

S1_RAW_Images

Figure S1

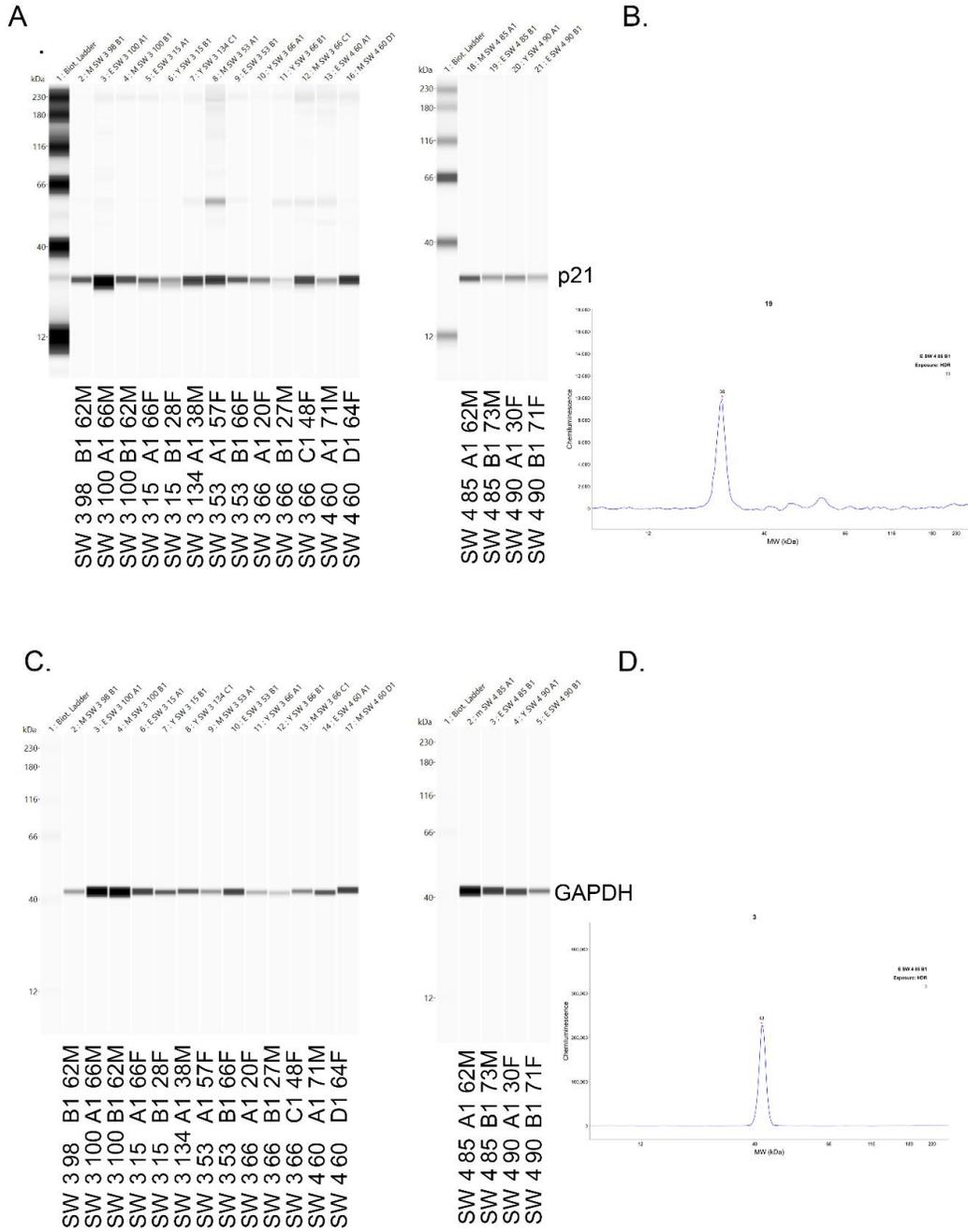
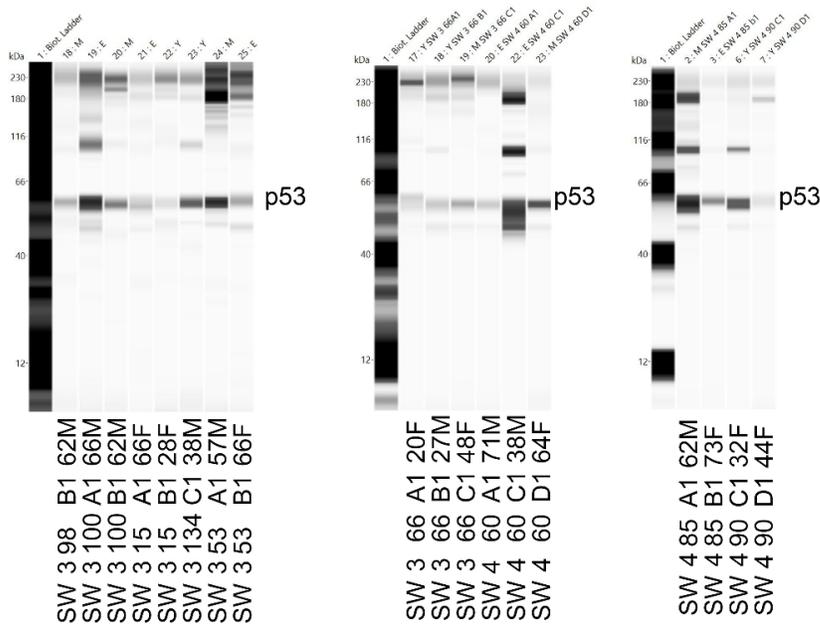
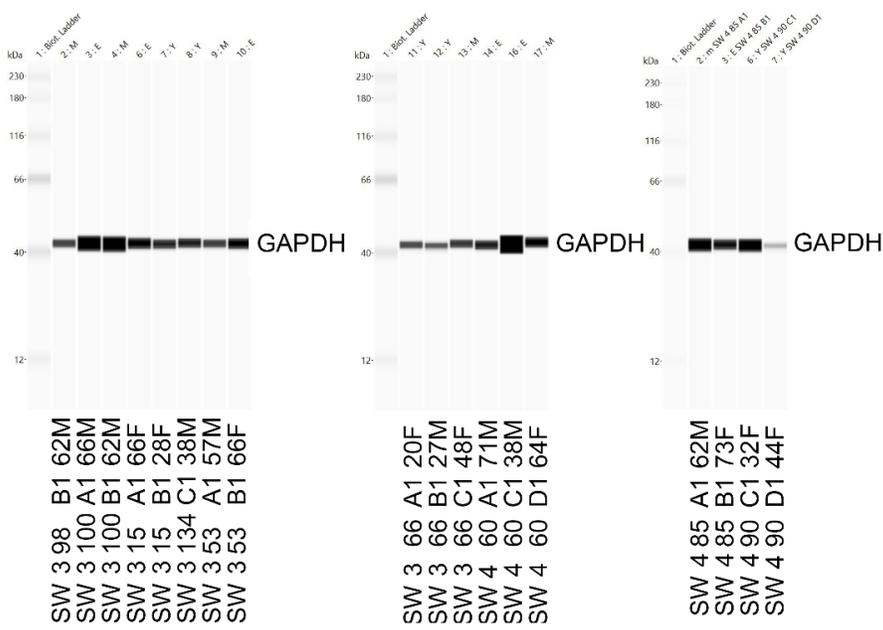


