

Table 4.2. Biological Pathway Analysis Criteria.
Criteria used for transcriptome analyses using Ingenuity Pathway Analysis.

			3h Comparison	
Tool	Criteria	Individual	Shared	Contrasting
Canonical pathways	z-score	• ≥1 or ≤-1	<ul style="list-style-type: none"> • same direction • one z-score ≥1 or ≤-1 • other ≥0.5 or ≤-0.5 	<ul style="list-style-type: none"> • opposing direction • one z-score ≥1/≤-1 • other ≥0.5/≤-0.5
	p-value	• p<0.1	• at least one z-score ≥1 or ≤-1 and p<0.05	<ul style="list-style-type: none"> • if only one z-score ≥1/≤-1, both z-scores p<0.05 • if both z-scores ≥1/≤-1, at least one p<0.05
Diseases and bio functions	z-score	• ≥2 or ≤-2	<ul style="list-style-type: none"> • same direction • one z-score ≥1 or ≤-1 • other ≥1.5/≤-1.5 	<ul style="list-style-type: none"> • opposing direction for both OR only appeared in one dataset • at least one z-score ≥1.5/≤-1.5 • other ≥1/≤-1
	p-value	• p<0.05	• at least one z-score is p<0.05	<ul style="list-style-type: none"> • if both z-scores meet criteria, both p<0.05 • if only appeared in one dataset, p<0.05
Regulator effects	Consistency score	<ul style="list-style-type: none"> • ≥2 or ≤-2 • Focus: top 10 dysregulated genes that meet consistency score 	<ul style="list-style-type: none"> • ≥2 or ≤-2 (both datasets) • if meet other criteria below, focus on (up to) top 20+/- up/down z-scores 	<ul style="list-style-type: none"> • ≥2 or ≤-2 (both datasets) • if meet other criteria below, focus on (up to) top 20+/- up/down z-scores (opposing or one, only)
	Known regulator-disease/ function relationship	• ≥20%	• ≥20% (if node total ≤25)	• ≥20% (if node total ≤25)
	Node total	• ≥25 <i>except</i> 48h (no limit)	• ≥25 (Known regulator... is ≤20%)	• ≥25 (Known regulator... is <20%)
Upstream regulators	z-score	• ≥2 or ≤-2	<ul style="list-style-type: none"> • same direction • one z-score is ≥0.8/≤-0.8 • other ≥2/≤-2 • focus on (up to) top 20+/- up/down z-scores meeting criteria, keep those appearing in top 20 of both datasets 	<ul style="list-style-type: none"> • opposing direction or only one dataset • one ≥1/≤-1 • other ≥1.5/≤-1.5 • focus on (up to) top 20+/- up/down z-scores meeting criteria
	p-value	• p<0.05	• both p<0.05	<ul style="list-style-type: none"> • if only appeared in one dataset, p≤0.05 • if both, one ≥1.5/≤-1.5and p≤0.05
Molecules	Fold-change	• top 10 up/down-regulated	<ul style="list-style-type: none"> • top 10 up/down-regulated each dataset • remove any not in top 20 of both datasets 	-

