# Compartment Switching Graphic Choices

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Summary:

- Goal: P3F/MYOD/K27ac association with discordant compartment.
- Methods: Distribution of binding sites per category (A-A, A-B, B-A, B-B).
- Problem: Compare per category or per 1000 binding sites?

    - For K27ac and MYOD, FP is quite comparable becauase they have similar number of binding sites in FP.
    - Normalizing by number of bins: P3F is about 1/9 binding sites of MYOD1, so it would sit lower than both (Fig1).
    - Normalize by binding sites: fraction is really low. (Fig 2)
    - Normalize by both: I feel like P3F is overblown. The fact that there are only 2000 or so consensus sites in FP means something. I am not sure if downscaling K27ac/MYOD is the right approach. (Fig 4)

- Additional graphical presentation choices: FP/FN as facets (Fig1-3), or Factor as facets (Fig4)?

Fig1: Normalize Per Compartment/Bin
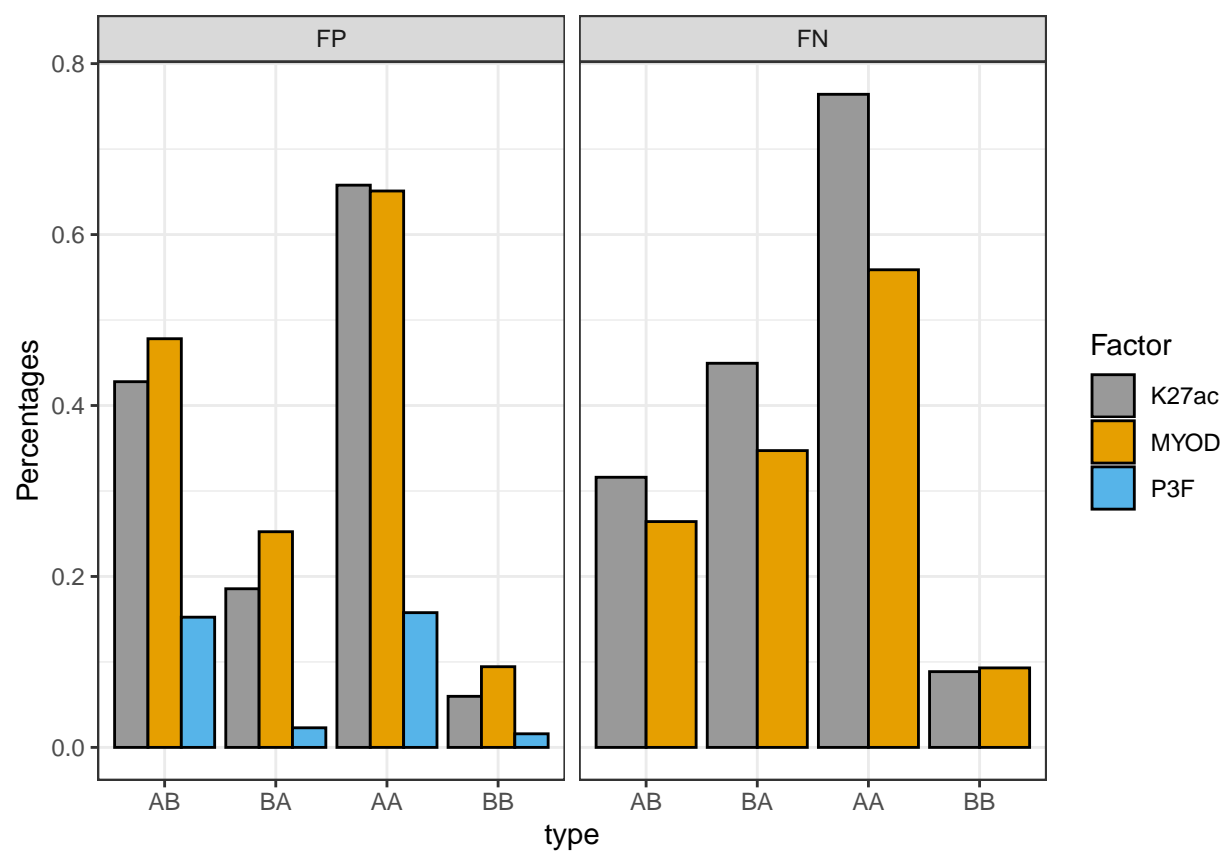
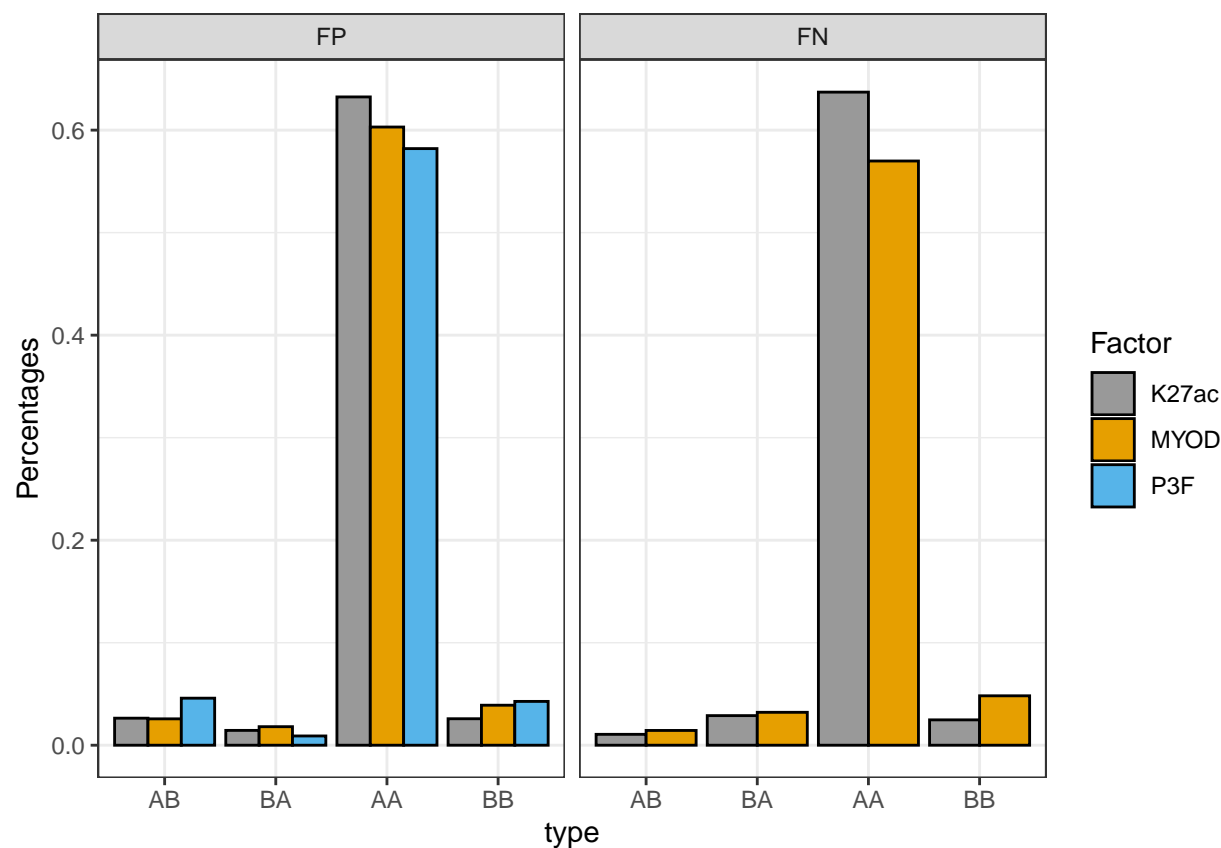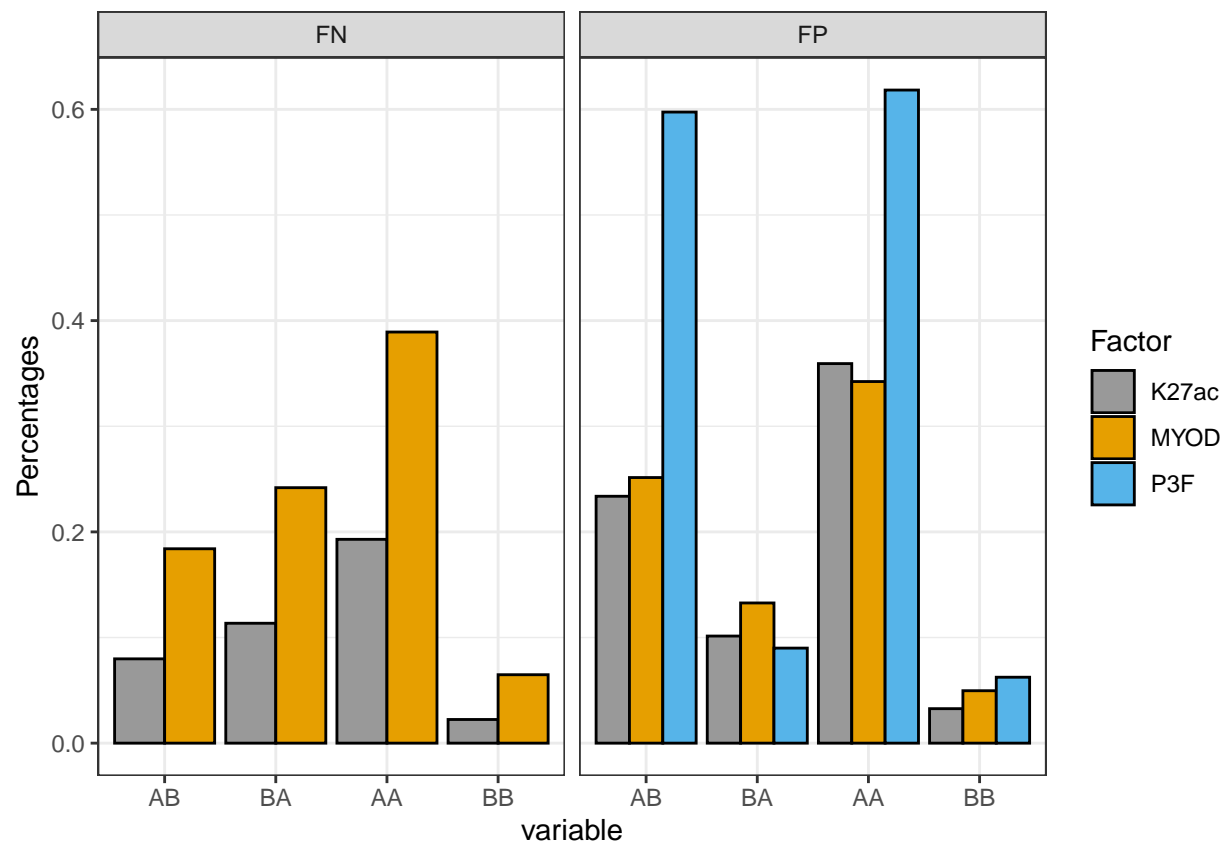**Fig2: Normalize by Number of binding sites (P3F has significantly fewer)**

Fig3: Normalize by Per Bin Per 10000 Binding Sites

Fig4: Factor as Facets (compare against Fig1)