

# of total hit	accession	custom cluster
1	cd17926	Helicase_ATP-bd
1	cd18012	Helicase_ATP-bd
2	PF00176	Helicase_ATP-bd
10	SM00487	Helicase_ATP-bd
4	cd18011	Helicase_ATP-bd
7	PS51192	Helicase_ATP-bd
1	cd17919	Helicase_ATP-bd
2	PF04851	Helicase_ATP-bd
330	PF01476	LysM
332	cd00118	LysM
333	PS51782	LysM
327	SM00257	LysM
46	cd00599	GH25
1	cd06417	GH25
61	cd06415	GH25
4	cd06414	GH25
3	cd06525	GH25
275	PF01183	GH25
207	SM00641	GH25
1	cd06522	GH25
24	cd06523	GH25
20	PF05036	SPOR
16	PS51724	SPOR
194	SM00646	Ami_3
209	cd02696	Ami_3
213	PF01520	Ami_3
4	PS50222	EF_HAND_2
1239	SM00644	Ami_2
202	SM00701	Ami_2
1173	cd06583	Ami_2
1407	PF01510	Ami_2
1	PF00565	SNase
1	PS50830	SNase
1	SM00318	SNase
1	cd02883	NUDIX
1	PF00293	NUDIX
1	PS51462	NUDIX
1	PF10908	YkuD
7	cd16913	YkuD
4	PF03734	YkuD

7	PS51194	Helicase_C
8	cd18793	Helicase_C
4	SM00490	Helicase_C
1	PS51348	SLT-related
12	cd16899	SLT-related
1	PF00062	SLT-related
14	cd13399	SLT-related
14	cd16896	SLT-related
837	PF01464	SLT-related
334	cd00254	SLT-related
46	cd13401	SLT-related
24	cd01021	SLT-related
15	cd16893	SLT-related
91	cd16894	SLT-related
50	cd13400	SLT-related
71	cd13403	SLT-related
182	cd13925	SLT-related
152	PF06737	SLT-related
462	cd13402	SLT-related
232	PF18013	SLT-related
94	cd14814	Peptidase_M15
2	cd14852	Peptidase_M15
47	PF02557	Peptidase_M15
1	cd14849	Peptidase_M15
131	cd14844	Peptidase_M15
156	PF08291	Peptidase_M15
228	PF06714	Gp5_OB_N
179	cd13926	GH108
172	PF05838	GH108
349	cd00737	Phage_lysozyme
1	cd16904	pesticin_lyz_like2
130	cd00736	Phage_lysozyme
282	cd16900	Phage_lysozyme
73	cd16901	Phage_lysozyme
1003	PF00959	Phage_lysozyme
422	cd00735	Phage_lysozyme
3	PF07669	MTases
3	cd02440	MTases
2	PF05175	MTases
21	cd16891	LT_GEWL_like
21	PF13702	LT_GEWL_like
42	cd00229	SGNH_hydro
42	PF13472	SGNH_hydro
2	PF02368	Big_2

4	SM00635	Big_2
136	PF08230	CPL7
136	SM01095	CPL7
7	cd00978	GH46
7	PF01374	GH46
6	cd16902	Pesticin_C
6	PF16754	Pesticin_C
473	cd00325	GH19
202	PF00182	GH19
380	cd14845	Peptidase_M15
428	PF13539	Peptidase_M15
14	cd14667	3D
7	PF06725	3D
1	cd14688	bZIP_YAP
31	PF13884	S74_ICA
43	PS51688	S74_ICA
70	cd06503	ATP-synt_Fo_b
2	cd18586	ABC_6TM_PrtD_like
1	cd18577	ABC_6TM_Pgp_ABCB1_D1_like
1	cd18028	Helicase_ATP-bd
1	cd17504	MFS_MMR_MDR_like
3	cd17477	MFS_YcaD_like
1	cd17330	MFS_SLC46_TetA_like
1	cd17324	MFS_NepI_like
2	cd17321	MFS_MMR_MDR_like
1	cd17040	Ubl_MoaD_like
7	cd17320	MFS_MdfA_MDR_like
12	cd14830	Delta_COP_N
1	cd08173	Gro1PDH
2	cd06180	MFS_YjiJ
3	cd06174	MFS
3	cd06173	MFS_MefA_like
1	cd04631	CBS_archAMPK_gamma-repeat
1	cd02775	MopB_CT
8	cd00890	Prefoldin
1	cd00063	FN3
1	cd00442	Lyz_like
1	PS51272	SLH
1	PS50861	AA_TRNA_LIGASE_II_GLYAB
1	PS51186	GNAT
4	PS50853	FN3
1	PS50817	INTEIN_N_TER
8	PS50163	RECA_3
7	PF18858	LPD39

5	PF18857	LPD38
2	PF18853	LPD37
3	PF18823	InPase
2	PF18809	PBECR1
1	PF18760	ART-PolyVal
5	PF18798	LPD3
17	PF18341	PSA_CBD
1	PF17969	Ldt_C
3	PF16838	Caud_tail_N
186	PF16775	ZoocinA_TRD
8	PF15711	ILEI
3	PF13810	DUF4185
1	PF13751	DDE_Tnp_1_6
1	PF13550	Phage-tail_3
1	PF13385	Laminin_G_3
156	PF13529	Peptidase_C39_2
1	PF13365	Trypsin_2
1	PF13354	Beta-lactamase2
1	PF13199	Glyco_hydro_66
19	PF12385	Peptidase_C70
6	PF12200	DUF3597
31	PF12123	Amidase02_C
90	PF11860	Muramidase
2	PF11650	Tail_accessory_Gp4
214	PF10145	Phage_tape_meas
37	PF10464	Peptidase_U40
2	PF09718	Phage_lambda_GpH_tape_mea
6	PF09588	YqaJ
157	PF09374	PG_3
23	PF08924	DUF1906
1	PF08481	GBS_Bsp-like
220	PF08310	LGFP
31	PF07902	Gp58
1	PF07833	Cu_amine_oxidN1
1	PF06832	BiPBP_C
32	PF07486	Hydrolase_2
1	PF02384	N6_Mtase
2	PF02018	CBM_4_9
1	PF01664	Reo_sigma1
339	PF01471	PG_1
36	PF01391	Collagen
1	PF01129	ART
1	PF00912	Transgly
1	PF00905	Transpeptidase

1	PF00395	SLH
1	PF00753	Lactamase_B
6	PF06791	TMP_2
230	PF06715	Gp5_C
1	PF05598	Transposase_Insh_N
4	PF05435	DNA_terminal_Gp3
231	PF05382	Ami_5
1	PF05203	Hom_end_hint
1	PF05106	Phage_lambda_GpS_holin
1	PF04965	IraD/Gp25-like
2	PF03330	RlpA-like_DPBB
1	PF04466	Terminase_L_N
84	PS50249	MPN
77	SM00232	MPN
185	cd08073	MPN
183	PF14464	MPN
469	PF00877	NLPC_P60
499	PF01551	Peptidase_M23
548	PF01473	CW
662	PS51170	CW
23	PS51257	PROKAR_LIPOPROTEIN
403	PF01832	Glucosaminidase
371	SM00047	Glucosaminidase
32	PF08239	SH3
321	PF08460	SH3
155	PS51781	SH3
290	SM00287	SH3
634	PF05257	CHAP
657	PS50911	CHAP

accession - [InterPro name - source db name]

average fraction of the overl

	cd17926	cd18012	PF00176	SM00487	cd18011	PS51192	cd17919	PF04851
cd17926- [DEXH-box helicase domain of DEAD-like helicase restrict	1			0		0		
cd18012- [DEAQ-box helicase domain of archaeal and bacterial SNF		1	0	0				
PF00176- [SNF2-related, N-terminal domain (SNF2_N) - SNF2 family		0	1	1	1	1		
SM00487- [Helicase superfamily 1/2, ATP-binding domain (Helicase	0	0	1	1	1	1	0	1
cd18011- [DEXH-box helicase domain of RapA (DEXDc_RapA)]			1	1	1	1		1
PS51192- [Helicase superfamily 1/2, ATP-binding domain (Helicase	0		1	1	1	1	0	1
cd17919- [DEXH/Q-box helicase domain of DEAD-like helicase Snf f				0		0	1	1
PF04851- [Helicase/UvrB, N-terminal (Helicase/UvrB_N) - Type III re				1	1	1	1	1
PF01476- [LysM domain (LysM_dom) - LysM domain (LysM)]								
cd00118- [LysM domain (LysM_dom) - Lysin Motif is a small domain								
PS51782- [LysM domain (LysM_dom) - LysM domain profile (LYSM)								
SM00257- [LysM domain (LysM_dom) - Lysin motif (LysM)]								
cd00599- [Endo-N-acetylmuramidases (muramidases) are lysozyme								
cd06417- [LysA is a cell wall endolysin produced by Lactobacillus fe								
cd06415- [Cpl-1 lysin (also known as Cpl-9 lysozyme / muramidase)								
cd06414- [The LytC lysozyme of Streptococcus pneumoniae is a bac								
cd06525- [Lyc muramidase is an autolytic lysozyme (autolysin) from								
PF01183- [Glycoside hydrolase, family 25 (Glyco_hydro_25) - Glyco								
SM00641- [Glycoside hydrolase, family 25 subgroup (Glyco_hydro_								
cd06522- [AtIA is an autolysin found in Gram-positive lactic acid ba								
cd06523- [PlyB is a bacteriophage endolysin that displays potent ly								
PF05036- [Sporulation-like domain (SPOR-like_dom) - Sporulation r								
PS51724- [Sporulation-like domain (SPOR-like_dom) - SPOR domain								
SM00646- [N-acetylmuramoyl-L-alanine amidase, catalytic domain								
cd02696- [N-acetylmuramoyl-L-alanine amidase, catalytic domain (
PF01520- [N-acetylmuramoyl-L-alanine amidase, catalytic domain (
PS50222- [EF-hand domain (EF_hand_dom) - EF-hand calcium-bind								
SM00644- [N-acetylmuramoyl-L-alanine amidase domain (Amidase								
SM00701- [Peptidoglycan recognition protein family domain, meta								
cd06583- [N-acetylmuramoyl-L-alanine amidase domain (Amidase_								
PF01510- [N-acetylmuramoyl-L-alanine amidase domain (Amidase_								
PF00565- [Staphylococcal nuclease (SNase-like), OB-fold (Staphyloc								
PS50830- [Staphylococcal nuclease (SNase-like), OB-fold (Staphyloc								
SM00318- [Staphylococcal nuclease (SNase-like), OB-fold (Staphylo								
cd02883- [Nudix hydrolase is a superfamily of enzymes found in all								
PF00293- [NUDIX hydrolase domain (NUDIX_hydrolase_dom) - NUD								
PS51462- [NUDIX hydrolase domain (NUDIX_hydrolase_dom) - Nuc								
PF10908- [Protein of unknown function DUF2778 (DUF2778) - Prot								
cd16913- [L,D-transpeptidases/carboxypeptidases similar to Bacillu								
PF03734- [L,D-transpeptidase catalytic domain (LD_TPept_cat_dom								

PS51194- [Helicase, C-terminal (Helicase_C) - Superfamilies 1 and 2
cd18793- [C-terminal helicase domain of the SNF family helicases (S
SM00490- [Helicase, C-terminal (Helicase_C) - helicase superfamily
PS51348- [Glycoside hydrolase, family 22 (Glyco_hydro_22) - Alpha
cd16899- [C-type invertebrate lysozyme (LYZ_C_invert)]
PF00062- [Glycoside hydrolase, family 22 (Glyco_hydro_22) - C-type
cd13399- [Slit35-like lytic transglycosylase (Slit35_like)]
cd16896- [Uncharacterized lytic transglycosylase subfamily with sim
PF01464- [Transglycosylase SLT domain 1 (Transglycosylase_SLT_do
cd00254- [Lytic transglycosylase (LT) and goose egg-white lysozyme
cd13401- [70kDa soluble lytic transglycosylase (Slit70) and similar p
cd01021- [Goose egg-white lysozyme (GEWL)]
cd16893- [Membrane-bound lytic murein transglycosylases MltC and
cd16894- [Membrane-bound lytic murein transglycosylase D and sim
cd13400- [IagB-like protein (LT_lagB_like)]
cd13403- [Membrane-bound lytic murein transglycosylase F (MLTF
cd13925- [Core lysozyme-like domain of resuscitation-promoting fa
PF06737- [Transglycosylase-like (Transglycosylas) - Transglycosylase
cd13402- [lytic transglycosylase-like domain of tail fiber-like protein
PF18013- [Phage tail lysozyme (Phage_lysozyme2) - Phage tail lysoz
cd14814- [Metalloproteases including zinc D-Ala-D-Ala carboxypep
cd14852- [L,D-carboxypeptidase DacB and LdcB, and related protei
PF02557- [Peptidase M15B (Pept_M15B) - D-alanyl-D-alanine carbo
cd14849- [D-Ala-D-Ala dipeptidase/D-Ala-D-Ala carboxypeptidase (C
cd14844- [Proteins similar to the zinc-containing D-Ala-D-Ala dipep
PF08291- [Peptidase M15A, C-terminal (Peptidase_M15A_C) - Pept
PF06714- [Protein Gp5, N-terminal OB-fold domain (Gp5_OB_N) - C
cd13926- [N-acetylmuramidase domain of the glycosyl hydrolase 10
PF05838- [Protein of unknown function DUF847 (DUF847) - Glycosy
cd00737- [Endolysin/autolysin (Endolysin_autolysin) - endolysin an
cd16904- [pesticin C-terminal-like domain of uncharacterized prote
cd00736- [Bacteriophage lambda lysozyme and similar proteins (lar
cd16900- [endolysin R21-like proteins (endolysin_R21_like)]
cd16901- [P1 lysozyme Lyz-like proteins (lyz_P1)]
PF00959- [Glycoside hydrolase, family 24 (Glyco_hydro_24) - Phage
cd00735- [Bacteriophage T4-like lysozymes (T4_like_lys)]
PF07669- [Restriction modification methylase Eco57I (RM_methyla
cd02440- [S-adenosylmethionine-dependent methyltransferases (S
PF05175- [Methyltransferase small domain (Small_mtfrase_dom) -
cd16891- [CwlT-like N-terminal lysozyme domain and similar doma
PF13702- [Lysozyme-like (Lysozyme_like)]
cd00229- [SGNH_hydrolase, or GDSL_hydrolase, is a diverse family
PF13472- [SGNH hydrolase-type esterase domain (SGNH_hydro) - C
PF02368- [Bacterial Ig-like, group 2 (Big_2) - Bacterial Ig-like domain

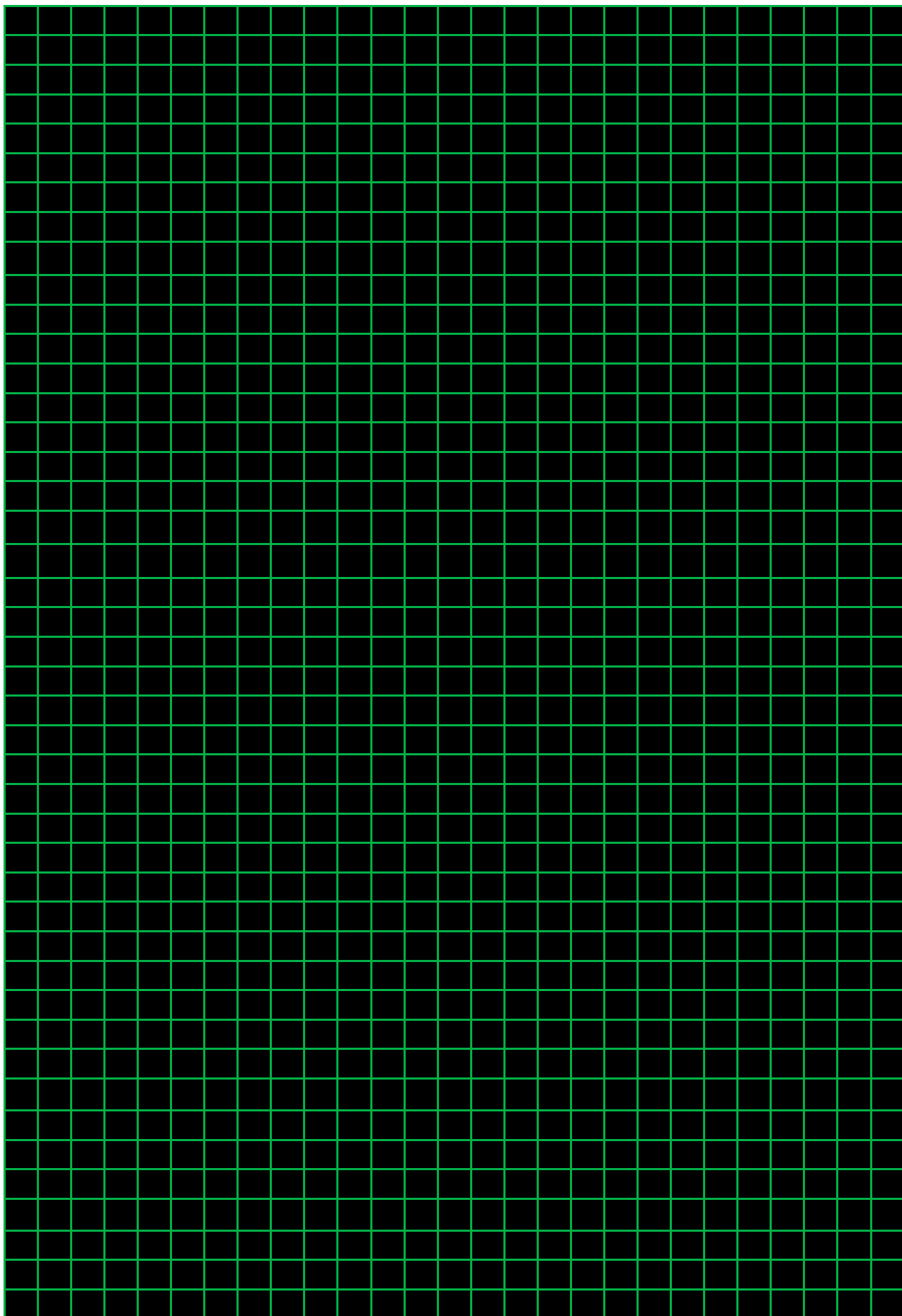
SM00635- [Bacterial Ig-like, group 2 (Big_2) - Bacterial Ig-like domain
PF08230- [Cpl-7 lysozyme, C-terminal (Cpl_7_lyso_C) - CW_7 repeat
SM01095- [Cpl-7 lysozyme, C-terminal (Cpl_7_lyso_C) - Cpl-7 lysozyme
cd00978- [Glycoside hydrolase, family 46 (Glyco_hydro_46) - chitinase
PF01374- [Glycoside hydrolase, family 46 (Glyco_hydro_46) - Glycoside
cd16902- [Lysozyme-like C-terminal domain of pesticin (pesticin_lyz
PF16754- [Bacterial toxin homologue of phage lysozyme, C-terminal
cd00325- [Glycoside hydrolase family 19, chitinase domain (chitinase
PF00182- [Glycoside hydrolase, family 19, catalytic (Glyco_hydro_1
cd14845- [L-Ala-D-Glu peptidase, also known as L-alanyl-D-glutamate
PF13539- [Peptidase M15C (Peptidase_M15C) - D-alanyl-D-alanine
cd14667- [Non-mltA associated 3D domain containing proteins, non-
PF06725- [3D domain (3D_dom) - 3D domain (3D)]
cd14688- [Basic leucine zipper (bZIP) domain of Yeast Activator Protein
PF13884- [Intramolecular chaperone auto-processing domain (S74_1
PS51688- [Intramolecular chaperone auto-processing domain (S74_1
cd06503- [F-type ATP synthase, membrane subunit b (ATP-synt_Fo
cd18586- [Six-transmembrane helical domain (6TM) domain of the
cd18577- [Six-transmembrane helical domain 1 (TMD1) of P-glycoprotein
cd18028- [DEXH-box helicase domain of archaeal Ski2-type helicase
cd17504- [Methylenomycin A resistance protein (also called MMR)
cd17477- [YcaD and similar transporters of the Major Facilitator Superfamily
cd17330- [Eukaryotic Solute carrier 46 (SLC46) family, Bacterial TetR
cd17324- [Purine ribonucleoside efflux pump NepI and similar transporters
cd17321- [Methylenomycin A resistance protein (also called MMR)
cd17040- [ubiquitin-like (Ubl) domain found in a group of small sulfotransferases
cd17320- [Multidrug transporter MdfA and similar multidrug resistance
cd14830- [delta subunit of the F-COPI complex, N-terminal domain
cd08173- [Sn-glycerol-1-phosphate dehydrogenase (Gro1PDH) catalytic
cd06180- [Uncharacterized protein YjiI and similar proteins of the MFS
cd06174- [Major Facilitator Superfamily (MFS)]
cd06173- [Macrolide efflux protein A and similar proteins of the MFS
cd04631- [CBS pair domains found in archeal 5'-AMP-activated protein kinase
cd02775- [Molybdopterin-Binding, C-terminal (MopB_CT) domain of molybdo-
cd00890- [Prefoldin is a hexameric molecular chaperone complex, formed by
cd00063- [Fibronectin type III (FN3_dom) - Fibronectin type 3 domain
cd00442- [Lysozyme-like domains (Lyz_like)]
PS51272- [S-layer homology domain (SLH_dom) - S-layer homology domain
PS50861- [Glycine-tRNA synthetase, heterodimeric (Gly-tRNA-synthetase
PS51186- [GNAT domain (GNAT_dom) - Gcn5-related N-acetyltransferase
PS50853- [Fibronectin type III (FN3_dom) - Fibronectin type-III domain
PS50817- [Intein N-terminal splicing region (Intein_N) - Intein N-terminal
PS50163- [DNA recombination and repair protein RecA, monomeric
PF18858- [Large polyvalent protein-associated domain 39 (LPD39) -

