

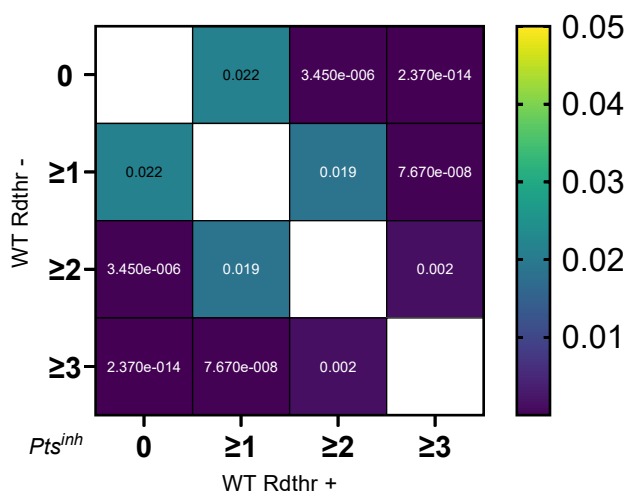
## Supplementary data

### Supplementary Table S2

#### Distribution of $Pts^{inh}$ based on WT readthrough

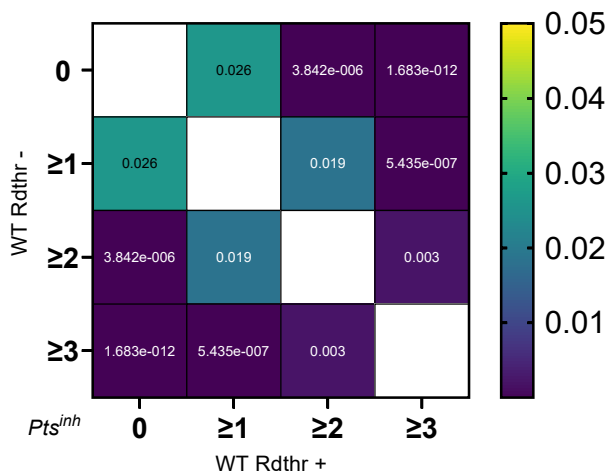
**A**

<i>WT Rdthr</i>	0	$\geq 1$	$\geq 2$	$\geq 3$
+	164	31	10	0
(%)	(20.1)	(13.4)	(6.0)	(0.0)
-	653	200	156	136
Total	817	231	166	136



**B**

<i>WT Rdthr</i>	0	$\geq 1$	$\geq 2$	$\geq 3$
+	116	31	10	0
(%)	(20.4)	(13.4)	(6.0)	(0.0)
-	454	200	156	136
Total	570	231	166	136



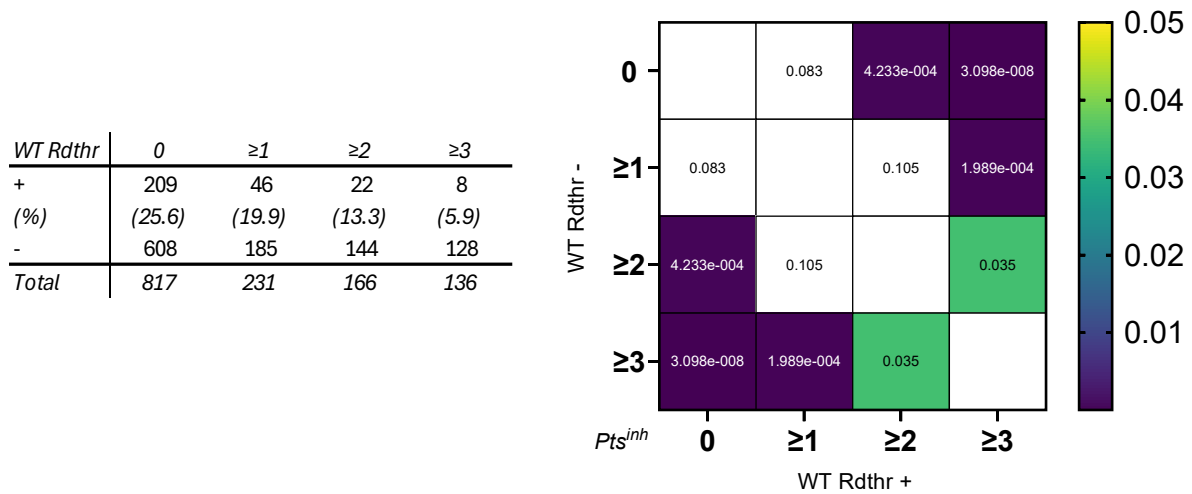
Data were obtained by the UAA=Tyr/Gln UGA= Trp and UAG=Tyr codification