		3v48h	
Tool	Criteria	Shared	Contrasting
Canonical pathways	z-score	<ul style="list-style-type: none"> • same direction for all • two z-scores ≥1/≤-1 • other ≥0.5/≤-0.5 	<ul style="list-style-type: none"> • time points opposing direction of z-score or appear only at one time point • for 3h: one ≥1/≤-1, other ≥0.5/≤-0.5 • for 48h: if ≥1/≤-1, both 3h p>0.05 and ≤1/≥-1 or meet above criteria for 3h
	p-value	• at least one z-score ≥1/≤-1 and p<0.05	<ul style="list-style-type: none"> • if only one z-score is ≥1/≤-1, both p<0.05 • if both z-scores are ≥1/≤-1, only one p<0.05
Diseases and bio functions	z-score	<ul style="list-style-type: none"> • same direction for all • one ≥1/≤-1 • other ≥1.5/≤-1.5 	<ul style="list-style-type: none"> • time points opposing direction of z-score or appear only at one time point • for 3h: one ≥1/≤-1, other ≥1.5/≤-1.5 • for 48h: ≥1.5/≤-1.5 and p<0.05
	p-value	• at least one z-score ≥1/≤-1 is p<0.05	<ul style="list-style-type: none"> • if both z-scores meet criteria, at least one p≤0.05 • if only appeared in one dataset, p<0.05
Regulator effects	Consistency score	<ul style="list-style-type: none"> • ≥2 or ≤-2 (both datasets, same direction) • if meet other criteria below, focus on (up to) top 20+/- up/down z-scores 	<ul style="list-style-type: none"> • ≥2 or ≤-2 (both datasets, opposing direction) • if meet other criteria below, focus on (up to) top 20+/- up/down z-scores (opposing or one time point, only)
	Known regulator-disease/ function relationship	• ≥20%	• ≥20%
	Node total	-	-
Upstream regulators	z-score	<ul style="list-style-type: none"> •same direction for all • one z-score is ≥0.8/≤-0.8 • others are ≥1/≤-1 • focus on (up to) top 20+/- up/down z-scores meeting criteria 	<ul style="list-style-type: none"> • opposing direction 3v48h • one is ≥0.8/-0.8 • one 1/≤-1 • other ≥1.5/≤-1.5 • focus on (up to) top 20+/- up/down z-scores meeting criteria
	p-value	• at least two datasets p<0.05	• at least two datasets p<0.05
Molecules	Fold-change	<ul style="list-style-type: none"> • top 10 up/down-regulated (each dataset) • same response (up/down) for fold-change • remove any not in top 20 for each individual dataset 	-

Table 4.7: PCR Array Analysis.

The array was comprised of 44 genes of interest normalized to two housekeeping genes. Gene names and symbols from the National Institute of Health (NIH) National Center of Biotechnology (NCBI) database, June 2015. Functions from NCBI, UniProt, Genecards, and published literature. Data are presented as fold change (exercise vs control leg, mean±SEM) and were analyzed as ΔΔC_t using repeated measures ANOVA, with significance based on false discovery rate: * p<0.002, effect of exercise.

