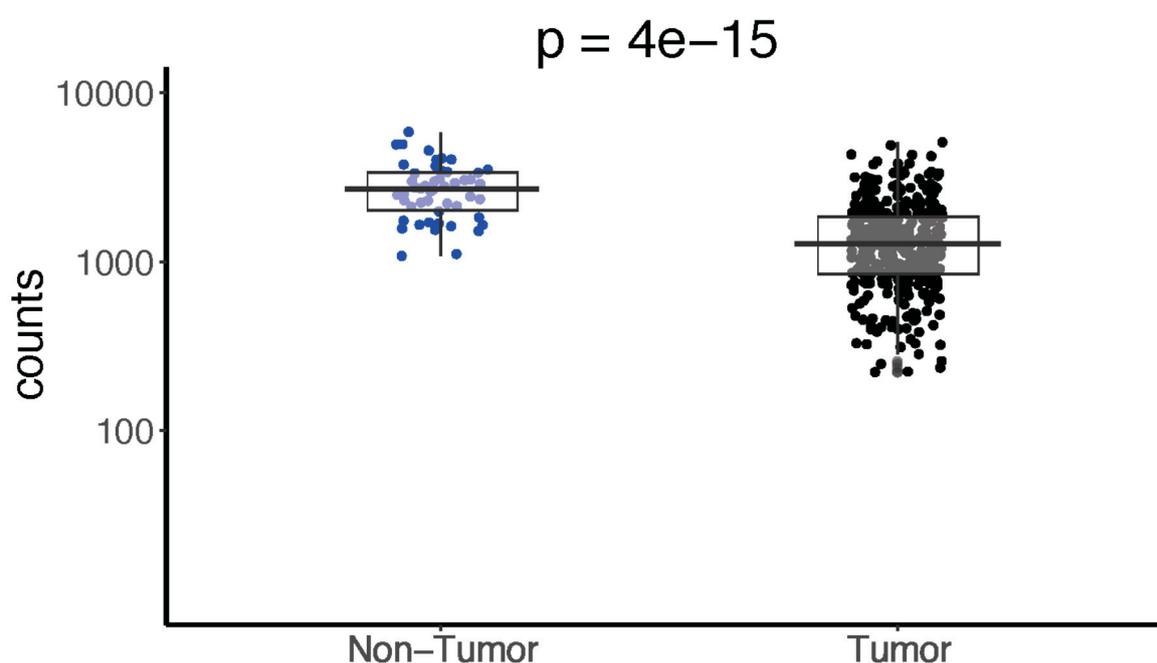
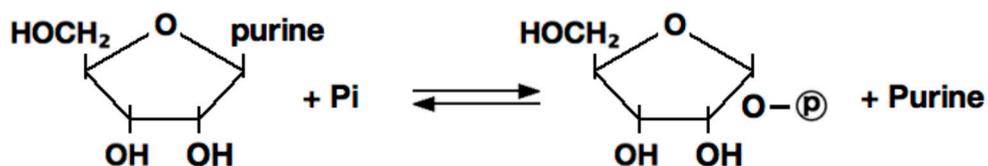


Supplementary Materials: [¹⁸F] Clofarabine for PET Imaging of Hepatocellular Carcinoma

Purine-nucleoside: orthophosphate ribosyltransferase (EC 2.4.2.1) ^{1,2)}



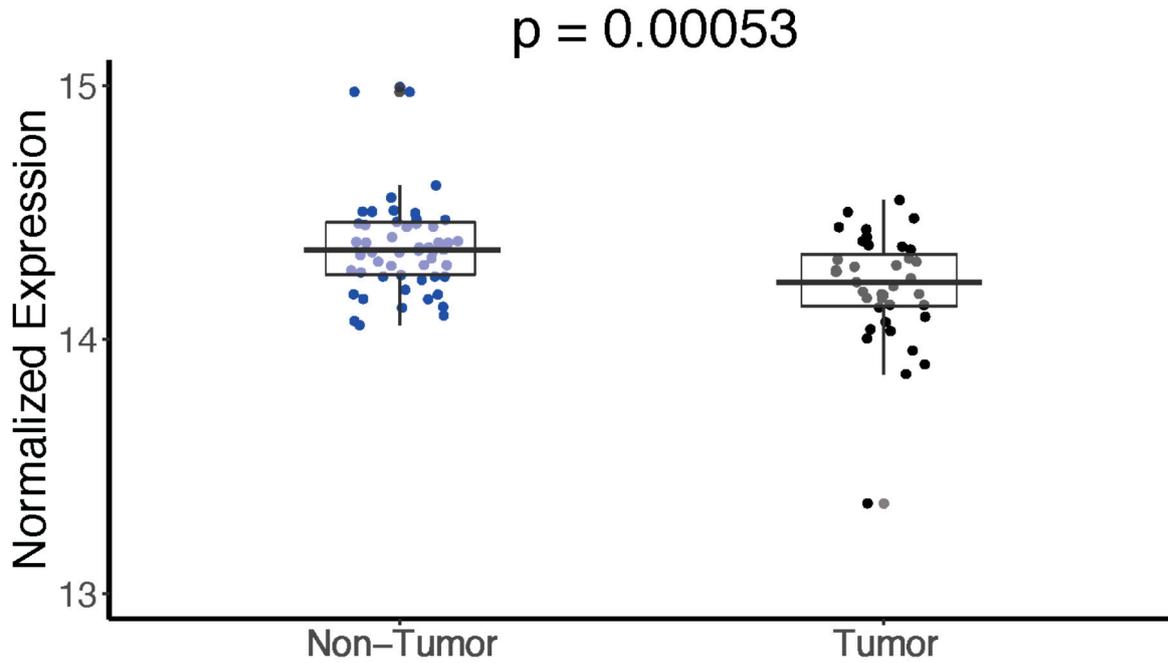


Figure S1. PNP levels in the liver. PNP has a significantly higher expression, in terms of the base main counts in either RNA-seq (human) or microarray (woodchuck) data, in the liver parenchyma than in HCC for human and woodchuck. The enzyme works reversibly in both directions.

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	MENGYTYEDYKNTAEWLLSHTKHRPQVAIICGSGLGGLTDKLTQAQIFDYGEIPNFPST	60
Sbjct 1	MEN +TYEDY+ TAEWLLS TKHRPQVA+ICGSGLGGLT+KLT+AQ FDY EIPNFP+ST	60
Query 61	VPGHAGRLVFGFLNGRACVMMQGRFHMIEGYPLWKVTFPVRVFLHLLGVDTLVVTNAAGGL	120
Sbjct 61	VPGHAGRLVFGFLN +ACVMMQGRFH YEGYPLWKVTFPVRVFLHLLGVDTLVVTNAAGGL	120
Query 121	NPKFEVGDIMLIRDHINLPGFSGQNPLRGPNDERFGDRFPAMSDAYDRMTMRQALSTWKQ	180
Sbjct 121	NP F+VGDIMLIRDHINLPG GQNPL+GPNDERFG RFPAMSDAYDR MR++ALSTWK	180
Query 181	MGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSL	240
Sbjct 181	MGENRELQEGTYVMVAGPSFETVAE 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	TTSHQPQDRYKAVWLIFFFMLGGLTLLPWNFFMTATQYFTNRLDMSQNVSLVTAELSKDAQ	61	
Sbjct	77	TTSHQPQDRYKAVWLIFFFMLGGLTLLPWNFFMTAT+YFTNRLDMSQNVSL A LSKD Q	136	
Query	62	ASAAPAAPLPERNSLSAIFNVMTLCAMPLLLFTYLNSFLHQRIPOSVRILGSLVAILL	121	
Sbjct	137	DPAVPTAPLPEQRSLSAIFNVMTLCAMPLLLF+ LNSFLHQRIPOSVRILGSLVAILL	196	