Figure S2

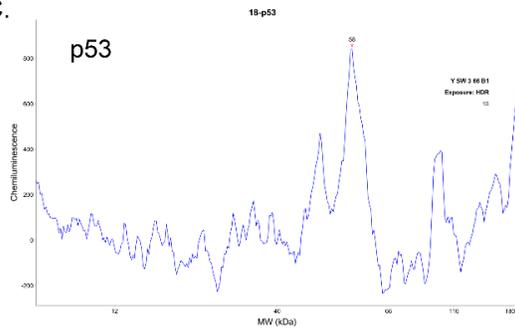
A.



B.



C.



D.

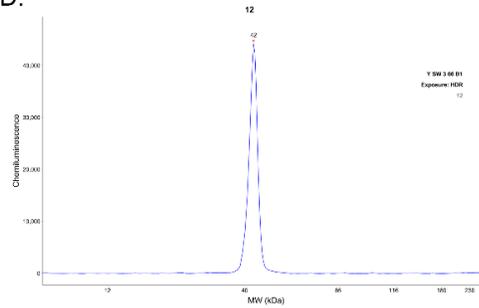


Figure S3

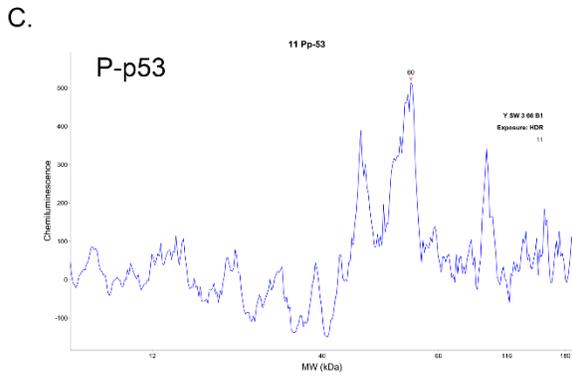
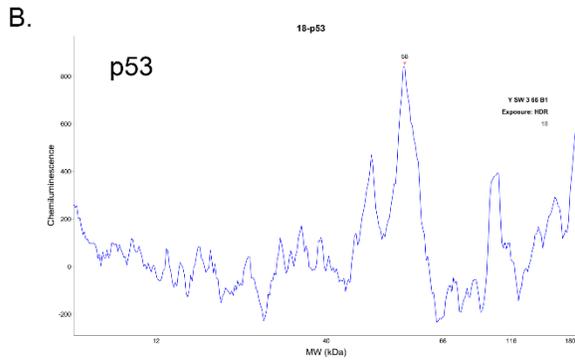
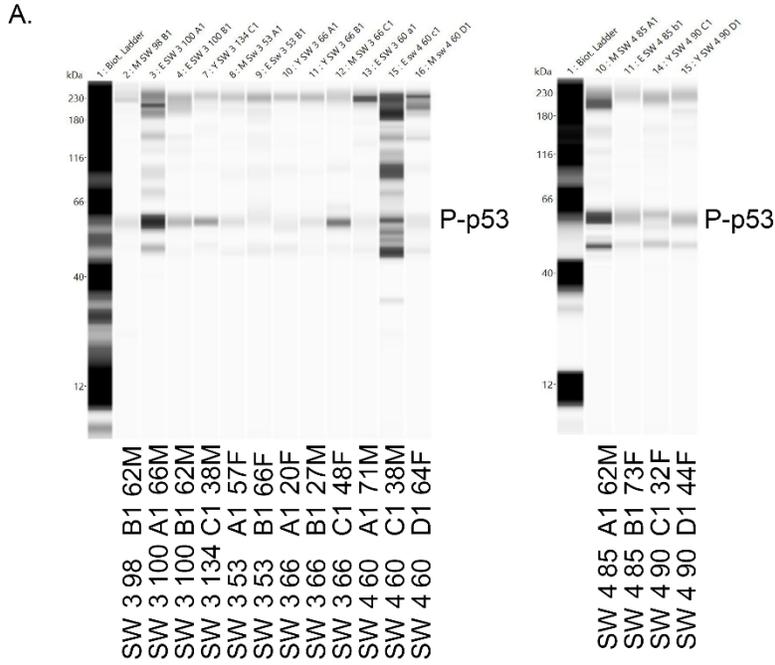
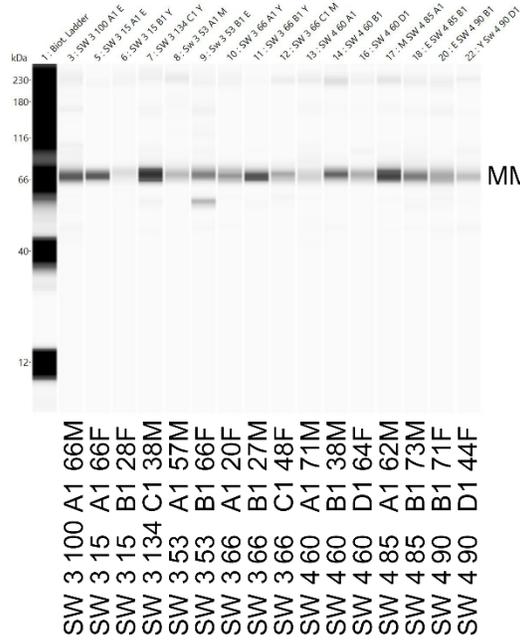
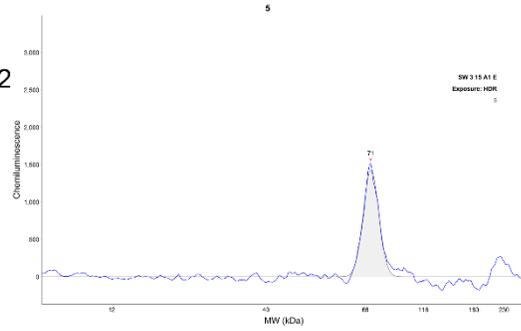


Figure S4

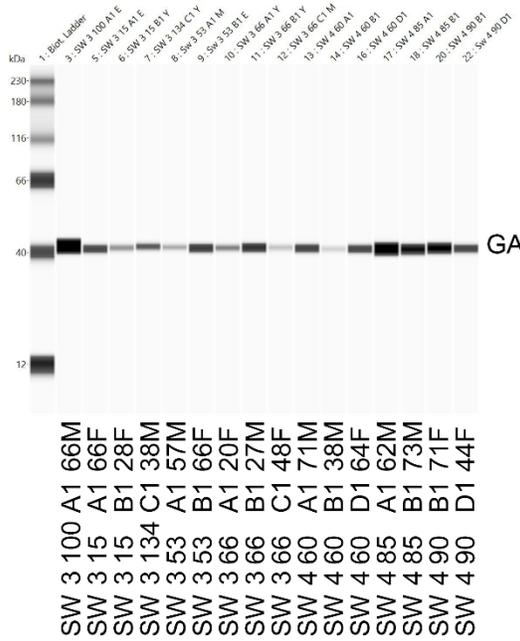
A.



