

# Supplementary Information

## **Co-evolution of Alpha-helical Transmembrane Protein Residues: Large-Scale Variant Profiling and Complete Mutational Landscape of 2277 known PDB Entries Representing 504 Unique Human Protein Sequences**

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**Supplementary Table 1. Comprehensive Dataset of Studied 504 UniProt Entries with RCSB PDB IDs, FASTA Sequences, and Functional Annotations**

This material is provided as a separate Excel file named "2-Supplementary\_Table\_1.xlsx".

**Supplementary Table 2. Comprehensive List of 2277 Relevant RCSB PDB Structures for Studied Proteins**

This material is provided as a separate Excel file named "3-Supplementary\_Table\_2.xlsx".

**Supplementary Table 3. Combined AlphaMissense Pathogenicity Scores Grouped by Initial Amino Acid in Studied Proteins**

This material is provided as a separate Excel file named "4-Supplementary\_Table\_3.xlsx".

**Supplementary Figure 1. Combined Topology Prediction Results for Studied Proteins**

These results show the topology predictions for the proteins studied using the Phobius tool, with the exception of DCD and PGAM5, where predictions failed to indicate transmembrane topology and were inconsistent with UniProt data.

This material is provided as a separate .PDF file named "5-Supplementary\_Figure\_1.pdf".

**Supplementary Figure 2. Combined Hydropathy Plots for Studied Proteins**

Hydropathy plots generated using the Kyte-Doolittle scale illustrate the hydrophobic properties of the protein sequences.

This material is provided as a separate .PDF file named "6-Supplementary\_Figure\_2.pdf".

**Supplementary Table 3a. Distribution of Potential Variants with Initial Hydrophobic Amino Acids Across Studied Proteins.**

<b>Amino acid change</b>	<b>Count</b>	<b>Z-score</b>	<b>MAD-score</b>
<b>A&gt;X</b>	427,603	0.6357	0.6941
<b>C&gt;X</b>	140,272	-1.1293	-1.3627
<b>F&gt;X</b>	311,370	-0.0783	-0.1379
<b>G&gt;X</b>	373,864	0.3056	0.3094
<b>I&gt;X</b>	349,913	0.1585	0.1379
<b>L&gt;X</b>	675,713	2.1598	2.4700
<b>M&gt;X</b>	143,550	-1.1091	-1.3392
<b>P&gt;X</b>	297,719	-0.1621	-0.2357
<b>V&gt;X</b>	422,136	0.6021	0.6549
<b>W&gt;X</b>	98,986	-1.3829	-1.6582

**Supplementary Table 3b. Descriptive Statistics for Data in Supplementary Table 3a.**

<b>Statistic</b>	<b>Value</b>
Total	3,241,126
Median	330,641.5
Mean	324,112.6
Standard deviation	162,795.50
Q1 (25th percentile)	182,092.25
Q3 (75th percentile)	410,068
IQR (Interquartile Range)	227,975.75
Lower Bound (5% tolerance margin)	-167,864.94
Upper Bound (5% tolerance margin)	789,633.20
MAD (Median Absolute Deviation)	139,702.43

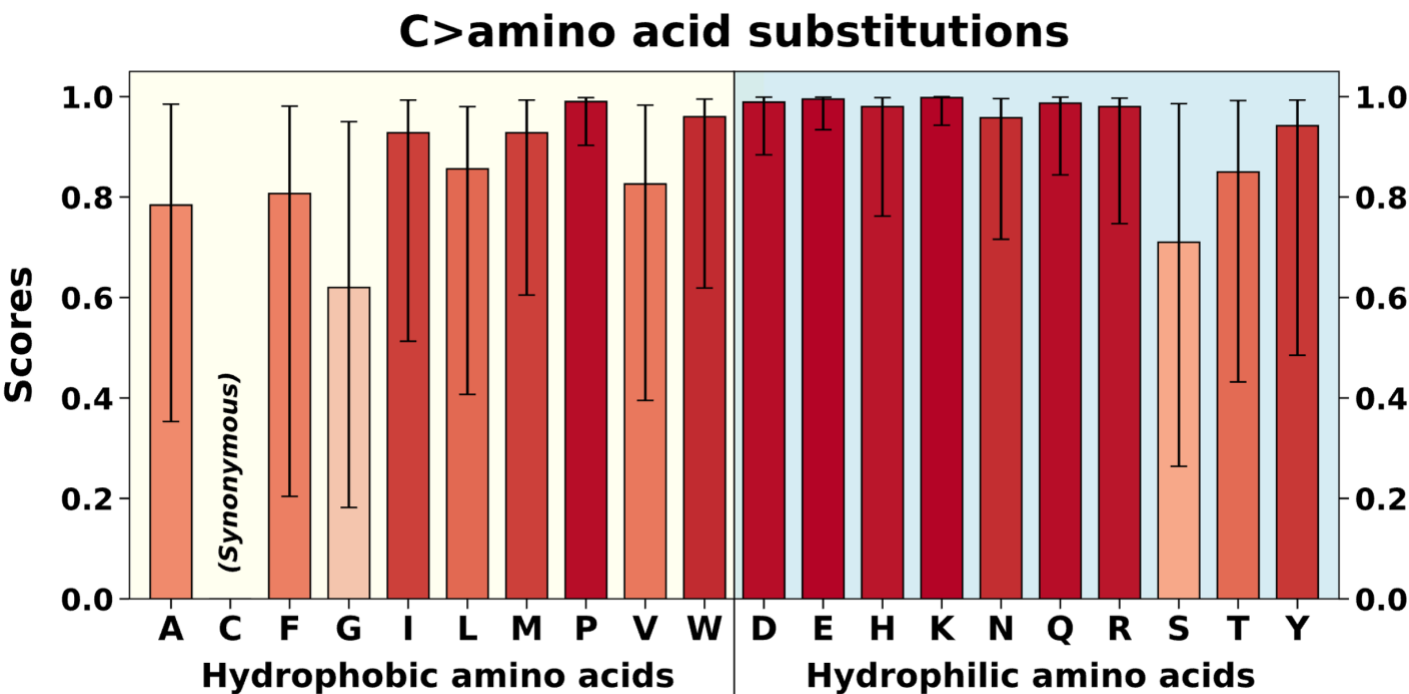
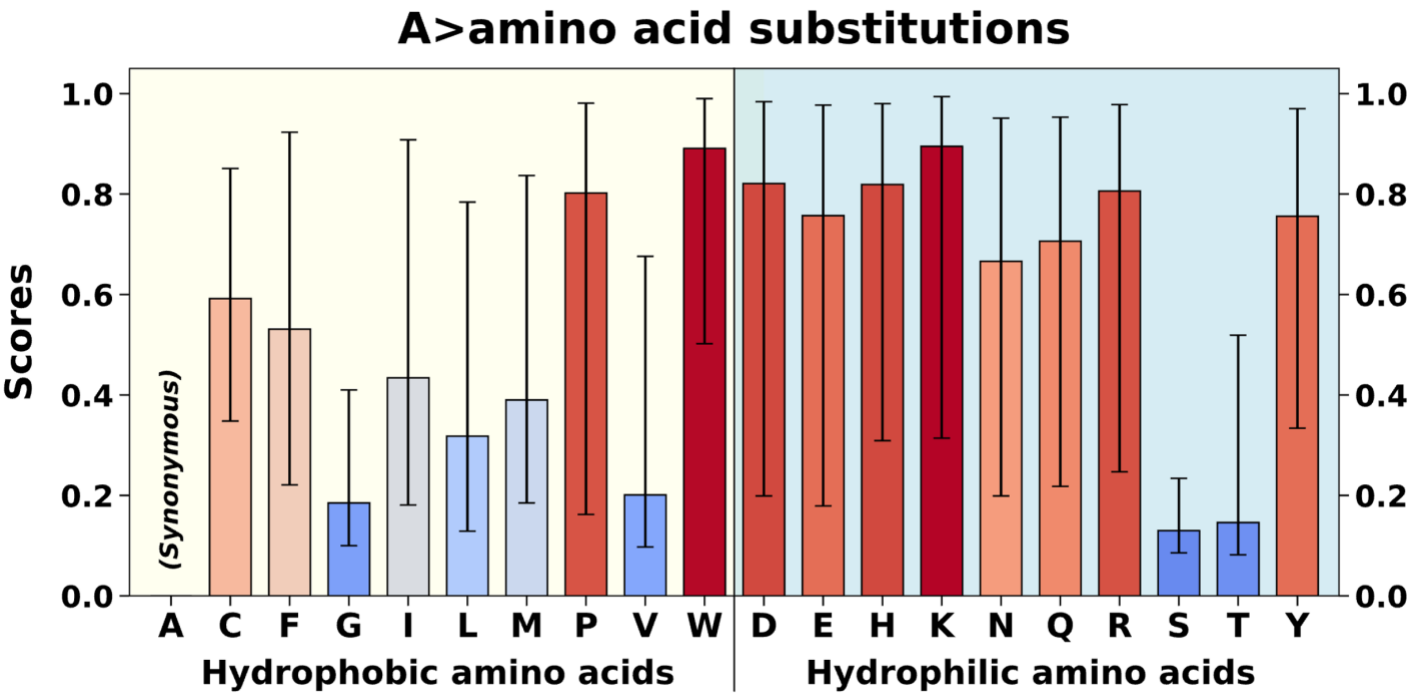
**Supplementary Table 4a. Distribution of Potential Variants with Initial Hydrophilic Amino Acids Across Studied Proteins.**