**A**  $Pts^{inh=0}$ , all patients for whom inhibitor was not reported or was reported as negative;

**B**  $Pts^{inh=0}$  only patients for whom the absence of inhibitor was reported in the database

### Supplementary Table S3

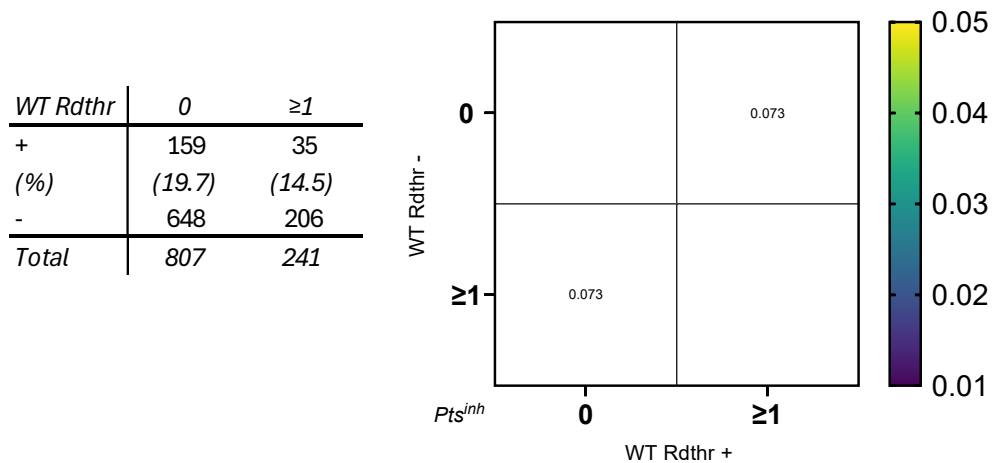
Distribution of  $Pts^{inh}$  based on WT readthrough (UAG=Gln).



Data were obtained by the UAA=Tyr/Gln UGA= Trp and UAG=Gln codification

### Supplementary Table S4

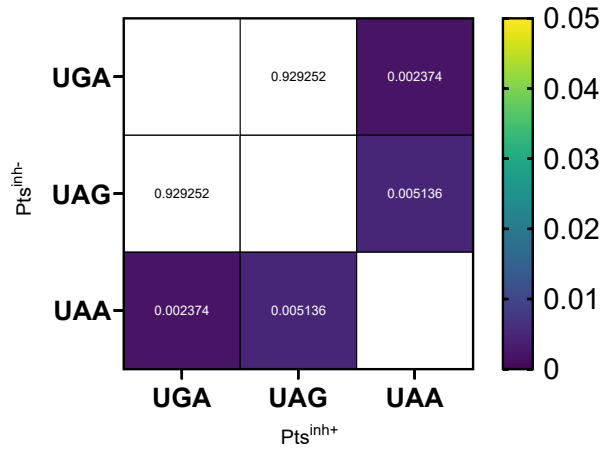
WT readthrough among  $Pts^{inh=0}$  and  $Pts^{inh \geq 1}$  after implementation with CHAMP database data



### Supplementary Table S5

Distribution of Pts<sup>inh</sup> for each PTC class.

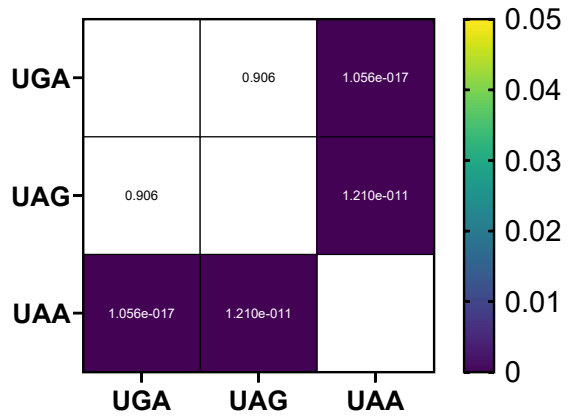
<i>Inh</i>	<i>UGA</i>	<i>UAG</i>	<i>UAA</i>	<i>Total</i>
+	146	59	26	231
(%)	(23.8)	(24.3)	(13.5)	
-	467	184	166	817
<i>Total</i>	613	243	192	1048



