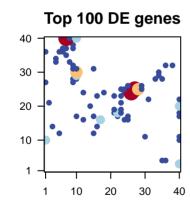
# Riesl\_warm\_r2

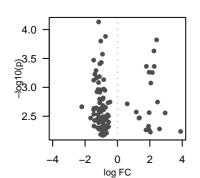
## **Global Summary**

%DE = 0 # genes with fdr < 0.2 = 0 (0+/0 -) # genes with fdr < 0.1 = 0 (0+/0 -) # genes with fdr < 0.05 = 0 (0+/0 -) # genes with fdr < 0.01 = 0 (0+/0 -)

<FC> = 0 <p-value> = 0.38 <fdr> = 1

# Portrait 40 30 20 10 1 10 20 30 40





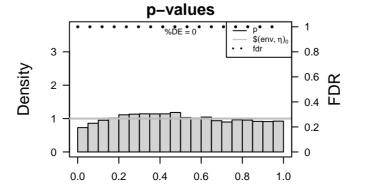
## Differentially expressed genes

log(FC)

Rank

_	ID .		p-va		Meta	90.10
	rexpressed					
1	Vitvi04g00533	2.42	2e-04	1	40 x 20	Any molecular function by which a gene product interacts sele
2 3	Vitvi11g00033	2.25	2e-04	1	40 x 20	A membrane-bounded organelle of eukaryotic cells in which
	Vitvi19g01432	1.78	4e-04	1	40 x 11	Binding to a metal ion.
1	Vitvi04g00493	2.27	4e-04	1	36 x 32	A membrane-bounded organelle of eukaryotic cells in which
5	Vitvi05g00520	1.96	5e-04	1	40 x 18	
6 7	Vitvi05g01450	2.15	6e-04	1	33 x 28	Binding to a protein.
	Vitvi11g00238	2.06	8e-04	1	35 x 4	Catalysis of the hydrolysis of various bonds, e.g. C-O, C-N,
3	Vitvi16g02059	2.47	2e-03	1	40 x 22	Binding to a metal ion.
)	Vitvi04g01157	0.6	2e-03	1	16 x 23	Binding to a metal ion.
0	Vitvi19g01806	1.16	3e-03	1	18 x 24	
1	Vitvi09g00448	1.96	3e-03	1	34 x 29	Binding to a metal ion.
2	Vitvi12g00368	2.94	3e-03	1	1 x 27	The component of a membrane consisting of the gene produc
3	Vitvi18g01132	1.36	3e-03	1	40 x 17	The space external to the outermost structure of a cell. For ce
4	Vitvi14g01178	1.32	3e-03	1	34 x 30	The part of the cytoplasm that does not contain organelles but
5	Vitvi03g00318	1.92	5e-03	1	40 x 10	A membrane-bounded organelle of eukaryotic cells in which
16	Vitvi01g00822	2.6	5e-03	1	40 x 3	Catalysis of the transfer of a glycosyl group from a UDP-suga
7	Vitvi01g00964	1.76	5e-03	1	38 x 32	The formation of a protein dimer, a macromolecular structure
8	Vitvi09g01543	1.96	6e-03	1	36 x 4	
9	Vitvi03g00325	3.9	6e-03	1	40 x 3	A transcription regulator activity that modulates transcription
20	Vitvi03g00442	2.03	6e-03	1	35 x 28	
Jnd	erexpressed					
1	Vitvi06g00651	-1.16	7e-05	1	26 x 24	The action of a molecule that contributes to the structural inte
2	Vitvi19g00696	-0.74	1e-04	1	15 x 17	A lipid bilayer along with all the proteins and protein complexe
3	Vitvi08g02415	-1.03	2e-04	1	25 x 26	
	Vitvi08g01508	-0.92	3e-04	1	27 x 25	The action of a molecule that contributes to the structural inte
)	Vitvi12g0070€	-1.47	3e-04	1	26 x 24	The import of proteins across the outer and inner mitochondr
ز	Vitvi12g01963	-1	4e-04	1	22 x 18	The conversion of a cytosine residue to uridine in an RNA mo
	Vitvi08g01212	-1.09	4e-04	1	26 x 25	A small, dense body one or more of which are present in the
}	Vitvi19g00485	-1.32	5e-04	1	10 x 28	
)	Vitvi13g00354	-1.4	6e-04	1	29 x 25	A semiautonomous, self replicating organelle that occurs in v
0	Vitvi12g00683	-1.12	7e-04	1	26 x 24	Binding to ATP, adenosine 5'-triphosphate, a universally impo
2	Vitvi07g00226	-1.29	7e-04	1	8 x 40	A small, dense body one or more of which are present in the
	Vitvi13g02518 Vitvi07g00581	-0.85	7e-04	1	22 x 18	The component of a membrane consisting of the gene production Binding to a protein.
3	Vitvi12g00479	-1.46 -1.17	8e-04 8e-04	1	10 x 30	Binding to a protein.
5	Vitvi05g00063	-1.17 -0.85	8e-04 1e-03	1	23 x 25 25 x 17	
6	Vitvi08g01955	-1.19	1e-03	1	6 x 37	Binding to a calcium ion (Ca2+).
7	Vitvi07g00315	-1.19	1e-03	1	12 x 16	Binding to a metal ion.
1	Vitvi09g00157	-0.77	1e-03	1	25 x 16	Any molecular function by which a gene product interacts sel
Ω	-	-1.26	1e-03	1	6 x 36	The contents of a cell excluding the plasma membrane and n
18 19	Vitvi01g01023					

