Supplementary Material

L. Donato et al., Atti Accad. Pelorit. Pericol. Cl. Sci. Fis. Mat. Nat., Vol. 96, No. S3, A7 (2018)

RETRACTED

ncRNA Type	*ref_id*	*GENE NAME*	*0h vs 1h (Untreated)*	*0h vs 1h (Treated)*	*1h (Treated vs Untreated)*	*2h (Treated vs Untreated)*	*4h (Treated vs Untreated)*	*6h (Treated vs Untreated)*
Small Cajal Body - Specific RNAs	U85	SCARNA10	0	0	0	0	0,861420257	0
	U89	SCARNA12	0	2,316707357	2,316707357	2,374522332	1,254837092	0
	U91	SCARNA17	0,959431461	0,693158945	-0,266272516	0,418405222	0,99798898	-0,342397111
	HBII-382	SCARNA2	-0,822538456	-0,822538456	0	0,574695422	-0,77887467	-0,343398174
	U90	SCARNA7	0,705595689	-0,362425696	-1,068021385	2,353347571	0	-1,192506663
	Z32	SCARNA9	0,800604673	-0,670232219	-1,470836893	-1,09258498	0,240963873	0,643210641
Small Nucleolar RNAs		SNORA1	0	0	0	0	0	3,745283054
	ACA10	SNORA10	-4,55574365	-4,55574365	0	3,939148892	0	-5,518788816
		SNORA11D	0	0	0	0	0	2,950035167
		SNORA14B	0	4,749975268	4,749975268	0	0	0
		SNORA18	0	6,82044253	6,82044253	8,132675289	0	7,885246432
		SNORA23	0	0	0	0	0	-2,94645689
		SNORA27	0	4,125149261	4,125149261	0	0	-4,809460029
		SNORA3	-4,665061566	-4,665061566	0	0	0	0
		SNORA32	5,091965925	5,85233427	0,760368344	5,349972796	0	5,606642391
		SNORA33	0	0	0	0	0	3,64011511
		SNORA4	4,494193877	3,734534481	-0,759659395	3,801227477	0	3,504516413
		SNORA40	4,604884627	5,53449373	0,929609102	0	4,541711827	3,853532534
	SNORA80E	SNORA42	0	0	0	0	0	-4,514108875
	SNORA3B	SNORA45	0	0	0	0	-4,53006481	0
		SNORA52	0	4,785759774	4,785759774	0	-4,422021022	3,605726744
		SNORA53	0	0	0	0	0	1,262030783
		SNORA56	0	4,014615419	4,014615419	0	0	0
		SNORA59A	0	2,405118584	2,405118584	0	2,456299935	0
		SNORA59B	0	2,405118584	2,405118584	0	2,456299935	0
		SNORA5A	0	3,837135914	3,837135914	-4,556188006	-5,387972497	0
		SNORA60	-4,449213897	-4,449213897	0	0	0	0
		SNORA62	0	0	0	0	4,740930042	0
		SNORA63	0	5,316954352	5,316954352	0	-4,386627288	0
	U64	SNORA64	0,080156317	-4,519928567	-4,600084884	-5,525195855	0	-4,514108875
	U65	SNORA65	4,529191644	0	-4,529191644	-4,485391275	0	-4,443407538
	U67	SNORA67	5,461825587	3,734534481	-1,727291106	0,29808953	5,3065835	5,002142028
	U70	SNORA70	-2,450160347	-1,69769349	0,752466857	0	1,714644649	-0,946389462
	U71a	SNORA71A	0	0	0	0	0	-4,373905132
		SNORA7B	0	3,667697445	3,667697445	0	0	0
		SNORA8	-5,309451579	-5,309451579	0	-4,381430611	3,72568794	-0,900955925
		SNORA80B	0	0	0	0	-4,351538229	3,537930664
		SNORA81	0	0	0	-0,598687969	0	0
	mgU6-77	SNORD10	0	0	0	0	0	-4,043539266
	U104	SNORD104	7,124678519	0	-7,124678519	0	-6,939864998	0
		SNORD109B	0	8,214957161	8,214957161	7,873199855	0	5,982672816
		SNORD110	-8,360783047	-8,360783047	0	0	0	6,400009203
		SNORD116-24	0	0	0	0	5,593695519	0
		SNORD116-6	0	0	0	0	0	5,085711535
		SNORD116-8	0	0	0	0	0	5,135330755
		SNORD11B	0	4,684942752	4,684942752	0	0	0
	U15B	SNORD15B	0	0	0	3,508753413	3,500418388	0
	U16	SNORD16	-5,93922164	-5,93922164	0	0	0	0
		SNORD17	-1,246865001	-0,502323194	0,744541807	1,585341366	1,658919953	1,65835924
		SNORD19B	7,369595427	0	-7,369595427	7,220638342	0	0
	U22	SNORD22	0,573883343	-0,214362221	-0,788245564	-0,236712265	-0,118182263	-0,031238155
		SNORD23	0	0	0	6,802510032	0	0
	U24	SNORD24	7,448377012	0	-7,448377012	0	0	0
	U26	SNORD26	0,083212006	1,271704971	1,188492965	0	-8,25857432	0
	U28	SNORD28	0	0	0	7,712115139	6,70992566	7,97353744
	U29	SNORD29	0	7,375986137	7,375986137	7,447540773	0	0
	U30	SNORD30	0	0	0	-0,68496928	0	0
	U31	SNORD31	0	0	0	0	0	6,895390921
	U32A	SNORD32A	0,08336779	-7,912525312	-7,995893102	-2,259158602	0	5,956384103
	U34	SNORD34	0	0	0	0	-0,554958038	0
	U35A	SNORD35A	0	5,967972981	5,967972981	0	0	0
	U35B	SNORD35B	6,707644854	5,911099836	-0,796545018	5,981909949	-0,550393501	-1,946161598
	U36A	SNORD36A	0	0	0	0	-0,55394053	0
	U36C	SNORD36C	0	0	0	0	0	-7,933069879
	U38B	SNORD38B	0	0	0	0	0	6,820927667
	U41	SNORD41	-7,714737001	-7,714737001	0	0	0	0
	U42A	SNORD42A	0	7,538372584	7,538372584	7,609972228	0	0
	U47	SNORD47	0	6,515948339	6,515948339	0,309127617	6,578113379	0
	U52	SNORD52	0	0	0	0	0	4,92410459
	U55	SNORD55	-0,500096871	0,013792395	0,513889266	9,582544559	-0,553554265	-1,547027395
	U57	SNORD57	0	0	0	6,924630653	0	7,597777941
	U58C	SNORD58C	-6,457235297	-6,457235297	0	0	0	0
