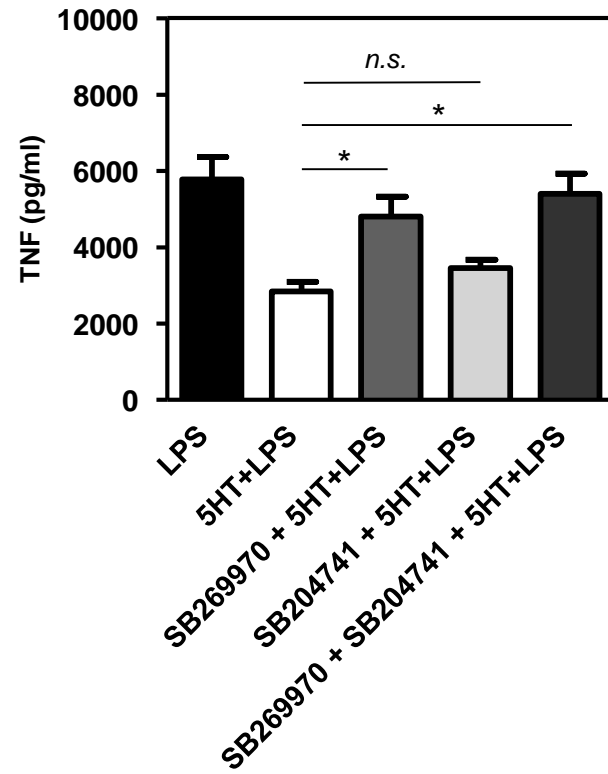


**Serotonin drives the acquisition of a profibrotic and anti-inflammatory gene profile through the 5-HT7R-PKA signaling axis**

