

Category	p-value	NG	NGR	Genes	Category	p-value	NG	NGR	Genes	
Group 1	ergosterol biosynthetic process [GO:0006696]	4.81E-10	11	23	ERG11 ERG20 ERG28 ERG26 ERG6 ERG12 ERG5 ERG2 ERG1 ERG13 HMG1	cytoplasmic translation [GO:0002181]	6.80E-34	40	171	RPS29A RPL22A RPL24B RPL36A RPL37B RPL6B RPS10B RPS11A RPS16A TIF3 RPS21A RPL11B RPL24A RPL4A RPP1A RPS1B RPL19A RPL7A RPL43B RPL33B RPS10A RPL12B RPL31B RPL11A RPL20B RPL18A RPL23B RPL9B RPS28B RPS13 RPS29B RPS26B DPS1 RPL42A RPL35A RPL27B RPS30A RPP2A RPS29A RPL22A RPL24B RPL26A RPL4B RPL36A RPL37B RPL6B TIF3 RPS21A RPL11B FRS1 RPL24A RPL4A RPS1B RPL7A GRS1 RPL33B RPL31B RPL11A RPL9B RPS28B RPS13 RPS29B RPS26B DPS1 RPL27B RPT1 RPS10B RPS10A RPS28B RPS26B RNA1
	sterol biosynthetic process [GO:0016126]	2.13E-09	11	27	ERG11 ERG20 ERG28 ERG26 ERG6 ERG12 ERG5 ERG2 ERG13 HMG1	translation [GO:0006412]	1.74E-14	28	242	FRS1 RPL24A RPL4A RPS1B RPL7A GRS1 RPL33B RPL31B RPL11A RPL9B RPS28B RPS13 RPS29B RPS26B DPS1 RPL27B RPT1
	steroid biosynthetic process [GO:0006694]	1.57E-08	10	25	ERG11 ERG20 ERG28 ERG26 ERG6 ERG12 ERG5 ERG2 ERG13 HMG1	rRNA export from nucleolus [GO:0006407]	4.69E-08	5	27	
	lipid biosynthetic process [GO:0006610]	2.33E-07	12	52	ERG12 ERG5 ERG2 ERG13 HMG1 HFA1 SFK1	pyridoxal 5'-phosphate salvage [GO:0009443]	1.31E-02	2	2	BUD17 BUD16
	oxidation-reduction process [GO:0055114]	5.94E-06	24	284	ERG11 MET8 CIR2 CTT1 AIM14 ERG26 ADH6 IDP2 COX8 CYB2 ERG5 MTR4 HMG1 AAD4 FET3 HFD1 ERG1 GND2 NDH1 TSA1 MSC7 DLD1 COX15 R1P1	Group 2				
aerobic respiration [GO:0009060]	7.30E-05	10	59	CBP1 QCR2 QCR7 MRPL51 COR1 COX4 PETS09 PET9 DLD1 R1P1						
electron transport chain [GO:0022900]	1.27E-04	9	50	CYB5 QCR2 QCR7 CIR2A IM14 CYB2 COR1 CVC1 R1P1						
isoprenoid biosynthetic process [GO:0008299]	2.30E-04	5	12	COQ2 ERG20 ERG12 HMG1 ERG13						
mitochondrial electron transport ubiquinol to cytochrome c [GO:0006122]	3.56E-08	4	11	QCR2 QCR7 CVC1 R1P1						
mitochondrial electron transport cytochrome c to oxygen [GO:0006123]	4.71E-08	4	12	COX6 COX8 COX4 CVC1	Group 3					
iron assimilation by reduction and transport [GO:0033215]	1.57E-02	2	2	FET3 FTR1						
protein insertion into mitochondrial membrane [GO:0051204]	1.57E-02	2	2	YUH47 MDM38						
ion transport [GO:0006811]	3.35E-02	9	109	CTR3 ATP17 CC2 ZRT1 AIM14 ATP14 ATP16 FET3 FTR1						
isopentenyl diphosphate biosynthetic process mevalonate pathway [GO:0019287]	3.98E-02	2	3	ERG12 HMG1						
cellular aldehyde metabolic process [GO:0006081]	4.36E-02	3	11	ADH6 AAD4 HFD1	Group 4					