B.



C.



D.

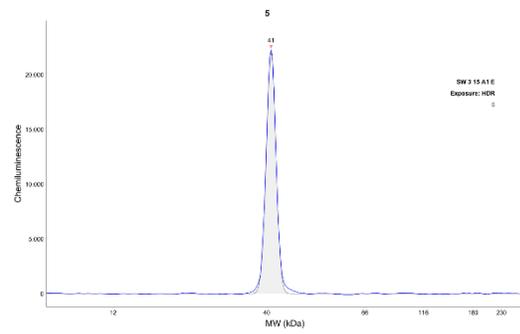


Figure S5

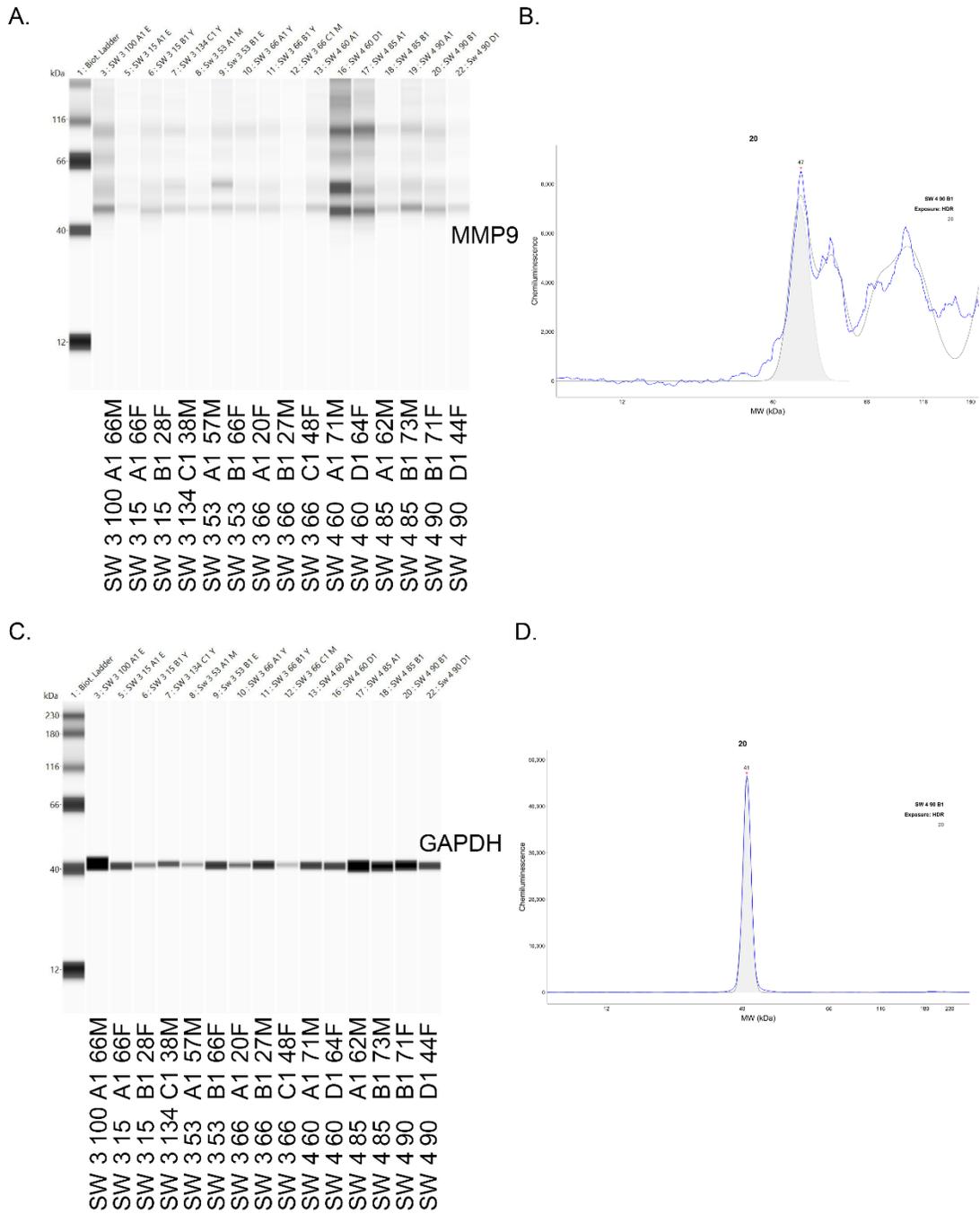


Figure S6

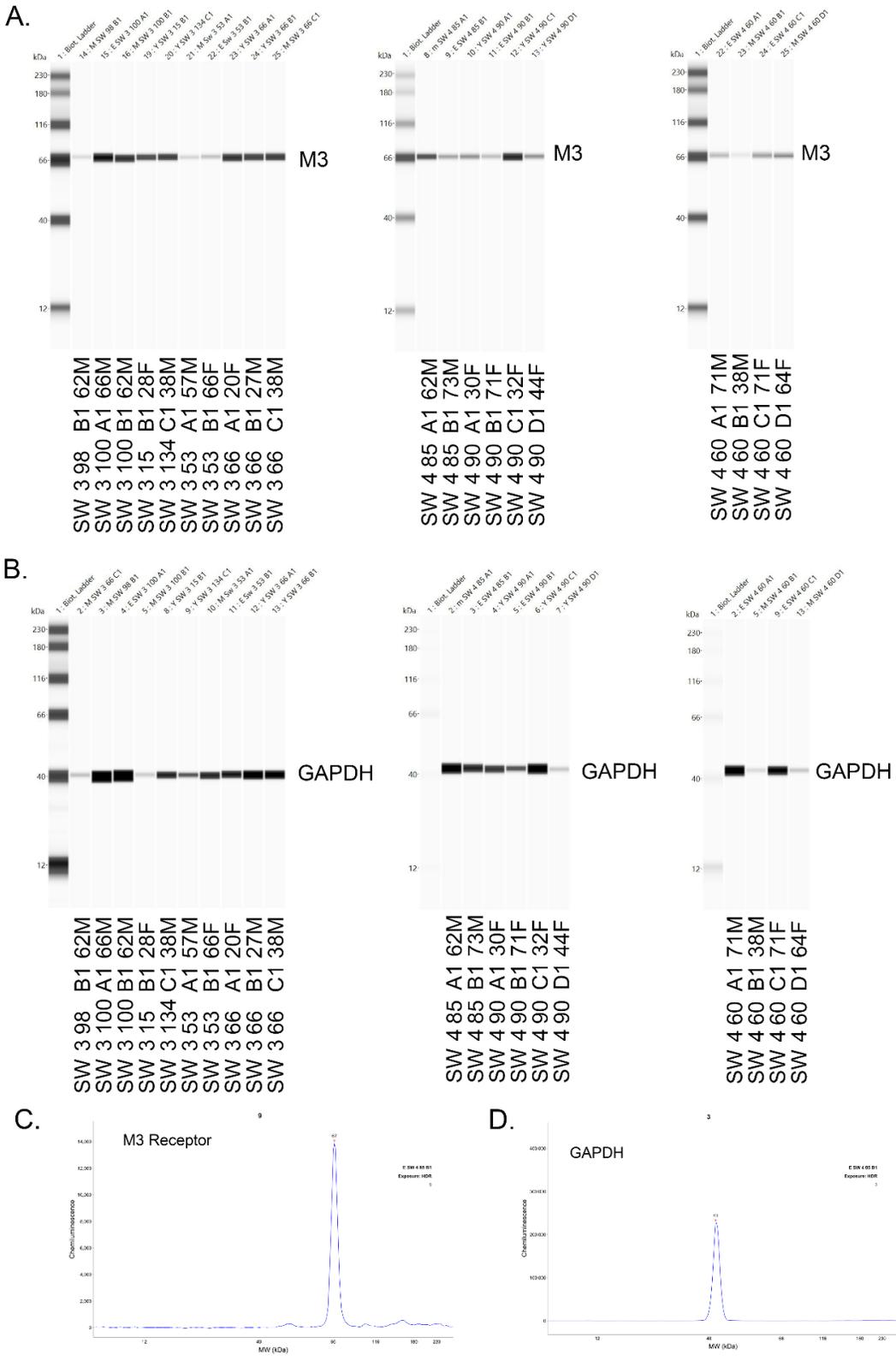