<b>Amino acid change</b>	<b>Count</b>	<b>Z-score</b>	<b>MAD-score</b>
<b>D&gt;X</b>	233,722	-0.3234	-0.1767
<b>E&gt;X</b>	304,628	0.5318	0.7202
<b>H&gt;X</b>	125,576	-1.6277	-1.5448
<b>K&gt;X</b>	261,662	0.0136	0.1767
<b>N&gt;X</b>	223,654	-0.4448	-0.3041
<b>Q&gt;X</b>	205,534	-0.6633	-0.5333
<b>R&gt;X</b>	297,756	0.4489	0.6333
<b>S&gt;X</b>	445,390	2.2294	2.5009
<b>T&gt;X</b>	316,328	0.6729	0.8682
<b>Y&gt;X</b>	191,117	-0.8372	-0.7157

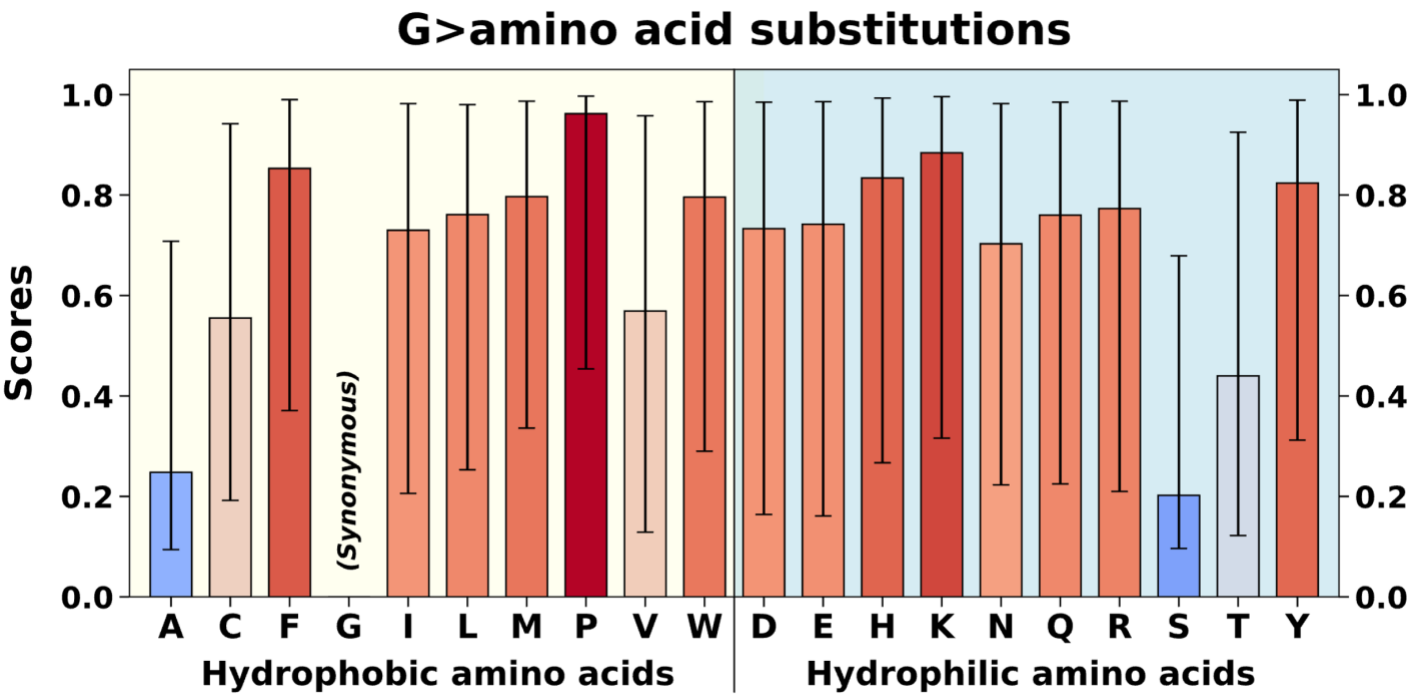
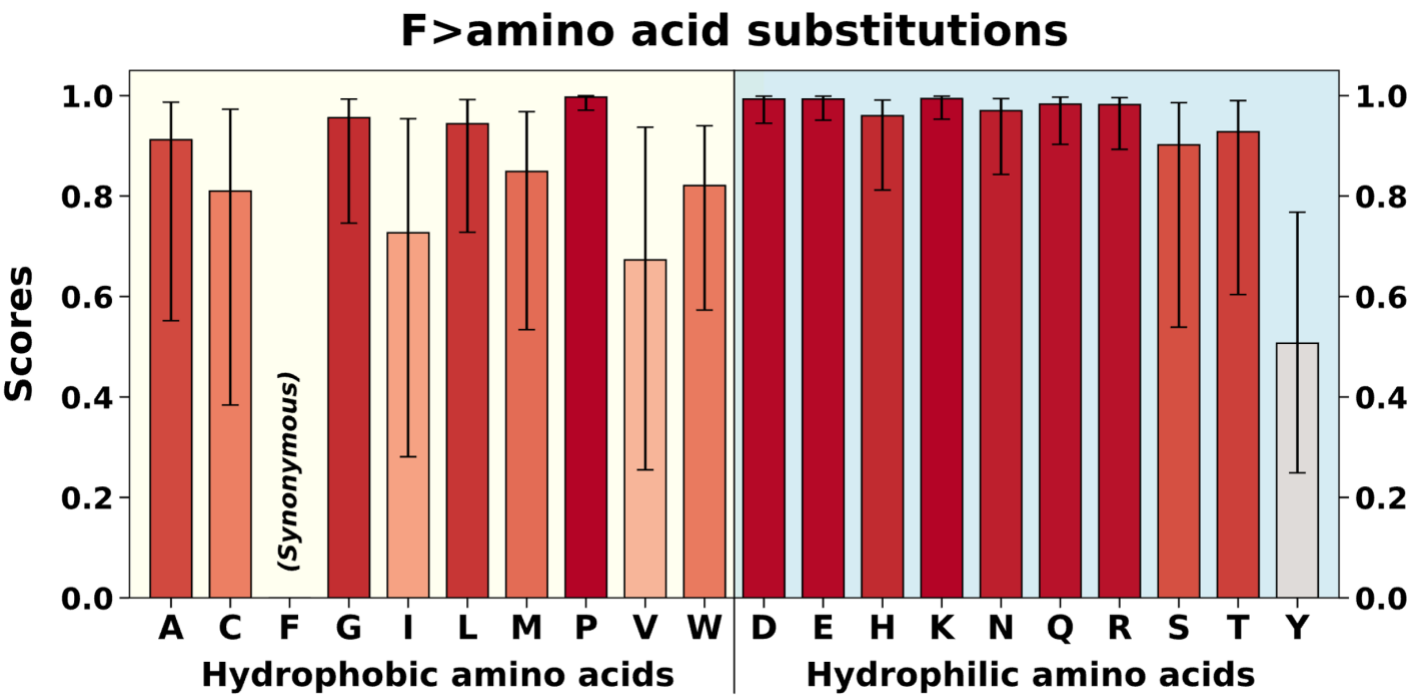
**Supplementary Table 4b. Descriptive Statistics for Data in Supplementary Table 4a.**

<b>Statistic</b>	<b>Value</b>
Total	2,605,367
Median	247,692
Mean	260,536.7
Standard deviation	82,916.91
Q1 (25th percentile)	210,064
Q3 (75th percentile)	302,910
IQR (Interquartile Range)	92,846
Lower Bound (5% tolerance margin)	74,334.75
Upper Bound (5% tolerance margin)	464,287.95
MAD (Median Absolute Deviation)	79,051.49

