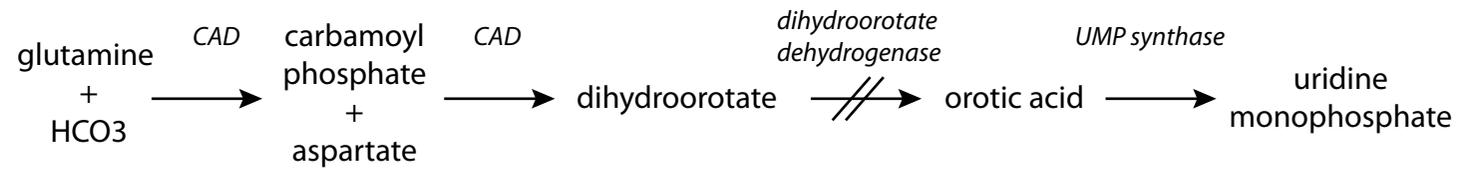


Supplementary Figure 2. Number of candidate genes vs. number of unaffected exomes in filter. The results of adding more unaffected exomes as a filter for novel variants is shown for the recessive model, i.e. requiring at least two novel variants for a gene to qualify as a candidate. For this analysis, either all twelve previously sequenced exomes (Ng et al., 2009) were used (top), or only the eight non-Yoruba exomes from the same study (bottom), and results from all possible combinations of the specified number of exomes are represented. Results of the same filtering with (orange) and without dbSNP129 (blue) are also shown. The single gene identified when using all twelve exomes was DHODH (top); when only non-Yoruba exomes were used, the list also included ESPNL.

Ng, S.B. et al. Targeted capture and massively parallel sequencing of 12 human exomes. *Nature* (2009).



Supplementary figure 3.

Enzymatic steps controlling *de novo* pyrimidine synthesis. Mutations in *DHODH* are predicted to diminish dihydroorotate dehydrogenase activity.