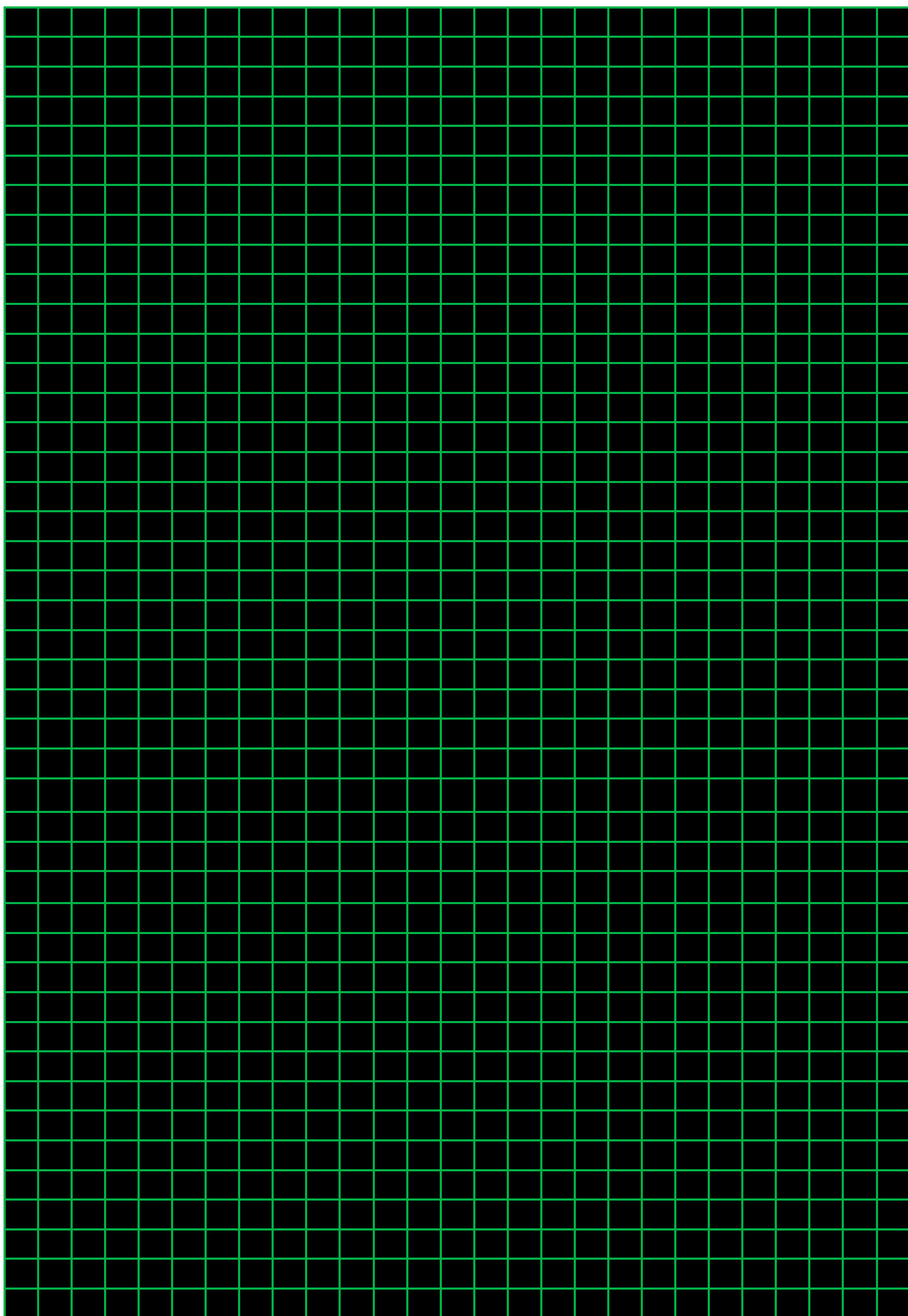
PF18857- [Large polyvalent protein associated domain 38 (LPD38) -
 PF18853- [Large polyvalent protein associated domain 37 (LPD37) -
 PF18823- [Inorganic pyrophosphatase domain (Inorganic_Pase) - In
 PF18809- [Phage-Barnase-EndoU-ColicinE5/D-ReLE-like nuclease (P
 PF18760- [ADP-Ribosyltransferase in polyvalent proteins (ART-Poly
 PF18798- [Large polyvalent protein-associated domain 3 (LPD3) - La
 PF18341- [PSA endolysin, cell wall binding domain (PSA_CBD) - PSA
 PF17969- [L,D-transpeptidase C-terminal domain (Ldt_C) - L,D-trans
 PF16838- [Distal tube protein, N-terminal (Caud_tail_N) - Caudovir
 PF16775- [Lytic exoenzyme, target recognition domain (ZoocinA_TI
 PF15711- [ILEI/PANDER domain (ILEI/PANDER_dom) - Interleukin-li
 PF13810- [Domain of unknown function DUF4185 (DUF4185) - Don
 PF13751- [Transposase DDE domain (Tnp_DDE_dom) - Transposase
 PF13550- [Tip attachment protein J (J_dom) - Putative phage tail pr
 PF13385- [Concanavalin A-like lectin/glucanases superfamily (Lamin
 PF13529- [Peptidase C39-like (Peptidase_C39-like) - Peptidase_C39
 PF13365- [Trypsin-like peptidase domain (Trypsin_2)]
 PF13354- [Beta-lactamase enzyme family (Beta-lactamase2)]
 PF13199- [Glycosyl hydrolase family 66 (Glyco_hydro_66) - Glycosy
 PF12385- [Peptidase C70, AvrRpt2 (Peptidase_C70_AvrRpt2) - Papa
 PF12200- [Domain of unknown function DUF3597 (DUF3597) - Don
 PF12123- [N-acetylmuramoyl-L-alanine amidase (Amidase02_C) - N
 PF11860- [N-acetylmuramidase (Muramidase) - N-acetylmuramidase
 PF11650- [Tail accessory factor GP4 (Tail_accessory_Gp4) - P22 tail
 PF10145- [Phage tail tape measure protein (Phage_tape_meas) - Pl
 PF10464- [Peptidase U40 (Peptidase_U40) - Peptidase U40 (Peptid
 PF09718- [Bacteriophage lambda, GpH, tail tape measure, C-termir
 PF09588- [Yqaj viral recombinase (Yqaj_viral_recombinase) - Yqaj-
 PF09374- [Peptidoglycan binding domain (Peptidoglycan-bd_3) - Pr
 PF08924- [Protein of unknown function DUF1906 (DUF1906) - Dom
 PF08481- [GBS Bsp-like (GBS_Bsp-like) - GBS Bsp-like repeat (GBS_B
 PF08310- [LGFP (LGFP) - LGFP repeat (LGFP)]
 PF07902- [Gp58-like (Gp58) - gp58-like protein (Gp58)]
 PF07833- [Copper amine oxidase-like, N-terminal (Cu_amine_oxida
 PF06832- [Penicillin-binding, C-terminal (PBP_C) - Penicillin-Binding
 PF07486- [Cell wall hydrolase, SleB (Cell_wall_hydrolase_SleB) - Ce
 PF02384- [DNA methylase, adenine-specific (DNA_methylase_A-5)]
 PF02018- [Carbohydrate-binding, CenC-like (CenC_carb-bd) - Carbo
 PF01664- [Viral attachment sigma 1, reoviral (Vir_attach_sigma1_r
 PF01471- [Peptidoglycan binding-like (Peptidoglycan-bd-like) - Puta
 PF01391- [Collagen triple helix repeat (Collagen) - Collagen triple h
 PF01129- [NAD:arginine ADP-ribosyltransferase, ART (ART) - NAD:a
 PF00912- [Glycosyl transferase, family 51 (Glyco_trans_51) - Transg
 PF00905- [Penicillin-binding protein, transpeptidase (PCN-bd_Tpep

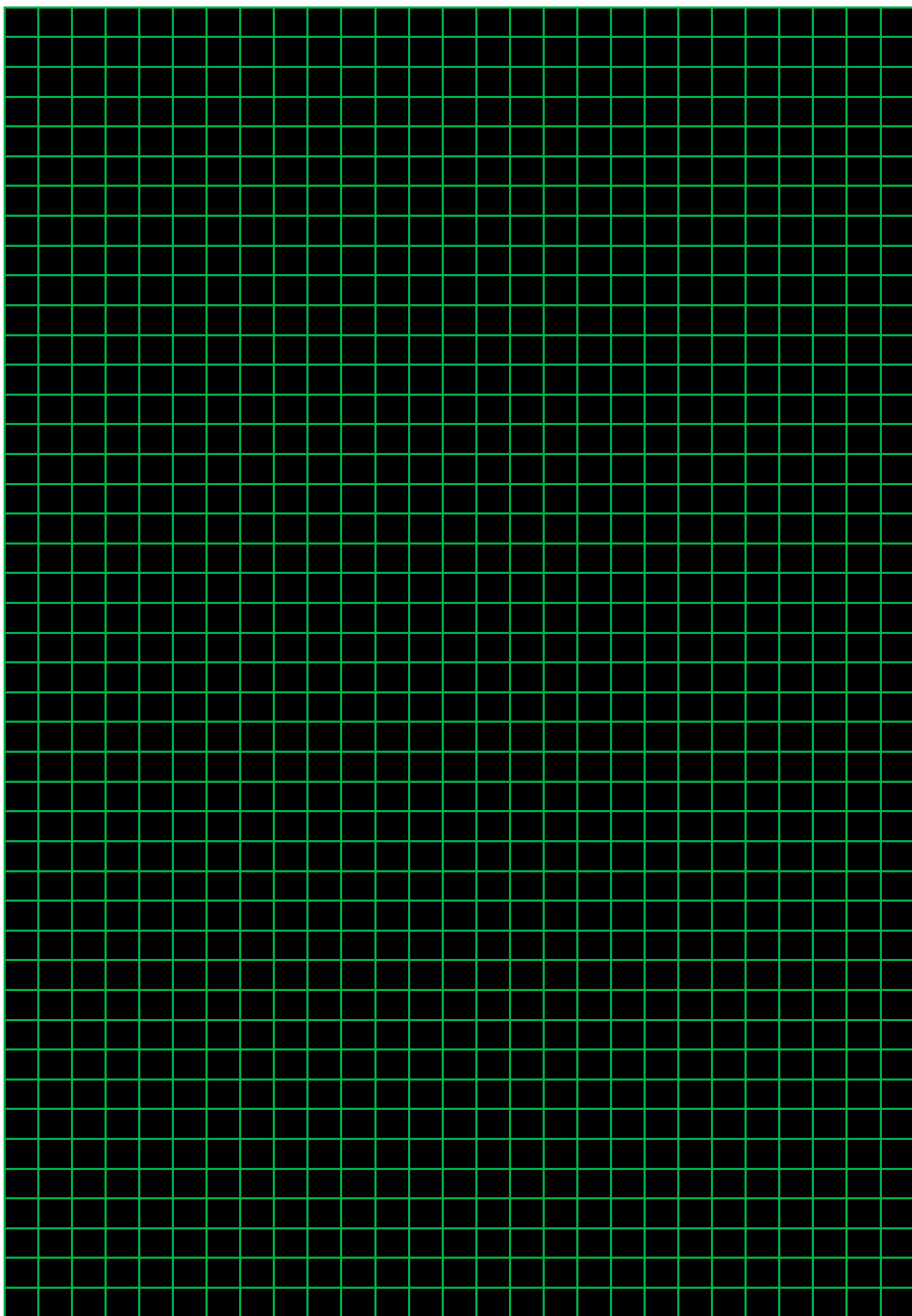
PF00395- [S-layer homology domain (SLH_dom) - S-layer homology
PF00753- [Metallo-beta-lactamase (Metallo-B-lactamas) - Metallo-
PF06791- [Bacteriophage lambda, GpH, tail tape measure, N-termi
PF06715- [Gp5, C-terminal (Gp5_C) - Gp5 C-terminal repeat (3 copi
PF05598- [Transposase InsH, N-terminal (Transposase_InsH_N) - Tr
PF05435- [DNA terminal protein Gp3 (DNA_terminal_Gp3) - Phi-29
PF05382- [Bacteriophage lysin (Phage_lysin) - Bacteriophage peptid
PF05203- [Hom-end-associated Hint (Hom_end_hint) - Hom_end-a
PF05106- [Bacteriophage lambda, GpS, holin (Phage_lambda_GpS_
PF04965- [IraD/Gp25-like (IraD/Gp25-like) - Gene 25-like lysozyme
PF03330- [RlpA-like protein, double-psi beta-barrel domain (RlpA-li
PF04466- [Phage terminase large subunit, N-terminal (Terminase_L
PS50249- [MPN domain (MPN) - MPN domain profile (MPN)]
SM00232- [JAB1/MPN/MOV34 metalloenzyme domain (JAMM/MP
cd08073- [Mpr1p, Pad1p N-terminal (MPN) domains with catalytic
PF14464- [JAB domain, prokaryotic (JAB_dom_prok) - Prokaryotic h
PF00877- [Endopeptidase, NLPC/P60 domain (NLP_P60_dom) - Nlp
PF01551- [Peptidase M23 (Peptidase_M23) - Peptidase family M23
PF01473- [Cell wall/choline-binding repeat (Cell_wall/Cho-bd_repe
PS51170- [Cell wall/choline-binding repeat (Cell_wall/Cho-bd_repe
PS51257- [Prokaryotic membrane lipoprotein lipid attachment site
PF01832- [Mannosyl-glycoprotein endo-beta-N-acetylglucosamidas
SM00047- [Mannosyl-glycoprotein endo-beta-N-acetylglucosamida
PF08239- [SH3-like domain, bacterial-type (SH3-like_bac-type) - Ba
PF08460- [SH3-like domain, bacterial-type (SH3-like_bac-type) - Ba
PS51781- [SH3-like domain, bacterial-type (SH3-like_bac-type) - SH
SM00287- [SH3-like domain, bacterial-type (SH3-like_bac-type) - Ba
PF05257- [CHAP domain (CHAP_dom) - CHAP domain (CHAP)]
PS50911- [CHAP domain (CHAP_dom) - CHAP domain profile (CHAP

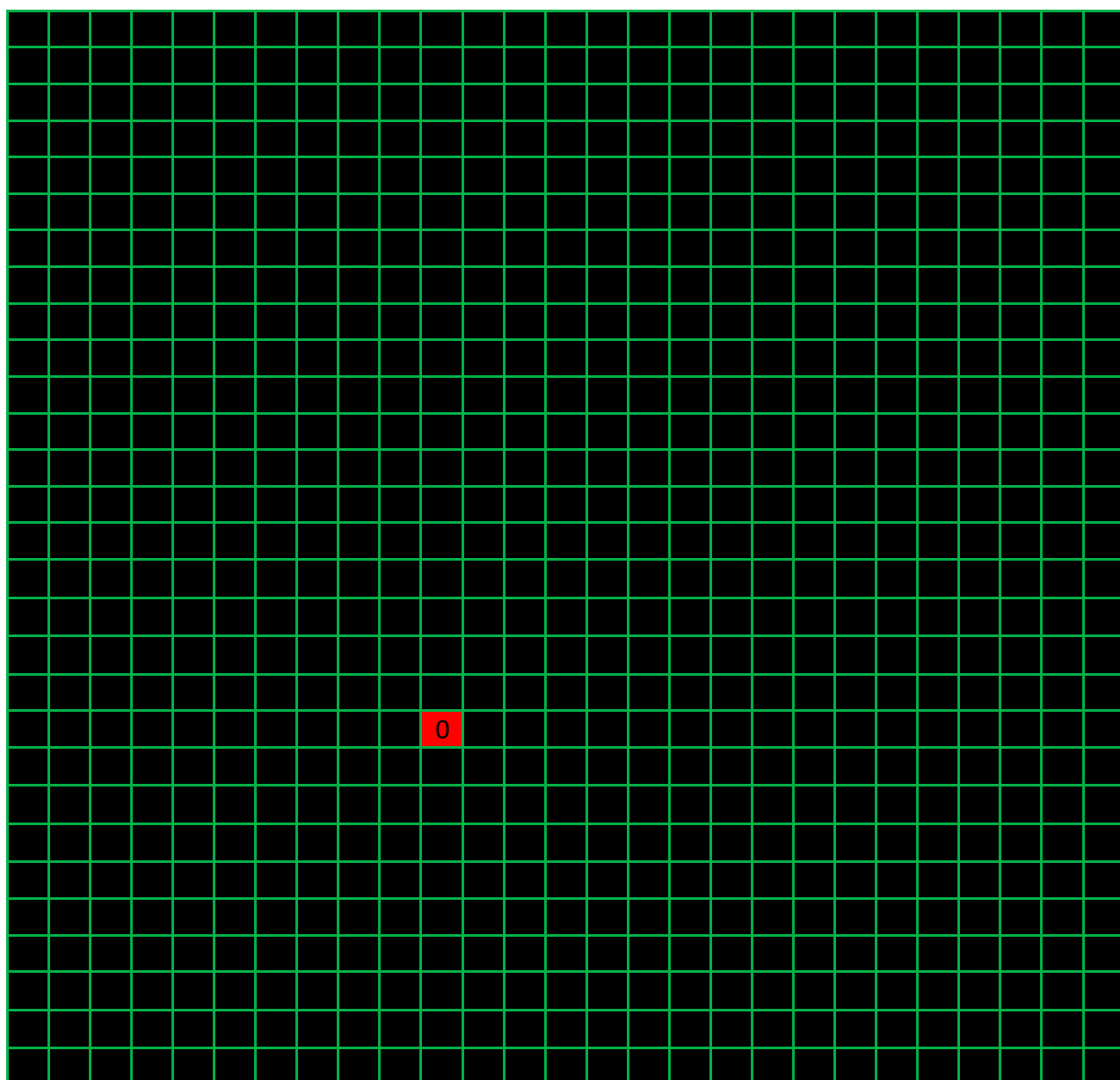
ap (average fraction between overlapping section en length of largest domain)

[illegible]

