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Prevalence and Significance of AGR2 Expression in Human Cancer

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ABSTRACT

Backround: Anterior gradient 2 (AGR2) is a resident endoplasmic reticulum (ER) protein with a vital role in embryonal development, mucus maturation, tissue regeneration, and wound healing.

Methods: To determine the prevalence and clinical significance of AGR2 expression in cancer, a tissue microarray containing 14,966 tumors from 134 different tumor types and subtypes as well as 608 samples of 76 different normal tissue types was analyzed by immunohistochemistry (IHC).

Results: AGR2 positivity was found in 103 of 134 tumor categories, and 83 tumor categories contained at least one strongly positive case. AGR2 expression was most frequently seen in tumors of the female genital tract, particularly adenocarcinomas (up to 100%), various breast cancer subtypes (57.1%–100%), urothelial carcinoma (74.6%–100%), adenocarcinomas of the upper and lower gastrointestinal tract (93.6%–99.6%), and pancreaticobiliary cancers (65.2%–98.2%). AGR2 positivity was slightly less common in squamous cell carcinomas (46.4%–77.3%) and mainly absent in mesenchymal and lymphoid tumors. While AGR2 expression was only weak or absent in the normal thyroid, it was moderate to strong in 46.0% of adenomas, 52.8% of follicular carcinomas, and 81.8% of papillary carcinomas of the thyroid. High AGR2 expression was strongly linked to poor ISUP ($p < 0.0001$), Fuhrman ($p < 0.0001$), and Thoenes ($p < 0.0001$) grades as well as advanced pT stage ($p = 0.0035$) in clear cell renal cell carcinoma (ccRCC). Low AGR2 expression was associated with high BRE grade in breast cancer $(p=0.0049)$, nodal metastasis $(p=0.0275)$ and RAS mutation ($p=0.0136$) in colorectal cancer, nodal metastasis ($p=0.0482$) in endometrioid endometrial carcinoma, high grade in noninvasive urothelial carcinoma ($p=0.0003$), and invasive tumor growth in urothelial carcinoma ($p < 0.0001$). **Conclusions:** It is concluded that AGR2 expression occurs in a broad range of different tumor entities and that AGR2 assessment may serve as a diagnostic aid for the distinction of thyroidal neoplasms and as a prognostic marker in various cancer types.

Nina Schraps and Jacob Constantin Port contributed equally to this work.

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1 | Introduction

Anterior gradient 2, AGR2, is a resident endoplasmic reticulum (ER) protein with a role in oxidative protein folding in the endoplasmic reticulum [\[1\]](#page-17-0). The protein is also termed Xenopus Anterior gradient 2 (XAG2) or secreted cement gland protein XAG-2 homolog because it was initially discovered in the African frog *Xenopus laevis*, where it plays a role in embryonic development and cement gland differentiation [\[1, 2](#page-17-0)]. AGR2 is not restricted to the ER, has protein disulfide isomerase (PDI) activity, and exerts physiological roles in embryonal development, mucus maturation, tissue regeneration, and wound healing [[1, 3–6](#page-17-0)]. Its mucus stabilizing role is critical for maintaining epithelial barrier function in the intestine, where AGR2 forms a heterodisulfide bond with cysteine residues of MUC2 [\[4, 7\]](#page-17-1). Disturbed AGR2 function causes intestinal pathology due to a disrupted mucin maturation [[4, 7, 8](#page-17-1)]. *AGR*2 knockout mice show a loss of intestinal mucus and develop ileitis and colitis [[8](#page-17-2)]. A critical role of AGR2 in gastrointestinal health is also supported by the observation of a human enteropathy caused by a loss-of-function variant of AGR2 which is associated with a disturbed processing of mucins, increased ER stress, and goblet cell loss [[7](#page-17-3)].