	U62A	SNORD62A	0	0	0	-5,733155956	0	0
		SNORD67	5,511278423	4,727937876	-0,783340548	-1,65281304	-5,32939309	0,031771911
		SNORD69	0	0	0	0	0	0
	U76	SNORD76	0	0	0	0	0	-6,973584311
	U79	SNORD79	0	0	0	0	0	6,017031816
	U83A	SNORD83A	6,273545933	0	-6,273545933	5,55100597	0	0
	U83B	SNORD83B	0	0	0	6,640504077	-1,538625431	0
	U84	SNORD84	0,079900879	-4,419792217	-4,499693097	0	0	0
		SNORD88B	0	0	0	5,449482041	0	5,135330755
		SNORD89	0,081639259	1,255180501	1,173541242	6,945149098	6,206950733	6,307402658
	U96a	SNORD96A	-7,571479761	-7,571479761	0	0	6,915565835	0
		SNORD99	7,124678519	0	-7,124678519	0	0	-7,035551377

Table 1. snoRNAS expression variations throughout all analyzed time points. All 84 selected snoRNAs showed particular fold – change trends, between treated and untreated samples, during considered time points (0h, 1h, 2h, 4h, 6h). The whole results were statistically validated by Bonferroni – corrected EDGE test, and p – values are all about 0 (values not shown).

Id	*HGNC Symbol*	*Length*	*Chrom*	*Chrom_Start*	*Chrom_End*	*Strand*	*Type*	*Genbank Acc. N°*	*Target RNA*	*Host Genes*
U85	SCARNA10	330	chr12	6489649	6489978	+	scaRNA	AF308283	U5 snRNA U46 and U5 snRNA C45	CNAP1
U89	SCARNA12	270	chr12	6946761	6947030	-	scaRNA	AY077739	U5 snRNA U46	REA
mgU12-22/U4-8	SCARNA17	421	chr18	45594391	45594811	+	scaRNA	BK005569	U4 snRNA C8 and U12 snRNA G22	Independent Transcriptional Unit
mgU2-25/61	SCARNA2	420	chr1	109444338	109444757	+	scaRNA	/	U2 snRNA G25 and U2 snRNA C61	Independent Transcriptional Unit
U90	SCARNA7	330	chr3	161715389	161715718	-	scaRNA	AY077740	U1 snRNA A70	KPNA4
mgU2-19/30	SCARNA9	353	chr11	93094328	93094680	+	scaRNA	BK005567	U2 snRNA G19 and U2 snRNA A30	AB051518 (KIAA1731)
ACA1	SNORA1	130	chr11	93104818	93104947	-	HAcaBox	/	28S rRNA U4441	TAF1D (AK128061)
ACA10	SNORA10	133	chr16	1952336	1952468	-	HAcaBox	AJ609432	18S rRNA U210 and 28S rRNA U4491	RPS2
SNORA11D	SNORA11D	128	chrX	51950457	51950584	+	HAcaBox	AM413018	unknown	MAGED4
ACA14b	SNORA14B	135	chr1	233357741	233357875	-	HAcaBox	AJ609457	18S rRNA U966	TOMM20
ACA18	SNORA18	132	chr11	93106280	93106411	-	HAcaBox	AJ609471	unknown	TAF1D (AK128061)
ACA23	SNORA23	189	chr11	9406889	9407077	+	HAcaBox	AJ609438	28S rRNA U3737 and 28S rRNA U4331	IPO7
ACA27	SNORA27	126	chr13	26727538	26727663	+	HAcaBox	AJ609439	28S rRNA U3694 and 28S rRNA U4522	RPL21
ACA3	SNORA3	130	chr11	8662350	8662479	+	HAcaBox	AJ609428	28S rRNA U3899 and 28S rRNA U3938	RPL27A
ACA32	SNORA32	121	chr11	93103793	93103913	-	HAcaBox	/	28S rRNA U1847	TAF1D (AK128061)
ACA33	SNORA33	133	chr6	133180051	133180183	+	HAcaBox	AJ609473	28S rRNA U4966	RPS12
ACA4	SNORA4	138	chr3	187988096	187988232	+	HAcaBox	AJ609452	18S rRNA U1347	EIF4A2
ACA40	SNORA40	127	chr11	93107924	93108050	-	HAcaBox	AJ609445	28S rRNA U4546 and 18S rRNA U1174	TAF1D (AK128061)
ACA42	SNORA42	134	chr1	154156324	154156457	-	HAcaBox	AJ609465	18S rRNA U572 and 18S rRNA U109	KIAA0907
ACA3-2	SNORA45	131	chr11	8663562	8663692	+	HAcaBox	AM055744	28SrRNA U3899	RPL27A
ACA52	SNORA52	134	chr11	801681	801814	+	HAcaBox	AJ609448	28S rRNA U1731	RPLP2
ACA53	SNORA53	250	chr12	97517544	97517793	+	HAcaBox	/	unknown	SLC25A3
ACA56	SNORA56	129	chrX	153656467	153656595	+	HAcaBox	AJ609449	28S rRNA U1664	DKC1
ACA59	SNORA59A	152	chr1	12489887	12490038	+	HAcaBox	AJ609481	unknown	VPS13D
ACA59B	SNORA59B	152	chr17	19401465	19401616	+	HAcaBox	AJ609481	unknown	SLC47A1 (FLJ10847)
ACA5	SNORA5A	134	chr7	45110473	45110606	-	HAcaBox	AJ609453	18S rRNA U1238 and 18S rRNA U1625	TBRG4 (KIAA0948)
ACA60	SNORA60	136	chr20	36511426	36511561	+	HAcaBox	AJ609469	18S rRNA U1004	SNHG11 (LOC128439)
E2	SNORA62	153	chr3	39427549	39427702	+	HAcaBox	L07383	28S rRNA U3830 and 28S rRNA U3832	RPSA
E3	SNORA63	123	chr3	187987782	187987916	+	HAcaBox	L07384	28S rRNA U4390	EIF4A2
U64	SNORA64	134	chr16	1952975	1953108	-	HAcaBox	Y11158	28S rRNA U4975	RPS2
U65	SNORA65	137	chr9	129250601	129250737	-	HAcaBox	Y11159	28S rRNA U4373 and 28S rRNA U4427	RPL12
U67	SNORA67	137	chr17	7421997	7422133	+	HAcaBox	Y11161	18S rRNA U1445	EIF4A1
U70	SNORA70	135	chrX	153281816	153281950	+	HAcaBox	Y11164	18S rRNA U1692	RPL10
U71a	SNORA71A	139	chr20	36489363	36489500	-	HAcaBox	Y11165	18S rRNA U406	AL080249.26
ACA7B	SNORA7B	139	chr3	130598743	130598881	-	HAcaBox	/	28S rRNA U1569 and 28S rRNA U1779	RPL32P3 (BC053996)
