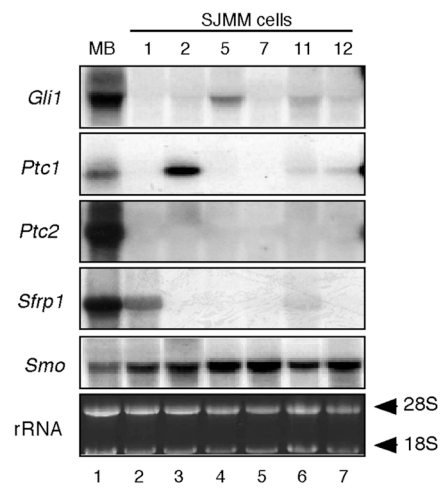


Supplemental Figure S1. Expression of Shh pathway genes in cultured medulloblastoma cells. Total RNA (10 μ g) was analyzed by northern blotting using antisense probes for *Gli1*, *Ptc1*, *Ptc2*, *Sfrp1* and *Smo* as indicated. Ethidium bromide staining of the 28S and 18S rRNA is shown as a loading control. MB, medulloblastoma from *Ptc1*^{+/-} mouse.

Supplemental Figure S1

CAN_05_4505
K Sasai et al.



Supplemental Table 1. The gene expression profiles of 18 samples (4 medulloblastoma tumors, 4 medulloblastoma cell cultures, 7 culture derived allografts and 3 direct allografts) were analyzed by cDNA microarray analyses. After normalization, each dataset was compared with all other samples. To identify changes in gene expression for each comparison, the numbers of probe sets scored as overexpressed (log ratio >1) and underexpressed (log ratio <1) were counted. The ratios of differentially expressed probe sets (including both over expressed and underexpressed probe sets) were also shown. Similar ratios (13-19%) of probe sets were differentially expressed in all “tumor versus direct allograft” comparisons (highlighted cells), and these ratios were similar to those of “tumor versus tumor” comparisons (17-21%).

