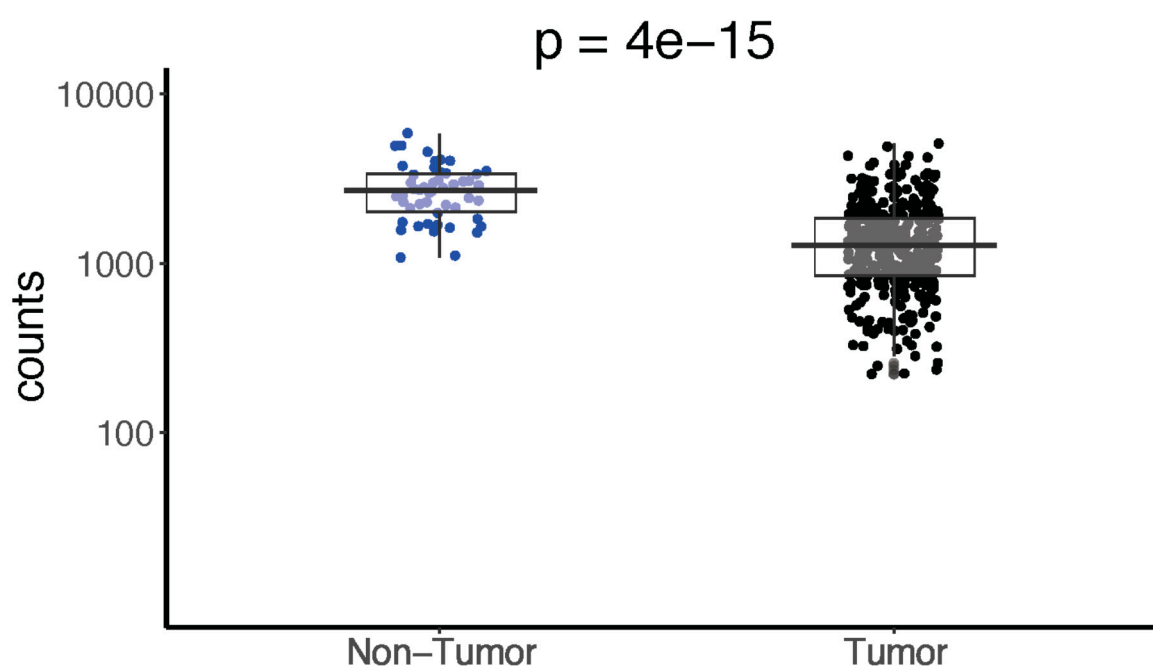
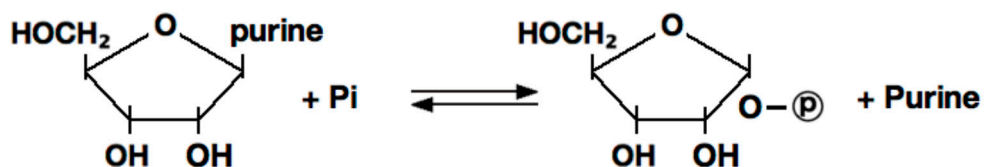
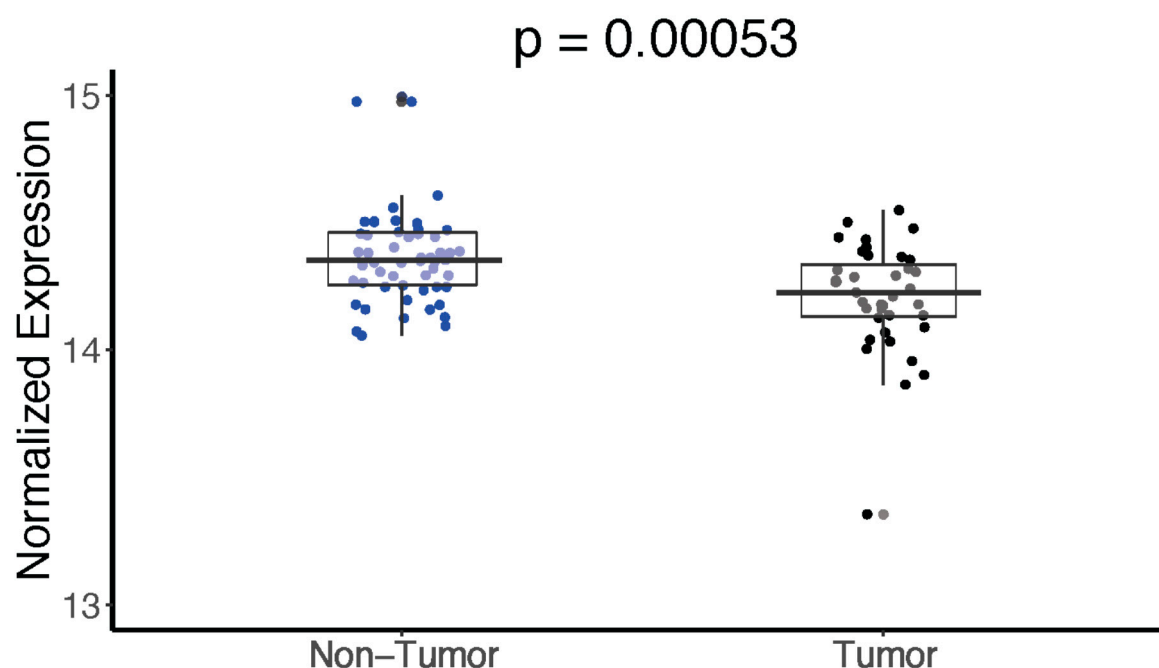


