Sham	23.1712	1	13617
1.19366	dnPI3K MI up vs Ntg Sham	0.00173923	1.47567	1.47567	dnPI3K Sham up vs Ntg Sham	9.59472	1	13617
1.1354	dnPI3K MI up vs Ntg Sham	0.0140511	1.47208	1.47208	dnPI3K Sham up vs Ntg Sham	4.66994	1	13617
1.72128	dnPI3K MI up vs Ntg Sham	2.46E-06	1.54908	1.54908	dnPI3K Sham up vs Ntg Sham	35.9949	1	16001
1.46731	dnPI3K MI up vs Ntg Sham	0.00653683	1.37463	1.37463	dnPI3K Sham up vs Ntg Sham	9.52372	1	16001
1.46297	dnPI3K MI up vs Ntg Sham	0.00815837	1.38486	1.38486	dnPI3K Sham up vs Ntg Sham	6.43945	1	16001
1.04483	dnPI3K MI up vs Ntg Sham	0.000703179	1.15601	1.15601	dnPI3K Sham up vs Ntg Sham	28.6392	1	100047666 /// 11651
-1.02512	dnPI3K MI down vs Ntg Sham	0.0239006	1.14993	1.14993	dnPI3K Sham up vs Ntg Sham	11.6373	1	100047666 /// 11651
2.03969	dnPI3K MI up vs Ntg Sham	2.26E-07	2.05658	2.05658	dnPI3K Sham up vs Ntg Sham	47.1402	1	16367
5.47878	dnPI3K MI up vs Ntg Sham	1.70E-05	8.22394	8.22394	dnPI3K Sham up vs Ntg Sham	27.9818	1	19716
-1.33479	dnPI3K MI down vs Ntg Sham	0.0121048	0.896062	-1.11599	dnPI3K Sham down vs Ntg Sham	25.7804	1	320951
1.33765	dnPI3K MI up vs Ntg Sham	0.453607	0.92627	-1.0796	dnPI3K Sham down vs Ntg Sham	3.96236	1	236604 /// 320951 ///
-1.09559	dnPI3K MI down vs Ntg Sham	0.531622	1.0472	1.0472	dnPI3K Sham up vs Ntg Sham	3.00815	1	320951 /// 66776
-1.05041	dnPI3K MI down vs Ntg Sham	0.424605	0.915829	-1.09191	dnPI3K Sham down vs Ntg Sham	0.685539	1	320951 /// 66776
-1.10476	dnPI3K MI down vs Ntg Sham	0.00135782	0.722851	-1.38341	dnPI3K Sham down vs Ntg Sham	14.4046	1	74596
-1.39068	dnPI3K MI down vs Ntg Sham	0.0163054	0.65903	-1.51738	dnPI3K Sham down vs Ntg Sham	7.33288	1	74596
-1.29275	dnPI3K MI down vs Ntg Sham	0.000463295	0.774065	-1.29188	dnPI3K Sham down vs Ntg Sham	14.84	1	329502
-4.42913	dnPI3K MI down vs Ntg Sham	7.21E-07	0.328992	-3.03959	dnPI3K Sham down vs Ntg Sham	58.6466	1	18784
1.05668	dnPI3K MI up vs Ntg Sham	0.0282571	0.84091	-1.18919	dnPI3K Sham down vs Ntg Sham	6.11565	1	19878
1.08151	dnPI3K MI up vs Ntg Sham	0.369197	0.934983	-1.06954	dnPI3K Sham down vs Ntg Sham	3.45707	1	19878
1.00311	dnPI3K MI up vs Ntg Sham	0.00489994	0.842384	-1.18711	dnPI3K Sham down vs Ntg Sham	11.2937	1	12476
1.03609	dnPI3K MI up vs Ntg Sham	0.0159089	0.879664	-1.1368	dnPI3K Sham down vs Ntg Sham	10.3634	1	12476
-1.06568	dnPI3K MI down vs Ntg Sham	0.00709198	0.848846	-1.17807	dnPI3K Sham down vs Ntg Sham	7.98581	1	12476
-1.01716	dnPI3K MI down vs Ntg Sham	0.0432581	0.870234	-1.14912	dnPI3K Sham down vs Ntg Sham	6.62948	1	12476