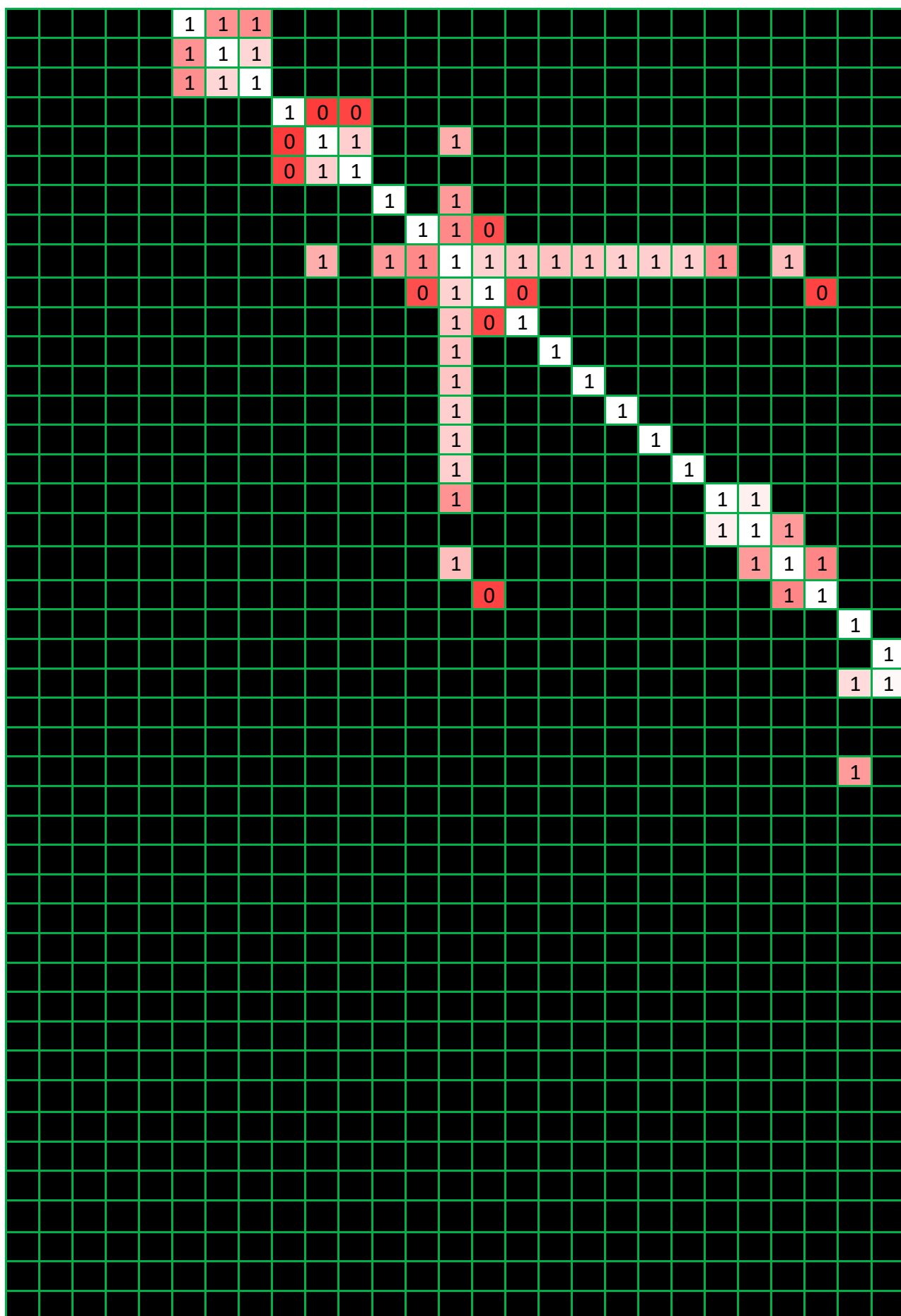


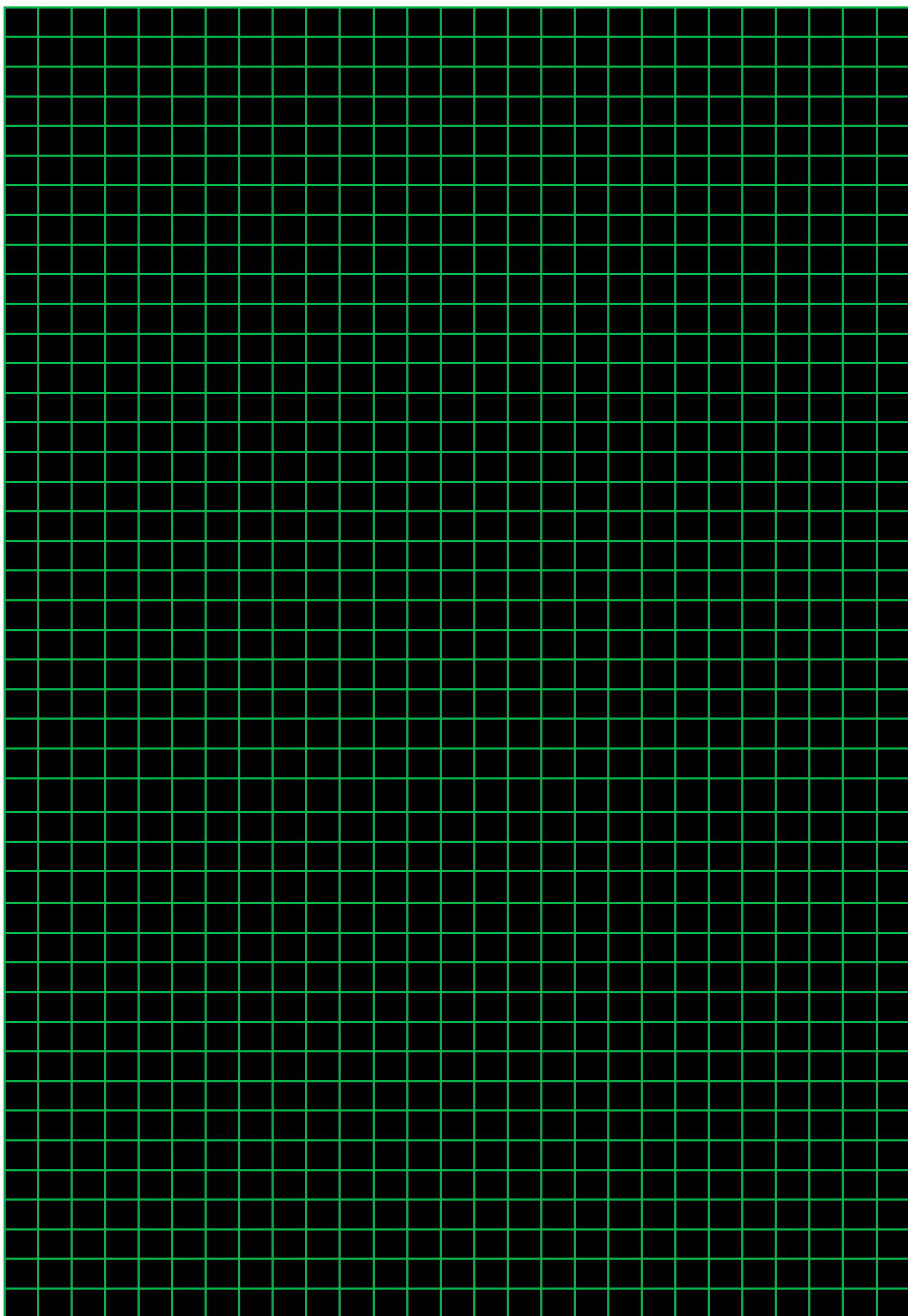


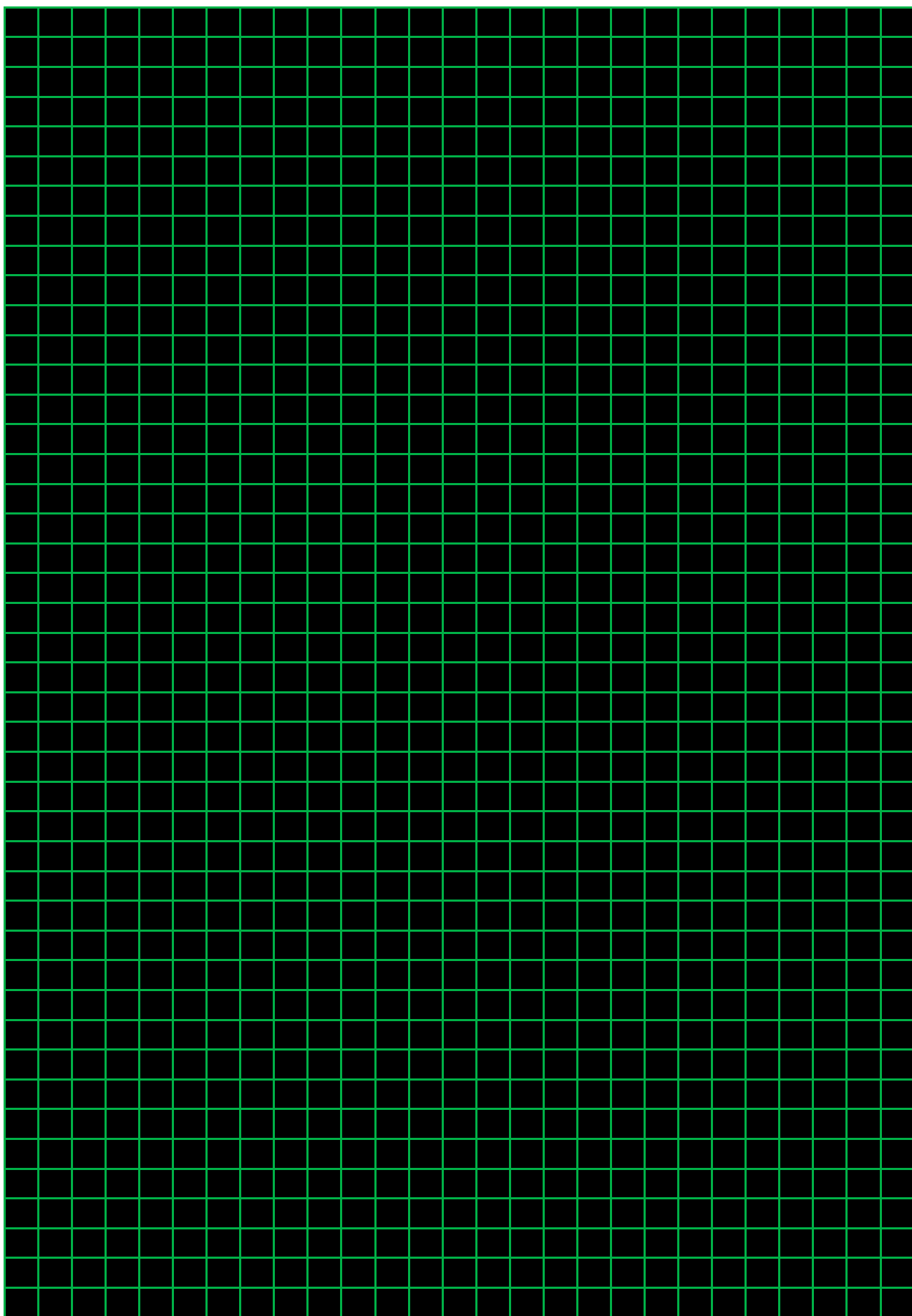


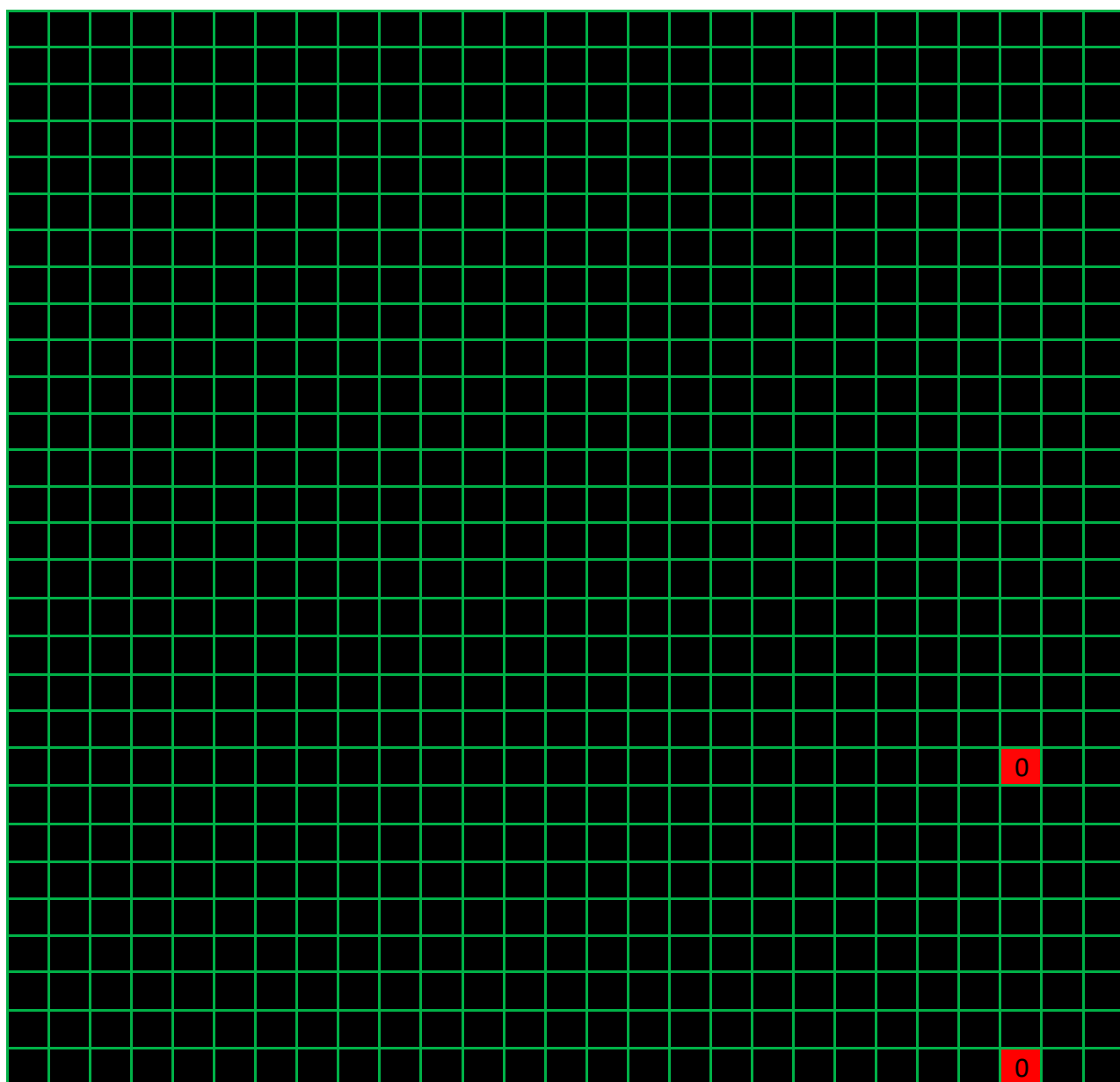


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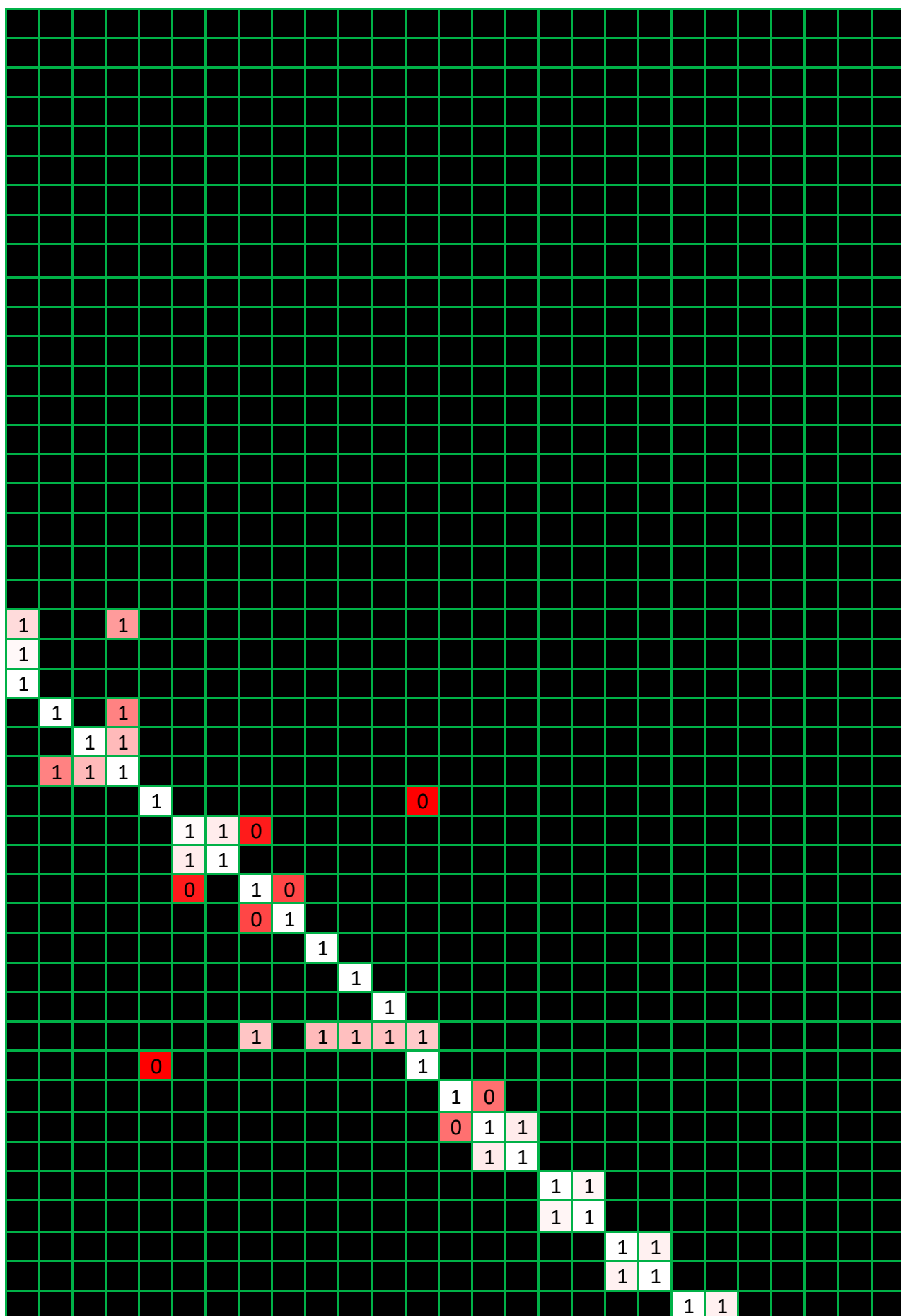