Figure S7

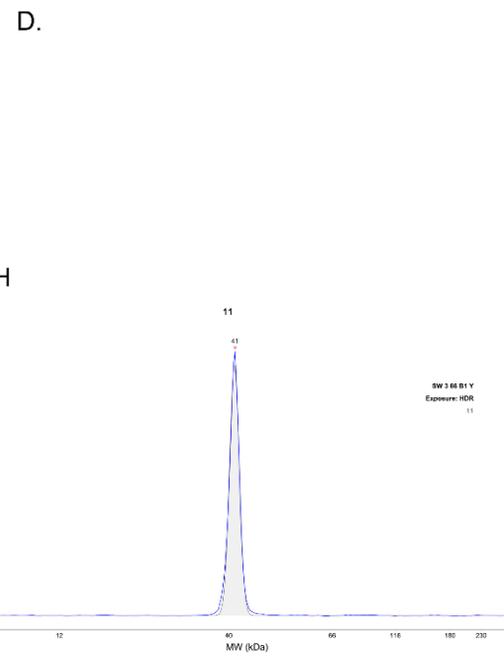
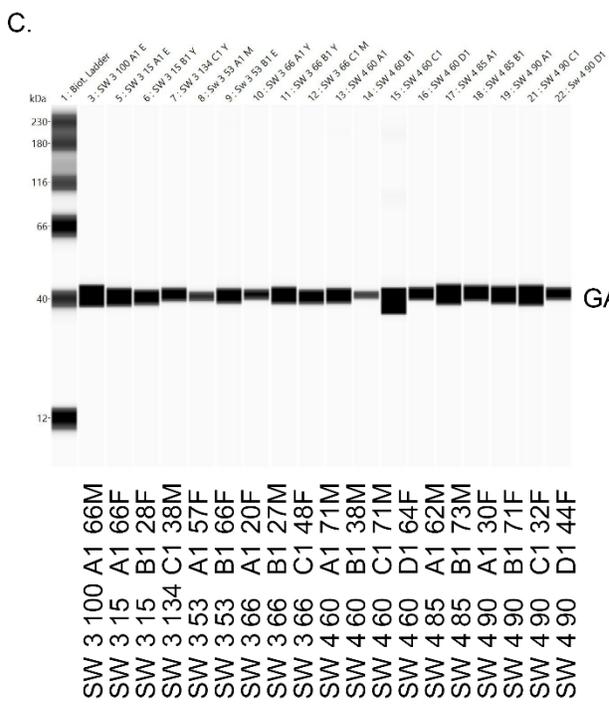
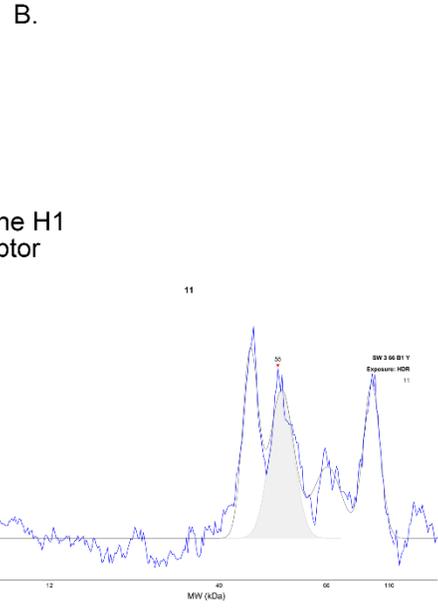
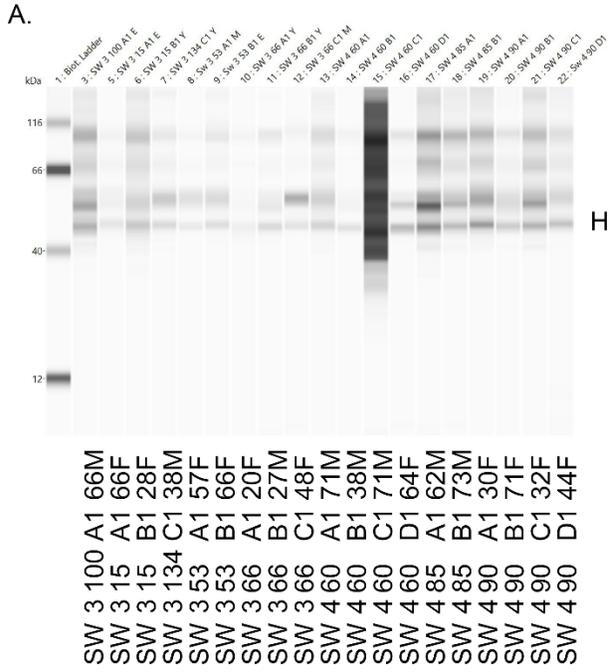


