Rules for sample naming

Sample names should be unique, short, and descriptive. Use underscore as a word separator.

Consider coding the following information in your sample names if relevant to the project:

(1) cell / tissue type;
(2) condition – temperature, exercise, treatment with an activator or inhibitor;
(3) perturbation – KO or OE;
(4) epitope – in case of, ChIP-Seq, it's very important to indicate the TF or the histone mark of interest; if control, use "WCE".
(5) time point – if you have multiple time points, use consistent time units;
(6) replicate ID – animal or cell ID.

Consider any future expansions of the project: Do you plan to add another parameter 6 months in the future? If yes, include it in the current set.
The indication of the replicate - a number - should always go last.

The result will look as follows:

tissue_condition_perturbation_epitope_time_replicate

Example 1. RNA-Seq, perturbation and condition:
`[Liv_HFD_KO_1, Liv_HFD_KO_2, Liv_Chow_KO_1, Liv_Chow_KO_2, Liv_HFD_WT_1, Liv_HFD_WT_2, Liv_Chow_WT_1, Liv_Chow_WT_2]`
Example 2. ChIP-Seq, histone mark and condition:
`[BAT_cold_27ac_1, BAT_cold_27ac_2, WAT_cold_27ac_1, WAT_cold_27ac_2, BAT_cold_WCE, WAT_cold_WCE]`
Example 3. RNA-Seq, time course and condition:
`[L1_WT_1, L1_WT_2, L1_Dex_d1_1, L1_Dex_d1_2, L1_TGFb_d1_1, L1_TGFb_d1_2, L1_Dex_d2_1, L1_Dex_d2_2]`
Example 4. ChIP-Seq, TF:
`[WAT_WT_PPARg_1, WAT_WT_PPARg_2, WAT_OE_PPARg_1, WAT_OE_PPARg_2, WAT_WT_WCE, WAT_OE_WCE]`

For technical reasons, sample name should have no words as follows:

1. "L00X" where X is a number
2. "001"
3. 6 to 8 consecutive ACTG letters
4. "SX" or "SXX" where Xs are numbers
5. "R1" or "R2"