### Supplementary Table S6

Distribution for each PTC class of Pts with PTCs undergoing WT Rdthr

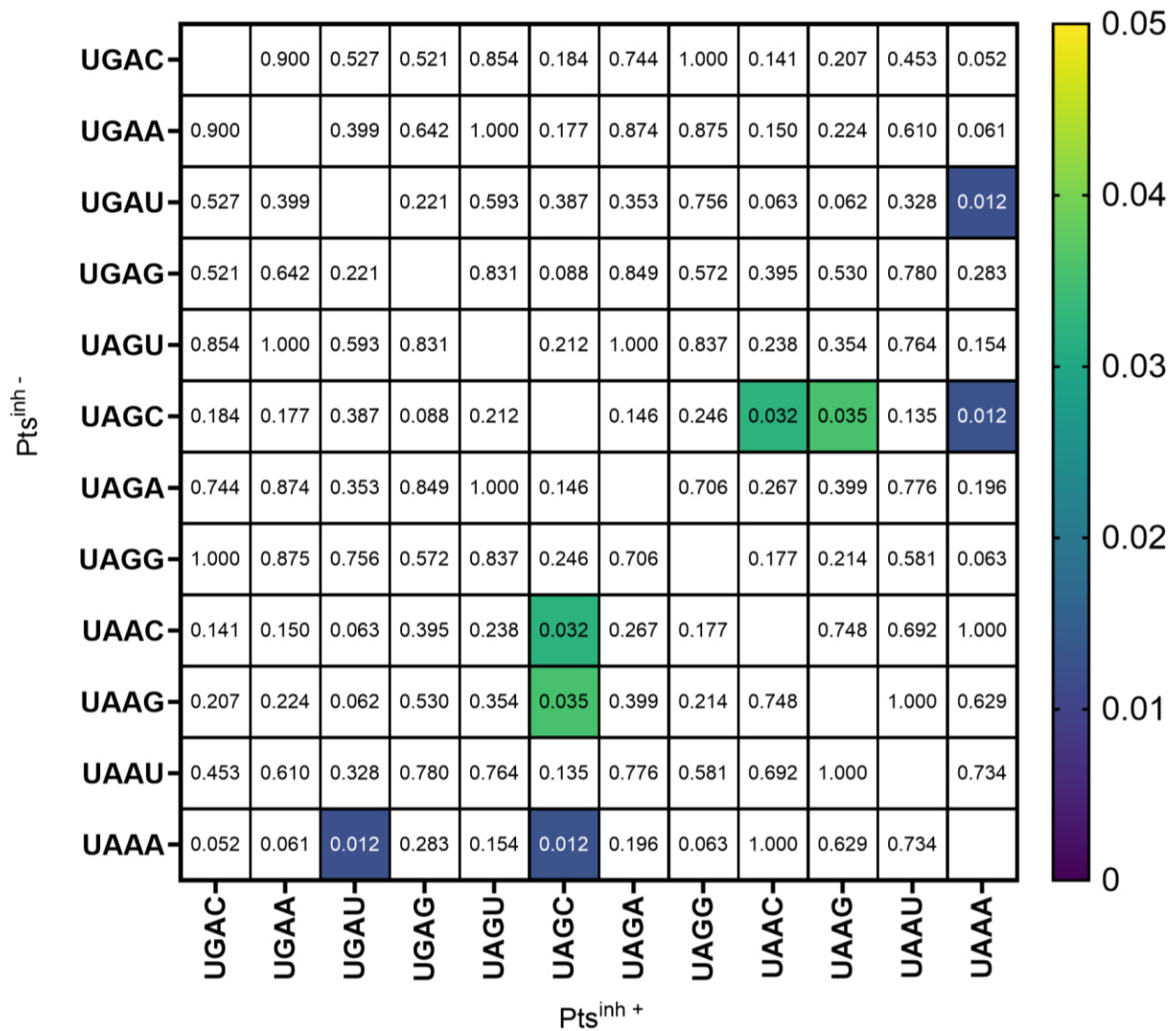
<i>WT Rdthr</i>	<i>UGA</i>	<i>UAG</i>	<i>UAA</i>	<i>Total</i>
+	69	28	98	195
(%)	(11.2)	(11.5)	(51.0)	
<i>Total</i>	613	243	192	1048