ACA8	SNORA8	139	chr11	93105175	93105313	-	HAcaBox	/	18S rRNA U1056 and 18S rRNA U1081	TAF1D (AK128061)
ACA67B	SNORA80B	136	chr2	10504291	10504426	-	HAcaBox	/	18S rRNA U109 and 18S rRNA U572	ODC1
HBI-61	SNORA81	178	chr3	187987158	187987335	+	HAcaBox	AM055745	28S rRNA U4606	EIF4A2
mgU6-77	SNORD10	148	chr17	7420853	7421000	+	CDBox	NR_002604	U6 snRNA C77 and 28S rRNA C3787	EIF4A1
U104	SNORD104	80	chr17	59577170	59577249	+	CDBox	AY349605	28S rRNA C1327	unknown
HBII-438B	SNORD109B	67	chr15	23074583	23074649	+	CDBox	AY055808	unknown	SNURF-SNRPN
HBII-55	SNORD110	75	chr20	2582858	2582932	+	CDBox	/	18S rRNA U1288	NOL5A (NOP56)
HBII-85-24	SNORD116-24	94	chr15	22890276	22890369	+	CDBox	NR_003338	unknown	SNURF-SNRPN
HBII-85-6	SNORD116-6	98	chr15	22861265	22861362	+	CDBox	NR_003321	unknown	SNURF-SNRPN
HBII-85-8	SNORD116-8	97	chr15	22866671	22866767	+	CDBox	NR_003323	unknown	SNURF-SNRPN
HBII-95B	SNORD11B	90	chr2	202864300	202864389	+	CDBox	AM413022	18S rRNA G509	NOP5/NOP58
U15B	SNORD15B	146	chr11	74793113	74793258	+	CDBox	/	28S rRNA A3764	RPS3
U16	SNORD16	101	chr15	64582203	64582303	-	CDBox	/	18S rRNA A484	RPL4
HBI-43	SNORD17	237	chr20	17891353	17891589	-	CDBox	/	28S rRNA U3797	SNX5
HBII-108B	SNORD19B	84	chr3	52699800	52699883	+	CDBox	AM413023	18S rRNA G683	GLN3
U22	SNORD22	126	chr11	62376958	62377083	-	CDBox	/	unknown	UHG (U22 host gene) (SNHG1)
HBII-115	SNORD23	110	chr19	52950922	52951031	+	CDBox	/	unknown	GLTSCR2
U24	SNORD24	75	chr9	135206072	135206146	+	CDBox	Z48764	28S rRNA C2338 and 28S rRNA C2352	RPL7A
U26	SNORD26	75	chr11	62379340	62379414	-	CDBox	/	28S rRNA A389	UHG (U22 host gene) (SNHG1)
U28	SNORD28	75	chr11	62378669	62378743	-	CDBox	/	18S rRNA C1391	UHG (U22 host gene) (SNHG1)
U29	SNORD29	65	chr11	62377952	62378016	-	CDBox	/	28S rRNA A4493	UHG (U22 host gene) (SNHG1)
U30	SNORD30	70	chr11	62377711	62377780	-	CDBox	/	28S rRNA A3804	UHG (U22 host gene) (SNHG1)
U31	SNORD31	71	chr11	62377373	62377443	-	CDBox	/	28S rRNA A4166	UHG (U22 host gene) (SNHG1)
U32A	SNORD32A	77	chr19	54685037	54685113	+	CDBox	/	18S rRNA G1328 and 28S rRNA A1511	RPL13A
U34	SNORD34	66	chr19	54685976	54686041	+	CDBox	/	28S rRNA U2824	RPL13A
U35A	SNORD35A	86	chr19	54686244	54686329	+	CDBox	/	28S rRNA C4506	RPL13A
U35B	SNORD35B	88	chr19	54692788	54692875	+	CDBox	/	28S rRNA C4506	RPS11
U36A	SNORD36A	72	chr9	135207132	135207203	+	CDBox	X97584	18S rRNA A668	RPL7A
U36C	SNORD36C	68	chr9	135207522	135207589	+	CDBox	X97587	28S rRNA A3703	RPL7A
U38B	SNORD38B	69	chr1	45016649	45016717	+	CDBox	X97583	28S rRNA A1858	RPS8
U41	SNORD41	70	chr19	12678263	12678332	-	CDBox	X96640	28S rRNA U4276	TNPO2
U42A	SNORD42A	58	chr17	24074579	24074636	+	CDBox	X96641	18S rRNA U116	RPL23A
U47	SNORD47	65	chr1	172100131	172100195	-	CDBox	X96647	28S rRNA C3866	GAS5 (AL110141, SNHG2)
U52	SNORD52	64	chr6	31912832	31912895	+	CDBox	X96651	28S rRNA U3904	C6orf48
U55	SNORD55	74	chr1	45014124	45014197	+	CDBox	X96654	28S rRNA C2791	RPS8
U57	SNORD57	72	chr20	2585585	2585656	+	CDBox	X96656	18S rRNA A99	NOL5A (NOP56)
U58C	SNORD58C	65	chr18	45269612	45269676	-	CDBox	AM413028	28S rRNA U4197 and 28S rRNA G4198	RPL17
U62A	SNORD62A	86	chr9	133350873	133350958	+	CDBox	U72851	18S rRNA A590	BAT2L (AB011087)
HBII-166	SNORD67	111	chr11	46740515	46740625	-	CDBox	/	U6 snRNA C60	CKAP5 (Ch-TOG)
HBII-210	SNORD69	77	chr3	52701792	52701868	+	CDBox	/	28S rRNA G4464	GLN3
U76	SNORD76	80	chr1	172102396	172102475	-	CDBox	AF141346	28S rRNA A2350	GAS5 (AL110141, SNHG2)
U79	SNORD79	85	chr1	172101109	172101193	-	CDBox	AF141346	28S rRNA A3809	GAS5 (AL110141, SNHG2)
U83A	SNORD83A	95	chr22	38041164	38041258	-	CDBox	AJ238852	unknown	RPL3
U83B	SNORD83B	93	chr22	38039770	38039862	-	CDBox	/	unknown	RPL3
U84	SNORD84	78	chr6	31616857	31616934	-	CDBox	AJ243199	unknown	BAT1
HBII-180B	SNORD88B	97	chr19	55994098	55994194	-	CDBox	/	28S rRNA C3680	MGC13170
HBII-289	SNORD89	114	chr2	101255830	101255943	-	CDBox	/	unknown	unknown
U96a	SNORD96A	72	chr5	180601424	180601495	-	CDBox	AY349595	5.8S rRNA G75	GNB2L1
HBII-420	SNORD99	80	chr1	28777842	28777921	-	CDBox	/	28S rRNA A2774	SNHG12

Table 2. Analyzed snoRNA target RNAs and host genes. Selected snoRNAs showed a wide range of target RNAs and host genes, suggesting a complex scenario in which they could be involved in.