Query	122	VFLITAILVKVQLDALPFFVITMIKIVLINSFGAILQGSFLGGLAGLLPASYPIMSGQG	181	
Sbjct	197	VFL+TAILVKVQLDALPFFV TMIKI+LINSFGAILQGSFLGGLAGLLPA+YTAPIMSGQG	256	
Query	182	LAGFFASVAMICAIASGSELSESAFGYFITACAVIILTIICYLGLPRLEFYRYQQQKLE	241	
Sbjct	257	LAGL FASVAMICAIASGSELSESAFGYFITAC V+IL IICYLGLPRLEFYRYQQQKLE	316	
Query	242	GPGEQETKLDLISK-----GEEPRAGKEESGVSVSNSOPTNESHSIKAILKNISVL	292	
Sbjct	317	GPGEQETKLDLISK GEEPR KEESGV NSQ T+ + SI+AILKNISVL	376	
Query	293	AFSVCFIPTITIGMFPVAVTVEVKSSIAGSSTWERYFIPVSCFLTFNIFDWLGRSLTAVFM	352	
Sbjct	377	ALSVCNFTVTIGLFPVAVTAEVKSSIAGTSAWGDYFIPVSCFLTFNIFDWLGRSLTAVFM	436	
Query	353	WPGKDSRWLPSLVLARLVFVPLLLLCNPKPRRYLTVVFEHDAWFIFMAAFASNGYLAS	412	
Sbjct	437	WPGKDS WLPVSLV+ARLVFVPLLLLCN+ PRRYL VVF+HDAW+IFFMAAFASNGYLAS	496	
Query	413	LCMCFGPKKVKPAAEETAGAIMAFFLCLGLALGAVFSFLFRAIV	456	
Sbjct	497	LCMCFGPKKVKPAAEETAGAIM 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	MSPGPPFSITMASVCFINSFSAVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALAMLL	180	
		MSPGPPFSITM SV FINSF AVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALAML+		
Sbjct	1	MSPGPPFSITMVSVWFINSFCAVLQGSILFGQLGTMPTSTYTLFLSGQGLAGIFAALMLM	60	
Query	181	SMASGVDAETSALGYFITPCVGIILMSIVCYLSLPHLKFARYYLANKSSQAQAQAELETKAE	240	
		SMASGVDA+TSALGYFITPCVGIILMSIVCYLSLPHL+FAARYLA K S++ ELETKAE		
Sbjct	61	SMASGVDAQTSALGYFITPCVGIILMSIVCYLSLPHLEFARYYLAKKPSRSPHELETKAE	120	
Query	241	LLQSDE-NGIPSSPQKVALTLDDLLEKEPESEPDEP--QKPGKPSVFTVFQKIWLTALCL	297	
		LLQ+DE NGIPSSPQ LTLDDL EKEPE EP+ QK KPSVF VFQKIWLTALCL		
Sbjct	121	LLQADEKNGIPSSPQVATLTLDDLLEKEPELEPELDEPQKLEKPSVFIVFQKIWLTALCL	180	
