**S3 Table: Contingency table showing the overlap of cattle stature genes from Bouwman *et al*. [12] with human height genes from Yengo *et al*. [10].**

|  |  |  |  |
| --- | --- | --- | --- |
|  | In Yengo *et al*. [10] | Not In Yengo *et al*. [10] | Marginal totals (rows) |
| In Bouwman *et al*. [12] | 30 | 47 | **77\*\*** |
| Not In Bouwman *et al*. [12] | 1,523 | 12,142 | **13,665** |
| Marginal totals (columns) | **1,553\*\*\*** | **12,189** | **13,742\*** |

\*Cattle genes with 1 to 1 orthologs in humans (after QC); \*\*Cattle genes within 10kb of the 164 lead SNPs from Bouwman *et al*. [12] that also have orthologs in humans; \*\*\*Human height genes prioritized as those that overlap with, or are within 10kbp either side of the 3,290 lead SNPs for height in Yengo *et al*. [10], that also have orthologs in cattle. The proportion 30/77 is more than can be expected by chance: Fisher’s exact test (odds ratio = 5.1, p-value = 3.1e-10).