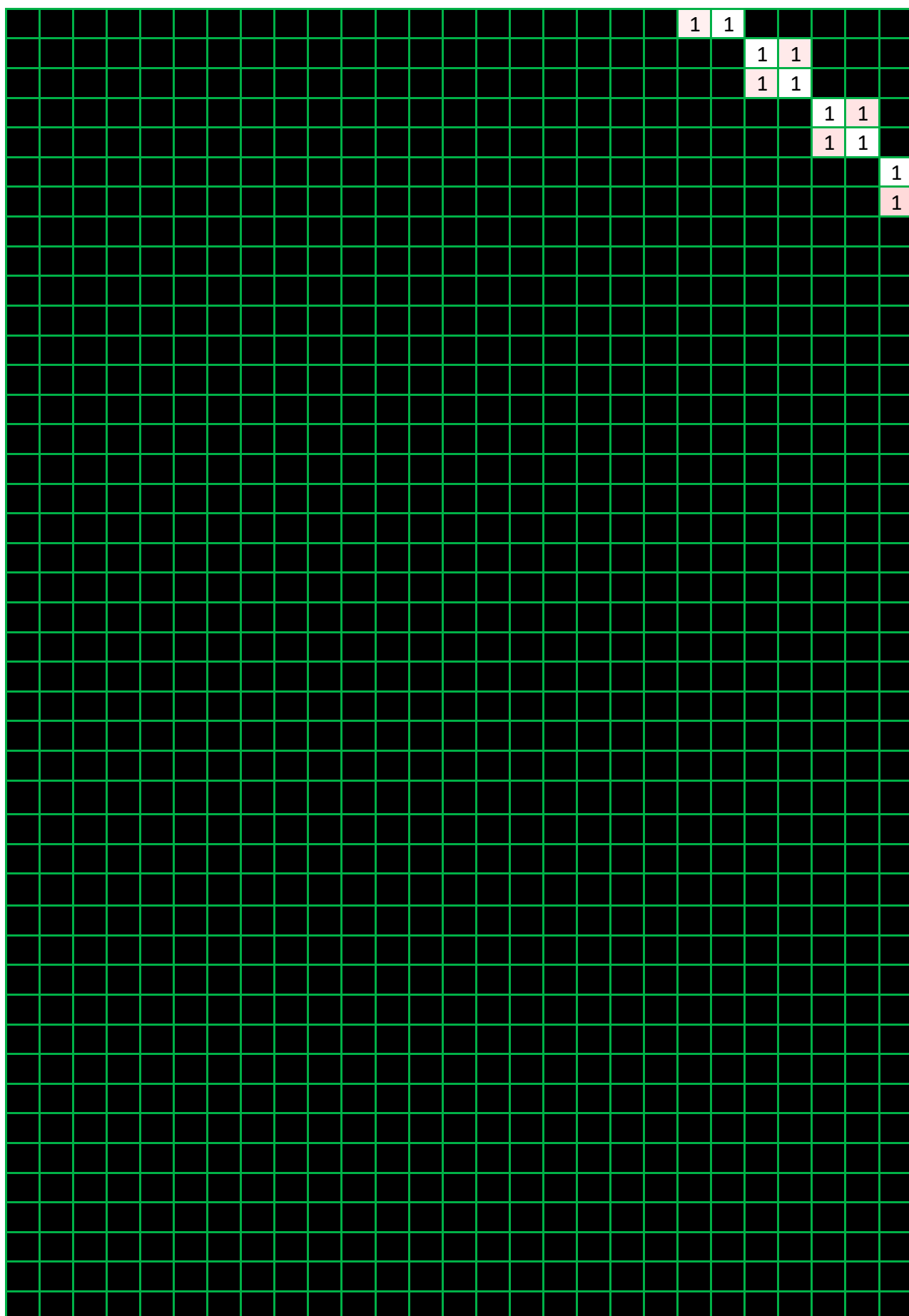


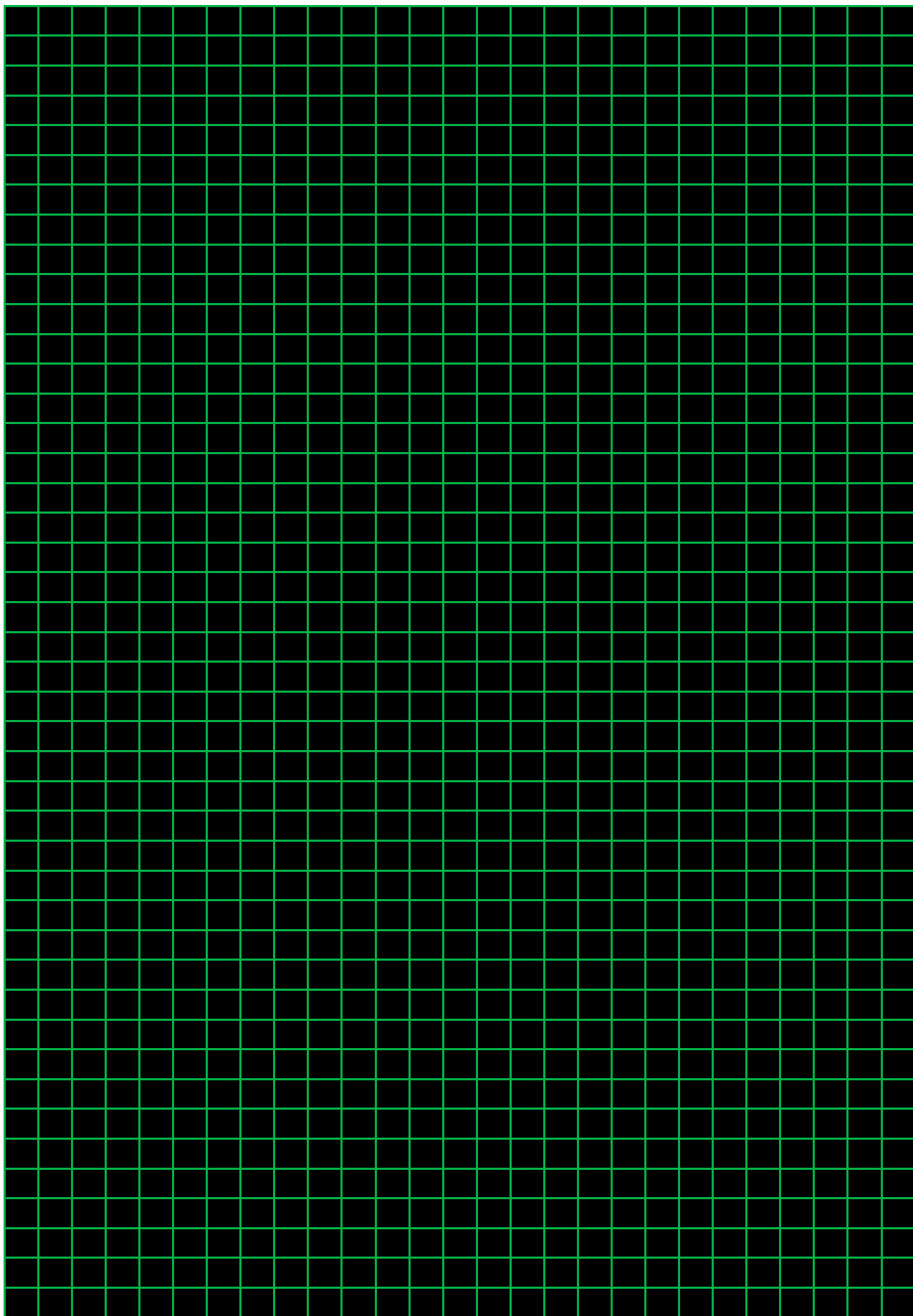


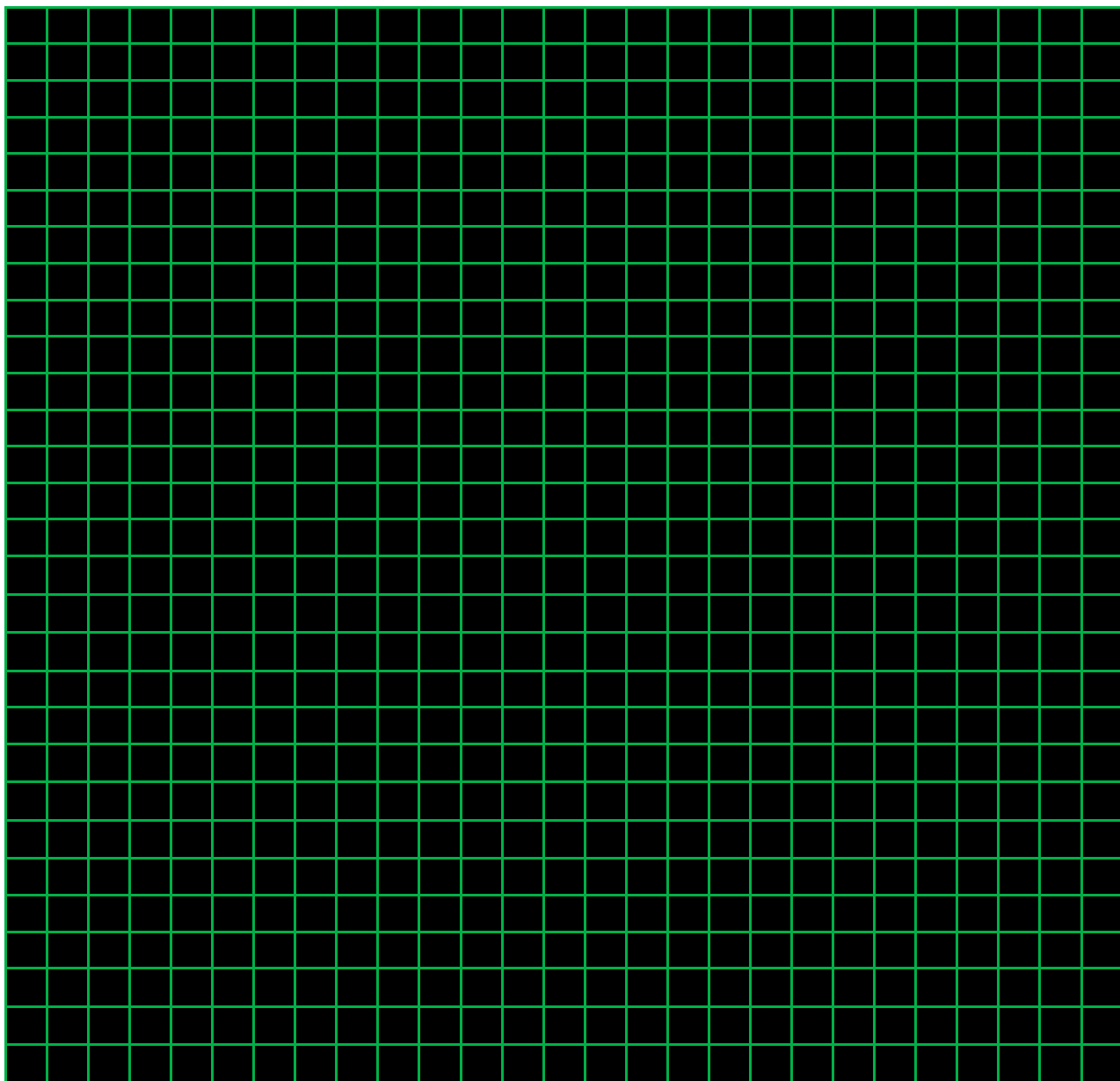


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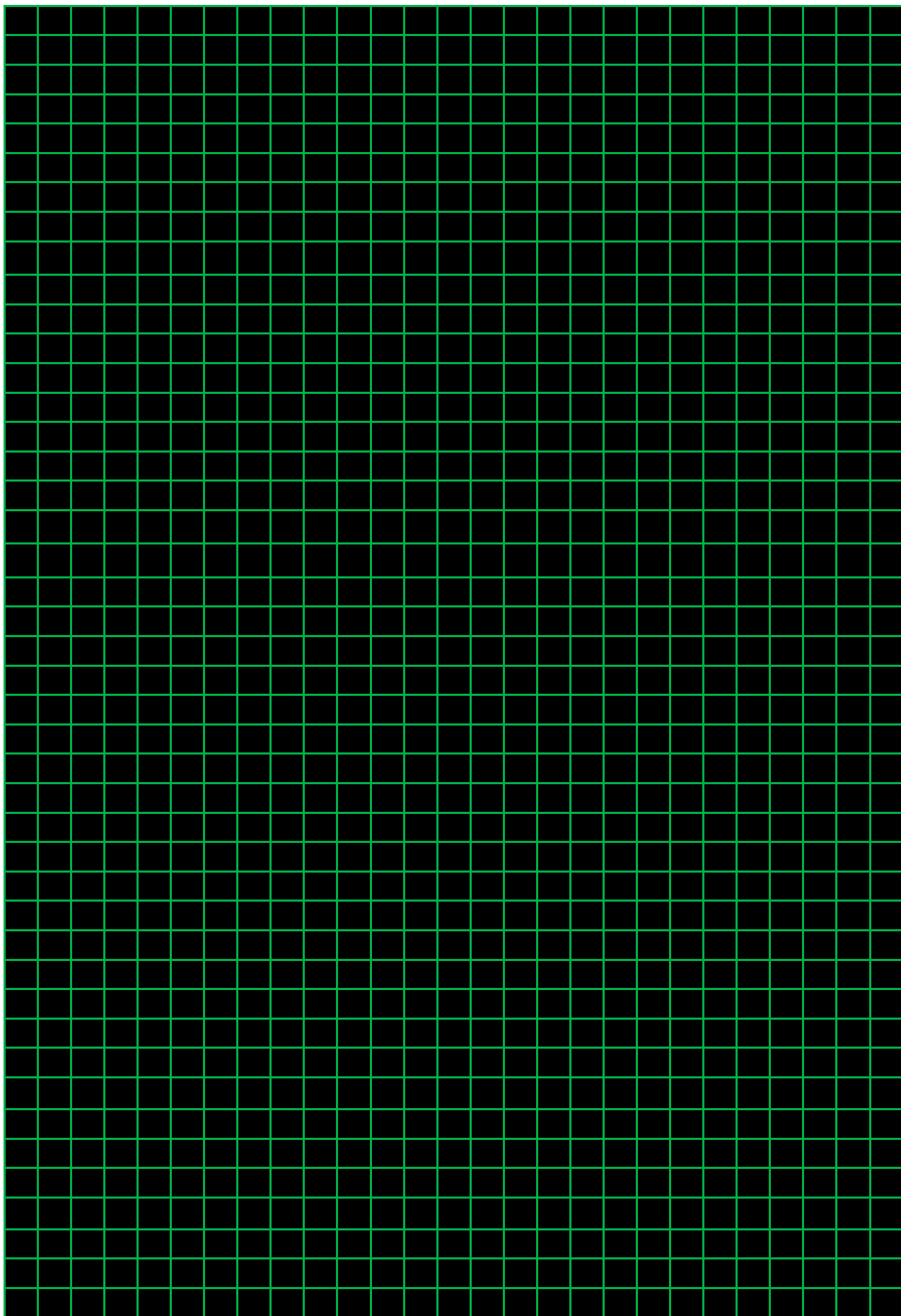


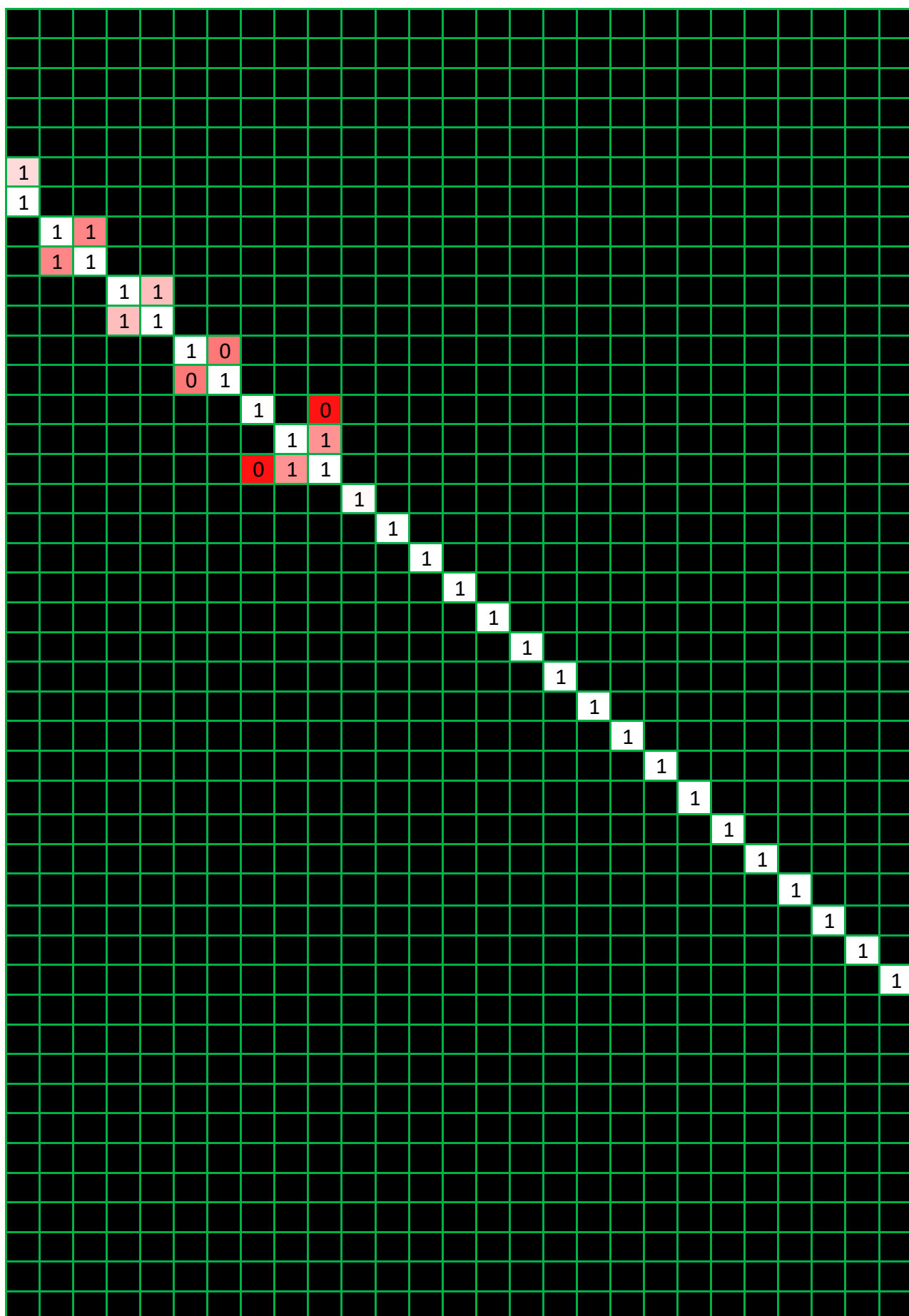


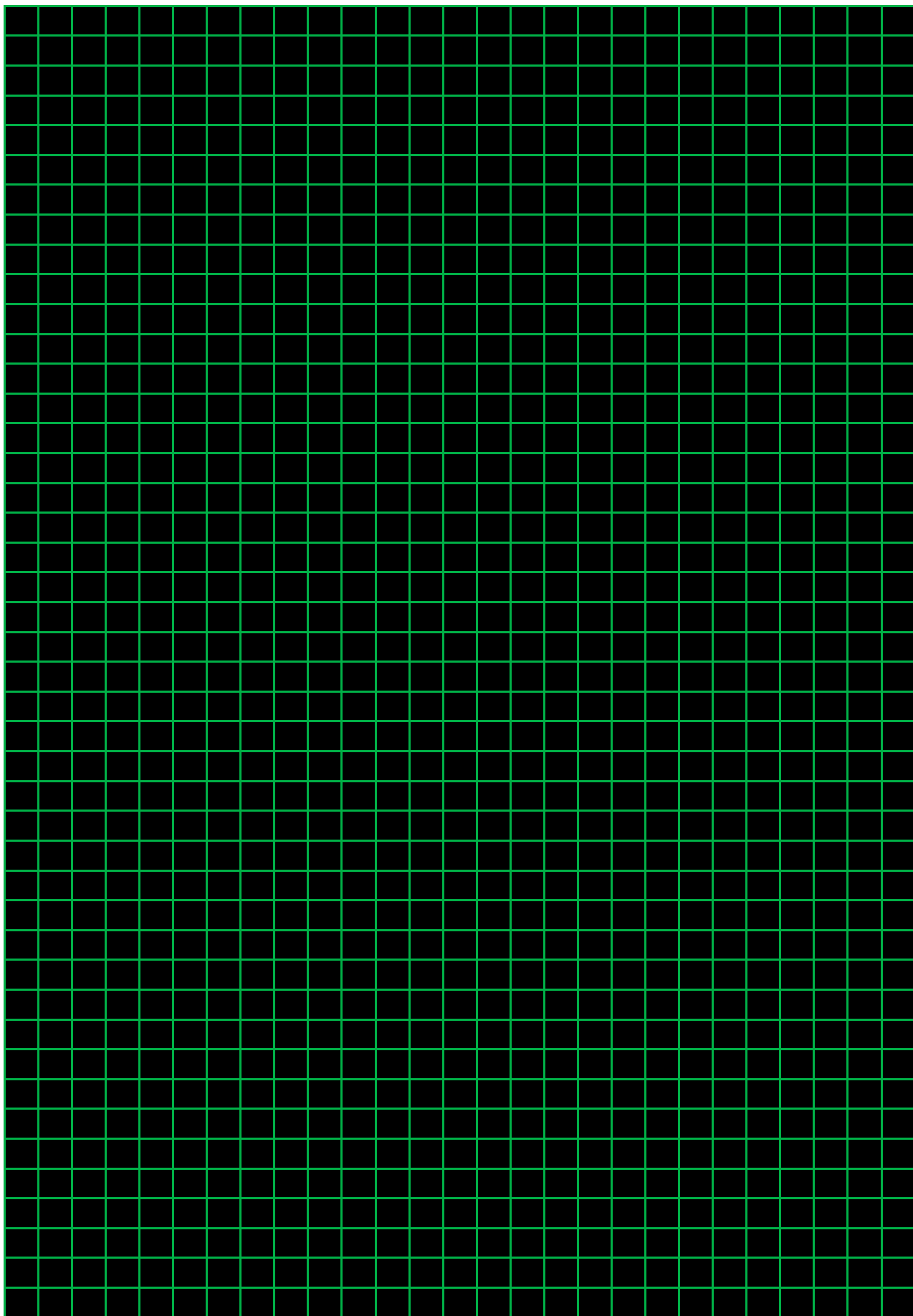


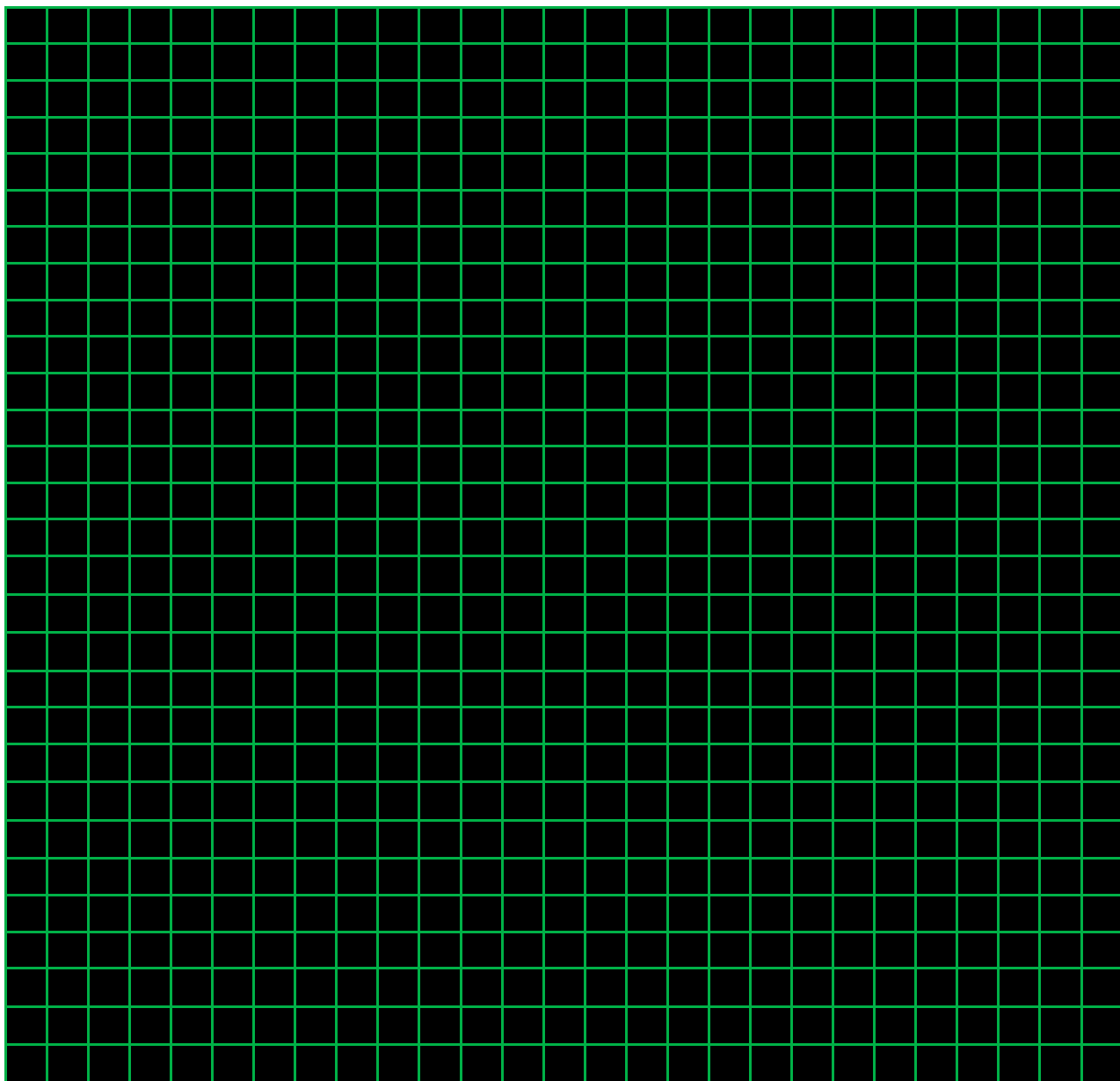


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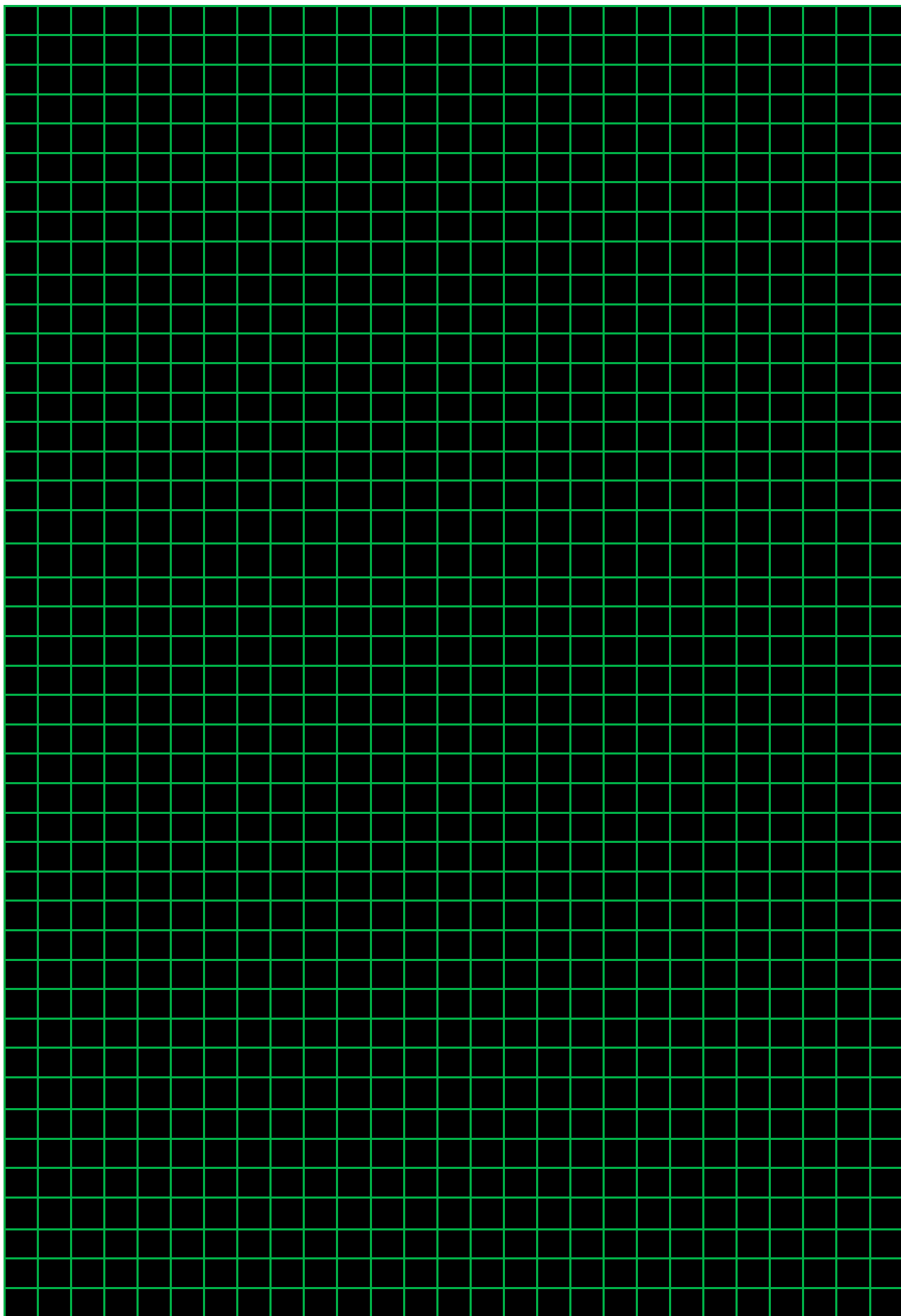