Altered expression of AGR2 has been implicated with several signal transduction pathways and cell functions related to cancer initiation, progression, and metastasis [[9–13](#page-17-4)]. For example, high AGR2 levels have been linked to downregulation of the p53 response $[14]$ $[14]$, increased cell migration $[13]$ $[13]$, and cell transformation in cancer cell lines [\[15\]](#page-17-7) although others have observed repression of cell growth and proliferation in case of high AGR2 levels [[16, 17](#page-17-8)]. In breast and prostate cancer, AGR2 expression has been linked to estrogen receptor [\[17–19\]](#page-17-9) and androgen receptor regulation [[20, 21](#page-17-10)]. Studies evaluating larger cohorts of cancers by immunohistochemistry (IHC) have identified associations between high AGR2 expression and unfavorable tumor phenotype or poor prognosis in adenocarcinoma of the lung [[10\]](#page-17-11), gastric adenocarcinoma [[22](#page-17-12)], and adenocarcinoma of the prostate [[23\]](#page-17-13). However, the number of studies analyzing AGR2 in cancer is still limited. In 34 studies using IHC, only 26 different tumor entities have so far been evaluated (Medline, May 2024). Moreover, in 12 cancer entities where multiple studies have been executed, the obtained results were sometimes considerably discrepant. For example, the range of reported AGR2-positive cases ranged from 56.8% to 100% in adenocarcinoma of the lung $[10, 24]$ $[10, 24]$, from 57.0% to 95.4% in prostate cancer [\[21, 23\]](#page-17-14), and from 19.0% to 46.1% in serous carcinoma of the ovary [\[13, 25](#page-17-6)]. Such conflicting results could be caused by the use of different antibodies, immunostaining protocols, and criteria to define positivity.

To better understand the prevalence and potential clinical significance of AGR2 expression in cancer, a comprehensive study analyzing a large number of neoplastic and nonneoplastic tissues under highly standardized conditions is needed. Therefore, AGR2 expression was analyzed in more than 14,000 tumor tissue samples from 134 different tumor types and subtypes as well as 76 nonneoplastic tissue categories by immunohistochemistry (IHC) in a tissue microarray (TMA) format in this study.

2 | Materials and Methods

2.1 | Tissue Microarrays (TMAs)

The normal tissue TMA was composed of eight samples from eight different donors for each of 76 different normal tissue types (608 samples on one slide). The cancer TMAs contained a total of 14,966 primary tumors from 134 tumor types and subtypes. Detailed histopathological data on grade, pT, or pN were available from subsets of colorectal cancer (*n*=2351), endometrioid endometrial carcinoma (*n*=182), clear cell (*n*=1224) and papillary renal cell carcinoma $(n=310)$, serous $(n=369)$ and endometrioid carcinoma of the ovary $(n=40)$, thyroid carcinoma $(n=518)$, urothelial carcinoma $(n=829)$, as well as pancreatic carcinomas ($n = 598$). Clinical follow-up data were available from 789 patients with ccRCC and from 177 patients with pRCC with a median follow-up time of 48.0 and 50.5months (range 1–250 and 1–247) and 254 patients with urothelial carcinoma with a median follow-up time of 14.0months (range 1–77). The composition of both normal and cancer TMAs is described in detail in the results section. All samples were from the archives of the Institutes of Pathology, University Hospital of Hamburg, Germany, the Institute of Pathology, Clinical Center Osnabrueck, Germany, and Department of Pathology, Academic Hospital Fuerth, Germany. Tissues were fixed in 4% buffered formalin and then embedded in paraffin. The TMA manufacturing process was described earlier in detail [[26, 27\]](#page-17-15). In brief, one tissue spot (diameter: 0.6mm) per patient was used. The use of archived remnants of diagnostic tissues for manufacturing of TMAs and their analysis for research purposes as well as patient data analysis has been approved by local laws (HmbKHG, §12) and by the local ethics committee (Ethics commission Hamburg, WF-049/09). All work has been carried out in compliance with the Helsinki Declaration.