Description



## Differentially expressed gene sets

Rank G	iSZ p−valı	ue #all	Geneset
--------	------------	---------	---------

	Overez	pressed			
sele	1	8.76	0e+00	206	Cell grow@cethgtrodeethhandCoethlatthall-Cell wall
ich	2	6.84	0e+00	47	Transporterarestaturger-datenisgort Televispoort celevidron carriers
	3	6.66	0e+00	134	Hormonelstigmating signatingsignating signaling
ich	4	6.52	0e+00	18	Energy m Etabrglismmeta Biblistons yn Placatios symtheres às paroteims a proteins
	5	6.32	0e+00	18	Photosyn Phesissy rathlesisa-proteinsa proteins
	6	6.3	0e+00	80	Cytoskele@ntoskeletotubulkisrotubules
Ν, (	7	6.21	0e+00	38	Photosyn <b>Plassis</b> synthesis
	8	5.89	0e+00	78	Energy mētadrglijsmetal Bhidsos yn Placaios synthesis
	9	5.58	0e+00	217	Cell motilitiell metilitlation exitation vitoskieleton
	10	5.58	0e+00	39	Pentose a Pachtolise canoda placin terro a teven terro as niversions
	11	5.56	0e+00	19	Transcription faldities A- AUXIAA
duc	12	5.19	0e+00	19	Aquaporin/aquaposimasilamelusralasionetet itala solutet eran [3] Contra its [TC:1.A.8]
r ce	13	5.14	0e+00	34	Peptidase Regardid ansless is transfer in Histories S1Ramily S10
s bu	14	5.07	0e+00	73	Transcription faction factorism fact
ich	15	4.59	0e+00	168	Plant hormalizante isternatura isternatura in statute in second
suga	16	4.58	0e+00	93	Transcription faction falcium - BHLH
ure	17	4.45	0e+00	78	Glycosyltr@injsfessylteens@erasteral@inlystarcdhoufyteaccharide
	18	4.27	0e+00	10	Photosyn Priestissymutreissis (Pitruteius ys Petroto(\$7750@noth)(\$770@noth)(\$770@noth)
on (	19	3.78	1e-04	140	Hormonelskigmaning signitalijhene signaling
	20	3.67	3e-04	40	Transport Transport Stylestenkoid Tlaybaktorid parthering pathway
				.0	
		expressed	d		
inte	1	-6.47	0e+00	116	RibosomeRitionsenessisionsenessisionsenessis Paetidies particles
lexe	2	-6.28	0e+00	62	RibosomeRitiogenessIsiog@@@spiartis@@sparticles
	3	-6.22	0e+00	64	RibosomeRibiosemesisiongenesisiongenesisyonesukaryotes
inte	4	-5.54	0e+00	75	TranslatioTranslatiosomeRibiosemesIsiongEndesisyioteEsukaryotes
ndri	5	-4.36	0e+00	24	Primary aletineatrya asspirote tersor [3] (Ca)
mc	<u>6</u>	-3.96	4e-05	165	Transcriptions Sipticerosome
he	7	-3.89	4e-05	126	Translatio Translatio transport
	8	-3.64	3e-04	247	TranslatioTranslationer@ibosome
n va	9	-3.6	4e-04	67	Replication
npc he	10	-3.56	5e-04	75	Mitochon dulieto dramsumi juttoum and pitems lantish framsitation factors  Glycan bi Odyodinelsio saynuthessisa botismoetallo e (Sityocan Voi Odyodinelsio saynuthessio).
duc	11 12	-3.46 -3.45	8e-04 8e-04	33 151	RNA poly <b>RtiAspellinspetane</b> II system
Juut	13	-3.43	9e-04	44	Proteasor Peoteasome
	14	-3.42	1e-03	144	RibosomeRib Estatameyote Esukaryotes
he	15	-3.34	1e-03	40	N-GlycarNbi@klycatmelsiesynthesis
	16	-3.27	1e-03	27	Enzyme -E2:26/mie:ans:26:6/militiganisfegeimpoisrggeuresus groups
	17	-3.26	1e-03	139	Spliceosome
sele	18	-3.25	1e-03	83	RNA deglaNatidegradation
d n	19	-3.19	2e-03	43	Mitochon dilitatore epitaliatore epitaliator
n va	20	-3.19	2e-03	42	Folding softolidignglesgonatidagtidengra?drattienasenffleoteasome