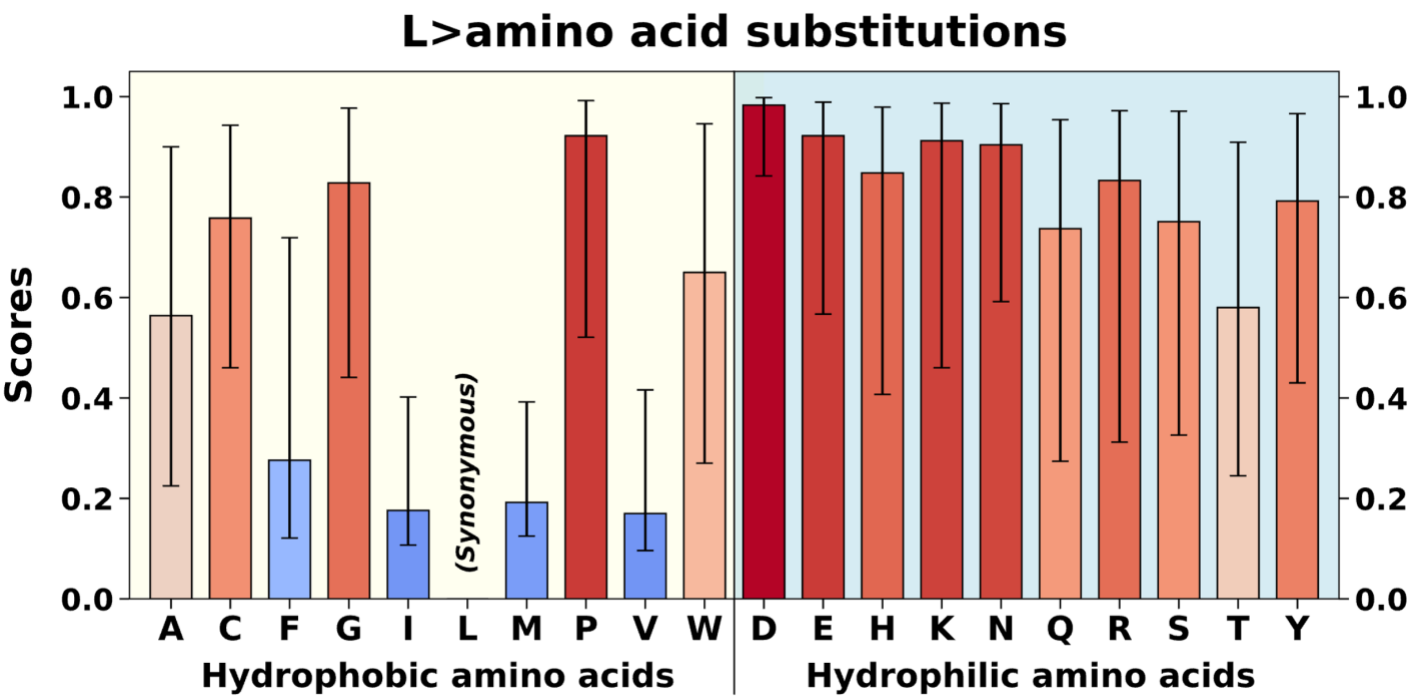
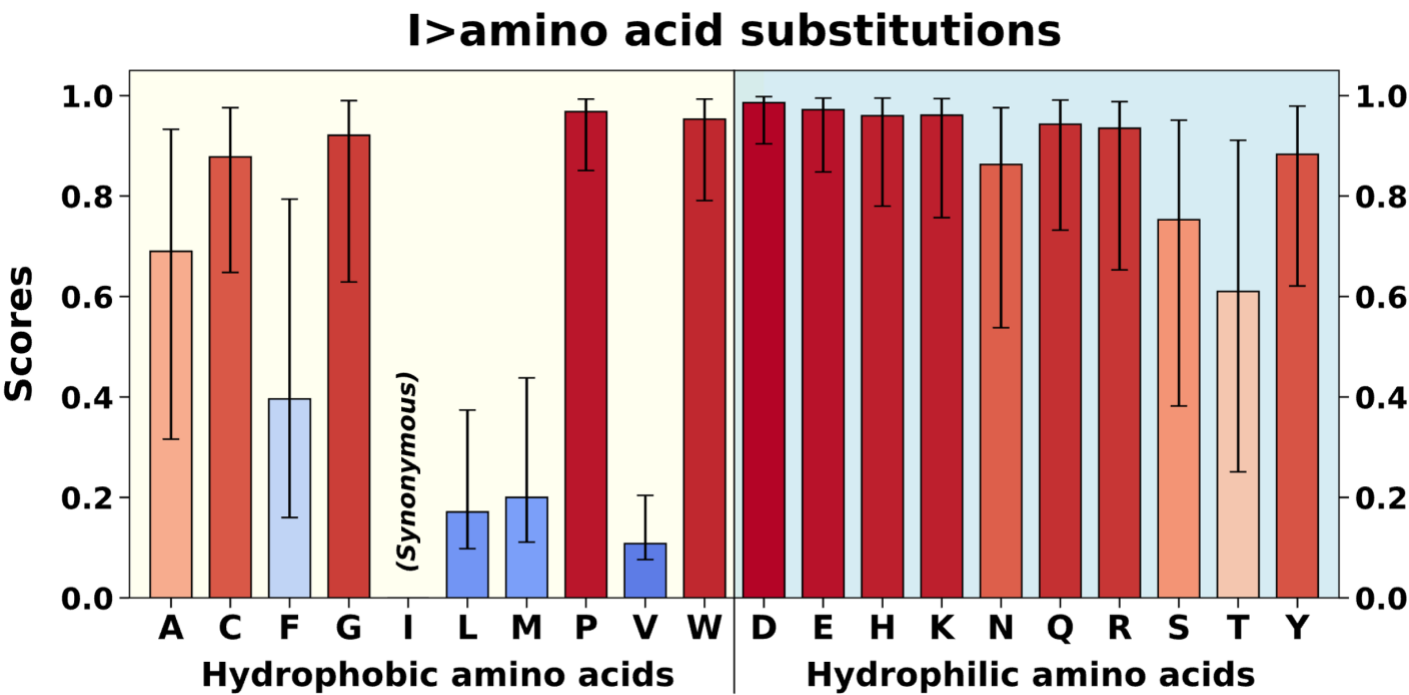
Supplementary Figure 3. Enlarged Panels of Figure 2.



Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.

