Supporting Information

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SI Text

We used 12 data sets, which we describe below:

- GLOBIN*17–144*, consists of 17 vertebrate sequences of the *beta*-globin gene (144 codons), taken from (1).
- ADH*23–254*, consists of alcohol dehydrogenase genes (254) taken from 23 species of *D*rosophila, also taken from (1).
- RHOD*38–300*, consists of 38 vertebrate rhodopsin genes, from ref. 2.
- GAPDH*26–207*, consists of a mammalian alignment of 26 sequence of glyceraldehyde phosphate dehydrogenase taken from ref. 3.
- SDHB*26–168*, consists of 26 sequences of succinate dehydrogenase subunit B, also taken from ref. 3.
- VWF*62–427*, consists of a mammalian alignment of 62 sequences of the von Will brand factor gene, taken from ref. 4.
- IRBP*62–433*, consists of 62 sequences of the interphotoreceptor retinoid binding protein gene, also taken from ref. 4.
- GHR*49–321*, consists of 49 sequences of the growth hormone receptor gene from rodents, taken from ref. 5.
- RAG*41–1002*, consists of 41 rodent sequences of the recombination activating-1 gene, also taken from ref. 5.
- TBR*42–240*, consists of an alignment of 42 ray-finned fishes T-box brain-1 genes, taken from ref. 6.
- GLYT*44–296*, consists of 44 sequences of glycosyltransferase, also taken from ref. 6.
- PPPCK*18–208*, consists of 18 insect sequences of phosphoenolpyruvate carboxykinase, taken from ref. 7.

For these last five data sets, we used the maximum likelihood tree topology returned by PhyML (8) under the WAG + Γ model, whereas for all other data sets, we used the same tree topologies as in their respective references.

We performed a simple posterior predictive diagnostic to assess the ability of the model to capture the overall intensity of selection. The diagnostic consists of contrasting the posterior distribution of the mean number of nonsynonymous events per site (obtained via substitution mapping) with the posterior predictive distribution on this statistic (obtained via unconstrained substitution mapping) (9). The detailed posterior predictive checks under the MG model (which assumes no selection, except against stop codons), the MG-NS model (which only distinguishes between synonymous and nonsynonymous events via a multiplicative parameter on nonsynonymous rate entries; e.g., see ref. 9) and the MG-MutSelDP model, for a dozen data sets, are reported in Figs. S1–S4, along with posterior predictive *P* values. A posterior predictive *P* value of 1 indicates that for all draws from the posterior distribution, the mean number of nonsynonymous events is higher in the predictive (unconstrained) substitution mapping than in the posterior (constrained) substitution mapping. Conversely, a posterior predictive *P* value of 0 indicates this statistic is lower in the predictive substitution mapping than in posterior substitution mapping, for all draws in our sample.

As reported in ref. 9, the MG model has a predictive distribution to the right of the posterior distribution (i.e., with *P* values ~1); because it assumes no selection, the model induces far too many nonsynonymous events in predictive substitution mappings, in comparison with the posterior substitution mappings (which are constrained to be consistent with the true data). The MG-NS model, on the other hand, explicitly parameterizes the overall effect of selection acting on the gene, and hence induces much fewer nonsynonymous events within predictive mappings than does the MG model. Also note that with the MG-NS model, the predictive mappings have fewer nonsynonymous events per site than the posterior mappings (i.e., with many data sets having a *P* value close to 0), which may in part be due to effects of the prior probability distribution, or model violations. With the MG-MutSelDP model, for some data sets there is a good corroboration between posterior and predictive distributions, whereas for other data sets the results are qualitatively similar to those under the MG-NS model, with the predictive distribution to the left of the posterior distribution (i.e., with *P* values approaching 0). We view these results as an additional indication that the MG-MutSelDP model is capturing features of selection. The predictive distribution being situated to the left of the posterior distribution for several data sets is indicative of remaining model violations, such as the fact that the MG-MutSelDP model cannot capture a substitution pattern under positive selection (with a nonsynonymous "flux" greater than the synonymous flux) (10). On the other hand, these results suggest that the MG-MutSelDP model likely provides a better account of less stringent overall purifying selection, because certain sites will be allowed to change within a reduced subset of amino acids.

