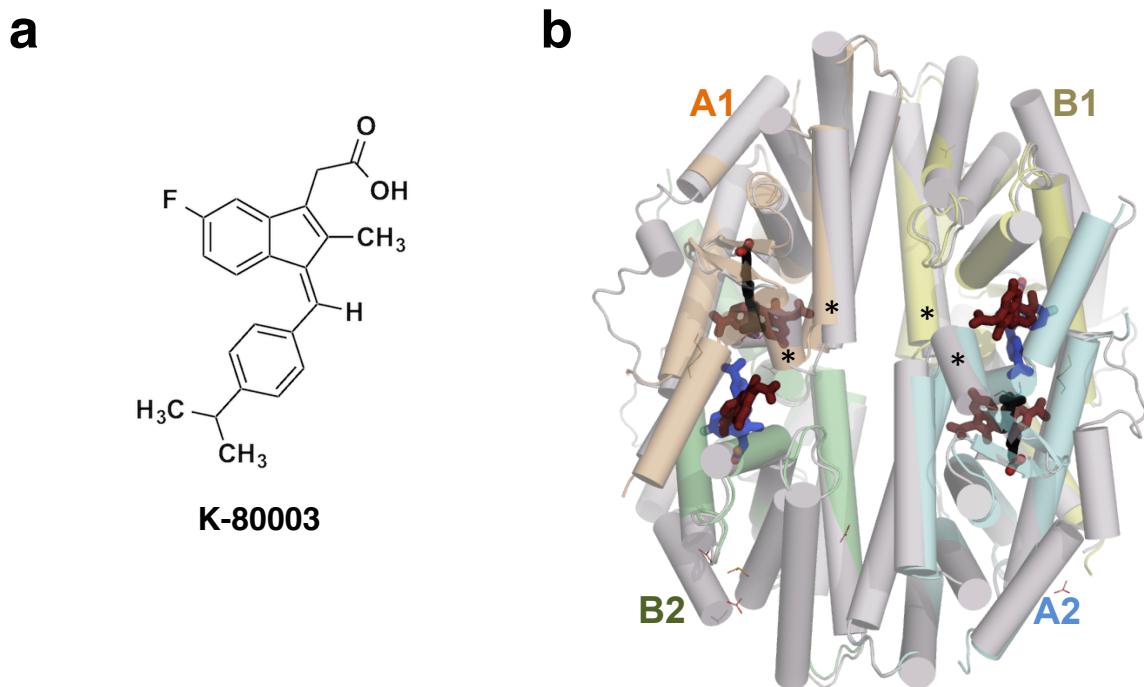


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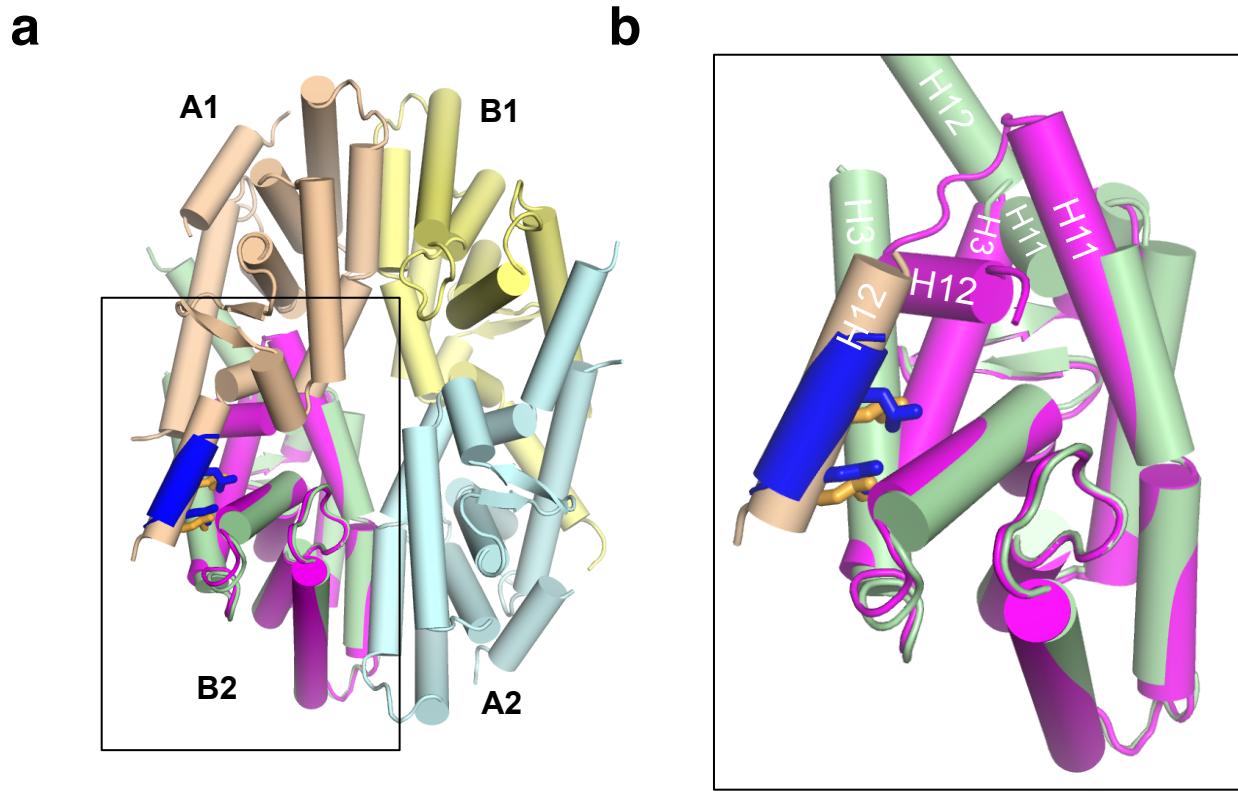
Description: Supplementary figures and supplementary table.



Supplementary Figure 1. Structure of RXR α -LBD in complex with K-80003

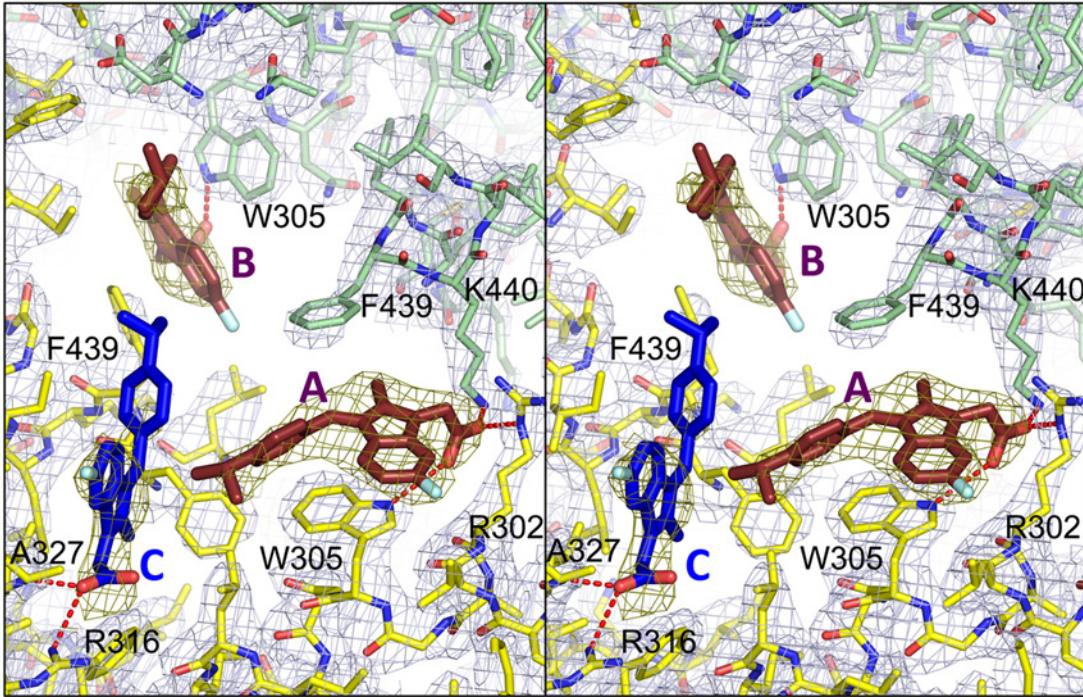
(a) Chemical structure of K-80003.