## Supplementary Materials: [<sup>18</sup>F] Clofarabine for PET Imaging of Hepatocellular Carcinoma

**Purine-nucleoside: orthophosphate ribosyltransferase (EC 2.4.2.1) <sup>1,2)</sup>**





**Figure S1.** PNP levels in the liver. PNP has a significantly higher expression, in terms of the base main counts in either RNA-seq (human) or microarray (woodchuck) data, in the liver parenchyma than in HCC for human and woodchuck. The enzyme works reversibly in both directions.

## The FASTA results

### 1. PNP alignment between

Query: NCBI Reference Sequence: NP\_000261.2; purine nucleoside phosphorylase [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015336353.1; PREDICTED: purine nucleoside phosphorylase [Marmota marmota marmota]

Identities	Positives	Gaps
251/288 (87%)	265/288 (92%)	0/288 (0%)
Query 1	MENGYTYEDYKNTAEWLLSHTKHPQVAIICGSLGGLTDKLTQAQIFDYGEIPNFPST	60
Sbjct 1	MEN +TYEDY+ TAEWLLS TKHRPQVA+ICGSLGGLT+KLT+AQ FDY EIPNFP+ST	60
Query 61	VPGHAGRLVFGFLNGRACVMMQGRFHYEGYPLWKVTFPVRVFHLLGVDTLVVTNAAGGL	120
Sbjct 61	VPGHAGRLVFGFLN +ACVMMQGRFH YEGYPLWKVTFPVRVF LLGVDTLVVTNAAGGL	120
Query 121	NPKFEVGDIMLIRDHINLPGFSGQNPLRGPNDRFGDRFPAMSDAYDRTMRQALSTWKQ	180
Sbjct 121	NP F+VGDIMLIRDHINLPG GQNPL+GPNDERFG RFPAMSDAYDR MR++ALSTWK	180
Query 181	MGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSL	240
Sbjct 181	MGE RELQEGTYVMVAGPSFETVAE R+LQ+LGADAVGMSTVPEVIVARHCGLRVFGFSL	240
Query 241	ITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSILMASIPLPKA	288
Sbjct 241	ITNKVIMDYESLEK HEEVL GKQAAQKLE+FVSILMASIP D A	288

## 2. ENT1 alignment between

Query: UniProtKB/Swiss-Prot: Q99808.3; S29A1\_HUMAN RecName: Full=Equilibrative nucleoside transporter 1; AltName: Full=Equilibrative nitrobenzylmercaptapurine riboside-sensitive nucleoside transporter; Short=Equilibrative NBMPR-sensitive nucleoside transporter; AltName: Full=Nucleoside transporter, es-type; AltName: Full=Solute carrier family 29 member 1

Sbjct: NCBI Reference Sequence: XP\_015342854.1; PREDICTED: equilibrative nucleoside transporter 1 [Marmota marmota marmota]  
222

