

<i>D. melanogaster - A. vulgare</i>		<i>D. melanogaster - C. capitata</i>		<i>D. melanogaster - H. saltator</i>	
Genes	Distances	Genes	Distances	Genes	Distances
Casein kinase	0,218	Neuroendocrine convertase II	0,165	ATPase B vacuole	0,186
ATP synthase	0,232	Ca/Calmodulin-dependent protein kinase 2	0,192	gluc-6-P 1-dehydrogenase	0,202
Alpha-spectrin 2	0,238	ATPase B vacuole	0,196	Elongation factor 1 alpha 48D	0,214
Protein kinase	0,27	glucose-6-phosphate 1-dehydrogenase	0,204	Myosin	0,253
mRNA splicing spliceosome associated protein	0,299	Casein kinase 2 alpha subunit	0,206	pre-mRNA splicing processing factor 8	0,269
Prohormone convertase	0,301	Translation elongation factor II	0,206	Casein kinase 2 alpha subunit	0,271
Acétyl-glucosaminyl transferase Super sexcombs	0,304	protein phosphatase PP2A 55kDa regulation subunit	0,215	Glycogene synthase activity	0,281
ARN pol	0,316	Oscillin (N-glucosamine-6-phosphate isomerase)	0,221	F-box 11	0,285
Alpha spectrin	0,322	Shibire dynamin	0,227	Rpd3 histone deacetylase	0,287
Neurofibromine	0,328	Clathrin heavy chain F	0,233	ATP depdt helicase activity	0,292
Proteasome subunit	0,332	DNA-directed RNA pol II subunit RPB1 (plus long)	0,241	DNA-directed RNA pol II subunit RPB1 (plus long)	0,296
Histone deacetylase	0,334	Alpha adaptin A (Cc : P2 subunit alpha)	0,246	RNA pol II	0,304
Arginin methyl-transferase	0,338	RNA pol II	0,246	Clathrin heavy chain F 2	0,308
RNA pol II	0,353	Super sexcombs B (Cc : UDP N-acetylglucosamine)	0,252	phosphatase protein kinase type 1	0,314
Glucose phosphate dehydrogenase	0,358	pre-mRNA splicing processing factor 8	0,253	pre-mRNA processing factor	0,325
F-box protein	0,367	Clathrin heavy chain F 2	0,257	mRNA splicing	0,326
Alpha adaptin	0,369	Myosin	0,257	DNA-directed RNA pol II subunit RPB1	0,327
Myosin	0,369	ATPase vacuole H+	0,259	RNA pol II	0,33
Clathrin heavy chain	0,37	RNA pol II	0,259	Super sexcombs B	0,354
ATP dependent Helicase activity RNA helicase	0,373	pre-mRNA processing factor 8	0,26	Alpha-spectrin D	0,355
ATPase	0,376	DNA-directed RNA pol II subunit RPB1	0,26	Arginine methyl-transferase 1	0,356
pre-mRNA processing factor 8	0,379	Alpha spectrin	0,266	Alpha adaptin A	0,362
Triose phosphate isomerase	0,386	Fbox 11	0,268	Clathrin heavy chain F	0,362
Elongation factor 1 alpha	0,39	Rpd3 histone deacetylase	0,27	ATPase vacuole H+	0,367
RNA pol II largest subunit	0,396	mRNA splicing (Cc : splicing factor 3B subunit 1)	0,273	Leu tRNA	0,374
Elongation factor 2	0,401	ATP dependent helicase activity	0,275	Oscillin	0,384
Carmine (clathrin adaptor)	0,403	Burgundy (Cc : GMP synthase)	0,278	transmembrane 9 superfamily member2	0,385
ATP dependent helicase activity RNA helicase	0,405	ATP dependent helicase activity	0,281	protein phosphatase PP2A 55kDa regulation subunit	0,393
protéine transmembranaire	0,408	Myosin	0,29	Neurofibromin 1	0,394
Protein kinase 1	0,41	Leu tRNA	0,296	Neuroendocrine convertase II	0,407
Shibire (dynamin)	0,411	Integrin linked protein kinase	0,299	insert cDNA	0,41
Clathrin heavy chain 2	0,412	Carmine (Cc : AP3 complex subunit mu 2)	0,301	Myosin	0,42
Protein phosphatase	0,421	elongation factor 1-alpha 48D	0,306	Replication licensing factor	0,424
Burgundy Glycine amidotransferase	0,423	Alanine tRNA synthetase	0,31	Pugilist E	0,425
RNA pol II largest subunit (autre)	0,425	Alpha spectrin D	0,31	Integrin linked-kinase	0,441
pre-mRNA splicing factor	0,427	Replication licensing factor	0,315	triose phosphate isomerase	0,521
Replication licensing factor	0,429	Arginine methyl-transferase 1	0,316	Burgundy	0,56
Oscillin glucose phosphate isomerase	0,433	Glycogen synthase activity	0,328		
Acetyl coenzyme A carboxylase	0,434	cAMP-depdt protein kinase type I regulation subunit	0,339		
Alpha-spectrin	0,441	Pugilist E (Cc : c-1-tetrahydrofolate synthase cytoplasmic	0,436		
Myosin	0,442	transmembrane 9 superfamily member2	0,457		
Leucine tRNA synthetase	0,451			Average	0,345
Alanine tRNA synthetase	0,464			Min	0,186
Glycogene synthase	0,471			Max	0,560
Pugilist E tetrahydrofolate synthetase	0,493				
Integrin-linked kinase	0,499				
Average	0,379				
Min	0,218				
Max	0,499				