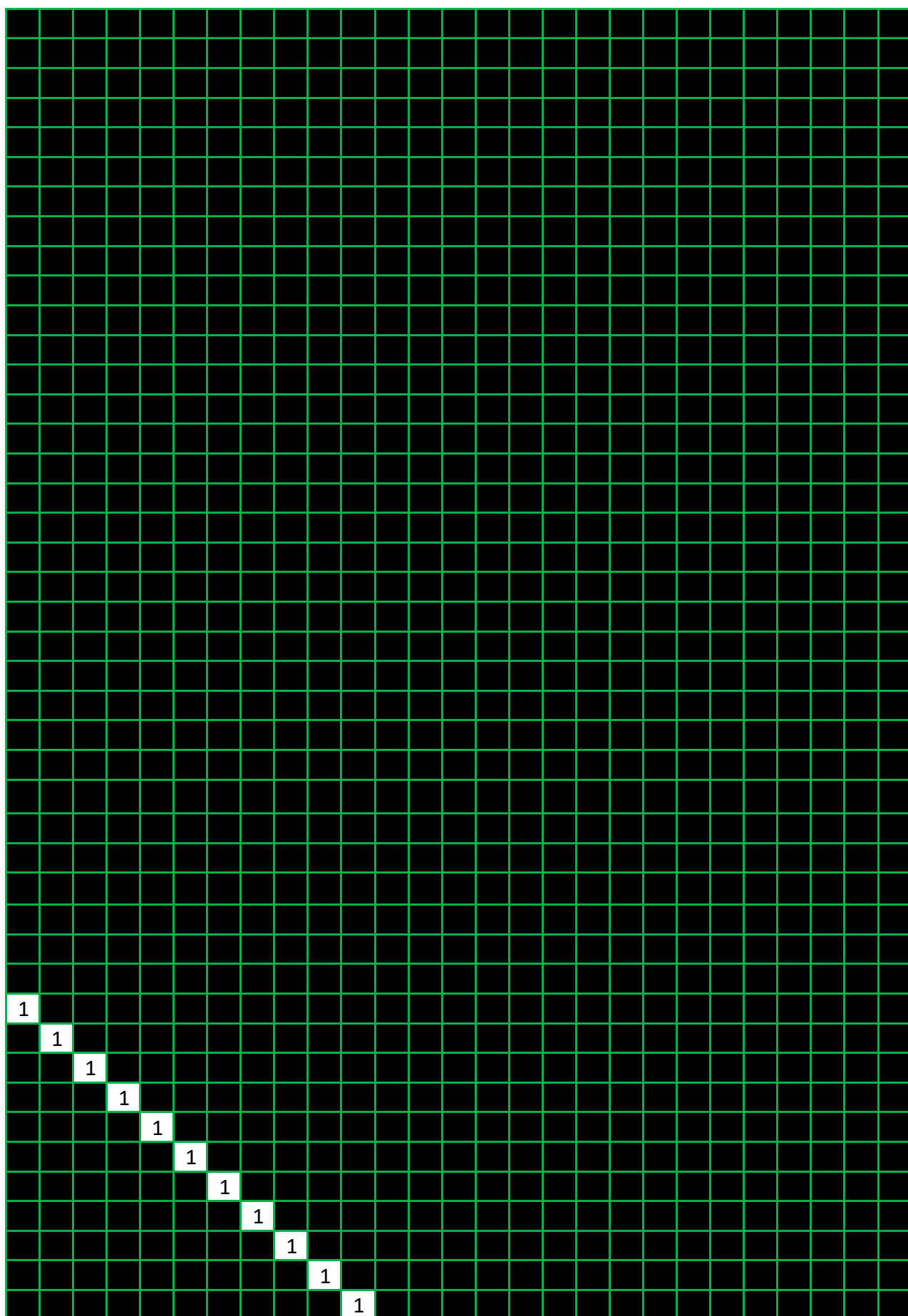


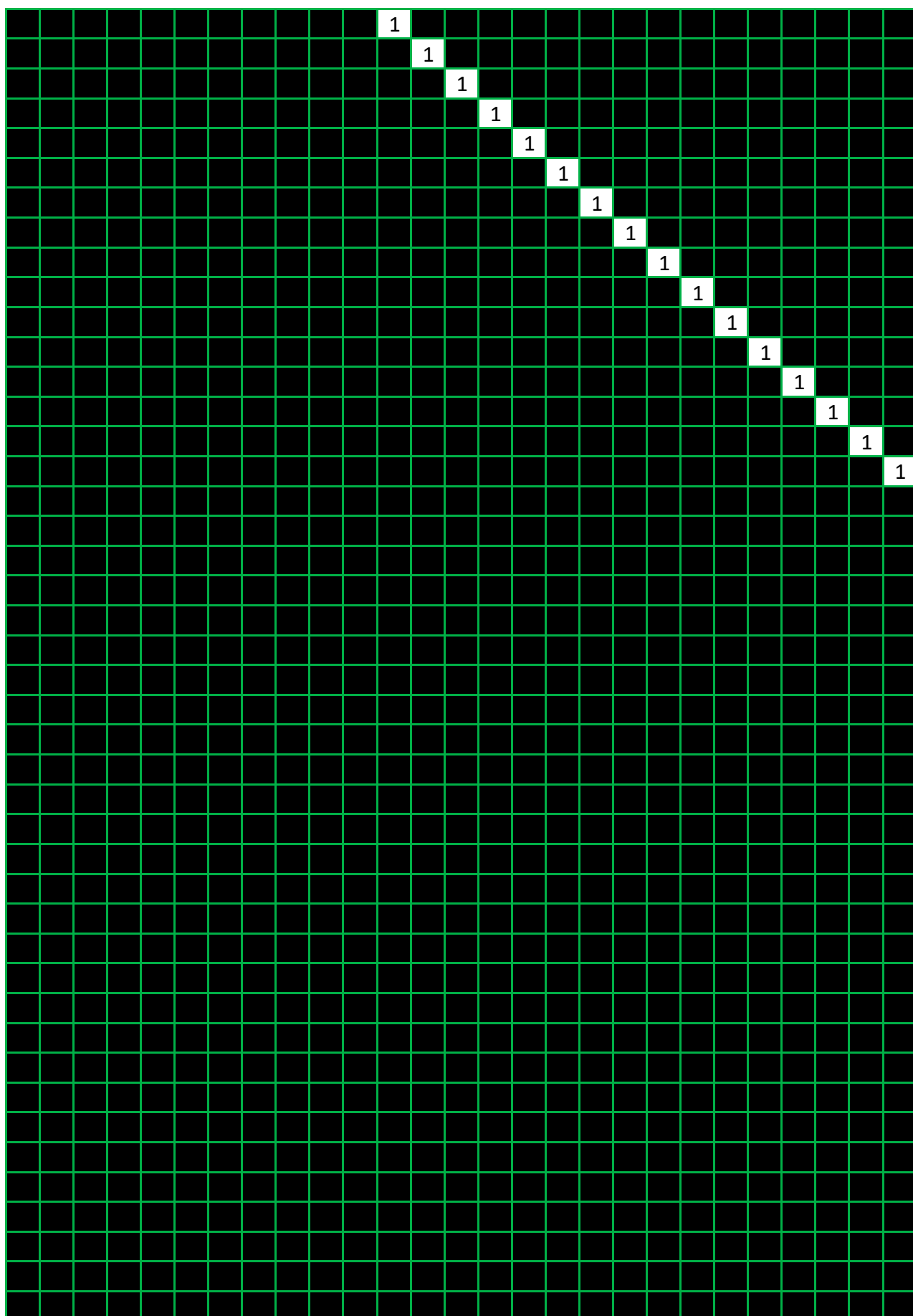


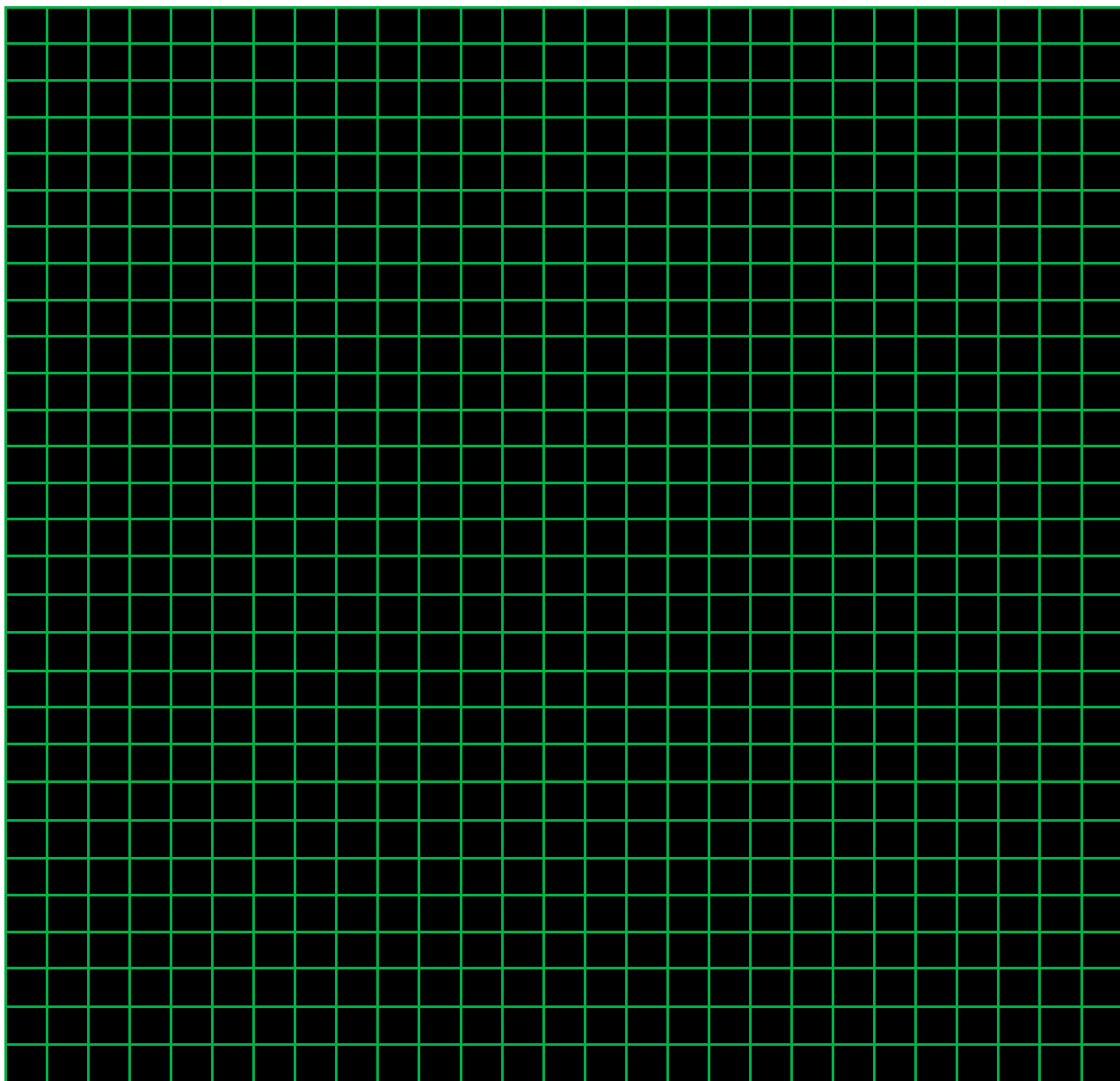


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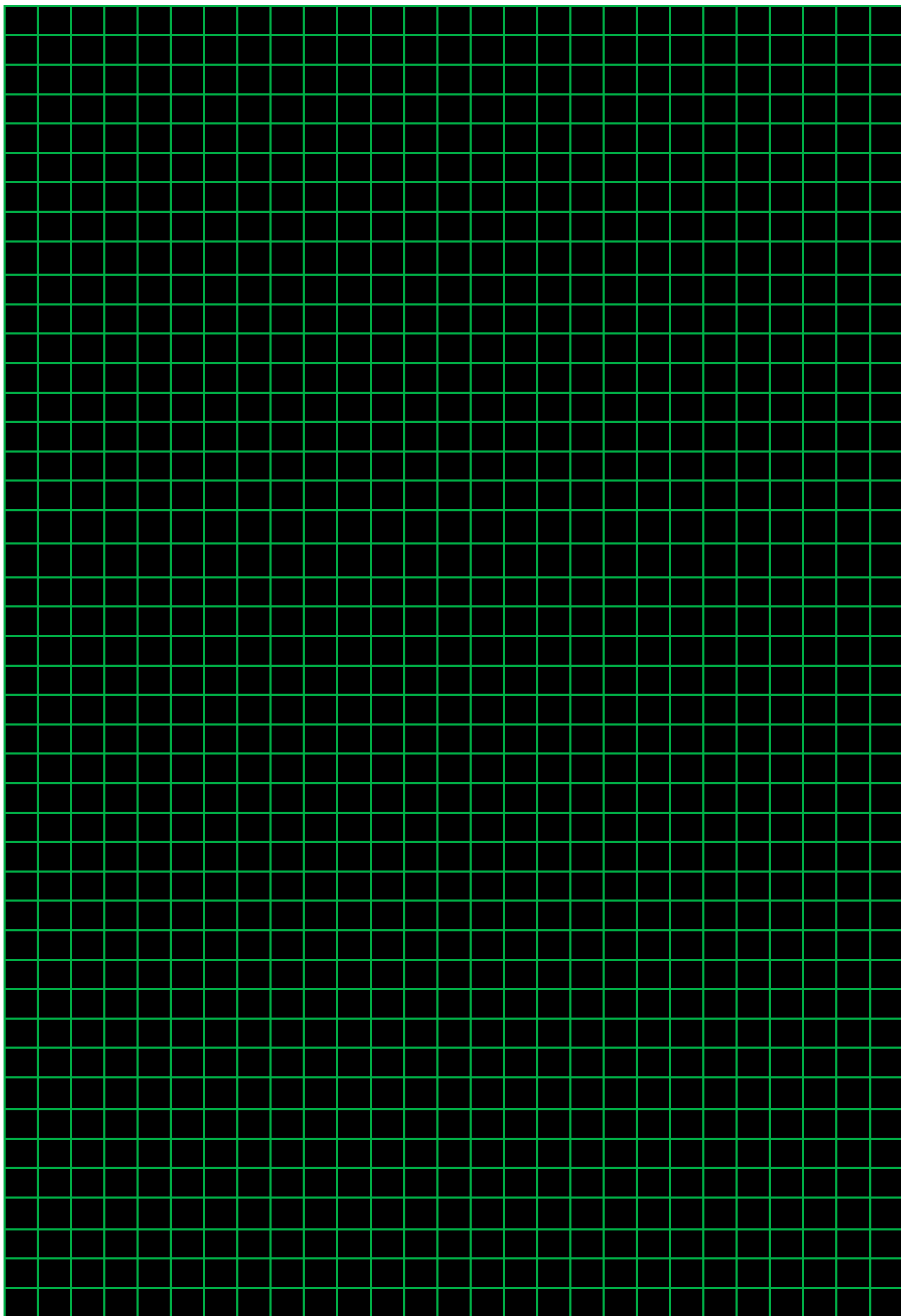