Supplemental Table 1

3612 4129	4978 3419	2538 3368	3558 3306	10892 6814	10370 6552	10164 7812	10772 6905	7986 9497	8215 7810	7652 7851	6677 6005	6228 6176	7152 10393	6687 9650	2545 5599	4811 3692	direct allograft 21
3256 4867	4151 3668	3365 5229	3120 2989	10351 6894	9557 6448	9452 7632	9918 6627	7291 9337	7630 7849	7192 7986	7298 7132	7399 7572	6334 10072	5994 9468	3484 7261	direct allograft 21	18.9%
4812 2641	4173 3943	5093 3232	4652 3810	12960 6367	12572 6205	11986 6903	12858 6375	9096 7704	10143 6926	9379 6780	9328 5431	9437 5735	7800 7895	7466 7496	direct allograft 2	23.8%	18.1%
8641 6840	10290 6152	8525 6494	8766 6079	12698 6133	12190 6021	11108 6034	12367 5731	8125 6544	9568 6255	8843 6106	10582 6500	11335 6825	4791 4803	SJMM-12 allograft	33.2%	34.3%	36.2%
9340 7331	11056 6590	9249 6891	9565 6496	13164 6623	12722 6545	11613 6623	12907 6268	8653 7075	10322 6812	9733 6709	11293 6939	12028 7329	SJMM-12 allograft	21.3%	34.8%	36.4%	38.9%
7007 8444	7418 6627	6011 7238	7043 7609	9893 6942	9733 7257	9328 8212	9988 7573	7122 10110	7315 7827	6632 7606	3814 3287	SJMM-2 allograft	42.9%	40.3%	33.6%	33.2%	27.5%
6616 8333	7347 6877	5741 7374	6460 7257	9999 6979	9512 6881	9220 7914	9981 7152	6527 9255	7015 7571	6326 7299	SJMM-2 allograft	15.7%	40.4%	37.9%	32.7%	32.0%	28.1%
7428 8266	8453 6870	7356 8069	7406 7145	9124 4861	9011 5143	8575 5867	9193 5159	4316 5615	5203 4445	SJMM-1 allograft	30.2%	31.6%	36.5%	33.1%	35.8%	33.7%	34.4%
7577 9032	8212 7231	7454 8802	7196 7542	8753 5184	8371 5049	8082 6180	8530 5072	4607 6652	SJMM-1 allograft	21.4%	32.3%	33.6%	38.0%	35.1%	37.8%	34.3%	35.5%
8830 8460	9885 7034	8949 8244	8626 7126	10559 4845	10062 4762	9437 5655	10419 4848	SJMM-1 allograft	25.0%	22.0%	35.0%	38.2%	34.9%	32.5%	37.2%	36.9%	38.8%
6654 11529	6594 9282	6650 11193	6025 9938	6631 6238	6260 6340	4864 6229	SJMM-12 cells	33.9%	30.2%	31.8%	38.0%	38.9%	42.5%	40.1%	42.6%	36.7%	39.2%
7371 10848	7602 8994	7406 10628	7018 9516	7628 5885	7408 6312	SJMM-12 cells	24.6%	33.5%	31.6%	32.0%	38.0%	38.9%	40.4%	38.0%	41.9%	37.9%	39.9%
6538 11270	6635 9261	6417 11054	6026 9743	5667 5276	SJMM-1 cells	30.4%	27.9%	32.9%	29.8%	31.4%	36.3%	37.7%	42.7%	40.4%	41.6%	35.5%	37.5%
6749 11776	6783 9728	6531 11454	6373 10434	SJMM-1 cells	24.3%	30.0%	28.5%	34.2%	30.9%	31.0%	37.6%	37.3%	43.9%	41.8%	42.9%	38.2%	39.3%
3867 4629	4663 3430	3816 4897	tumor-21	37.3%	35.0%	36.7%	35.4%	34.9%	32.7%	32.3%	30.4%	32.5%	35.6%	32.9%	18.8%	13.5%	15.2%
4053 3705	6115 3423	tumor-12	19.3%	39.9%	38.7%	40.0%	39.6%	38.1%	36.0%	34.2%	29.1%	29.4%	35.8%	33.3%	18.4%	19.1%	13.1%
3169 5541	tumor-2	21.1%	17.9%	36.6%	35.2%	36.8%	35.2%	37.5%	34.2%	34.0%	31.5%	31.1%	39.1%	36.5%	18.0%	17.3%	18.6%
tumor-1	19.3%	17.2%	18.8%	41.1%	39.5%	40.4%	40.3%	38.3%	36.8%	34.8%	33.1%	34.3%	37.0%	34.3%	16.5%	18.0%	17.2%

Number of B over A	B
Number of B under A	% of differentially expressed probe sets
A	

Supplemental Table 2

pathway	Total *	direct allograft			culture			culture-derived allograft		
		over tumor			over tumor			over culture		
		No. of probe sets			No. of probe sets			No. of probe sets		
		over	under	(ratio [†])	over	under	(ratio)	over	under	(ratio)
apoptosis	215	6	2	(3.7%)	30	33	(29%)	36	14	(23%)
cell cycle	202	3	9	(5.9%)	11	53	(32%)	16	20	(18%)
G protein	227	5	14	(8.4%)	23	60	(37%)	47	5	(23%)
integrin	245	7	3	(4.1%)	57	48	(43%)	41	26	(27%)
MAP kinase	91	2	9	(12%)	10	29	(43%)	14	2	(18%)
MMP	50	3	0	(6.0%)	27	7	(68%)	11	14	(50%)
TGF β	120	5	0	(4.2%)	34	7	(34%)	11	17	(23%)
Wnt	165	8	13	(13%)	24	37	(37%)	31	24	(33%)

The lists of pathway related genes were downloaded from the NETAFFX ANALYSIS CENTER website (<http://www.affymetrix.com/analysis>). The numbers of differentially overexpressed (log ratio >1) and underexpressed (log ratio <1) probe sets were counted for each comparison (direct allograft over tumor, culture over tumor, and culture-derived allograft over culture).

* Total number of probe sets in each gene list

[†] Ratio of differentially expressed probe sets (including both overexpressed and underexpressed probe sets)