Gene symbol	Gene name	Refseq ID	Primary function	Other functions	Fold change	p-value
CASP9	Caspase 9, apoptosis-related cysteine peptidase	NM_001229	Apoptosis	-	1.17±0.18	0.81
MAPK8	Mitogen-activated protein kinase 8 (JNK)	NM_002750		Hyperalgesia	1.08±0.12	0.47
JUN	Jun proto-oncogene	NM_002228	Cell cycle	-	0.94±0.08	0.47
PRKCZ	Protein kinase C, zeta	NM_002744		Inflammation Hyperalgesia	1.21±0.19	0.65
RASA1	RAS p21 protein activator (GTPase activating protein) 1	NM_002890		Inflammation	1.06±0.10	0.91
REL	V-rel avian reticuloendotheliosis viral oncogene homolog	NM_002908		Inflammation	1.02±0.14	0.69
HSPA4	Heat shock 70kDa protein 4	NM_002154		Muscle stress response	1.34±0.10	0.03
AKT2	V-akt murine thymoma viral oncogene homolog 2	NM_001626		Myogenesis	1.14±0.22	0.74
CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_000389			2.85±0.67	0.01
IGF1	Insulin-like growth factor 1 (somatomedin C)	NM_000618		Myogenesis Hyperalgesia	1.16±0.17	0.79
MTOR	Mechanistic target of rapamycin	NM_004958			1.14±0.16	0.84
PDK2	Pyruvate dehydrogenase kinase, isozyme 2	NM_002611			0.82±0.13	0.13
PTEN	Phosphatase and tensin homolog	NM_000314		Myogenesis Inflammation Hyperalgesia	1.28±0.14	0.09
AKT1 *	V-akt murine thymoma viral oncogene homolog 1	NM_005163			1.51±0.07	0.00
MAP2K1 *	Mitogen-activated protein kinase kinase 1	NM_002755			2.48±0.36	0.00
MAPK1	Mitogen-activated protein kinase 1	NM_002745			1.26±0.12	0.04
MAPK3	Mitogen-activated protein kinase 3	NM_002746			1.50±0.43	0.88
PDPK1	3-phosphoinositide dependent protein kinase 1	NM_002613			1.20±0.08	0.13
PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	NM_006218			1.26±0.13	0.1
PIK3CG	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma	NM_002649			1.51±0.31	0.3
PIK3R3	Phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_003629			0.94±0.19	0.26
PRKAR1B	Protein kinase, cAMP-dependent, regulatory, type I, beta	NM_002735			1.39±0.32	0.98
RHEB	Ras homolog enriched in brain	NM_005614			1.19±0.10	0.22
PPP3CA	Protein phosphatase 3, catalytic subunit, alpha isozyme	NM_000944		Myogenesis Inflammation Apoptosis	1.04±0.15	0.74
CAMK1	Calcium/calmodulin-dependent protein kinase I	NM_003656		Myogenesis Nitric oxide signaling	1.11±0.15	0.86
CHUK	Conserved helix-loop-helix ubiquitous kinase	NM_001278	Inflammation	-	1.23±0.30	0.67
CCL2	Chemokine (C-C motif) ligand 2	NM_002982		Hyperalgesia	2.29±0.66	0.4
NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NM_020529			1.17±0.14	0.46
PTGS2	Prostaglandin-endoperoxide synthase 2	NM_000963		Cell cycle Myogenesis Hyperalgesia	1.35±0.52	0.44
MAPK14	Mitogen-activated protein kinase 14 (p38 MAPK)	NM_001315			1.11±0.09	0.87
ACTA1	Actin, alpha 1, skeletal muscle	NM_001100	Muscle structure	-	0.99±0.05	0.77
COL4A1	Collagen, type IV, alpha 1	NM_001845			1.14±0.20	0.95
DES	Desmin	NM_001927			1.17±0.11	0.37
PXN	Paxillin	NM_002859			1.24±0.12	0.16
FOXO1	Forkhead box O1	NM_002015	Myogenesis	-	1.35±0.24	0.23
DLG4	Discs, large homolog 4 (Drosophila)	NM_001365	Nitric oxide signaling	-	1.11±0.21	0.72
NOS1	Nitric oxide synthase 1 (neuronal)	NM_000620			1.06±0.27	0.35
NOS3	Nitric oxide synthase 3 (endothelial cell)	NM_000603		Hyperalgesia	1.03±0.22	0.5
FIGF	C-fos induced growth factor (vascular endothelial growth factor D)	NM_004469	Vascular health and angiogenesis	-	1.60±0.15	0.02
FLT1	Fms-related tyrosine kinase 1	NM_002019			0.99±0.11	0.66
FLT4	Fms-related tyrosine kinase 4	NM_002020			1.22±0.32	0.66
VEGFA	Vascular endothelial growth factor A	NM_003376			0.83±0.16	0.15
VEGFB	Vascular endothelial growth factor B	NM_003377			1.16±0.13	0.4
VEGFC	Vascular endothelial growth factor C	NM_005429			1.35±0.35	0.75

Table 5.1: *In Silico* Expression Profile Analysis.

CCL2, chemokine (C-C motif) ligand 2; CXCL1 chemokine (C-X-C motif) ligand 1; CXCL10, chemokine (C-X-C motif) ligand 10; CXCL2, chemokine (C-X-C motif) ligand 2; IKBKB, inhibitor of kappa light polypeptide gene enhancer in B-cells, kinas beta; IL18, interleukin-18; IL1R1, interleukin-1 receptor 1; IL6, interleukin-6; IL6R, interleukin-6 receptor; MAP3K14, mitogen activated kinase kinase kinase 14 (NIK); MAP3K8, mitogen activated kinase kinase kinase 8 (COT); NFKBIA, nuclear ;; NGF, nerve growth factor; NGFR (p75^{NTR}), nerve growth factor receptor; NTRK1 (TrkA), neurotrophin receptor kinase 1; TGFB1, transforming growth factor beta 1; TRAF6, TNF receptor-associated factor 6.