1. Yang Z, Nielsen R, Goldman N, Pedersen A-MK (2000) Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics* 155:431–449.
2. Yokoyama S, Tada T, Zhang H, Britt L (2008) Elucidation of phenotypic adaptations: Molecular analyses of dim-light vision proteins in vertebrates. *Proc Natl Acad Sci USA* 105:13480–13485.
3. Kullberg MK, Nilsson MA, Arnason U, Harley EH, Janke A (2006) Housekeeping genes for phylogenetic analysis of eutherian relationships. *Mol Biol Evol* 23:1493–1503.
4. Poux C, Chevret P, Huchon D, de Jong WW, Douzery EJ (2006) Arrival and diversification of caviomorph rodents and playrrhine primates in South America. *Syst Biol* 55:228–244.
5. Steppan SJ, Adkins RM, Anderson J (2004) Phylogeny and divergence-date estimates of rapid radiations in muroid rodents based on multiple nuclear genes. *Syst Biol* 53: 533–553.
6. Li C, Lu G, Ortí G (2008) Optimal data partitioning and a test case for ray-finned fishes (Actinopterygii) based on ten nuclear loci. *Syst Biol* 57:519–539.
7. Friedlander TP, Regier JC, Mitter C, Wagner DL (1996) A nuclear gene for higher level phylogenetics: Phosphoenolpyruvate carboxykinase tracks mesozoic-age divergences within Lepidoptera (Insecta). *Mol Biol Evol* 13:594–604.
8. Guindon S, Gascuel O (2003) A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol* 52:696–704.
9. Rodrigue N, Kleinman CL, Philippe H, Lartillot N (2009) Computational methods for evaluating phylogenetic models of coding sequence evolution with dependence between codons. *Mol Biol Evol* 26:1663–1676.
10. Halpern AL, Bruno WJ (1998) Evolutionary distances for protein-coding sequences: Modeling site-specific residue frequencies. *Mol Biol Evol* 15:910–917.

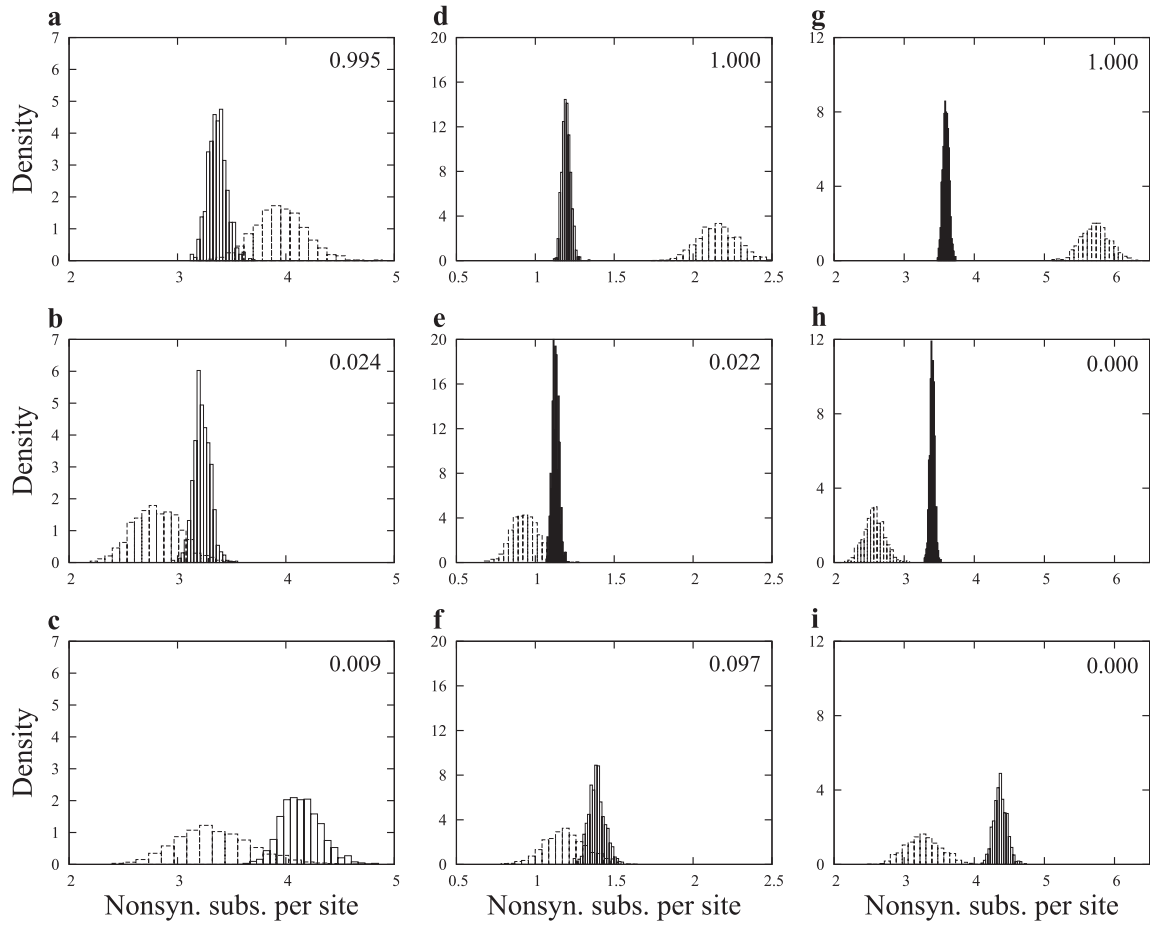

Fig. S1. Posterior predictive checks of the mean number of nonsynonymous events across sites. (*A*–C) Globin*17–144* set. (*D–F*) Adh*23–254* data set. (*G–I*) Rhod*38–300* data set. (*A*, *D*, and *G*) The MG model. (*B*, *E*, and *H*) The MG-NS model. (*C*, *F*, and *I*) The MG-MutSelDP model. The posterior predictive *P* value is displayed in the top right corner of each panel.