### Supplementary Table S7

#### Distribution of Pts<sup>inh</sup> for each tetranucleotide class.

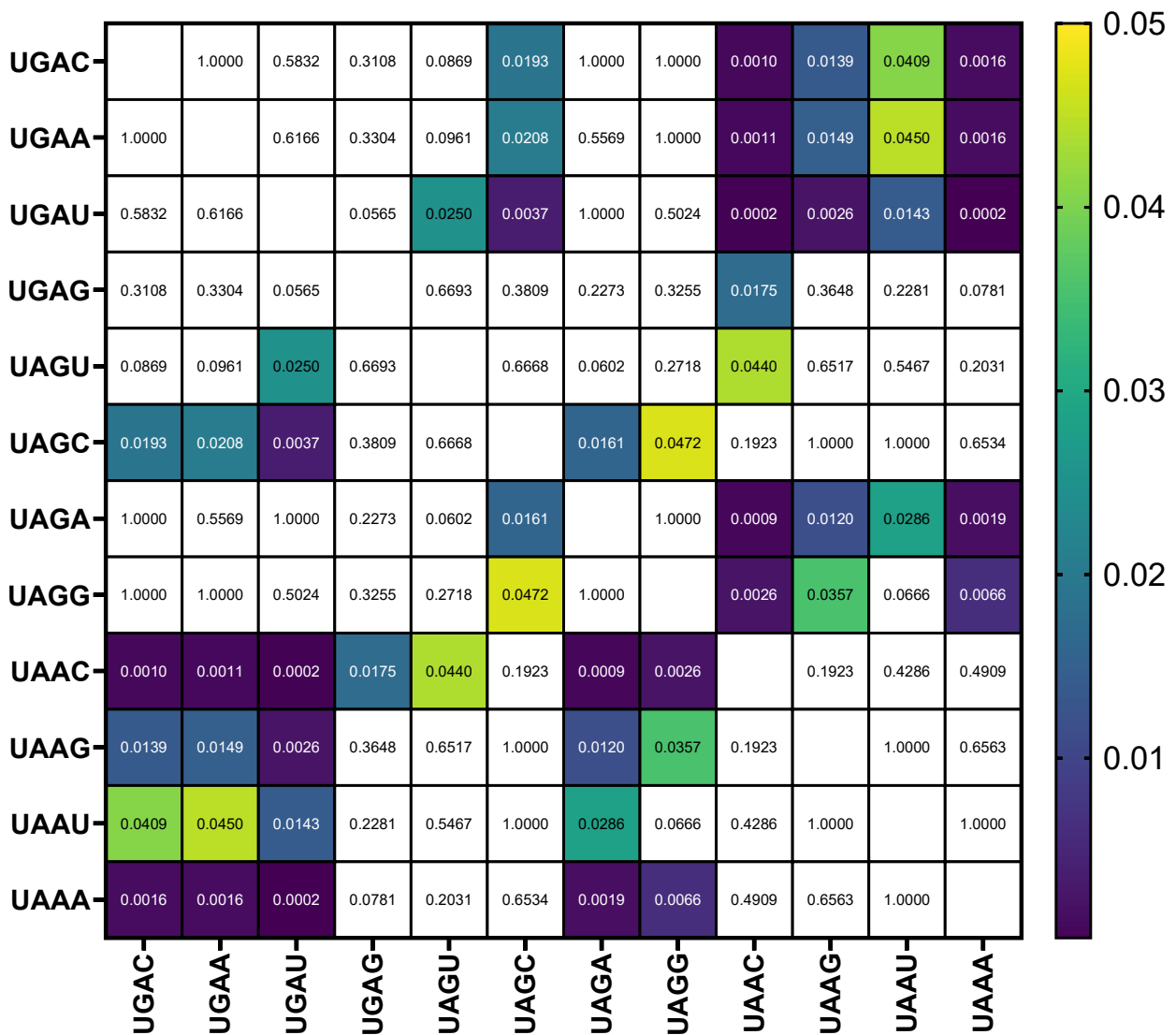
Inh	UGAC	UGAA	UGAU	UGAG	UAGU	UAGC	UAGA	UAGG	UAAC	UAAG	UAUU	UAAA	Total
+	37	46	46	17	12	11	17	19	3	10	4	9	231
(%)	(24)	(23)	(27)	(19)	(22)	(35)	(21)	(24)	(10)	(15)	(16)	(12)	
-	118	155	124	70	42	20	63	59	26	55	21	64	817
Total	155	201	170	87	54	31	80	78	29	65	25	73	1048



### Supplementary Table S8

Distribution of Pts with WT Rdthr for each tetranucleotide class.