	Muscle			Smoking			Pain		
Target	Muscle response	GEO identifiers	Models	Smoking response	GEO identifiers	Models	Pain response	GEO identifiers	Models
CCL2	Elevated	GDS236, GDS394, GDS638, GDS639, GDS641, GDS703, GDS2701	Eccentric/isometric contractions; MDX (regeneration, diaphragm, hindlimb muscles, skeletal muscle profiles, extraocular and leg muscle); contraction/freeze-injured muscle	Elevated	GDS3746, GDS5061, GDS5062	Tracheal explants; nasal respiratory epithelium; lung parenchyma	Elevated	GDS2664, GDS3605	Peripheral nerve injury; spared nerve injury (dorsal root ganglion; dornal horn spinal cord)
CXCL1	Elevated	GDS394, GDS638, GDS703	Eccentric/isometric contractions; MDX (diaphragm, extraocular and leg muscles)	Suppressed	GDS3493	Bronchial epithelial cells			
				Elevated	GDS5061	Nasal respiratory epithelium			
CXCL10	No difference	GDS236, GDS2153	MDX (regeneration); dermatomyositis	Elevated	GDS3493, GDS3746	Bronchial epithelial cells; tracheal explants			
	Elevated	GDS2158, GDS2701	Emery-Dreifuss dystrophy model; contraction/freeze-injured muscle						
CXCL2	Elevated	GDS394, GDS2701	Eccentric/isometric contractions; contraction/freeze-injured muscle (elevated freeze only)	Elevated	GDS2194, GDS3494, GDS5061, GDS5062	Lung response; bronchial epithelial cells; nasal respiratory epithelium; lung parenchyma			
	Suppressed	GDS4843	Tibial muscular dystrophy	Suppressed	GDS3493, GDS3494	Bronchial epithelial cells			
IKBKB				Suppressed	GDS3746	Tracheal explants			
IL18				Elevated	GDS5061, GDS2194	Nasal respiratory epithelium; lung	Elevated	GDS2664, GDS3605	Peripheral nerve injury; spared nerve injury (dorsal root ganglion; dornal horn spinal cord)
IL1A				Suppressed (early)/elevated (later)	GDS3493	Bronchial epithelial cells			
IL1B	Elevated; established in literature			Suppressed	GDS3493	Bronchial epithelial cells	Elevated; established in literature		
				Elevated	GDS1348, GDS3493, GDS3494	Bronchial epithelial cells			
IL1R1	Elevated	GDS2153	Dematomyositis						
IL6	Elevated	GDS614; literature	MDX (extraocular muscle)	Suppressed	GDS3493	Bronchial epithelial cells	Elevated; established in literature		
	No difference			Elevated	GDS5061	Nasal respiratory epithelium			
IL6R	Elevated	GDS2158; literature	Emery-Dreifuss dystrophy model; eccentric exercise	Elevated	GDS3054, GDS3493, GDS3494, GDS3706, GDS5061	Buccal epithelium; bronchial epithelial cells; lung fibroblasts; nasal respiratory epithelium	No difference	GDS3605	Spared nerve injury (dornal horn spinal cord)
	No difference	GDS2153	Dematomyositis						
MAP3K14	No difference	GDS611	Duchenne muscular dystrophy	Elevated	GDS3493	Bronchial epithelial cells			
MAP3K8	No difference	GDS2153	Dermatomyositis	Elevated	GDS3309, GDS3494	Bronchial epithelial cells	No difference	GDS3605	Spared nerve injury (dornal horn spinal cord)
NFKBIA	Elevated	GDS394, GDS2153	Eccentric/isometric contractions; dermatomyositis	Elevated	GDS1348, GDS3493, GDS3494, GDS4609, GDS5061	Bronchial epithelial cells; lungs (second-hand); nasal respiratory epithelium			
	Suppressed	Literature	Eccentric contractions (early)	Suppressed	GSD3493	Bronchial epithelial cells			
NGF	Suppressed (trend)	GDS2153	Dermatomyositis	Elevated; established in literature			Elevated; established in literature		
	Elevated	GDS2701	Contraction/freeze-injured muscle (contraction only)						
NGFR (p75 ^{NTR})	No difference	GDS2153	Dermatomyositis	Suppressed	GDS3746	Tracheal explants	Elevated	GDS3605	Spared nerve injury (dornal horn spinal cord)
				Elevated	GDS5061	Nasal respiratory epithelium			
NTRK1 (TrkA)	Suppressed	GDS2153	Dermatomyositis				No difference	GDS3605	Spared nerve injury (dornal horn spinal cord)
TGFB1	Elevated	GDS394, GDS639	Eccentric/isometric contractions; MDX (hindlimb muscles)	Elevated (trend)	GDS5061	Nasal respiratory epithelium	Elevated	GDS3605	Spared nerve injury (dornal horn spinal cord)
	Suppressed	GDS639, GDS1247, GSD2996	MDX (hindlimb muscles); dystrophy (dysferlin deficiency, cardiac muscle; dystrophin deficiency, cardiac muscle)						
TRAF6	Elevated	GDS2153	Dermatomyositis	Elevated	GDS3493, GDS5061	Bronchial epithelial cells; nasal respiratory epithelium			
	Suppressed		Dystrophy (dysferlin deficiency, skeletal muscle)						

