Additional	Data File	5			
	In situ component				
Gene		of DCIS-IDC x pure			
Symbol	Gene ID	DCIS (Fold Change)	Functional Process		
ADFP	123	-2.79	unknown		
A1 N4O4	70.40	2.0	visual perception, sensory perception of		
ALMS1	7840	-3.8	sound, response to stimulus cell division, ubiquitin cycle, cell cycle,		
ANAPC13	25847	-2.19	mitosis,		
ANKRD6	22881	-2.01	unknown		
			regulation of protein secretion,		
			intracellular protein transport,		
ARFIP1	27236	-2.55	biological_process		
ARHGAP19	84986	-2.2	signal transduction		
ARHGAP9	64333	-2.92	signal transduction		
ATF2	1386	-2.07	transcription, regulation of transcription, DNA-dependent,		
BCHE	590	-2.62	cocaine metabolic process		
BIN2	51411	-2.08	unknown		
BOP1	23246	-2.1	rRNA processing		
C10orf26	54838	-4.06	unknown		
C13orf23	80209	2.41	unknown		
C13orf24	10464	-2.49	unknown		
			apoptotic program, tumor necrosis factor- mediated signaling pathway, biological_process, induction of apoptosis, DNA damage response, signal transduction by p53 class mediator		
C16orf5	29965	-5.45	resulting in induction of apoptosis		
C1orf66	51093	-5.32	unknown		
C20orf23	55614	-3.6	microtubule-based movement, cell communication,		
C20orf42	55612	-4.26	cell adhesion		
C3AR1	719	-3.04	inflammatory response, G-protein coupled receptor protein signaling pathway, elevation of cytosolic calcium ion concentration, cell motility, signal transduction, chemotaxis, smooth muscle contraction, blood circulation,		
C7orf24	79017	2.12	unknown		
CAS	764	-2.18	ane-carbon compound metabolic presses		
CA3 CAMP	761 820	-2.18 -2.84	one-carbon compound metabolic process defense response to bacterium		
CAIVIP	620	-2.04	четенье тевронѕе то растенит		
CAV1	857	-2.08	cholesterol transport, vesicle organization and biogenesis, cholesterol homeostasis, regulation of blood coagulation,		
CCT5	22948	2.4	protein folding		
CDC45L	8318	-2.9	DNA replication initiation, DNA replication, cell cycle, DNA replication checkpoint,		

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			regulation of membrane potential,
			synaptic transmission, cholinergic, signal transduction, muscle contraction, cation
CHRNB1	1140	-5.11	transport
OTIKINDI	1140	0.11	carbohydrate metabolic process, cell
CHST10	9486	-5.07	adhesion,
CIRBP	1153	-2.04	response to cold
CLINT1	9685	-2.5	endocytosis
CLINTT	9000	-2.5	endocytosis
			protein compley accombly anotomical
			protein complex assembly, anatomical structure morphogenesis, receptor-
			mediated endocytosis, intracellular protein
CLTCL1	8218	-2.07	transport, vesicle-mediated transport
		-	cell-matrix adhesion, phosphate transport,
COL17A1	1308	-2.52	epidermis development
			lipid metabolic process, vesicle-mediated
CPNE3	8895	-2.38	transport,
			glucose metabolic process, lipid
			metabolic process, eating behavior,
			transport, regulation of insulin secretion,
			fatty acid beta-oxidation, fatty acid
CPT1A	1374	-2.06	metabolic process
CTSZ	1522	-2.21	proteolysis
CTTNDDONI	FF047	4.04	a line assum
CTTNBP2NL	55917	-4.84	unknown
			inflammatory response, G-protein coupled receptor protein signaling
			pathway, immune response, signal
			transduction, chemotaxis, cell-cell
CXCL9	4283	2.7	signaling, cellular defense response
DHRS12	79758	-2.45	metabolic process
DHX35	60625	-3.07	RNA splicing, mRNA processing,
			1 3, 1 3,
			elevation of cytosolic calcium ion
			concentration, heart development, brain
			development, signal transduction, small
EPOR	2057	-2.99	GTPase mediated signal transduction
			protein transport, positive regulation of
			anti-apoptosis, activation of NF-kappaB
			transcription factor, multicellular
			organismal development, I-kappaB
	00005	0.00	phosphorylation, regulation of
ERC1	23085	-3.86	transcription, DNA-dependent
			biological_process, mesodermal cell fate
			specification, metabolic process,
			multicellular organismal development, transcription, regulation of transcription,
ETNK2	55224	-2.23	DNA-dependent
EYA2	2139	-2.08	multicellular organismal development
FAM40B	57464	-2.77	unknown
	σ. 10 T		2
FCGR2B	2213	-3.39	immune response, signal transduction,
FCGR3A	2214	-2.7	immune response
			opsonization, phosphate transport, signal
FCN1	2219	-3.79	transduction
FN3K	64122	-6.3	fructoselysine metabolic process
CDCT4	26204	4.06	glycolipid biosynthetic process,
GBGT1	26301	-4.06	carbohydrate metabolic process,