Query	298	VLVFTVTLVSVFPAITAMVTSSTSPGKWSQFFNPICCFLLFNIMDWLGRSLTSYFLWPDED	357	
		VLVFTVTLVSVFPAITAMVTSSTSPGKWSQFFNPICCFLLFN+MDWLGRSLTSYFLWPDED		
Sbjct	181	VLVFTVTLVSVFPAITAMVTSSTSPGKWSQFFNPICCFLLFNMDWLGRSLTSYFLWPDED	240	
Query	358	SRLPLLVCLRFLFVPLFMLCHVPQRSRLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL	417	
		SRLPLLVCLRFLFVPLFMLCHVP+R+RLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL		
Sbjct	241	SRLPLLVCLRFLFVPLFMLCHVPERARLPILFPQDAYFITFMLLFAVSNGYLVSLTMCL	300	
Query	418	APRQVLPHHEREVAGALMTFFLALGLSCGASLSFLFKALL	456	
		APRQVLPHHEREVAGALMTFFLALGLSCGASLSFLFKALL		
Sbjct	301	APRQVLPHHEREVAGALMTFFLALGLSCGASLSFLFKALL	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	MAVESQGG RPLVLG LLLC VLG P VVSHAG KILLIPVDG SHWLSMLG AIQQLQ ORGHEIVVL	60
Sbjct 1	MAV SQG L+L G LLLC V L P +SHA K+L+IPVDG SHWLSM+G IQQLQ+RGHE+VV+	60
Query 61	APDASLYIRDGAFYTLKTYVPV FQREDVKESFVSLGHNVFENDSFLQ RVIKTYKKIKKDS	120
Sbjct 61	P+AS++I++ +FY+LK YPV FQ+EDV+ SF LG FEN FLQ V K Y+K +KDS	120
Query 121	AMLLSGCSHLLHNKELMASLAESSFDV MLTDPFLPCSPIVAQYLSLPTVFFLHALPCSLE	180
Sbjct 121	A+LLSGCSHLLHNKE MASL ES FD +LTD PFLPC IVAQYL LP V FL+ALPC L+	180
Query 181	FEATQCPNPF SYVPRPLSSHSDHMTFLQ RVKNM LIAFSQNF LCDVVYSPYATLASEFLQR	240
Sbjct 181	+ATQCP+P SYVPR LSS+SDHMTFLQ RVKNM LIA +NFLC +VYSPYA LAS+ LQR	240
Query 241	EVTVQDLLSSASVWLFRSDFVKDYPRPIMP NMV FVGGINCLHQ NPLSQEF EAYINASGEH	300
Sbjct 241	++T+QDLLSSASVWL R DFVKDYP PIMP NMV FVGGINCLH P+SQEF EAY+NASGEH	300
Query 301	GIVV FSLGSMVSEIPEKKAMAIADALGKIPQTVLWRYTGT RPSNL ANNTILVKWLPQNDL	360