Table 5.5: Gene Expression after Eccentric Exercise.

Arrays were comprised of 44 genes of interest, normalized to two housekeeping genes. Gene names and symbols from the National Institute of Health (NIH) National Center of Biotechnology (NCBI) database, June 2015. Functions from NCBI, UniProt, Genecards, and published literature. Data are presented as fold change (exercise vs control leg) and were analyzed as ΔΔC_t using repeated measures ANOVA, with significance based on false discovery rate (FDR): * p<0.007, effect of exercise; § p<0.003, interaction (group*exercise). No genes were significant (p<0.002) for the effect of group (smoke).

					Fold change		Significance (p-value)		
Gene symbol	Gene name	Refseq ID	Primary function	Other functions	Non-smokers	Smokers	Smoke	Exercise	Exercise*Smoke
CASP9	Caspase 9, apoptosis-related cysteine peptidase	NM_001229	Apoptosis	-	1.17±0.18	0.75±0.12	0.36	0.16	0.09
MAPK8	Mitogen-activated protein kinase 8 (JNK)	NM_002750		Hyperalgesia	1.08±0.12	0.68±0.06	0.78	0.02	0.01
JUN	Jun proto-oncogene	NM_002228	Cell cycle	-	0.94±0.08	1.23±0.30	0.13	0.75	0.64
REL	V-rel avian reticuloendotheliosis viral oncogene homolog	NM_002908		Inflammation	1.02±0.14	0.79±0.14	0.56	0.08	0.22
PRKCZ	Protein kinase C, zeta	NM_002744		Inflammation Hyperalgesia	1.21±0.19	1.25±0.28	0.46	0.64	0.87
RASA1	RAS p21 protein activator (GTPase activating protein) 1	NM_002890			1.06±0.10	0.91±0.07	0.73	0.4	0.33
HSPA4	Heat shock 70kDa protein 4	NM_002154		Muscle stress response	1.34±0.10	0.93±0.07	0.22	0.2	0.01
AKT2	V-akt murine thymoma viral oncogene homolog 2	NM_001626		Myogenesis	1.14±0.22	0.81±0.11	0.93	0.21	0.45
CDKN1A *	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	NM_000389			2.85±0.67	3.25±1.12	0.77	0.00*	0.76
IGF1	Insulin-like growth factor 1 (somatomedin C)	NM_000618			1.16±0.17	0.95±0.14	0.61	0.65	0.38
MTOR	Mechanistic target of rapamycin	NM_004958		Myogenesis Hyperalgesia	1.14±0.16	0.82±0.09	0.43	0.27	0.15
PDK2 *	Pyruvate dehydrogenase kinase, isozyme 2	NM_002611			0.82±0.13	0.59±0.07	0.66	0.00 *	0.2
PTEN	Phosphatase and tensin homolog	NM_000314			1.28±0.14	0.94±0.10	0.71	0.61	0.07
PPP3CA	Protein phosphatase 3, catalytic subunit, alpha isozyme	NM_000944		Myogenesis Inflammation Apoptosis	1.04±0.15	0.65±0.06	0.34	0.01	0.03
AKT1 *	V-akt murine thymoma viral oncogene homolog 1	NM_005163		Myogenesis Inflammation Hyperalgesia	1.51±0.07	1.21±0.10	0.53	0.00 *	0.02
MAP2K1 *	Mitogen-activated protein kinase kinase 1	NM_002755			2.48±0.36	2.05±0.36	0.74	0.00 *	0.3
MAPK1	Mitogen-activated protein kinase 1	NM_002745			1.26±0.12	1.01±0.07	0.69	0.15	0.1
