

Supplementary Tables 3+4. Results of PAML analyses

Supplementary Table 3. Sperm phosphoproteins with (with) and without Y phosphorylation (without) in human probands: Results of PAML analyses

Protein	Y phos- phorylation	l_{M8A}	l_{M8}	$2\Delta l$ (LRT)	P	dN/dS (M8a)	aa distance (JTT)
ACADS	without	-3359.655	-3359.263	0.784	>0.010	0.084	0.089
ACRBP	with	-5096.052	-5095.310	1.483	>0.010	0.191	0.188
ACTA2	with	-2662.297	-2662.297	0.000	1.000	0.007	0.005
AK8	without	-3075.259	-3074.451	1.616	>0.010	0.219	0.205
ANXA1	with	-2841.260	-2841.254	0.012	>0.010	0.167	0.110
APEH	without	-5554.810	-5554.810	0.000	1.000	0.134	0.080
CAPZA1	with	-1708.410	-1708.410	0.000	1.000	0.055	0.022
CAPZB	without	-1402.024	-1393.784	16.479	<0.010**	0.011	0.004
CRISP1	without	-3306.755	-3304.448	4.614	>0.010	0.515	0.459
DNAJB11	with	-2265.394	-2265.383	0.023	>0.010	0.041	0.021
ECI1	with	-3275.550	-3275.550	0.000	1.000	0.226	0.258
ENO1	without	-3191.276	-3191.275	0.000	1.000	0.052	0.041
GDI2	without	-3283.128	-3283.127	0.002	>0.010	0.027	0.030
GK2	without	-5087.027	-5086.710	0.634	>0.010	0.212	0.146
GLUL	without	-2677.369	-2677.369	0.000	1.000	0.051	0.044
GOT1	without	-3878.461	-3878.461	0.000	1.000	0.188	0.119
GSTM3	with	-2037.902	-2037.902	0.000	1.000	0.185	0.232
HIBADH	with	-2451.975	-2451.948	0.055	>0.010	0.110	0.066
HSPA1L	with	-4855.114	-4855.114	0.000	1.000	0.031	0.036

Protein	Y phos- phorylation	l_{M8A}	l_{M8}	$2\Delta l$ (LRT)	P	dN/dS (M8a)	aa distance (JTT)
HSPA9	without	-4566.448	-4566.448	0.000	1.000	0.026	0.016
HSPD1	without	-3711.347	-3711.347	0.000	1.000	0.034	0.022
IDH3A	without	-2510.243	-2510.243	0.000	1.000	0.032	0.020
LAP3	without	-4239.762	-4239.762	0.000	1.000	0.111	0.085
LZTFL1	without	-2242.124	-2242.124	0.000	1.000	0.113	0.071
MPST	with	-2713.497	-2713.178	0.638	>0.010	0.085	0.140
NME5	without	-733.235	-733.185	0.100	>0.010	0.146	0.075
NME7	without	-2126.723	-2126.723	0.000	1.000	0.128	0.101
ODF1	without	-1629.074	-1628.605	0.937	>0.010	0.019	0.021
PARK7	with	-1760.435	-1759.903	-1.065	>0.010	0.143	0.093
PCYT2	without	-3212.773	-3212.770	0.006	>0.010	0.088	0.093
PDHB	without	-2622.500	-2622.419	0.162	>0.010	0.075	0.052
PHB	without	-1845.918	-1845.918	0.000	1.000	0.002	0.002
PPP1CB	without	-1854.085	-1854.085	0.001	>0.010	0.000	0.000
PRDX4	without	-1795.878	-1795.878	0.000	1.000	0.105	0.050
PSMA1	without	-1723.276	-1723.276	0.000	1.000	0.017	0.015
PSMA6	without	-1429.224	-1429.224	0.000	1.000	0.007	0.003
PSMB2	without	-1347.091	-1347.091	0.000	1.000	0.047	0.029
PSMB3	without	-1364.632	-1364.334	0.597	>0.010	0.027	0.018
PSMC2	without	-2868.020	-2868.020	0.000	1.000	0.001	0.001
PSMD11	with	-2401.510	-2401.510	0.000	1.000	0.005	0.002
PSMD13	without	-2626.978	-2626.978	0.000	1.000	0.035	0.027
PSMD14	with	-1721.882	-1721.882	0.000	1.000	0.000	0.000

Protein	Y phos- phorylation	l_{M8A}	l_{M8}	$2\Delta l$ (LRT)	P	dN/dS (M8a)	aa distance (JTT)
ROPN1	with	-1746.853	-1746.853	0.000	1.000	0.141	0.107
SDHA	with	-5614.220	-5614.220	0.000	1.000	0.073	0.063
SPAG6	without	-3705.312	-3705.312	0.000	1.000	0.036	0.029
TEKT1	with	-3816.973	-3816.932	0.080	>0.010	0.164	0.141
TUBA1A	without	-2947.934	-2947.934	0.000	1.000	0.006	0.006
TUBB2A	without	-3478.649	-3478.625	-0.048	>0.010	0.024	0.041
TUBB2C	with	-2725.630	-2725.630	0.000	1.000	0.000	0.000
UQCRC1	with	-4031.202	-4031.202	0.000	1.000	0.147	0.104
YWHAZ	without	-1339.842	-1339.842	0.000	1.000	0.004	0.002

aa, amino acid; Δl , log likelihood difference; dN/dS, ratio of non-synonymous to synonymous substitution rates; JTT, JTT substitution matrix; l , log likelihood; M8A, null version of beta model M8; M8, alternative version of beta model M8; P , probability of alpha error; PAML, Phylogenetic Analysis by Maximum Likelihood v. 4.4. Analyses were carried out based on orthologs of six mammalian species. Asterisks (**) highlight significance at the 1% level of significance.

Supplementary Table 4. Sperm proteins that were non-phosphorylated in human probands: Results of PAML analyses

Protein	l_{M8A}	l_{M8}	$2\Delta l$ (LRT)	P	dN/dS (M8a)	aa distance (JTT)
ALDH9A1	-4471.859	-4468.178	7.363	<0.010**	0.184	0.105
CRISP2	-2456.411	-2451.860	9.102	<0.010**	0.351	0.236
DLD	-3494.111	-3494.111	0.000	1.000	0.073	0.046
DNAJB8	-1984.602	-1984.340	0.524	>0.010	0.053	0.111
ECHS1	-2624.481	-2624.326	0.309	>0.010	0.158	0.129
PRDX2	-1536.979	-1536.376	1.206	>0.010	0.079	0.074
SPESP1	-3929.851	-3920.146	19.409	<0.010**	0.572	0.398
TEKT2	-3510.132	-3510.132	0.000	1.000	0.153	0.114

aa, amino acid; Δl , log likelihood difference; dN/dS, ratio of non-synonymous to synonymous substitution rates; JTT, JTT substitution matrix; l , log likelihood; M8A, null version of beta model M8; M8, alternative version of beta model M8; P , probability of alpha error; PAML, Phylogenetic Analysis by Maximum Likelihood v. 4.4. Analyses were carried out based on orthologs of six mammalian species. Asterisks (**) highlight significance at the 1% level of significance.