**Table S4. Software tools for motif analysis of ChIP-seq peaks and their uses.**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Category*** | ***Software tool*** | ***Web Server*** | ***Obtain peak regions*** | ***Motif discovery*** | ***Motif comparison*** | ***Central motif enrichment analysis*** | ***Local motif enrichment analysis*** | ***Motif spacing analysis*** | ***Motif prediction/mapping*** |
| **Obtaining sequences** | **Galaxy [50-52]** | X | X |  |  |  |  |  |  |
| **RSAT [53]** | X | X |  |  |  |  |  |  |
| **UCSC Genome Browser [54]** | X | X |  |  |  |  |  |  |
| **Motif discovery + more** | **ChIPMunk [55]** | X |  | X |  |  |  |  |  |
| **CisGenome [56]** |  |  | X | X |  |  |  |  |
| **CompleteMOTIFS [48]** | X |  | X | X |  |  |  |  |
| **MEME-ChIP [57]** | X |  | X | X | X |  |  |  |
| **peak-motifs [58]** | X |  | X | X |  |  |  | X |
|  | **Cistrome [49]** | X | X | X |  | X | X |  | X |
| **Motif comparison** | **STAMP [59]** | X |  |  | X |  |  |  |  |
| **TOMTOM [60]** | X |  |  | X |  |  |  |  |
| **Motif enrichment/spacing** | **CentriMo [61]** | X |  |  |  | X | X |  |  |
| **SpaMo [62]** | X |  |  |  |  |  | X |  |
| **Motif prediction/mapping** | **FIMO [63]** | X |  |  |  |  |  |  | X |
| **PATSER [64]** | X |  |  |  |  |  |  | X |