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| --- | --- | --- |
|  |  | **Table S12: Classification of core promoters** |
| Sigma 1 | DBTBS 2 | Comp 3 | Pred 4 | Recov 5 | Var %6 | R-sq7 | Expl %8 |
| SigA | 352 | 6 | 1868 | 282/296 | 30.3 | 0.236 | 7.15 |
| SigB | 63 | 1 | 170 | 46/48 | 7.3 | 0.760 | 5.55 |
| SigD | 30 | 1 | 68 | 24/26 | 1.5 | 0.774 | 1.16 |
| SigE, *F* | 70,*25* | 1 | 262 | 54/63,*7/22* | 21.6 | 0.917 | 19.81 |
| SigG, *F* | 55,*25* | 1 | 185 | 50/51,*11/22* | 16.7 | 0.889 | 14.84 |
| SigH | 25 | 1 | 72 | 12/17 | 1.7 | 0.690 | 1.17 |
| SigI | 1 | 1 | 13 | 1/1 | 0.3 | 0.389 | 0.12 |
| SigK | 52 | 1 | 207 | 42/46 | 18.6 | 0.858 | 15.96 |
| SigL | 6 | 1 | 11 | 6/6 | 0.8 | 0.263 | 0.21 |
| SigW,X,M,Y | 34,15,3,2 | 1 | 79 | 45/50 | 1.2 | 0.418 | 0.50 |
| **Total** | 758 | 15 | **2935** | 580/648 | 100 | n.r. | **66.47** |

(1)Sigma factors. (2) Number of promoters for the corresponding sigma factor(s) in DBTBS (detailed in Table S13). (3) Number of clusters associated with this category of promoters identified by unsupervised sequence classification. (4) Total number of up-shifts predicted to be controlled by the sigma factor (posterior probability Pcomp > 0.5, Table S4). (5) Recovery of DBTBS information by our classification. The sigma factor binding sites reported in DBTBS but not associated with up-shifts were excluded from the denominator. (6) Percentage of the genome-wide promoter activity variance accounted for by promoters of this category. (7) R-squared value corresponds to the fraction of the variance that can be explained by regulation at the cluster level. (8) Percentage of explained variance per cluster. Note that the ‘explained fraction’ integrates all regulatory levels modulating sigma factor activity (including the well-known role of anti-sigma factors) because it is based on regulon activity and not on sigma expression level. n.r., not relevant.