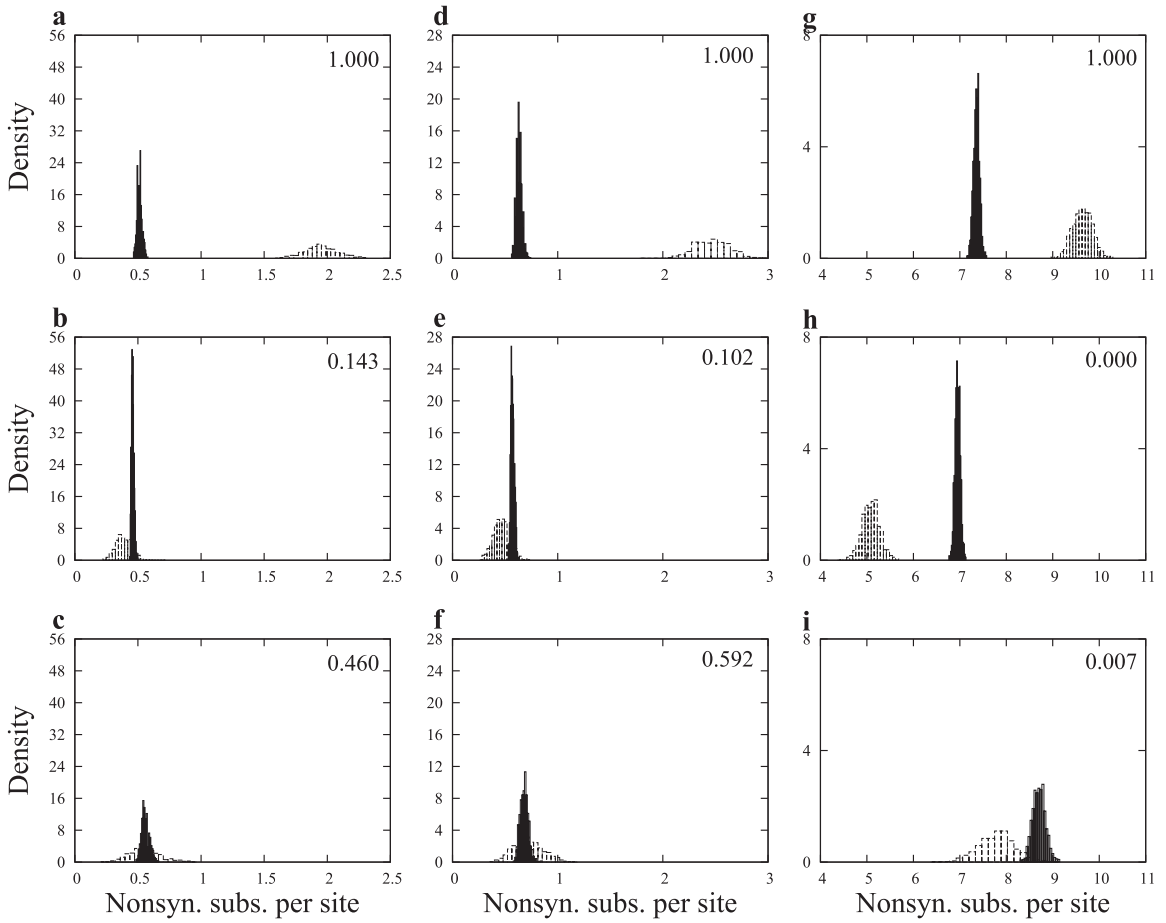

Fig. S2. Posterior predictive checks of the mean number of nonsynonymous events across sites. (*A*–*C*) GAPDH*26–168* data set. (*D*–*F*) SDHB*26–168* data set. (*G*–*I*) VWF*62–427* data set. (*A*, *D*, and *G*) The MG model. (*B*, *E*, and *H*) The MG-NS model. (*C*, *F*, and *I*) The MG-MutSelDP model. The posterior predictive *P* value is displayed in the top right corner of each panel.

