Msig-DB URL:
http://www.gsea-msigdb.org/gsea/msigdb/search.jsp

Gene set URL:
https://www.gsea-msigdb.org/gsea/msigdb/cards/KRAS.LUNG.BREAST_UP.V1_DN

Size of gene set: 141

Gene Set:

ACKR3
ADAMTS20
ADD2
ADGRE1
AKAP6
AKR1B10
ALDH5A1
ALOX12B
AMBN
ANKRD1
APOB
ART1
ATP6V1B1
BDKRB1
C5AR2
CACNA1I
CALCB
CALML3
CALML5
CCDC121
CD248
CD36
CD6
CDH12
CDH16
CLCA2
CLDN8
COBL
COL2A1
COL5A2
CRABP2
CXCL14
CYP21A2
DEFB1
DPT
DTNB
DTX2
EPB41L4A
EPHX2
ERAP2
FGFR3
FLT1
FMO6P
FRAS1
GABRA4
GADD45G
GAMT
GDNF
GLS2
GLYAT
H3C1
HCN2
HHLA1
HRK
HTR1B
HTR1E
IFI44L
IFNA16
IGF2-AS
IGFBP2
IL5RA
INPP5D
IVL
KCNMB1
KIF25
KRT13
KRT16
KRT38
KRT4
LGALS7
LGALS9
LY6D
MAP2K6
MAST3
MEGF8
METTL7A
MMP28
MTHFR
MXD3
MXRA8
MYL9
NCR3
NOS1
NOX5
NSUN6
NTF3
NYNRIN
OLFML2A
P2RX1
PAQR6
PARP3
PBX1
PCDHB1
PDE3A
PDE6B
PGGHG
PIK3C2B
PLBD1
PROC
PTPRU
PVALB
RAG1
RAMP3
RARRES2
RBM17
RPL13P5
RTP4
RUNDC3B
RYR1
S100A7
SCARF1
SCN7A
SERPINA10
SERPINB13
SIDT1
SLC12A3
SLC3A1
SLC6A9
SOBP
SOX11
SPAG11A
SPTBN2
SYNDIG1
TAS2R4
TBR1
TGM1
THNSL2
TM4SF4
TNFSF10
TNNI3
TRIM48
TRIM9
TRPM2
TSBP1
TSHB
TTLL1
UPK3B
VAV3
VAX2
VPS50
YPEL1

DAVID URL:
https://david.ncifcrf.gov/

Functional annotation Chart:

Functional Annotation Chart

Help and Manual

Current Gene List: List_1
Current Background: Homo sapiens
141 DAVID IDs
Options

Rerun Using Options | Create Sublist

166 chart records

Download File

Sublist	Category	Term	RT	Genes	Count	%	P-Value	Benjamini
	UP_SEQ_FEATURE	TOPO_DOM:Extracellular	RT		40	28,4	1,5E-5	1,1E-2
	UP_KW_LIGAND	Calcium	RT		23	16,3	1,8E-5	4,9E-4
	GOTERM_BP_DIRECT	signal transduction	RT		22	15,6	1,1E-4	1,1E-1
	UP_SEQ_FEATURE	TOPO_DOM:Cytoplasmic	RT		45	31,9	1,2E-4	4,4E-2
	GOTERM_CC_DIRECT	integral component of plasma membrane	RT		24	17,0	1,2E-4	1,3E-2
	GOTERM_CC_DIRECT	extracellular space	RT		28	19,9	1,2E-4	1,3E-2
	KEGG_PATHWAY	cAMP signaling pathway	RT		10	7,1	1,3E-4	2,3E-2
	UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine	RT		49	34,8	1,9E-4	4,7E-2
	UP_KW_PTM	Glycoprotein	RT		55	39,0	2,2E-4	4,8E-3
	GOTERM_CC_DIRECT	extracellular region	RT		29	20,6	2,4E-4	1,7E-2
	KEGG_PATHWAY	Calcium signaling pathway	RT		10	7,1	2,4E-4	2,3E-2
	UP_KW_BIOLOGICAL_PROCESS	Cell adhesion	RT		12	8,5	2,7E-4	1,4E-2
	UP_KW_CELLULAR_COMPONENT	Secreted	RT		30	21,3	3,3E-4	1,1E-2
	GOTERM_BP_DIRECT	cell adhesion	RT		13	9,2	4,0E-4	2,0E-1
	UP_KW_PTM	Disulfide bond	RT		46	32,6	4,9E-4	5,4E-3
	GOTERM_BP_DIRECT	sodium ion transmembrane transport	RT		6	4,3	8,0E-4	2,6E-1
	GOTERM_MF_DIRECT	calcium ion binding	RT		15	10,6	8,2E-4	2,7E-1
	UP_KW_DOMAIN	Signal	RT		49	34,8	9,4E-4	1,7E-2
	GOTERM_BP_DIRECT	chemotaxis	RT		6	4,3	1,5E-3	3,7E-1
	GOTERM_CC_DIRECT	plasma membrane	RT		49	34,8	2,7E-3	1,4E-1
	KEGG_PATHWAY	Lipid and atherosclerosis	RT		8	5,7	2,8E-3	1,7E-1
	GOTERM_BP_DIRECT	muscle contraction	RT		5	3,5	3,0E-3	5,9E-1
	UP_KW_BIOLOGICAL_PROCESS	Ion transport	RT		12	8,5	3,1E-3	8,3E-2
	GOTERM_MF_DIRECT	NADP binding	RT		4	2,8	3,2E-3	5,2E-1
	INTERPRO	EF-hand-like domain	RT		8	5,7	3,6E-3	1,0E0
	GOTERM_CC_DIRECT	endoplasmic reticulum lumen	RT		8	5,7	4,1E-3	1,6E-1
	GOTERM_BP_DIRECT	response to lipopolysaccharide	RT		6	4,3	4,2E-3	6,4E-1
	GOTERM_CC_DIRECT	basal plasma membrane	RT		4	2,8	4,5E-3	1,6E-1
	GOTERM_BP_DIRECT	positive regulation of ERK1 and ERK2 cascade	RT		7	5,0	4,6E-3	6,4E-1
	GOTERM_MF_DIRECT	scavenger receptor activity	RT		4	2,8	5,2E-3	5,7E-1
	KEGG_PATHWAY	Vascular smooth muscle contraction	RT		6	4,3	6,4E-3	3,0E-1
	GOTERM_CC_DIRECT	extracellular matrix	RT		7	5,0	7,2E-3	2,2E-1
	INTERPRO	Ion transport domain	RT		5	3,5	7,3E-3	1,0E0
	UP_KW_MOLECULAR_FUNCTION	Ion channel	RT		9	6,4	7,4E-3	4,3E-1
	GOTERM_BP_DIRECT	keratinocyte differentiation	RT		4	2,8	7,8E-3	9,6E-1
	UP_SEQ_FEATURE	DOMAIN:EF-hand 1	RT		6	4,3	8,4E-3	8,6E-1