Identities		Positives	Gaps
404/464(87%)		421/464(90%)	9/464(1%)
Query	2	TTSHQPQDRYKAVWLIFFMLGLGTLTPWNFFMTATQYFTNRLDMSQNVSLVTAELSKDAQ	61
Sbjct	77	TTSHQPQDRYKAVWLIFFMLGLGTLTPWNFFMTAT+YFTNRLDMSQNVSL A LSKD Q	136
Query	62	ASAAPAAPLPERNSLSAIFNNVMTLCAMPLPLLLFTYLNSFLHQRIPQSVRILGSLVAILL	121
Sbjct	137	A P APLPE+ SLSAIFNNVMTLCAMPLPLLLF+ LNSFLHQRIPQSVRILGSLVAILL	196
Query	122	VFLITAILVKVQLDALPFFVITMIKIVLINSFGAILQGSFLFGLAGLLPASYPIMSGQG	181
Sbjct	197	VFL+TAILVKVQLDALPFFV TMIKI+LINSFGAILQGSFLFGLAGLLPA+YTAPIMSGQG	256
Query	182	LAGFFASVAMICAIASGSELSAFAFYFITACAVIILTIICYLGLPRLEFYRYQQQKLE	241
Sbjct	257	LAG FASVAMICAIASGSELSAFAFYFITAC V+IL IICYLGLPRLEFYRYQQQKLE	316
Query	242	GPGEQETKLDLISK-----GEEPRAGKEESGVSVSNSOPTNESHSHKAILKNISVL	292
Sbjct	317	GPGEQETKLDLISK GEEPR KEESGV NSQ T+ + SI+AILKNISVL	376
Query	293	AFSVCFIPTITIGMFPAVTVEVKSSIAGSSTWERYFIPVSCFLTFFNIFDWLGRSLTAVFM	352
Sbjct	377	A SVC FT+TIG+FPAAVT EVKSSIAG+S W YFIPVSCFLTFFNIFDWLGRSLTAVFM	436
Query	353	WPGKDSRWLPSLVARLVFVPLLLLCNIPRRYLTVVFEHDAWFIFMAAFASFNGYLAS	412
Sbjct	437	WPGKDS WLPVLV+ARLVFVPLLLLCN+ PRRYL VVF+HDAW+IFFMAAFASFNGYLAS	496
Query	413	LCMCFGPKKVKPAEAETAGAIMAFFLCLGLALGAVFSFLFRAIV	456
Sbjct	497	LCMCFGPKKVKPAEAETAGAIM FFL LGLALGAV SFL RAIV	540

### 3. ENT2 alignment between

Query: NCBI Reference Sequence: NP\_001523.2 equilibrative nucleoside transporter 2 isoform a; SLC29A2 [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015358637.1 PREDICTED: equilibrative nucleoside transporter 2 isoform X1 [Marmota marmota marmota]

Identities		Positives		Gaps	
308/339(91%)		318/339(93%)		3/339(0%)	
Query	121	MSPGPFFSITMASVCFINSFSAVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALAMLL	180		
		MSPGPFFSITM SV FINSF AVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALAML+			
Sbjct	1	MSPGPFFSITMVSVMFINSFCAVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALMLM	60		
Query	181	SMASGVDAETSALGYFITPCVGILMSIVCYLSLPHLKFARYYLANKSSQAQAQAELETKAE	240		
		SMASGVDA+TSALGYFITPCVGILMSIVCYLSLPHL+FARYYLA K S++ ELETKAE			
Sbjct	61	SMASGVDAQTSALGYFITPCVGILMSIVCYLSLPHLEFARYYLAKKPSRSPTHELETKAE	120		
Query	241	LLQSDE-NGIPSSPQKVALTLDLDLEKEPESEPDEP--QKPGKPSVFTVFQKIWLTAALCL	297		
		LLQ+DE NGIPSSPQ LTLDLD EKEPE EP+ QK KPSVF VFQKIWLTAALCL			
Sbjct	121	LLQADEKNGIPSSPQVATLTLDLDPEKEPELEPELDEPQKLEKPSVFIVFQKIWLTAALCL	180		
Query	298	VLVFTVTLVSFPAITAMVTSSTSPGKWSQFFNPICCFLLFNIMDWLGRSLTSYFLWPDED	357		
		VLVFTVTLVSFPAITAMVTSSTSPGKWSQFFNPICCFLLFN+MDWLGRSLTSYFLWPDED			
Sbjct	181	VLVFTVTLVSFPAITAMVTSSTSPGKWSQFFNPICCFLLFNMDWLGRSLTSYFLWPDED	240		
Query	358	SRLPLLVCLRFLFVPLFMLCHVPQRSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL	417		
		SRLPLLVCLRFLFVPLFMLCHVP+R+RLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL			
Sbjct	241	SRLPLLVCLRFLFVPLFMLCHVPERARLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL	300		
Query	418	APRQVLPHEREVAGALMTFFLALGLSCGASLSFLFKALL	456		
		APRQVLPHEREVAGALMTFFLALGLSCGASLSFLFKALL			
Sbjct	301	APRQVLPHEREVAGALMTFFLALGLSCGASLSFLFKALL	339		

## 4. UGT1A1 alignment between

Query: NCBI Reference Sequence: NP\_000454.1; UDP-glucuronosyltransferase 1-1 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015337083.1; PREDICTED: UDP-glucuronosyltransferase 1-1 isoform X2 [Marmota marmota marmota]