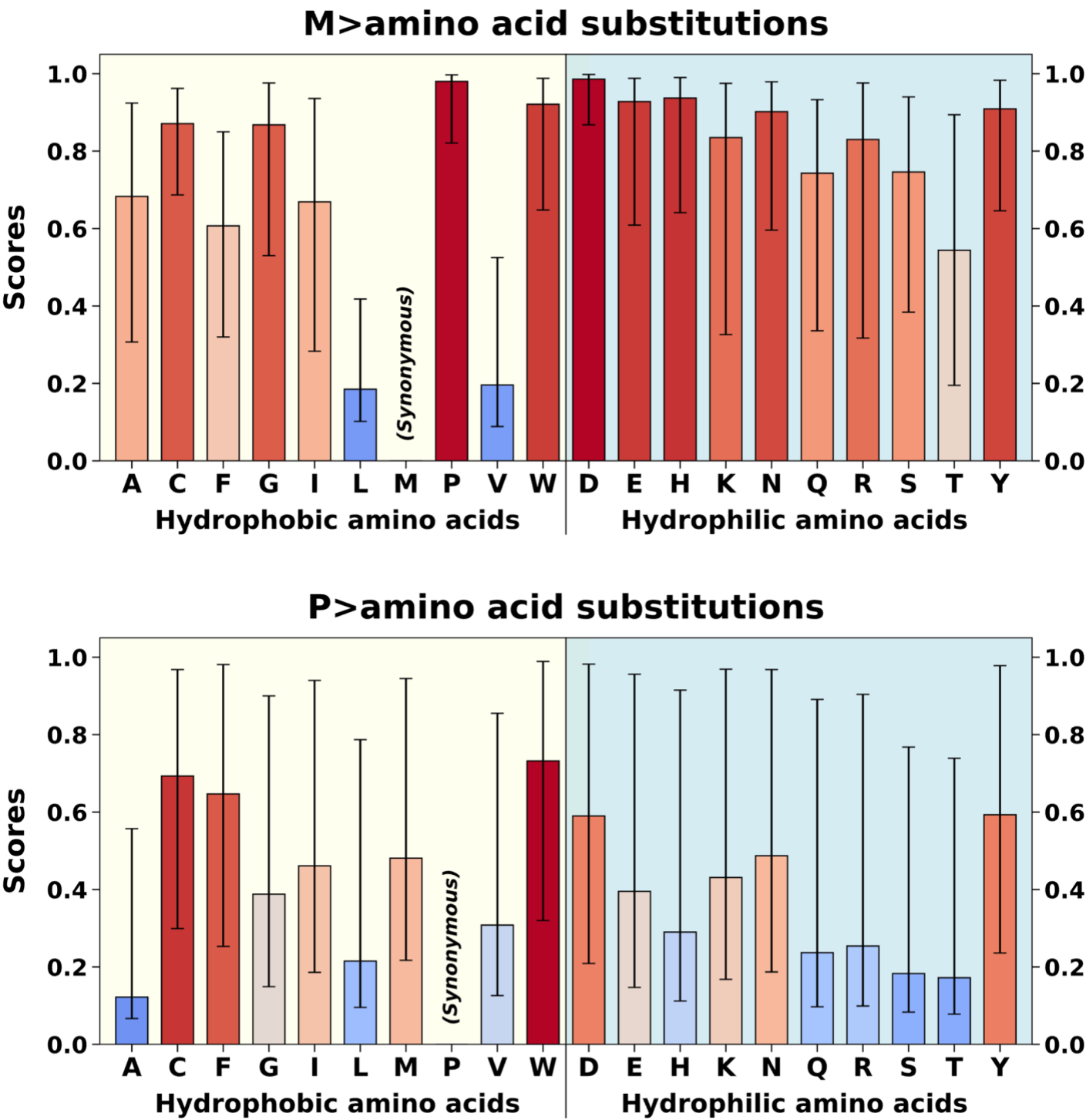


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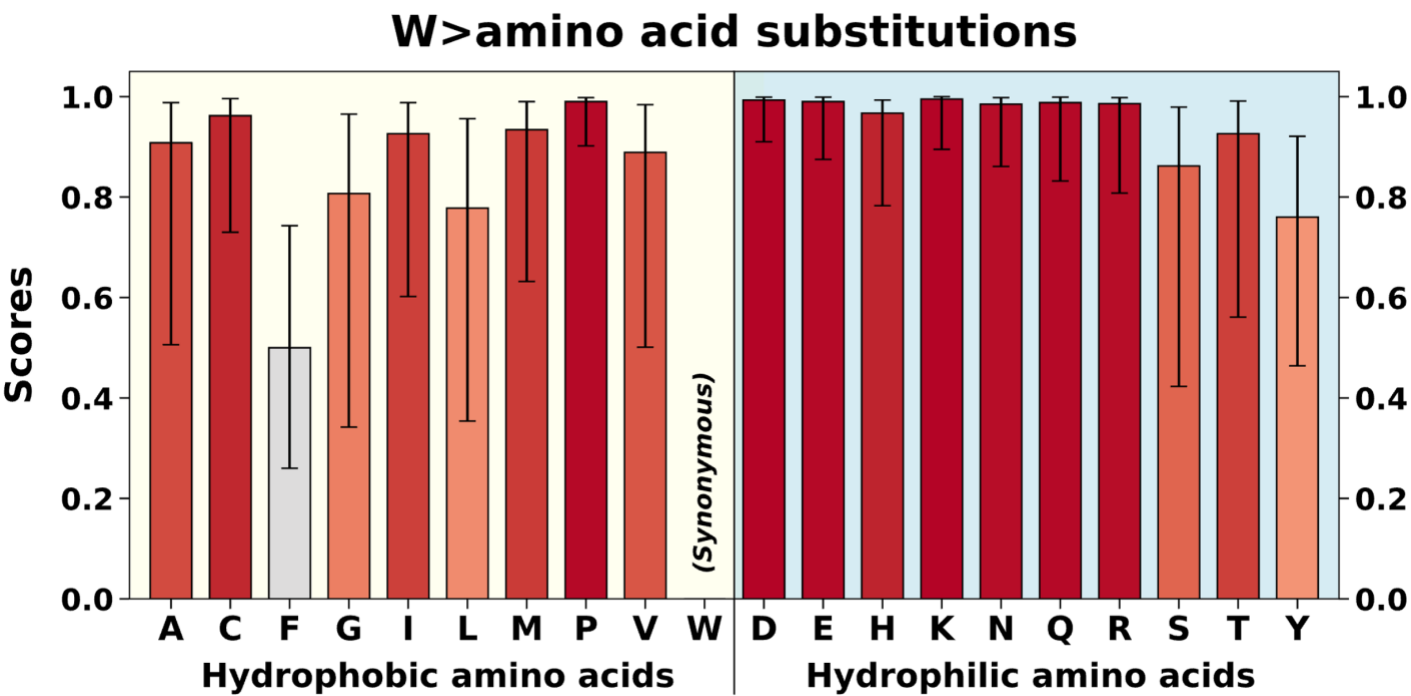
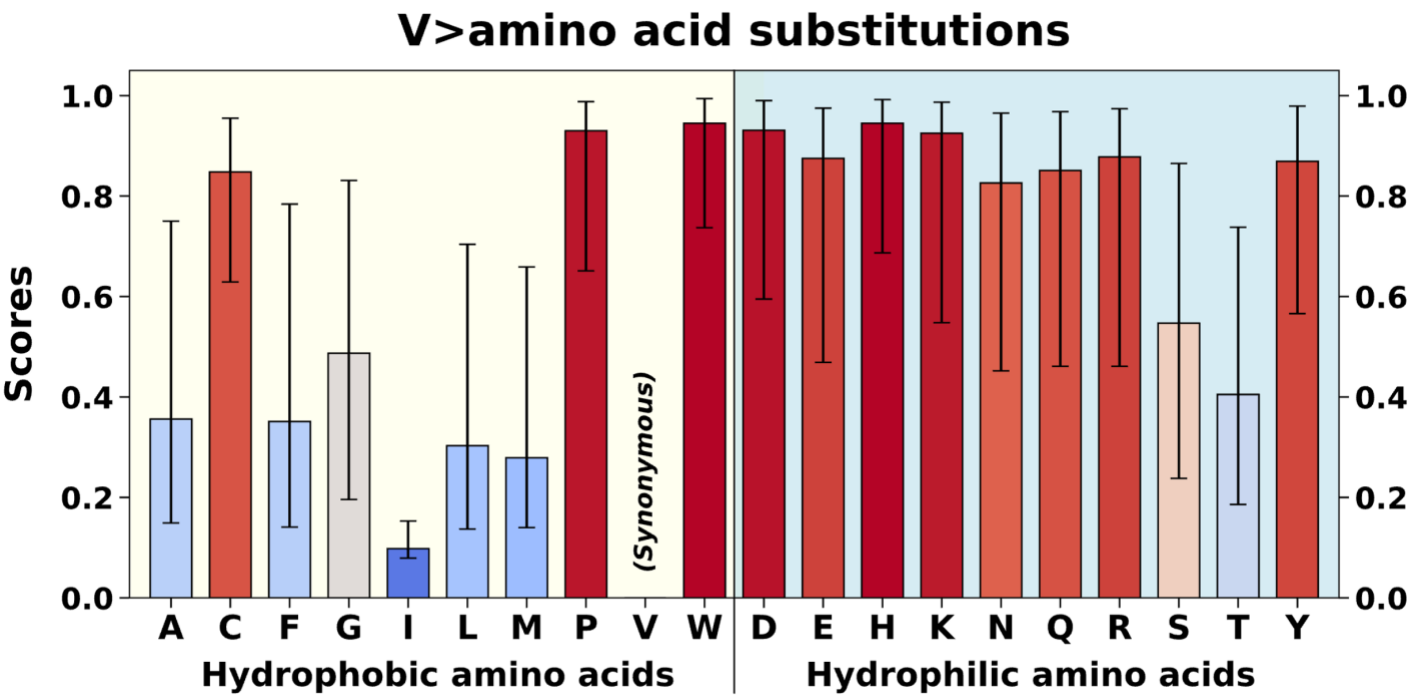




