Table SI. The mammalian FABP family: tissue distribution, ligands, principal functions and coverage in this review.

Isoform (alternative name)	Locus[a]	Principal tissue distribution	Main ligands	Principal physiological function	Established non-cancer biomarker use	Coverage in this review
FABP1 (L-FABP)	2p11.2	Liver, small intestine, pancreas, kidney	Two long-chain fatty acids simultaneously; bile acids; heme; monoacylglycerols; endocannabinoids	Uniquely large binding pocket; buffers excess free fatty acids, supports hepatic β-oxidation, bile-acid transport into canaliculi and VLDL biogenesis	Urinary and serum L-FABP in renal and hepatic injury (137-139)	Contextual; discussed where hepatic lipid handling bears on the metabolic liver axis
FABP2 (I-FABP)	4q26	Enterocytes	Long-chain fatty acids	Intestinal fatty acid absorption	None established	Not discussed; no FABP-specific evidence at more than one point of an inflammation-cancer continuum
FABP3 (H-FABP)	1p35.2	Heart, skeletal muscle, mammary gland, brain	Long-chain fatty acids	Collisional transfer of long-chain fatty acids to mitochondria for β-oxidation; cardiac fuel selection; binds cholesterol and facilitates lysosomal egress	Serum H-FABP as an early marker of acute myocardial infarction, often detectable 3-6 h after symptom onset (1,133-136)	Contextual; cited in Section 6 to show that biomarker maturity is disease-specific and does not transfer to cancer
FABP4 (A-FABP, aP2)	8q21.13	Adipocytes, macrophages, dendritic cells, endothelium	Long-chain fatty acids	Intracellular fatty acid shuttle; nucleocytoplasmic shuttling to PPARγ; non-classical secretion as a circulating adipokine	Serum FABP4 as an index of systemic metabolic-inflammatory burden (5,7,127-132)	Principal focus
FABP5 (E-FABP)	8q21.13	Epidermis, macrophages, dendritic cells, T cells, tumor cells	Long-chain fatty acids; retinoic acid; anandamide and related N-acylethanolamines	Delivers retinoic acid and fatty acids to PPARβ/δ; the FABP5:CRABPII ratio partitions retinoic acid between PPARβ/δ and RAR; carries a Cys120-Cys127 disulfide within the binding cavity	None established	Principal focus

FABP6 (Il-FABP)	5q33.3	Ileal enterocytes	Bile acids	Ileal bile-acid reabsorption and enterohepatic recycling; epithelial barrier and microbiota interaction	None established	Contextual; retained in Section 5 as a worked example of unconnected physiological and cancer-associated observations
FABP7 (B-FABP)	6q22.31	Brain, radial glia, neural stem cells, glioblastoma stem-like cells	Polyunsaturated fatty acids, including arachidonic acid and docosahexaenoic acid	Establishes the radial glial fiber system during neurogenesis; delivers polyunsaturated fatty acids to RXRα; binds cholesterol	None established	Principal focus, restricted to neural-lineage tumor
FABP8 (M-FABP, PMP2)	8q21.13	Peripheral nerve, myelin-producing cells	Long-chain fatty acids	Peripheral myelin lipid homeostasis; binds cholesterol and facilitates lysosomal egress	None established	Not discussed; minimal direct evidence in inflammation or cancer
FABP9 (T-FABP)	8q21.13	Testis, spermatozoa	Long-chain fatty acids	Not well defined outside reproductive biology	None established	Not discussed; noted in Section 7 only as an isoform whose capacity to compensate is unknown
FABP12	8q21.13	Retina, testis and selected tissues	Not well characterized	Not well defined	None established	Not discussed; noted in Section 7 only as an isoform whose capacity to compensate is unknown

[a]FABP4, FABP5, FABP8, FABP9 and FABP12 lie within a single tandem-duplication cluster at 8q21.13; the remaining isoforms map to separate loci (1,27). Nomenclature reflects the tissue in which each isoform was first identified and does not imply exclusivity: most tissues express more than one isoform (9,20). A-FABP, adipocyte FABP; aP2, adipocyte protein 2; B-FABP, brain FABP; CRABPII, cellular retinoic acid-binding protein II; E-FABP, epidermal FABP; FABP, fatty acid-binding protein; H-FABP, heart-type FABP; I-FABP, intestinal FABP; Il-FABP, ileal FABP; L-FABP, liver-type FABP; M-FABP, myelin FABP; PMP2, peripheral myelin protein 2; PPAR, peroxisome proliferator-activated receptor; RAR, retinoic acid receptor; RXRα, retinoid X receptor α; T-FABP, testis fatty acid-binding protein; VLDL, very low-density lipoprotein.

