

## Supplementary Tables

Supplementary tables describe eight results predicted by PROCOMOSS using Lin Jiang and Kappa measure in each of the datasets MIPS and DIP. Column 6 and 7 of each table describes the most Most Significant GO-terms and GO-id under biological process category. The two tables constructed using the results of PROCOMOSS\_Lin\_bp in Dip dataset and PROCOMOSS\_Kappa\_mf for MIPS dataset are found in main text.

### 1 In MIPS Dataset

Table 1: Protein complexes predicted by PROCOMOSS in MIPS dataset using Kappa measure (biological process)

Sl No.	Real Protein Complex	Com-	Predicted Protein Complex	p-value	% of protein covered	Most Significant GO-term	Go-id
1	mRNA decapping complex		Dcp1 Dcp2 Edc3 Kem1 Rpm2 Ybr094w	1.87E-14	66.67	RNA catabolic process	GO:0006401
2	Actin capping complex		Cap1 Cap2 Yer071c Yir003w	1.80E-14	75.00	covalent chromatin modification	GO:0016569
3	RNA polymerase II general transcription factor TFIID		Taf1 Taf10 Taf2 Taf5 Taf6 Taf7 Taf8 Tef4	7.83E-23	75.00	RNA polymerase II transcriptional preinitiation complex assembly	GO:0051123
4	Kel1/Lte1 complex		Bem2 Fks1 Lte1	1.35E-15	75.00	organelle fission	GO:0048285
5	SBF, SWI4-SWI6-dependent cell cycle box binding factor complex		Swi4 Swi6	2.20E-24	66.67	covalent chromatin modification	GO:0016569
6	Clathrin-associated protein AP-3 complex		Apl5 Apl6 Apm3	1.47E-16	75.00	biological regulation	GO:0065007
7	Complex 346		Gcn5 Ngg1 Pdr1 Sgf29 Spt15 Spt20 Taf1 Taf12 Tao3	1.24E-23	60.00	biological regulation	GO:0065007
8	Sec62/Sec63 complex		Anp1 Fks1 Sec66 Sec72	1.35E-15	66.67	organelle fission	GO:0048285
9	Anaphase-promoting complex, cyclosome		Apc1 Apc2 Apc4 Apc5 Apc9 Cdc16 Cdc23 Cdc27	1.07E-24	88.89	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	GO:0031145
10	Retromer subcomplex		Vps29 Vps35 Vps5	1.47E-16	100	biological regulation	GO:0065007
11	Ric1/Rgp1 complex		Rgp1 Ric1	2.20E-24	66.67	covalent chromatin modification	GO:0016569
12	Gim complexes		Gim3 Pac10 Yke2	1.35E-15	100	organelle fission	GO:0048285
13	Vps27/Hse1 protein complex		Hse1 Vps27	5.15E-22	100	organelle fission	GO:0048285

Table 2: Protein complexes predicted by PROCOMOSS in MIPS dataset using Kappa measure (cellular component)

Sl No.	Real plex	Protein Com-plex	Predicted Protein Complex	p-value	% of protein covered	Most Significant GO-term	Go-id
1	mRNA decapping complex		Dcp1 Dcp2 Edc3 Kem1	1.23E-14	66.67	histone acetylation	GO:0016573
2	Act1/Sac6 complex		Act1 Sac6	1.65E-32	66.67	mitotic cell cycle	GO:0000278
3	Ctf19 protein complex		Chl4 Ctf19 Ctf3 Mcm21 Mcm22 Okp1	7.75E-26	75.00	organelle fission	GO:0048285
4	RNA polymerase II general transcription factor TFIID		Taf1 Taf10 Taf2 Taf5 Taf6 Taf8	6.96E-22	75.00	chromosome organization	GO:0051276
5	SBF, SWI4-SWI6-dependent cell cycle box binding factor complex		Swi4 Swi6	1.25E-27	66.67	covalent chromatin modification	GO:0016569
6	Clathrin-associated protein AP-3 complex		Apl5 Apl6 Apm3	5.67E-16	75	protein localization	GO:0008104
7	Retromer subcomplex		Vps29 Vps35 Vps5	7.90E-16	100	protein acylation	GO:0043543
8	Ric1/Rgp1 complex		Rgp1 Ric1	1.25E-27	66.67	covalent chromatin modification	GO:0016569
9	Gim complexes		Gim3 Pac10 Yke2	6.96E-22	100	chromosome organization	GO:0051276
10	HAP subcomplex of elongator complex		Elp2 Elp3 Elp4 Iki3	1.11E-31	66.67	regulation of transcription	GO:0045449