(b) Superposition of K-80003 bound RXR α -LBD tetramer (same colors as in Fig. 1a) and RXR α -LBD/tRA-isomer (grey cartoon/black sticks, PDB entry 1G5Y) RMS deviation for C α atoms between PDB entries 1G5Y and 1G1U is 0.20 Å. RMS deviation for C α atoms between the K-80003-complex and 1G1U (or 1G5Y) is 1.20 Å. The noteable changes (marked with *) are around the tetramer interface.

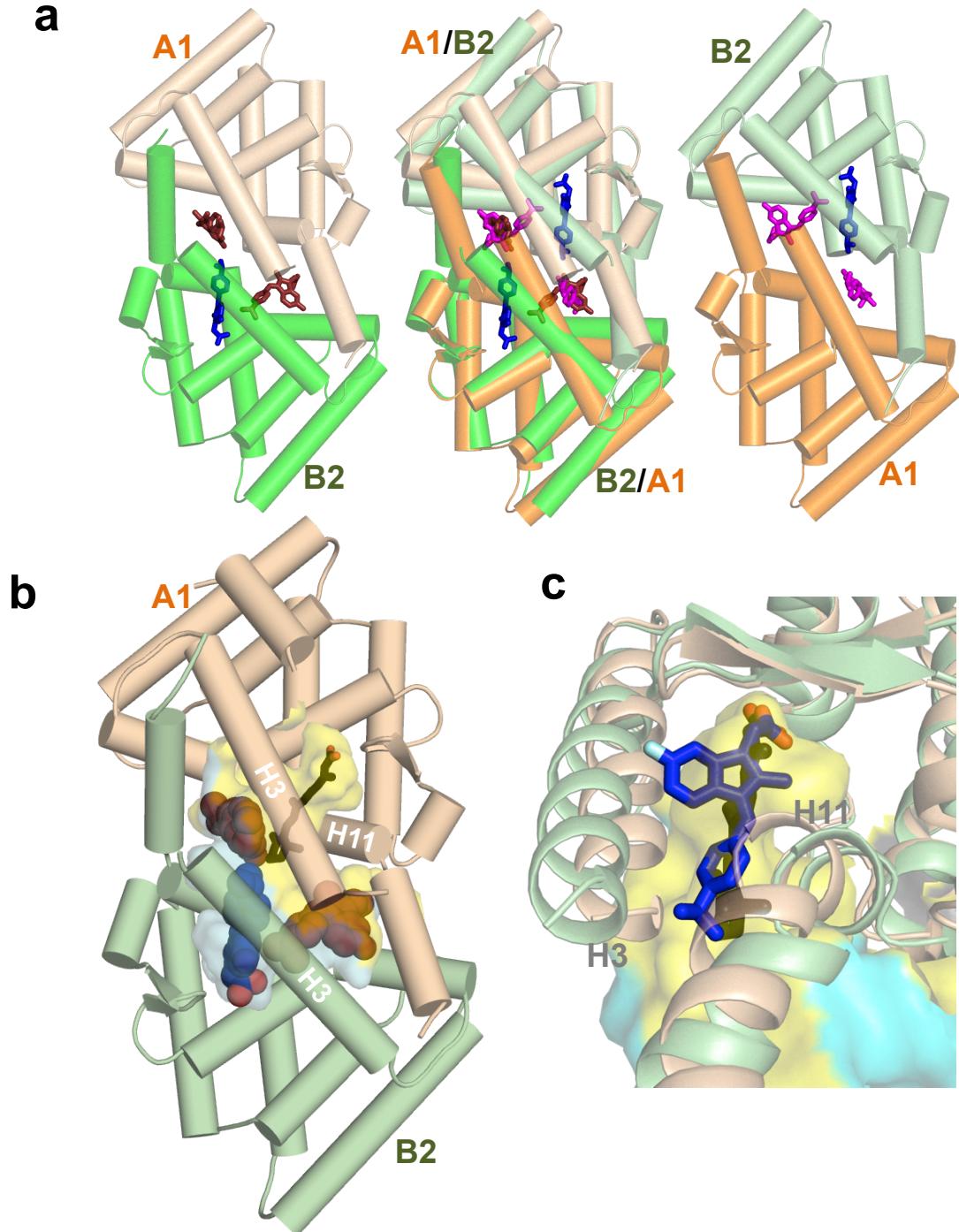


Supplementary Figure 2. Superposition of the agonist and coactivator peptide bound RXR α -LBD.

- (a) Superposition of the agonist and coactivator peptide bound RXR α -LBD (PDB entry 3FUG) shown as magenta cartoon with one subunit of K-80003 bound RXR α -LBD tetramer (same orientation and same colors as in the Fig. 1a).
- (b) Enlarged area around the superimposed molecules. The bound coactivator peptide in 3FUG is shown in blue, occupying a region that overlaps with H12 from the adjacent monomer. Hydrophobic side chains of the LMEML portion of the H12 (shown in orange) and the LxxLL motif of the coactivator peptide (shown in blue) are shown in sticks.



Supplementary Figure 3. Stereo view of the electron density map (2Fo-Fc, 0.8 σ cut-off) around three K-80003 molecules that bind to the cavity in subunit A1/B2 (A1, green; a B2, yellow). The density mesh for the protein and the ligands have different colors for clarity. K-80003A and K-80003B (brown sticks) are bound to symmetry related sites at the interface between A1 and B2. Hydrogen bonds from the K-80003 molecules to protein are shown with red dash lines. K-80003C (blue) is bound to the site similar to the canonical ligand-binding site.

