Supplementary Figure 1 Sequence: IEAAMDRK, Charge: +2, Monoisotopic m/z: 467.24777 Da (+2.99 mmu/+6.4 ppm), MH+: 933.48827 Da, RT: 18.60 min, Identified with: SEQUEST (v1.12); XCorr:2.25, Probability:5.45, Ions matched by search engine: 9/14 Display Options Fragment match tolerance used for search: 0.8 Da Charge Detail Level: Fragments used for search: b; b-H₂O; b-NH₃; y; y-H₂O; y-NH₃ Value Type: Delta Mass [mmu] 2.0 % of base peak Ion Series Neutral Losses Precursor Ions ✓ Use search settings 69.04 -363.52 +5.28 +210.89 -108.47 -48.68 -41.67 +4.89 -81.28 B +355.77 A Match Tolerance +33.11 A -216.66 5 +3.44 M -39.91 4 -171.10 D -294.64 3 -294.64 -131.16 2 - 1 -147.89 F -H,0 ₽b ₽v Extracted from: XILabDataWelos-orbi082510lBuckInstitute-GelSlice-SL_100826072828.RAW #1905 RT: 18.60 ITMS, CID, z=+2, Mono m/z=467.24777 Da, MH+=933.48827 Da, Match Tol.=0.8 Da ▼ Precursor y₆* 691.40 [M+2H]²⁺-H₂O, [M+2H]²⁺-NH₃ b₂⁺ 243.21 394.66 у₅* 620.36 y₄2* 275.25 b₃* 314.24 b₄*-H₂O y₆*-H₂O 367.28 b5*-H2O 673.37 498.33

Supplementary Figure 1: Fragmentation spectrum of MLL protein. Eight of fourteen possible fragment ions match under 100 mmu (milli mass units) mass error.

y, y-H₂O, y-NH₃

OK Help

Pre+H, Precursor, Precursor-H₂O, Precursor-H₂O-NH₃, Precursor-NH₃, Pre-H b, b-H₂O, b-NH₃

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