Gene Ontology Biological Process	Gene Ontology Cellular Component	Gene Ontology Molecular Function	MGI Name	
0006006 // glucose metabolic process // infer	0005622 // intracellular // inferred from elec	0004197 // cysteine-type endopeptidase a	107437	
0002011 // morphogenesis of an epithelial sh	0005576 // extracellular region // inferred fr	0005509 // calcium ion binding // inferred	101864	
0002011 // morphogenesis of an epithelial sh	0005576 // extracellular region // inferred fr	0005509 // calcium ion binding // inferred	101864	
0002011 // morphogenesis of an epithelial sh	0005576 // extracellular region // inferred fr	0005509 // calcium ion binding // inferred	101864	
0030029 // actin filament-based process // tra	0005737 // cytoplasm // inferred from electr	0003779 // actin binding // traceable auth	95557	
0030029 // actin filament-based process // tra	0005737 // cytoplasm // inferred from electr	0003779 // actin binding // traceable auth	95557	
0006631 // fatty acid metabolic process // inf	0005634 // nucleus // inferred from direct as	---	1925571	
0007169 // transmembrane receptor protein t	0005625 // soluble fraction // inferred from	0005212 // structural constituent of eye le	88516	
0007169 // transmembrane receptor protein t	0005625 // soluble fraction // inferred from	0005212 // structural constituent of eye le	88516	
0007229 // integrin-mediated signaling pathw	0030018 // Z disc // inferred from direct ass	0005509 // calcium ion binding // inferred	1353420	
---	0005737 // cytoplasm // inferred from electr	0005080 // protein kinase C binding // inf	1344412	
---	0005634 // nucleus // inferred from electron	0003779 // actin binding // not recorded /	2153070	
---	0005634 // nucleus // inferred from electron	0003779 // actin binding // not recorded /	2153070	
---	0005737 // cytoplasm // inferred from electr	0003779 // actin binding // inferred from	1916010	
---	0005737 // cytoplasm // inferred from electr	0003779 // actin binding // inferred from	1916010	
---	0005737 // cytoplasm // inferred from electr	0003779 // actin binding // inferred from	1916010	
0001569 // patterning of blood vessels // infe	0005886 // plasma membrane // inferred fro	0001584 // rhodopsin-like receptor activit	105923	
0001569 // patterning of blood vessels // infe	0005886 // plasma membrane // inferred fro	0001584 // rhodopsin-like receptor activit	---	
0001569 // patterning of blood vessels // infe	0005886 // plasma membrane // inferred fro	0001584 // rhodopsin-like receptor activit	105923	
0001569 // patterning of blood vessels // infe	0005886 // plasma membrane // inferred fro	0001584 // rhodopsin-like receptor activit	105923	
0006468 // protein amino acid phosphorylatio	0016020 // membrane // inferred from elect	0000166 // nucleotide binding // inferred	---	
0006468 // protein amino acid phosphorylatio	0016020 // membrane // inferred from elect	0000166 // nucleotide binding // inferred	96433	
0006468 // protein amino acid phosphorylatio	0016020 // membrane // inferred from elect	0000166 // nucleotide binding // inferred	96433	
0000060 // protein import into nucleus, transl	0005634 // nucleus // inferred from electron	0000166 // nucleotide binding // inferred	87986 /// 87986	
0000060 // protein import into nucleus, transl	0005634 // nucleus // inferred from electron	0000166 // nucleotide binding // inferred	87986 /// 87986	
0002053 // positive regulation of mesenchym	0005634 // nucleus // inferred from direct as	0004871 // signal transducer activity // in	---	
0002052 // positive regulation of neuroblast p	0005634 // nucleus // inferred from direct as	0005515 // protein binding // inferred fro	1328321	
0008654 // phospholipid biosynthetic process	0005739 // mitochondrion // inferred from e	0004609 // phosphatidylserine decarboxyl	2445114	
0008654 // phospholipid biosynthetic process	0005739 // mitochondrion // inferred from e	0004609 // phosphatidylserine decarboxyl	1914026 /// 1914026 /// 1914026	
0008654 // phospholipid biosynthetic process	0005739 // mitochondrion // inferred from e	0004609 // phosphatidylserine decarboxyl	1914026 /// 1914026	
0008654 // phospholipid biosynthetic process	0005739 // mitochondrion // inferred from e	0004609 // phosphatidylserine decarboxyl	1914026 /// 1914026	
0008654 // phospholipid biosynthetic process	0005783 // endoplasmic reticulum // inferre	0000287 // magnesium ion binding // infe	1921846	
0008654 // phospholipid biosynthetic process	0005783 // endoplasmic reticulum // inferre	0000287 // magnesium ion binding // infe	1921846	
0008152 // metabolic process // inferred from	0005737 // cytoplasm // inferred from direc	0004620 // phospholipase activity // infer	1919144	
0006644 // phospholipid metabolic process //	0005576 // extracellular region // inferred fr	0004623 // phospholipase A2 activity // in	101899	
0000910 // cytokinesis // inferred from electr	0005622 // intracellular // inferred from elec	0000166 // nucleotide binding // inferred	---	
0000910 // cytokinesis // inferred from electr	0005622 // intracellular // inferred from elec	0000166 // nucleotide binding // inferred	107926	
0001701 // in utero embryonic development /	0005634 // nucleus // inferred from direct as	0003676 // nucleic acid binding // inferred	1096360	
0001701 // in utero embryonic development /	0005634 // nucleus // inferred from direct as	0003676 // nucleic acid binding // inferred	1096360	
0007601 // visual perception // inferred from	0016020 // membrane // inferred from elect	---	1096360	
0007601 // visual perception // inferred from	0016020 // membrane // inferred from elect	---	1096360	