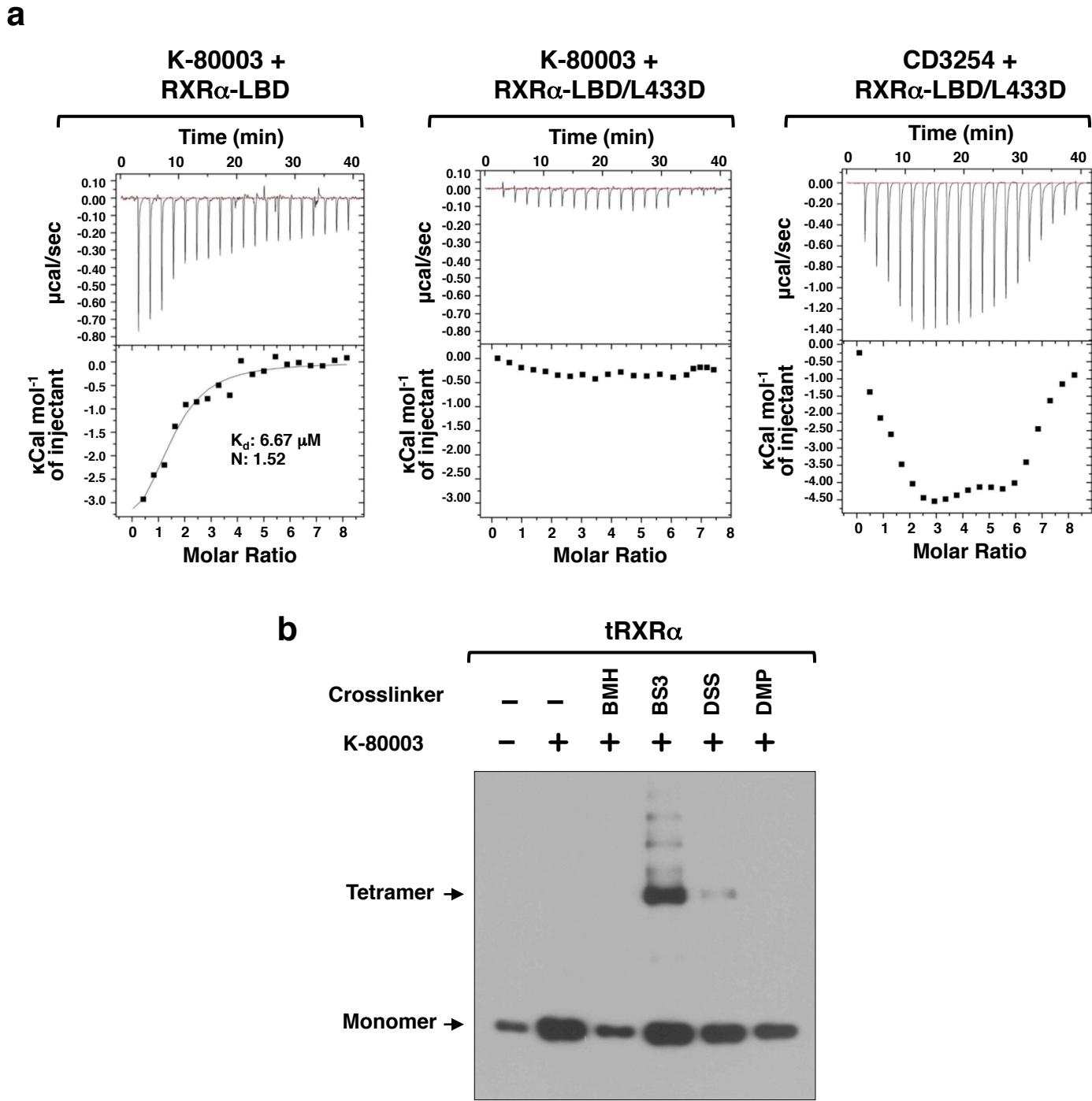


Supplementary Figure 4. Asymmetry of the cavity in A1/B2 subunit of the RXR α -LBD tetramer.

(a) Superposition of A1 and B2 subunits of the RXR α -LBD tetramer on themselves. K-80003 is shown as sticks. Colors are the same as Fig. 1b.

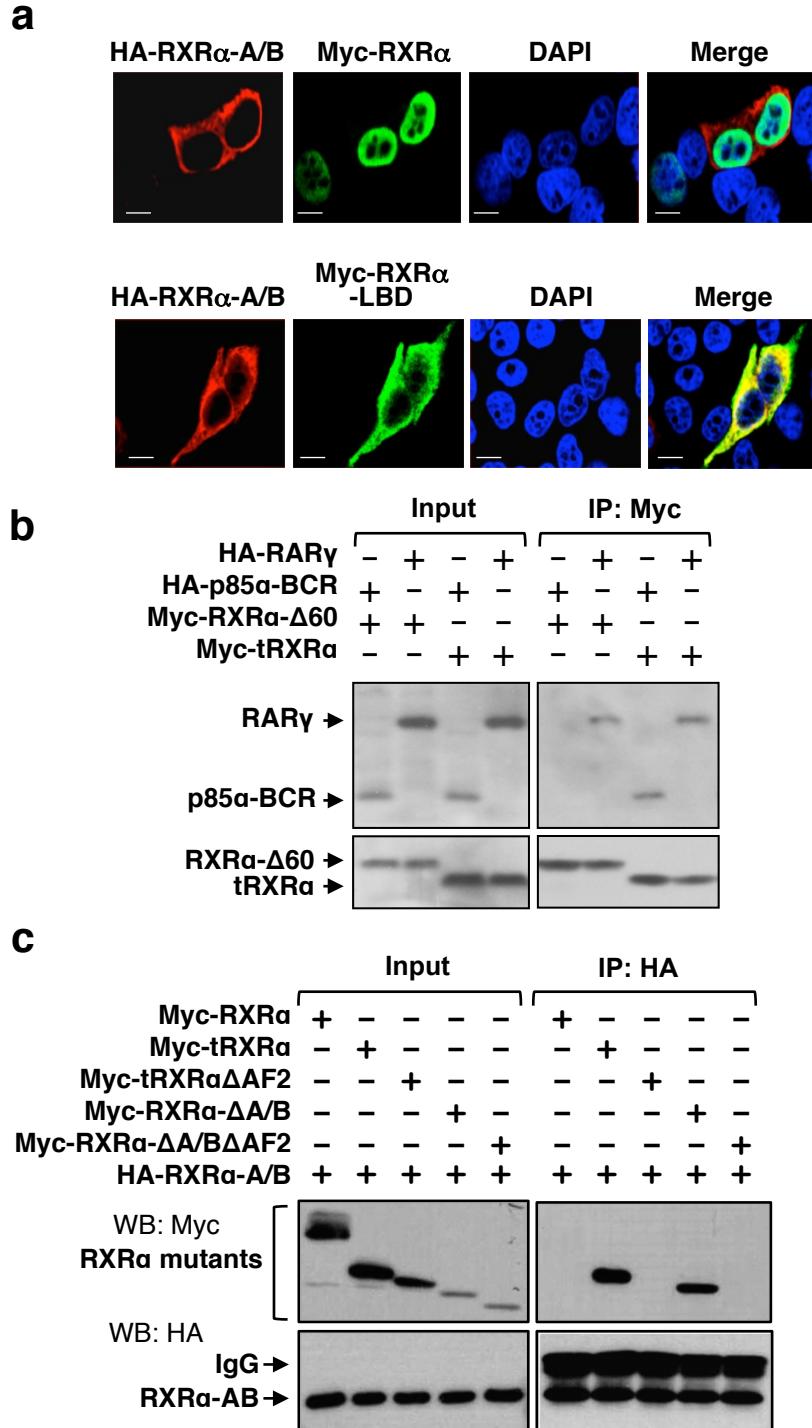
(b) Superposition of the molecule tRA-isomer (black sticks) from RXR α -LBD tetramer (pdb entry 1G5Y) on the A1/B2 subunit with bound K-80003 (spheres). The ligand-binding cavity is shown as a VDW surface.

(c) The superposition of the subunit B2 on A1 enlarged around the binding site for tRA-isomer (black sticks). The helices H3 and H11 of the subunit A1 (wheat) are much closer to each other than in the subunit B2 (green). As a result, the cavity of the subunit A1 is capable to bind tRA-isomer (black sticks) but does not fit K-80003 (blue sticks).



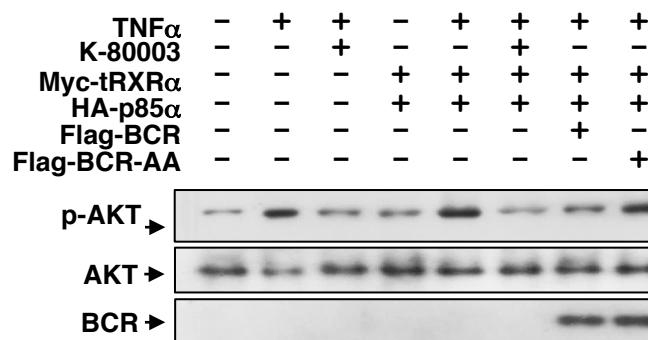
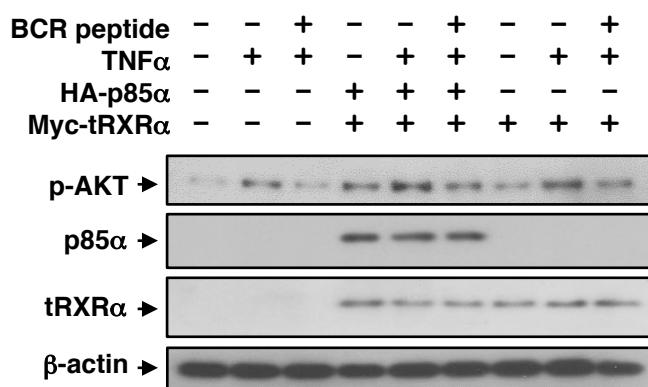
Supplementary Figure 5. Characterization of RXR α mutant and chemical crosslinkers.