2.2 | Immunohistochemistry (IHC)

Freshly cut TMA sections were immunostained on 1day and in one experiment. Slides were deparaffinized with xylol, rehydrated through a graded alcohol series and exposed to heatinduced antigen retrieval for 5min in an autoclave at 121°C in pH7.8 Tris-EDTA-Citrat (TEC) puffer. Endogenous peroxidase activity was blocked with Dako REAL Peroxidase-Blocking Solution (Agilent Technologies, Santa Clara, CA, USA; #S2023) for 10min. Primary antibody-specific against AGR2 protein (rabbit recombinant, HMV-325, ardoci GmbH, Hamburg, Germany) was applied at 37°C for 60min at a dilution of 1:150. For the purpose of antibody validation, the normal tissue TMA was also analyzed by the rabbit recombinant AGR2 antibody EPR3278 (ab76473, Abcam Limited, Cambridge CB2 0AX, GB) at a dilution of 1:1800 and an otherwise identical protocol. Bound antibody was then visualized using the Dako REAL EnVision Detection System Peroxidase/DAB+, Rabbit/Mouse kit (Agilent Technologies, Santa Clara, CA, USA; #K5007) according to the manufacturer's directions. The sections were counterstained with hemalaun. For tumor tissues, the percentage of AGR2 positive tumor cells was estimated, and the staining intensity was semi-quantitatively recorded (0, 1+, 2+, 3+). For statistical analyses, the staining results were categorized into four groups as follows: negative: no staining at all, weak staining: staining

intensity of 1+ in $\langle 70\% \rangle$ or staining intensity of 2+ in $\langle 30\% \rangle$ of tumor cells, moderate staining: staining intensity of 1+ in $>70\%$, staining intensity of 2+ in $>30\%$ but in $\leq 70\%$ or staining intensity of $3+$ in $\leq 30\%$ of tumor cells, strong staining: staining intensity of $2+$ in $>70\%$ or staining intensity of $3+$ in $>30\%$ of tumor cells. The evaluation was performed by an experienced pathologist (SB).

2.3 | Statistics

Statistical calculations were performed with JMP17 software (SAS, Cary, NC, USA). Contingency tables and the chi-squared test were performed to search for associations between AGR2 staining and tumor phenotype. The log-rank test was applied to detect significant differences between groups.

3 | Results

3.1 | Technical Issues

A total of 12,434 (83.1%) of 14,966 tumor samples were interpretable in our TMA analysis. Noninterpretable samples demonstrated a lack of unequivocal tumor cells or a lack of entire tissue spots. A sufficient number of samples (≥ 4) of each normal tissue type was evaluated.

3.2 | AGR2 Immunostaining in Normal Tissues

A strong, predominantly cytoplasmic AGR2 staining occurred in various epithelial cell types such as from the colorectum, stomach (except parietal cells), gallbladder, pancreas (intercalated ducts and excretory ducts), seminal vesicle, urothelium, respiratory epithelium, lung (a large subset of pneumocytes), breast (a subset of luminal cells), endocervix, endometrium, and the fallopian tube. A somewhat less intense AGR2 staining also occurred in glandular (especially mucinous) and excretory duct cells of salivary glands, Brunner glands of the duodenum, a small subset of tubuli/collecting ducts of the kidney, a subset of epithelial cells in the epididymis, and a subset of epithelial cells of the adenohypophysis. Staining was variable ranging from absent to strong in pancreatic acinar cells as well as in acinar and basal cells of the prostate. AGR2 staining was mostly absent in squamous epithelial cells except in the tonsil, a fraction of cells of corpuscles of Hassall's, and the inner (Huxley) layers of hair follicles of the skin. In the thyroid, AGR2 staining was mostly absent although a weak to moderate staining occasionally was seen. Representative images are shown in Figure [1.](#page-2-0) All cell types found to be positive by HMV-325 were also confirmed as AGR2 positive by EPR3278 (Figure [S1](#page-19-0)). AGR2 staining was always absent in hepatocytes, testis, ovary, placenta, adrenal gland, parathyroid, brain, mesenchymal tissues, and in hematolymphatic cells.