Figure S8

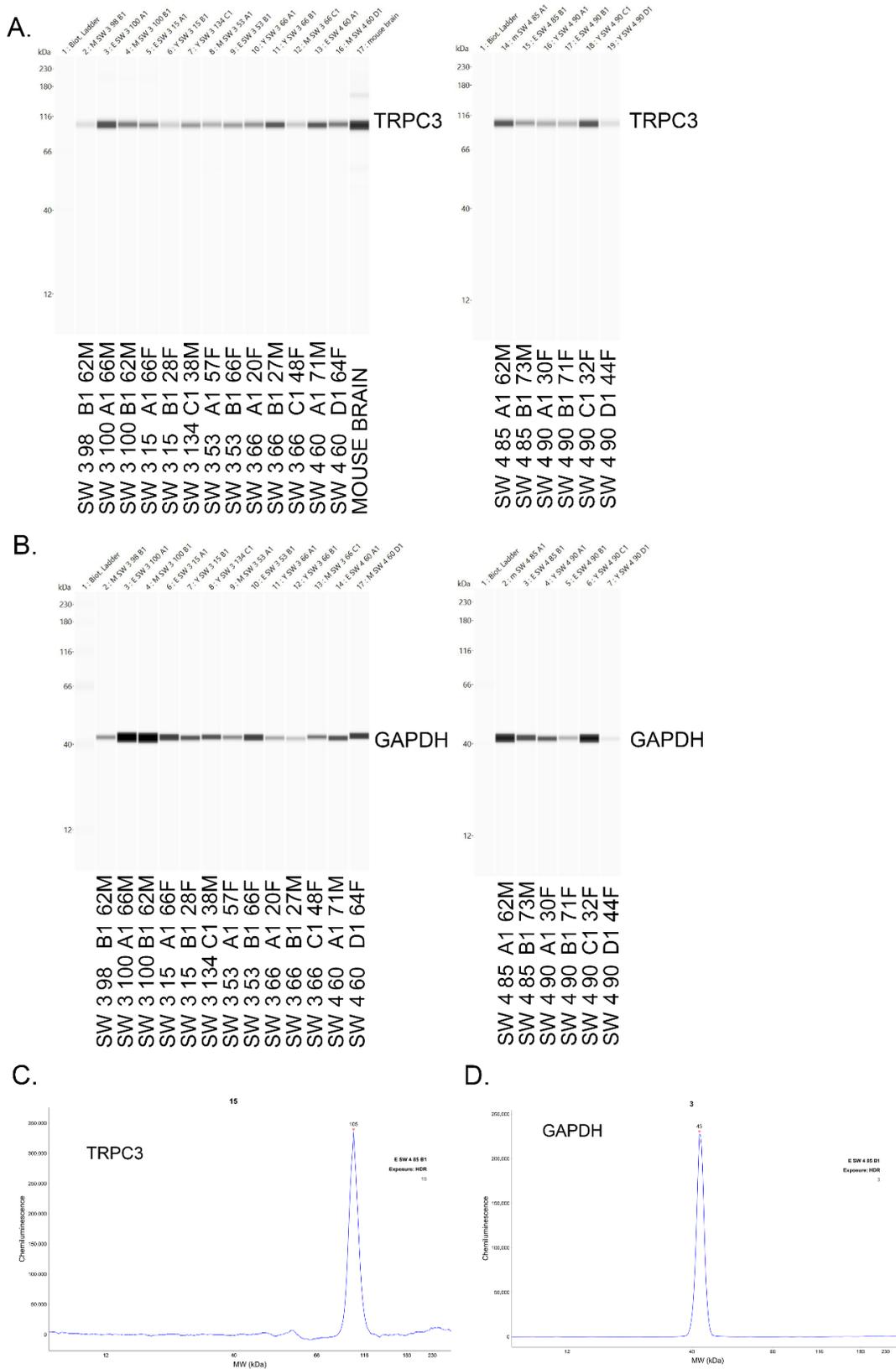
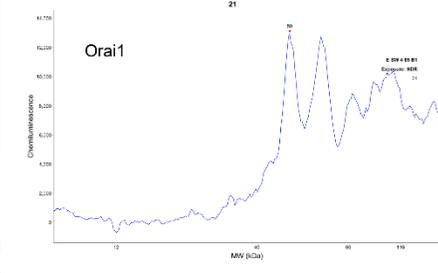
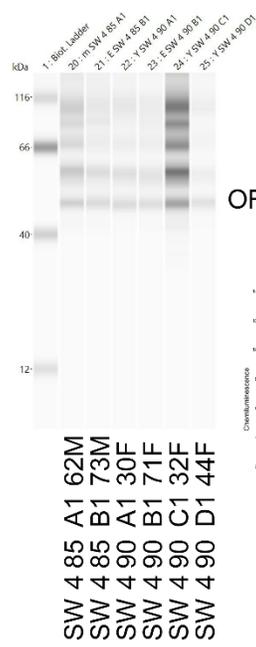
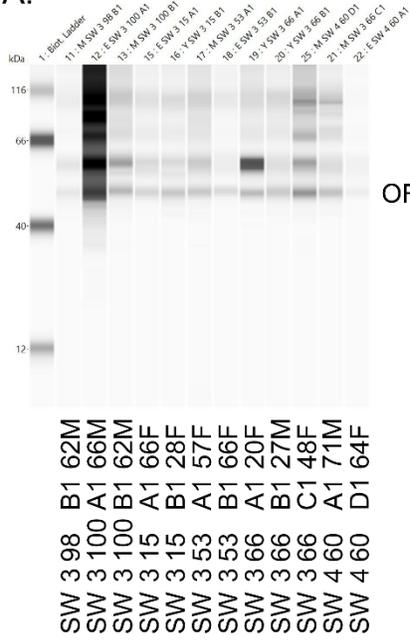


Figure S9

A.



B.