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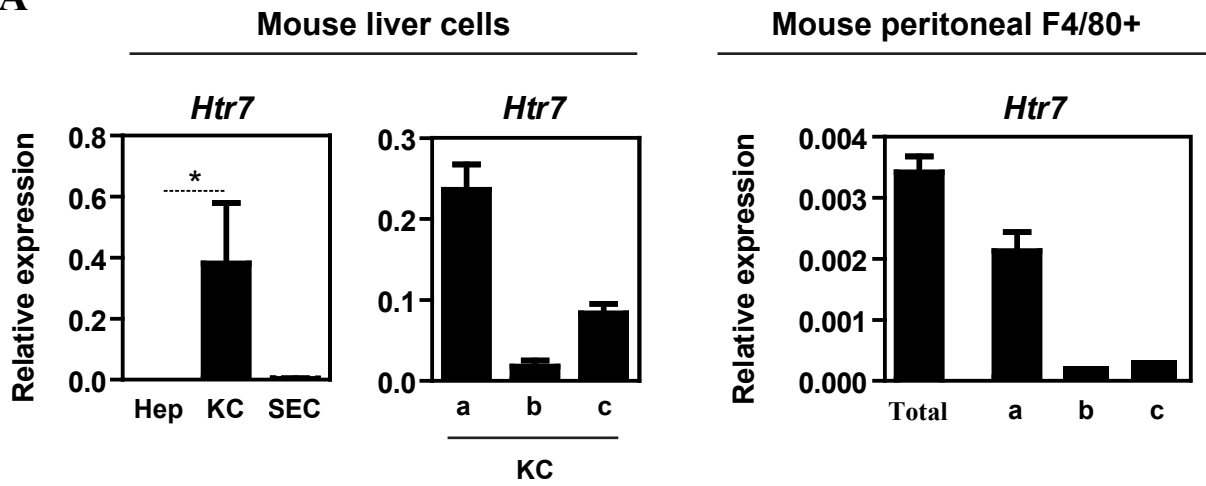
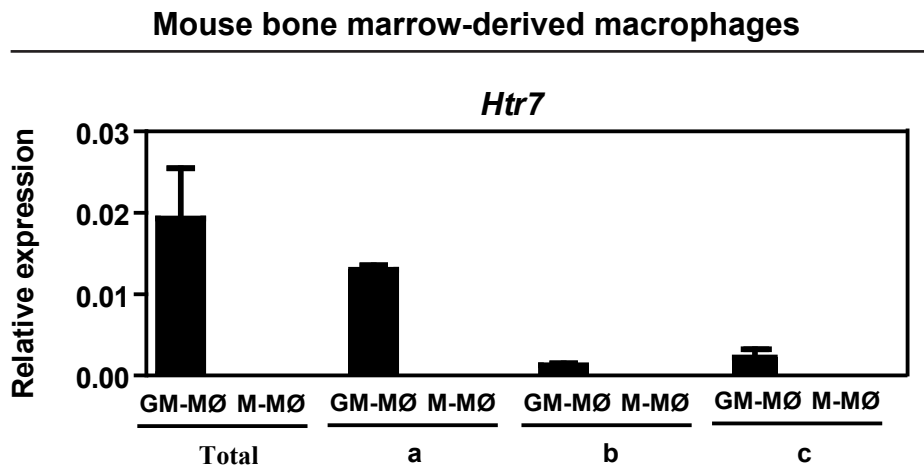
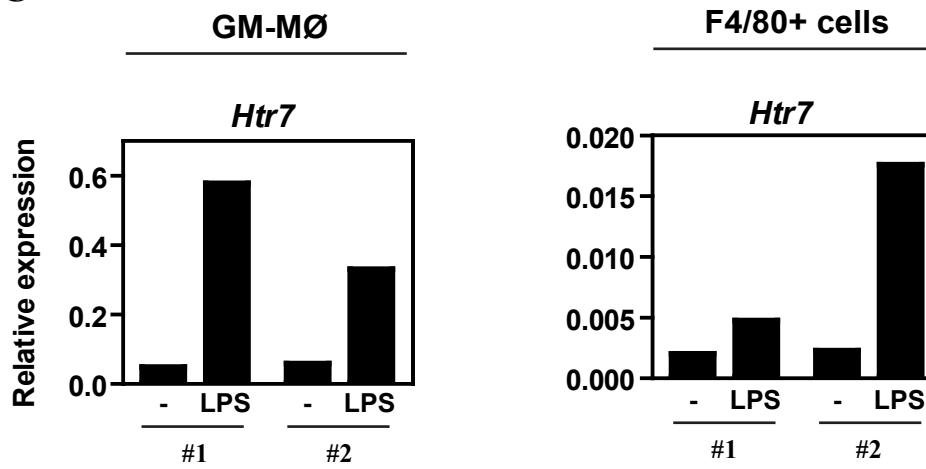


