**S8** **Table.** Genomic correlation between 2017 and 2018 in each environment for trait EV\_V4 for KE (blue numbers) and PE (red numbers). The blue and red bold numbers with stars indicate which proportion of interactions in bivariate sERRBLUP maximized the predictive ability based on haplotype blocks in each environment for KE and PE, respectively.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Bivariate Models | EIN | ROG | GOL | TOM |
| GBLUP | 0.855 / 0.592 | 0. 890/ 0.716 | 0.873 / 0.980 | 0.959 / 0.755 |
| sERRBLUP top 10% | **0.855**\* / **0.625\*** | 0.897 / **0.666\*** | 0.809 / 0.844 | 0.946 / **0.681\*** |
| sERRBLUP top 5% | 0.881 / 0.677 | 0.892 / 0.715 | 0.792 / 0.829 | 0.994 / 0.661 |
| sERRBLUP top 1% | 0.941 / 0.793 | 0.892 / 0.816 | **0.783**\* / **0.834\*** | 0.977 / 0.636 |
| sERRBLUP top 0.1% | 0.934 / 0.831 | **0.905**\* / 0.930 | 0.807 / 0.879 | **0.966\*** / 0.643 |
| sERRBLUP top 0.01% | 0.902 / 0.871 | 0.914 / 0.681 | 0.854 / 0.901 | 0.909 / 0.683 |
| sERRBLUP top 0.001% | 0.272 / 0.220 | -6.818 / 0.435 | 0.718 / 0.537 | 0.504 / 0.746 |