

Supplement Tables

Suppl. Table 1. General linear model results from comparison between mean peptide reactivity in different libraries (for library designation see Table 1).

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
pep5pred - pep5 == 0	0.040685	0.036587	1.112	0.9502
pepneg - pep5 == 0	-0.101131	0.039385	-2.568	0.1563
pepneglo - pep5 == 0	-0.001002	0.075444	-0.013	1
pepnegrnd - pep5 == 0	-0.390134	0.036239	-10.766	< 0.0010 ***
pepoth5 - pep5 == 0	0.059812	0.03348	1.786	0.6110
peppos - pep5 == 0	0.081682	0.03848	2.123	0.3810
peprnd - pep5 == 0	-0.115647	0.036324	-3.184	0.0286 *
pepneg - pep5pred == 0	-0.141816	0.037469	-3.785	0.0035 **
pepneglo - pep5pred == 0	-0.041687	0.074462	-0.56	0.9992
pepnegrnd - pep5pred == 0	-0.430819	0.034148	-12.616	< 0.0010 ***
pepoth5 - pep5pred == 0	0.019127	0.031204	0.613	0.9985
peppos - pep5pred == 0	0.040997	0.036517	1.123	0.9477
peprnd - pep5pred == 0	-0.156332	0.034237	-4.566	< 0.0010 ***
pepneglo - pepneg == 0	0.100129	0.075876	1.32	0.8832
pepnegrnd - pepneg == 0	-0.289003	0.037129	-7.784	< 0.0010 ***
pepoth5 - pepneg == 0	0.160943	0.034442	4.673	< 0.0010 ***
peppos - pepneg == 0	0.182813	0.03932	4.649	< 0.0010 ***
peprnd - pepneg == 0	-0.014516	0.037212	-0.39	1
pepnegrnd - pepneglo == 0	-0.389132	0.074292	-5.238	< 0.0010 ***
pepoth5 - pepneglo == 0	0.060814	0.072986	0.833	0.9903
peppos - pepneglo == 0	0.082684	0.07541	1.096	0.9539
peprnd - pepneglo == 0	-0.114645	0.074333	-1.542	0.7706
pepoth5 - pepnegrnd == 0	0.449946	0.030795	14.611	< 0.0010 ***
peppos - pepnegrnd == 0	0.471816	0.036168	13.045	< 0.0010 ***
peprnd - pepnegrnd == 0	0.274487	0.033865	8.105	< 0.0010 ***
peppos - pepoth5 == 0	0.02187	0.033404	0.655	0.9978
peprnd - pepoth5 == 0	-0.175459	0.030895	-5.679	< 0.0010 ***
peprnd - peppos == 0	-0.197329	0.036253	-5.443	< 0.0010 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

Suppl. Table 2. GLM results from comparison of mean nearest neighbor distance between peptide profiles in different libraries (for library designation see Table 1).

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: glm(formula = log(value) ~ L1, data = mc10c1nndist)