Supplementary Figure 1

<b>Upregulated</b>	<b>FDR q-val</b>
Hallmark Angiogenesis	0.129
Hallmark Hypoxia	0.2
Hallmark Inflammatory response	0.216
Hallmark DNA repair	0.228
Hallmark Glycolysis	0.238

<b>Downregulated</b>	<b>FDR q-val</b>
Hallmark Cholesterol homeostasis	0.0
Hallmark Fatty Acid metabolism	0.012
Hallmark Androgen response	0.015
Hallmark Oxydative phosphorylation	0.018
Hallmark mTORC1 signaling	0.103
Hallmark Myc targets	0.103
Hallmark Estrogen Response late	0.112

**Supplementary Figure 2**

**A****B****C****Supplementary Figure 3**

Supplementary Table I

probeid	M-MØ	M-MØ+5HT	log2.fold M-MØ+5HT/M-MØ	t	pval	adj.pval	genesymbol
A_23_P401106	154.79	2069.16	3.68	14.6249	0	0.192	PDE2A
A_23_P19333	80.05	344.74	2.08	16.5371	0	0.192	TREM1
A_24_P349547	218.04	750.66	1.97	9.8847	2.0000E-04	0.2138	
A_33_P3322288	101.13	372.80	1.95	9.6901	2.0000E-04	0.2138	AZI2
A_23_P68031	99.87	385.92	1.92	5.8015	0.0024	0.2918	STAT4
A_23_P359245	36.35	139.40	1.78	4.6261	0.0062	0.3294	MET
A_33_P3262694	146.55	434.36	1.76	6.2628	0.0017	0.2733	
A_33_P3236267	228.15	690.87	1.74	6.4271	0.0015	0.2733	KCNQ1OT1
A_23_P76969	785.27	2508.70	1.60	7.4097	8.0000E-04	0.2392	SIPA1L1
A_23_P132515	102.95	300.13	1.55	12.9583	1.0000E-04	0.2092	SIDT1
A_23_P170453	4108.14	10205.73	1.49	7.968	6.0000E-04	0.2193	CST5
A_33_P3257150	930.53	2405.95	1.45	5.6793	0.0026	0.3013	CDC42
A_24_P179013	29.76	82.16	1.44	4.446	0.0072	0.3315	
A_33_P3372727	54.20	141.80	1.44	6.8087	0.0012	0.2668	SEMA5A
A_23_P416711	51.15	137.60	1.44	14.5716	0	0.192	ST6GALNAC3
A_23_P41344	22.46	64.52	1.43	4.6314	0.0061	0.3294	EREG
A_33_P3422294	101.01	288.34	1.42	7.6364	7.0000E-04	0.2392	
A_24_P245379	51.84	148.73	1.41	8.8935	3.0000E-04	0.2138	SERPINB2
A_23_P201979	541.13	1528.58	1.40	4.4274	0.0074	0.3315	CREM
A_23_P208900	275.45	686.62	1.33	14.3717	0	0.192	SEMA6B
A_23_P428129	407.37	1022.43	1.32	8.6251	4.0000E-04	0.2138	CDKN1C
A_33_P3317431	1153.70	2714.24	1.31	7.5237	8.0000E-04	0.2392	
A_23_P72117	446.16	1126.78	1.30	8.8485	4.0000E-04	0.2138	SMPDL3A
A_23_P102731	127.71	316.19	1.28	8.6233	4.0000E-04	0.2138	SMOX
A_23_P85453	45.04	102.33	1.26	10.2964	2.0000E-04	0.2138	CD244
A_24_P32085	269.48	651.45	1.26	10.2497	2.0000E-04	0.2138	MOB3B
A_33_P3294133	870.49	1877.56	1.25	5.9258	0.0022	0.2918	EIF4B
A_23_P32404	410.56	963.29	1.24	13.1219	1.0000E-04	0.2092	ISG20
A_23_P145529	31.66	75.46	1.20	6.385	0.0016	0.2733	PKIB
A_33_P3308115	990.35	1966.88	1.18	5.2919	0.0035	0.311	
A_23_P257649	331.87	745.56	1.18	12.2964	1.0000E-04	0.2138	RBP1
A_23_P154605	3414.30	7447.51	1.16	10.6682	2.0000E-04	0.2138	SULF2
A_24_P49260	120.84	254.30	1.14	11.5085	1.0000E-04	0.2138	SPTLC3
A_23_P419714	19.58	42.63	1.14	9.2799	3.0000E-04	0.2138	BTBD11
A_24_P677642	30.48	61.09	1.14	5.2716	0.0036	0.311	FLJ31813
A_33_P3407230	27.08	57.92	1.13	5.0078	0.0044	0.3173	
A_23_P404481	116.49	243.45	1.11	8.5894	4.0000E-04	0.2138	S1PR1
A_33_P3258977	35.31	72.61	1.11	8.2306	5.0000E-04	0.2193	CLEC4D
A_33_P3333436	78.19	169.81	1.10	9.9911	2.0000E-04	0.2138	SGSM3
A_23_P373724	55.60	115.94	1.10	11.7738	1.0000E-04	0.2138	PPFIBP1
A_33_P3323722	2078.85	4415.23	1.10	7.9589	6.0000E-04	0.2193	ARL4C
A_23_P79518	166.63	375.23	1.10	7.111	0.001	0.2435	IL1B
A_24_P23245	1433.40	2910.16	1.10	5.095	0.0041	0.3145	NDUFA6
A_33_P3412716	154.06	380.19	1.08	5.0541	0.0043	0.3168	
A_23_P25503	2952.57	6154.31	1.06	8.4164	5.0000E-04	0.2138	FNDC3A
A_33_P3382560	7622.06	15383.62	1.06	8.424	4.0000E-04	0.2138	RPL23A
A_24_P759477	36.54	77.03	1.05	8.6302	4.0000E-04	0.2138	ITGB8
A_33_P3229390	496.15	987.05	1.05	5.6149	0.0027	0.3038	
A_33_P3275055	18.28	36.20	1.03	6.2679	0.0017	0.2733	ST6GALNAC3