- (a) Analysis of RXR α -LBD/L433D for binding to K-80003 and RXR α agonist CD3254 by ITC assay.
Data acquisition and analysis were performed using MicroCal Origin software (version 7.0).
- (b) Characterization of chemical crosslinkers for their effect on tRXR α oligomerization. HEK293T cells transfected with Myc-tRXR α were treated with or without K-80003. Cell lysates were subjected to crosslink by the indicated chemical crosslinkers as recommended by the manufacturer, and analyzed by Western Blotting using anti-Myc antibody. HMH:bismaleimidohexane; BS3: bis(sulfosuccinimidyl)suberate; DSS: disuccinimidyl suberate; DMP: dimethyl pimelimidate,



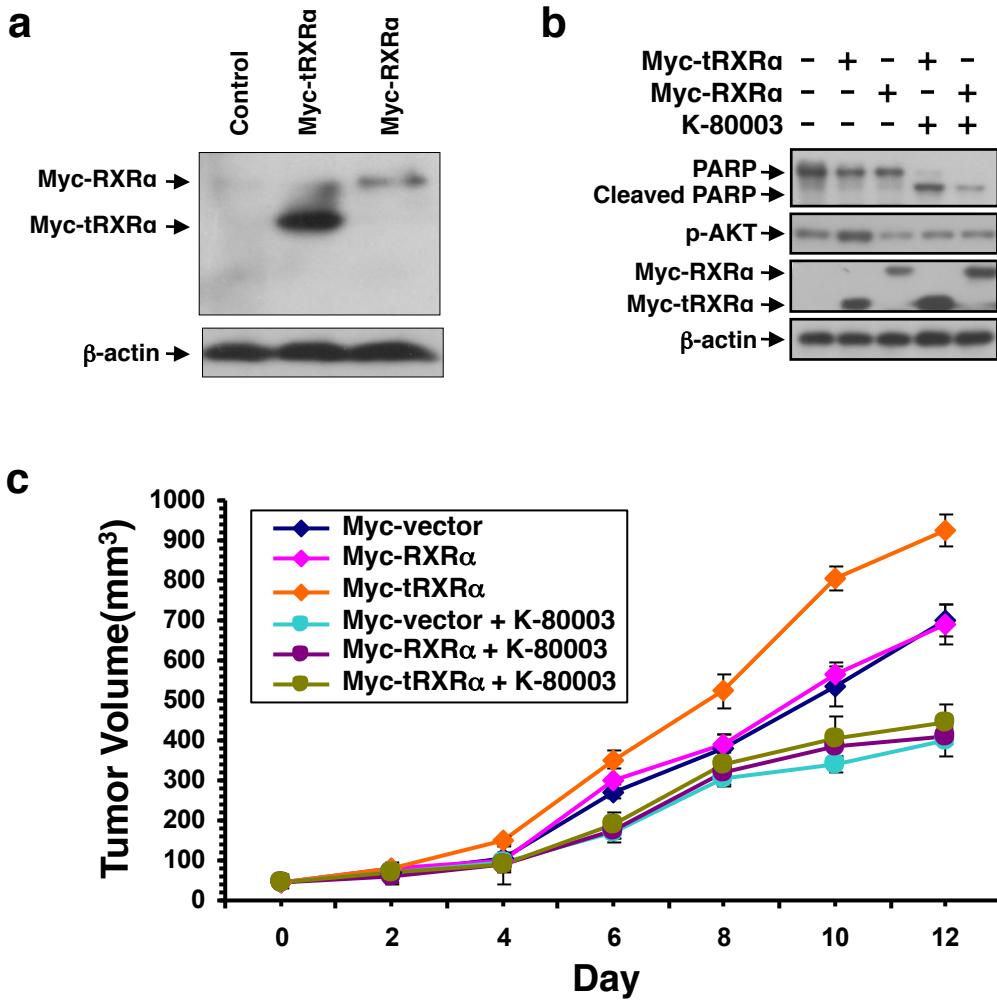
Supplementary Figure 6. Characterization of RXR α A/B domain and the LxxLL motif in p85 α .

- (a) Colocalization of RXR α A/B domain with RXR α -LBD but not RXR α revealed by immunostaining. HEK293T cells cotransfected with the indicated expression vectors were immunostained with anti-Myc or anti-HA antibody, and examined by confocal microscopy. Scale bar, 10 μ m.
- (b) RXR α - Δ 60 interacts with RAR γ but not RXR α -A/B. RXR α - Δ 60 and tRXR α tagged with Myc epitope were transfected into HEK293T cells with HA-p85 α -BCR or HA-RAR γ , and their interaction was analyzed by coIP using anti-Myc antibody.
- (c) AF2 in RXR α is required for binding A/B region. HA-RXR α -A/B and Myc-tagged RXR α mutants were transfected together in to HEK293T cells, and their interaction was analyzed by coIP.

a**b**

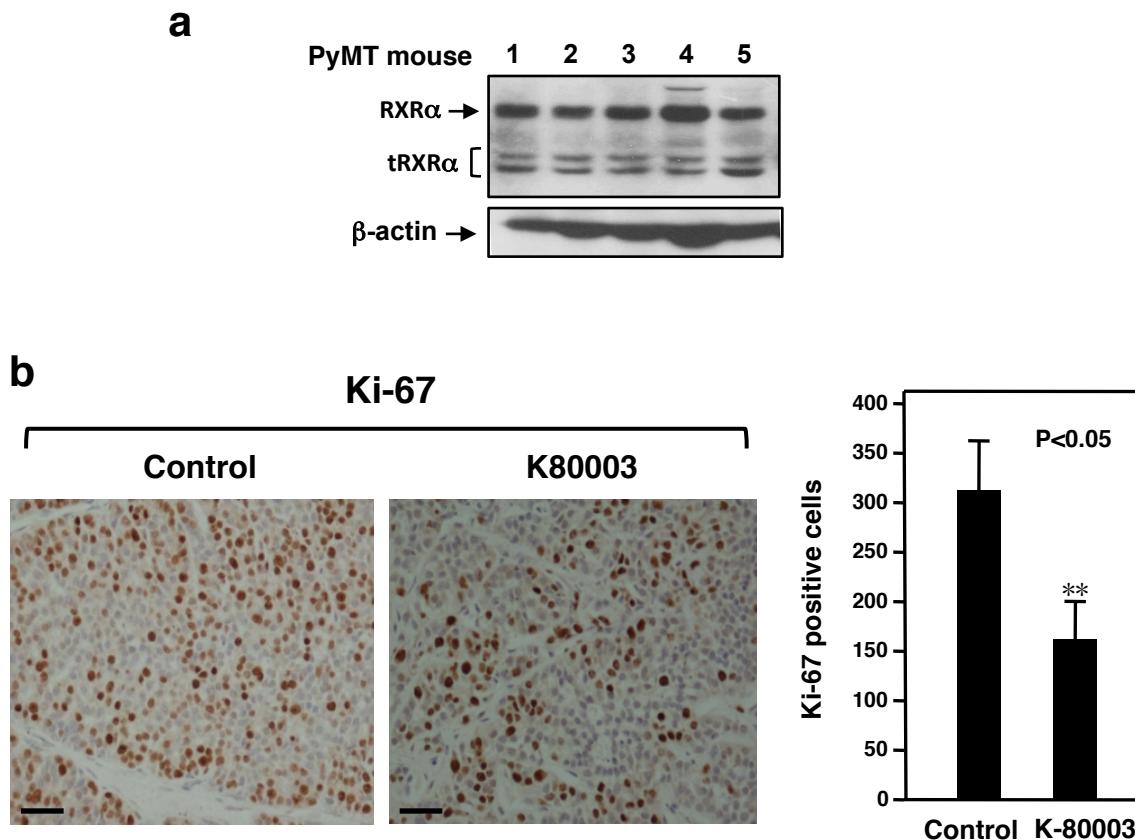
Supplementary Figure 7. Characterization of the LxxLL motif in BCR of p85 α .