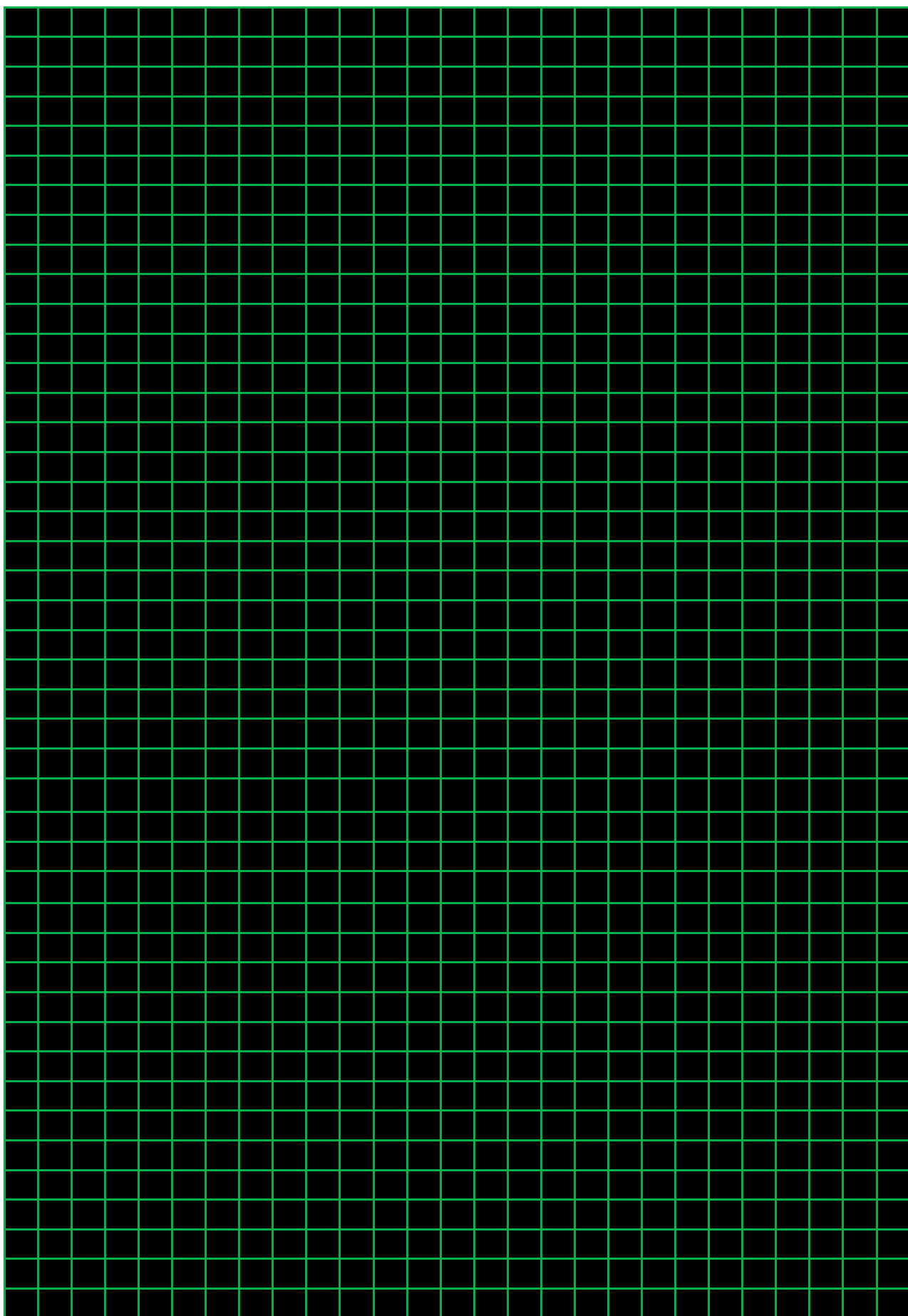


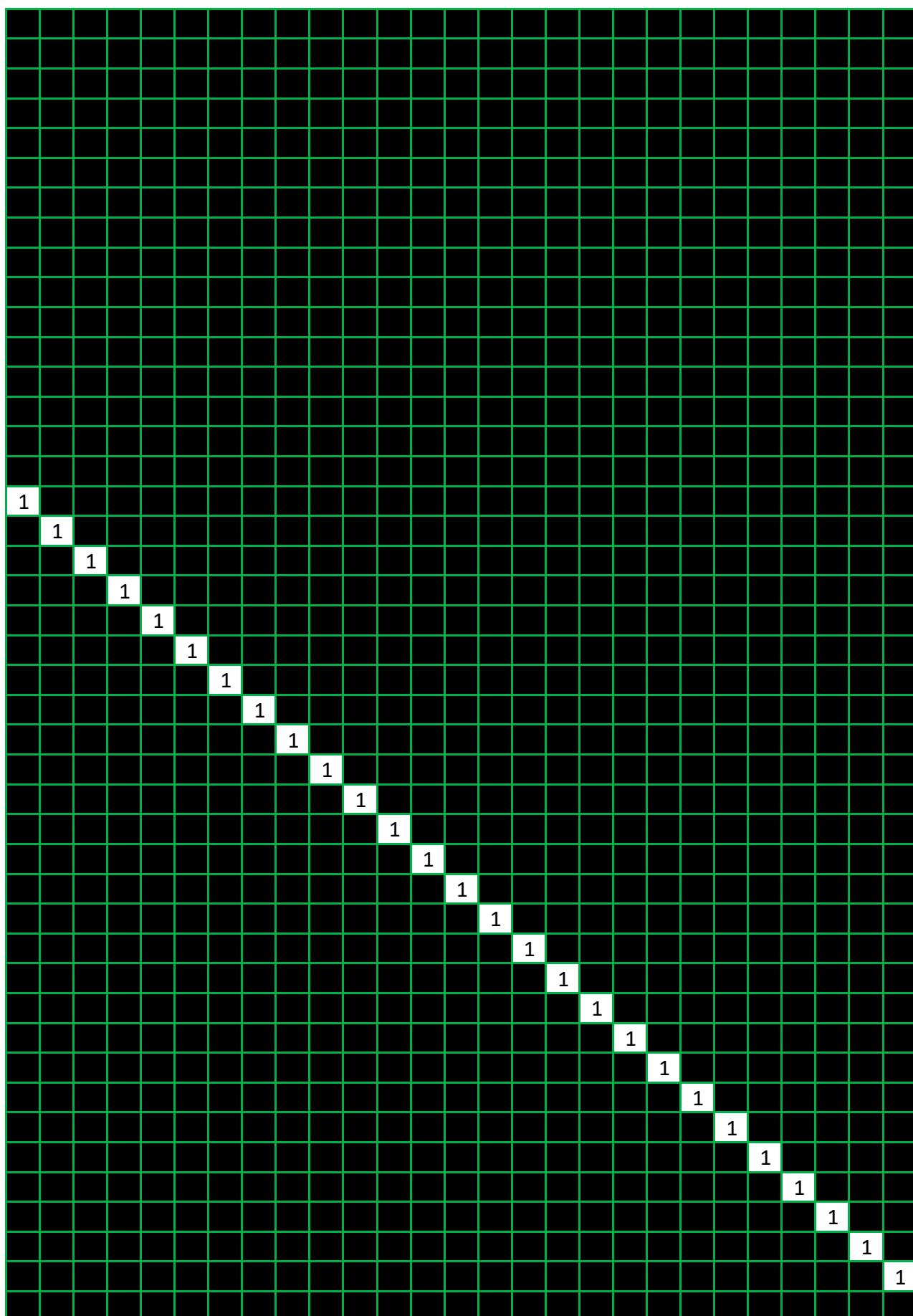


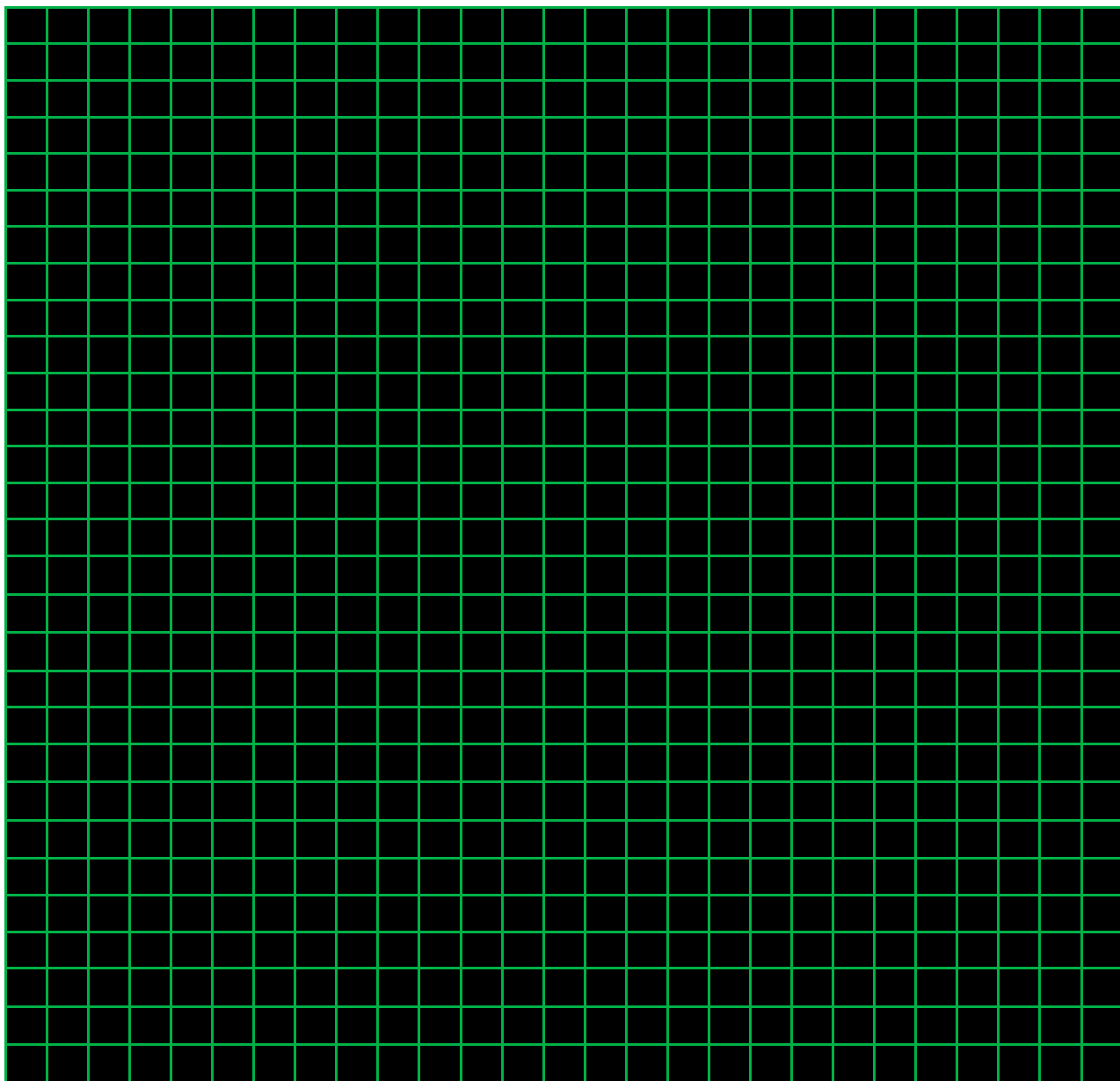


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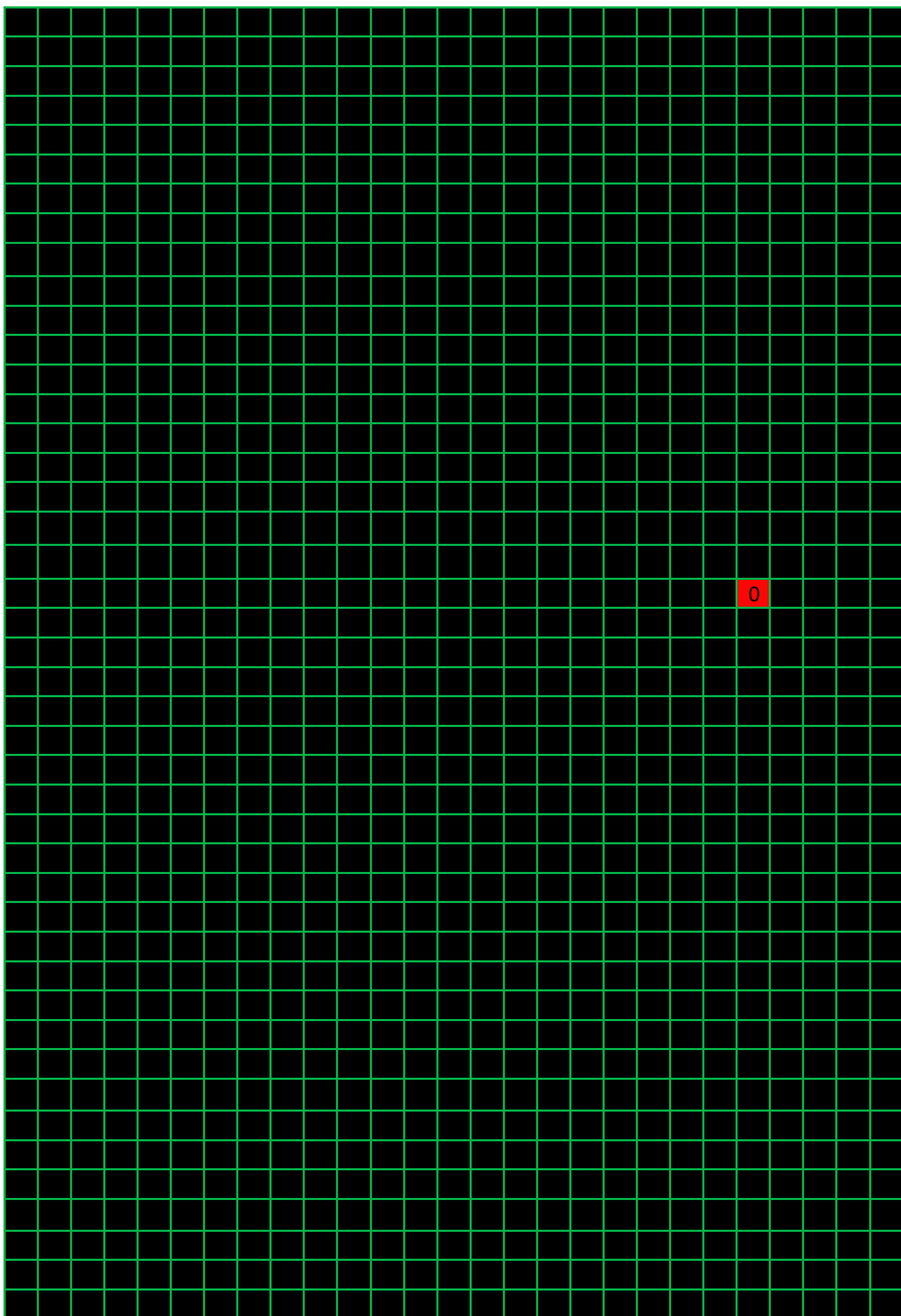


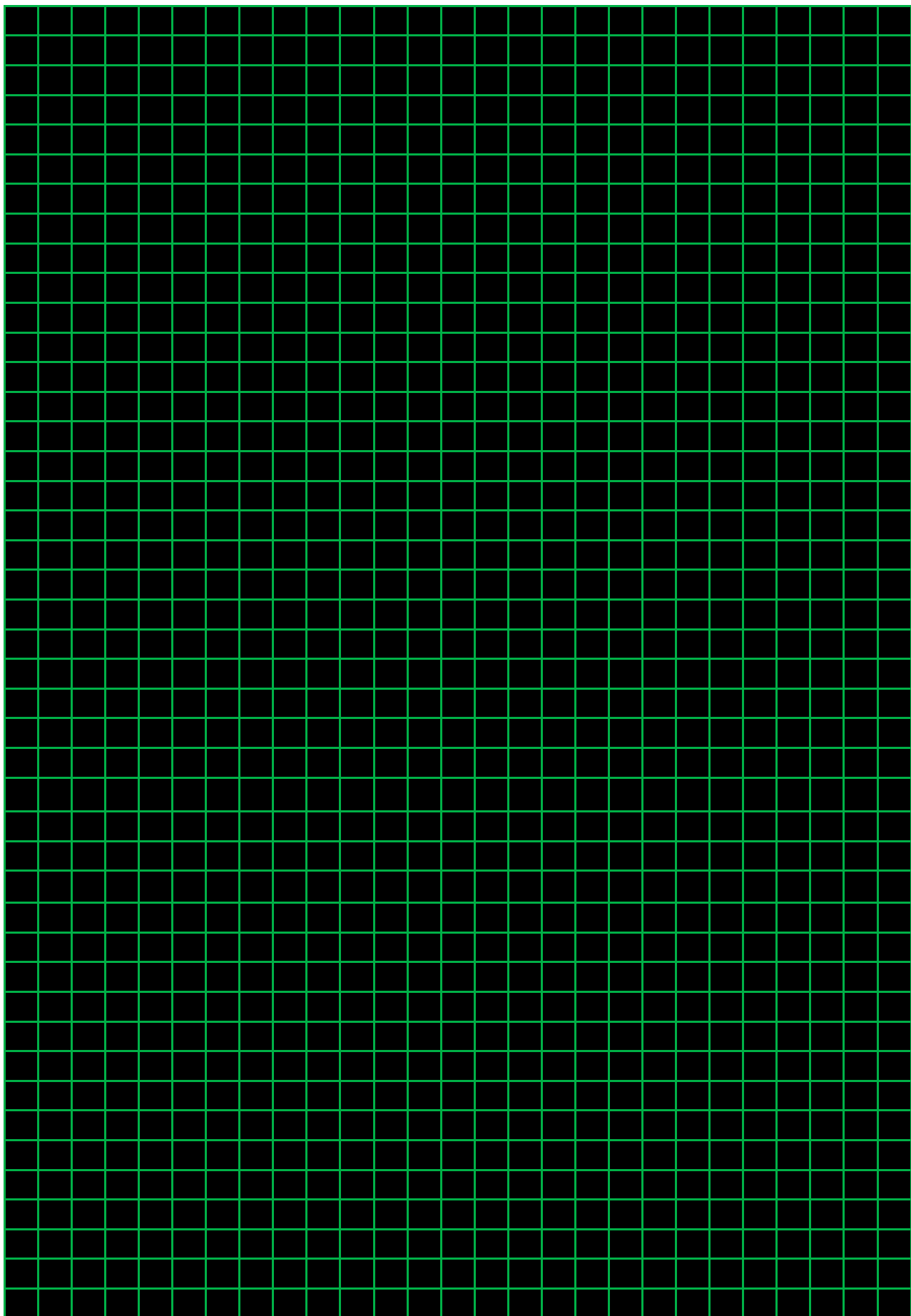


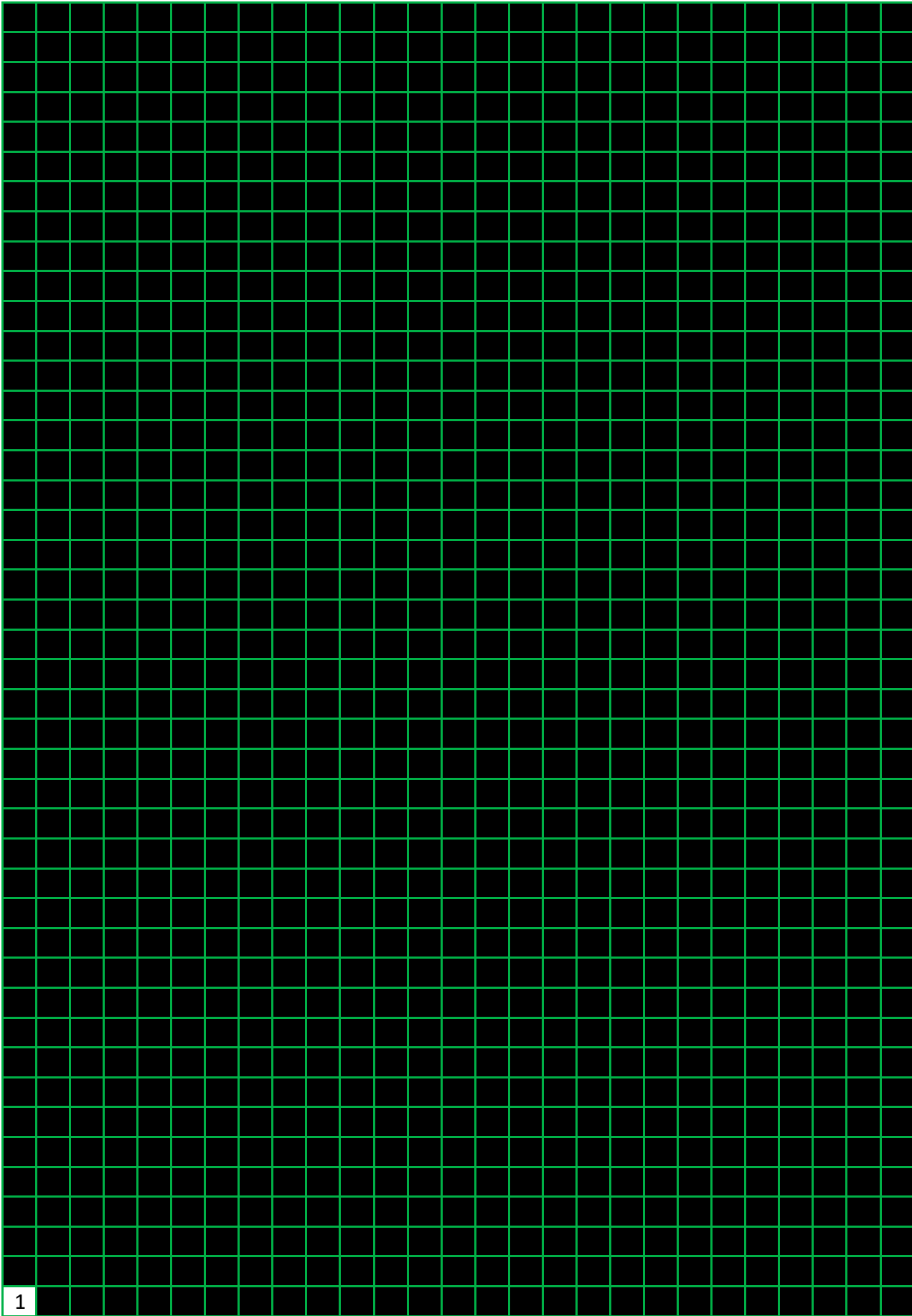


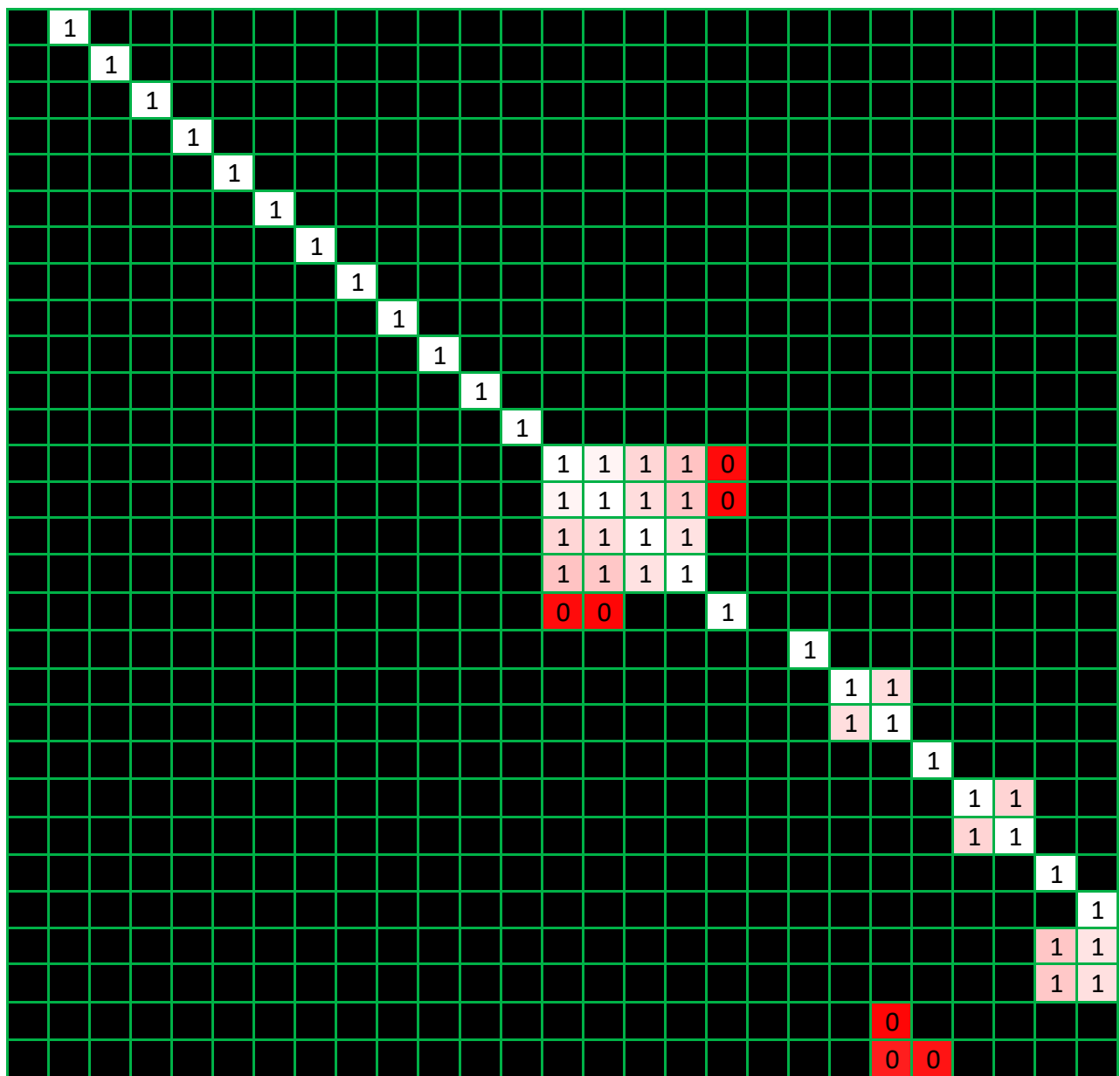


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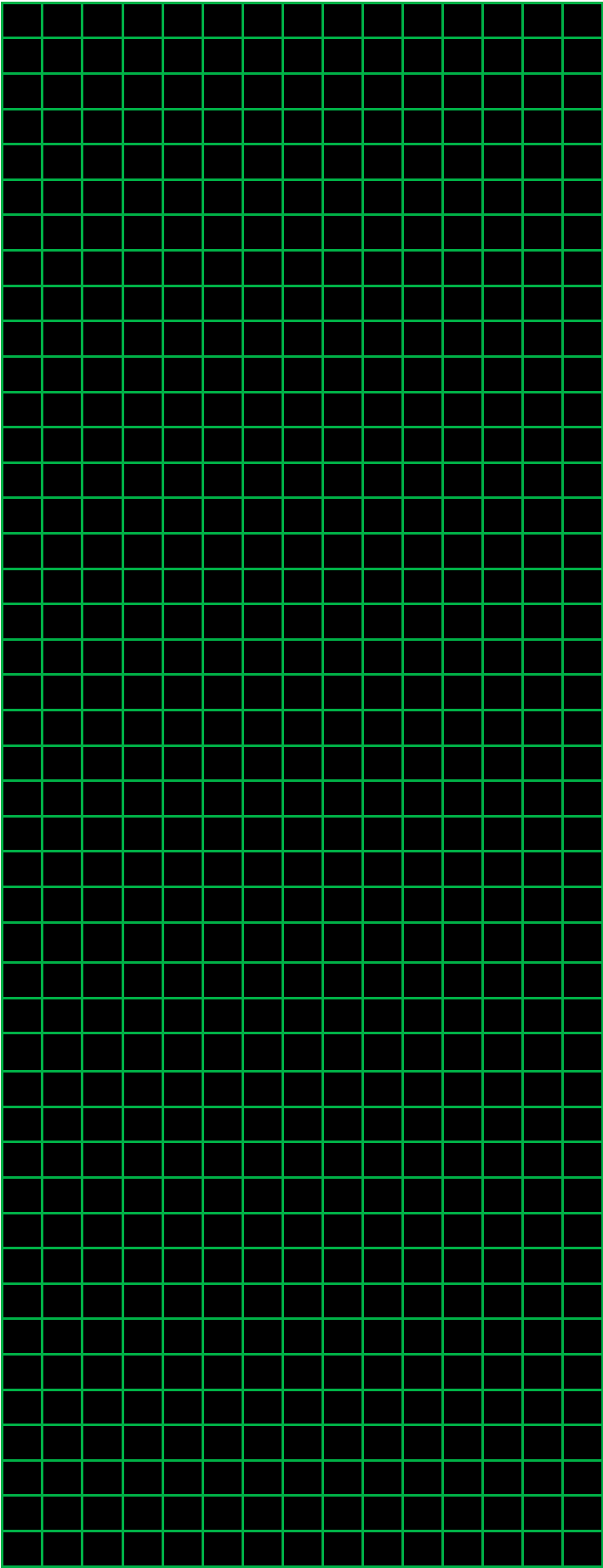
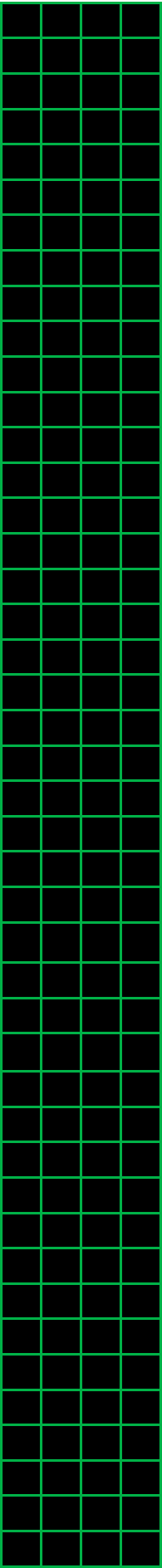