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GOID	GOTerm	Ontology Source	Term PValue
GO:0022613	ribonucleoprotein complex biogenesis	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0042254	ribosome biogenesis	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0016072	rRNA metabolic process	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:72312	rRNA processing	REACTOME_Pathways_20.11.2017	0,00
R-HSA:886877	rRNA processing in the nucleus and cytosol	REACTOME_Pathways_20.11.2017	0,00
GO:0006401	RNA catabolic process	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0034470	ncRNA processing	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0006364	rRNA processing	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:156827	L13a-mediated translational silencing of Ceruloplasmin expression	REACTOME_Pathways_20.11.2017	0,00
R-HSA:679122	Major pathway of rRNA processing in the nucleolus and cytosol	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72613	Eukaryotic Translation Initiation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72706	GTP hydrolysis and joining of the 60S ribosomal subunit	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72737	Cap-dependent Translation Initiation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72766	Translation	REACTOME_Pathways_20.11.2017	0,00
GO:0006413	translational initiation	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0006402	mRNA catabolic process	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0000956	nuclear-transcribed mRNA catabolic process	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:71291	Metabolism of amino acids and derivatives	REACTOME_Pathways_20.11.2017	0,00
GO:0090150	establishment of protein localization to membrane	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0005840	ribosome	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0044391	ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0006605	protein targeting	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
KEGG:03010	Ribosome	KEGG_20.11.2017	0,00
R-HSA:141671	Polypeptide release from the eRF3-GDP:eRF1:mRNA:80S Ribosome complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:141673	GTP Hydrolysis by eRF3 bound to the eRF1:mRNA:polypeptide:80S Ribosome complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:141691	GTP bound eRF3:eRF1 complex binds the peptidyl tRNA:mRNA:80S Ribosome complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:156842	Eukaryotic Translation Elongation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:156902	Peptide chain elongation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:156907	Aminoacyl-tRNA binds to the ribosome at the A-site	REACTOME_Reactions_20.11.2017	0,00
R-HSA:156912	Peptide transfer from P-site tRNA to the A-site tRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:156915	Translocation of ribosome by 3 bases in the 3' direction	REACTOME_Reactions_20.11.2017	0,00
R-HSA:156923	Hydrolysis of eEF1A:GTP	REACTOME_Reactions_20.11.2017	0,00
R-HSA:168254	Influenza Infection	REACTOME_Pathways_20.11.2017	0,00
R-HSA:168255	Influenza Life Cycle	REACTOME_Pathways_20.11.2017	0,00
R-HSA:168273	Influenza Viral RNA Transcription and Replication	REACTOME_Pathways_20.11.2017	0,00
R-HSA:179932	Signal-containing nascent peptide translocates to endoplasmic reticulum	REACTOME_Reactions_20.11.2017	0,00
R-HSA:179932	Signal peptidase hydrolyzes signal peptide from ribosome-associated nascent protein	REACTOME_Reactions_20.11.2017	0,00
R-HSA:179933	The SRP receptor binds the SRP:nascent peptide:ribosome complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:179933	Nascent polypeptide:mRNA:ribosome complex binds signal recognition particle (SRP)	REACTOME_Reactions_20.11.2017	0,00
R-HSA:179933	Synthesis of nascent polypeptide containing signal sequence	REACTOME_Reactions_20.11.2017	0,00
R-HSA:179933	SRP-dependent cotranslational protein targeting to membrane	REACTOME_Pathways_20.11.2017	0,00
R-HSA:192704	Synthesis of PB1-F2	REACTOME_Reactions_20.11.2017	0,00
R-HSA:192823	Viral mRNA Translation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:192841	Viral Protein Synthesis	REACTOME_Reactions_20.11.2017	0,00
R-HSA:240852	Selenoamino acid metabolism	REACTOME_Pathways_20.11.2017	0,00