Supplementary Table II

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	mmu03010:Ribosome	18	2.17918	3.85E-08	RPL18,RPS9,RPS4X,RPS5,RPS7,RPS3,RPS25,RPS27,RPL7,RPL23,RPL18A,RPS17,RPLP0,RPLP1,RPS15,RPL11,RPL12,RPS21	225	89	5738	5.157752809	5.82E-06	5.82E-06	4.61E-05
BIOCARTA	m_igf1rPathway:Multiple antiapoptotic pathways from IGF-1R signaling lead to BAD phosphorylation	5	0.60533	0.004093	IGF1R,GRB2,RAF1,BAD,IRS1	44	19	1171	7.003588517	0.36308614	0.3630861	4.527815
KEGG_PATHWAY	mmu04510:Focal adhesion	16	1.93705	0.010107	MYL7,ROCK2,GRB2,MYLK3,RAF1,BAD,MAPK10,FLNC,IGF1R,PPP1CA,LAMB3,CCND2,ITGB6,LAMB1-1,EGF,COL11A1	225	198	5738	2.060785634	0.78430494	0.5355702	11.43605
KEGG_PATHWAY	mmu04910:Insulin signaling pathway	12	1.45278	0.018519	PPP1R3D,PPP1CA,EIF4EBP1,PHKB,PYGL,GRB2,PRKAG1,FASN,RAF1,MAPK10,BAD,IRS1	225	138	5738	2.217584541	0.94054618	0.6097048	20.02652
BIOCARTA	m_igf1Pathway:IGF-1 Signaling Pathway	4	0.48426	0.038674	IGF1R,GRB2,RAF1,IRS1	44	21	1171	5.069264069	0.98694498	0.8857414	35.9574
BIOCARTA	m_il2rbPathway:IL-2 Receptor Beta Chain in T cell Activation	5	0.60533	0.039473	GRB2,RAF1,JAK1,BAD,IRS1	44	36	1171	3.696338384	0.98808577	0.7716039	36.55606
KEGG_PATHWAY	mmu00564:Glycerophospholipid metabolism	7	0.84746	0.045646	DGKZ,PCYT1A,PISD,CDS1,CHPT1,PLA2G4E,PLA2G5	225	67	5738	2.664411277	0.99913676	0.8285912	42.79696

Supplementary Table III: Boolean descriptive index

Descriptive logic (1-2-3-4-5)

- this describes the comparisons performed and number (1-5) indicates each comparison

o 1 = capi3k/dnpi3k Sham vs. Ntg Sham
o 2 = capi3k/dnpi3k MI vs. Ntg MI
o 3 = Sham only (i.e. significant only in sham)
o 4 = MI only (i.e. significant only in MI)
o 5 = Sham and MI (significant in both)

1 = Boolean descriptor for presence (being significant and present) of pattern of interest and A, B, C, D = pattern where necessary. (0 = absence of pattern/significance).

- A = up-down (reciprocal)
- B = down-up (reciprocal)
- C = up-up (uni-directional)
- D = down-down (uni-directional)

IDENTIFIER	Descriptive_logic(1-2-3-4-5)
0610009B22Rik	'01A000'
0610009L18Rik	'01A000'
Asb5	'01A000'
Bphl	'01A000'
Cacybp	'01A000'
Chpt1	'01A000'
Dhx32	'01A000'
Gm410	'01A000'
Hspe1	'01A000'
LOC100044161 /// Sema3a	'01A000'
Lyrm5	'01A000'
Ormdl1	'01A000'
Amn1	'01A001A'
Cops7b	'01A001A'
Skp1a	'01A001A'
1700025G04Rik /// LOC545371	'01B000'
Ahnak	'01B000'
B4galt6 /// LOC675709	'01B000'
Ccnd2	'01B000'
Etv5	'01B000'
Fgl2	'01B000'
Gnptab	'01B000'
Hn1	'01B000'
Ik	'01B000'
LOC100046056 /// Pbxip1	'01B000'
Ndrg4	'01B000'
Tac1	'01B000'
Tmbim1	'01B000'
Upp1	'01B000'

Gcnt2	'01B001B'
Myo1c	'01B001B'
Nrd1	'01B001B'
Rab17	'01B001B'
Rusc2	'01B001B'
Spats1	'01B001B'
4921527H02Rik	'01C000'
4930534B04Rik	'01C000'
Aen	'01C000'
Ard1a	'01C000'
Atp5o /// LOC100047429	'01C000'
Bbox1	'01C000'
Ckap2l	'01C000'
Cmtm8	'01C000'
Cnot2	'01C000'
Dynlrb1	'01C000'
Gstm5	'01C000'
L2hgdh	'01C000'
LOC100047123	'01C000'
LOC100049077	'01C000'
Mapbpip	'01C000'
Mipol1	'01C000'
Mrpl35	'01C000'
Mrpl48	'01C000'
Myl7	'01C000'
Naif1	'01C000'
Prkag1	'01C000'
Prps1	'01C000'
Ptgfr	'01C000'
Sec14l4	'01C000'
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