Sbjct 301	GIVV FSLGSMVSEIPEKKAM IADALG+IPQTVLWRYTGT PSNLA NT LVKWLPQNDL	360
Query 361	LGHPMTRAFITHAGSHGVYESICNGVPMVM MP LFGDQMDNAKRMETKGAGVTLNVLEMTS	420
Sbjct 361	LGHPKTRAFITHAGSHGVYEGICNGVPMVM MP LFGDQMDNAKRMETRGAGVTLNVLEMTS	420
Query 421	EDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPA AHD	480
Sbjct 421	+DL NALKAVINDKSYKENIMRLS LHKDRP+EPLDLAVFWVEFVMRHKGAPHLRPA AHD	480
Query 481	LTWYQYHSLDVIGFLLAVVLTVA FIFTKCCAYGYR KCLGKKGRVKKAHKSKTH	533
Sbjct 481	LTWYQYHSLDVIGFLLA+VL VAFI FKCCAYG RKC GKKG VKK HSK H	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
Sbjct 10	LPLCVCLLL A+AGKLLVVPMDGSHWFTMRSVVEKL+ RG+EVV VMPEVSWQLG+S	69
Query 70	LNCTVKTYSTSYTLEDLDREFKAFAHAQWKAQVRSIYSLLMGSYNDIFDLFFSNCRSLFK	129
Sbjct 70	LNFTVKTYSTSYTLEDLDLDRGFFVDTQWKTPQSMYSAAMGSSKAFFDITFSRCRSLFN	129
Query 130	DKKLVEYLKESFSDAVFLDPDNCGLIVAKYFSLPSVVFARGILCHYLEEGAQCPAPLSY	189
Sbjct 130	DKKLVEYLKESFSDAVFLDPD CGL+VAKYFSLPSVVFAR + C++LE+GAQCP+PLSY	189
Query 190	VPRILLGFSDAMTFKERVNRNIMHLEEHLLCHRFFKNALEIASEILQTPVTEYDLYSHTS	249
Sbjct 190	VPRVFLMSSDALSFMERIRNHLNLYEYLFQPYFFQTALEVASEILRTPVTIGDLFSQIS	249
Query 250	IWLLRTDFVLDYPKVMPNMIFIGGINCHQKPLPMEFEAYINASGEHGIVVFSLGSMVS	309
Sbjct 250	IWLLRTDFVLEYPVMPNMIF+GGINCHQ KPLP EFEAY+NASGEHGIVVFSLGSMVS	309
Query 310	EIPEKKAMAIADALGKIPQTVLWRYTGTRPSNLANNITLVKWLQPNDLLGHPMTRAFITH	369
Sbjct 310	EIPEKKAMEIADALGRIPQTVLWRYTGTPPSNLAKNTKLVKWLQPNDLLGHPKTRAFITH	369
Query 370	AGSHGVYESICNGVPMVMMPFLFGDQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVIN	429
Sbjct 370	AGSHGVYE ICNGVPMVMMPFLFGDQMDNAKRMET+GAGVTLNVLEMTS+DL NALKAVIN	429