- (a) Dominant-negative effect of BCR on tRXR α activation of AKT. A549 cells were transfected with the indicated expression vector prior to exposure to K-80003 (5×10^{-6} M) for 3 h. Phosphorylated AKT and total AKT were analyzed by Western blotting.
- (b) BCR peptide inhibits AKT activation. A549 cells were transfected with HA-p85 α and/or tRXR α prior to exposure to BCR peptide for 12 h, and analyzed by Western blotting.



Supplementary Figure 8. Characterization of the inhibitory effect of K-80003 on the tumor promoting activity of tRXR α in nude mice.

- (a) MCF-7 cells stably expressing tRXR α and RXR α analyzed by Western blotting.
- (b) Effect of K-80003 on PARP cleavage and AKT activation in MCF-7 cells expressing tRXR α or RXR α . Cells stably expressing either RXR α or tRXR α were treated with or without K-80003 for 24 h, and analyzed by Western blotting.
- (c) Effect of K-80003 on the growth of MCF-7 cells in nude mice. MCF-7 cells stably expressing tRXR α or RXR α were injected into nude mice. Mice were then administered with K-80003 (20 mg/kg), and the growth of tumor measured. Data are presented as the mean \pm standard deviation (n=6 in each group).



Supplementary Figure 9. Characterization of the inhibitory effect of K-80003 on the growth of mammary tumor in MMTV-PyMT transgenic mice.

- (a) Expression of tRXR α in MMTV-PyMT mammary tumors analyzed by Western blotting using Δ N197 anti-RXR α antibody.
- (b) Tumor sections from MMTV-PyMT mice fed with vehicle or K-80003 were immunostained with anti-Ki-67 antibody. Ki-67 positive cells were scored from 500 cells. Scale bar, 20 μ m.

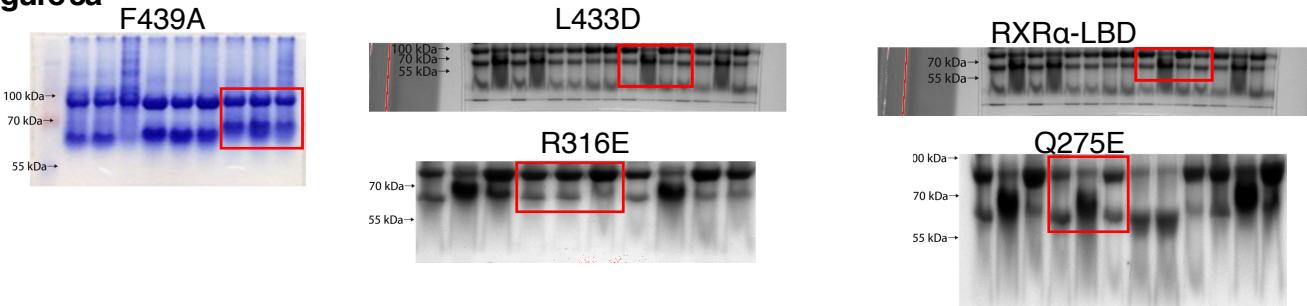
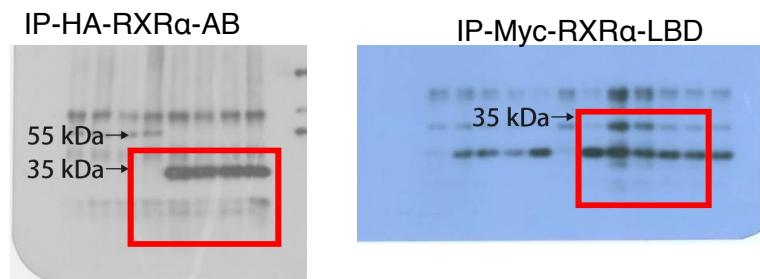
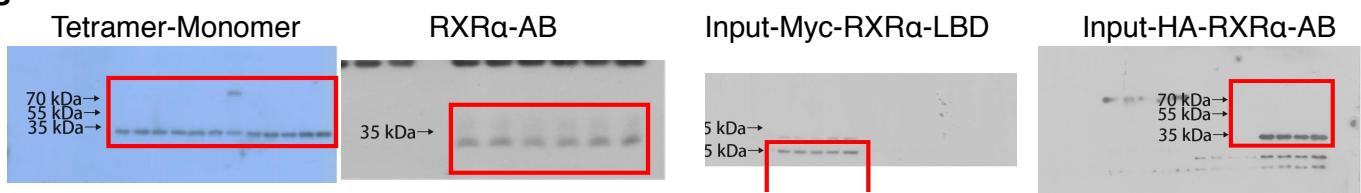
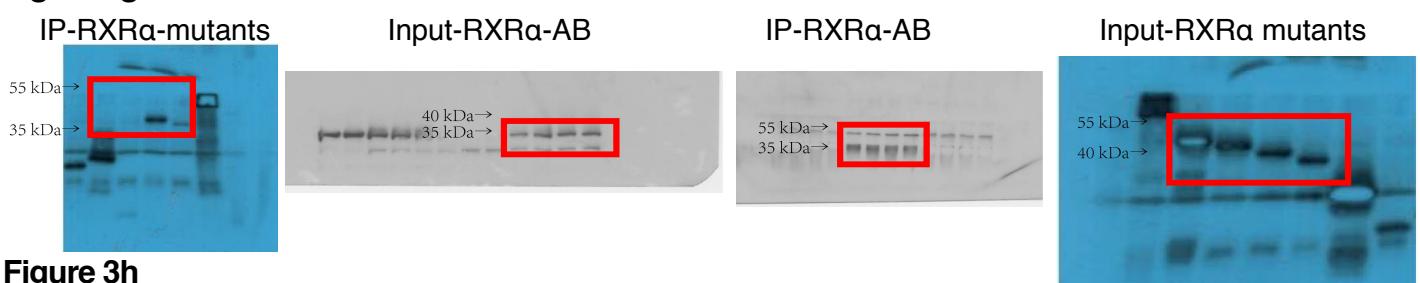
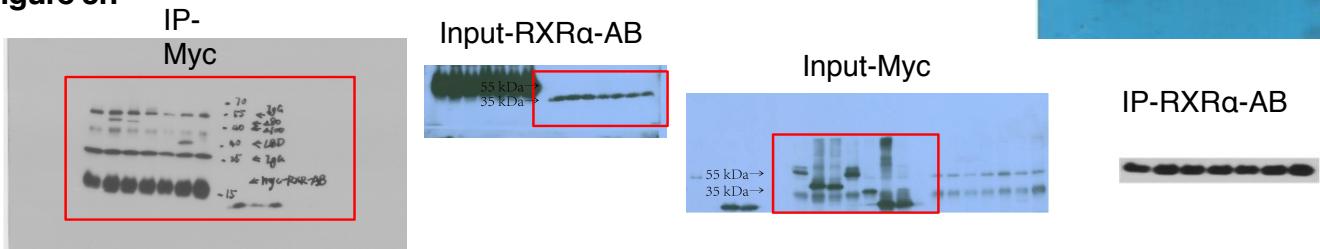
Figure 3a**Figure 3c****Figure 3e****Figure 3f****Figure 3g****Figure 3h****Figure 3i****Supplementary Figure 10.** Uncropped Western blot images for Figure 3.