3.3 | AGR2 Immunostaining in Neoplastic Tissues

A cytoplasmic AGR2 immunostaining was observed in 7514 (60.4%) of 12,434 analyzable tumors including 732 (5.9%) with weak, 874 (7.0%) with moderate, and 5908 (47.5%) with strong staining intensity. We did not see any membranous or extracellular staining of AGR2. Representative images are shown in Figure [2.](#page-3-0) At least an occasional weak AGR2 positivity was detected in 103 of 134 tumor types and tumor subtypes and 83

FIGURE 1 | AGR2 immunostaining of normal tissues. The panels show a strong cytoplasmic AGR2 immunostaining of all epithelial cells of the stomach except parietal cells (a), as well as of all epithelial cells of the duodenal mucosa (b), the colorectal mucosa (c), the endocervical epithelium (d), the endometrium of the pregnant uterus (e), the cauda epididymis (f), and the seminal vesicle (g). Most epithelial cells of a prostate sample are also AGR2 positive (h).

FIGURE 2 | AGR2 immunostaining in cancer. AGR2 staining was cytoplasmic. The panels show a strong AGR2 positivity in cancer cells of adenocarcinoma of colon (a), gastric adenocarcinoma (b), adenocarcinoma of the pancreas (c), urothelial carcinoma (d), follicular thyroid carcinoma (e) and clear cell renal cell carcinoma (f), AGR2 immunostaining is absent in mesothelioma (g), and seminoma (h).

entities included at least one case with strong AGR2 positivity (Table [1\)](#page-4-0). AGR2 expression was most frequently seen in tumors of the female genital tract, particularly adenocarcinoma of the cervix (100%) and mucinous carcinoma of the ovary (100%), various subtypes of breast cancer (57.1%–100%), urothelial carcinoma (74.6%–100%), adenocarcinoma of the upper and lower gastrointestinal tract (93.6%–99.6%), as well as in pancreaticobiliary cancers (65.2%–98.2%). AGR2 positivity was slightly less common in neuroendocrine neoplasms (20.0%–100%) and in squamous cell carcinoma (46.4%–77.3%). AGR2 staining was only rarely seen in adrenocortical tumors (4.3%–9.3%) and in renal cell carcinoma (7.8%–26.5%), and mainly absent in melanoma, seminoma, embryonal carcinoma, adrenocortical neoplasms, tumors of the hematopoietic and lymphoid tissues, as well as mesenchymal tumors. A graphical representation of a ranking order of AGR2 positive and strongly positive cancers is given in Figure [3.](#page-11-0) The relationship between AGR2 expression and tumor phenotype in different cancer types is summarized in Table [2.](#page-12-0) High AGR2 expression was strongly linked to poor ISUP $(p<0.0001)$, Fuhrman $(p<0.0001)$, and Thoenes (p <0.0001) grades as well as advanced pT stage (p =0.0035) in clear cell renal cell carcinoma (ccRCC). AGR2 staining was associated with shortened recurrence-free survival $(p=0.0275)$ in ccRCC. That AGR2 staining was unrelated to overall survival in ccRCC ($p = 0.1826$), may be due to the low number of positive cases (Figure [S2](#page-19-0)). A reduced AGR2 expression was significantly associated with high BRE grade in breast cancer $(p=0.0049)$, nodal metastasis ($p=0.0275$) and RAS mutation ($p=0.0136$) in colorectal cancer, nodal metastasis (*p*=0.0482) in endometrioid endometrial carcinoma, high grade in noninvasive urothelial carcinoma ($p = 0.0003$), and with invasive tumor growth in urothelial carcinoma (*p*<0.0001). In urothelial carcinoma, AGR2 staining was unrelated to overall and recurrence-free

survival ($p > 0.1$). AGR2 immunostaining was unrelated to parameters of tumor aggressiveness in pancreatic, ovarian, and thyroidal cancer as well as papillary renal cell carcinoma although tumors with lower AGR2 expression often tended to exhibit more unfavorable tumor features.