WT Rdthr	UGAC	UGAA	UGAU	UGAG	UAGU	UAGC	UAGA	UAGG	UAAC	UAAG	UAAU	UAAA	Total
+	2	3	1	3	3	4	0	1	3	4	2	5	31
(%)	(5.4)	(6.5)	(2.2)	(18)	(25)	(36)	(0.0)	(5.3)	(100)	(40)	(50)	(55.6)	
-	35	43	45	14	9	7	17	18	0	6	2	4	200
Total	37	46	46	17	12	11	17	19	3	10	4	9	231



### Supplementary Table S9

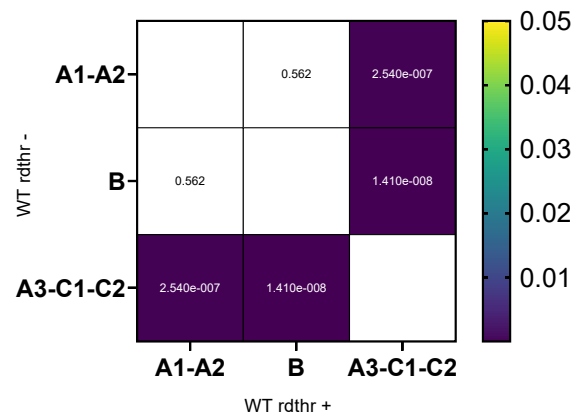
Distribution of Pts<sup>inh</sup> for domain localization of PTCs and for PTC classes.

Inh	All PTC				UGA			UAG			UAA		
	A1-A2	B	A3-C1-C2	Total	A1-A2	B	A3-C1-C2	A1-A2	B	A3-C1-C2	A1-A2	B	A3-C1-C2
+	42	34	157	230	24	15	106	14	10	35	4	9	13
(%)	(14.7)	(12.9)	(32.1)	(22.4)	(14.8)	(15.6)	(31.6)	(17.9)	(15.9)	(34.3)	(8.7)	(8.6)	(30.9)
-	244	229	322	795	138	81	229	64	53	67	42	95	29
Total	286	263	479	1028	162	96	335	78	63	102	46	104	42

### Supplementary Table S10

Distribution of Pts WT Rdthr based on FVIII domain localization of PTCs.

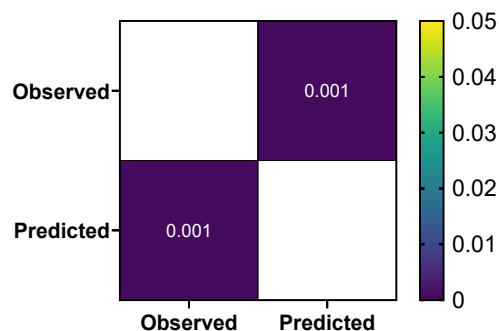
WT Rdthr	A1-A2	B	A3-C1-C2	Total
+	72	72	51	195
(%)	(25.2)	(27.4)	(10.6)	
-	214	191	428	833
Total	286	263	479	1028



### Supplementary Table S11

Distribution of WT Rdthr for PTCs observed (EAHAD) and predicted (never reported) as single nucleotide variants.

WT Rdthr	Observed	Predicted	Total
+	105	144	249
(%)	(31)	(22)	(25)
-	230	518	748
Total	335	662	997