Table 3: Protein complexes predicted by PROCOMOSS in MIPS dataset using Jiang measure (cellular component)

Sl No.	Real plex	Protein Com-plex	Predicted Protein Complex	p-value	% of protein covered	Most significant GO-terms	GO-id
1	Act1/Sac6 complex		Mgs1 Sac6	1.24E-19	66.67	cellular response to stress	GO:0033554
2	Ctf19 protein complex		Chl4 Ctf19 Ctf3 Mcm21 Mcm22 Nkp1	1.80E-35	66.67	organelle fission	GO:0048285
3	RNA polymerase II general transcription factor TFIID		Taf1 Taf10 Taf2 Taf6 Taf8	5.31E-24	62.50	RNA polymerase II transcriptional preinitiation complex assembly	GO:0051123
4	TRAPP II complex		Bet3 Bet5 Gsg1 Kre11 Trs120 Trs130 Trs20 Trs23 Trs31 Trs33	1.30E-12	83.33	cellular nitrogen compound biosynthetic process	GO:0044271
5	Retromer subcomplex		Vps29 Vps35	2.16E-24	66.67	organelle fission	GO:0048285
6	Ric1/Rgp1 complex		Rgp1 Ric1	4.14E-33	66.67	M phase	GO:0000279
7	Gim complexes		Gim3 Pac10 Yke2	6.59E-07	100	tubulin complex assembly	GO:0007021
8	HAP subcomplex of elongator complex		Elp2 Elp3 Elp4 Iki3	1.80E-35	66.67	organelle fission	GO:0048285
9	Vps27/Hse1 protein complex		Hse1 Vps27	2.62E-18	100	M phase of mitotic cell cycle	GO:0000087
10	Complex 479		Msn5 Num1	1.80E-35	66.67	organelle fission	GO:0048285

Table 4: Protein complexes predicted by PROCOMOSS in MIPS dataset using Lin measure (molecular function)

Sl No.	Real Protein Complex	Predicted Protein Complex	p-value	% of protein covered	Most significant GO-terms	GO-id
1	mRNA decapping complex	Dcp1 Dcp2 Edc3 Kem1	1.53E-20	66.67	histone acetylation	GO:0016573
2	Ctf19 protein complex	Chl4 Ctf19 Ctf3 Mcm21 Mcm22 Nkp1 Okp1	1.43E-36	77.78	organelle fission	GO:0048285
3	RNA polymerase II general transcription factor TFIID	Taf1 Taf10 Taf2 Taf5 Taf6 Taf8	7.83E-23	75	RNA polymerase II transcriptional preinitiation complex assembly	GO:0051123
4	Kell/Lte1 complex	Bem2 Kell Lte1	7.42E-27	75	cellular component organization at cellular level	GO:0071842
5	Spindle pole body	Spc72 Spc97 Spc98 Tub4	1.19E-17	80	histone acetylation	GO:0016573
6	SBF, SWI4-SWI6-dependent cell cycle box binding factor complex	Swi4 Swi6	1.78E-19	66.67	mitotic cell cycle	GO:0000278
7	Clathrin-associated protein AP-3 complex	Apl5 Apl6 Apm3	2.05E-16	75	protein localization	GO:0008104
8	Anaphase-promoting complex, cyclosome	Apc1 Apc2 Apc4 Apc5 Apc9 Cdc16 Cdc23 Cdc27	2.40E-27	88.89	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	GO:0031145
9	Retromer subcomplex	Vps29 Vps35 Vps5	2.05E-16	100	protein localization	GO:0008104
10	Ric1/Rgp1 complex	Rgp1 Ric1	1.78E-19	66.67	mitotic cell cycle	GO:0000278
11	Gim complexes	Gim3 Pac10 Yke2	8.70E-27	100	mitotic cell cycle	GO:0000278
12	HAP subcomplex of elongator complex	Elp2 Elp3 Elp4 Iki3	9.83E-31	66.67	mitotic cell cycle	GO:0000278
13	Complex 479	Msn5 Num1	9.83E-31	66.67	mitotic cell cycle	GO:0000278

## 2 In DIP Dataset

Table 5: Protein complexes predicted by PROCOMOSS in DIP dataset using Lin measure (cellular component)