A_24_P291826	173.38	346.79	1.02	5.8185	0.0023	0.2918	SYTL3
A_32_P4985	21.76	43.44	1.01	5.5752	0.0028	0.3038	CAMTA1
A_33_P3273885	409.11	870.16	1.01	7.9645	6.0000E-04	0.2193	
A_32_P84605	14673.78	28072.13	1.00	4.8911	0.0049	0.3196	RPS23
A_33_P3319905	23.59	46.75	0.99	10.9177	1.0000E-04	0.2138	TREM1
A_33_P3366053	276.73	534.19	0.99	5.9429	0.0021	0.2918	ADPRH
A_33_P3395314	647.87	1272.55	0.99	5.3382	0.0034	0.3095	
A_23_P144959	43.39	85.50	0.98	10.5655	2.0000E-04	0.2138	VCAN
A_23_P166297	227.26	450.70	0.98	8.6544	4.0000E-04	0.2138	ABCG1
A_23_P74278	162.12	299.62	0.98	4.4996	0.0069	0.3315	PDE4B
A_32_P117464	190.00	365.73	0.97	7.6492	7.0000E-04	0.2392	MB21D2
A_23_P251075	111.82	212.26	0.97	4.835	0.0051	0.3231	MAMLD1
A_23_P414654	56.39	113.19	0.96	8.9112	3.0000E-04	0.2138	RAB37
A_23_P23438	741.59	1400.56	0.96	7.4906	8.0000E-04	0.2392	SEMA4A
A_24_P62505	31.16	59.65	0.96	4.9374	0.0047	0.3196	COLGALT2
A_23_P59637	957.90	1874.73	0.96	7.9163	6.0000E-04	0.2193	DOCK4
A_24_P296508	702.06	1395.79	0.95	8.7928	4.0000E-04	0.2138	SLC43A2
A_24_P381604	1672.70	2917.42	0.95	5.128	0.004	0.3145	ITM2B
A_23_P321354	389.53	744.31	0.95	10.037	2.0000E-04	0.2138	TMEM71
A_24_P270460	30.36	63.95	0.94	6.9762	0.0011	0.2531	IFI27
A_23_P60565	62.44	113.57	0.94	5.3352	0.0034	0.3095	ZNF354A
A_24_P132383	491.79	927.06	0.94	9.3149	3.0000E-04	0.2138	GIMAP8
A_33_P3352578	74.65	140.30	0.93	10.043	2.0000E-04	0.2138	CLEC4D
A_23_P39550	38.95	68.20	0.92	4.7259	0.0056	0.3294	TMEM163
A_23_P571	246.24	421.15	0.91	4.9355	0.0047	0.3196	SLC2A1
A_33_P3413840	121.69	228.70	0.91	6.8214	0.0012	0.2668	GK
A_33_P3273919	33.02	62.25	0.90	5.8288	0.0023	0.2918	RNF212
A_23_P91850	27.53	52.53	0.90	5.0045	0.0044	0.3173	IL20RB
A_23_P31858	98.63	174.64	0.90	4.9561	0.0046	0.3196	ST18
A_33_P3240843	170.64	314.95	0.88	8.4384	4.0000E-04	0.2138	TMEM71
A_23_P214139	349.66	647.84	0.88	7.2258	9.0000E-04	0.2392	REV3L
A_23_P69109	1470.47	2684.51	0.87	9.957	2.0000E-04	0.2138	PLSCR1
A_32_P161762	69.56	124.60	0.87	8.7471	4.0000E-04	0.2138	RUNX2
A_23_P208334	48.63	87.49	0.87	7.2443	9.0000E-04	0.2392	PDE4A
A_23_P68601	54.52	97.95	0.87	6.3335	0.0016	0.2733	CST7
A_33_P3375934	679.07	1219.59	0.86	5.0331	0.0043	0.3173	NAMPT
A_23_P81760	25.62	45.18	0.86	6.4934	0.0014	0.2733	QKI
A_33_P3389653	22.84	39.46	0.85	4.6774	0.0059	0.3294	PDE4D
A_23_P167920	117.43	211.91	0.85	7.7999	6.0000E-04	0.2296	DLL1
A_23_P66432	239.80	437.52	0.85	5.49	0.003	0.3082	TTYH2
A_23_P425502	53.16	94.05	0.84	6.4028	0.0015	0.2733	DONSON
A_23_P24077	2990.99	5175.59	0.84	6.2178	0.0018	0.2772	C10orf54
A_24_P315184	9659.77	16932.61	0.83	7.7041	7.0000E-04	0.2387	NBEAL1
A_23_P115011	59.66	102.35	0.83	7.3499	8.0000E-04	0.2392	ADAMTSL4
A_33_P3259557	296.93	544.75	0.83	7.1249	0.001	0.2435	TMEM198B
A_33_P3279456	1040.31	1927.41	0.82	5.8947	0.0022	0.2918	
A_23_P55356	279.95	489.77	0.82	7.2414	9.0000E-04	0.2392	VMO1
A_24_P93703	371.19	656.60	0.82	8.9764	3.0000E-04	0.2138	TMEM198B
A_24_P141332	475.35	791.34	0.82	4.2302	0.0088	0.3318	CAMK2G
A_23_P55649	43.70	76.22	0.81	7.4754	8.0000E-04	0.2392	FPR2
A_33_P3287348	460.32	754.77	0.81	5.3999	0.0032	0.3095	CHN2
A_24_P417606	8592.71	14024.86	0.81	4.3835	0.0077	0.3318	
A_23_P110445	129.59	225.31	0.81	7.5107	8.0000E-04	0.2392	APBB3