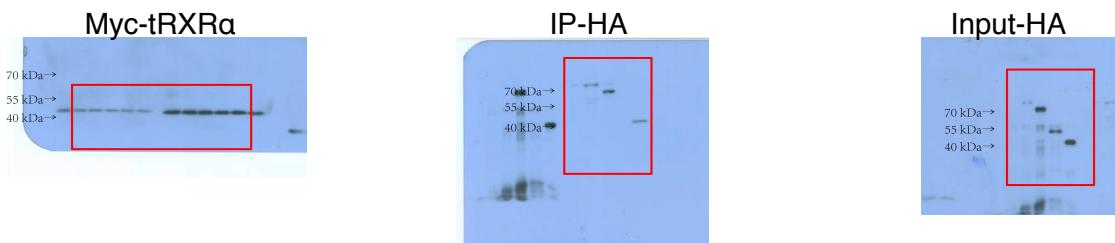
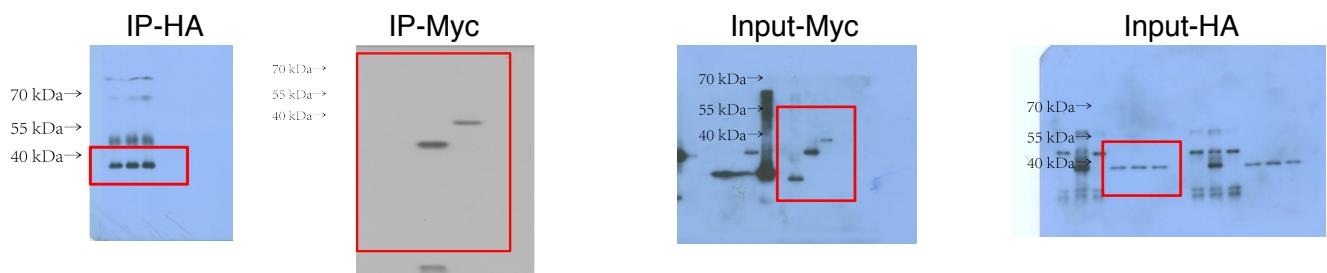
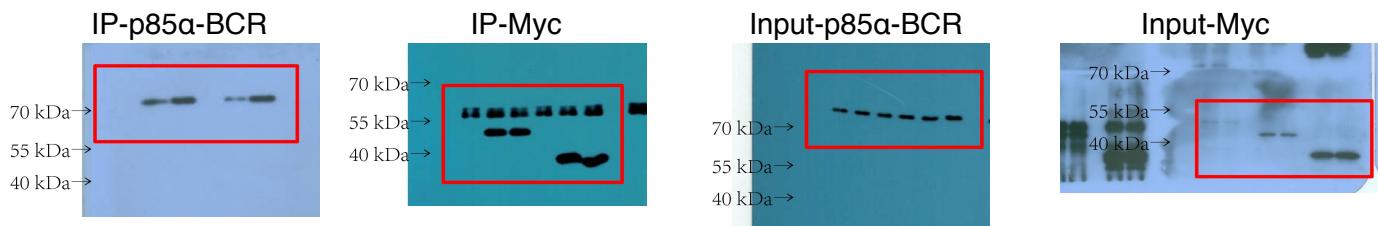
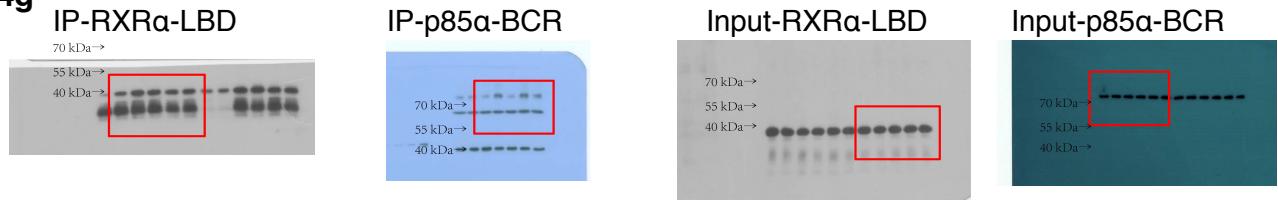
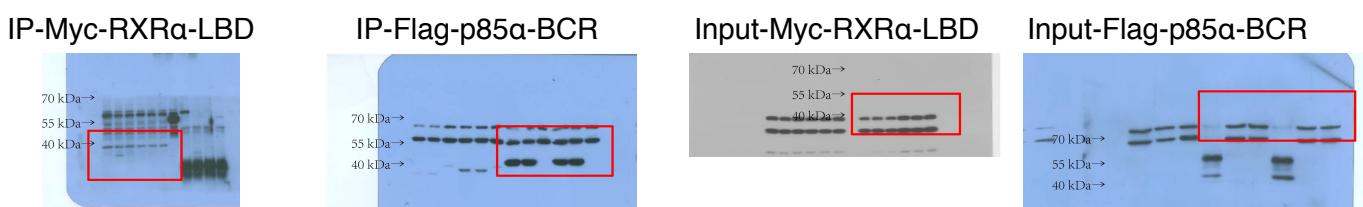
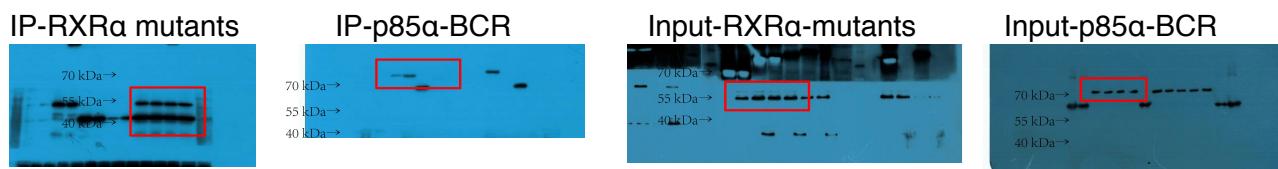
Figure 4b**Figure 4c****Figure 4f****Figure 4g****Figure 4h****Figure 4i****Supplementary Figure 11.** Uncropped Western blot images for Figure 4.