### Supplementary Table S12

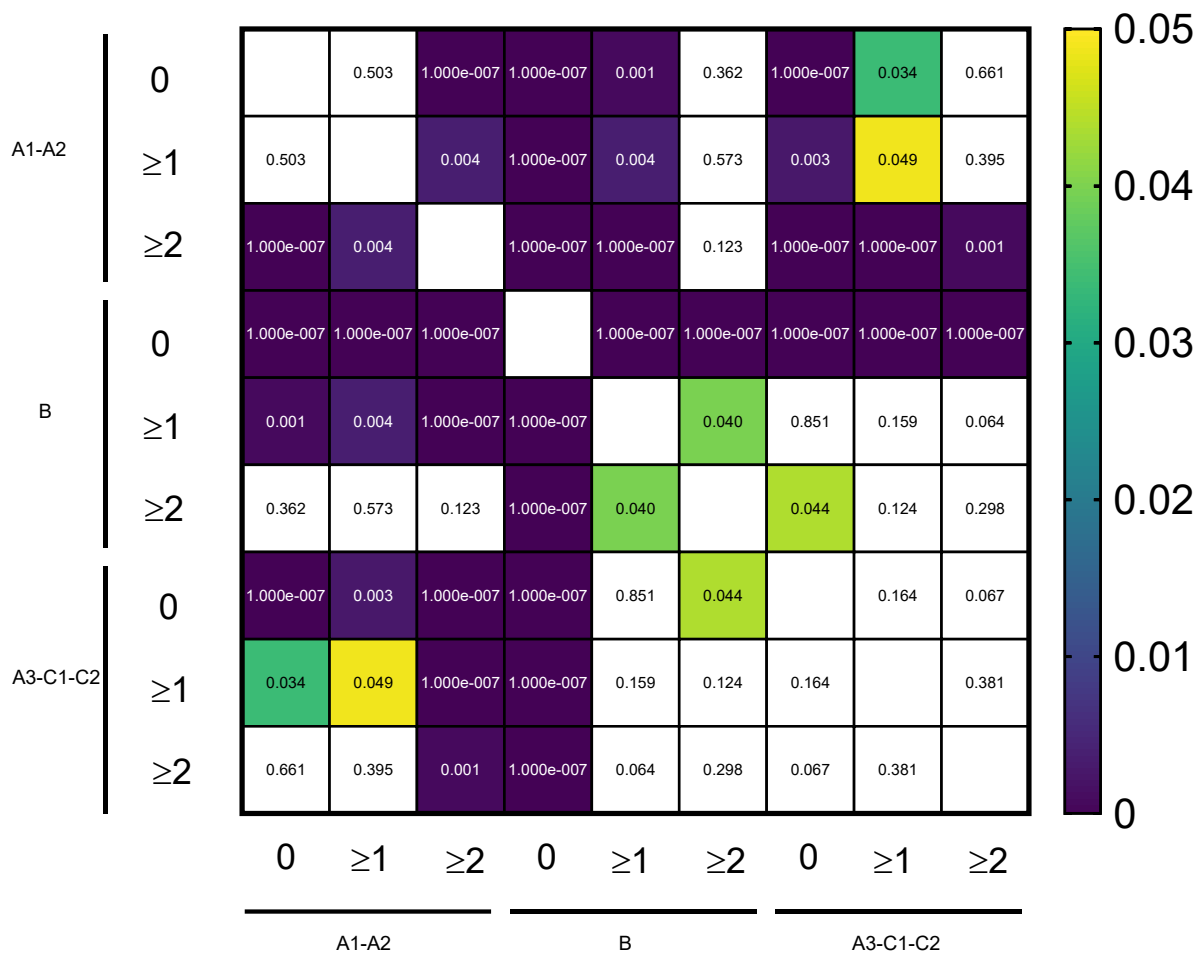
Distribution for each PTC class of PTCs observed (EAHAD) and predicted (never reported) as single nucleotide variants.

	<i>Observed</i> <i>n(%)</i>	<i>Predicted</i> <i>n(%)</i>	<i>Total</i> <i>n(%)</i>
<i>UGA</i>	88(27)	160(24)	248(25)
<i>UAG</i>	122(36)	223(34)	345(35)
<i>UAA</i>	125(37)	279(42)	404(41)
<i>Total</i>	335	662	997