A_23_P400378	512.19	844.84	0.81	6.8421	0.0011	0.2668	GPBAR1
A_33_P3559138	690.61	1148.55	0.81	5.3174	0.0034	0.3095	
A_24_P413126	50.01	87.03	0.80	7.4007	8.0000E-04	0.2392	PMEP1
A_23_P38795	1232.70	2077.44	0.80	6.7376	0.0012	0.2692	FPR1
A_33_P3226050	548.01	953.06	0.80	8.4776	4.0000E-04	0.2138	GATSL3
A_23_P91390	1169.22	2064.74	0.80	5.3811	0.0033	0.3095	THBD
A_23_P201747	114.55	205.24	0.79	6.4307	0.0015	0.2733	PADI2
A_33_P3232557	119.84	206.66	0.78	6.5667	0.0014	0.2733	DLGAP3
A_33_P3415191	182.14	313.76	0.78	6.6105	0.0013	0.2733	ATP8B1
A_24_P324674	492.95	846.92	0.78	8.9556	3.0000E-04	0.2138	LY9
A_23_P86653	11484.56	19458.03	0.77	8.3019	5.0000E-04	0.2193	SRGN
A_23_P15108	532.44	913.10	0.77	8.1222	5.0000E-04	0.2193	YPEL3
A_23_P89570	551.51	948.42	0.76	8.0314	6.0000E-04	0.2193	ZMYND15
A_33_P3353259	19313.92	31984.65	0.76	5.2107	0.0038	0.3134	
A_33_P3238685	85.84	142.42	0.76	4.8244	0.0052	0.3237	TET2
A_24_P397817	26.80	49.85	0.76	4.5795	0.0064	0.3315	LEP
A_23_P210253	455.64	781.74	0.76	5.7366	0.0025	0.298	DGKD
A_33_P3421695	672.37	1171.67	0.76	4.1928	0.0091	0.3318	CTNNB1
A_24_P33156	80.86	135.90	0.75	4.889	0.0049	0.3196	AFMID
A_23_P10559	264.88	447.64	0.75	8.4521	4.0000E-04	0.2138	AATK
A_23_P152791	163.03	270.51	0.75	6.851	0.0011	0.2668	SLC16A6
A_23_P37375	217.10	359.90	0.74	8.0574	5.0000E-04	0.2193	RPS6KA5
A_23_P380998	165.10	269.18	0.74	6.4024	0.0015	0.2733	R3HDM1
A_33_P3227716	820.46	1369.66	0.73	7.4591	8.0000E-04	0.2392	GATSL3
A_24_P189739	38.88	64.36	0.73	4.5853	0.0064	0.3315	DUSP16
A_23_P154849	87.31	145.08	0.73	7.9088	6.0000E-04	0.2193	OLIG1
A_23_P258108	11895.64	19363.83	0.73	6.3718	0.0016	0.2733	
A_33_P3294524	90.88	148.39	0.72	5.3412	0.0034	0.3095	ANKRD12
A_23_P42116	264.29	453.39	0.72	4.936	0.0047	0.3196	PPT2
A_24_P58620	89.92	144.32	0.72	4.1773	0.0093	0.3318	GRAMD1B
A_24_P370172	236.53	391.70	0.72	7.0777	0.001	0.2457	LILRA5
A_23_P53588	24.99	41.18	0.72	5.2053	0.0038	0.3134	WNT5B
A_33_P3390708	37.54	64.61	0.72	4.439	0.0073	0.3315	TMEM2
A_33_P3242623	865.18	1305.65	0.72	4.3188	0.0081	0.3318	SLC7A11
A_32_P222961	30.14	49.40	0.72	7.198	9.0000E-04	0.2392	SPIN4
A_33_P3290955	5568.64	9146.74	0.71	5.3543	0.0033	0.3095	KIAA1875
A_23_P353316	31.74	50.36	0.71	5.2575	0.0036	0.311	SMURF1
A_33_P3328619	6678.08	11020.05	0.71	4.7319	0.0056	0.3294	
A_23_P215744	91.56	144.62	0.71	6.3883	0.0016	0.2733	CTTNBP2
A_23_P25566	4726.99	7713.17	0.71	6.3212	0.0016	0.2733	GPR183
A_33_P3258988	17.45	29.52	0.71	4.9046	0.0048	0.3196	GDI2
A_23_P166508	549.11	889.84	0.70	5.2813	0.0035	0.311	
A_33_P3236177	703.17	1139.93	0.70	7.9894	6.0000E-04	0.2193	ANG
A_24_P261383	202.16	310.89	0.70	4.2333	0.0088	0.3318	TAF1D
A_23_P85716	2690.03	4201.95	0.69	6.8414	0.0011	0.2668	FCGR2A
A_23_P371011	48.04	75.06	0.69	5.4183	0.0032	0.3095	ZNF227
A_24_P54131	247.63	380.98	0.69	4.5339	0.0067	0.3315	DCLRE1B
A_23_P99625	27.67	44.38	0.69	4.9355	0.0047	0.3196	FITM1
A_33_P3351775	79.06	130.10	0.69	7.4673	8.0000E-04	0.2392	
A_24_P342807	23.75	39.53	0.69	5.9989	0.0021	0.2918	SLC30A6
A_32_P87697	29475.87	46802.86	0.68	7.3421	8.0000E-04	0.2392	HLA-DRA
A_24_P313418	68.68	118.09	0.68	5.7423	0.0025	0.298	CCL22
A_24_P237586	275.01	447.66	0.68	5.0103	0.0044	0.3173	ANKRD37