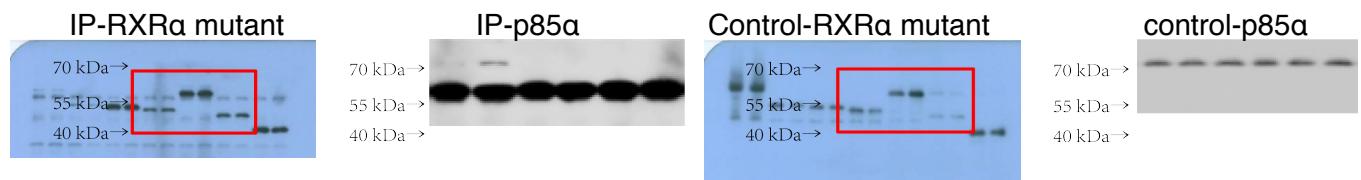
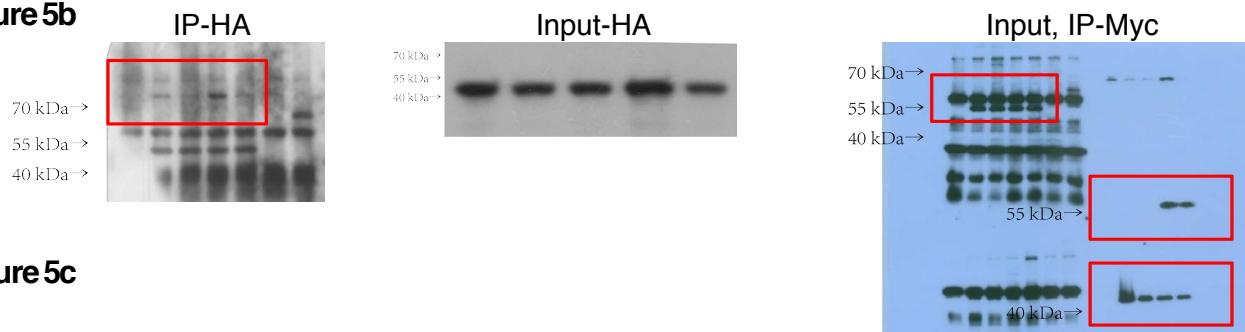
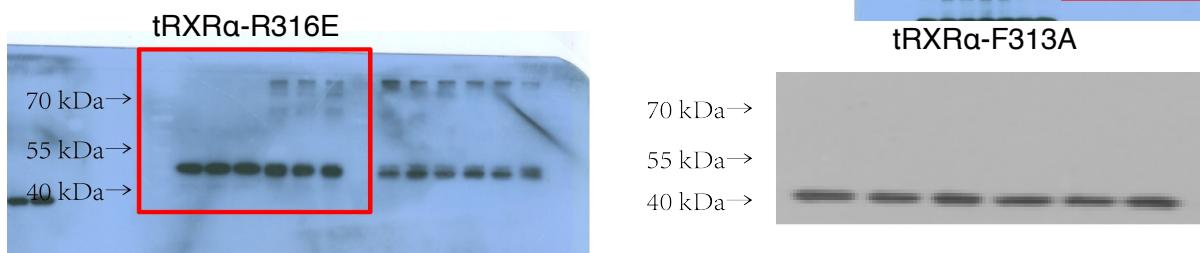
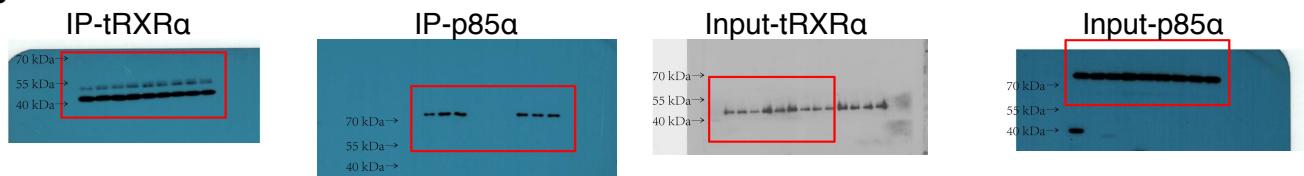
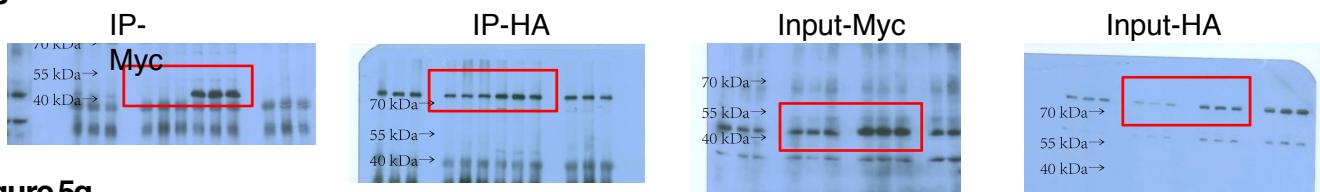
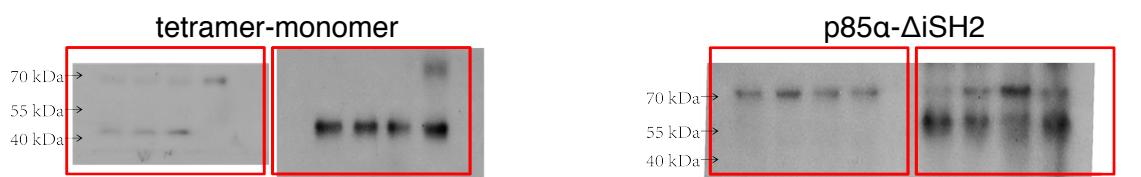
Figure 5a**Figure 5b****Figure 5c****Figure 5d****Figure 5e****Figure 5g****Figure 5h****Supplementary Figure 12.** Uncropped Western blot images for Figure 5.