4 | Discussion

The successful analysis of 12,434 tumors from 134 different tumor categories provides a comprehensive overview on AGR2 expression in cancer. The data show that the AGR2 findings in tumors largely mirror the observations in normal tissues. A significant AGR2 expression was found in large fractions of cases in virtually all epithelial tumor entities but only rarely in nonepithelial neoplasms. That adenocarcinomas are more commonly positive than squamous cell carcinomas reflects the limited AGR2 expression in normal squamous epithelium. That only few renal cell carcinomas were AGR2 positive also parallels our normal tissue findings as only few tubuli and collecting ducts had shown AGR2 staining in the normal kidney. For the few tumor entities that were previously analyzed for AGR2 expression, our positivity rates were generally in the upper range of earlier data (Figure [4\)](#page-16-0). This demonstrates a comparatively high sensitivity of our assay. Accordingly, we found higher positivity rates for squamous cell carcinomas of the lung (77.3%) than the 49% of Fritzsche et al. [\[28](#page-18-0)] and the 45% of Pizzi et al. [\[24\]](#page-17-16), for squamous cell carcinomas of the esophagus (64.3%) than the 28.4% of Takabatake et al. [\[29](#page-18-1)] and the 37% of DiMaio et al. [\[30\]](#page-18-2) for clear cell carcinomas of the ovary (90%) than the 45% of Armes et al. [\[25](#page-17-17)] and the 11.1% of Darb-Esfahani et al. [\[31\]](#page-18-3) and for serous high-grade carcinomas of the ovary (67.2%) than the 32.3% of Darb-Esfahani et al. [\[31](#page-18-3)], the 50% of Park et al. [\[13](#page-17-6)], and

 $(Continuous)$ (Continues)

TABLE 1 | AGR2 immunostaining in human tumors. **TABLE 1** | AGR2 immunostaining in human tumors.

 $(Continuous)$

the 19% of Armes et al. [[25](#page-17-17)]. We also found an AGR2 positivity in 38.6% of our 277 hepatocellular carcinomas, a cancer type where Lepreux et al. [\[32](#page-18-4)] had previously not found AGR2 staining in a cohort of 12 cancers. Possible reasons that might have caused these discrepancies include differences in the staining protocols and antibodies used as well as different definitions of thresholds to determine positivity.

The comprehensive analysis of a broad range of cancer types and their corresponding normal tissues is an important prereq uisite to assess the potential diagnostic utility of an IHC assay. The most striking diagnostic aspect for AGR2 was its significant upregulation in a large number of thyroidal neoplasms. While AGR2 expression was weak or absent in our normal thyroid, a moderate to strong AGR2 staining was observed in 46% of ade nomas, 52.8% of follicular carcinomas, 81.8% of papillary carci nomas, and 31.6% of anaplastic carcinomas of the thyroid. AGR2 IHC may therefore be helpful for the distinction of neoplastic from nonneoplastic thyroidal tissues, which is especially chal l[enging](#page-18-5) in cytology where sensitivity ranges from 45% to 95.2% [\[33–38\]](#page-18-5) depending on the subtype. Other potential diagnostic applications of AGR2 IHC may include the distinction of renal cell carcinomas (usually negative) from urothelial carcinomas (usually positive) from the kidney and mesotheliomas (usually negative) from adenocarcinomas (usually positive) of the lung. However, all these potential diagnostic applications need to be further evaluated.

The availability of large subsets of tumors from various import ant cancer entities enabled us to also address the clinical/prog nostic relevance of AGR2 expression in diverse cancers. These data demonstrate that the prognostic role of AGR2 is cancer-type dependent. In most cancers derived from tissues with high AGR2 expression in normal cells, such as the colorectum, the breast, the endometrium, and the urothelium, a reduced expression paralleled morphological parameters of tumor aggressiveness such as high histologic grade and advanced stage. These find ings are in line with earlier data. Associations between reduced AGR2 expression and unfavorable tumor features have been de scribed for colorectal cancer [\[39](#page-18-6)], ductal adenocarcinoma of the pancreas [\[40\]](#page-18-7), prostate cancer [\[41](#page-18-8)], ovarian cancer [\[16, 25\]](#page-17-8), and adenocarcinoma of the lung [\[42\]](#page-18-9) although other groups could not confirm these findings for ovarian [\[31](#page-18-3)] and lung cancer [\[28\]](#page-18-0) and others even found a link between low AGR expression and favorable tumor features for lung [\[10\]](#page-17-11), ovarian, [\[31](#page-18-3)] and pros tate cancer [\[23](#page-17-13)]. The reasons for the role of AGR2 loss in tumor progression are not clear. Functional studies have suggested a higher resistance to apoptosis [[43\]](#page-18-10) and a reduction of cellular adhesion [\[40, 43](#page-18-7)]. Alternatively, it is possible that reduced AGR2 expression in tumors derived from AGR2-expressing normal cells just reflects tumor cell dedifferentiation which usually par allels cancer progression.

