

**Table S2. Mobility parameters of wild-type and mutated EGFP-RAR with different diffusion models. Data represent the best-fit parameters to the one-component anomalous**

100 nM AM580		2-component free diffusion		
		_1 (ms)	_2 (ms)	r2
EGFP-RAR	-	2.64 ± 0.65	97 ± 57	29% ± 7%
EGFP-RAR	+	2.87 ± 0.99	89 ± 45	43% ± 9%
EGFP-RAR-A392R (activator binding mutant)	-	2.69 ± 0.73	108 ± 81	27% ± 8%
	+	2.83 ± 0.92	92 ± 56	39% ± 11%
EGFP-RAR-W225A (repressor binding mutant)	-	2.64 ± 1.07	119 ± 81	22% ± 8%
	+	2.54 ± 0.5	127 ± 80	26% ± 7%
EGFP-RAR-V395A (cofactor non-binding mutant)	-	2.66 ± 1.29	120 ± 112	20% ± 8%
	+	2.65 ± 0.84	116 ± 121	19% ± 9%
EGFP-RAR-dH12 (Helix-12 deleted mutant)	-	2.83 ± 0.81	120 ± 62	26% ± 7%
	+	3.17 ± 0.84	124 ± 58	27% ± 7%
EGFP-RAR-mZn (Zinc-finger mutant)	-	2.89 ± 0.7	105 ± 61	29% ± 6%
	+	3.40 ± 0.99	111 ± 61	35% ± 9%
EGFP-RAR-LBD (ligand binding domain only)	-	1.62 ± 0.62	99 ± 101	17% ± 11%
	+	2.05 ± 1.20	114 ± 138	27% ± 15%