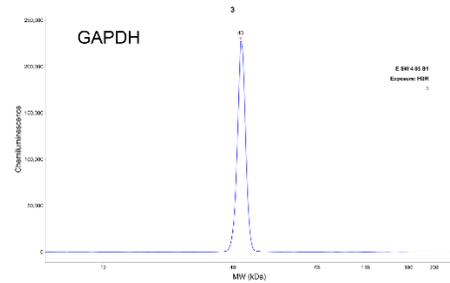
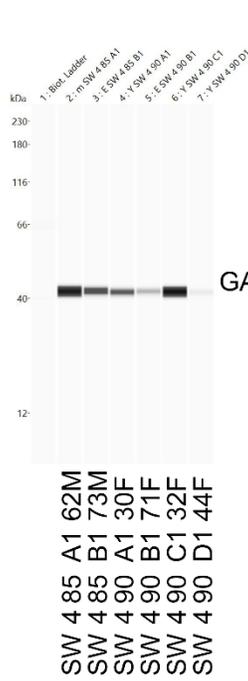
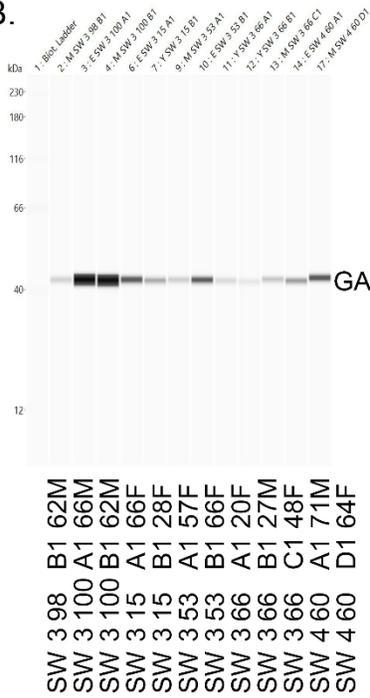