Elevated AGR2 expression was associated with unfavorable tumor features in only one of our cancer entities. The strong link of high AGR2 with high grade and advanced stage in clear cell renal cell carcinoma (ccRCC) is in line with RNA data from the Cancer Genome Atlas (TCGA) which also suggested a poor prognosis in case of high AGR2 expression levels [\[44\]](#page-18-11). Although the number of AGR2-positive cases was low (7.8%) in this cancer entity, AGR2 expression analysis might become clinically useful

FIGURE 3 | Ranking order of AGR2-positive immunostaining in different human tumors. Orange dots show the percentage of strongly stained samples, whereas blue dots show the percentage of positive samples of any intensity.

in this cancer type because patients with high-risk renal cell carcinomas are increasingly subjected to adjuvant chemotherapy, and risk assessment by histology alone is not sufficient for a safe individual risk assessment. Elevated levels of AGR2 expression have earlier also been linked to unfavorable tumor features in breast cancer [\[12\]](#page-17-18), prostate cancer [\[23\]](#page-17-13), head and neck squamous cell carcinoma [\[45](#page-18-12)], and squamous cell carcinoma of the esophagus [\[29\]](#page-18-1).

Potential cancer promoting effects of AGR2 upregulation include a stimulating role on cell proliferation [\[29, 46, 47\]](#page-18-1), migration [\[47, 48\]](#page-18-13), epithelial–mesenchymal transition [\[48\]](#page-18-14), invasion $[49, 50]$, and chemoresistance $[47]$ $[47]$. Arumugam et al. $[47]$ reported that AGR2 stimulated the proliferation, migration, invasion, and chemoresistance of pancreatic ductal adenocarcinoma cells by interacting with the metastasis-associated protein C4.4A that is co-expressed on the cell surface. Jia et al. [\[51\]](#page-18-16) found that AGR2 directly interacts with VEGFA and enhances VEGFR/VEGFR2 signaling in prostate cancer cells, leading to the acquisition of a mesenchymal phenotype in vivo and in vitro, which is associated with increased invasiveness and metastatic growths. Fessart et al. [\[46\]](#page-18-17) described a mechanism by which secreted AGR2 acts like a growth factor and stimulates cell proliferation in lung cancer cells by repressing cyclin-dependent kinase inhibitor 1A (CDKN1A). Zhang et al. [[48\]](#page-18-14) reported that intracellular but not extracellular AGR2 promotes the expression of the SNAIL and SLUG transcription factors through direct transcriptional activation and histone 3 acetylation. This drives epithelial–mesenchymal transition in colorectal cancer cells [\[48](#page-18-14)], an important cellular process leading to increased migratory capability and invasive potential [\[52\]](#page-18-18). Others have found that extracellular AGR2 may promote cell migration and metastasis in CRC through noncanonical Wnt signaling [\[53\]](#page-18-19). Takabatake et al. [\[29\]](#page-18-1) described a direct interaction of AGR2 with the p53 tumor suppressor that results in attenuation of p53 activity and increased cell proliferation in esophageal squamous cell carcinoma cells. Again, it cannot be excluded that AGR2 neo-expression in tumors derived from non-AGR2-expressing normal cells is caused by random alterations occurring because of tumor cell dedifferentiation.