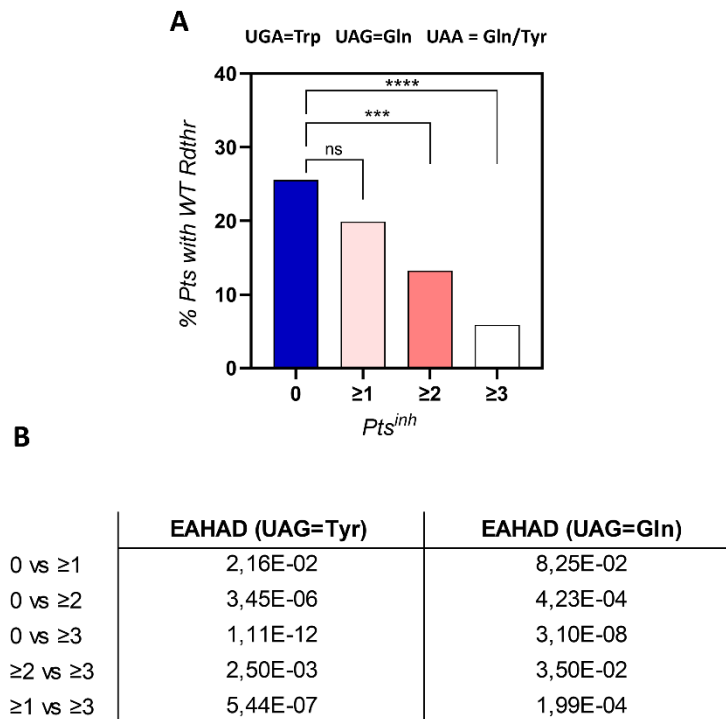
### Supplementary Table S13

Mean differential affinity, expressed as percentile ranking, of peptides obtained from WT Rdthr- PTCs grouped by PTC<sup>inh</sup> status and FVIII domain location.

PTC <sup>inh</sup>	A1-A2			B			A3-C1-C2		
	0	≥1	≥2	0	≥1	≥2	0	≥1	≥2
Mean	0,53	0,80	3,00	-2,25	-0,55	1,32	-0,48	-0,04	0,34
Standard error	0,16	0,37	0,66	0,19	0,29	0,86	0,23	0,21	0,38
Count	1768	364	156	2574	728	104	1144	1118	442
Variants number	68	14	6	99	28	4	44	43	17



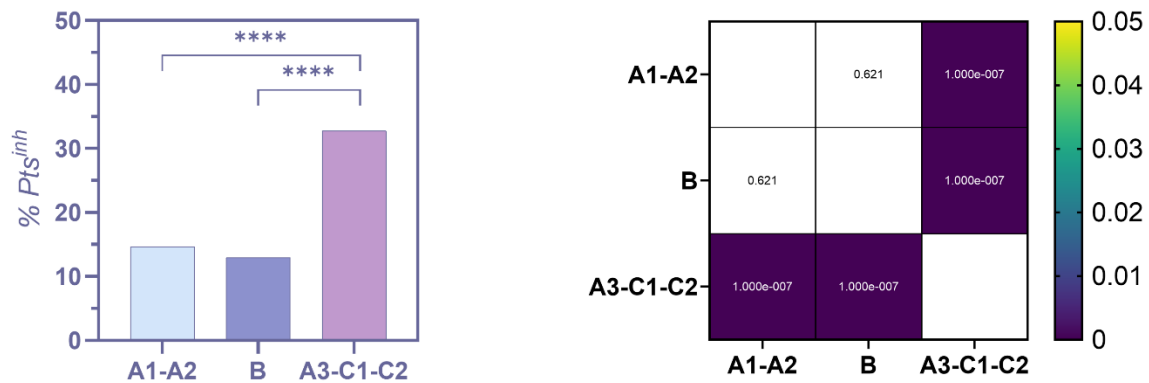
## Supplementary Figure S1



### Insertion of WT amino acid upon readthrough in the UAG=Gln model

A) HA patients with *F8* PTCs predicted to undergo WT readthrough, exploring Gln at UAG, were classified in accordance with PTCs associated with an increasing number of inhibitor-positive cases ( $Pts^{inh=0}$ , patients with PTCs never found in patients with inhibitors;  $Pts^{inh\geq 1}, Pts^{inh\geq 2}, Pts^{inh\geq 3}$ , patients affected by PTCs found in 1,2,3 or more patients with inhibitors). B) Statistical comparison between models with Tyr or Gln reinsertion at UAG. Statistical significance of Fisher's exact test.

