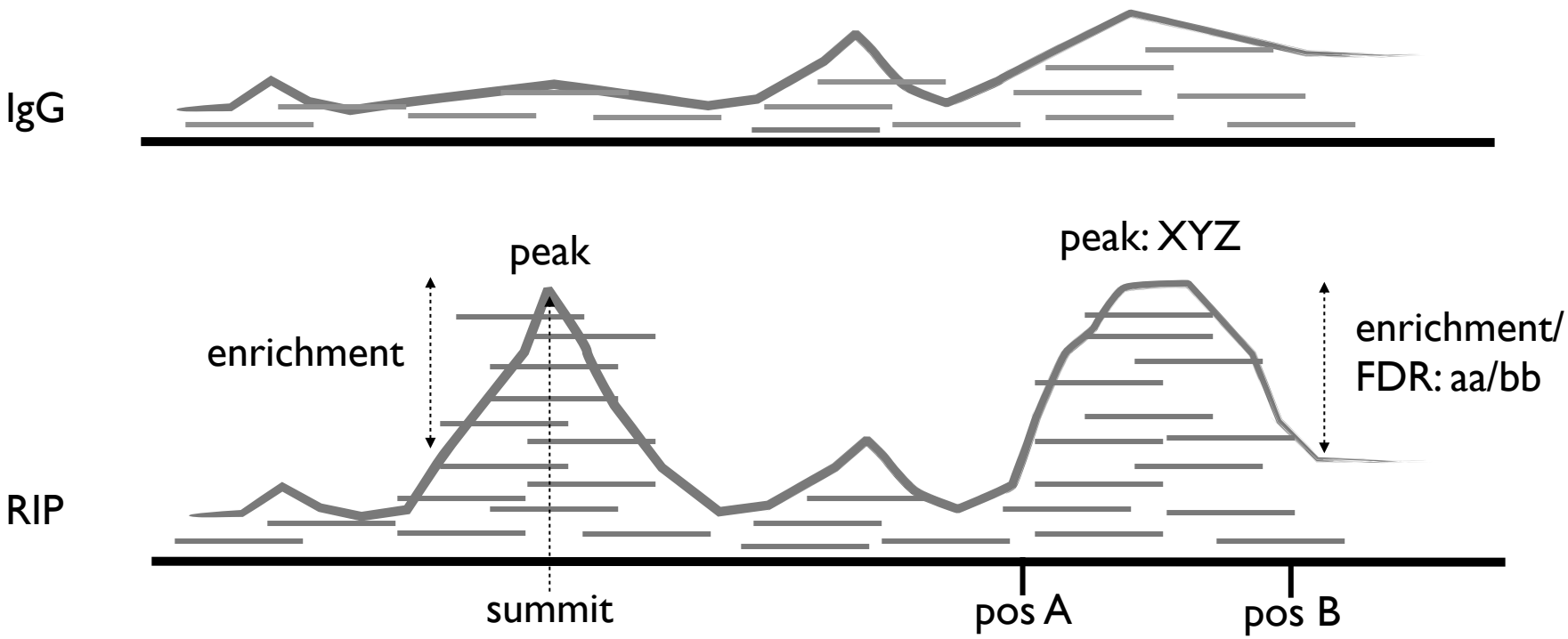
Comparing two seq samples



IgG: 1 1 1 1 1 2 2 1 1 1 1 3 3 3 2 2 2 3 3 2 1 3 2 3 4 3 2 1 2 2 2 2 2 2 2 3 3 4 1 1 1 1 1 5 2 1 3 4 4 4 4 2 3 3 2 3 4 3 2 1 1 0 0 0 0

RIP: 1 1 1 1 1 2 2 1 1 1 1 3 3 3 5 5 7 8 9 9 9 8 8 7 5 3 2 1 2 2 2 2 2 2 2 3 3 4 1 1 1 1 1 5 5 5 6 7 8 9 9 9 8 9 7 6 4 3 2 1 1 0 0 0 0

RIP-IgG: 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 3 5 6 6 7 8 5 6 4 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 3 4 3 3 4 5 5 7 5 6 5 3 0 0 0 0 0 0 0 0 0

- all based on reads and coverage

<u>.bed file basic format</u>: chr/start/end/peakID/score/strand