A_33_P3263666	2204.73	3570.41	0.68	4.4619	0.0071	0.3315	ANKRD9
A_23_P110196	173.85	287.18	0.68	5.9138	0.0022	0.2918	HERC5
A_33_P3295333	26.76	42.54	0.68	5.155	0.0039	0.3134	CLEC1A
A_33_P3236392	249.82	382.87	0.67	5.8762	0.0022	0.2918	PVRL4
A_23_P2745	17.93	29.77	0.67	5.7744	0.0024	0.2953	GJB6
A_23_P402319	337.02	507.54	0.67	5.1038	0.0041	0.3145	GAPT
A_24_P477051	23.51	37.44	0.67	6.1669	0.0018	0.2816	
A_24_P288993	162.96	270.55	0.66	4.2925	0.0083	0.3318	
A_33_P3386132	397.26	623.42	0.66	6.3502	0.0016	0.2733	C2orf49
A_23_P10077	443.79	705.56	0.66	6.2905	0.0017	0.2733	PNPLA2
A_24_P22079	225.45	352.04	0.66	5.9146	0.0022	0.2918	FOXO1
A_23_P57760	101.41	159.07	0.66	7.4768	8.0000E-04	0.2392	ACPL2
A_24_P212819	3107.33	4788.86	0.65	6.2808	0.0017	0.2733	
A_24_P390060	219.39	346.68	0.65	5.6028	0.0028	0.3038	IQCD
A_24_P195724	1585.50	2347.11	0.65	4.3066	0.0082	0.3318	
A_23_P24044	47.34	73.82	0.65	7.3834	8.0000E-04	0.2392	CNNM2
A_23_P37359	168.99	253.57	0.65	5.0175	0.0044	0.3173	CIDEB
A_23_P49499	279.35	414.74	0.65	4.651	0.006	0.3294	ST6GALNAC2
A_23_P82128	17218.41	26359.21	0.64	5.9828	0.0021	0.2918	RPS12
A_33_P3234472	60.21	97.99	0.64	5.1275	0.004	0.3145	LOC284751
A_33_P3417589	25.18	40.08	0.64	4.3282	0.0081	0.3318	
A_33_P3352098	11435.65	17831.64	0.64	6.7192	0.0012	0.2692	MS4A7
A_23_P60166	395.34	627.24	0.64	6.3945	0.0016	0.2733	DEPTOR
A_33_P3284883	48.11	74.30	0.64	6.3034	0.0017	0.2733	MOB3B
A_24_P110273	676.36	1044.92	0.63	6.3217	0.0016	0.2733	
A_33_P3327799	3260.03	5077.60	0.63	5.9058	0.0022	0.2918	
A_23_P26024	4892.64	7101.14	0.63	4.5079	0.0068	0.3315	C15orf48
A_33_P3272090	154.84	239.22	0.63	4.7594	0.0055	0.3288	PDE4DIP
A_33_P3295650	61.03	95.87	0.62	5.5974	0.0028	0.3038	APBA1
A_32_P135818	7584.21	11366.12	0.62	5.2381	0.0037	0.3121	RPS3A
A_23_P217428	62.29	97.58	0.62	5.0527	0.0043	0.3168	ARHGAP6
A_24_P332341	227.80	367.39	0.62	4.3021	0.0082	0.3318	POLR2J4
A_33_P3382031	70.26	108.03	0.62	6.2503	0.0017	0.2736	TMEM236
A_23_P9883	1124.10	1674.39	0.62	5.326	0.0034	0.3095	NLRP3
A_23_P41114	878.89	1323.40	0.62	6.4491	0.0015	0.2733	CSTA
A_23_P55020	656.97	1013.28	0.61	6.659	0.0013	0.2725	CD300LF
A_23_P422851	605.75	902.87	0.61	5.8119	0.0024	0.2918	CABLES1
A_23_P140848	324.38	493.00	0.61	4.9716	0.0046	0.3196	MPHOSPH6
A_24_P63136	107.12	161.75	0.61	6.2917	0.0017	0.2733	P2RY13
A_24_P363548	31.41	47.43	0.61	6.2105	0.0018	0.2772	HIP1
A_23_P70398	47.75	70.80	0.61	4.3648	0.0078	0.3318	VEGFA
A_33_P3216427	523.77	813.73	0.61	4.8868	0.0049	0.3196	DGKQ
A_33_P3367994	385.69	568.55	0.60	5.8335	0.0023	0.2918	TAF8
A_24_P48408	98.56	142.17	0.60	4.5112	0.0068	0.3315	RNMT
A_32_P217750	49.31	78.60	0.60	4.2311	0.0088	0.3318	IL3RA
A_33_P3315320	70.38	106.96	0.60	6.7149	0.0012	0.2692	CNTD1
A_23_P64343	2067.77	3068.07	0.60	5.7079	0.0025	0.3005	TIMM10
A_23_P343398	58.18	85.73	0.60	5.3014	0.0035	0.3105	CCR7
A_23_P62967	1743.65	1144.21	-0.60	-6.7737	0.0012	0.2689	DISC1
A_33_P3317168	418.46	276.28	-0.60	-4.5822	0.0064	0.3315	EPS8L3
A_23_P372096	49.48	33.26	-0.60	-4.1053	0.0099	0.3318	C20orf112
A_23_P18119	83.37	52.02	-0.61	-4.2356	0.0088	0.3318	IMPG2
A_23_P125204	492.06	317.00	-0.61	-6.4729	0.0015	0.2733	OR10G8