Table SII. Study-level extraction underlying the claim-level evidence map in Table I[a].

ID[b]	Claim as stated in the review	Isoform; disease context	System, species and manipulation	Outcome actually measured (class)[c]	Direction of result	Principal limitation	(Refs.)
S-01	FABP5 suppresses colorectal cancer progression by lowering FASN	FABP5; colorectal carcinoma	Human cell lines HCT116 and SW620; BALB/c nude mouse xenograft. Stable overexpression and shRNA knockdown; cycloheximide chase; MG132; FASN-ubiquitin co-immunoprecipitation; FASN shRNA and orlistat rescue	Proliferation, colony formation, migration and invasion; FASN protein and ubiquitination; LC3 and Beclin1; phospho-mTOR; xenograft volume and weight (established tumor growth)	FABP5 up → FASN down → tumor growth down	Two cell lines. The in vivo arm is described as SW620 in the Results but as HCT116 in the Fig. 7 legend, so model identity is internally inconsistent in the source. Subcutaneous xenograft only; no orthotopic or colitis-associated model	(16)
S-02	FABP5 promotes pancreatic neuroendocrine neoplasm progression by stabilizing FASN	FABP5; pancreatic neuroendocrine neoplasm	QGP-1, PNET and STC-1 cells; mouse xenograft. Stable overexpression and knockdown; FASN co-immunoprecipitation; MG132 chase; ubiquitination assay; orlistat rescue	Proliferation, migration and invasion; FASN protein and ubiquitination; lipid droplets by Nile red; WNT/β-catenin targets; xenograft growth (established tumor growth)	FABP5 up → FASN up → tumor growth up	Same laboratory as S-01 and contemporaneous, with the opposite direction for the same interaction and the same read-out; neither paper cites the other. Tumor type differs, so this is cross-tumor heterogeneity rather than contradiction, but the determining variable is untested	(91)
S-03	Tumor-intrinsic FABP5 drives colon cancer growth via HIF-1	FABP5; colorectal adenoma and carcinoma	Human cell lines HCT116, WiDr, HT29, Caco-2; no in vivo experiment. Transient siRNA knockdown with two sequences; normoxia 21% versus hypoxia 1% O2; oxygen-permeable three-dimensional culture chip, 7 days; gene-set enrichment analysis of a	Hypoxia-induced HIF-1α protein; HIF-1 target transcripts VEGF, CA9, LOX, PDK1 and BNIP3L; spheroid diameter; FABP5 mRNA in tissue (established tumor growth; premalignant change for the tissue series)	FABP5 knockdown → HIF-1α down and spheroid growth down, i.e. protumorigenic	No in vivo work. Loss of function only, with no overexpression arm. Transient silencing, so adaptation is untested. The paired tissue series cited (GSE8671, n = 32) is a colorectal adenoma set, not carcinoma, although described as colon cancer tissue. No survival analysis was performed despite the prognostic claim	(17)

			public paired expression series				
S-03R	Cross-study comparison: the colorectal directional conflict between S-01 and S-03	FABP5; colorectal adenoma and carcinoma	Structured comparison of design variables; not an experiment	Not applicable	Not applicable	Both studies used HCT116, so cell line does not explain the difference. Four candidate variables remain untested as the determining factor: disease stage (adenoma versus carcinoma), analyte (transcript versus protein), oxygen tension, and perturbation kinetics (transient versus stable, one direction versus both)	(16,17)
S-04	Acute loss of FABP5 function in regulatory T cells enhances suppression via mtDNA, cGAS-STING and IL-10	FABP5; tumor immunity and autoimmunity	Mouse in vitro-differentiated and ex vivo regulatory T cells; human blood-derived regulatory T cells; E.G7-OVA mouse tumor. Acute BMS309403 or Fabp5 shRNA; cGAS and STING siRNA; IFNAR knockout; Opa1 knockout control; anti-IL-10 blockade; washout	Oxygen consumption and extracellular acidification; electron transport chain complexes; cardiolipin; cristae width; cytosolic mtDNA; phospho-STAT1; Il10; suppression of responder proliferation (inflammatory phenotype)	FABP5 function down → IL-10 up → suppression up	The pharmacological arm is not isoform-selective; the inhibitor engages FABP3, FABP4 and FABP5. Fabp4/Fabp5 double-knockout cells showed the opposite metabolic phenotype, attributed to compensatory Fabp3. The tumor arm is descriptive: no in vivo FABP5 perturbation, one model at one time point, and type I interferon production by tumor regulatory T cells was not directly demonstrated. Anti-IL-10 abolished suppression regardless of FABP5 inhibition	(67)
S-05	Tumor regulatory T cells are FABP5-high yet display the phenotype of FABP5 loss of function	FABP5; breast carcinoma and transplantable lymphoma	Reanalysis of published human breast-carcinoma regulatory T-cell RNA-seq; mouse E.G7-OVA tumor; lipid-depleted culture to test the proposed explanation	FABP5, IL10, ISG15, IFI44 and RSAD2 expression; tumor interstitial lipid content; C16-BODIPY uptake (biomarker association)	FABP5 expression up; tumor interstitium lipid-poor; substrate scarcity proposed to produce a functional deficit	The reconciling step is a proposal supported by correlative measurements and has not been tested causally. Omitting it, however, makes the relationship read as FABP5-high causing IL-10, which the source does not support	(67)