Sl No.	Real plex	Protein Com-	Predicted Protein Complex	p-value	% of protein covered	Most significant GO-terms	Go-id
1	Mitochondrial ribosomal small subunit		Ehd3 Mrp13 Mrp17 Mrp4 Mrp51 Mrps16 Mrps18 Mrps28 Mrps5 Mrps9 Nam9 Psd2 Rsm10 Rsm22 Rsm23 Rsm24 Rsm25 Rsm26 Rsm27 Rsm7 Ubp10	6.98E-52	70	RNA splicing, via transesterification reactions	GO:0000375
2	Complex 54		Aar2 Brr1 Bud31 Csn12 Cwc2 Lsm4 Msl1 Prp11 Prp19 Prp4 Prp45 Prp9 Smd3 Snu114 Snu23 Snu66 Syf1	1.02E-51	60.71	RNA splicing, via transesterification reactions	GO:0000375
3	Act1/Sac6 complex		Act1 Sac6	3.56E-42	66.67	RNA splicing, via transesterification reactions	GO:0000375
4	Complex 170		Hmg1 Rad51	3.19E-23	66.67	establishment of localization	GO:0051234
5	Complex 173		Ehd3 Mrp13 Mrp17 Mrp4 Mrp51 Mrps16 Mrps18 Mrps28 Mrps5 Mrps9 Nam9 Psd2 Pus7 Rsm10 Rsm22 Rsm23 Rsm24 Rsm26 Rsm7 Ubp10	6.98E-52	74.07	RNA splicing, via transesterification reactions	GO:0000375
6	Ku complex		Yku70 Yku80	3.56E-42	100	RNA splicing, via transesterification reactions	GO:0000375
7	Complex 187		Brr1 Hta1	3.56E-42	100	RNA splicing, via transesterification reactions	GO:0000375
8	Complex 206		Bem2 Ecm16 Ehd3 Mrp13 Mrp17 Mrp4 Mrp51 Mrps18 Mrps28 Mrps5 Psd2 Pus7 Rsm10 Rsm22 Rsm23 Rsm26 Rsm27 Ubp10	6.98E-52	81.81	RNA splicing, via transesterification reactions	GO:0000375
9	Complex 207		Aar2 Bud31 Snt309	8.80E-96	75	RNA splicing, via transesterification reactions	GO:0000375
10	SBF, SWI4-SWI6-dependent cell cycle box binding factor complex		Swi4 Swi6	5.20E-53	66.67	RNA splicing, via transesterification reactions	GO:0000375
11	Complex 263		Aar2 Snu66	9.94E-67	66.67	RNA splicing, via transesterification reactions	GO:0000375
12	Complex 288		Ret1 Rpc17 Rpc19 Rpc25 Rpc37 Rpc53	9.94E-67	75	RNA splicing, via transesterification reactions	GO:0000375
13	cAMP-dependent protein kinase complex		Bcy1 Tpk2	1.02E-51	100	RNA splicing, via transesterification reactions	GO:0000375
14	Complex 317		Kar2 Scj1	3.56E-42	100	RNA splicing, via transesterification reactions	GO:0000375
15	Sec62/Sec63 complex		Anp1 Sec63 Sec66 Sec72	3.77E-25	66.67	transmembrane transport	GO:0055085
16	Complex 411		Aar2 Brr1 Bud31 Cwc2 Ecm2 Isy1 Lea1 Msl1 Prp19 Prp4 Prp45 Rse1 Smd2 Smd3 Snt309 Snu114 Snu23	8.80E-96	65.38	RNA splicing, via transesterification reactions	GO:0000375
17	Complex 436		Brr1 Cbc2 Csn12 Cus1 Lsm4 Prp11 Prp40 Prp42 Prp9 Rse1 Smd1 Smd2 Snp1 Snu56 Snu66 Snu71	1.02E-51	66.67	RNA splicing, via transesterification reactions	GO:0000375

Table 6: Protein complexes predicted by PROCOMOSS in DIP dataset using Lin measure (molecular function)