Query 430	DKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI	489
Sbjct 430	DKSYKENIMRLSRLHKDRPIEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI	489
Query 490	GFLLAIVLTVAFITFKCCAYGRKCLGKKGRVKKAHKSKTH 530	
Sbjct 490	GFLLAIVLTVAFI AFKCCAYGRKCFGKKGSVKKGHKSKAH 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	MAKADIWLIRNYWDFQFPHPLLPNVEFVGGHLHCKPAKPLPKEMEEFVQSSGENGVVVFSL	309
Sbjct 1	MAKADIWLI YWD +F H LPNV+ VGGLHC+PAK LP	40
Query 310	GSMVNTSEERANVIASALAKIPQKVLWRFVGNKPDTLGLNTRLYKWIPQNDLLG	364
Sbjct 41	-----KILWRFVGNKPDTLGLNIQLYKWIPKGDLLG	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]

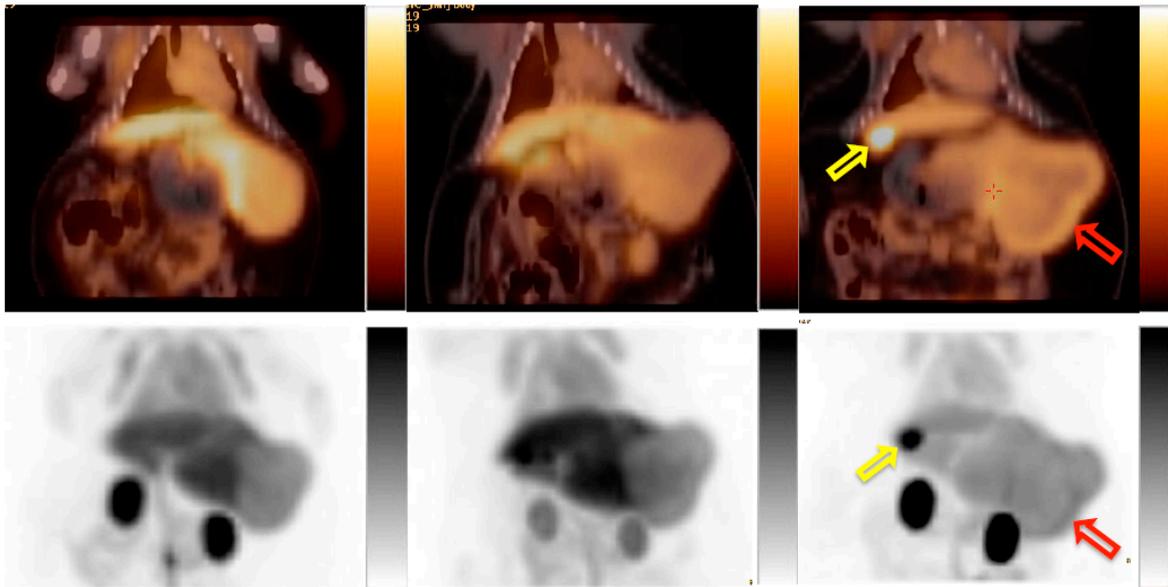
Identities	Positives	Gaps
388/530 (73%)	455/530 (85%)	2/530 (0%)
Query 1	MSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSHWMNIKTILDELVQRGHEVTVLASSA	60
	MS+K S LLLIQL CYFSSGSCGKVLVWPTE+SHW+NIK ILDEL+QRGHEVTVL S+A	
Sbjct 1	MSVKRNSVLLLIQLMICYFSSGSCGKVLVWPTEYSHWINIKAILDELLQRGHEVTVLSTA	60
Query 61	SISFDPNPSTLKFVYVPSLTKTEFEDIKQLVKRWA-ELPKDTFWSYFSQVQEIMWTF	119
	SI +PN+ S + FEVYP +K E+ + + W + PKD FW ++S VQ++ +	
Sbjct 61	SILINPNTTSAINFEVYPAPSSKQHLERFSKWIHEWIYDTPKDDFWEFYSLVQKVFVDY	120
Query 120	NDILRKFKCDIVSNKKLMMKQLQESRFDVVLADAVFPFGELLAELLKIPFVYSLRFSPTYA	179
	+D + + C+++V NKKLM KL ES+FDVVLADAV P GELLAELLKIPFVY+LRF+ GY	
Sbjct 121	SDTIEQLCRNVVLNKKLMMKLLHESKFDVVLADAVGPCGELLAELLKIPFVYTLRFTFYGT	180
Query 180	IEKHSGLLFPSPYVPMVSELSQMTFIERVKNMIYVLYFEFQIFDMKKWDQFYSEV	239
	EK+SGGL PPSYVP+VMSELSQMTF+ERVKN +Y+LYF+FWFQIFD+K+W+QFYSEV	