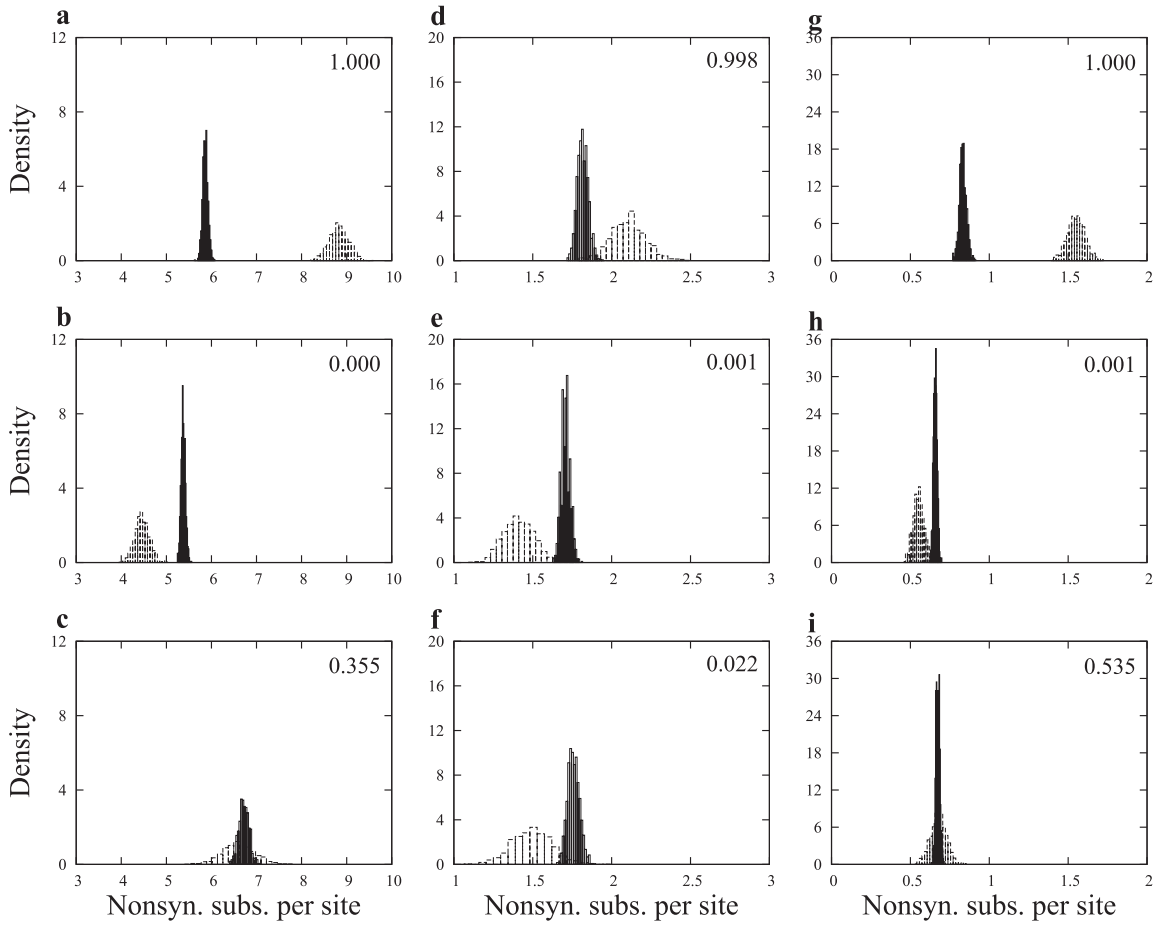

Fig. S3. Posterior predictive checks of the mean number of nonsynonymous events across sites. (*A–C*) IRBP*62–433* data set. (*D–F*) GHR*49–321* data set. (*G–I*) RAG*41–1002* data set. (*A*, *D*, and *G*) The MG model. (*B*, *E*, and *H*) The MG-NS model. (*C*, *F*, and *I*) The MG-MutSelDP model. The posterior predictive *P* value is displayed in the top right corner of each panel.