			G-protein coupled receptor protein
GIPC1	10755	-2.74	signaling pathway
			5 51 7
			neuropeptide signaling pathway,
			photoreceptor cell maintenance, cell-cell
			adhesion, sensory perception of sound,
			signal transduction, neurological system
			process, nervous system development,
GPR98	84059	-2.21	maintenance of organ identity, ,
HN1	51155	2.3	unknown
			regulation of apoptosis, caspase
			activation, transcription, regulation of
IFT57	55081	-3.3	transcription, DNA-dependent,
IMMT	10989	-2.92	biological_process
INOC1	54617	-2.11	chromatin remodeling
			immune response, myeloid cell
			differentiation, negative regulation of
			transcription from RNA polymerase II
			promoter, transcription, regulation of
IRF8	3394	-4.33	transcription, DNA-dependent
			neutrophil chemotaxis, inflammatory
			response, apoptosis, cell-matrix adhesion,
			leukocyte adhesion, cell-cell signaling,
			cell adhesion, regulation of peptidyl-
ITGB2	3689	-3.27	tyrosine phosphorylation, ,
ITPKC	80271	-3.26	unknown
	40004	0.40	ubiquitin cycle, striated muscle
KBTBD10	10324	-2.42	contraction,
			transmembrane receptor protein tyrosine
			kinase signaling pathway, protein amino
			acid phosphorylation, cell differentiation,
KDD	0704	2.55	angiogenesis, multicellular organismal
KDR	3791	-2.55	development
KIAA0664	23277	-3.45	translation
KIAA0748	9840	-2.38	unknown
KIAA1211	57482	2.3	unknown
KIF1A	547	-2.71	anterograde axon cargo transport, microtubule-based movement,
LETMD1	25875	-2.32	
LETIVIDT	20070	-2.32	unknown protein complex assembly, signal
LPXN	9404	-3.2	transduction, cell adhesion
LRCH2	57631	-2.33	unknown
LTBP3	4054	-2.74	unknown
2.510	1001		cell division, signal transduction, cell
			cycle, cell proliferation, cellular defense
MAPRE2	10982	-2.62	response, mitosis
MARCH8	220972	2.45	immune response, ubiquitin cycle,
MARK3	4140	-4.91	protein amino acid phosphorylation
			transcription, regulation of transcription,
MBD3	53615	-4.58	DNA-dependent,
			transcription, regulation of transcription,
MED10	84246	2.15	DNA-dependent,
	0000	. –	transcription, regulation of transcription,
MGC21874	93624	-4.7	DNA-dependent,
MRPS17	51373	-2.23	transport, translation,
NCDN	23154	-5.19	unknown

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NCOA4	8031	2.34	androgen receptor signaling pathway, transmembrane receptor protein tyrosine kinase signaling pathway, positive regulation of transcription, DNA-dependent, male gonad development, transcription
NEDD9	4739	-6.02	cell division, regulation of cell growth, actin filament bundle formation, signal transduction, cell cycle, cell adhesion, integrin-mediated signaling pathway, cytoskeleton organization and biogenesis,
NGDN	25983	-2.59	rRNA processing, regulation of translation,
NMU	10874	4.12	NMU, neuropeptide signaling pathway, regulation of smooth muscle contraction, digestion, signal transduction,
NOX4	50507	2.35	inflammatory response, cell morphogenesis, cell aging, oxygen and reactive oxygen species metabolic process, superoxide release, negative regulation of cell proliferation
NUP50	10762	-2.5	protein transport, intracellular transport, mRNA transport, intracellular protein transport across a membrane,
OSBPL7	114881	-4.91	steroid metabolic process, lipid transport,
P4HA1	5033	2.2	protein metabolic process
Р4НВ	5034	-3.01	peptidyl-proline hydroxylation to 4- hydroxy-L-proline, cell redox homeostasis,
PCDH10	57575	-3.01	homophilic cell adhesion, cell adhesion,
PCLKC	54825	-2.75	homophilic cell adhesion, cell adhesion, negative regulation of cell growth
PEPD	5184	-3.65	collagen catabolic process, proteolysis, amino acid metabolic process
PHTF1	10745	2.42	transcription, regulation of transcription, DNA-dependent,
PIAS2	9063	-2.43	androgen receptor signaling pathway, ubiquitin cycle, positive regulation of transcription, DNA-dependent, transcription,
PITPNM2	57605	-4.28	metabolic process, transport,
PLEKHC1	10979	-2.05	actin cytoskeleton organization and biogenesis, cell adhesion, regulation of cell shape
PMPCA	23203	-4.2	proteolysis
POLD3	10714	-2.69	mismatch repair, DNA synthesis during DNA repair,
POMGNT1	55624	-2.25	protein amino acid O-linked glycosylation, protein amino acid N-linked glycosylation,