Figure 6b

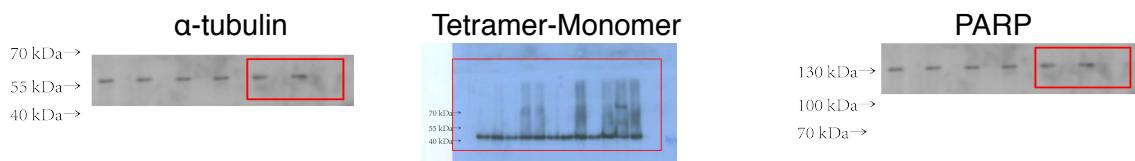


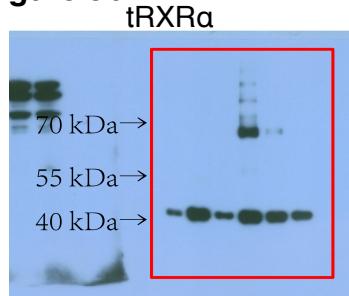
Figure 6d



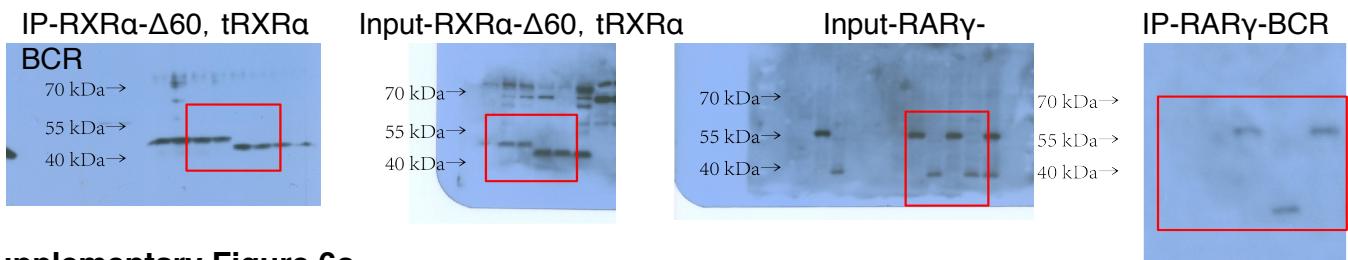
Figure 6g



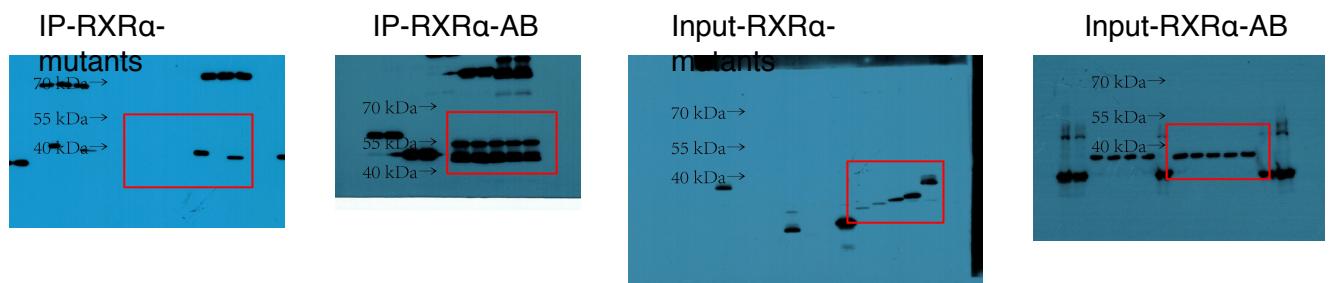
Supplementary Figure 5b



Supplementary Figure 6b

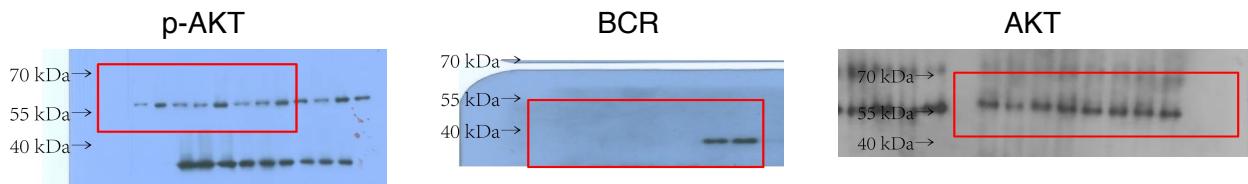


Supplementary Figure 6c

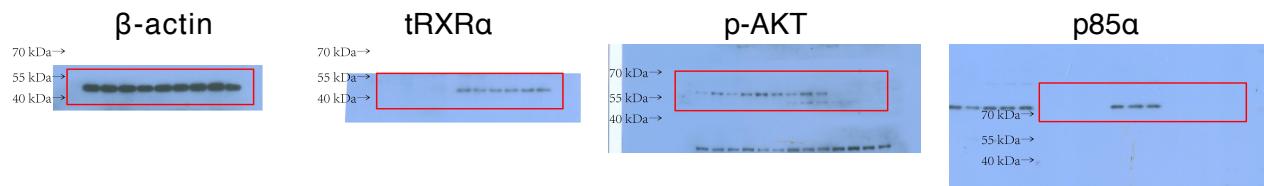


Supplementary Figure 13. Uncropped Western blot images for Figure 6 and Supplementary Figures 5 and 6.

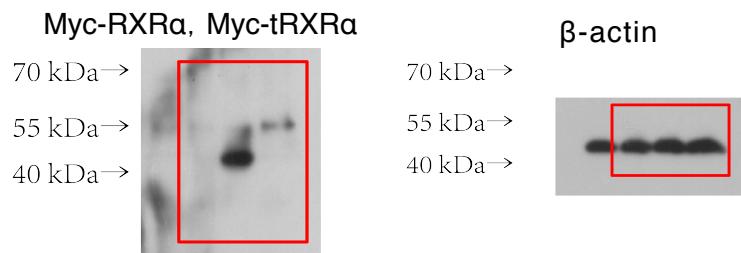
Supplementary Figure 7a



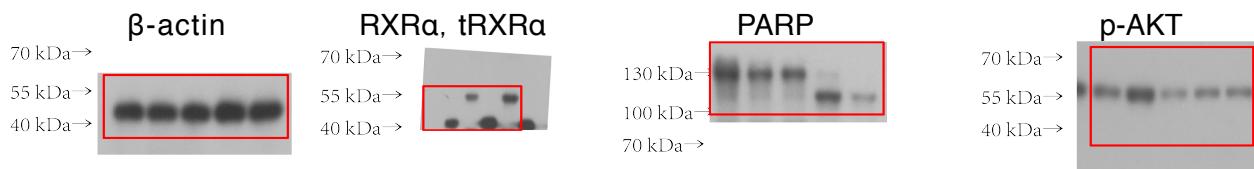
Supplementary Figure 7b



Supplementary Figure 8a



Supplementary Figure 8b



Supplementary Figure 9a



Supplementary Figure 14. Uncropped Western blot images for Supplementary Figures 7, 8, and 9.

Supplementary Table 1. Primers used for constructing expression plasmids

Plasmid	Forward	Reverse
Myc-RXR α	CCGGAATTGGATGGACACCAAACATTCCTGC	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-RXR α - Δ 40	CCGGAATTGGATGGCATGGCTCCCGGGACAGC	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-RXR α - Δ 60	CCGGAATTGGATGGGCCGCTTCCTGC	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-tRXR α	CCGGAATTGGACCACACCCACCCCTGGC	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-RXR α - Δ 100	CCGGAATTGGGTCAAGCAGCAGCGAGGAC	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-RXR α - Δ AF2	CCGGAATTGGATGGACACCAAACATTCCTGC	CCGCTCGAGGTCAATGGGTGTGCCCCGATG
Myc-RXR α - Δ A β	CCGGAATTGGTCTGCATCTGGGG	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-RXR α - Δ A β AF2	CCGGAATTGGTCTGCATCTGGGG	CCGCTCGAGGTCAATGGGTGTGCCCCGATG
Myc-RXR α -LBD	CCGGAATTGGAGCAGGCCAACGAGGACATGCCGT	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
Myc-tRXR α - Δ AF2	CCGGAATTGGACCACACCCACCCCTGGC	CCGCTCGAGGTCAATGGGTGTGCCCCGATG
Myc-RXR α -1-235	CCGGAATTGGATGGACACCAAACATTCCTGC	CCGCTCGAGCTAGATCCTCTCCACCGGATGCTCCTC
Myc-RXR α -AB	CCGGAATTGGATGGACACCAAACATTCCTGC	CCGCTCGAGCTAGATGTGCTGGTGAAGGAAGCCATG
Myc-RXR α -LBD/W305Q	TGCGGGCAGGCCAGAATGAGCTGCTCAT	ATGAGCAGCTATTGGCCTGCCG
Myc-tRXR α /R316E	CCTTCTCCCACGAGTCCATCGCCGTGAA	TTCACGGCGATGGACTCGTGGAGAAGG
Myc-tRXR α /F313A	CTCATGGCTCCGCTCCACCGCTCCA	TGGAGCGGTGGGAGGCGGAGGCATGAG
HA-RXR α -AB	CCGGAATTGGATGGACACCAAACATTCCTGC	CCGCTCGAGCTAGATGTGCTGGTGAAGGAAGCCATG
HA-RAR γ	CCGGAATTGGATGGCACCAATAAGGAG	CCGCTCGAGTCAGGCTGGGACTTCAG
HA-p85 α	CCGGAATTGGATGAGTGCTGAGGGTACCAAGTAC	ATAGTTAGCGGCCCTCATGCCCTGCTGTGCATATAC
HA-p85 α -NIC	CCGGAATTGGAGCTGTATAACTGAAAACCTCA	ATAGTTAGCGGCCCTCATGCCCTGCTGTGCATATAC
HA-p85 α -SH3	CCGGAATTGGATGAGTGCTGAGGGTACCAAGTAC	CTCGAGCCTCCAATATATTCTACGTA
HA-p85 α -BCR	CCGGAATTGGAAAAAAATCTGCCCTCCACACCAA	ATAGTTAGCGGCCCTCAGGCTGCTGAGAATCTGAAAAGCATAG
Flag-p85 α -BCR	CCGGAATTGGAAAAAAATCTGCCCTCCACACCAA	CGGGATCCTCAGGCTGCTGAGAATCTGAAAAGCATAG
Flag-p85 α -BCR-LxxAA	AGAATTACGACAGGCTGCTGATTGTGATACACC	GGTGTATCACAATCAGCAGCCTGCTGTAATTCT
His-RXR α -LBD	GGAATTCCATATGAGCAGGCCAACGAGGACATGCCGT	CCGCTCGAGCTAAGTCATTGGTGCAGCGCCTC
His-RXR α -LBD/L433D	GGCTCAAATGCGACGAACATCTCTTCTT	AAGAAGAGATGTTCGTCGCATTGAGCC
His-RXR α -LBD/R316E	CCTTCTCCCACGAGTCCATCGCCGTGAA	TTCACGGCGATGGACTCGTGGGAGAAGG
His-RXR α -LBD/Q275E	AGCAGCCGACAAAGAGCTTTCACCTG	CAGGGTAAAAGCTTGTGCGCTGCT
His-RXR α -LBD/F439A	ACATCTCTTCGCAAGCTCATGGG	CCCCGATGAGCTGGCGAAGAAGAGATGT