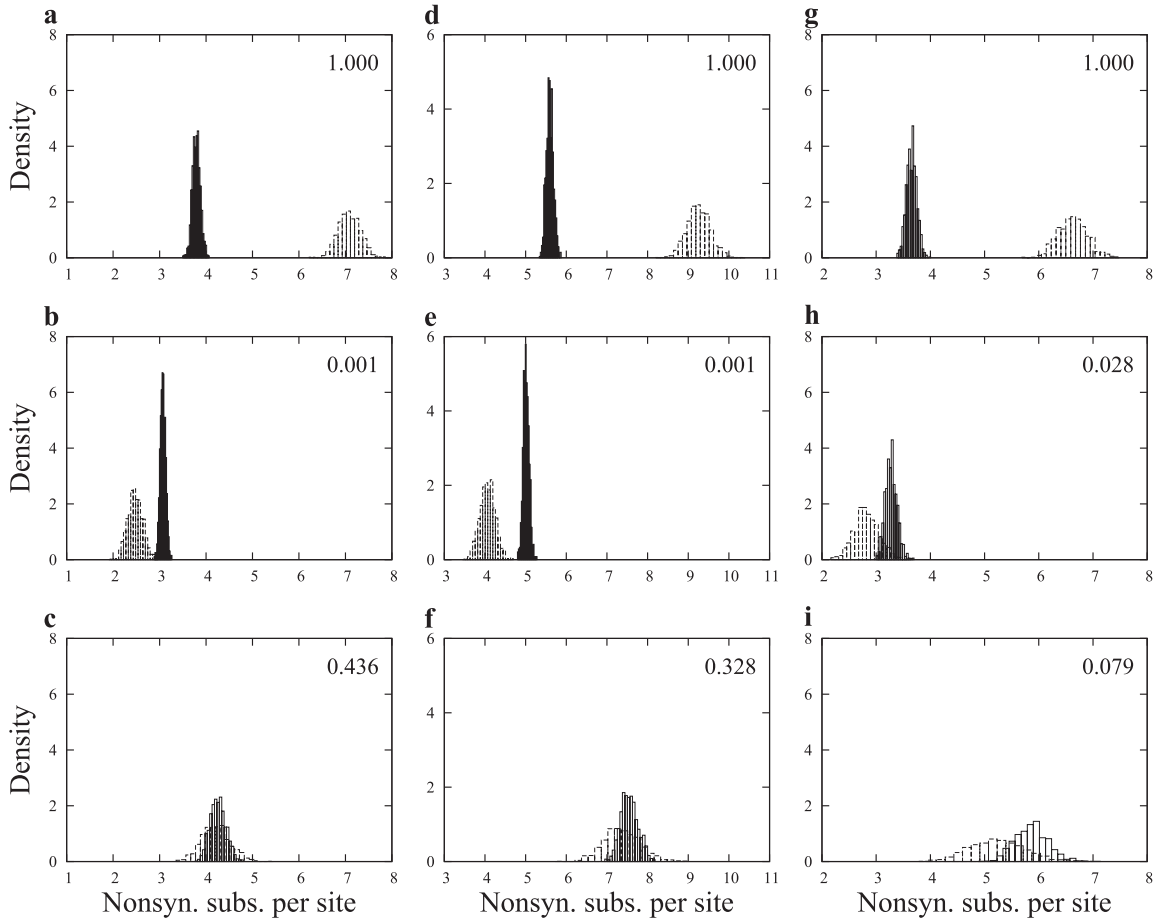

Fig. S4. Posterior predictive checks of the mean number of nonsynonymous events across sites. (*A–C*) TBR*42–240* data set. (*D–F*) GLYT*44–296* data set. (*G–I*) FRIED*18–208* data set. (*A*, *D*, and *G*) The MG model. (*B*, *E*, and *H*) The MG-NS model. (*C*, *F*, and *I*) The MG-MutSelDP model. The posterior predictive *P* value is displayed in the top right corner of each panel.

Table S1. Posterior mean and 95% credibility intervals of parameters governing the substitution process under the MG-MutSelDP model, inferred from the GLOBIN*17–144*, ADH*23–254*, and RHOD*38–300* data sets

	GLOBIN*17–144*	ADH*23–254*	RHOD*38–300*
φ_A	0.098 (0.079–0.119)	0.093 (0.076–0.110)	0.104 (0.092–0.118)
φ_C	0.372 (0.335–0.411)	0.398 (0.363–0.434)	0.499 (0.472–0.527)
φ_G	0.262 (0.221–0.303)	0.287 (0.252–0.327)	0.255 (0.229–0.283)
φ_T	0.267 (0.233–0.303)	0.223 (0.194–0.251)	0.141 (0.128–0.156)
ϱ_{AC}	0.159 (0.117–0.208)	0.191 (0.148–0.239)	0.112 (0.094–0.133)
ϱ_{AG}	0.300 (0.245–0.360)	0.237 (0.190–0.287)	0.267 (0.237–0.296)
ϱ_{AT}	0.179 (0.113–0.248)	0.228 (0.168–0.294)	0.235 (0.195–0.280)
ϱ_{CG}	0.069 (0.047–0.092)	0.076 (0.056–0.099)	0.067 (0.056–0.080)
ϱ_{CT}	0.194 (0.154–0.234)	0.185 (0.152–0.226)	0.182 (0.160–0.204)
ϱ_{GT}	0.099 (0.070–0.131)	0.083 (0.055–0.116)	0.137 (0.115–0.162)
α	5.665 (2.796–9.460)	7.505 (3.898–12.34)	12.273 (8.054–17.483)
Ψ_{Ala}	0.058 (0.027–0.102)	0.055 (0.029–0.090)	0.054 (0.034–0.077)
Ψ_{Cys}	0.036 (0.015–0.070)	0.029 (0.015–0.052)	0.043 (0.026–0.072)
Ψ_{Asp}	0.059 (0.021–0.111)	0.050 (0.023–0.093)	0.029 (0.018–0.047)
Ψ_{Glu}	0.073 (0.031–0.132)	0.062 (0.027–0.118)	0.058 (0.033–0.092)
Ψ_{Phe}	0.045 (0.021–0.083)	0.042 (0.018–0.081)	0.089 (0.055–0.135)
Ψ_{Gly}	0.040 (0.018–0.073)	0.041 (0.020–0.075)	0.031 (0.018–0.051)
Ψ_{His}	0.051 (0.022–0.097)	0.042 (0.021–0.075)	0.033 (0.02–0.051)
Ψ_{Ile}	0.045 (0.018–0.089)	0.044 (0.019–0.092)	0.059 (0.033–0.091)
Ψ_{Lys}	0.095 (0.035–0.187)	0.086 (0.032–0.176)	0.052 (0.028–0.081)
Ψ_{Leu}	0.048 (0.021–0.083)	0.048 (0.025–0.078)	0.045 (0.028–0.069)
Ψ_{Met}	0.049 (0.020–0.093)	0.050 (0.024–0.093)	0.116 (0.068–0.175)
Ψ_{Asn}	0.109 (0.050–0.190)	0.073 (0.029–0.142)	0.059 (0.034–0.095)
Ψ_{Pro}	0.025 (0.013–0.045)	0.034 (0.018–0.057)	0.025 (0.015–0.039)
Ψ_{Gln}	0.044 (0.017–0.094)	0.055 (0.025–0.105)	0.039 (0.024–0.063)
Ψ_{Arg}	0.026 (0.013–0.048)	0.028 (0.015–0.050)	0.025 (0.016–0.038)
Ψ_{Ser}	0.034 (0.014–0.065)	0.052 (0.027–0.085)	0.047 (0.029–0.07)
Ψ_{Thr}	0.048 (0.021–0.085)	0.072 (0.035–0.126)	0.053 (0.032–0.079)
Ψ_{Val}	0.047 (0.022–0.085)	0.043 (0.022–0.075)	0.047 (0.029–0.071)
Ψ_{Try}	0.027 (0.011–0.064)	0.038 (0.017–0.073)	0.044 (0.024–0.078)
Ψ_{Tyr}	0.029 (0.012–0.063)	0.045 (0.021–0.086)	0.043 (0.022–0.074)
ε	3.336 (2.545–4.402)	2.309 (1.812–2.859)	2.365 (2.045–2.764)