peutic target. Wu et al. [\[54](#page-18-20)] showed inhibition of breast cancer growth in vitro using the first developed monoclonal antibody directed against AGR2, termed 184A. Subsequent studies showed the potential therapeutic benefit of a humanized version of 184A in ovarian cancer xenografts [\[55\]](#page-18-21) and improved survival in lung cancer in mice [\[56\]](#page-18-22). Further therapeutic strategies are targeting the influence of AGR2 on chemotherapy resistance. Studies have shown that AGR2 is involved in cellular survival and the development of tamoxifen resistance in breast cancer [\[57\]](#page-18-23). Antibodies directed against AGR2 were able to reduce tumor growth in endocrine therapy-resistant breast cancer [\[58\]](#page-18-24).

Additional interest in AGR2 is based on its potential as a thera-

Considering the large scale of our study, our assay was extensively validated according to the recommendations of the international working group of antibody validation (IWGAV) [\[59\]](#page-18-25) by comparing our IHC findings in normal tissues with data obtained by another independent anti-AGR2 antibody and RNA data derived from three different publicly accessible databases [\[60–63\]](#page-18-26). To ensure an as broad as possible range of proteins to be tested for a possible cross-reactivity, 76 different normal tissue categories were included in this analysis. These diverse tissues are likely to contain a large fraction of the proteins expressed in cells of adult humans all of which are screened for potential cross-reactivities of antibodies. Our normal tissue analysis revealed AGR2 immunostaining in all organs for which RNA expression had been described (salivary glands, stomach, duodenum small intestine, appendix, colorectum, gallbladder, urinary bladder, lung, pituitary gland, epididymis, prostate, seminal vesicle, breast, cervix, and fallopian tube). While significant RNA expression had not been reported for other tissues with IHC-positive cell types, such as endometrium, intercalated ducts and acinar cells of the pancreas, a subset of tubuli/collecting ducts of the kidney, squamous epithelial cells of the tonsil, hair follicles, and of corpuscles of Hassall's of the thymus, these staining obtained by our assay were confirmed by an independent second AGR2 antibody. It is likely that these cell types are made up of too small fractions of their entire organs to be detected in RNA

AGR2 immunostaining

analysis of disintegrated tissues. Overall, these validation data document a high level of specificity for our AGR2 IHC assay.

In summary, our data provide a comprehensive overview of AGR2 expression in different tumor entities, identify AGR2 IHC as a potential diagnostic aid for the identification of thyroidal neoplasms, and demonstrate a potential prognostic role of AGR2 in various cancer types.

Author Contributions

Nina Schraps: conceptualization (equal), data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), visualization (equal), writing – original draft (equal). **Jacob Constantin Port:** conceptualization (equal), data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), visualization (equal), writing – original draft (equal). **Anne Menz:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Florian Viehweger:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Seyma Büyücek:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), visualization (equal), writing – review and editing (supporting). **David Dum:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Ria Schlichter:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Andrea Hinsch:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Christoph Fraune:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Christian Bernreuther:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Martina Kluth:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Claudia Hube-Magg:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing – review and editing (supporting). **Katharina Möller:** data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), resources (equal), writing

FIGURE 4 | AGR2 protein expression in cancer (own findings vs. literature data). Graphical representation of AGR2 data from this study (X) compared to the previous literature. The colors of the dots represent the number of tumors analyzed in these studies: Red: $n \le 20$, yellow: $n = 21$ to 100, green: *n*>100. For raw data and references, see Table [S1](#page-19-0).

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Ethics Statement

The use of archived remnants of diagnostic tissues for manufacturing of TMAs and their analysis for research purposes as well as patient data analysis has been approved by local laws (HmbKHG, §12) and by the local ethics committee (Ethics commission Hamburg, WF-049/09), allowing the use of leftover diagnostic tissues and corresponding clinical data for scientific research without the patients written consent. All work has been carried out in compliance with the Helsinki Declaration.

Conflicts of Interest

The AGR2 antibody clone HMV-325 was provided by ardoci GmbH (owned by a family member of G.S.).

Data Availability Statement

All data generated or analyzed during this study are included in this published article.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.