Identities		Positives	Gaps	
433/533(81%)		472/533(88%)	0/533(0%)	
Query	1	MAVESQGGRLVLGLLLCVLGPVSHAGKILLIPVDGSHWLSMLGAIQQLQQRGHEIVVL	60	
		MAV SQG L+LGLLLCVL P +SHA K+L+IPVDGSHWLSM+G IQQLQ+RGHE+VV+		
Sbjct	1	MAVVSQGPCTLLLGLLLCVLNPSISHAEKLLIIPVDGSHWLSMVGVIQQLQQRGHEMVVI	60	
Query	61	APDASLYIRDGAFYTLKTYPVFPQREDVKESFVSLGHNVFENDSFLQRVIKTYKKIKKDS	120	
		P+AS++I++ +FY+LK YPVFPQ+EDV+ SF LG FEN FLQ V K Y+K +KDS		
Sbjct	61	TPEASIIHKEASFYSLKKYPVPFQKEDVETSFAELGFYAFENVFPFLQGVAKMYEKAQKDS	120	
Query	121	AMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPCSLE	180	
		A+LLSGCSHLLHNKE MASL ES FD +LTDPFPLC IVAQYL LP V FL+ALPC L+		
Sbjct	121	AVLLSGCSHLLHNKEFMASLVESDFDAVLTDPFPLPCGSIVAQYLDLPVFNFLNALPCGLD	180	
Query	181	FEATQCPNPFSSYVPRPLSSSDHMTFLQRVKNMLIAFSQNFCDVVYSPYATLASEFLQR	240	
		+ATQCP+P SYVPR LSS+SDHMTFLQRVKNMLIA +NFLC +VYSPYA LAS+ LQR		
Sbjct	181	LKATQCPSPLSYVPRALSSNSDHMTFLQRVKNMLIALLENFLCSMVYSPYAALASQVLQR	240	
Query	241	EVTVDLLSSASVWLFVDFKDYPRPIMPNMVVFVGGINCLHQNPLSQEFEAYINASGEH	300	
		++T+QDLLSSASVWL R DFVKDYP PIMPNMVVFVGGINCLH P+SQEFEAY+NASGEH		
Sbjct	241	DLTLQDLLSSASVWLMRKDFVKDYPMPIMPNMVVFVGGINCLHTKPISQEFEAYVNASGEH	300	
Query	301	GIVVFSGLSMVSEIPEKKAMAIADALGKIPQTVLWRYTGTRPSNLNNTILVKWLPQNDL	360	
		GIVVFSGLSMVSEIPEKKAM IADALG+IPQTVLWRYTGT PSNLA NT LVKWLQNDL		
Sbjct	301	GIVVFSGLSMVSEIPEKKAMEIADALGRIPQTVLWRYTGTPPSNLAKNTKLKWLQNDL	360	
Query	361	LGHPMTRAFITHAGSHGVYESICNGVPMVMMPFLFGDQMDNAKRMETKGAGVTNLVLEMTS	420	
		LGHP TRAFITHAGSHGVYE ICNGVPMVMMPFLFGDQMDNAKRMET+GAGVTNLVLEMTS		
Sbjct	361	LGHPKTRAFITHAGSHGVYEGICNGVPMVMMPFLFGDQMDNAKRMETRGAGVTNLVLEMTS	420	
Query	421	EDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPAHD	480	
		+DL NALKAVINDKSYKENIMRLS LHKDRP+EPLDLAVFWVEFVMRHKGAPHLRPAHD		
Sbjct	421	DDLANALKAVINDKSYKENIMRLSRLHKDRPIEPLDLAVFWVEFVMRHKGAPHLRPAHD	480	
Query	481	LTWYQYHSLDVIGFLLAVLTVAFITFKCCAYGYRKCLGKKGRVKKAHKSKTH	533	
		LTWYQYHSLDVIGFLLA+VL VAFI FKCCAYG RKC GKKG VKK HSK H		
Sbjct	481	LTWYQYHSLDVIGFLLAIVLGVAFAFKCCAYGCRKCFGKKGSVKKGHKSKAH	533	



## 5. UGT1A9 alignment between

Query: NCBI Reference Sequence: NP\_066307.1; UDP-glucuronosyltransferase 1-9 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015337084.1; PREDICTED: UDP-glucuronosyltransferase 1-9 isoform X3 [Marmota marmota marmota]