R-HSA:240852	Sec-tRNA(Sec):EEFSEC:GTP binds to 80S Ribosome	REACTOME_Reactions_20.11.2017	0,00
R-HSA:240855	Selenocysteine synthesis	REACTOME_Pathways_20.11.2017	0,00
R-HSA:376176	Signaling by ROBO receptors	REACTOME_Pathways_20.11.2017	0,00
R-HSA:533361	80S:Met-tRNAi:mRNA:SECISBP2:Sec-tRNA(Sec):EEFSEC:GTP is hydrolysed to 80S:Met-tRNAi:mRNA:SECISBP2:Sec and EEFSEC:GD	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72671	eIF5B:GTP is hydrolyzed and released	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72672	The 60S subunit joins the translation initiation complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72673	Release of 40S and 60S subunits from the 80S ribosome	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72689	Formation of a pool of free 40S subunits	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72764	Eukaryotic Translation Termination	REACTOME_Pathways_20.11.2017	0,00
R-HSA:901055	Regulation of expression of SLITs and ROBOs	REACTOME_Pathways_20.11.2017	0,00
R-HSA:901461	Translation of ROBO3.2 mRNA initiates NMD	REACTOME_Reactions_20.11.2017	0,00
R-HSA:901465	Translation of ROBO3.2 mRNA is negatively regulated by NMD	REACTOME_Reactions_20.11.2017	0,00
R-HSA:927789	Formation of UPF1:eRF3 complex on mRNA with a premature termination codon and no Exon Junction Complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:927802	Nonsense-Mediated Decay (NMD)	REACTOME_Pathways_20.11.2017	0,00
R-HSA:927813	p-4S-UPF1 recruits SMG5, SMG7, SMG6, PNRC2, DCP1A, and PP2A	REACTOME_Reactions_20.11.2017	0,00
R-HSA:927832	UPF1 binds an mRNP with a termination codon preceding an Exon Junction Complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:927836	SMG6 hydrolyzes mRNA with premature termination codon	REACTOME_Reactions_20.11.2017	0,00
R-HSA:927889	SMG1 phosphorylates UPF1 (enhanced by Exon Junction Complex)	REACTOME_Reactions_20.11.2017	0,00
R-HSA:975956	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	REACTOME_Pathways_20.11.2017	0,00
R-HSA:975957	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	REACTOME_Pathways_20.11.2017	0,00
WP:477	Cytoplasmic Ribosomal Proteins	WikiPathways_20.11.2017	0,00
GO:0019080	viral gene expression	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0019083	viral transcription	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0044445	cytosolic part	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0070972	protein localization to endoplasmic reticulum	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0072599	establishment of protein localization to endoplasmic reticulum	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0022626	cytosolic ribosome	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0006612	protein targeting to membrane	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0045047	protein targeting to ER	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0006613	cotranslational protein targeting to membrane	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:156826	Dissociation of L13a from the 60s ribosomal subunit	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679121	12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA	REACTOME_Reactions_20.11.2017	0,00
GO:0015934	large ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0022625	cytosolic large ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
R-HSA:156826	Dissociation of L13a from the 60s ribosomal subunit	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679121	12S pre-rRNA is nucleolytically processed to yield 5.8S rRNA	REACTOME_Reactions_20.11.2017	0,00
GO:0015934	large ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0022625	cytosolic large ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
R-HSA:156823	Association of phospho-L13a with GAIT element of Ceruloplasmin mRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:156808	Formation of translation initiation complexes yielding circularized Ceruloplasmin mRNA in a 'closed-loop' conformation	REACTOME_Reactions_20.11.2017	0,00
