



Figure S1. Yam bean root images including the origin and accession numbers of each cultivar, which were grown and investigated at the University of Western Australia. S1) *P. tuberosus* (Pt-CIP-209013) from Peru. S2) *P. tuberosus* (Pt-CIP-209014) from Peru. S3) *P. tuberosus* (Pt-CIP-209015) from Peru. S4) *P. erosus* (Pe-CIP-209016) from Guatemala. S5) *P. erosus* (Pe-CIP-209046) from Cartago Costa Rica. S6) *P. erosus* (Pe-CIP-209051) from Mexico.

Table S1. Assembly statistics of the yam bean genome assembled by MaSuRCA 3.2.2. N50 of the assembly was 6687 across 18,412 sequences.

| | Average bp | Number of sequences (n=) |
|----------------|-------------|--------------------------|
| N50 | 18,412 | 6687 |
| N60 | 13,530 | 9590 |
| N70 | 8991 | 13,736 |
| N80 | 4712 | 20,673 |
| N90 | 1301 | 39,256 |
| N100 | 300 | 127,163 |
| Total sum | 460,035,745 | 127,163 |
| Predicted size | 550Mbp | N/A |

Table S2. The BUSCO (Benchmarking Universal Single-Copy Orthologs) analysis results for the yam bean MaSuRCA assembly.

| | Number of BUSCO hits | Percentage of Total BUSCOs |
|-----------------------|--|--|
| Complete BUSCOs | 1255 (1197 single-copy and 58 duplicated) | 87.1 (83.1% single-copy and 4.0% duplicated) |
| Fragmented BUSCOs | 74 | 5.1 |
| Missing BUSCOs | 111 | 7.8 |
| Total BUSCOs searched | 1440 | N/A |

Table S3. The singleton/non-duplicated statistics of the yam bean genome assembled by MaSuRCA 3.2.2. compared to other six other Pachyrhizus cultivars using bcftools.

| | Number of BUSCO hits | Percentage of Total BUSCOs |
|-----------------------|--|--|
| Complete BUSCOs | 1255 (1197 single-copy and 58 duplicated) | 87.1 (83.1% single-copy and 4.0% duplicated) |
| Fragmented BUSCOs | 74 | 5.1 |
| Missing BUSCOs | 111 | 7.8 |
| Total BUSCOs searched | 1440 | N/A |