Sl No.	Real Protein Complex	Com- Predicted Protein Complex	p-value	% of protein covered	Most significant GO-terms	GO-id
1	Complex 26	Atp2 Met18 Rad3 Rpt6 Tfp1 Tub1 Ydj1	7.36E-37	77.78	rRNA processing	GO:0006364
2	19/22S regulator	Ecm29 Mlh2 Pre1 Pre5 Pre9 Rad50 Rpn1 Rpn10 Rpn11 Rpn12 Rpn2 Rpn5 Rpn6 Rpn7 Rpn8 Rpt1 Rpt2 Rpt3 Rpt5 Rpt6 Ubp6 Yku70 Yku80	2.79E-15	67.74	proteolysis involved in cellular protein catabolic process	GO:0051603
3	Ku complex		1.05E-11	100	cellular component biogenesis	GO:0044085
4	Complex 187	Brr1 Hta1	5.09E-66	100	RNA splicing, via transesterification reactions	GO:0000375
5	Complex 207	Aar2 Bud31 Snt309	8.81E-90	75	RNA splicing, via transesterification reactions	GO:0000375
6	Complex 210	Dbp9 Pre8 Spa2 Ymr310c	5.06E-21	100	modification-dependent macromolecule catabolic process	GO:0043632
7	Complex 216	Dbp9 Mds3 Pre5 Pse1 Rpt5 Rrp12 Slx9 Spa2 Ymr310c Yra1	5.06E-21	62.5	modification-dependent macromolecule catabolic process	GO:0043632
8	Complex 238	Dbp9 Spa2	5.06E-21	100	modification-dependent macromolecule catabolic process	GO:0043632
9	Complex 266	Dip2 Mpp10 Nop1 Nop58 Pwp2 Rok1 Utp22 Utp30 Utp6 Utp7 Ylr003c	7.36E-37	68.75	rRNA processing	GO:0006364
10	Complex 307	Nop13 Rlp7	2.11E-31	100	rRNA processing	GO:0006364
11	Sec62/Sec63 complex	Fks1 Sec63 Sec66 Sec72	4.54E-15	66.67	localization	GO:0051179
12	Complex 384	Idh2 Lys12 Rvb2	1.05E-11	75	ribosomal large subunit biogenesis	GO:0042273
1	Complex 411	Aar2 Bud31 Cdc40 Cwc2 Ecm2 Hsh49 Isy1 Lea1 Msl1 Prp19 Prp4 Prp45 Rse1 Smd2 Smd3 Snt309 Snu114	8.81E-90	65.38	RNA splicing, via transesterification reactions	GO:0000375
13	Complex 436	Brr1 Cbc2 Cus1 Lsm4 Prp11 Prp40 Prp42 Prp9 Rse1 Smd1 Smd2 Snp1 Snu56 Snu66 Snu71	5.09E-66	62.50	RNA splicing, via transesterification reactions	GO:0000375
14	Complex 440	Brx1 Drs1 Mak21 Nip7 Noc2 Noc3 Nop4 Spb4 Ytm1	4.23E-33	64.28	rRNA processing	GO:0006364
15	Complex 447	Imp3 Ylr003c	7.36E-37	100	rRNA processing	GO:0006364
16	Complex 473	Ecm29 Rpn1 Rpn10 Rpn11 Rpn12 Rpn3 Rpn6 Rpn8 Rpt2 Ura7	2.79E-15	71.43	proteolysis involved in cellular protein catabolic process	GO:0051603
17	Complex 477	Cct8 Tdh2 Tef1 Ufd4	4.57E-20	66.67	rRNA processing	GO:0006364

Table 7: Protein complexes predicted by PROCOMOSS in DIP dataset using Kappa measure (biological process)