Figure S10

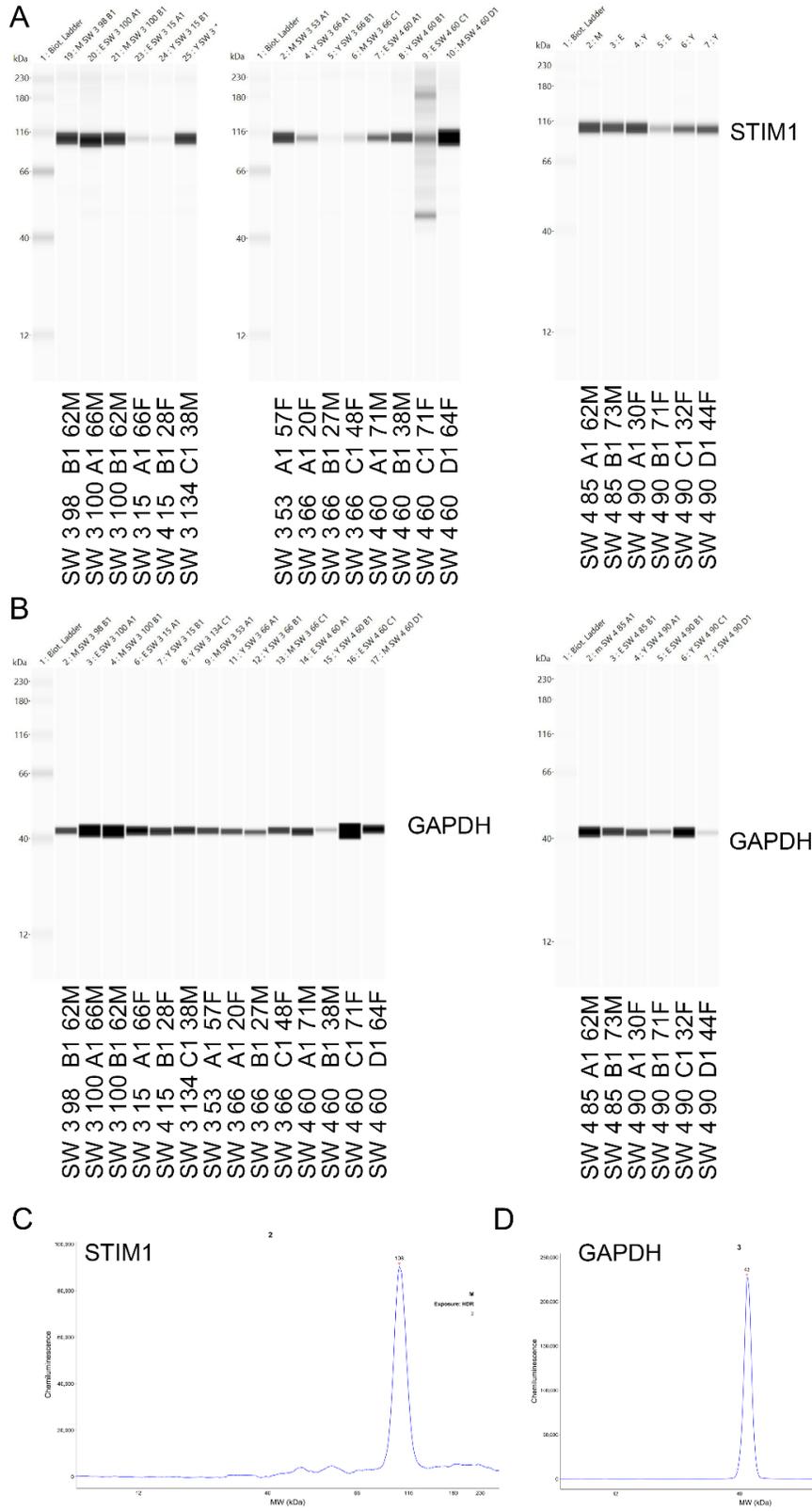


Figure S11

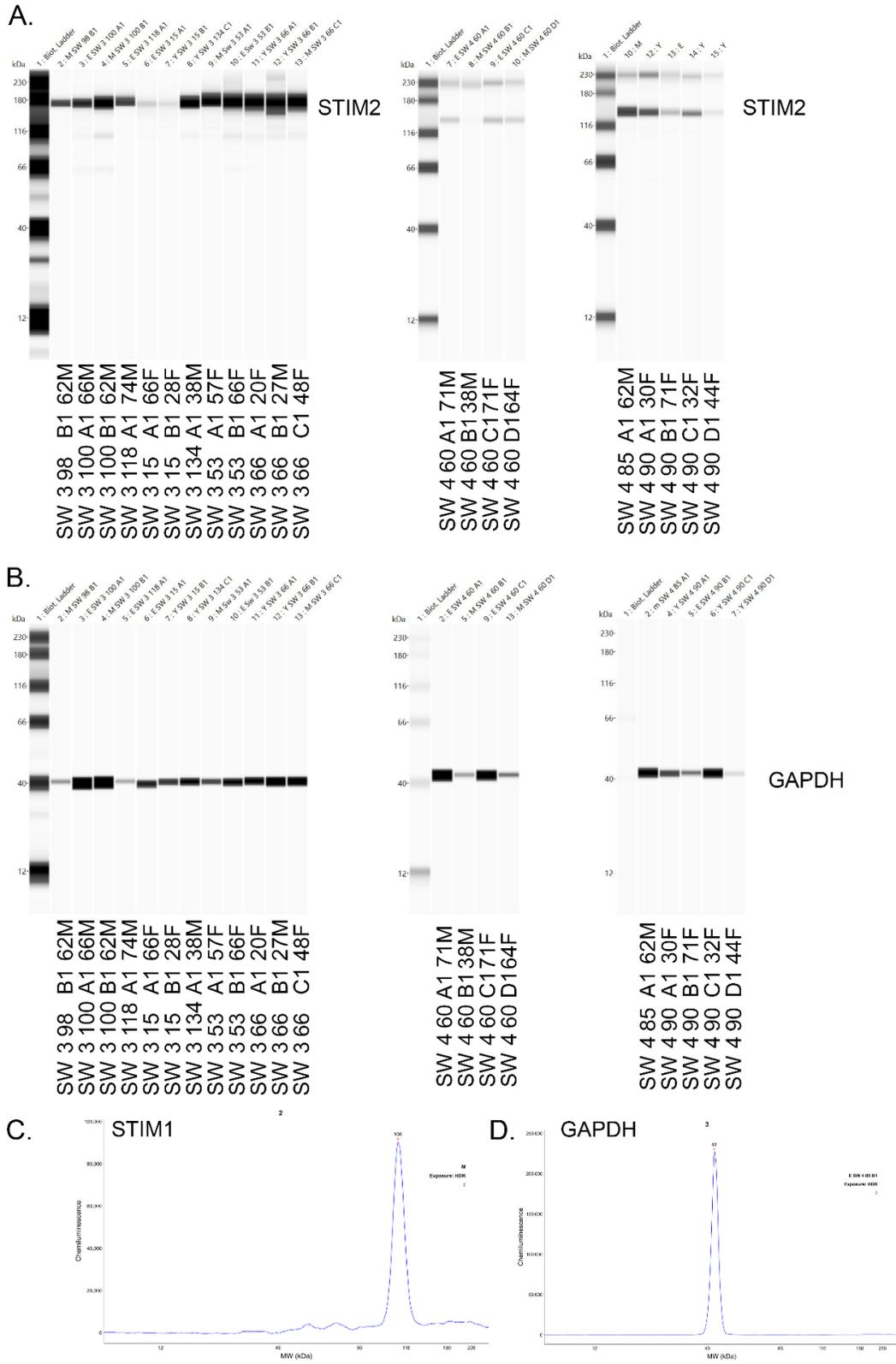
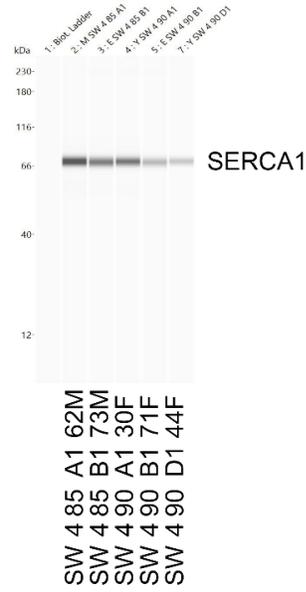
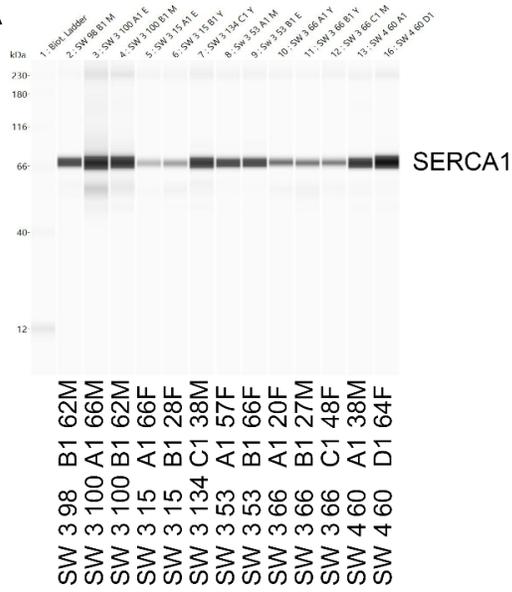
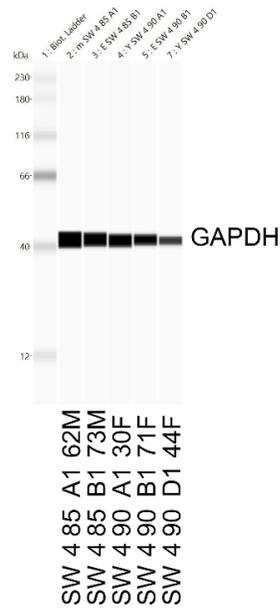
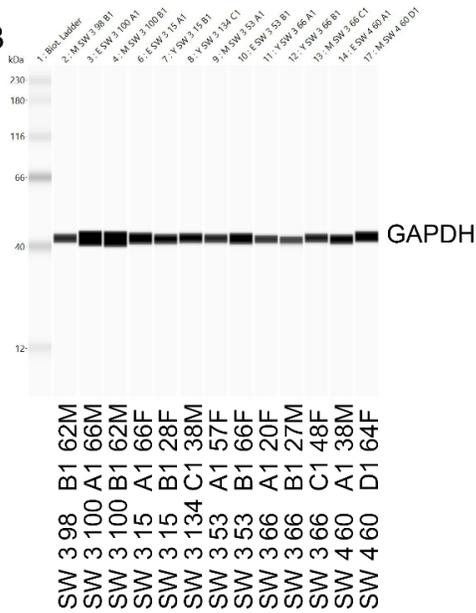