DDM4H	F7400	-2.02	
PPM1H	57460		unknown
PPP2R3A	5523	-2.48	protein amino acid dephosphorylation
PPTC7	160760	-2.92	unknown
PTBP2	58155	2.84	RNA splicing, mRNA processing,
DAD54AD4	40005	2.00	DNA repair, double-strand break repair
RAD51AP1	10635	2.96	via homologous recombination,
RARRES3	5920	-3.64	negative regulation of cell proliferation
101111200	0020	0.01	meiotic recombination, meiosis,
			spermatogenesis, sister chromatid
REC8L1	ND	-3.37	cohesion,
			positive regulation of transcription, signal
			transduction, BMP signaling pathway, cell
RGMB	285704	-2.28	adhesion,
RNF43	54894	-2.23	unknown
RPL3	6122	-4.02	translation
RPL41	6171	-3.52	translation
RSL1D1	26156	-2	translation
RUNDC1	146923	2.76	unknown
SAMD4A	23034	-4.11	positive regulation of translation
			positive regulation of cell proliferation,
			regulation of cell growth, regulation of
			epidermal growth factor receptor activity,
			intracellular signaling cascade, epidermal
			growth factor receptor signaling pathway,
01101	0.40.4	0.54	activation of MAPK activity, positive
SHC1	6464	-2.54	regulation of mitosis
			signal transduction, transcription from RNA polymerase II promoter, multicellular
SKIL	6498	2.34	organismal development
SLC6A20	54716	-3.54	neurotransmitter transport
02007120	34710	0.01	sodium ion transport, ion transport,
SLC9A5	6553	-2.32	regulation of pH
			regulation of transcription from RNA
			polymerase II promoter, chromatin
SMARCA3	ND	-2.84	modification, transcription
			anatomical structure morphogenesis,
			regulation of transcription, DNA-
SOX13	9580	-3.58	dependent,
			extracellular matrix organization and
SDOOKS	0000	2.24	biogenesis, synaptogenesis, regulation of
SPOCK2	9806	-2.24	cell differentiation
			signal transduction, response to oxidative stress, protein amino acid
STK25	10494	-2	phosphorylation
511.20	.0707	<u>-</u>	p.noopnoryidaon
			intracellular protein transport, membrane
STX11	8676	-3.18	fusion, vesicle-mediated transport
			·
			apoptosis, metabolic process, heparan
SULF1	23213	3.92	sulfate proteoglycan metabolic process
SV2B	9899	-2.21	neurotransmitter transport
		· · · · · · · · · · · · · · · · · · ·	synaptic transmission, neurotransmitter
SYN1	6853	-2.97	secretion,

			RNA splicing, transcription from RNA
			polymerase II promoter, mRNA
			processing, transcription, mitosis,
TARDBP	23435	-4.03	regulation of transcription, DNA- dependent
TBC1D9B	23433	-4.03 -2.14	
TRAP1	10131		regulation of Rab GTPase activity
		-3.5 -6	biological_process, protein folding,
TXNDC11	51061		cell redox homeostasis
TXNL2	10539	-4.24	cell redox homeostasis
UBXD1	80700	-3.63	biological_process
			skeletal development, ubiquitin cycle,
UFD1L	7353	-3.01	ubiquitin-dependent protein catabolic
OFDIL	1303	-3.01	process
UTP20	27340	-3.16	negative regulation of cell proliferation
020	27010	00	transcription, regulation of transcription,
ZBTB5	9925	-2.82	DNA-dependent,
			mRNA catabolic process, deadenylation-
			dependent decay, regulation of mRNA
			stability, vasculogenesis, regulation of
ZFP36L1	677	-2.4	translation,
			receptor-mediated endocytosis, vesicle
RABEPK	10244	-4.94	docking during exocytosis,
DUOL	50400	2.42	small GTPase mediated signal
RHOU	58480	-3.12	transduction
			G-protein coupled receptor protein signaling pathway, signal transduction,
GPR77	27202	-2.52	chemotaxis, biological_process,
KCTD15	79047	-2.35	potassium ion transport
ROIDIS	73047	-2.00	transcription, regulation of transcription,
AOF2	23028	-2.46	DNA-dependent,
LSM4	25804	-2.85	RNA splicing, mRNA processing,
	2000 !		immune response, cell surface receptor
IGSF6	10261	2.32	linked signal transduction,
CORO1C	23603	3.05	signal transduction, phagocytosis,
			immune response, antigen processing
AZGP1	563	-2.94	and presentation, cell adhesion
DENND3	22898	-3.51	unknown
DGCR2	9993	-2.96	cell adhesion, organ morphogenesis,
I/DMA	00000	0.00	NLS-bearing substrate import into
KPNA6	23633	-2.32	nucleus, intracellular protein transport,
B4GALT5	9334	-2.77	carbohydrate metabolic process
			transmembrane receptor protein tyrosine
			kinase signaling pathway, collagen fibril
			organization, protein modification process, elastic fiber assembly, blood
LOX	4015	2.01	vessel development, lung development
20/	7010	2.01	protein transport, retrograde transport,
VPS54	51542	-2.25	endosome to Golgi,
			<u> </u>
			signal transduction, negative regulation
FGFBP1	9982	-3.28	of cell proliferation, cell-cell signaling
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			ER to Golgi vesicle-mediated transport,
			intracellular protein transport, membrane
GOSR2	9570	-3.97	fusion