Sbjct 181	YEKYSGLTVPPSYVPIVMSELSQMTFMERVKNTVYMLYDFWFQIFDVKRWNQFYSEV	240
Query 240	LGRPTTLSETMAKADIWLIRNYWDFQFPHPLLPNVEFVGGHLHCKPAKPLPKEMEEFVQSS	299
	LGRPTT+ ETM KAD WLIR YWD +FP PLLPN +FVGGHLHCKPAKPLPKEMEEFVQSS	
Sbjct 241	LGRPTTIYETMGKADFWLIRTYWDFPRPLLPNDFVGGHLHCKPAKPLPKEMEEFVQSS	300
Query 300	GENGVVVFSLGSMVSNSTSEERANVIASALAKIPQKVLWRFDGNKPDTLGLNTRLYKWIPQ	359
	GENG+VVVSLG+MVSN EE+AN+IA ALA+IPQKV+WRF+G KPD LG NT++Y+WIPQ	
Sbjct 301	GENGIVVVFSLGTMVSNMPEEKANMIAFALAQIPQKVIWRFNGKPKDCLGPNTQIYEWIPQ	360
Query 360	NDLLGHPKTRAFITHGGANGIYEAIYHGIPVMGVPLFADQPDNIAHMKAGAAVSLDFHT	419
	NDLLGHPKT+AFITHGG NG+YEAIYHG+PMVG+PLFADQPDNIAH+KAKGAA+ LD+	
Sbjct 361	NDLLGHPKTKAFITHGGTNGVYEAIYHGVPVMGIPFADQPDNIAHVAKAGAAIRLDYRI	420
Query 420	MSSTDLLNALKTVINDPLYKENAMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA	479
	++S DLL AL+ VINDP YKENAM+LSRI HDQPVKPLDRAVFWIEFVMRHKGAKHL+VA	
Sbjct 421	LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA	480
Query 480	AHDLTWFQYHSLDVTGFLACVATVIFIIITK-CLFCVWKFVRTGKKGKRD 528	
	AHDL+WFQY+SLDV GFLACVATV+FII+K CLFC F +TGKK KR+	
Sbjct 481	AHDLSWFQYHSLDVIGFLACVATVMFIIISKCCCLFCFQMFVKTKGKKEKRE 530	

8. UGT2B15 alignment

Query: NCBI Reference Sequence: NP_001067.2; UDP-glucuronosyltransferase 2B15 precursor [Homo sapiens]

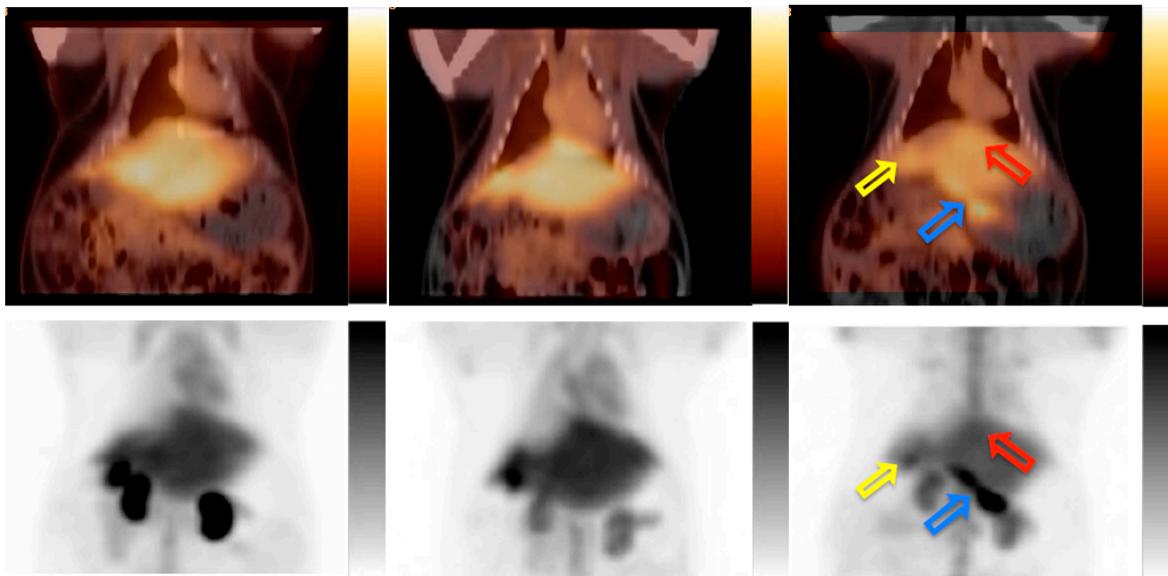
Sbjct: NCBI Reference Sequence: XP_015360783.1; PREDICTED: UDP-glucuronosyltransferase 2B15-like [Marmota marmota marmota]

Identities	Positives	Gaps
392/530 (74%)	459/530 (86%)	0/530 (0%)
Query 1	MSLKWTSVFLLIQLSCYFSSGSCGKVLVWPTEYSHWINMKTILEELVQRCHEVTVLTSSA	60