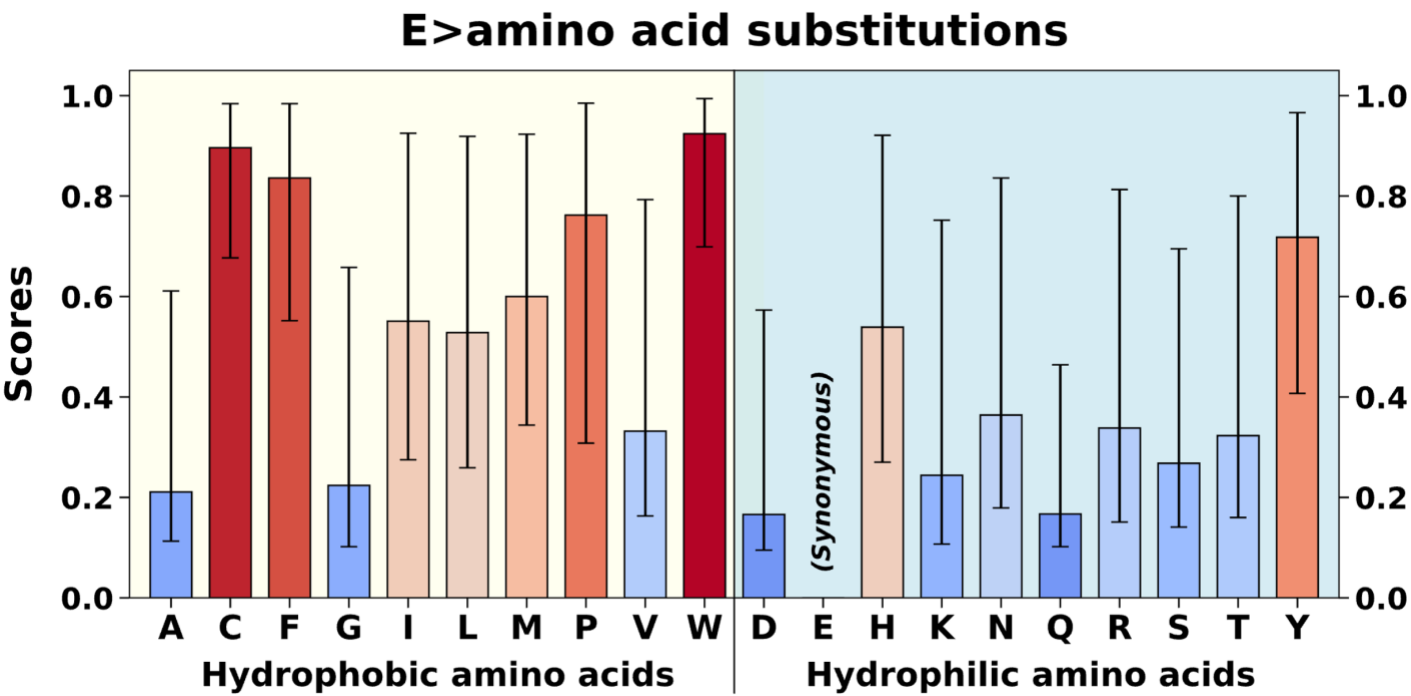
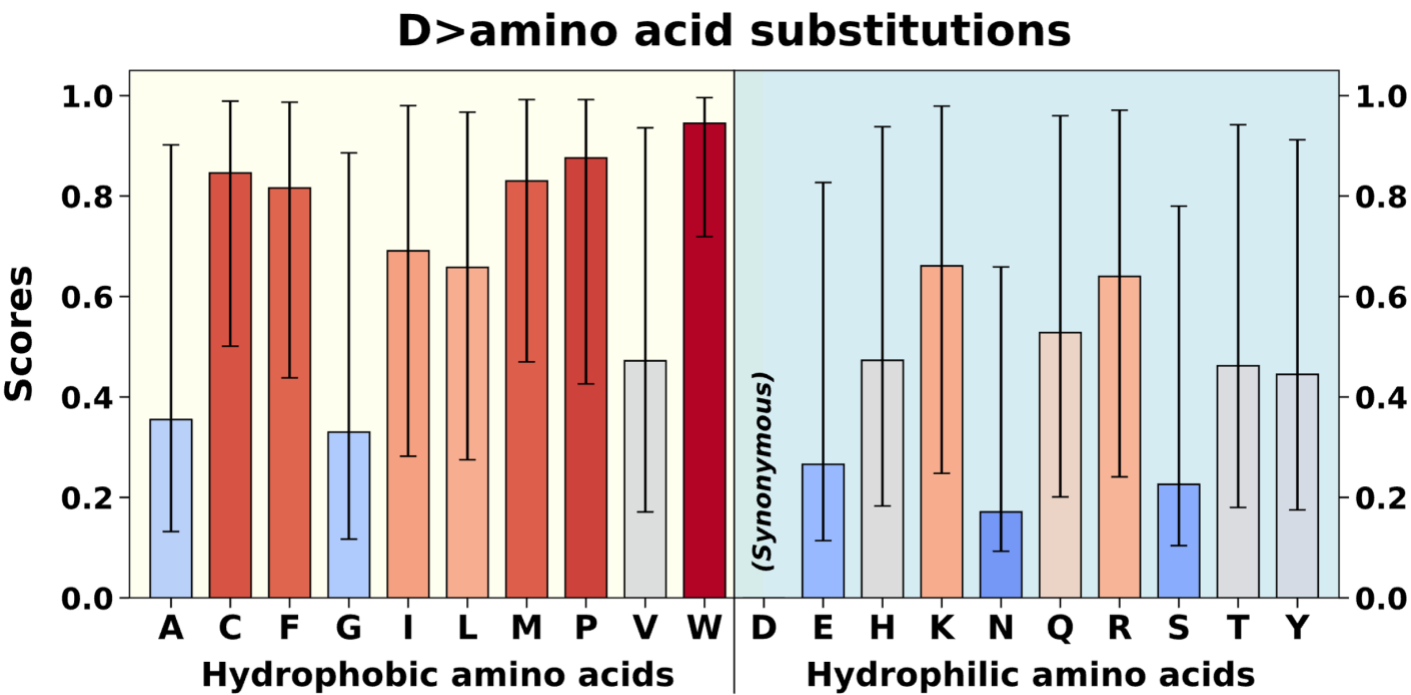
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



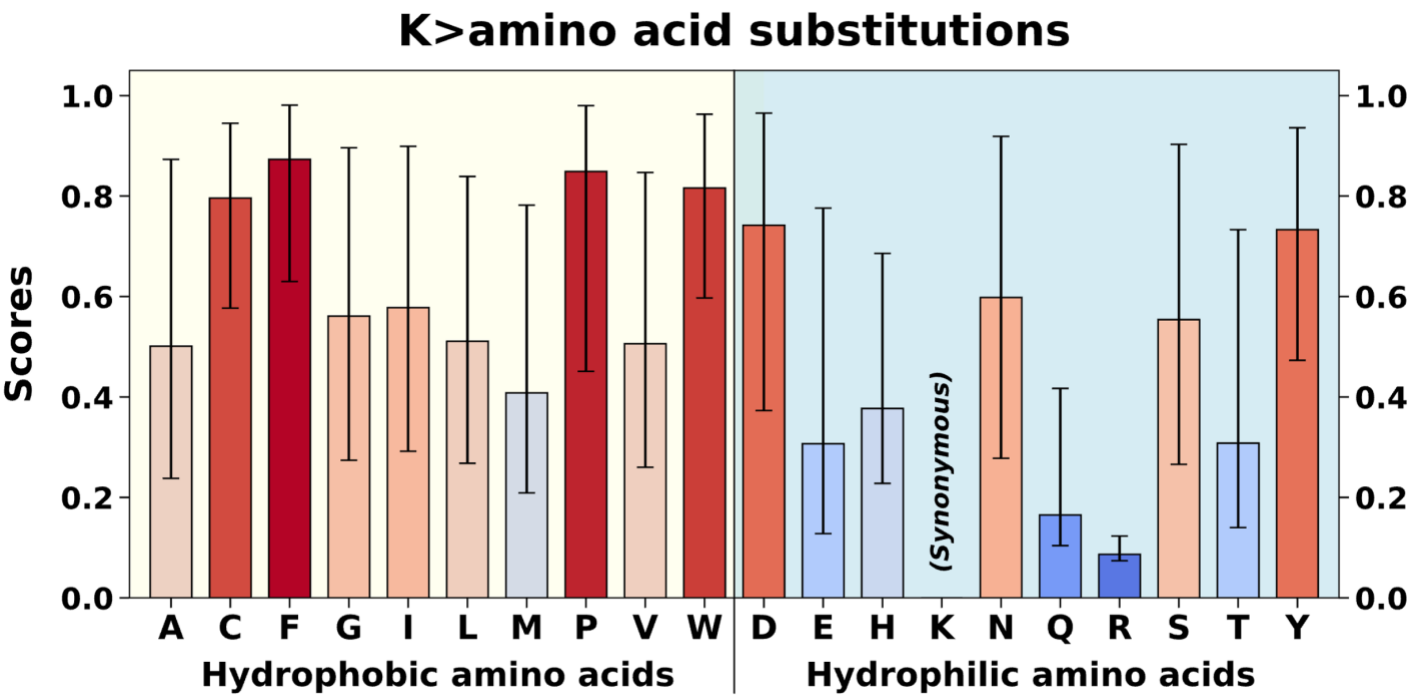
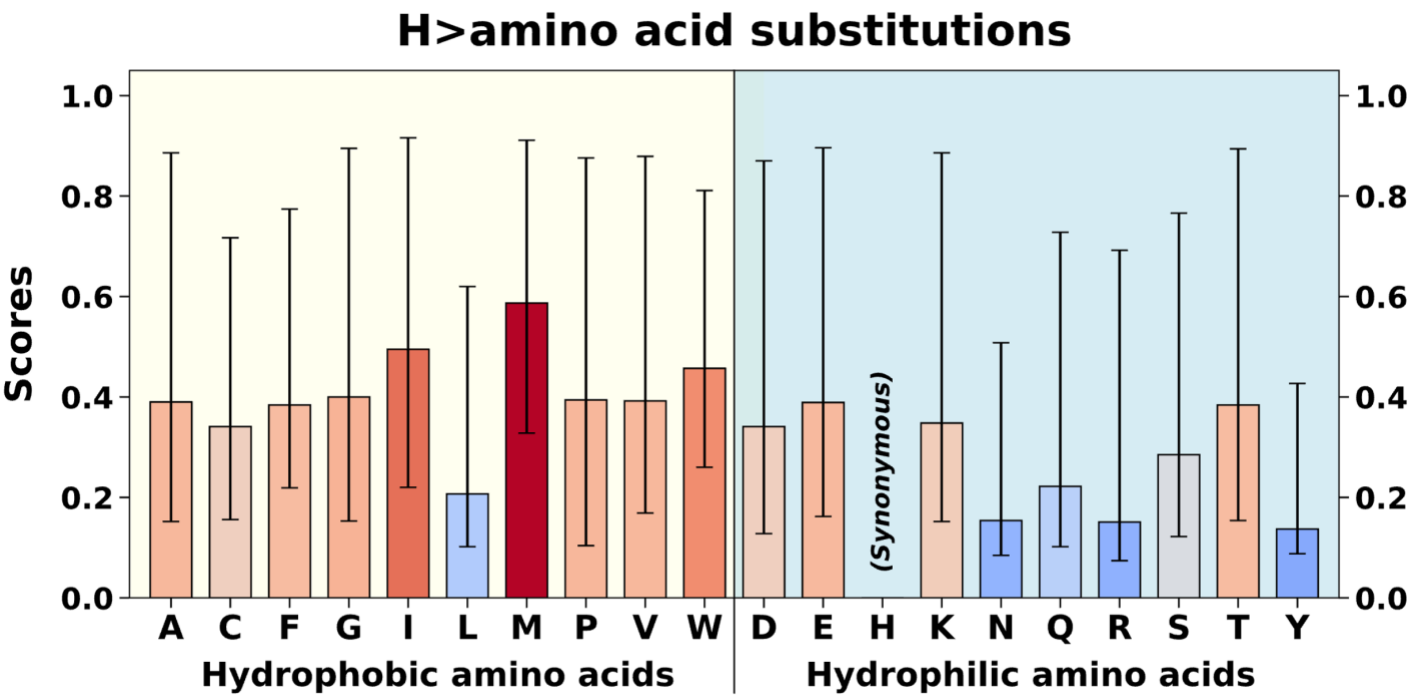
Supplementary Figure 3 (Continued). Enlarged Panels of Figure 2.



