				protein-protein interaction							co-citation							mips						
networks	pairs	p<=0.01	p>0.01	+	-	tp	fp	tn	fn		+	-	tp	fp	tn	fn		+	-	tp	fp	tn	fn	
in-silico vs. *in-silico*	471	33	438	1	279	0	17	262	1	0.0%	36	346	3	18	328	33	8.3%	0	29	0	2	27	0	
in-silico vs. mutant	2873	22	2851	6	1424	0	13	1411	6	0.0%	53	1505	3	14	1491	50	5.7%	1	239	0	1	238	1	0.0%
in-silico vs. ChIP	2342	25	2317	7	1040	1	17	1023	6	14.3%	77	1512	8	14	1498	69	10.4%	8	145	3	3	142	5	37.5%
mutant vs. mutant	4278	578	3700	20	1750	4	216	1534	16	20.0%	56	1484	23	221	1263	33	41.1%	14	421	7	46	375	7	50.0%
mutant vs. ChIP	7664	49	7615	15	2957	1	32	2925	14	6.7%	80	3505	7	33	3472	73	8.8%	4	625	0	1	624	4	0.0%
ChIP vs. ChIP	3414	174	3240	11	1225	6	78	1147	5	54.5%	85	2005	22	84	1921	63	25.9%	15	199	7	10	189	8	46.7%

Comparison of target sets from ChIP networks are best for the prediction of protein-protein interactions, whereas comparion of target sets from the mutant network are better for the identification of MIPS complexes or co-citations in Medline abstracts. pairs: number of target sets from the indicated networks which were compared; the number of similar target sets (threshold for p-value = 0.01); +(-): number of pairs that are (not) connected in the respective reference network; tp true-positives, i.e. correctly predicted pairs, fp: false-positives falsly predicted pairs, tn true-negatives correctly not-predicted pairs, fn false-negatives missed pairs; the percentage given is the ratio of correctly predicted pairs over all pairs to be identified (tp/+); ChIP networks are combined increase the data basis, if one source gene is present in several ChIP networks, then the comparison result with the lowest p-value was used