*Supplementary Material*

Exploring deep learning for complex trait genomic prediction in polyploid outcrossing species

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**Table S1:** Optimum hyperparameter choice in strawberry data.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Activation function CNN / MLP | # CNN Layers /  # Filters | # MLP layers /  # Neurons | Weight decay | Dropout rate CNN / MLP |
| Brix | Linear / relu | 1 / 128 | 3 / 12 | 0.001 | 0.1 / 0.0 |
| MktWtE | Linear / linear | 1 / 128 | 10 / 4 | 0.001 | 0.1 / 0.0 |
| MktWtT | Linear / linear | 1 / 128 | 1 / 32 | 0.001 | 0.2 / 0.001 |
| AveWtT | Linear / linear | 1 / 128 | 10 / 8 | 0.001 | 0.2 / 0.01 |
| CulsTPer | Linear / relu | 1 / 128 | 1 / 128 | 0.01 | 0.01 / 0.0 |

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| Learning rate was 0.0025 except for CulsTPer (lr = 0.01). |