Sl No.	Real Protein Complex	Com- Predicted Protein Complex	p-value	% of protein covered	Most significant GO-term	GO-id
1	20S core particle of the proteasome	Ecm29 Pre1 Pre10 Pre3 Pre5 Pre6 Pre8 Pre9 Pup3 Rpn2 Rpn8	2.14E-31	61.11	proteolysis involved in cellular protein catabolic process	GO:0051603
2	Complex 26	Atp2 Met18 Rad3 Tfp1 Tub1 Ydj1	7.90E-18	66.67	tRNA transcription from RNA polymerase III promoter	GO:0042797
3	RNA polymerase I	Ams1 Cdc14 Rpa12 Rpa190 Rpa49 Rpb10 Rpc31 Rpc40 Rpo26 Sro7	7.90E-18	62.50	tRNA transcription from RNA polymerase III promoter	GO:0042797
4	19/22S regulator	Ecm29 Pre1 Pre5 Rad50 Rpn1 Rpn10 Rpn11 Rpn12 Rpn13 Rpn2 Rpn5 Rpn6 Rpn7 Rpn8 Rpt1 Rpt2 Rpt3 Rpt5 Rpt6 Ubp6 Rpt3 Tub3	2.37E-11	64.51	ubiquitin-dependent protein catabolic process	GO:0006511
5	Complex 109		1.15E-11	100	proteolysis involved in cellular protein catabolic process	GO:0051603
6	Ku complex	Yku70 Yku80	7.90E-18	100	tRNA transcription from RNA polymerase III promoter	GO:0042797
7	Complex 187	Brr1 Hta1	7.36E-49	100	RNA splicing, via transesterification reactions	GO:0000375
8	Complex 204	Psk1 Vas1	7.90E-18	66.67	tRNA transcription from RNA polymerase III promoter	GO:0042797
9	Complex 263	Aar2 Snu66	1.98E-78	66.67	RNA splicing, via transesterification reactions	GO:0000375
10	Complex 288	Ret1 Rpc17 Rpc19 Rpc25 Rpc37 Rpc53	7.90E-18	75	tRNA transcription from RNA polymerase III promoter	GO:0042797
11	Complex 307	Nop13 Rlp7	1.54E-24	100	cellular component biogenesis at cellular level	GO:0071843
12	Complex 384	Idh2 Lys12 Rvb2	2.37E-11	75	ubiquitin-dependent protein catabolic process	GO:0006511
13	Complex 440	Brx1 Drs1 Mak21 Nip7 Noc2 Noc3 Nop4 Spb4 Ytm1	1.33E-31	64.28	rRNA processing	GO:0006364
14	Complex 446	Aro1 Rps0a	1.15E-11	66.67	proteolysis involved in cellular protein catabolic process	GO:0051603
15	Complex 450	Ams1 Rpa190 Rpa49 Rpb10 Rpc31 Rpc40 Rpc82 Rpo31 Sro7	7.90E-18	75	tRNA transcription from RNA polymerase III promoter	GO:0042797
16	Complex 473	Ecm29 Rpn1 Rpn10 Rpn11 Rpn12 Rpn3 Rpn6 Rpn8 Rpt2 Ura7	2.37E-11	71.43	ubiquitin-dependent protein catabolic process	GO:0006511
17	Complex 474	Hta1 Tos4	1.33E-31	100	rRNA processing	GO:0006364
18	Complex 480	Cys4 Sse1	1.74E-64	66.67	RNA splicing, via transesterification reactions	GO:0000375

Table 8: Protein complexes predicted by PROCOMOSS in DIP dataset using Jiang measure (molecular function)

Sl No.	Real Protein Complex	Predicted Protein Complex	p-value	% of protein covered	Most significant GO-term	GO-id
1	20S core particle of the proteasome	Ecm29 Pre1 Pre10 Pre2 Pre3 Pre5 Pre6 Pre8 Pre9 Pup3 Rpn2 Rpn8	2.06E-29	66.67	proteolysis involved in cellular protein catabolic process	GO:0051603
2	Complex 26	Atp2 Met18 Rad3 Rpt6 Tfp1 Tub1 Ydj1	5.07E-19	77.77	proteolysis involved in cellular protein catabolic process	GO:0051603
3	19/22S regulator	Ecm29 Pre1 Pre5 Pre9 Rpn1 Rpn11 Rpn12 Rpn13 Rpn2 Rpn5 Rpn6 Rpn7 Rpn8 Rpt1 Rpt2 Rpt3 Rpt5 Rpt6 Ubp6	5.07E-19	61.29	proteolysis involved in cellular protein catabolic process	GO:0051603
4	Complex 102	Npl3 Nrp1	2.61E-37	66.67	rRNA processing	GO:0006364
5	Ku complex	Yku70 Yku80	3.77E-16	100	cellular response to stress	GO:0033554
6	Complex 250	Bms1 Ecm16 Utp7 Ygr054w	7.78E-57	66.67	rRNA processing	GO:0006364
7	Complex 264	Ade6 Pet123	5.37E-25	100	rRNA processing	GO:0006364
8	Complex 270	Clu1 Ura7	5.37E-25	100	rRNA processing	GO:0006364
9	Complex 307	Nop13 Rlp7	5.37E-25	100	rRNA processing	GO:0006364
10	Complex 440	Brx1 Drs1 Mak21 Nip7 Noc2 Noc3 Nop4 Spb4 Ytm1	5.37E-25	64.29	rRNA processing	GO:0006364
11	Complex 472	Dbp10 Dbp9 Drs1 Nip7 Nop13 Nop4 Pol5 Rix7 Rlp7 Rrp12	5.37E-25	66.67	rRNA processing	GO:0006364
12	Complex 473	Ecm29 Rpn1 Rpn11 Rpn12 Rpn3 Rpn6 Rpn8 Rpt2 Ura7	5.07E-19	64.29	proteolysis involved in cellular protein catabolic process	GO:0051603