UP_SEQ_FEATURE	REGION:Coil 2	RT	4	2,8	8,8E-3	8,6E-1
UP_SEQ_FEATURE	REGION:Linker 12	RT	4	2,8	8,8E-3	8,6E-1
UP_SEQ_FEATURE	DOMAIN:EF-hand 2	RT	6	4,3	9,1E-3	8,6E-1
INTERPRO	EF-Hand 1, calcium-binding site	RT	6	4,3	9,8E-3	1,0E0
INTERPRO	Intermediate filament protein, conserved site	RT	4	2,8	1,0E-2	1,0E0
GOTERM_BP_DIRECT	intermediate filament organization	RT	4	2,8	1,0E-2	1,0E0
KEGG_PATHWAY	Circadian entrainment	RT	5	3,5	1,0E-2	3,9E-1
UP_SEQ_FEATURE	REGION:Coil 1B	RT	4	2,8	1,1E-2	8,6E-1
GOTERM_MF_DIRECT	voltage-gated sodium channel activity	RT	3	2,1	1,1E-2	8,0E-1
UP_SEQ_FEATURE	REGION:Coil 1A	RT	4	2,8	1,1E-2	8,6E-1
UP_SEQ_FEATURE	REGION:Linker 1	RT	4	2,8	1,1E-2	8,6E-1
GOTERM_MF_DIRECT	flavin adenine dinucleotide binding	RT	4	2,8	1,2E-2	8,0E-1
UP_SEQ_FEATURE	REGION:Head	RT	4	2,8	1,3E-2	8,6E-1
UP_SEQ_FEATURE	REGION:Tail	RT	4	2,8	1,4E-2	8,6E-1
UP_SEQ_FEATURE	DOMAIN:IF rod	RT	4	2,8	1,5E-2	8,6E-1
GOTERM_BP_DIRECT	keratinization	RT	4	2,8	1,5E-2	1,0E0
UP_KW_DISEASE	Disease variant	RT	35	24,8	1,5E-2	4,1E-1
INTERPRO	Insulin-like growth factor binding protein, N-terminal	RT	5	3,5	1,6E-2	1,0E0
SMART	EGF	RT	6	4,3	1,7E-2	8,4E-1
UP_SEQ_FEATURE	METAL:Calcium	RT	6	4,3	1,7E-2	9,2E-1
GOTERM_CC_DIRECT	extracellular exosome	RT	24	17,0	1,7E-2	4,6E-1
UP_KW_CELLULAR_COMPONENT	Intermediate filament	RT	4	2,8	1,8E-2	2,6E-1
GOTERM_BP_DIRECT	positive regulation of phosphatidylinositol 3-kinase activity	RT	3	2,1	2,0E-2	1,0E0
GOTERM_BP_DIRECT	cell-cell signaling	RT	6	4,3	2,0E-2	1,0E0
GOTERM_BP_DIRECT	neuronal action potential	RT	3	2,1	2,1E-2	1,0E0
SMART	SM01391	RT	4	2,8	2,1E-2	8,4E-1
UP_KW_MOLECULAR_FUNCTION	Sodium channel	RT	3	2,1	2,1E-2	4,6E-1
KEGG_PATHWAY	Renin secretion	RT	4	2,8	2,3E-2	6,9E-1
UP_SEQ_FEATURE	DOMAIN:VWFC	RT	3	2,1	2,3E-2	1,0E0
INTERPRO	Keratin, type I	RT	3	2,1	2,3E-2	1,0E0
UP_KW_CELLULAR_COMPONENT	Cell membrane	RT	38	27,0	2,3E-2	2,6E-1
UP_KW_MOLECULAR_FUNCTION	Ligand-gated ion channel	RT	4	2,8	2,4E-2	4,6E-1
GOTERM_BP_DIRECT	cAMP-mediated signaling	RT	3	2,1	2,5E-2	1,0E0
INTERPRO	EF-hand domain	RT	6	4,3	2,6E-2	1,0E0
GOTERM_BP_DIRECT	extracellular matrix organization	RT	5	3,5	2,6E-2	1,0E0
GOTERM_BP_DIRECT	epithelial cell differentiation	RT	4	2,8	2,6E-2	1,0E0
UP_KW_BIOLOGICAL_PROCESS	Chemotaxis	RT	4	2,8	2,6E-2	4,3E-1
GOTERM_CC_DIRECT	cytoskeleton	RT	9	6,4	2,6E-2	6,1E-1
UP_KW_PTM	Cleavage on pair of basic residues	RT	7	5,0	2,6E-2	1,9E-1
UP_KW_LIGAND	NADP	RT	6	4,3	2,6E-2	3,6E-1
KEGG_PATHWAY	Phototransduction	RT	3	2,1	2,7E-2	6,9E-1
GOTERM_BP_DIRECT	skin development	RT	3	2,1	2,7E-2	1,0E0
INTERPRO	Epidermal growth factor-like domain	RT	6	4,3	2,8E-2	1,0E0
GOTERM_BP_DIRECT	angiogenesis	RT	6	4,3	2,8E-2	1,0E0
GOTERM_BP_DIRECT	embryonic limb morphogenesis	RT	3	2,1	2,8E-2	1,0E0
UP_KW_BIOLOGICAL_PROCESS	Detoxification	RT	2	1,4	3,2E-2	4,3E-1
SMART	EFh	RT	5	3,5	3,2E-2	8,4E-1
GOTERM_CC_DIRECT	collagen type XI trimer	RT	2	1,4	3,2E-2	6,7E-1