Table 1. Association of *COMT* SNPs with Postoperative Pain and Oxycodone Consumption

| SNP | postoperative pain during movement when needing the first oxycodone dose | | | | | | | | | total oxycodone mg/kg | | | | | | | | |
| | additive | | | dominant | | | recessive | | | additive | | | dominant | | | recessive | | |
	perm P-value	β	SNP cor P-value	perm P-value	β	SNP cor P-value	perm P-value	β	SNP cor P-value	perm P-value	β	SNP cor P-value	perm P-value	β	SNP cor P-value	perm P-value	β	SNP cor P-value
rs6518591	0.739	0.028	1.000	0.928	-0.009	1.000	0.215	0.319	0.960	0.762	0.003	1.000	0.793	0.003	1.000	0.805	0.007	1.000
rs737866	0.669	0.036	1.000	0.624	0.049	1.000	0.996	0.001	1.000	0.209	0.012	0.917	0.355	0.010	0.994	0.179	0.039	0.921
rs737865	0.672	0.035	1.000	0.628	0.048	1.000	0.998	0.001	1.000	0.202	0.012	0.908	0.345	0.010	0.993	0.178	0.039	0.919
rs1544325	0.867	0.012	1.000	0.905	-0.013	1.000	0.688	0.045	1.000	0.503	-0.005	1.000	0.923	-0.001	1.000	0.318	-0.013	0.993
rs8185002	0.981	-0.002	1.000	0.840	0.020	1.000	0.543	-0.156	1.000	0.324	0.009	0.985	0.426	0.009	0.999	0.374	0.026	0.998
rs174675	0.848	-0.014	1.000	0.999	0.000	1.000	0.674	-0.067	1.000	0.847	-0.002	1.000	0.944	0.001	1.000	0.587	-0.010	1.000
rs5993882	0.874	0.013	1.000	0.911	0.011	1.000	0.858	0.041	1.000	0.718	0.003	1.000	0.714	0.004	1.000	0.904	0.003	1.000
rs740603	0.709	0.026	1.000	0.744	0.032	1.000	0.779	0.037	1.000	0.122	0.012	0.742	0.185	0.015	0.906	0.249	0.017	0.975
rs4646312	0.041	0.148	0.376	**0.008**	0.248	0.118	0.897	0.020	1.000	0.263	0.009	0.959	0.174	0.014	0.899	0.846	0.003	1.000
rs4633	0.151	0.095	0.830	0.158	0.145	0.877	0.388	0.101	0.998	0.989	0.0001	1.000	0.812	0.003	1.000	0.805	-0.003	1.000
rs2239393	**0.021**	0.188	0.221	**0.010**	0.281	0.134	0.371	0.151	0.998	0.237	0.011	0.939	0.111	0.019	0.781	0.955	0.001	1.000
rs4818	**0.044**	0.146	0.399	**0.009**	0.243	0.134	0.893	0.021	1.000	0.301	0.008	0.977	0.206	0.013	0.937	0.866	0.003	1.000
rs4680	0.174	0.091	0.864	0.158	0.146	0.875	0.449	0.089	1.000	0.843	0.002	1.000	0.605	0.006	1.000	0.819	-0.003	1.000
rs4646316	0.404	0.066	0.996	0.428	0.078	0.999	0.629	0.105	1.000	0.885	-0.001	1.000	0.900	0.001	1.000	0.515	-0.016	1.000
rs165774	0.127	-0.119	0.765	0.149	-0.138	0.852	0.400	-0.174	0.999	0.151	0.013	0.820	0.120	0.017	0.792	0.685	0.009	1.000
rs174696	0.630	-0.033	1.000	0.328	-0.094	0.990	0.620	0.069	1.000	0.103	-0.013	0.697	0.608	-0.005	1.000	0.012	-0.040	0.152
rs9306235	0.789	-0.037	1.000	0.982	-0.003	1.000	0.176	-0.944	0.931	0.308	-0.016	0.978	0.365	-0.015	0.995	0.404	-0.065	9.999
rs9332377	0.726	0.037	1.000	0.581	0.061	1.000	0.540	-0.259	1.000	0.520	0.007	1.000	0.537	0.008	1.000	0.727	0.016	1.000
rs165599	0.887	0.010	1.000	0.571	-0.053	1.000	0.212	0.196	0.953	0.851	-0.002	1.000	0.684	-0.004	1.000	0.775	0.005	1.000
rs887199	0.703	-0.031	1.000	0.569	-0.057	1.000	0.745	0.077	1.000	0.410	-0.008	0.997	0.511	-0.007	1.000	0.453	-0.019	1.000
rs2518824	0.369	0.160	0.992	0.372	0.160	0.996	1.000	NA	1.000	0.834	-0.004	1.000	0.839	-0.004	1.000	1.000	NA	1.000
rs887200	0.882	-0.013	1.000	0.829	-0.022	1.000	0.900	0.038	1.000	0.456	-0.008	0.999	0.529	-0.007	1.000	0.522	-0.020	1.000