R-HSA:157849	Formation of translation initiation complexes containing mRNA that does not circularize	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72619	eIF2:GTP is hydrolyzed, eIFs are released	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72621	Ribosomal scanning	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72649	Translation initiation complex formation	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72662	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	REACTOME_Pathways_20.11.2017	0,00
R-HSA:72697	Start codon recognition	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72702	Ribosomal scanning and start codon recognition	REACTOME_Pathways_20.11.2017	0,00
GO:0019843	rRNA binding	GO_MolecularFunction-EBI-QuickGO-GOA_20.11.2017_(	0,00
GO:0015935	small ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0042273	ribosomal large subunit biogenesis	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0042255	ribosome assembly	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:679122	18SE pre-rRNA in pre-40S particles is nucleolytically processed during translocation from the nucleus to the cytosol	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72676	eIF3 and eIF1A bind to the 40S subunit	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72691	Formation of the 43S pre-initiation complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72695	Formation of the ternary complex, and subsequently, the 43S complex	REACTOME_Pathways_20.11.2017	0,00
GO:0022627	cytosolic small ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
R-HSA:679122	18SE pre-rRNA in pre-40S particles is nucleolytically processed during translocation from the nucleus to the cytosol	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72676	eIF3 and eIF1A bind to the 40S subunit	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72691	Formation of the 43S pre-initiation complex	REACTOME_Reactions_20.11.2017	0,00
R-HSA:72695	Formation of the ternary complex, and subsequently, the 43S complex	REACTOME_Pathways_20.11.2017	0,00
GO:0022627	cytosolic small ribosomal subunit	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0042273	ribosomal large subunit biogenesis	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0002181	cytoplasmic translation	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0000027	ribosomal large subunit assembly	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
R-HSA:679122	30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679122	30S pre-rRNA is nucleolytically processed at site 1 to yield 21S pre-rRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679090	rRNA modification in the nucleus and cytosol	REACTOME_Pathways_20.11.2017	0,00
CORUM:5380	TRBP containing complex (DICER, RPL7A, EIF6, MOV10 and subunits of the 60S ribosomal particle)	CORUM_CORUM-FunCat-MIPS_20.11.2017	0,00
GO:0003724	RNA helicase activity	GO_MolecularFunction-EBI-QuickGO-GOA_20.11.2017_(	0,00
GO:0010501	RNA secondary structure unwinding	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00
GO:0004004	ATP-dependent RNA helicase activity	GO_MolecularFunction-EBI-QuickGO-GOA_20.11.2017_(	0,00
R-HSA:679090	EMG1 of the SSU processome methylates pseudouridine-1248 of 18S rRNA yielding N(1)-methylpseudouridine-1248	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679122	21S pre-rRNA is nucleolytically processed at site E (site2a) to yield 18SE pre-rRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679122	47S pre-rRNA is nucleolytically processed at A' (01,A1), site A0, and site 02 (site 6) to yield 45S pre-rRNA	REACTOME_Reactions_20.11.2017	0,00
R-HSA:679122	45S pre-rRNA is nucleolytically processed at site 2 (site 2b) to yield 30S pre-rRNA and 32S pre-rRNA	REACTOME_Reactions_20.11.2017	0,00
GO:0005732	small nucleolar ribonucleoprotein complex	GO_CellularComponent-EBI-QuickGO-GOA_20.11.2017_	0,00
GO:0030515	snoRNA binding	GO_MolecularFunction-EBI-QuickGO-GOA_20.11.2017_(	0,00
GO:0000154	rRNA modification	GO_BiologicalProcess-EBI-QuickGO-GOA_20.11.2017_0	0,00

Supplementary Material

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RETRACTED

Term PValue Corrected with Bonferroni step	GOLevels	% Associated Gen	Nr. Genes	Associated Genes Found
0,00	[3]	4,45	22,00	[DDX39B, DKC1, NOP53, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2,
0,00	[4]	6,03	21,00	[DKC1, NOP53, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3,