A 33 P3371109	51.32	33.28	-0.62	-5.701	0.0026	0.3005	LOC100130597
A 33 P3404097	2144.26	1411.17	-0.63	-5.0479	0.0043	0.3169	PGM5P2
A 33 P3380850	47.45	30.57	-0.63	-7.2047	9.0000E-04	0.2392	PAX2
A 24 P376787	499.87	337.10	-0.64	-4.73	0.0056	0.3294	ZNF496
A 23 P146284	2607.18	1715.24	-0.64	-4.2267	0.0088	0.3318	SQLE
A 33 P3315824	105.26	67.94	-0.64	-4.5628	0.0065	0.3315	
A 33 P3381827	432.23	287.12	-0.65	-4.5535	0.0066	0.3315	OSBPL2
A 32 P134290	1591.48	1022.82	-0.65	-6.7639	0.0012	0.2689	ZCCHC2
A 23 P150903	261.74	167.82	-0.65	-5.3154	0.0035	0.3095	FAR2
A 33 P3297978	21265.37	13729.91	-0.65	-5.547	0.0029	0.3038	MYO1E
A 24 P587443	38.51	23.78	-0.66	-4.2511	0.0086	0.3318	
A 23 P340848	1536.35	979.80	-0.67	-7.0574	0.001	0.246	PTGIR
A 23 P48784	34.89	21.22	-0.67	-4.8737	0.005	0.3196	CYP46A1
A 33 P3310296	406.56	256.02	-0.67	-5.7208	0.0025	0.2994	
A 33 P3242039	594.73	354.94	-0.67	-4.1768	0.0093	0.3318	
A 23 P500400	118.89	76.68	-0.67	-4.5846	0.0064	0.3315	ABCA6
A 23 P32006	45.87	28.63	-0.68	-7.1463	9.0000E-04	0.2435	OR13D1
A 33 P3324786	283.86	169.49	-0.69	-4.8484	0.0051	0.3212	
A 23 P250619	2274.92	1342.70	-0.72	-5.3412	0.0034	0.3095	ZDHHC14
A 33 P3281468	55.49	33.39	-0.73	-4.8617	0.005	0.3197	STARD9
A 33 P3397348	136.33	80.84	-0.73	-4.7319	0.0056	0.3294	LOC149134
A 33 P3512350	675.48	399.65	-0.76	-6.9789	0.0011	0.2531	LOC339807
A 33 P3214314	1141.14	713.42	-0.76	-4.3225	0.0081	0.3318	CCSER2
A 23 P81441	1493.93	874.24	-0.76	-8.7105	4.0000E-04	0.2138	C5orf20
A 23 P328545	440.40	259.98	-0.76	-8.0807	5.0000E-04	0.2193	GABRP
A 33 P3274134	777.16	461.18	-0.77	-4.3718	0.0077	0.3318	TMEM151B
A 33 P3232955	920.03	555.00	-0.77	-6.662	0.0013	0.2725	F2RL3
A 33 P3263867	5610.72	3207.27	-0.79	-4.7778	0.0054	0.3285	P2RX7
A 23 P97394	1334.01	788.36	-0.80	-5.3565	0.0033	0.3095	BCAR3
A 33 P3380383	4374.93	2579.19	-0.81	-8.8739	4.0000E-04	0.2138	TIFAB
A 23 P58009	32.28	18.15	-0.82	-8.8114	4.0000E-04	0.2138	C3orf52
A 23 P34345	116.89	68.07	-0.83	-4.8014	0.0053	0.3267	VCAM1
A 23 P91095	523.44	291.00	-0.84	-9.6298	2.0000E-04	0.2138	CD28
A 23 P103034	214.84	114.56	-0.91	-7.2742	9.0000E-04	0.2392	CRYBA4
A 23 P67896	269.49	137.51	-0.92	-6.3894	0.0016	0.2733	SCN3A
A 33 P3393655	103.21	52.60	-0.93	-5.5633	0.0028	0.3038	LGI2
A 23 P390116	389.38	221.87	-0.98	-4.4755	0.007	0.3315	SPATA13
A 32 P155666	716.76	350.13	-1.07	-9.703	2.0000E-04	0.2138	ECEL1
A 23 P404162	100.99	46.26	-1.08	-8.2829	5.0000E-04	0.2193	HDAC9
A 33 P3304998	197.28	94.61	-1.09	-4.7524	0.0055	0.3291	LOC101930176
A 24 P41706	77.88	21.11	-1.81	-7.2246	9.0000E-04	0.2392	OFCC1