S-06	Circulating FABP4 contributes causally to colorectal cancer risk	FABP4; colorectal cancer	Human; EPIC cohort and GECCO, CORECT and CCFR consortia. Prospective nested case-control; two-sample Mendelian randomization with one cis and two trans variants; cis-only analysis; colocalization; mediation analysis	Incident colorectal cancer (cancer incidence)	Null. RR 1.01 (0.92-1.12) per SD adjusted for body size; Mendelian randomization OR 1.10 (0.95-1.27); cis-only estimate in women 1.56 (1.09-2.23), not surviving correction	Instruments explain about 1% of FABP4 variance and the minimum detectable OR was 1.17 per SD, so a small effect is not excluded. Applies to the circulating protein and to colorectal cancer overall, not to colitis-associated disease, not to breast cancer and not to tissue FABP4	(119)
S-07	FABP4 binds PPARγ and shuttles agonists to the nucleus	FABP4; not disease-specific	COS1 and COS7 cells; recombinant protein. Wild-type and non-ligand-binding R126Q and Y19F mutants; confocal localization; pull-down with PPARα, β, γ1 and γ2 and with PPARγ DEF, ABC and AB domains	Nuclear versus cytosolic distribution; receptor binding (mechanism only)	Ligand binding enhances nuclear retention, but FABP4-PPARγ binding is ligand-independent and occurs at both the DNA-binding and ligand-binding regions	Heterologous overexpression in COS cells; no disease model. This study concerns adipocyte-type FABP (FABP4) and contains no FABP5 experiment	(42)
S-08	FABP4 promotes ubiquitination and proteasomal degradation of PPARγ	FABP4; adipose tissue and adipogenesis	Adipocytes, preadipocytes, 293T and NIH-3T3 cells; mouse adipose tissue. FABP4 overexpression and FABP4-null cells; HA-ubiquitin co-transfection with immunoprecipitation; proteasome inhibition; PPRE-luciferase reporter with and without	PPARγ protein level and half-life; mono- versus polyubiquitinated PPARγ; PPRE transactivation, basal and agonist-induced; adipocyte differentiation (inflammatory phenotype, mechanism)	FABP4 up → PPARγ polyubiquitination up, protein down, transactivation down; FABP4-null adipocytes have higher PPARγ	Largely overexpression and heterologous systems. The authors state that the interaction occurs through a site on FABP4 distinct from its fatty-acid pocket, and that inhibitor blockade may therefore be an indirect allosteric effect; they frame the whole as a negative feedback loop	(43)

			rosiglitazone; p53 as specificity control				
S-09	FABP5 carries a Cys120-Cys127 disulfide unique among mammalian intracellular lipid-binding proteins	FABP5; not disease-specific	Human recombinant protein; X-ray crystallography at 2.05 Å	Presence of the disulfide; cavity volume; ligand affinity (structure)	Six cysteines; only Cys120 and Cys127 form a disulfide; Cys67 and Cys87 are proximal but do not	A single structure. The antioxidant function is an inference from this structure and requires the separate 4-hydroxynonenal study (S-13)	(32)
S-10	Epidermal FABP prevents chemical-induced skin tumorigenesis	FABP5; cutaneous squamous carcinogenesis	Mouse two-stage DMBA/TPA model. Germline E-FABP knockout versus wild-type littermates; A-FABP (FABP4) knockout as isoform control; keratinocyte expression analysis	Tumor latency, incidence and number per mouse; TPA-induced IFN-β and IFN-λ; IFN-induced p53 response; SOX2 expression (cancer incidence)	E-FABP loss → skin tumor earlier, more frequent and more numerous; FABP4 loss has no such effect	A single carcinogenesis model with germline rather than skin-specific deletion, and chemical rather than inflammation-driven carcinogenesis, so it does not directly model psoriasis-associated cancer. It is nonetheless the only carcinogenesis experiment reported in skin	(167)
S-11	Intestinal epithelial FABP6 loss worsens colitis through a bile acid-microbiota-barrier mechanism	FABP6; dextran sulfate sodium-induced colitis	Mouse. Intestinal-epithelium-specific Fabp6 deletion versus control; dextran sulfate sodium-induced colitis; rescue by oral *Ligilactobacillus murinus* or taurodeoxycholic acid	Colitis severity; bile acid composition; microbiota composition (inflammatory phenotype)	Fabp6 loss → altered bile acids and dysbiosis → colitis worse; rescued by *L. murinus* or taurodeoxycholic acid	Extracted from the published Methods and Results rather than from the full report. A colitis model only, with no neoplastic endpoint. The loss-of-function direction is the opposite of the one a tumor-driver role would predict.	(116)
S-12	FABP6 is overexpressed in colorectal cancer and is detectable from the adenoma stage	FABP6; colorectal cancer	Human. Paired tumor and matched normal colorectal tissue; expression measurement only, with no perturbation	FABP6 mRNA level (biomarker association in the absence of perturbation)	FABP6 elevated in most paired tumor samples; detectable from the adenoma stage	Extracted from the published Methods and Results rather than from the full report. Expression only, so no causal inference is possible, and the data do not address whether FABP6	(117)

