Supplementary Table S1. Characteristics of the source GWAS

Source study (locus prefix)	Cohort / setting	Surgical population	Sample size	CPSP phenotype and pain measure	Assessment time	Ancestry	Loci contributed → retained
Parisien et al., Br J Anaesth 2024 (PAR)	Six prospective cohorts: HYS (4 hospitals, Netherlands); ABKNEE (3 hospitals, Italy); PMPS and TKR (Pittsburgh, USA); HRN (Denmark); TANK (Iowa, USA). Seven GWAS by surgery type plus a meta-analysis	Hysterectomy (PAR-A); abdominal surgery (PAR-B); mastectomy (no loci); open hernia repair (PAR-D); knee arthroplasty (PAR-E); meta-analysis of all cohorts (PAR-F)	1,350 after QC: hysterectomy 325, abdominal 90, mastectomy 450, hernia 182, knee 303; 75.8% female	Pain at the surgical site as a continuous trait: highest pain in the last week, 0–10 NRS (HYS, ABKNEE, PMPS, HRN); worst pain in the last 24 h, Brief Pain Inventory (TKR, TANK)	3 months (hysterectomy, abdominal, ABKNEE knee); 6 months (hernia, TKR, TANK); mean 38 months (mastectomy)	European (Caucasian)	24 → 22
Li et al., Anaesthesia 2025 (LI)	UK Biobank; first abdominal surgery recorded 1997–2015	Abdominal surgery: digestive, urinary, female genital tract, arteries/veins, soft tissue, diagnostic laparoscopy	27,603 (1,044 cases; 26,559 controls)	Case: analgesic (mainly NSAID/opioid) prescription records in more than 3 of the 12 months after surgery; control: ≤3 months. Excluded: >3 months of analgesic records in the year before surgery, another abdominal surgery within 1 year. No pain intensity measure	12 months after surgery	Not stated in main text	11 → 11
Li et al., Br J Anaesth 2025 (GLR)	UK Biobank; first surgery recorded 1997–2015; separate GWAS after major and minor surgery, meta-analyzed	Major and minor surgery: visceral, musculoskeletal, nervous system, otorhinolaryngology and eye, vascular	95,931 (2,923 cases; 93,008 controls)	Case: ≥4 months of analgesic (mainly NSAID/opioid) prescription records in the 12 months after surgery; control: ≤3 months. Excluded: >3 months of analgesic records in the year before surgery. No pain intensity measure	12 months after surgery	White British	10 → 8

Source study (locus prefix)	Cohort / setting	Surgical population	Sample size	CPSP phenotype and pain measure	Assessment time	Ancestry	Loci contributed → retained
Warner et al., Eur J Hum Genet 2017 (WAR)	Nottinghamshire, UK; secondary care	Total hip or knee replacement for osteoarthritis	613 (109 cases; 504 controls)	Possible neuropathic pain: painDETECT score >12 (0–39 scale)	Not reported	Not reported	1 → 1
Peres et al., J Pain 2026 (UKB)	UK Biobank; index surgery from 2000 onward in hospital records	Surgery across 12 specialty categories, mainly orthopedic and general surgery; controls matched to cases on surgery type and year	47,836 after QC (2,490 cases; 45,346 controls); GWAS training set 38,268 (1,992 cases; 36,276 controls)	Self-reported physician-diagnosed CPSP (Field 120005) linked to a hospital-recorded index surgery. No pain intensity measure	Not applicable (lifetime self-report)	European (Pan-UK Biobank genetic ancestry, Field 30079)	4 → 3

NRS, numeric rating scale; NSAID, non-steroidal anti-inflammatory drug; QC, quality control.

Supplementary Table S2. Source-Study Gene Labels That Differ from the Assigned Nearest Gene (11 Loci)

Positional correction: the source-reported gene was not the nearest protein-coding gene at the variant's coordinates. **Dual-label resolution:** the source reported two candidate genes; the nearer was assigned. **HGNC nomenclature update:** same gene, current approved symbol. **Reported gene excluded:** the source-reported gene lies far from the variant, and no protein-coding gene was found within 500 kb. LI-8 (rs185545327), for which the source study reported no gene, was assigned to NKX2-6 (28.2 kb) and is not listed.

Locus	rsID	Source-reported gene	Assigned gene	Type of difference
PAR-A4	rs117244643	FHL5	GPR63	Positional correction
PAR-F2	rs114837251	MAP9	GUCY1A1	Positional correction
LI-11	rs4843341	FOXF1	IRF8	Positional correction
PAR-D2	rs7946537	LRP5	PPP6R3	Positional correction
PAR-D3	rs76991866	SLC52A1	ZFP3	Positional correction
PAR-A11	rs79423608	LINC02175 (lncRNA)	LCMT1	Positional correction
PAR-A10	rs4347600	IQGAP1/CRTC3	CRTC3	Dual-label resolution
PAR-B2	rs112030385	CDH2/DSC3	DSC3	Dual-label resolution
PAR-A5	rs10488532	SAMD9/SAMD9L	SAMD9L	Dual-label resolution
PAR-A7	rs78326996	AAED1	PRXL2C	HGNC nomenclature update
PAR-A6	rs10969869	LINGO2	None within 500 kb	Reported gene excluded

Supplementary Table S3. Exploratory subgroup and leave-one-study-out analyses

(A) Each locus set compared with the full background sets (cCRE: 500 random autosomal positions, dELS 264/500 = 52.8%, CTCF-bound 152/500 = 30.4%; PheWAS: 500 random protein-coding genes, Moderate-or-above 162/500 = 32.4%). Two-sided Fisher's exact test; Woolf 95% CI (Haldane correction for zero cells).