Identities	Positives	Gaps
429/521(82%)	463/521(88%)	0/521(0%)
Query 10	LPLCVCLLLTCGFAEAGKLLVVPMDGSHWFTMRSVVEKLILRGHEVVVVMPPEVSWQLGRS	69
	LPLCVCLLL A+AGKLLVVPMDGSHWFTMRSVVEKL+ RG+EVV VMPEVSWQLG+S	
Sbjct 10	LPLCVCLLLASSSAQAGKLLVVPMDGSHWFTMRSVVEKLVHRGNEVVAVMPEVSWQLGQS	69
Query 70	LNCTVKTYSTSYTLEDLDREFKAFHAHQWKAQVRSIYSLLMGSYNDIFDLFFSNCRSLFK	129
	LN TVKTYSTSYTLEDLDR F F QWK +S+YS MGS FD+ FS CRSLF	
Sbjct 70	LNFTVKTYSTSYTLEDLDRGFNFVDTQWKTPQSMYSAAMGSSKAFFDITFSRCRSLFN	129
Query 130	DKKLVEYLKESSFDAVFLDPDNCGLIVAKYFSLPSVVFARGILCHYLEEGAQCPAPLSY	189
	DKKLVEYLKE+SFDAVFLDPFD CGL+VAKYFSLPSVVFAR + C++LE+GAQCP+PLSY	
Sbjct 130	DKKLVEYLKETSFDAVFLDPDVCGLVVAKYFSLPSVVFARVVCNLFEDGAQCPSPLSY	189
Query 190	VPRILLGFSDAMTFKERVNRHIMHLEEHLLCHRFKNALEIASEILQTPVTEYDLYSHTS	249
	VPR+ L SDA++F ER+RNH+ +LEE+L C FF+ ALE+ASEIL+TPVT DL+S S	
Sbjct 190	VPRVFLMSSDALSFMERIRNHLNLYEEYLFQPYFFQTALVASEILRTPVTIGDLFSQIS	249
Query 250	IWLLRTDFVLDYPKVMPNMIFIGGINCHQKPLPMEFEAYINASGEHGIVVFSLGSMVS	309
	IWLLRTDFVL+YP+PVMNMF+GGINCHQ KPLP EFEAY+NASGEHGIVVFSLGSMVS	
Sbjct 250	IWLLRTDFVLEYPRVMPNMIFVGGINCHQKPLPKEFEAYVNASGEHGIVVFSLGSMVS	309
Query 310	EIPEKKAMAIADALGKIPQTVLWRYTGTRPSNLANTILVKWLPQNDLLGHPMTRAFITH	369
	EIPEKKAM IADALG+IPQTVLWRYTGT PSNLA NT LVKWLPQNDLLGHP TRAFITH	
Sbjct 310	EIPEKKAMEIADALGRIPQTVLWRYTGTTPPSNLAKNTKLKWLPQNDLLGHPKTRAFITH	369
Query 370	AGSHGVYESICNGVPMVMMPFLFGDQMDNAKRMETKGAGVTNLVLEMTSEDLENALKAVIN	429
	AGSHGVYE ICNGVPMVMMPFLFGDQMDNAKRMET+GAGVTNLVLEMTS+DL NALKAVIN	
Sbjct 370	AGSHGVYEGICNGVPMVMMPFLFGDQMDNAKRMETRGAGVTNLVLEMTSDDLANKAVIN	429
Query 430	DKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI	489
	DKSYKENIMRLS LHKDRP+EPDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI	
Sbjct 430	DKSYKENIMRLSRLHKDRPIEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI	489
Query 490	GFLLAIVLTVAFITFKCCAYGYRKCLGKKGRVKKAHKSKTH	530
	GFLLA+VL VAFI FKCCAYG RKC GKKG VKK HSK H	
Sbjct 490	GFLLAIVLGVAFI AFKCCAYGCRKCFGKKGSVKKGHKS KA H	530

## 6. UGT2B4 alignment between

Query: NCBI Reference Sequence: NP\_066962.2; UDP-glucuronosyltransferase 2B4 isoform 1 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015337650.1 PREDICTED: UDP-glucuronosyltransferase 2B4-like [Marmota marmota marmota]

Identities	Positives	Gaps
54/115(47%)	60/115(52%)	44/115(38%)
Query 250	MAKADIWLIRNYWDFQFPHPLLPNVEFVGGLHCKPAKPLPKEME EFVQSSGENGVVVFSL	309
	MAKADIWLI YWD +F H LPNV+ VGGLHC+PAK LP	
Sbjct 1	MAKADIWLICTYWDLEFSHSTLPNVDIVGGLHCRPAKSLP-----	40
Query 310	GSMVNTSEERANVIASALAKIPQKVLWRFDGNKPD TLGLNTRLYKWIPQNDLLG	364
	K+LWRFDG KPD TLGLN +LYKWIP+ DLLG	
Sbjct 41	-----KILWRFDGKKPD TLGLNIQLYKWIPKGDLLG	71

## 7. UGT2B4 alignment (alternative)

Query: NCBI Reference Sequence: NP\_066962.2; UDP-glucuronosyltransferase 2B4 isoform 1 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015360783.1; PREDICTED: UDP-glucuronosyltransferase 2B15-like [Marmota marmota marmota]

