

Supporting Table S2: Average heterozygosity at microsatellite loci among offspring from single clone cultures and the position in of the microsatellites with respect to the centromere

| Locus | Scaffold (<i>D. magna</i> assembly 2.4) | Position on scaffold (base pairs) | Linkage group (v4.0.1) | Distance from centromere (cM) | <i>N</i>^a | Heterozygosity (confidence limits) |
|--------------|--|--|-------------------------------|--------------------------------------|-----------------------------|---|
| B008 | scaffold03124 | 1781052 | 6 | 25.8 | 5 | 0 (0 – 0.40) |
| B030 | scaffold00243 | 463057 | 3 | 32.9 | 27 | 0.59 (0.41 – 0.76) |
| B050 | scaffold02066 | 483524 | 3 | 77.6 | 22 | 0.77 (0.56 – 0.90) |
| B064 | scaffold00443 | 151077 | 1 | 37.9 | 27 | 0.63 (0.44 – 0.79) |
| B074 | contig23904 | 1149 | unmapped | NA | 27 | 0.78 (0.59 – 0.90) |
| B096 | scaffold01005 | 1506200 | 9 | 3.6 | 22 | 0.36 (0.20 – 0.57) |
| B107 | scaffold00763 | 136826 | 1 | 100.0 | 22 | 0.59 (0.30 – 0.77) |

^a*N* refers to the number of genotyped offspring from heterozygous parents