						contributes to the adenoma-carcinoma transition.	
S-13	Cys120 is the principal site of 4-hydroxynonenal modification of FABP5	FABP5; not disease-specific	Recombinant protein; rat retina and retinal pigment epithelium. MALDI-TOF/TOF adduct mapping; C120A, C127A and double mutants; guanidine denaturation; two-dimensional gels of retinal pigment epithelial extracts from E-FABP-null and wild-type mice	Site of modification; conformational stability; extent of 4-hydroxynonenal modification of other proteins in FABP5-null cells (mechanism)	Cys120 is the major modification site; modification is potentiated by bound fatty acid; the modified protein is more stable; FABP5-null cells show increased modification of other proteins	The stability increase belongs to the 4-hydroxynonenal adduct, not to the disulfide itself, and the in vivo evidence is retinal and retinal pigment epithelial rather than epidermal	(33)
S-14	Myeloid FABP5 restricts tumor growth	FABP5; tumor immunity	Mouse tumor models. E-FABP knockout and a small-molecule E-FABP activator	Tumor growth; IFN-β response in tumor-associated macrophages (established tumor growth)	FABP5 activity up → IFN-β up → tumor growth down	This anti-tumor myeloid direction has not been tested in the same system as the protumorigenic tumor-cell roles described elsewhere in the review, and the two should not be summed into a single directional statement	(59,61)

[a]Rows record what was read in the primary report, not what a secondary source states about it. [b]For all entries except S-11 and S-12 the primary report was obtained and read in full during revision; for S-11 and S-12 the extraction was made from the published Methods and Results sections, and this is stated in the limitation column of those two rows. [c]Outcome classes are inflammatory or immune phenotype; growth or spread of an already established tumor; premalignant change; cancer incidence; and biomarker association in the absence of perturbation. Where a study measured more than one class, each is named. A-FABP, adipocyte FABP; BNIP3L, BCL2-interacting protein 3-like; BODIPY, boron dipyrromethene; CA9, carbonic anhydrase 9; CCFR, Colon Cancer Family Registry; cGAS, cyclic GMP-AMP synthase; CORECT, Colorectal Transdisciplinary Study; DMBA, 7,12-dimethylbenz[a]anthracene; E-FABP, epidermal FABP; EPIC, European Prospective Investigation into Cancer and Nutrition; FABP, fatty acid-binding protein; FASN, fatty acid synthase; GECCO, Genetics and Epidemiology of Colorectal Cancer Consortium; HA, hemagglutinin; HIF-1, hypoxia-inducible factor 1; IFI44, IFN-induced protein 44; IFNAR, IFN α/β receptor; ISG15, IFN-stimulated gene 15; LC3, microtubule-associated protein 1 light chain 3; LOX, lysyl oxidase; MALDI-TOF/TOF, matrix-assisted laser desorption/ionization tandem time-of-flight mass spectrometry; mtDNA, mitochondrial DNA; mTOR, mammalian target of rapamycin; OPA1, mitochondrial dynamin-like GTPase OPA1; OR, odds ratio; PDK1, pyruvate dehydrogenase kinase 1; PPAR, peroxisome proliferator-activated receptor; PPRE, peroxisome proliferator-activated receptor response element; RNA-seq, RNA sequencing; RR, relative risk; RSAD2, radical S-adenosyl methionine domain-containing protein 2; SD, standard deviation; shRNA, short hairpin RNA; siRNA, small interfering RNA; STING, stimulator of interferon genes; TPA, 12-O-tetradecanoylphorbol-13-acetate; VEGF, vascular endothelial growth factor; WNT, Wingless/Int-1.