S11 Table. Estimates of power to detect an association between the *EGLN1* SNP rs186996510 and Hb in our data set. We used effect size estimates from multiple studies, ranging from 0.386 to 1.676 g/dL per allele. Power was calculated using the observed allele frequency (maf = 0.336), sample size (n=649) and standard deviation of Hb residuals after regressing out covariates (1.330 g/dL), assuming a single test (α = 0.05).

| Source | Effect size (g/dL/allele) | Power |
|--|---------------------------|-------|
| Simonson et al. (mixed gender) [1] | 1.676 | 1.000 |
| Xiang et al. (male only) [2] | 0.620 | 1.000 |
| This study (top EPAS1 SNP rs372272284) | 0.386 | 0.999 |
| An estimate for 99% power | 0.332 | 0.990 |
| An estimate for 95% power | 0.280 | 0.950 |
| An estimate for 90% power | 0.252 | 0.900 |
| An estimate for 80% power | 0.218 | 0.800 |

References

- 1. Simonson TS, Yang Y, Huff CD, Yun H, Qin G, Witherspoon DJ et al. (2010) Genetic evidence for high-altitude adaptation in Tibet. *Science* 329: 72-75.
- 2. Xiang K, Peng Y, Yang Z, Zhang X, Cui C, Zhang H et al. (2013) Identification of a Tibetan-specific mutation in the hypoxic gene *EGLN1* and its contribution to high-altitude adaptation. *Mol Biol Evol* 30: 1889-1898.