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)	
pep5pred - pep5 == 0	-0.0463163	0.0204399	-2.266	0.29596	
pepneg - pep5 == 0	-0.0314013	0.0220028	-1.427	0.83374	
pepneglo - pep5 == 0	0.2372490	0.0421481	5.629	< 0.001	***
pepnegrnd - pep5 == 0	-0.0576799	0.0202455	-2.849	0.07630	.
pepoth5 - pep5 == 0	-0.0583229	0.0187041	-3.118	0.03474	*
peppos - pep5 == 0	0.0708564	0.0214974	3.296	0.01993	*
peprnd - pep5 == 0	-0.0260619	0.0202927	-1.284	0.89734	
pepneg - pep5pred == 0	0.0149150	0.0209328	0.713	0.99629	
pepneglo - pep5pred == 0	0.2835652	0.0415995	6.817	< 0.001	***
pepnegrnd - pep5pred == 0	-0.0113636	0.0190771	-0.596	0.99882	
pepoth5 - pep5pred == 0	-0.0120067	0.0174327	-0.689	0.99701	
peppos - pep5pred == 0	0.1171727	0.0204009	5.744	< 0.001	***
peprnd - pep5pred == 0	0.0202544	0.0191272	1.059	0.96175	
pepneglo - pepneg == 0	0.2686503	0.0423893	6.338	< 0.001	***
pepnegrnd - pepneg == 0	-0.0262786	0.0207429	-1.267	0.90381	
pepoth5 - pepneg == 0	-0.0269216	0.0192415	-1.399	0.84765	
peppos - pepneg == 0	0.1022577	0.0219666	4.655	< 0.001	***
peprnd - pepneg == 0	0.0053394	0.0207890	0.257	1.00000	
pepnegrnd - pepneglo == 0	-0.2949288	0.0415043	-7.106	< 0.001	***
pepoth5 - pepneglo == 0	-0.2955719	0.0407746	-7.249	< 0.001	***
peppos - pepneglo == 0	-0.1663925	0.0421291	-3.950	0.00185	**
peprnd - pepneglo == 0	-0.2633108	0.0415273	-6.341	< 0.001	***
pepoth5 - pepnegrnd == 0	-0.0006431	0.0172043	-0.037	1.00000	
peppos - pepnegrnd == 0	0.1285363	0.0202060	6.361	< 0.001	***
peprnd - pepnegrnd == 0	0.0316180	0.0189192	1.671	0.68953	
peppos - pepoth5 == 0	0.1291794	0.0186614	6.922	< 0.001	***
peprnd - pepoth5 == 0	0.0322611	0.0172599	1.869	0.55321	
peprnd - peppos == 0	-0.0969183	0.0202533	-4.785	< 0.001	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)

Suppl. Table 3. GLM results from comparison between z-score transformed mean correlation between patient profiles in different libraries (for library designation see Table 1).

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: glm(formula = value ~ variable, data = corptzm)

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z)	
pep5pred - pep5 == 0	0.010342	0.027400	0.377	0.99995	
pepneg - pep5 == 0	-0.024782	0.027400	-0.904	0.98574	
pepneglo - pep5 == 0	-0.114978	0.027400	-4.196	< 0.001	***
pepnegrnd - pep5 == 0	-0.059773	0.027400	-2.181	0.36269	
pepoth5 - pep5 == 0	-0.003980	0.027400	-0.145	1.00000	
peppos - pep5 == 0	-0.133697	0.027400	-4.879	< 0.001	***
peprnd - pep5 == 0	-0.051258	0.027400	-1.871	0.57126	
pepneg - pep5pred == 0	-0.035123	0.027400	-1.282	0.90583	
pepneglo - pep5pred == 0	-0.125319	0.027400	-4.574	< 0.001	***
pepnegrnd - pep5pred == 0	-0.070115	0.027400	-2.559	0.17162	
pepoth5 - pep5pred == 0	-0.014322	0.027400	-0.523	0.99955	
peppos - pep5pred == 0	-0.144039	0.027400	-5.257	< 0.001	***
peprnd - pep5pred == 0	-0.061600	0.027400	-2.248	0.32313	
pepneglo - pepneg == 0	-0.090196	0.027400	-3.292	0.02225	*
pepnegrnd - pepneg == 0	-0.034991	0.027400	-1.277	0.90753	
pepoth5 - pepneg == 0	0.020801	0.027400	0.759	0.99505	
peppos - pepneg == 0	-0.108915	0.027400	-3.975	0.00182	**
peprnd - pepneg == 0	-0.026476	0.027400	-0.966	0.97906	
pepnegrnd - pepneglo == 0	0.055204	0.027400	2.015	0.47168	
pepoth5 - pepneglo == 0	0.110997	0.027400	4.051	0.00127	**
peppos - pepneglo == 0	-0.018719	0.027400	-0.683	0.99744	
peprnd - pepneglo == 0	0.063720	0.027400	2.325	0.28004	
pepoth5 - pepnegrnd == 0	0.055793	0.027400	2.036	0.45724	
peppos - pepnegrnd == 0	-0.073924	0.027400	-2.698	0.12324	
peprnd - pepnegrnd == 0	0.008515	0.027400	0.311	0.99999	
peppos - pepoth5 == 0	-0.129717	0.027400	-4.734	< 0.001	***
peprnd - pepoth5 == 0	-0.047278	0.027400	-1.725	0.67064	
peprnd - peppos == 0	0.082439	0.027400	3.009	0.05339	.

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)