Identities		Positives	Gaps
388/530 (73%)		455/530 (85%)	2/530 (0%)
Query	1	MSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSHWMNIKTILDELVQRGHEVTVLASSA	60
Sbjct	1	MSVKRNSVLLLIQLMCFSSGSCGKVLVWPTEYSHWINIKAILDELLQRGHEVTVLSTA	60
Query	61	SISFDPNSPSTLKFVYPVSLTKTEFEDIKQLVKRWA-ELPKDTFWSYFSQVQEIMWTF	119
Sbjct	61	SI +PN+ S + FEVYP +K E+ + + W + PKD FW ++S VQ++ +	120
Query	120	NDILRKFCCKDIVSNKKLMKKLQESRFDVVLADAVFPFGELLAELLKIPFVYSLRFSPTYA	179
Sbjct	121	SDTIEQLCRNVVLNKKLMMKLHESKFDVVLADAVGPCGELLAELLKIPFVYTLRFTFGYT	180
Query	180	IEKHSGLLFPSPSYVPMSELSQMTFIERVKNMIYVLYFEFWFQIFDMKKWDQFYSEV	239
Sbjct	181	YEKYSGLTVPPSYVPIVSELSQMTFMERVKNVTYMLYFDFWFQIFDVKRWQFYSEV	240
Query	240	LGRPTTLSETMAKADIWLIRYWDFFQPHPLLPNVEFVGGLHCKPAKPLPKEMEETFVQSS	299
Sbjct	241	LGRPTTIYETMGKADFWLIRTYWDLFPRPLLPNFDVVGGLHCKPAKPLPKEMEETFVQSS	300
Query	300	GENGVVVFSLGSMVSNSTSEERANVIASALAKIPQKVLWRFDGKPDTLGLNTRLYKWIPQ	359
Sbjct	301	GENGIVVVFSLGTMVSNMPEEKANMIAFALAIQIPQVIWRFNGKKPKDGLPNTQIYEWIPQ	360
Query	360	NDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGVPPLFADQPDNIAHMKAKGAASLDFT	419
Sbjct	361	NDLLGHPKTAFITHGGTNGVYEAIYHGVPVMPGIPPLFADQPDNIAHVAKAGAAIRLDYRI	420
Query	420	MSSTDLLNALKTVINDPLYKENAMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA	479
Sbjct	421	++S DLL AL+ VINDP YKENAM+LSRI HDQPVKPLDRAVFWIEFVMRHKGAKHL+VA	480
Query	480	LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA	530
Query	480	AHDLTWFQYHSLDVTGFLACVATVIFIITK-CLFCVWKVVRTGKKGKRD	528
Sbjct	481	AHDL+WFQY+SLDV GFLACVATV+FII+K CLFC F +TGKK KR+	530

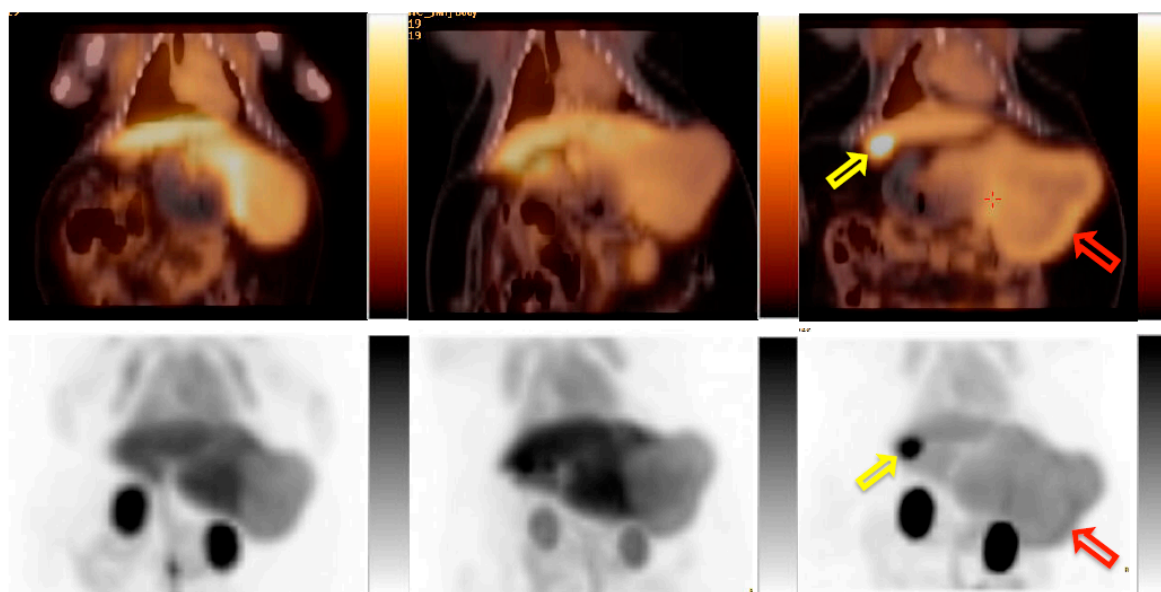
## 8. UGT2B15 alignment

Query: NCBI Reference Sequence: NP\_001067.2; UDP-glucuronosyltransferase 2B15 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP\_015360783.1; PREDICTED: UDP-glucuronosyltransferase 2B15-like [Marmota marmota marmota]