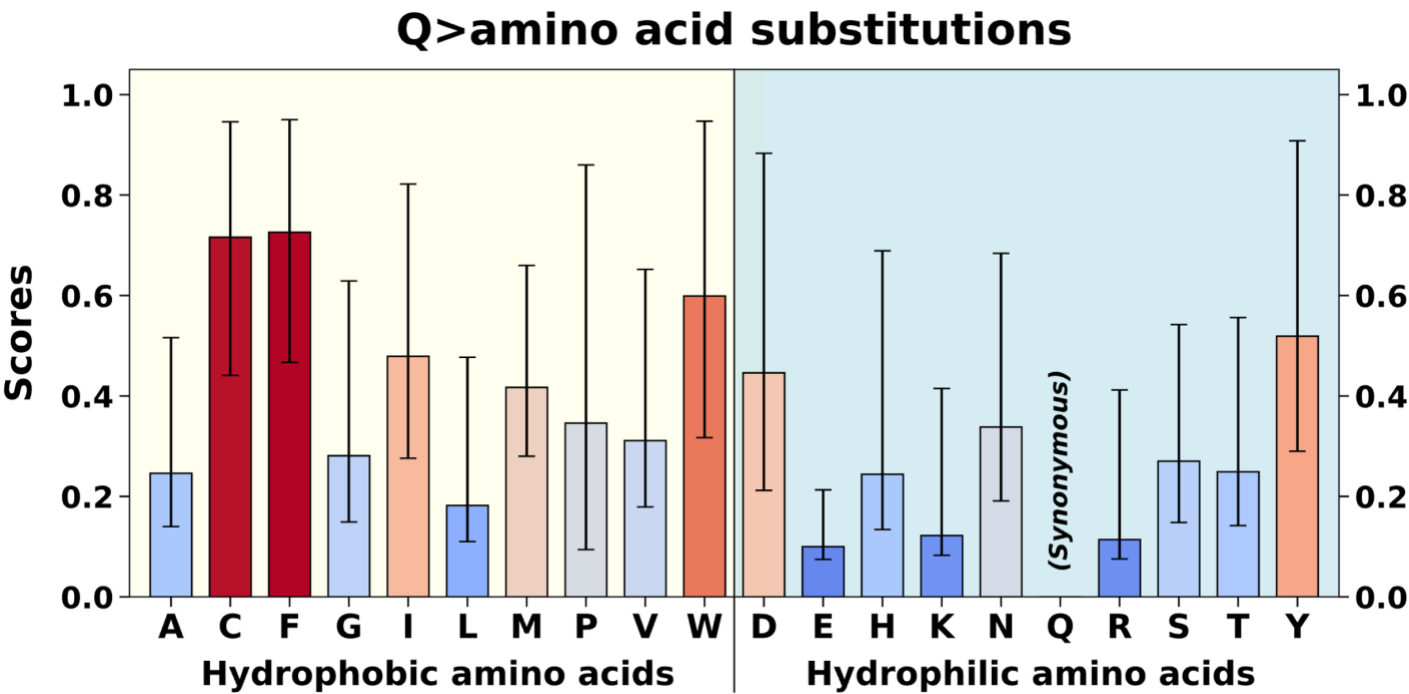
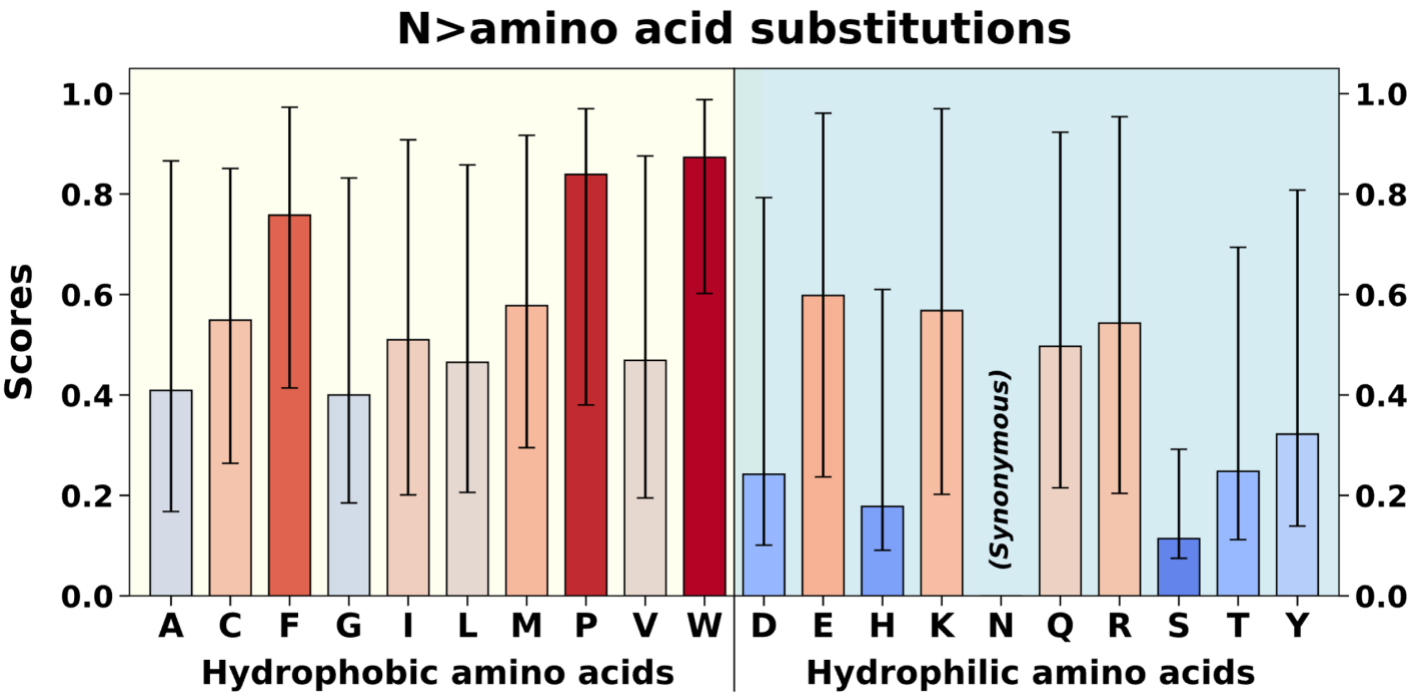
Supplementary Figure 4. Enlarged Panels of Figure 3.



