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| **Table S8:** OAS gene family evolutionary summary for 11 primate species using PAML. | | | |  |
| Gene | P-value | Branches\* | Sites (>95%)\*\* |  |
| OAS1 | < 0.001 | 8 | 22 |  |
| OAS2 | < 0.014 | 4 | 2 |  |
| OAS3 | < 0.08 | 2 | 0 |  |
| OASL | ~ 0.99 | 1 | 0 |  |
| \*The number of branches (red) with *d*N/*d*S > 1 identified by Free Ratio analyses in PAML (see Figure). | | | |  |
|  |
| \*\*The number of amino acid sites with 95% or greater statistical signifcance identified by Bayes Emprical Bayes analysis in PAML NSsites (M7 vs. M8). | | | |  |
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