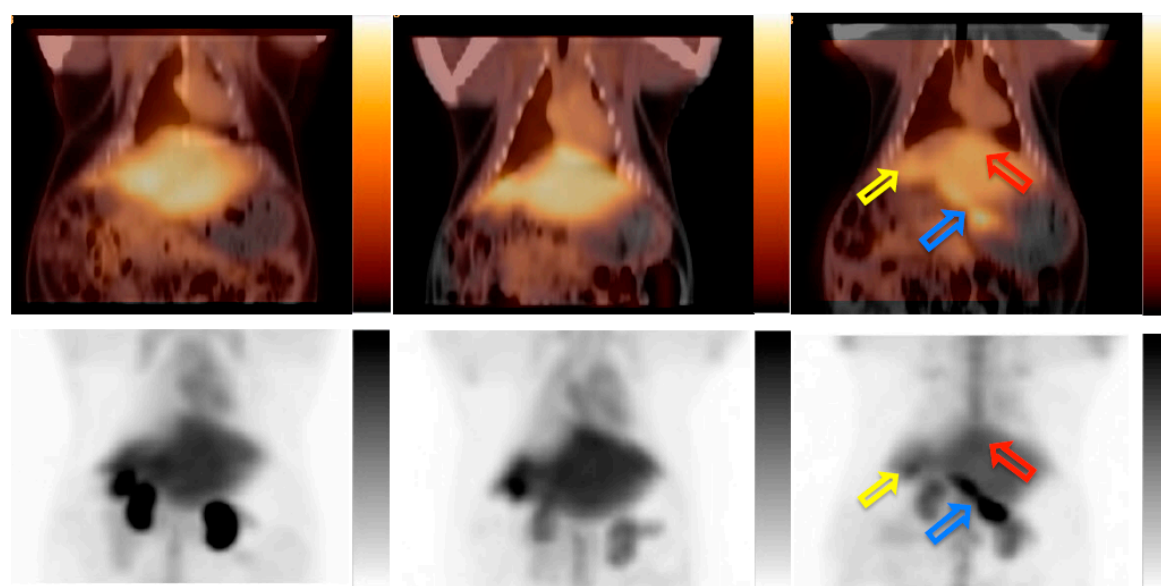
Identities		Positives	Gaps	
392/530 (74%)		459/530 (86%)	0/530 (0%)	
Query	1	MSLKWTSVFLLIQLSCYFSSGSCGKVLVWPTEYSHWINMKTILEELVQRGHEVTVLTSSA	60	
		MS+K SV LLIQL CYFSSGSCGKVLVWPTEYSHWIN+K IL+EL+QRGHEVTVLTSA+A		
Sbjct	1	MSVKRNSVLLLIQLMCYFSSGSCGKVLVWPTEYSHWINIKAILDELLQRGHEVTVLTSTA	60	
Query	61	STLVNASKSSAIKLEVYPTSLTKNYLEDSSLKILDRWIYGVSKNTFWSYFSQLQELCWEY	120	
		S L+N + +SAI EVYP +K +LE+ K + WIY K+ FW ++S +Q++ +Y		
Sbjct	61	SILINPNTTSAINFEVYPAPSSKQHLEERFSKWIHEWIYDTPKDDFEFYSLVQKVKDY	120	
Query	121	YDYSNKLCKDAVLNKKLMMKLQESKFDVILADALNPCGELLAELFNIPFLYSLRFSVGYT	180	
		D +LC++ VLNKKLMMKL ESKFDV+LADA+ PCGELLAEL IPF+Y+LRF+ GYT		
Sbjct	121	SDTIEQLCRNVVLNKKLMMKLHESKFDVVLADAVGPCGELLAELLKIPFVYTLRFTFGYT	180	
Query	181	FEKNGGGFLFPPSYVPVVMSELSQDMIFMERIKNMIHMLYFDFWFQIYDLKKWDQFYSEV	240	
		+EK GG PPSYVP+VMSELSQDM FMER+KN ++MLYFDFWFQI+D+K+W+QFYSEV		
Sbjct	181	YEKYSGLTVPPSYVPIVMSELSQDMTFMERVKNTVYMLYFDFWFQIFDVKRWNQFYSEV	240	
Query	241	LGRPTTLFETMGKAEMWLIRTYWDFEFPRPFLPNVDFVGGGLHCKPAKPLPKEMEETFVQSS	300	
		LGRPTT++ETMGKA+ WLIRTYWD EFPRP LPN DFVGGGLHCKPAKPLPKEMEETFVQSS		
Sbjct	241	LGRPTTIYETMGKADFWLIRTYWDLEFPRPLLPNDFVGGGLHCKPAKPLPKEMEETFVQSS	300	
Query	301	GENGIVVFSLSGSMISNMSEESANMIASALAQIPQKVLWRFDGKKPNTLGSNTRLYKWLPQ	360	
		GENGIVVFSLG+M+SNM EE ANMIA ALAQIPQKV+WRF+GKKP+ LG NT++Y+W+PQ		
Sbjct	301	GENGIVVFSLGTVMVSNMPEEKANMIAFALAQIPQKVIWRFNKGKPKDKLPNTQIYEWIPQ	360	
Query	361	NDLLGHPKTKAFITHGGTNGIYEAIYHGIPMVGIPFLFADQHDNIAHMKAKGAALSVDIRT	420	
		NDLLGHPKTKAFITHGGTNG+YEAIYHG+PMVGIPFLFADQ DNIAH+KAKGAA+ +D R		
Sbjct	361	NDLLGHPKTKAFITHGGTNGVYEAIYHGVPMVGIPFLFADQPDNIAHVAKAKGAIRLDYRI	420	
Query	421	MSSRDLLNALKSVINDPVYKENVMKLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVA	480	
		++S DLL AL+ VINDP YKEN M+LSRI HDQP+KPLDRAVFWIEFVMRHKGAKHL+VA		
Sbjct	421	LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA	480	
Query	481	AHNLTWIIQYHSLDVIAFLLACVATVIFIITKFLCFRKLAKKGKKKKRD	530	
		AH+L+W QY+SLDVI FLLACVATV+FII+K CLFCF+ K GKK+KR+		
Sbjct	481	AHDLWFQYYSLDVIGFLLACVATVMFIISKCLFCFQMFCKTGKKEKRE	530	