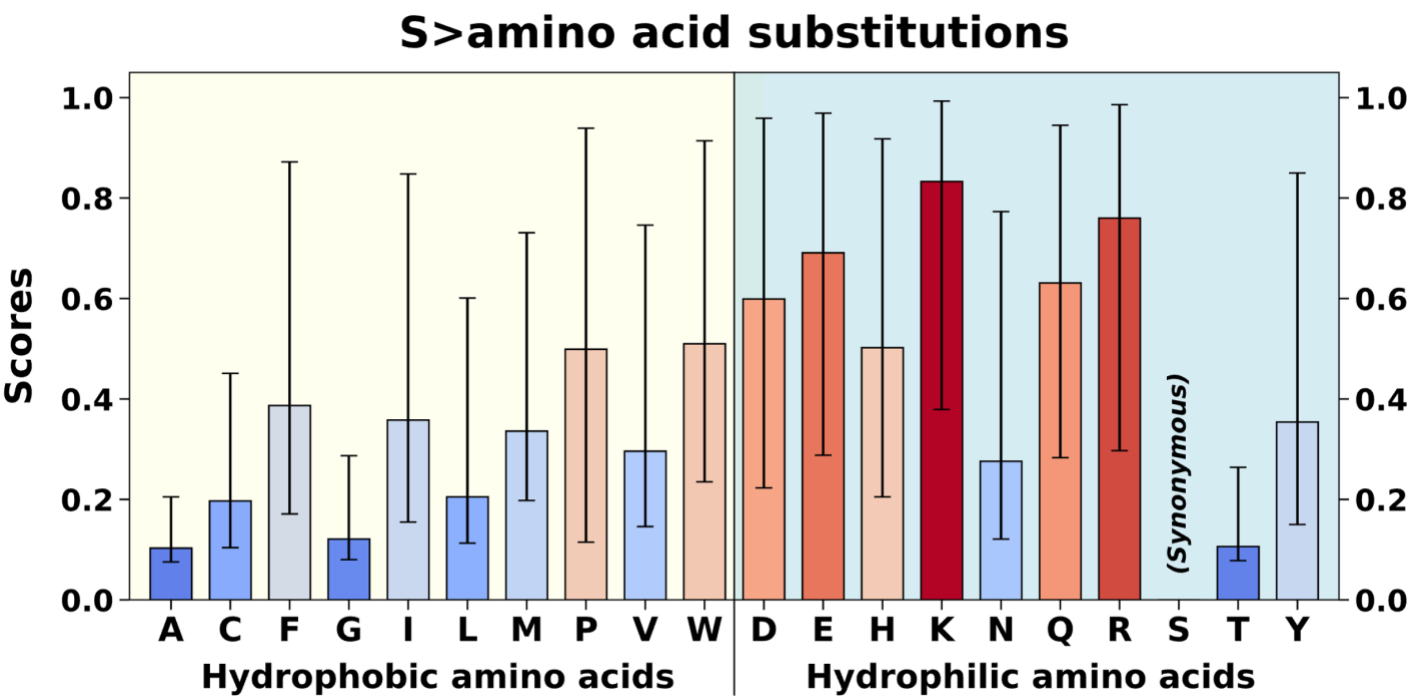
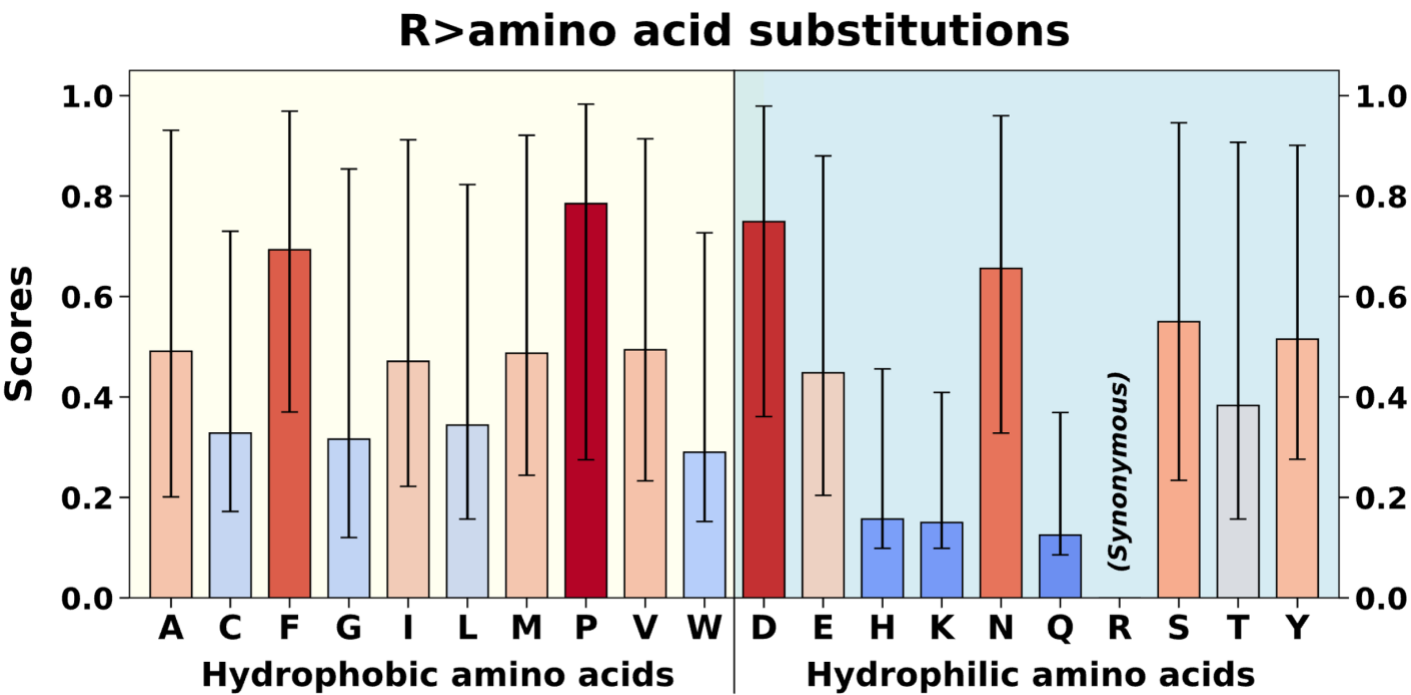
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



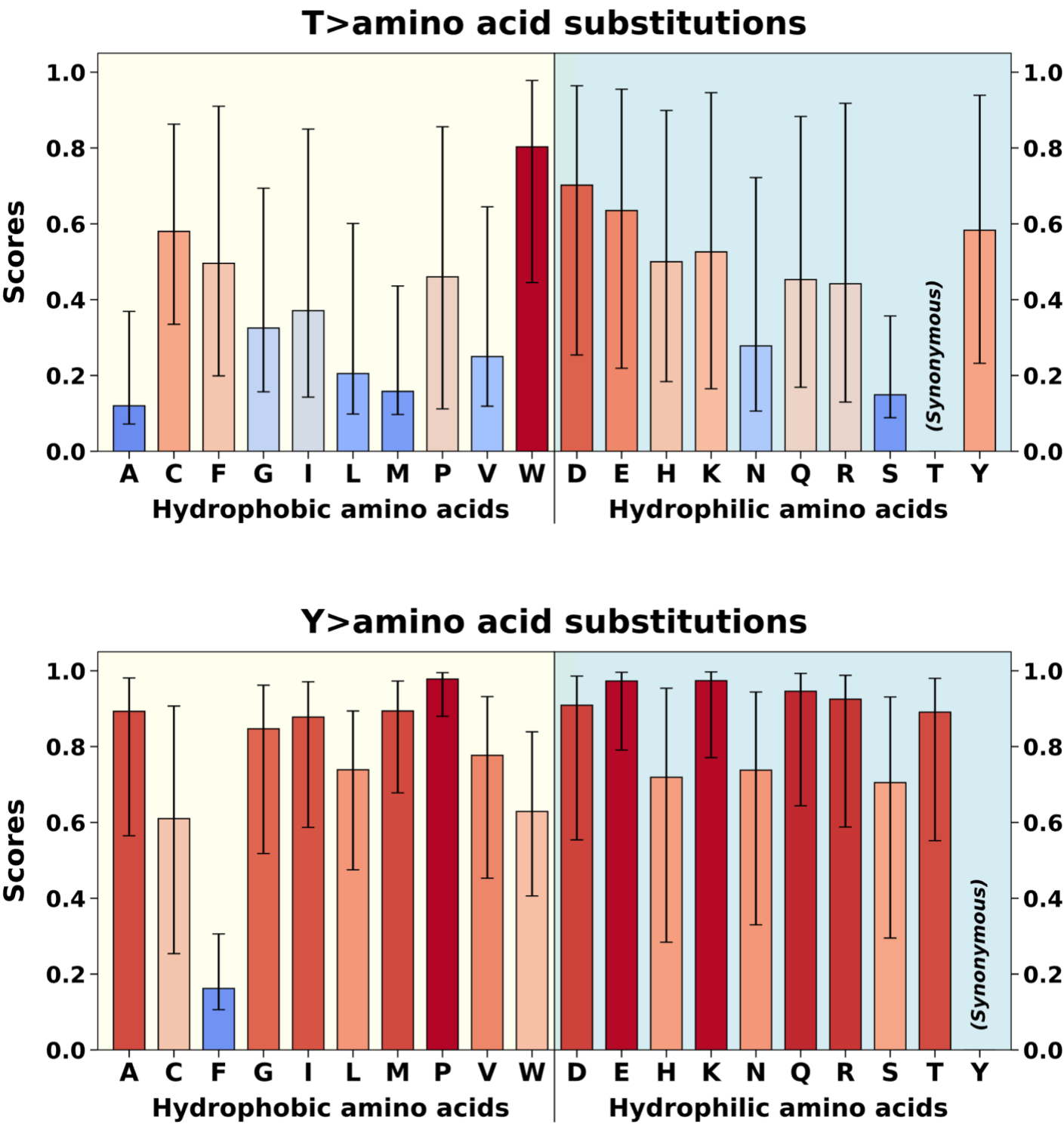
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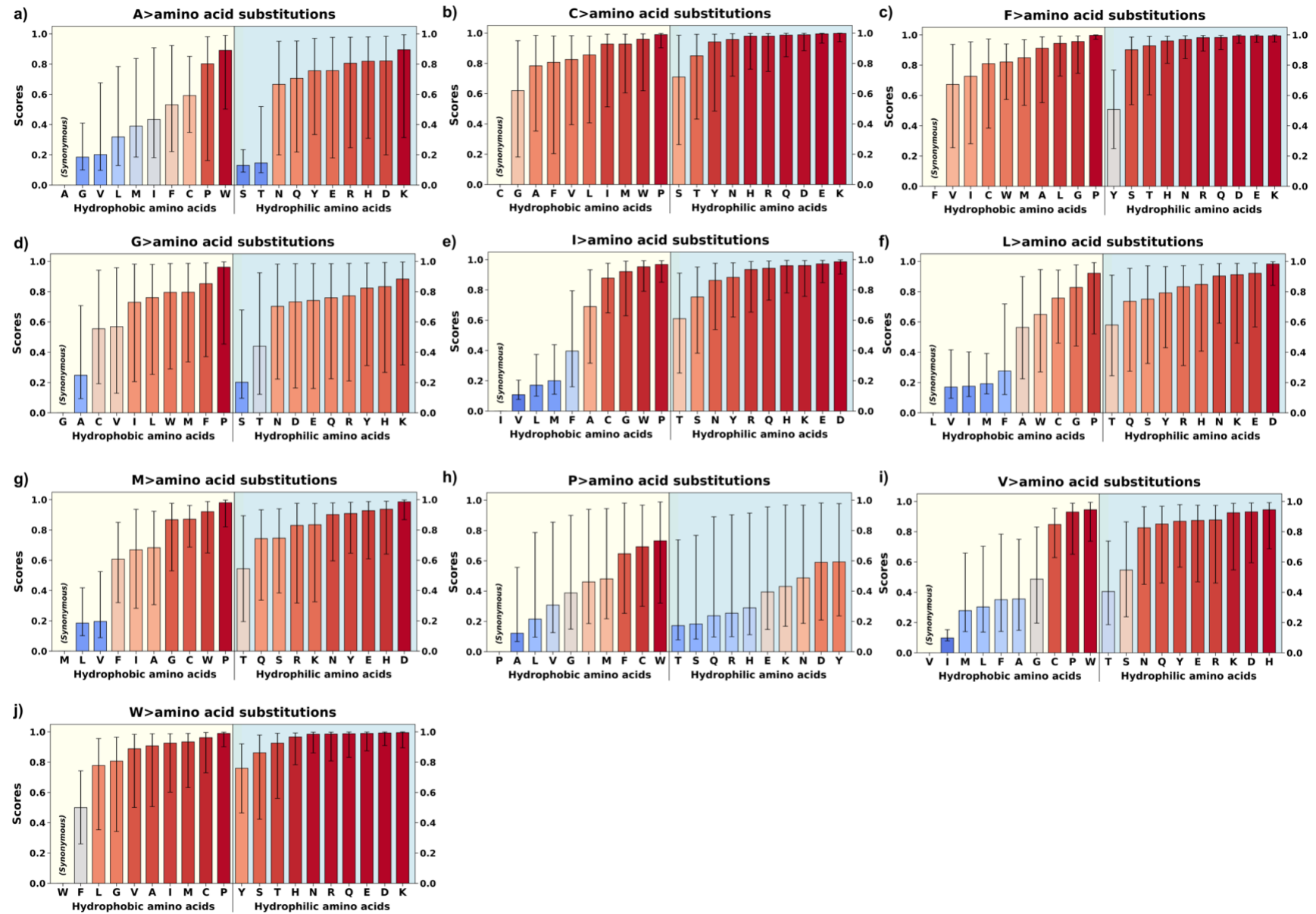
Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.