Sbjct 1	MS+K SV LLIQL CYFSSGSCGKVLVWPTEYSHWIN+K IL+EL+QRCHEVTVLTS+A	60
Query 61	MSVKNRSVLLLIQLMCFSSGSCGKVLVWPTEYSHWINIKAILDELLQRCHEVTVLTSTA	60
Sbjct 61	MSVKNRSVLLLIQLMCFSSGSCGKVLVWPTEYSHWINIKAILDELLQRCHEVTVLTSTA	60
Query 121	STLVNASKSSAIKLEVYPTSLTKNYLEDSELLKILDRWIYGVSKNTFWSYFSQLQELCWEY	120
Sbjct 121	S L+N + +SAI EVYP +K +LE+ K + WIY K+ FW ++S +Q++ +Y	120
Query 181	SILINPNTTSAINFEVYPAPSSKQHLERFSKWIHEWIYDTPKDDFWFYSLVQVKFKDY	120
Sbjct 181	SILINPNTTSAINFEVYPAPSSKQHLERFSKWIHEWIYDTPKDDFWFYSLVQVKFKDY	120
Query 241	YDYSNKLCKDAVLNKKLMMKLQESKFDVILADALNPCGELLAELFNIPFLYSLRFSVGYT	180
Sbjct 241	D +LC++ VLNKKLMMKL ESKFDV+LADA+ PCGELLAEL IPF+Y+LRF+ GYT	180
Query 301	SDTIEQLCRNVVLNKKLMMKLHESKFDVVLDADAVGPCGELLAELLKIPFVYTLRFTFGYT	180
Sbjct 301	SDTIEQLCRNVVLNKKLMMKLHESKFDVVLDADAVGPCGELLAELLKIPFVYTLRFTFGYT	180
Query 361	FEKNGGGFLFPPSYVPPVVMSELSQDMIFMERIKNMIHMLYFDFWFQIYDLKKWDQFYSEV	240
Sbjct 361	+EK GG PPSYVP+VMSELSQDM FMER+KN ++MLYFDFWFQI+D+K+W+QFYSEV	240
Query 421	YEKYSGLTVPPSYVPIVMSELSQDMTFMERVKNTVYMLYFDFWFQIFDVKRWNQFYSEV	240
Sbjct 421	YEKYSGLTVPPSYVPIVMSELSQDMTFMERVKNTVYMLYFDFWFQIFDVKRWNQFYSEV	240
Query 481	LGRPTTLFETMGKAEMWLIRTYWDFEFPFPLPNVDFVGGGLHCKPAKPLPKEMEEFVQSS	300
Sbjct 481	LGRPTT++ETMGKA+ WLIRTYWD EFPFPLPN DFVGGGLHCKPAKPLPKEMEEFVQSS	300
Query 541	LGRPTTIYETMGKADFWLIRTYWDFEFPFPLPNVDFVGGGLHCKPAKPLPKEMEEFVQSS	300
Sbjct 541	LGRPTTIYETMGKADFWLIRTYWDFEFPFPLPNVDFVGGGLHCKPAKPLPKEMEEFVQSS	300
Query 601	GENGIVVFSLSGSMISNMSEESANMIASALAQIPQKVLWRFDGKKPNTLGSNTRLYKWLPO	360
Sbjct 601	GENGIVVFSLSG+M+SNM EE ANMIA ALAQIPQKV+WRF+GKKP+ LG NT++Y+W+PQ	360