## SUPPLEMENTARY FIGURES

**Supplementary Figure 1. Lack of effect of 5-HT<sub>2</sub>BR blockade on the inhibitory effect of 5-HT on the LPS-induced TNF $\alpha$  production.** Production of LPS-stimulated TNF $\alpha$  by M-M $\emptyset$  non-treated or pretreated with 5-HT (6 h) in the presence or absence of the 5-HT<sub>7</sub>R antagonist SB269970 (10  $\mu$ M) or the 5-HT<sub>2</sub>BR antagonist SB204741 (10  $\mu$ M) (n=3; \*, p < 0.05; \*\*, p < 0.01; ns, non-significant ).

**Supplementary Figure 2. GSEA Hallmark gene sets significantly regulated upon M-M $\emptyset$  exposure to 5-HT.** Results of GSEA on the “t statistic-ranked” list of genes obtained from the 5-HT-treated M-M $\emptyset$  versus M-M $\emptyset$  limma analysis, and using the “Hallmark gene sets” contained in the Molecular Signature databases available at the GSEA website. The gene sets significantly upregulated or down-regulated in the transcriptome of 5HT-treated M-M $\emptyset$  are shown. The False Discovery Rate (FDR q-val) for each GSEA is indicated.

**Supplementary Figure 3. Htr7 mRNA expression in *ex vivo*-isolated and *in vitro*-generated mouse macrophages.** A. Relative expression of the Htr7 mRNA and Htr7 splicing isoforms (a,b,c) in mouse liver cells (Hep, Hepatocytes; KC, Kupffer Cells; SEC, Sinusoidal Endothelial Cells) and mouse peritoneal F4/80<sup>+</sup> (n=3, \*, p < 0.05). B. Relative expression of the Htr7 mRNA and Htr7 splicing isoforms (a,b,c) in mouse bone marrow-derived GM-M $\emptyset$  and M-M $\emptyset$  (n=3). C. Relative Htr7 mRNA expression in untreated (-) or LPS-stimulated mouse bone marrow-derived GM-M $\emptyset$  (upper panel) and peritoneal F4/80<sup>+</sup> cells (lower panel). Two independent experiments were performed and both are shown. In all cases (A-C), results are expressed as the Htr7 mRNA level relative to the Tbp mRNA level in the same sample.

**Supplementary Table I. Gene expression analysis on untreated or 5-HT-treated (10  $\mu$ M, 6h) M-MØ.** List of 170 upregulated annotated genes ( $p < 0.01$ ;  $\log_2$  ratio 5-HT/untreated  $\geq 0.6$ ) and 41 downregulated genes ( $p < 0.01$ ;  $\log_2$  ratio 5-HT/untreated  $\leq -0.6$ ).