Supplementary Figure 4 (Continued). Enlarged Panels of Figure 3.

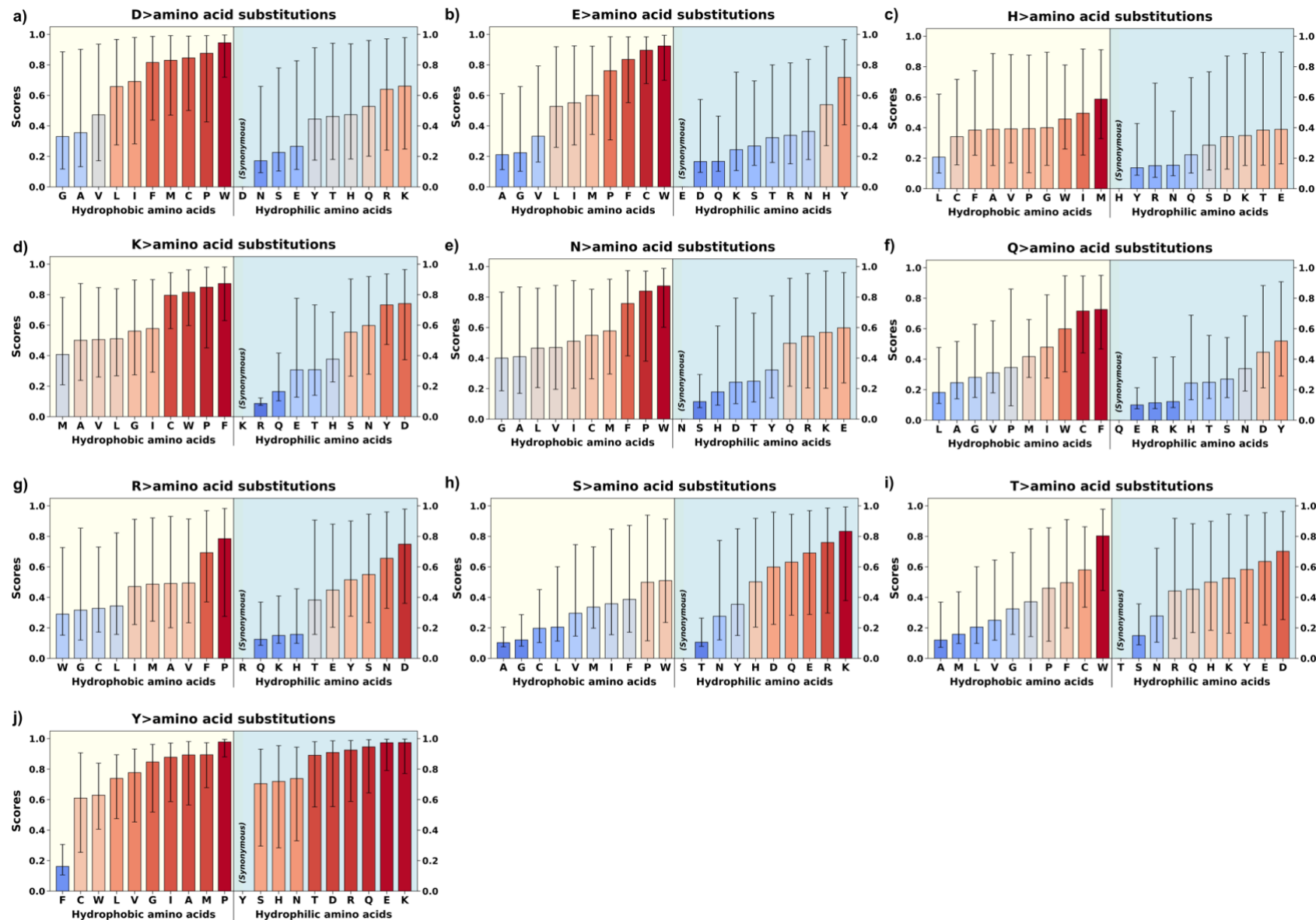


**Supplementary Figure 5. Re-ordered version of Figure 2, with amino acid scores arranged in ranked order instead of alphabetical order in each panel.**





**Supplementary Figure 6. Re-ordered version of Figure 3, with amino acid scores arranged in ranked order instead of alphabetical order in each panel.**



**Supplementary Table 5. Spearman Correlation Results of 74679 Residue frequencies.**  
**(Please refer to Table 1 in the main article for partial correlation data.)**

<b>Pair</b>	<b>Spearman's Rho</b>	<b>p-value</b>
F and Y	0.4662	< 0.001
W and Y	0.3457	< 0.001
I and T	0.2521	< 0.001
M and T	0.2618	< 0.001
A and T	0.4816	< 0.001
V and T	0.3158	< 0.001
G and T	0.2999	< 0.001
G and S	0.4527	< 0.001
A and S	0.4960	< 0.001
I and S	-0.0243	< 0.001
L and S	-0.0716	< 0.001
V and S	0.0527	< 0.001
C and S	0.1996	< 0.001
L and R	-0.0528	< 0.001
L and Q	-0.0084	0.0208
M and Q	0.0867	< 0.001
G and N	0.3351	< 0.001
A and N	0.1940	< 0.001
A and H	0.1280	< 0.001