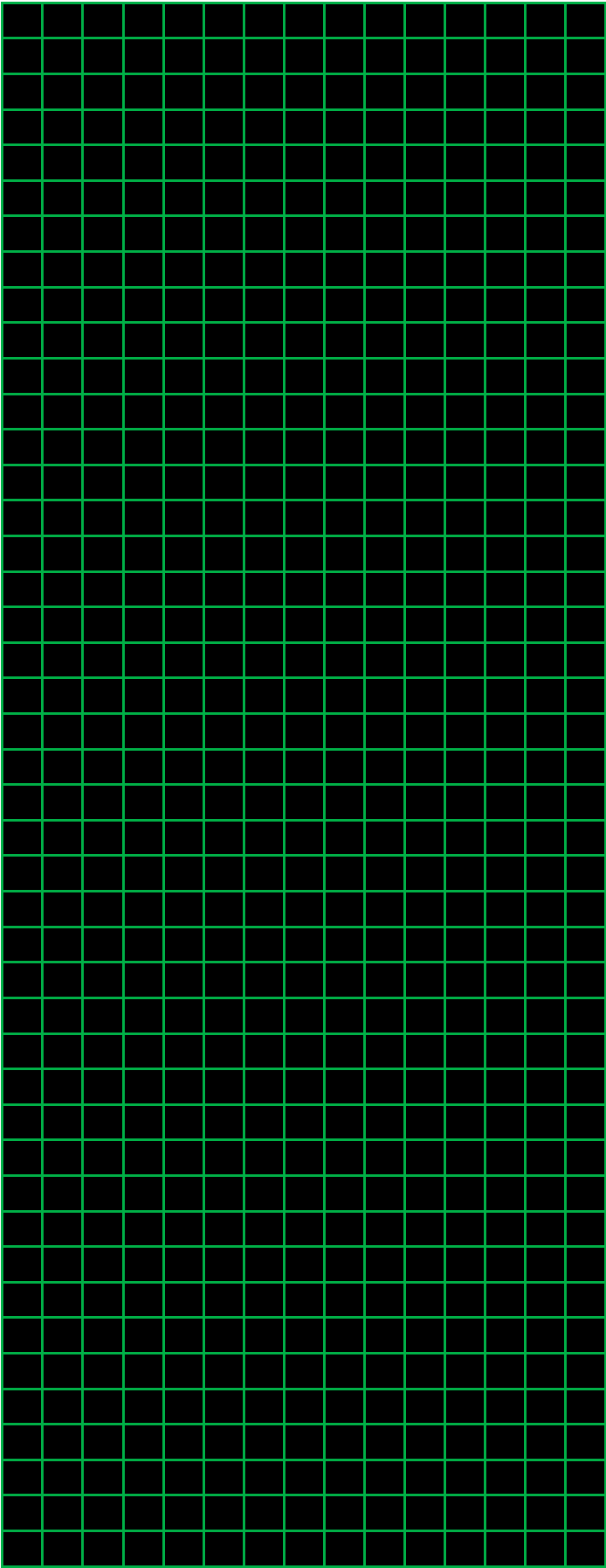
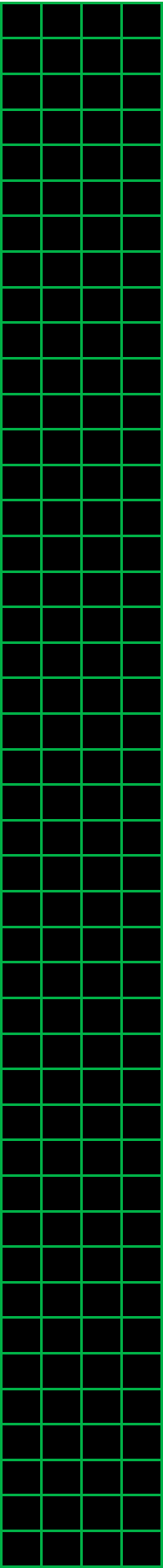




absolute number of overlaps between each pair of do

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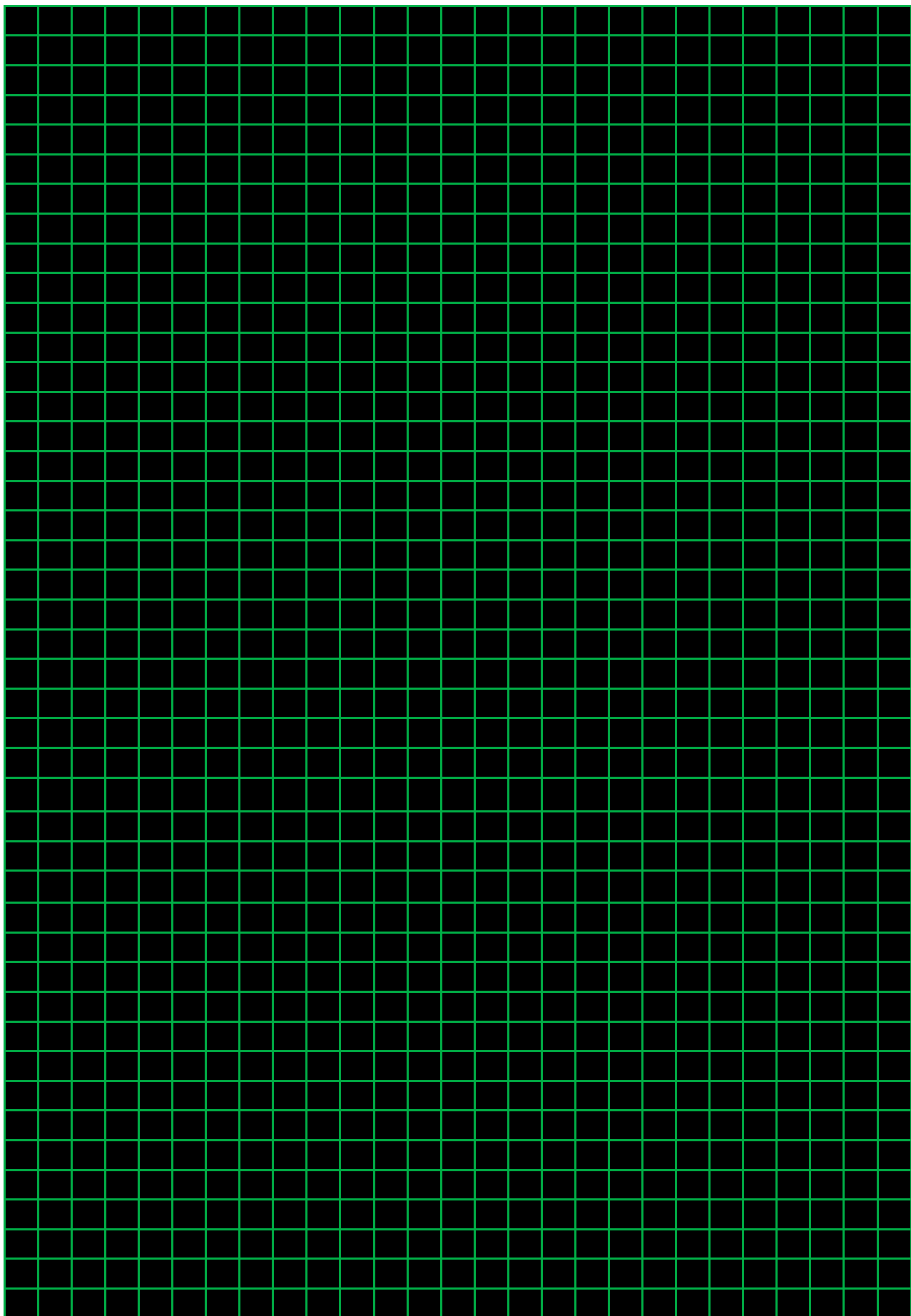


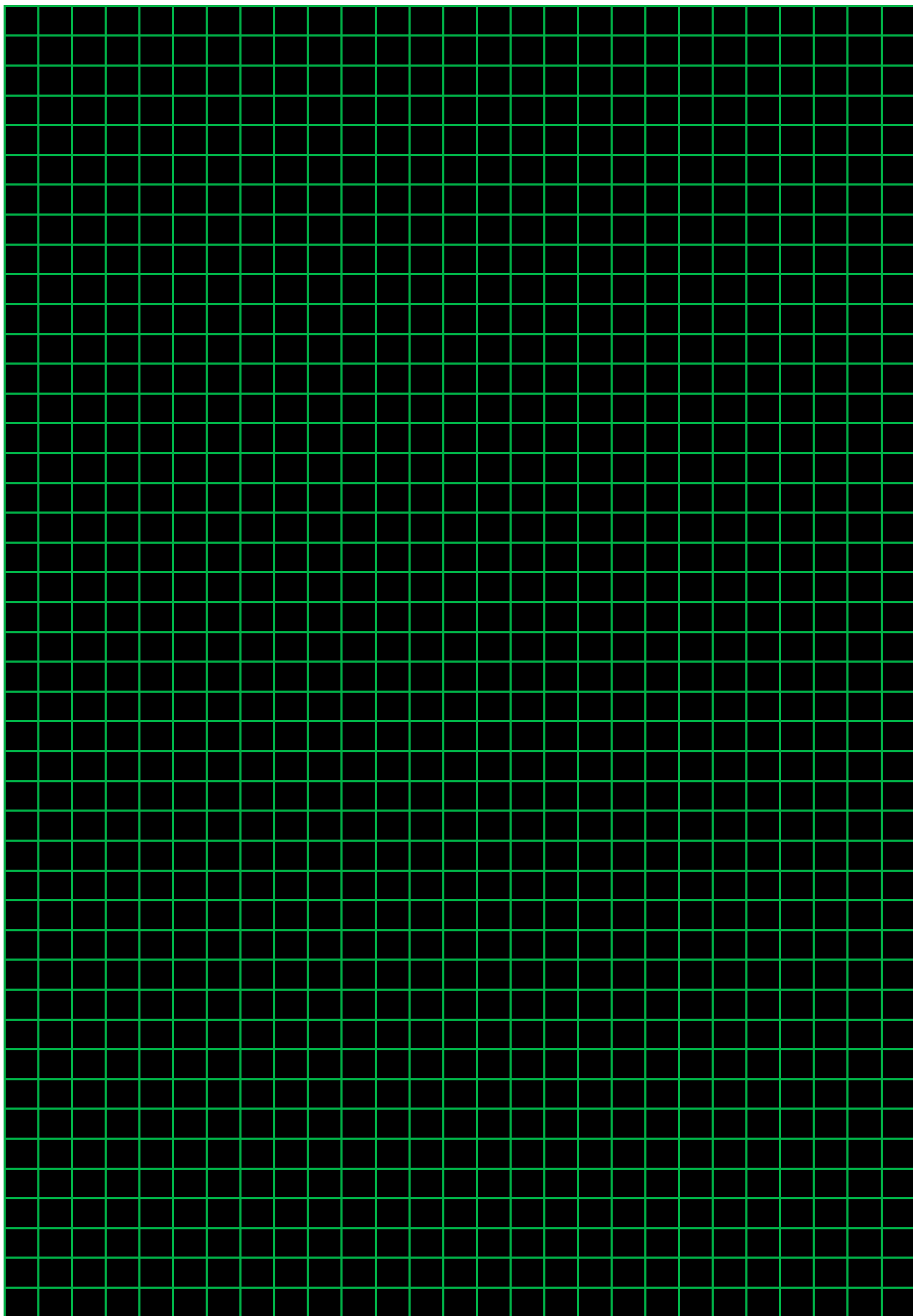
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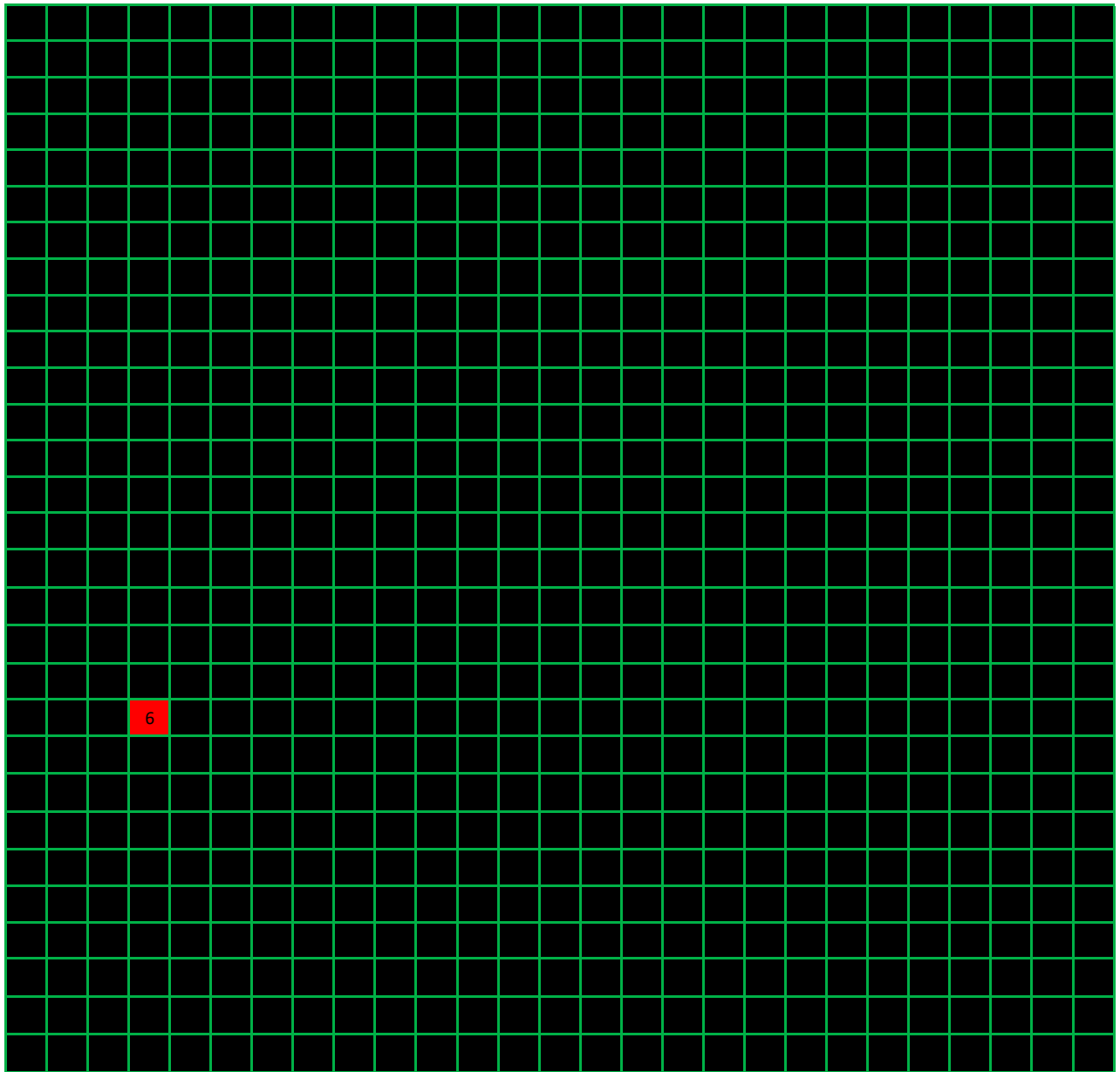
main profiles in PhaLP

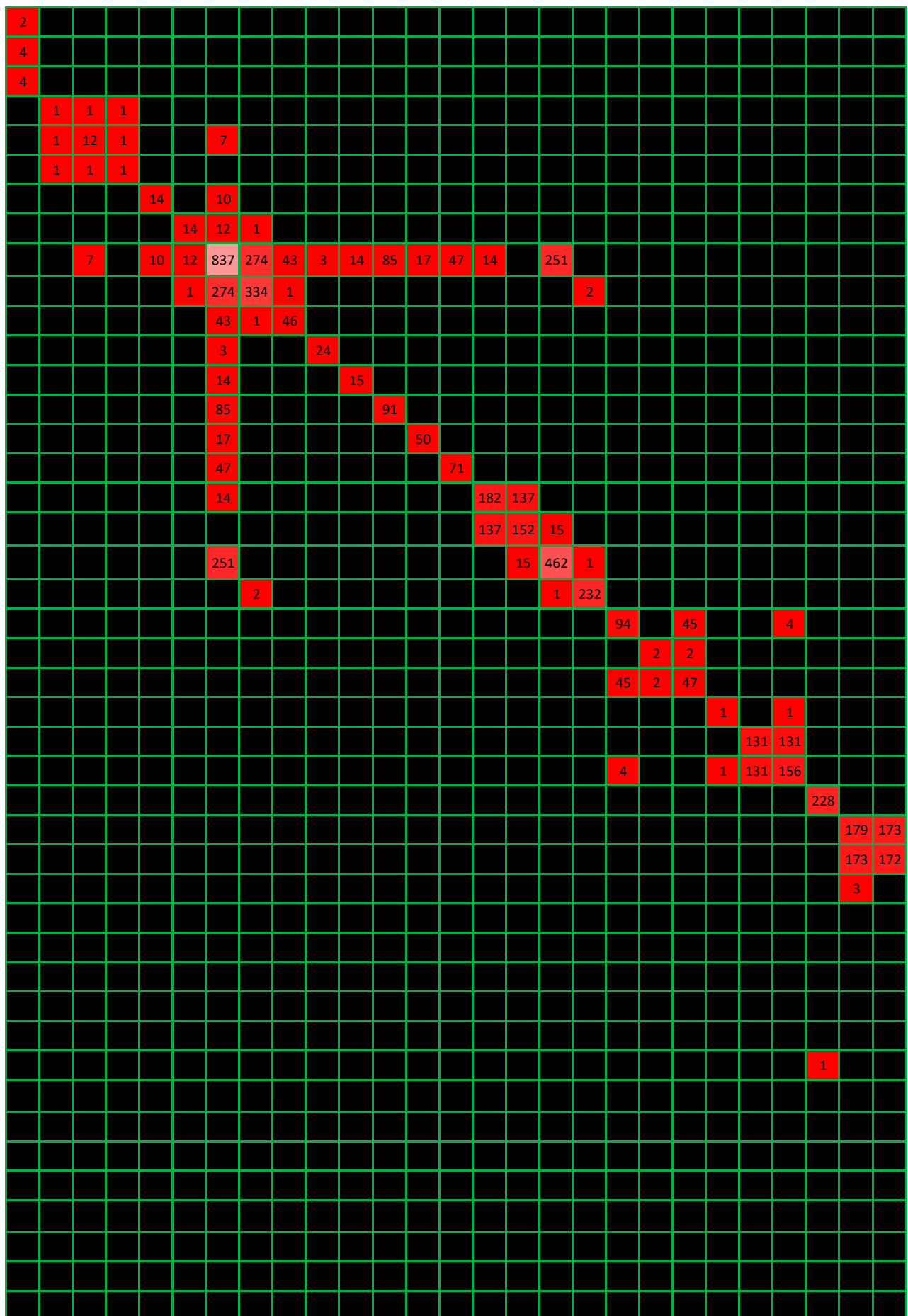
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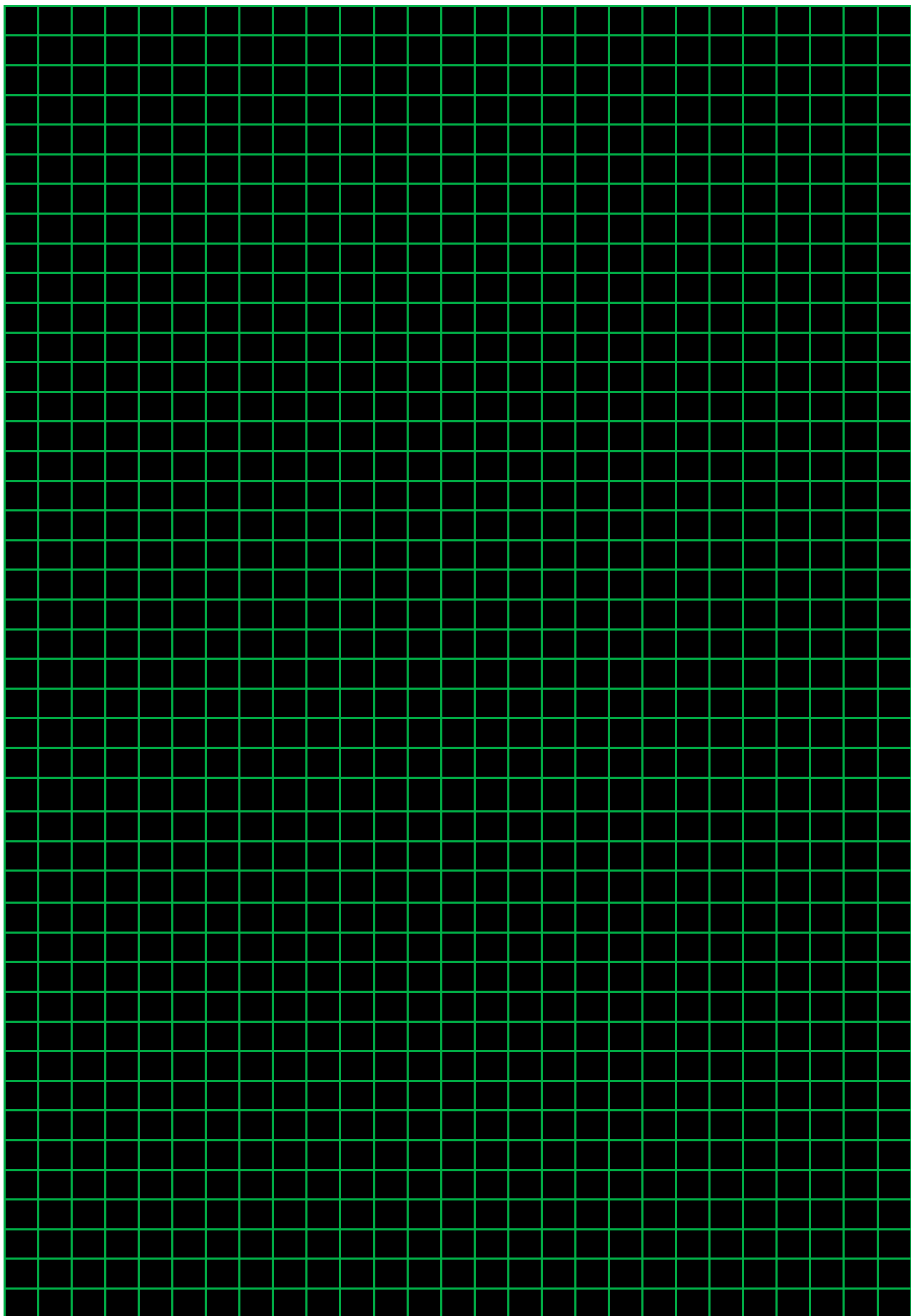
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2	4