0,00	[6, 7, 8]	6,60	21,00	[DKC1, NOP53, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3,
0,00	[-1]	9,62	20,00	[DKC1, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	10,10	20,00	[DKC1, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7]	5,06	20,00	[DKC1, EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[6, 7, 8]	4,69	20,00	[DKC1, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 7, 8, 9]	7,22	20,00	[DKC1, NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,81	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	10,11	19,00	[NOP56, NOP58, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,70	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,67	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,70	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	6,51	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[3, 6, 7, 8]	9,31	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8]	5,31	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[6, 7, 8, 9]	8,72	19,00	[EIF4A1, EIF4A2, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	4,93	18,00	[ODC1, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[4, 5, 6]	6,08	18,00	[RACK1, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[4, 5, 6, 7]	7,41	18,00	[RACK1, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[3, 4, 5, 6, 7, 8]	9,28	18,00	[RACK1, RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8, 9]	4,25	18,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA, TOMM20]
0,00	[-1]	11,04	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,68	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,68	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,68	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,09	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,89	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,32	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,89	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	10,24	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	10,97	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,72	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,74	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,19	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	17,71	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,09	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,32	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,04	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,83	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	17,00	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	14,29	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,89	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,09	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	7,76	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,89	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,89	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,50	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	18,09	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	9,88	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,35	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	16,35	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	17,71	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	14,66	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	14,66	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,74	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,32	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	15,74	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	17,71	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	14,66	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	19,10	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5]	8,25	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6]	8,90	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[4, 5, 6, 7, 8]	6,64	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[6]	12,59	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7]	15,04	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8, 9]	13,93	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8, 9, 10]	9,55	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[6, 7, 8, 9, 10]	15,60	