Figure S12

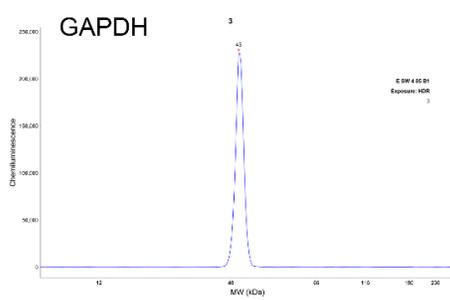
A



B



C



D

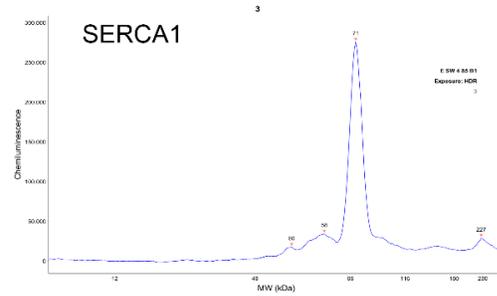


Figure S13

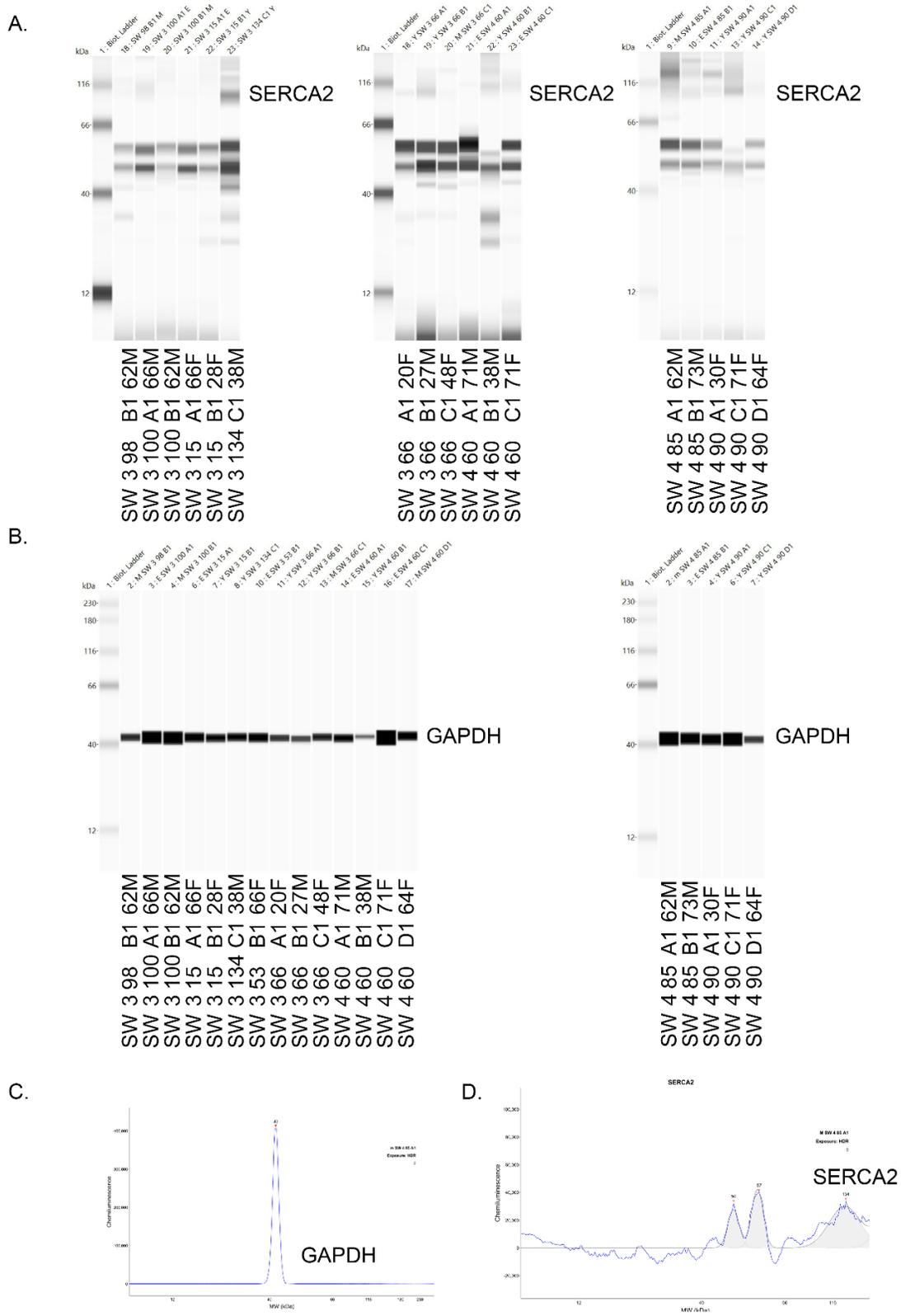


Figure S1. P21 western blot generated using WES a capillary western system. The wes system creates a figure that looks like a traditional western blot (A). Representative trace for p21 (B) and GAPDH (D). p21 protein expression was quantified by measuring the area under the curve for p21(B) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S2. P53 western blot generated using WES a capillary western system. The wes system creates a figure that looks like a traditional western blot (A). Representative trace for p53 (C) and GAPDH (D). p53 protein expression was quantified by measuring the area under the curve for p53(C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S3. Western blot for phospho p53 (P-p53) (A). A representative trace for p53 (B) and Pp53 (C). The sample age and name are annotated below each lane. P-p53 was quantified to P53 data shown in Figure S2. The age and sample ID has been annotated below each lane.

Figure S4. Western blot for MMP2 was generated via WES Simple Western. GAPDH used to normalize MMP2 gene expression is shown in (C). MMP2 expression was quantified by measuring the area under the curve for MMP2 (B) vs area under the curve for GAPDH (D). The age and sample ID has been annotated below each lane.

Figure S5. Western blot for MMP9 was generated via WES Simple Western. GAPDH used to normalize MMP9 gene expression is shown in (C). MMP9 expression was quantified by measuring the area under the curve for MMP9 (B) vs area under the curve for GAPDH (D). The age and sample ID has been annotated below each lane.

Figure S6. Western blot for M3 muscarinic receptor was generated via WES Simple Western. GAPDH used to normalize M3 muscarinic receptor expression is shown in (B). M3 muscarinic receptor expression was quantified by measuring the area under the curve for M3 (C) vs area under the curve for GAPDH (D). The age and sample ID has been annotated below each lane.

Figure S7 Western blot for histamine H1 receptor generated via WES simple western (A). H1R expression was normalized to GAPDH (C). Representative trace showing how protein expression was quantified by area under the curve of histamine H1R (B) normalized to GAPDH (D). The age and sample ID is annotated below each lane.

Figure S8. TRPC3 western blot generated using WES a capillary western system. The wes system creates a figure that looks like a traditional western blot (A). Representative trace for TRPC3 (C) and GAPDH (D). TRPC3 protein expression was quantified by measuring the area under the curve for TRPC3(C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S9. Western blot for Orai1 was generated via WES Simple Western. GAPDH used to normalize Orai1 expression is shown in (C). Orai1 protein expression was quantified by measuring the area under

the curve for Orai1 (B) vs area under the curve for GAPDH (D). The age and sample ID has been annotated below each lane.

Figure S10. STIM1 western blot generated using WES a capillary western system (A). Representative trace for STIM1 (C) and GAPDH (D). STIM1 protein expression was quantified by measuring the area under the curve for STIM1(C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S11. STIM2 western blot generated using WES a capillary western system(A). Representative trace for STIM2 (C) and GAPDH (D). STIM2 protein expression was quantified by measuring the area under the curve for STIM2(C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S12. SERCA1 western blot generated using WES a capillary western system. The wes system creates a figure that looks like a traditional western blot (A). Representative trace for SERCA1 (C) and GAPDH (D). SERCA1 protein expression was quantified by measuring the area under the curve for SERCA1 (C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.

Figure S13. SERCA2 western blot generated using WES a capillary western system. The wes system creates a figure that looks like a traditional western blot (A). Representative trace for SERCA2 (C) and GAPDH (D). SERCA2 protein expression was quantified by measuring the area under the curve for SERCA2 (C) normalized to the area under the curve for GAPDH (D). The sample name and age has been annotated below each lane.