φ_A is the parameter associated with the propensity of nucleotide A; ϱ_{AC} is the parameter associated with the exchangeability of nucleotides A and C (reversibly); α is the parameter governing the "granularity" of the Dirichlet process; the Ψ vector governs the base prior of the Dirichlet process, in this case representing the mean amino acid profile of the Dirichlet process, and with ε governing the dispersal around the mean.

Table S2. Posterior mean and 95% credibility intervals of parameters governing the substitution process under the MG-MutSelDP model, inferred from the GAPDH*26–168*, SDHB*26–168*, and VWF*62–427* data sets

	GAPDH*26–168*	SDHB*26–168*	VWF*62–427*
φ_A	0.079 (0.063–0.099)	0.156 (0.124–0.188)	0.085 (0.077–0.093)
φ_C	0.467 (0.422–0.513)	0.385 (0.340–0.430)	0.391 (0.371–0.411)
φ_G	0.247 (0.201–0.298)	0.281 (0.237–0.327)	0.440 (0.418–0.463)
φ_T	0.207 (0.177–0.238)	0.178 (0.151–0.209)	0.084 (0.078–0.090)
ϱ_{AC}	0.121 (0.088–0.159)	0.093 (0.063–0.127)	0.089 (0.078–0.100)
ϱ_{AG}	0.385 (0.317–0.451)	0.323 (0.268–0.385)	0.285 (0.265–0.306)
ϱ_{AT}	0.244 (0.176–0.315)	0.059 (0.024–0.107)	0.173 (0.140–0.208)
ϱ_{CG}	0.032 (0.019–0.048)	0.067 (0.043–0.098)	0.029 (0.025–0.033)
ϱ_{CT}	0.169 (0.133–0.210)	0.299 (0.248–0.352)	0.341 (0.315–0.368)
ϱ_{GT}	0.049 (0.029–0.075)	0.159 (0.109–0.218)	0.084 (0.072–0.098)
α	4.981 (2.401–8.714)	5.875 (2.886–10.068)	15.732 (10.652–21.723)
Ψ_{Ala}	0.043 (0.019–0.083)	0.043 (0.022–0.076)	0.041 (0.028–0.058)
Ψ_{Cys}	0.033 (0.016–0.061)	0.039 (0.019–0.077)	0.020 (0.013–0.031)
Ψ_{Asp}	0.043 (0.020–0.084)	0.061 (0.029–0.115)	0.043 (0.025–0.065)
Ψ_{Glu}	0.059 (0.025–0.103)	0.062 (0.031–0.111)	0.059 (0.031–0.085)
Ψ_{Phe}	0.040 (0.020–0.075)	0.042 (0.020–0.076)	0.052 (0.029–0.09)
Ψ_{Gly}	0.039 (0.017–0.074)	0.041 (0.018–0.072)	0.028 (0.018–0.041)
Ψ_{His}	0.051 (0.024–0.095)	0.033 (0.017–0.062)	0.056 (0.037–0.079)
Ψ_{Ile}	0.040 (0.019–0.073)	0.057 (0.027–0.102)	0.071 (0.043–0.101)
Ψ_{Lys}	0.089 (0.030–0.196)	0.063 (0.029–0.116)	0.071 (0.040–0.108)
Ψ_{Leu}	0.048 (0.024–0.081)	0.037 (0.018–0.068)	0.050 (0.031–0.072)
Ψ_{Met}	0.059 (0.024–0.136)	0.073 (0.033–0.130)	0.073 (0.041–0.112)
Ψ_{Asn}	0.084 (0.036–0.154)	0.059 (0.026–0.115)	0.072 (0.044–0.105)
Ψ_{Pro}	0.035 (0.017–0.058)	0.034 (0.017–0.062)	0.025 (0.016–0.036)
Ψ_{Gln}	0.068 (0.029–0.128)	0.076 (0.033–0.140)	0.074 (0.050–0.105)
Ψ_{Arg}	0.032 (0.017–0.055)	0.034 (0.017–0.063)	0.027 (0.018–0.039)
Ψ_{Ser}	0.051 (0.024–0.088)	0.044 (0.023–0.082)	0.050 (0.033–0.071)
Ψ_{Thr}	0.047 (0.022–0.088)	0.058 (0.026–0.105)	0.052 (0.033–0.075)
Ψ_{Val}	0.045 (0.023–0.085)	0.040 (0.019–0.076)	0.056 (0.037–0.077)
Ψ_{Try}	0.043 (0.020–0.086)	0.044 (0.020–0.088)	0.021 (0.012–0.033)
Ψ_{Tyr}	0.042 (0.018–0.082)	0.048 (0.022–0.097)	0.049 (0.026–0.086)
ε	1.761 (1.363–2.287)	1.781 (1.428–2.155)	3.985 (3.500–4.683)

φ_A is the parameter associated with the propensity of nucleotide A; ϱ_{AC} is the parameter associated with the exchangeability of nucleotides A and C (reversibly); α is the parameter governing the "granularity" of the Dirichlet process; the Ψ vector governs the base prior of the Dirichlet process, in this case representing the mean amino acid profile of the Dirichlet process, and with ε governing the dispersal around the mean.