P-values that have been corrected taking into account both SNPs, models and phenotypes tested are not shown but are 1.00 in all cases.

Variables have been adjusted for type of surgery, age, BMI, anxiety (STAI score) and presence of preoperative chronic pain condition.

BMI = body mass index, COMT = catechol-O-methyltransferase, NA = not available, SNP = single nucleotide polymorphism, STAI = state and trait anxiety inventory

perm *P*-value = empirical *P*-value produced using permutations

SNP cor P-value = permuted and experimental-wise corrected p-value (taking into account the number of independent SNPs)

Table 2. Association between Experimental Pain and COMT Haplotypes

Haploblock	Haplotype	Frequency	Heat Pain Intensity, 48 °C			Cold Withdrawal Time			Cold Pain Intensity, NRS at		
			perm P-value	β	cor P-value	perm P-value	β	cor P-value	perm P-value	β	cor P-value
1	AATATCT	0.49	0.625	0.055	1.000	0.129	-2.160	0.825	0.535	0.088	1.000
1	AGCGGCT	0.20	0.064	-0.250	0.592	0.053	3.380	0.511	0.422	-0.138	0.999
1	GATGTTG	0.17	0.940	0.010	1.000	0.800	-0.481	1.000	0.728	-0.062	1.000
1	AATGTTG	0.03	0.080	0.554	0.655	0.089	-7.090	0.704	0.202	0.524	0.934
1	AATGTTT	0.11	0.848	0.035	1.000	0.245	2.540	0.973	0.797	-0.055	1.000
2	TTACACA	0.24	**0.014**	-0.314	0.188	0.215	2.040	0.952	0.131	-0.242	0.825
2	CCGGGCG	0.13	0.925	0.016	1.000	0.922	-0.211	1.000	0.442	0.163	0.999
2	TTACACG	0.28	0.308	0.123	0.989	0.400	-1.280	0.998	0.819	-0.034	1.000
2	CCGGGTG	0.18	0.534	0.087	1.000	0.294	-1.900	0.987	0.059	0.329	0.554
2	TTACATG	0.02	0.934	-0.033	1.000	0.258	-5.920	0.976	0.996	-0.002	1.000
2	TCACGCG	0.14	0.486	0.112	1.000	0.210	2.500	0.948	0.421	-0.155	0.999
3	CGAGC	0.02	0.737	0.134	1.000	0.221	6.240	0.955	0.122	-0.771	0.801
3	CGATC	0.14	0.407	0.147	0.999	0.136	3.290	0.840	0.704	-0.080	1.000
3	TGGGT	0.01	0.048	1.090	0.481	0.057	-13.900	0.538	0.157	0.985	0.893
3	CGATT	0.04	0.905	0.038	1.000	0.754	-1.120	1.000	0.550	0.210	1.000
3	TGGTT	0.11	0.519	-0.117	1.000	0.680	-0.986	1.000	0.572	0.130	1.000
3	CAGTT	0.67	0.328	-0.116	0.992	0.581	-0.834	1.000	0.817	-0.034	1.000

COMT = catechol-O-methyltransferase, NRS = numerical rating scale

perm P-value = empirical P-value produced using permutations

cor P-value = permuted and experimental-wise corrected p-value (taking into account the number of haplotypes tested)