		Table 8. Correlation between X= marker profile for MTR3 and Y= any gene profile
Gene Y	CORR	Gene Information
YOR300W	0.616	Up in Starvation
PBP1	0.509	Poly(A)-binding protein binding protein
YOR081C	0.498	Protein of unknown function, localizes to lipid particles; potential Cdc28p substrate
ACH1	0.480	acetyl CoA hydrolase
SSA4	0.464	HSP70 family
CIT1	0.463	citrate synthase
HSP26	0.462	heat shock protein 26
GSY2	0.450	glycogen synthase (UDP-glucose-starch glucosyltransferase)
CIN5	0.448	bZIP (basic-leucine zipper) protein can activate transcription from a promoter containing a Yap recognition site
YPL230W	0.445	Up in Starvation
HAP4	0.444	transcriptional activator protein of CYC1 (component of HAP2/HAP3 heteromer)
YPR152C	0.440	-
SOD2	0.437	Mn-containing superoxide dismutase
CDC15	0.429	protein kinase domain
YPL014W	0.423	-
MSN4	0.422	zinc finger protein
YDL197C	0.418	-
RPI1	0.413	ras inhibitor
YMR279C	0.413	-
ECM30	0.407	Non-essential protein of unknown function
BIO2	-0.530	biotin synthase
PHO81	-0.488	Positive regulatory protein of phosphate pathway
MTR3	-0.481	Involved in mRNA transport
YGR154C	-0.475	-
PDH1	-0.451	prpD homologue; (62% identical to the prpD genes of Escherichia coli and Salmonella typhimurium, which play an unknown but essential role in propionate catabolism)
YLR334C	-0.449	-
STB6	-0.412	binds Sin3p in two-hybrid assay
VPS33	-0.409	vacuolar sorting protein essential for vacuolar morphogenesis and function
MET8	-0.396	Bifunctional dehydrogenase and ferrochelatase, involved in the biosynthesis of siroheme; also involved in the expression of PAPS reductase and sulfite reductase
YDR415C	-0.388	-
CHS7	-0.385	The seventh gene identified that is involved in chitin synthesis; involved in Chs3p export from the ER
YOL166C	-0.382	-
YOL164W	-0.381	-
YGL050W	-0.381	-
YAL035C-A	-0.380	-
MFA1	-0.376	a-factor mating pheromone precursor
YDL114W	-0.376	-
YNL170W	-0.372	Sporulation
YBR190W	-0.371	Protein required for cell viability
PTC1	-0.369	serine-threonine protein phosphatase