Table S3. Posterior mean and 95% credibility intervals of parameters governing the substitution process under the MG-MutSelDP model, inferred from the IRBP*62–433*, GHR*49–321*, and RAG*41–1002* data sets

	IRBP*62–433*	GHR*49–321*	RAG*41–1002*
φ_A	0.134 (0.123–0.145)	0.268 (0.233–0.306)	0.208 (0.190–0.227)
φ_C	0.377 (0.354–0.400)	0.263 (0.232–0.295)	0.287 (0.268–0.308)
φ_G	0.384 (0.359–0.408)	0.180 (0.154–0.210)	0.270 (0.247–0.292)
φ_T	0.106 (0.097–0.114)	0.289 (0.254–0.324)	0.235 (0.216–0.253)
ϱ_{AC}	0.073 (0.065–0.083)	0.075 (0.057–0.096)	0.109 (0.093–0.127)
ϱ_{AG}	0.283 (0.259–0.307)	0.386 (0.338–0.436)	0.306 (0.277–0.335)
ϱ_{AT}	0.171 (0.147–0.195)	0.057 (0.041–0.074)	0.043 (0.032–0.056)
ϱ_{CG}	0.028 (0.024–0.031)	0.120 (0.094–0.150)	0.080 (0.065–0.097)
ϱ_{CT}	0.368 (0.343–0.398)	0.269 (0.229–0.314)	0.367 (0.337–0.397)
ϱ_{GT}	0.077 (0.066–0.089)	0.094 (0.068–0.123)	0.096 (0.079–0.113)
α	13.030 (8.523–18.484)	6.906 (3.467–11.659)	7.151 (3.762–11.413)
Ψ_{Ala}	0.043 (0.028–0.060)	0.061 (0.030–0.105)	0.051 (0.027–0.093)
Ψ_{Cys}	0.019 (0.011–0.029)	0.045 (0.019–0.084)	0.032 (0.017–0.056)
Ψ_{Asp}	0.045 (0.027–0.069)	0.070 (0.033–0.119)	0.043 (0.021–0.078)
Ψ_{Glu}	0.066 (0.040–0.099)	0.083 (0.034–0.152)	0.072 (0.031–0.129)
Ψ_{Phe}	0.038 (0.019–0.066)	0.029 (0.013–0.057)	0.052 (0.028–0.089)
Ψ_{Gly}	0.041 (0.025–0.060)	0.055 (0.025–0.095)	0.033 (0.018–0.055)
Ψ_{His}	0.048 (0.029–0.075)	0.031 (0.012–0.060)	0.059 (0.028–0.099)
Ψ_{Ile}	0.051 (0.027–0.080)	0.036 (0.015–0.068)	0.055 (0.029–0.093)
Ψ_{Lys}	0.064 (0.035–0.097)	0.049 (0.021–0.090)	0.060 (0.031–0.107)
Ψ_{Leu}	0.043 (0.027–0.064)	0.049 (0.023–0.084)	0.041 (0.020–0.069)
Ψ_{Met}	0.084 (0.053–0.124)	0.053 (0.025–0.098)	0.050 (0.025–0.085)
Ψ_{Asn}	0.057 (0.031–0.089)	0.045 (0.018–0.084)	0.067 (0.031–0.113)
Ψ_{Pro}	0.027 (0.017–0.041)	0.050 (0.021–0.089)	0.037 (0.019–0.065)
Ψ_{Gln}	0.082 (0.053–0.122)	0.077 (0.034–0.131)	0.063 (0.028–0.106)
Ψ_{Arg}	0.038 (0.024–0.055)	0.032 (0.014–0.058)	0.045 (0.022–0.076)
Ψ_{Ser}	0.055 (0.036–0.081)	0.056 (0.025–0.095)	0.047 (0.026–0.074)
Ψ_{Thr}	0.059 (0.037–0.084)	0.062 (0.031–0.107)	0.056 (0.029–0.092)
Ψ_{Val}	0.053 (0.033–0.077)	0.047 (0.022–0.084)	0.052 (0.024–0.093)
Ψ_{Try}	0.027 (0.015–0.049)	0.037 (0.014–0.072)	0.032 (0.018–0.054)
Ψ_{Tyr}	0.050 (0.024–0.083)	0.024 (0.010–0.048)	0.045 (0.024–0.078)
ε	3.649 (3.135–4.246)	4.659 (3.564–5.953)	2.502 (2.092–2.921)

φ_A is the parameter associated with the propensity of nucleotide A; ϱ_{AC} is the parameter associated with the exchangeability of nucleotides A and C (reversibly); α is the parameter governing the "granularity" of the Dirichlet process; the Ψ vector governs the base prior of the Dirichlet process, in this case representing the mean amino acid profile of the Dirichlet process, and with ε governing the dispersal around the mean.