Query 661	GENGIVVFSLGTVMVSNMPEEKANMIAFALAQIPQKVIWRFNGKPKDKLGPNTQIYEWIPQ	360
Sbjct 661	GENGIVVFSLGTVMVSNMPEEKANMIAFALAQIPQKVIWRFNGKPKDKLGPNTQIYEWIPQ	360
Query 721	NDLLGHPKTKAFITHGGTNGIYEAIYHGIPMVGIPLFADQHDNIAHMKAKGAALSVDIRT	420
Sbjct 721	NDLLGHPKTKAFITHGGTNG+YEAIYHG+PMVGIPLFADQ DNIAH+KAKGAA+ +D R	420
Query 781	NDLLGHPKTKAFITHGGTNGVYEAIYHGVPMVGIPLFADQPDNIAHVKAKGAAIRLDYRI	420
Sbjct 781	NDLLGHPKTKAFITHGGTNGVYEAIYHGVPMVGIPLFADQPDNIAHVKAKGAAIRLDYRI	420
Query 841	MSSRDLLNALKSVINDPVYKENVMKLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVA	480
Sbjct 841	++S DLL AL+ VINDP YKEN M+LSRI HDQP+KPLDRAVFWIEFVMRHKGAKHL+VA	480
Query 901	LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA	480
Sbjct 901	LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA	480
Query 961	AHNLTWIIQYHSLDVIAFLLACVATVIFIIITKFLCFRKLAKKGKKKKRD	530
Sbjct 961	AH+L+W QY+SLDVI FLLACVATV+FII+K CLFCF+ K GKK+KR+	530
Query 1021	AHDLWFQYYSLDVIGFLLACVATVMFIIISKCLFCFQMFVKTKGKKEKRE	530
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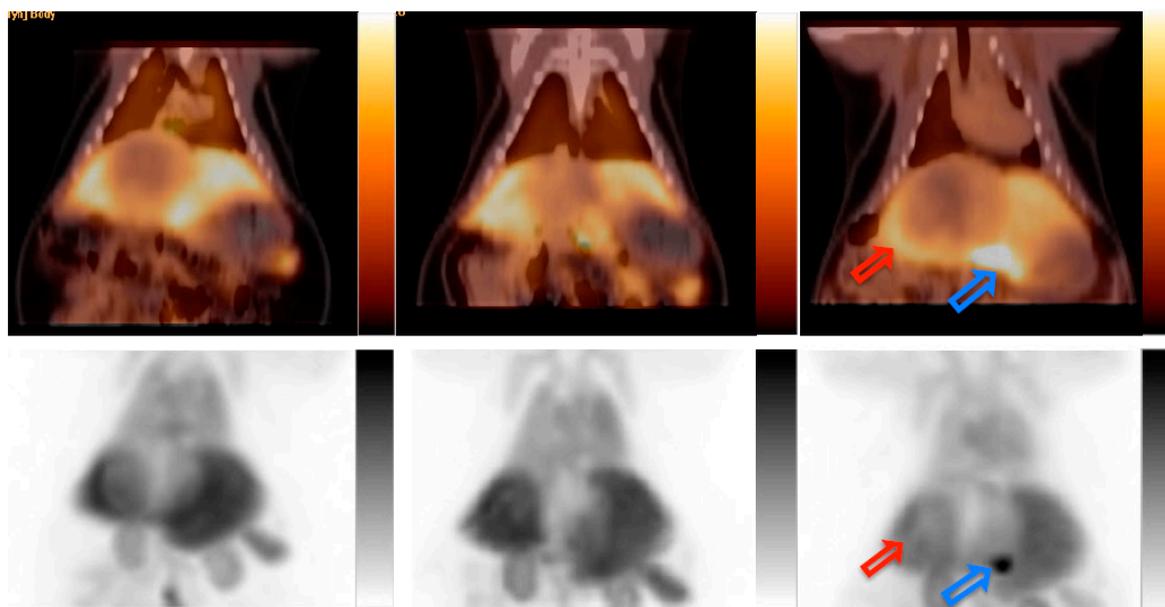


Animal C: In this animal, liver background uptake is much higher than tumor uptake. Only after cold CFA application, the uptake around the tumor rim (red arrow) can be perceived. Gallbladder (GB, yellow arrow) is clearly displayed from the PET/CT overlay and MIP (yellow arrow) with cold CFA application,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

Figure S2. Three-way comparison of $[^{18}\text{F}]\text{CFA}$ 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).