Locus set	n	dELS n (%)	dELS OR [95% CI]	p	CTCF-bound n (%)	CTCF OR [95% CI]	p	PheWAS Mod+ n (%)	PheWAS OR [95% CI]	p
All loci	45	29/45 (64.4%)	1.62 [0.86–3.06]	0.160	15/45 (33.3%)	1.14 [0.60–2.19]	0.736	14/45 (31.1%)	0.94 [0.49–1.82]	1.000
Hysterectomy (PAR–A)	12	7/12 (58.3%)	1.25 [0.39–4.00]	0.776	5/12 (41.7%)	1.64 [0.51–5.23]	0.526	2/12 (16.7%)	0.42 [0.09–1.93]	0.354
Abdominal surgery (LI, PAR–B)	13	9/13 (69.2%)	2.01 [0.61–6.62]	0.274	4/13 (30.8%)	1.02 [0.31–3.36]	1.000	5/13 (38.5%)	1.30 [0.42–4.05]	0.765
Hernia repair (PAR–D)	5	2/5 (40.0%)	0.60 [0.10–3.60]	0.671	2/5 (40.0%)	1.53 [0.25–9.23]	0.643	2/5 (40.0%)	1.39 [0.23–8.41]	0.662
Joint replacement (PAR–E1, WAR–1)	2	1/2 (50.0%)	0.89 [0.06–14.37]	1.000	1/2 (50.0%)	2.29 [0.14–36.85]	0.517	1/2 (50.0%)	2.09 [0.13–33.57]	0.544
Mixed / all surgery (UKB, GLR, PAR–F)	13	10/13 (76.9%)	2.98 [0.81–10.96]	0.098	3/13 (23.1%)	0.69 [0.19–2.53]	0.763	4/13 (30.8%)	0.93 [0.28–3.06]	1.000
UK Biobank studies (UKB, LI, GLR)	22	17/22 (77.3%)	3.04 [1.10–8.37]	0.028	6/22 (27.3%)	0.86 [0.33–2.24]	1.000	7/22 (31.8%)	0.97 [0.39–2.43]	1.000
Non–UK Biobank studies (PAR, WAR)	23	12/23 (52.2%)	0.98 [0.42–2.25]	1.000	9/23 (39.1%)	1.47 [0.62–3.47]	0.365	7/23 (30.4%)	0.91 [0.37–2.26]	1.000
Excluding Peres et al. (UKB)	42	26/42 (61.9%)	1.45 [0.76–2.77]	0.265	14/42 (33.3%)	1.14 [0.59–2.24]	0.728	14/42 (33.3%)	1.04 [0.53–2.04]	0.866
Excluding Li et al., Anaesthesia (LI)	34	21/34 (61.8%)	1.44 [0.71–2.95]	0.376	12/34 (35.3%)	1.25 [0.60–2.59]	0.567	10/34 (29.4%)	0.87 [0.41–1.86]	0.850

Locus set	n	dELS n (%)	dELS OR [95% CI]	p	CTCF-bound n (%)	CTCF OR [95% CI]	p	PheWAS Mod+ n (%)	PheWAS OR [95% CI]	p
Excluding Li et al., Br J Anaesth (GLR)	37	23/37 (62.2%)	1.47 [0.74–2.92]	0.308	13/37 (35.1%)	1.24 [0.62–2.50]	0.581	11/37 (29.7%)	0.88 [0.43–1.83]	0.856

Benjamini-Hochberg correction across the 30 subgroup tests: minimum p_FDR = 0.85. Heterogeneity across the five surgical subgroups (permutation chi-square, 20,000 permutations): dELS p = 0.64, CTCF-bound p = 0.86, PheWAS Moderate-or-above p = 0.75; UK Biobank vs. non-UK Biobank: p = 0.12, 0.53, and 1.00, respectively. Subgroup analyses were not pre-specified and are exploratory.

(B) Post-hoc power: minimum detectable odds ratio (MDOR) at 80% power, two-sided Fisher's exact test, 500 background units

Comparison	Background proportion	MDOR, 45 loci (α = 0.05)	MDOR, 45 loci (α = 0.05/8)	Power at OR = 1.62, 45 loci	MDOR, 25 GWS loci (α = 0.05)	MDOR, 25 GWS loci (α = 0.05/8)
dELS	52.8%	2.58 (74.3%)	3.52	30%	3.70	6.11
CA	17.2%	2.72	3.44	25%	3.56	4.80
CTCF-bound	30.4%	2.45	3.14	31%	3.22	4.56
PheWAS Moderate-or-above	32.4%	2.44	3.11	32%	3.26	4.58

Power computed by exact enumeration over binomial outcomes in both groups. GWS, genome-wide significant ($p < 5 \times 10^{-8}$).