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[7, 8, 9, 10]	13,18	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[6, 7, 8, 9, 10, 11]	16,19	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[7, 8, 9, 10, 11, 1	17,00	17,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	20,75	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[-1]	14,67	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[4, 5, 6, 7, 8, 9]	9,40	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[5, 6, 7, 8, 9, 10]	17,19	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[-1]	20,75	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[-1]	14,67	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[4, 5, 6, 7, 8, 9]	9,40	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[5, 6, 7, 8, 9, 10]	17,19	11,00	[RPL10, RPL12, RPL13A, RPL17, RPL21, RPL23A, RPL27A, RPL3, RPL4, RPL7A, RPLP2]
0,00	[-1]	14,75	9,00	[EIF4A1, EIF4A2, RPL13A, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,33	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,56	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,33	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,56	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,33	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,11	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,33	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	13,33	8,00	[EIF4A1, EIF4A2, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5]	10,77	7,00	[NOP53, RPL12, RPL17, RPL23A, RPL3, RPS11, RPS3]
0,00	[4, 5, 6, 7, 8, 9]	8,86	7,00	[RACK1, RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[4, 5]	8,57	6,00	[NOP53, RPL10, RPL12, RPL23A, RPL3, RPL7A]
0,00	[5, 6, 7]	9,09	6,00	[NOP53, RPL10, RPL12, RPL23A, RPL3, RPSA]
0,00	[-1]	11,11	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	12,00	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,32	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,32	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8, 9, 10]	11,76	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,11	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	12,00	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,32	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[-1]	11,32	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[5, 6, 7, 8, 9, 10]	11,76	6,00	[RPS11, RPS12, RPS2, RPS3, RPS8, RPSA]
0,00	[4, 5]	8,57	6,00	[NOP53, RPL10, RPL12, RPL23A, RPL3, RPL7A]
0,00	[6, 7, 8]	7,58	5,00	[RPL13A, RPL27A, RPL4, RPLP2, RPS3]
0,00	[5, 6, 7, 8]	16,13	5,00	[NOP53, RPL10, RPL12, RPL23A, RPL3]
0,00	[-1]	7,81	5,00	[NOP56, NOP58, RPS11, RPS2, RPS8]
0,00	[-1]	7,81	5,00	[NOP56, NOP58, RPS11, RPS2, RPS8]
0,00	[-1]	6,25	4,00	[DKC1, NOP56, NOP58, RPS2]
0,00	[2, 3]	16,00	4,00	[RPL12, RPL21, RPL7A, RPLP2]
0,00	[3, 8]	4,35	3,00	[DDX39B, EIF4A1, EIF4A2]
0,00	[5, 6, 7]	6,38	3,00	[DDX39B, EIF4A1, EIF4A2]
0,00	[4, 9, 10]	4,41	3,00	[DDX39B, EIF4A1, EIF4A2]
0,00	[-1]	5,77	3,00	[NOP56, NOP58, RPS2]
0,00	[-1]	4,76	3,00	[NOP56, NOP58, RPS2]
0,00	[-1]	5,45	3,00	[NOP56, NOP58, RPS2]
0,00	[-1]	5,36	3,00	[NOP56, NOP58, RPS2]
0,00	[4, 5, 6]	11,11	3,00	[DKC1, NOP56, NOP58]
0,00	[5]	8,82	3,00	[DKC1, NOP56, NOP58]
0,00	[6, 7, 8, 9, 10]	7,32	3,00	[DKC1, NOP56, NOP58]

RETRACTED

Table 3: ClueGO detailed pathway analysis of snoRNAs host genes from snoRNABase and snOPY. ClueGO functionally grouped annotation network represents the relationships between the terms based on the similarity of their associated genes, coming from miRTarBase and microT databases. GO ID: ID of Gene Ontology. GO Term: specific Gene Ontology Term. Ontology Source: source ontology for Gene Ontology. Term p-value: term significance. Term p-value corrected with Bonferroni step-down: term significance after Bonferroni step-down correction. GO Levels: due to complex structure of GO tree (directed acyclic graph), the GO terms can be placed in several levels. Percentage of Associated Genes: percentage of the genes from the uploaded cluster that were associated with the term, compared with all the genes associated with the term. Nr. Genes: number of the genes from the uploaded cluster that were associated with the term. Associated Genes Found: genes from the uploaded cluster that were associated with the term.