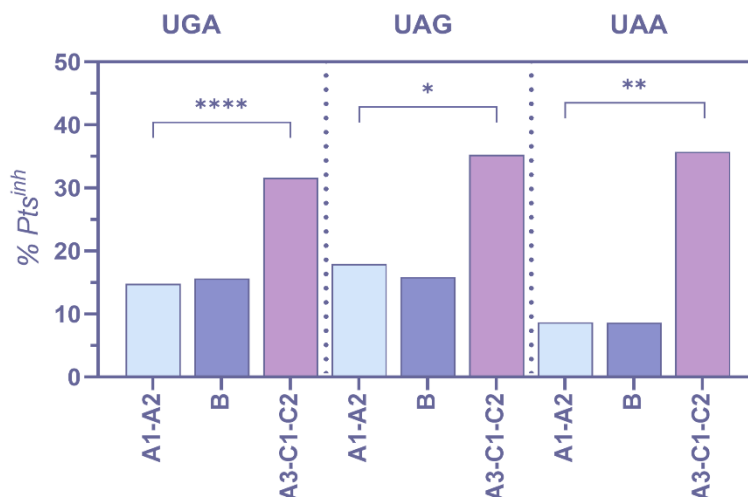
## Supplementary Figure S2



### Comparison of the percentage of Pts<sup>inh</sup> with PTCs in FVIII domains.

*Left panel.* Distribution of Pts<sup>inh</sup> with PTCs in grouped FVIII domains. *Right panel.* Statistical Comparison

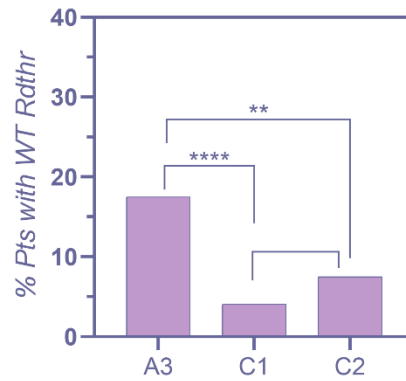
## Supplementary Figure S3



### Comparison of the percentage of Pts<sup>inh</sup> for PTCs in FVIII domains.

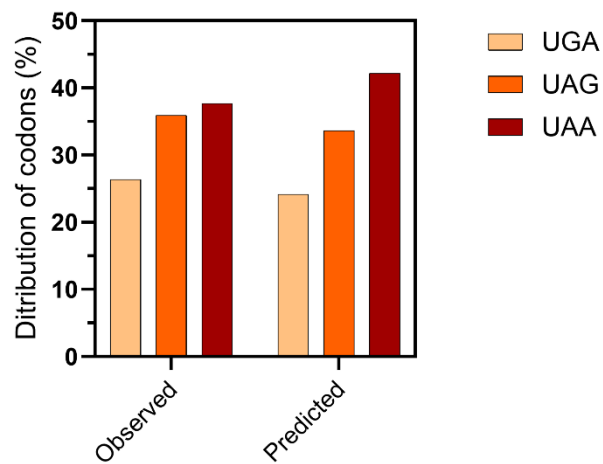
Distribution of Pts<sup>inh</sup> in relation to FVIII domain location of PTC classes (UGA/UAG/UAA).

### Supplementary Figure S4



Comparison of the percentage of Pts with PTCs with WT Rdthr in single FVIII domains (A3, C1 and C2)

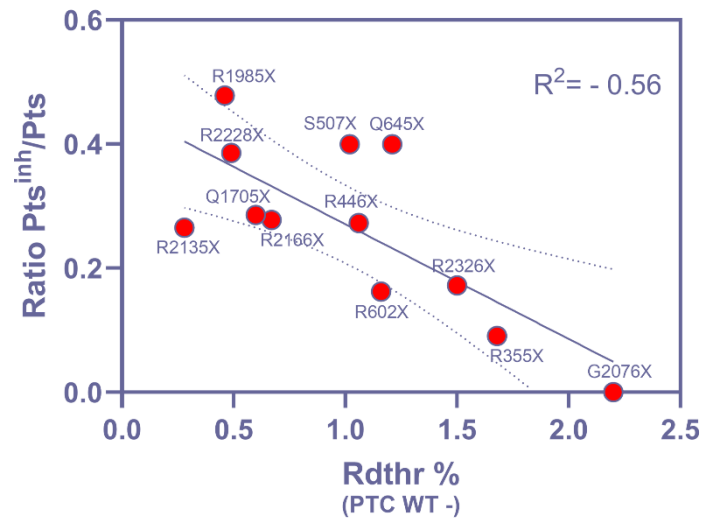
### Supplementary Figure S5



Comparison of observed (EAHAD) and predicted (never reported before) PTCs for each PTC class (UGA, UAG, UAA).

Prediction of PTCs produced by single nucleotide variants (SNV).

## Supplementary Figure S6



**Correlation between recombinant Rdthr output and ratio of patients with inhibitor on total number of patients for WT Rdthr- PTCs.**

Inverse relation between readthrough over PTCs WT –, excluding those within B domain, and ratio of patients with inhibitor on total number of patients for 12 PTCs WT – (red dots).