Table S4. Posterior mean and 95% credibility intervals of parameters governing the substitution process under the MG-MutSelDP model, inferred from the TBR*42–240*, GLYT*44–296*, and FRIED*18–208* data sets

	TBR*42–240*	GLYT*44–296*	FRIED*18–208*
φ_A	0.134 (0.120–0.148)	0.181 (0.167–0.196)	0.291 (0.269–0.314)
φ_C	0.430 (0.400–0.461)	0.326 (0.307–0.345)	0.277 (0.256–0.297)
φ_G	0.305 (0.276–0.334)	0.302 (0.283–0.322)	0.181 (0.164–0.199)
φ_T	0.131 (0.117–0.147)	0.191 (0.177–0.206)	0.251 (0.231–0.272)
ϱ_{AC}	0.121 (0.102–0.144)	0.096 (0.082–0.113)	0.126 (0.097–0.157)
ϱ_{AG}	0.322 (0.291–0.355)	0.272 (0.251–0.298)	0.223 (0.189–0.264)
ϱ_{AT}	0.186 (0.151–0.226)	0.196 (0.169–0.226)	0.145 (0.105–0.186)
ϱ_{CG}	0.076 (0.065–0.089)	0.073 (0.061–0.087)	0.156 (0.114–0.200)
ϱ_{CT}	0.181 (0.158–0.206)	0.271 (0.249–0.294)	0.239 (0.198–0.288)
ϱ_{GT}	0.114 (0.091–0.140)	0.092 (0.074–0.111)	0.112 (0.065–0.163)
α	8.941 (5.221–13.716)	15.023 (9.987–20.959)	10.504 (6.455–15.809)
Ψ_{Ala}	0.079 (0.046–0.123)	0.063 (0.043–0.087)	0.084 (0.051–0.126)
Ψ_{Cys}	0.035 (0.020–0.061)	0.025 (0.016–0.038)	0.039 (0.022–0.065)
Ψ_{Asp}	0.039 (0.021–0.071)	0.037 (0.023–0.057)	0.050 (0.027–0.087)
Ψ_{Glu}	0.052 (0.026–0.092)	0.043 (0.027–0.065)	0.076 (0.041–0.127)
Ψ_{Phe}	0.043 (0.022–0.075)	0.046 (0.028–0.069)	0.040 (0.023–0.061)
Ψ_{Gly}	0.063 (0.035–0.097)	0.039 (0.025–0.056)	0.058 (0.032–0.093)
Ψ_{His}	0.035 (0.019–0.060)	0.035 (0.022–0.054)	0.035 (0.020–0.060)
Ψ_{Ile}	0.035 (0.019–0.059)	0.054 (0.033–0.084)	0.040 (0.022–0.063)
Ψ_{Lys}	0.038 (0.020–0.065)	0.086 (0.053–0.122)	0.060 (0.033–0.096)
Ψ_{Leu}	0.037 (0.022–0.060)	0.045 (0.025–0.070)	0.047 (0.027–0.075)
Ψ_{Met}	0.073 (0.038–0.124)	0.089 (0.055–0.130)	0.055 (0.027–0.094)
Ψ_{Asn}	0.061 (0.030–0.103)	0.048 (0.030–0.071)	0.048 (0.028–0.079)
Ψ_{Pro}	0.055 (0.032–0.087)	0.031 (0.019–0.047)	0.031 (0.018–0.049)
Ψ_{Gln}	0.037 (0.020–0.062)	0.067 (0.044–0.101)	0.059 (0.033–0.096)
Ψ_{Arg}	0.029 (0.017–0.046)	0.039 (0.024–0.059)	0.038 (0.023–0.058)
Ψ_{Ser}	0.078 (0.044–0.119)	0.055 (0.037–0.077)	0.053 (0.032–0.083)
Ψ_{Thr}	0.070 (0.041–0.110)	0.058 (0.038–0.084)	0.049 (0.027–0.083)
Ψ_{Val}	0.050 (0.027–0.085)	0.059 (0.037–0.087)	0.037 (0.023–0.061)
Ψ_{Try}	0.047 (0.024–0.080)	0.033 (0.020–0.053)	0.053 (0.027–0.096)
Ψ_{Tyr}	0.034 (0.019–0.059)	0.039 (0.024–0.057)	0.038 (0.024–0.058)
ε	2.043 (1.696–2.482)	2.638 (2.192–3.275)	2.167 (1.769–2.657)

φ_A is the parameter associated with the propensity of nucleotide A; ϱ_{AC} is the parameter associated with the exchangeability of nucleotides A and C (reversibly); α is the parameter governing the "granularity" of the Dirichlet process; the Ψ vector governs the base prior of the Dirichlet process, in this case representing the mean amino acid profile of the Dirichlet process, and with ε governing the dispersal around the mean.