MAPK3	Mitogen-activated protein kinase 3	NM_002746			1.50±0.43	0.58±0.13	0.99	0.08	0.13
PDPK1 §	3-phosphoinositide dependent protein kinase 1	NM_002613			1.20±0.08	0.85±0.06	0.94	0.84	0.00 §
PIK3CA	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit alpha	NM_006218			1.26±0.13	1.06±0.11	0.81	0.17	0.22
PIK3CG	Phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic subunit gamma	NM_002649			1.51±0.31	1.28±0.24	0.16	0.36	0.49
PIK3R3	Phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	NM_003629			0.94±0.19	0.70±0.09	0.59	0.02	0.29
PRKAR1B	Protein kinase, cAMP-dependent, regulatory, type I, beta	NM_002735			1.39±0.32	0.57±0.08	0.45	0.08	0.08
RHEB	Ras homolog enriched in brain	NM_005614			1.19±0.10	0.94±0.13	0.42	0.97	0.09
CAMK1	Calcium/calmodulin-dependent protein kinase I	NM_003656		Myogenesis Nitric oxide signaling	1.11±0.15	0.89±0.11	0.17	0.4	0.28
CHUK	Conserved helix-loop-helix ubiquitous kinase	NM_001278	Inflammation	-	2.29±0.66	0.51±0.13	0.41	0.16	0.02
MAPK14	Mitogen-activated protein kinase 14 (p38 MAPK)	NM_001315		Cell cycle Myogenesis Hyperalgesia	1.11±0.09	0.89±0.06	0.63	0.54	0.08
CCL2	Chemokine (C-C motif) ligand 2	NM_002982		Hyperalgesia	1.23±0.30	0.78±0.19	0.3	0.13	0.33
NFKBIA	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	NM_020529			1.17±0.14	0.91±0.14	0.21	0.6	0.16
PTGS2	Prostaglandin-endoperoxide synthase 2	NM_000963			1.35±0.52	0.68±0.14	0.59	0.07	0.46
ACTA1 * §	Actin, alpha 1, skeletal muscle	NM_001100	Muscle structure	-	0.99±0.05	0.76±0.04	0.39	0.00 *	0.00 §
COL4A1	Collagen, type IV, alpha 1	NM_001845			1.14±0.20	1.06±0.21	0.1	0.6	0.71
DES	Desmin	NM_001927			1.17±0.11	0.82±0.07	0.18	0.39	0.02
PXN	Paxillin	NM_002859			1.24±0.12	0.95±0.10	0.51	0.7	0.1
FOXO1	Forkhead box O1	NM_002015	Myogenesis	-	1.35±0.24	0.75±0.14	0.32	0.31	0.02
DLG4	Discs, large homolog 4 (Drosophila)	NM_001365	Nitric oxide signaling	-	1.11±0.21	0.62±0.08	0.89	0.03	0.11
NOS1	Nitric oxide synthase 1 (neuronal)	NM_000620			1.06±0.27	0.63±0.14	0.9	0.03	0.31
NOS3	Nitric oxide synthase 3 (endothelial cell)	NM_000603		Hyperalgesia	1.03±0.22	0.84±0.13	0.52	0.12	0.5
FIGF §	C-fos induced growth factor (vascular endothelial growth factor D)	NM_004469	Vascular health and angiogenesis	-	1.60±0.15	0.89±0.13	1	0.24	0.00 §
FLT1	Fms-related tyrosine kinase 1	NM_002019			0.99±0.11	0.75±0.08	0.78	0.02	0.08
FLT4	Fms-related tyrosine kinase 4	NM_002020			1.22±0.32	0.75±0.15	0.28	0.11	0.31
VEGFA *	Vascular endothelial growth factor A	NM_003376			0.83±0.16	0.48±0.07	0.24 *	0	0.1
VEGFB	Vascular endothelial growth factor B	NM_003377			1.16±0.13	0.72±0.07	0.39	0.1	0.01
VEGFC	Vascular endothelial growth factor C	NM_005429			1.35±0.35	0.67±0.12	0.89	0.11	0.23