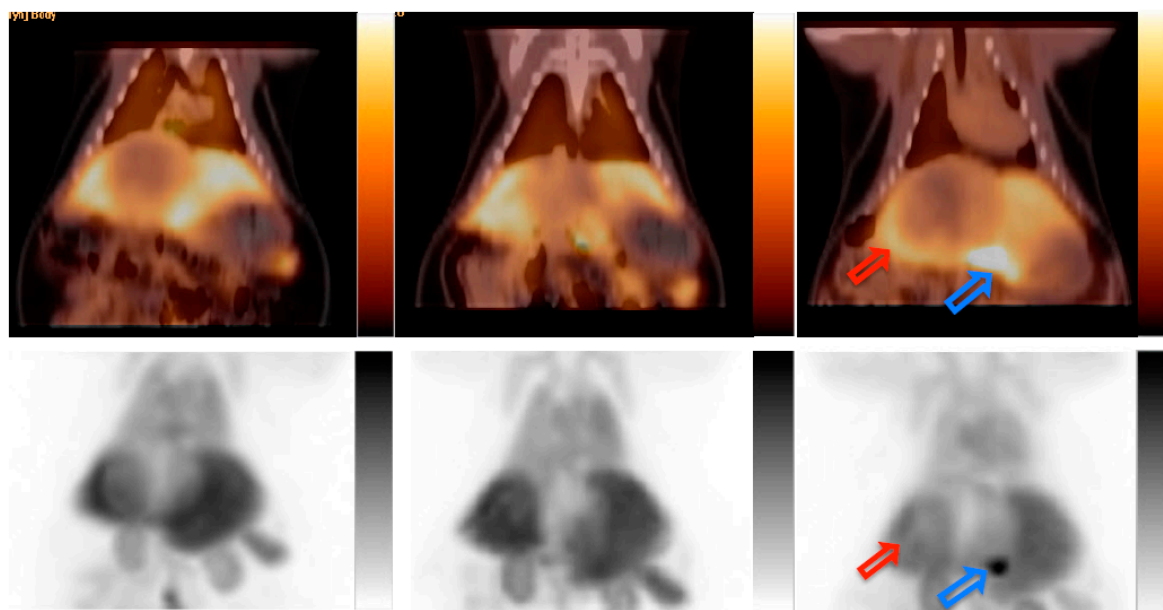


Animal C: In this animal, liver background uptake is much higher than tumor uptake. Only after cold CFA application, the uptake around the tumor rim (red arrow) can be perceived. Gallbladder (GB, yellow arrow) is clearly displayed from the PET/CT overlay and MIP (yellow arrow) with cold CFA application, which can be weakly identified from the middle panel with probenecid application.

**Figure S2.** Three-way comparison of  $[^{18}\text{F}]$ CFA uptake in tumor (red arrow) and liver. From the left: baseline, post UGT inhibitor probenecid application, and after cold CFA application. In each column, the upper panel is PET/CT overlay while the lower panel is the maximal intensity projection (MIP).



Animal D: Right column: Gallbladder (GB, yellow arrow) can be discerned from the image after cold CFA application. Cold CFA application also caused strong intestinal accumulation (blue arrow).



Animal E: The tumor's uptake in the proliferative rim (red arrow) with no GB but intestinal accumulation.

**Figure S3.** Three-way comparison of  $[^{18}\text{F}]\text{CFA}$  uptake in tumor (red arrow) and liver. From the left: baseline, post PNP inhibitor forodesine application, and after cold CFA application. In each column, the upper panel is PET/CT overlay while the lower panel is the maximal intensity projection (MIP).