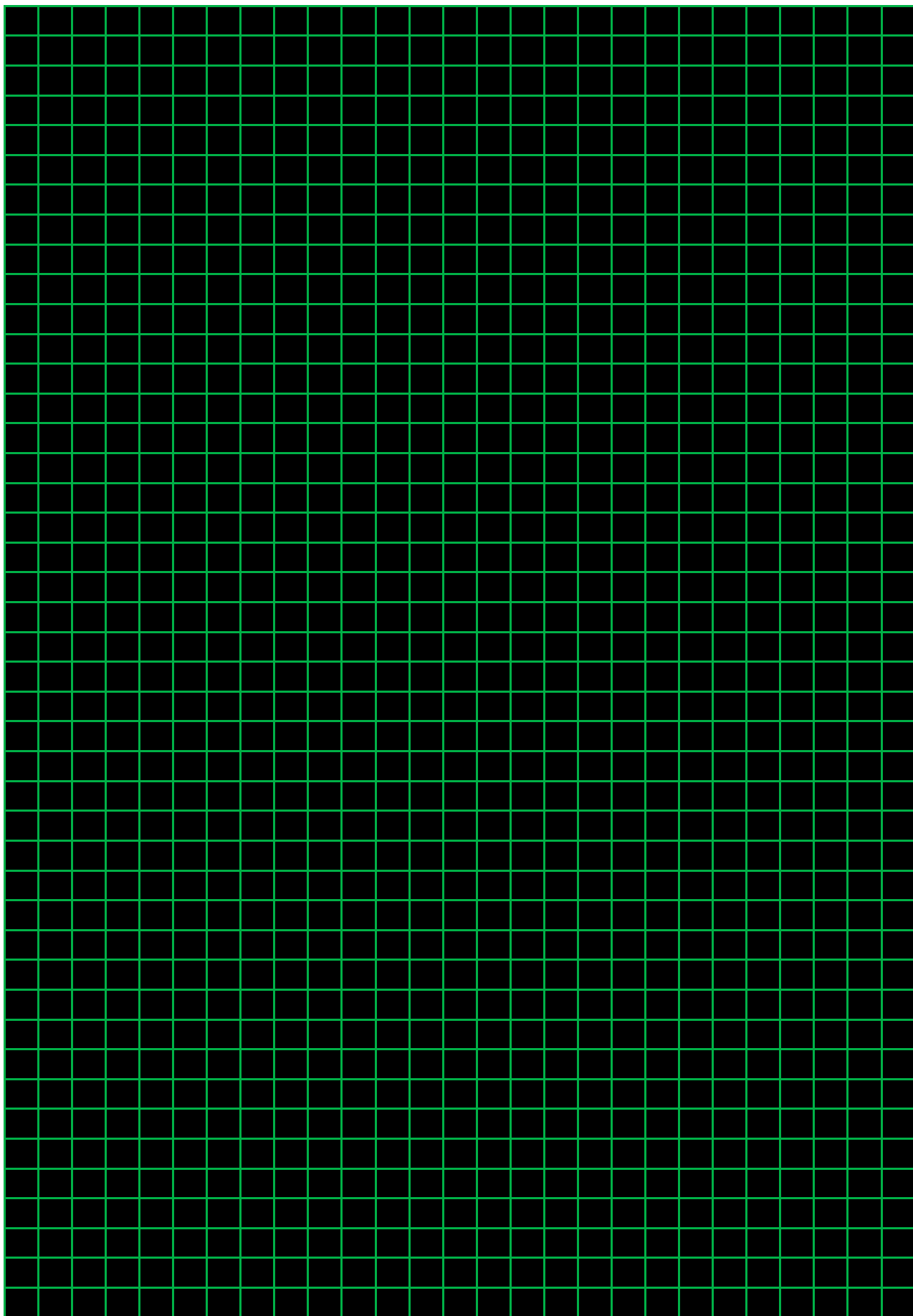


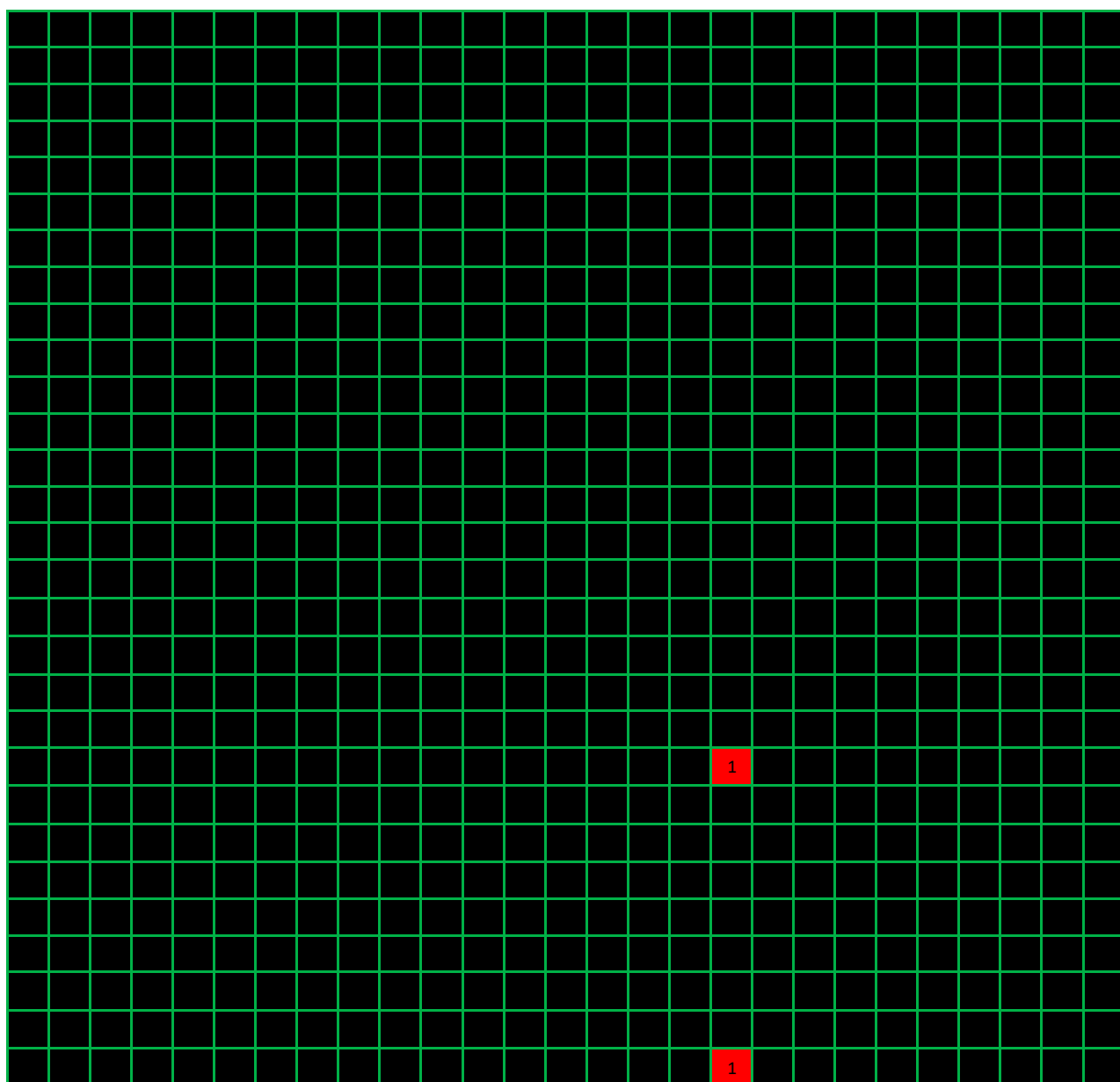




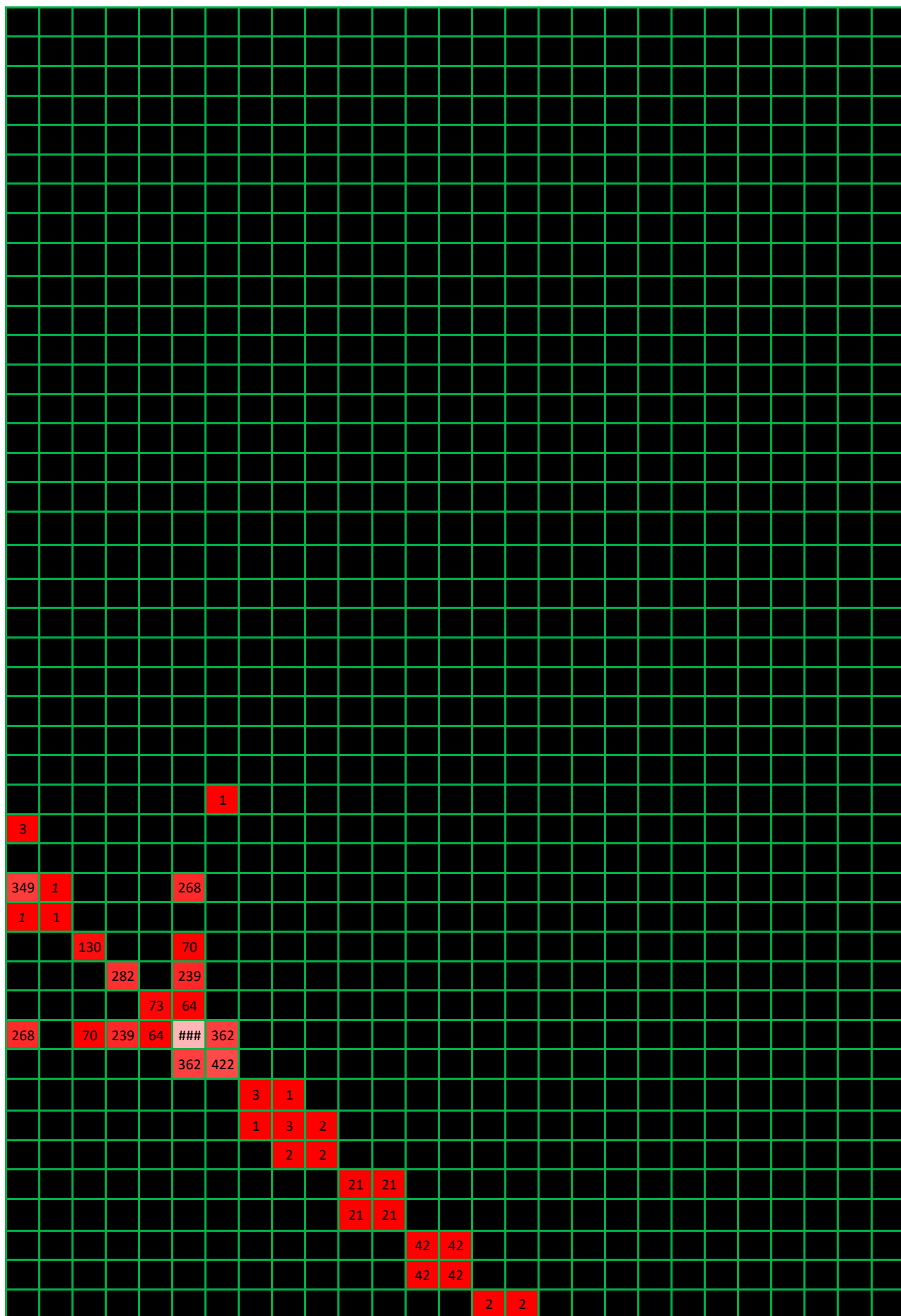


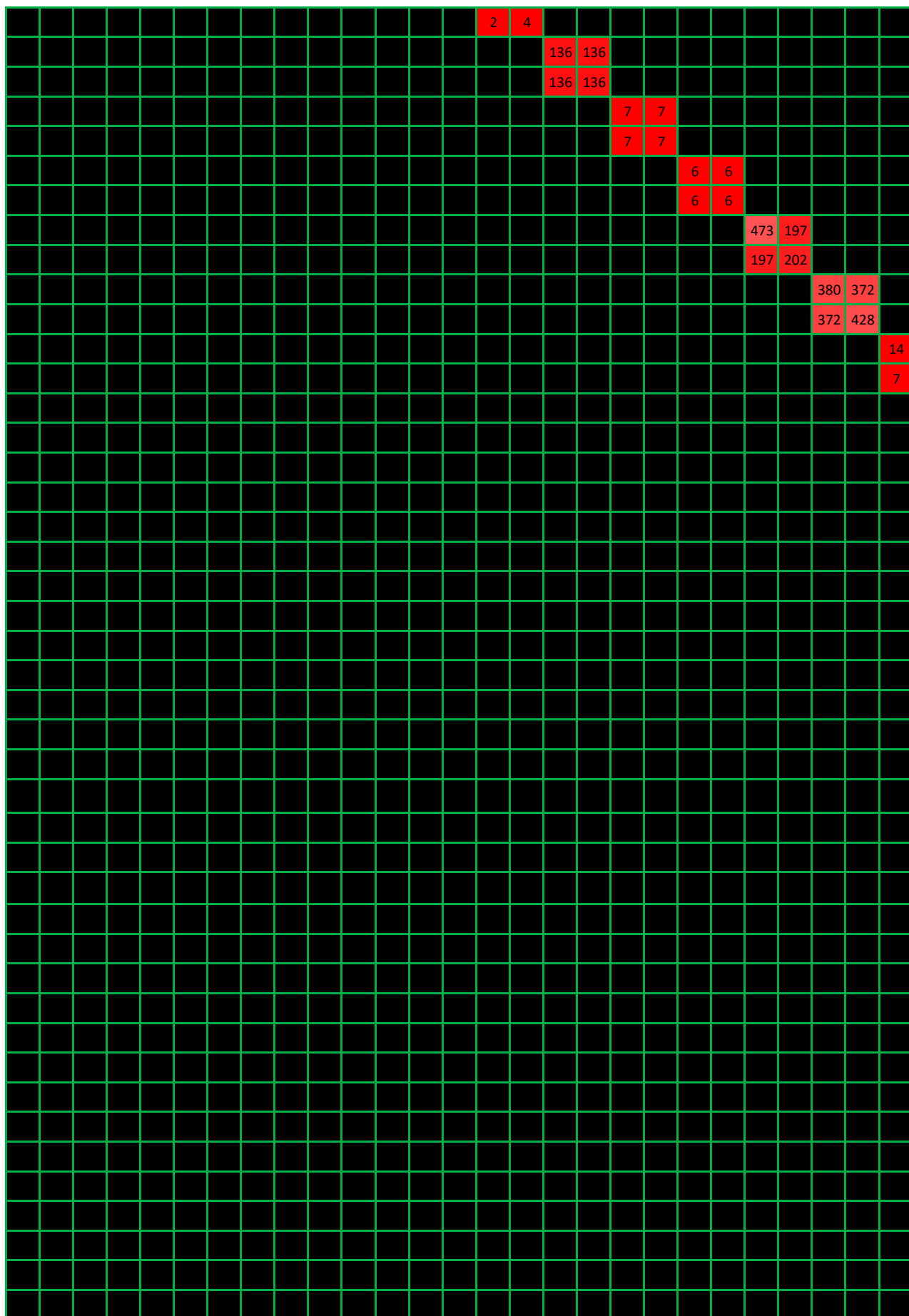


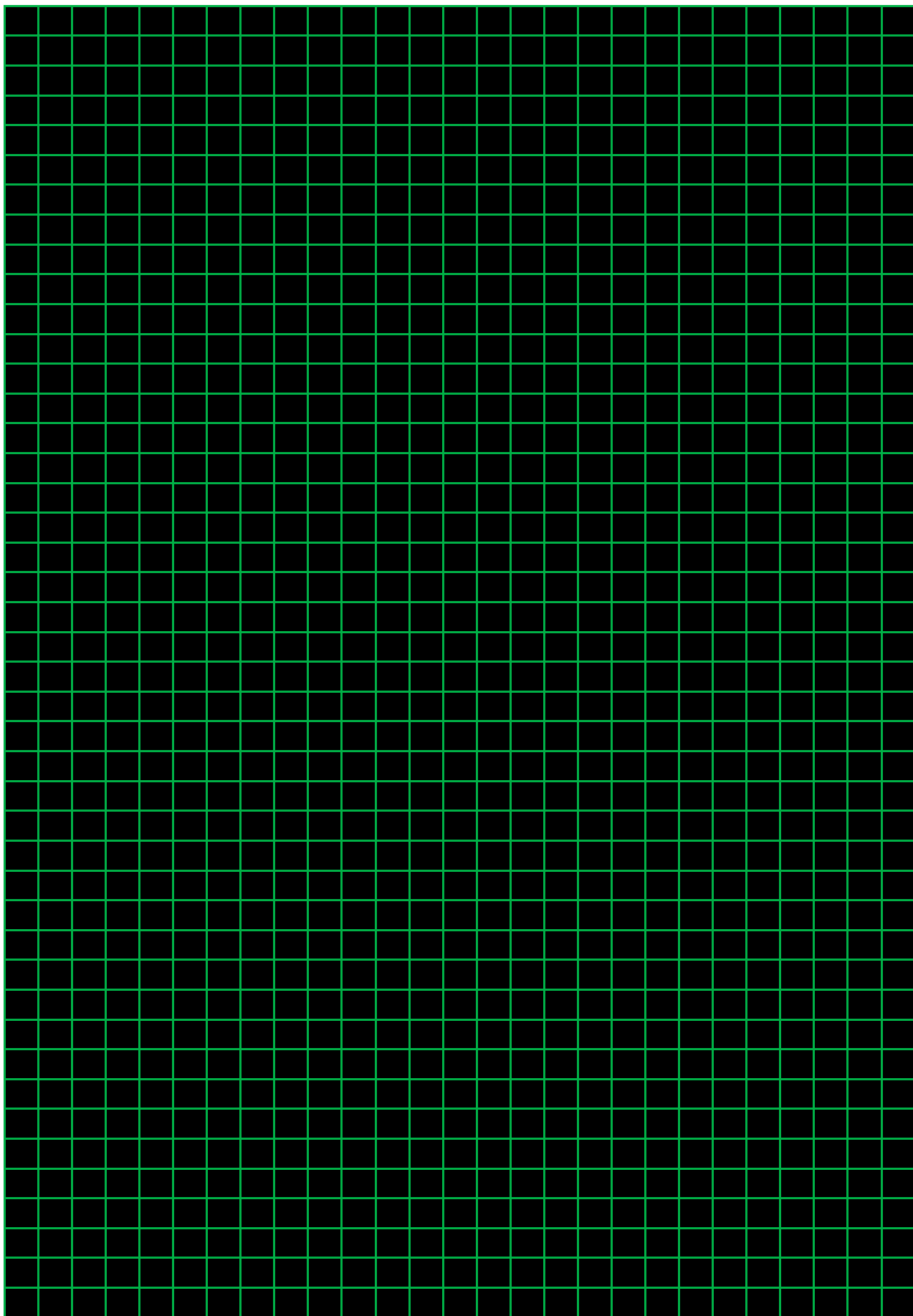


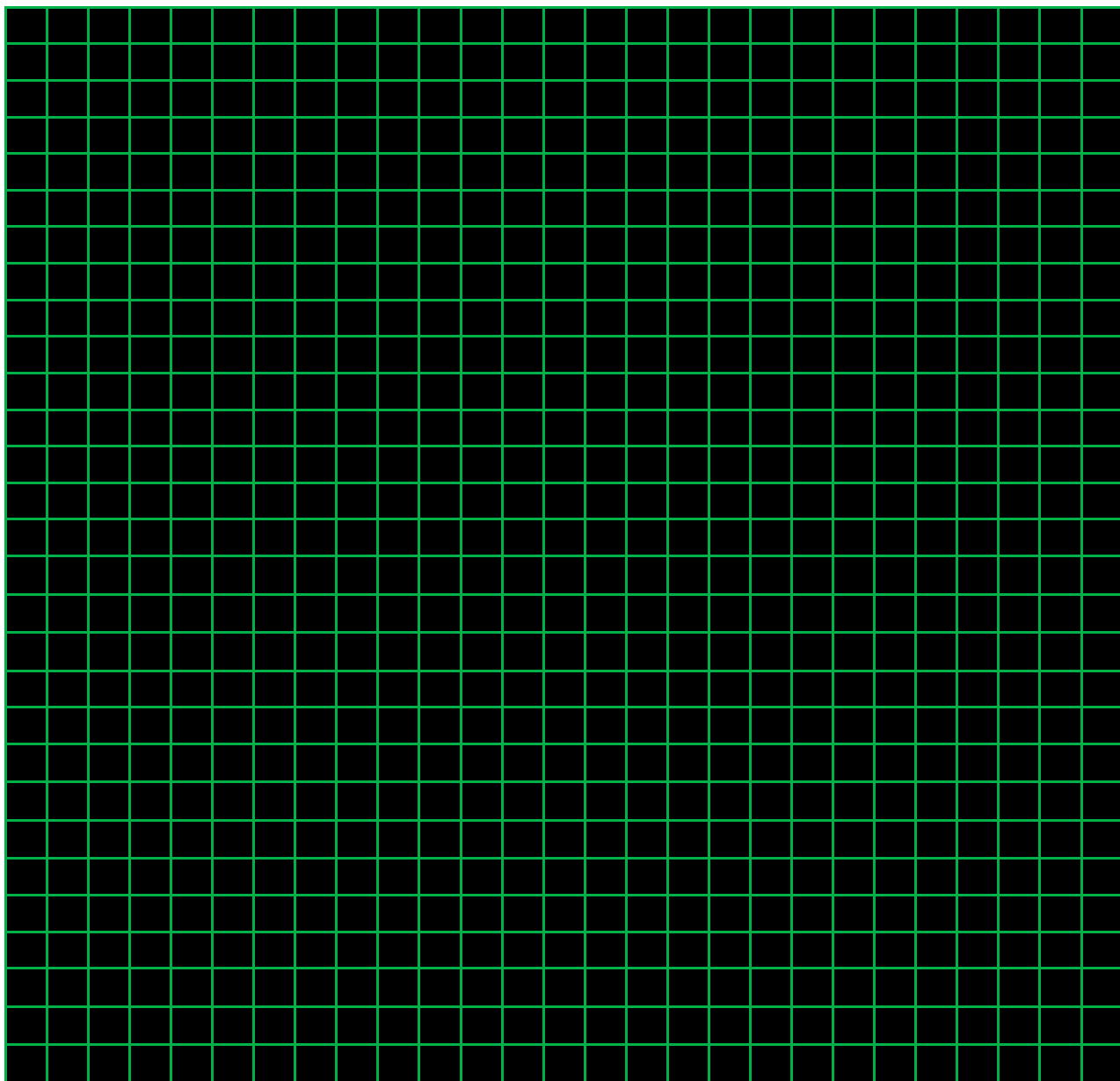


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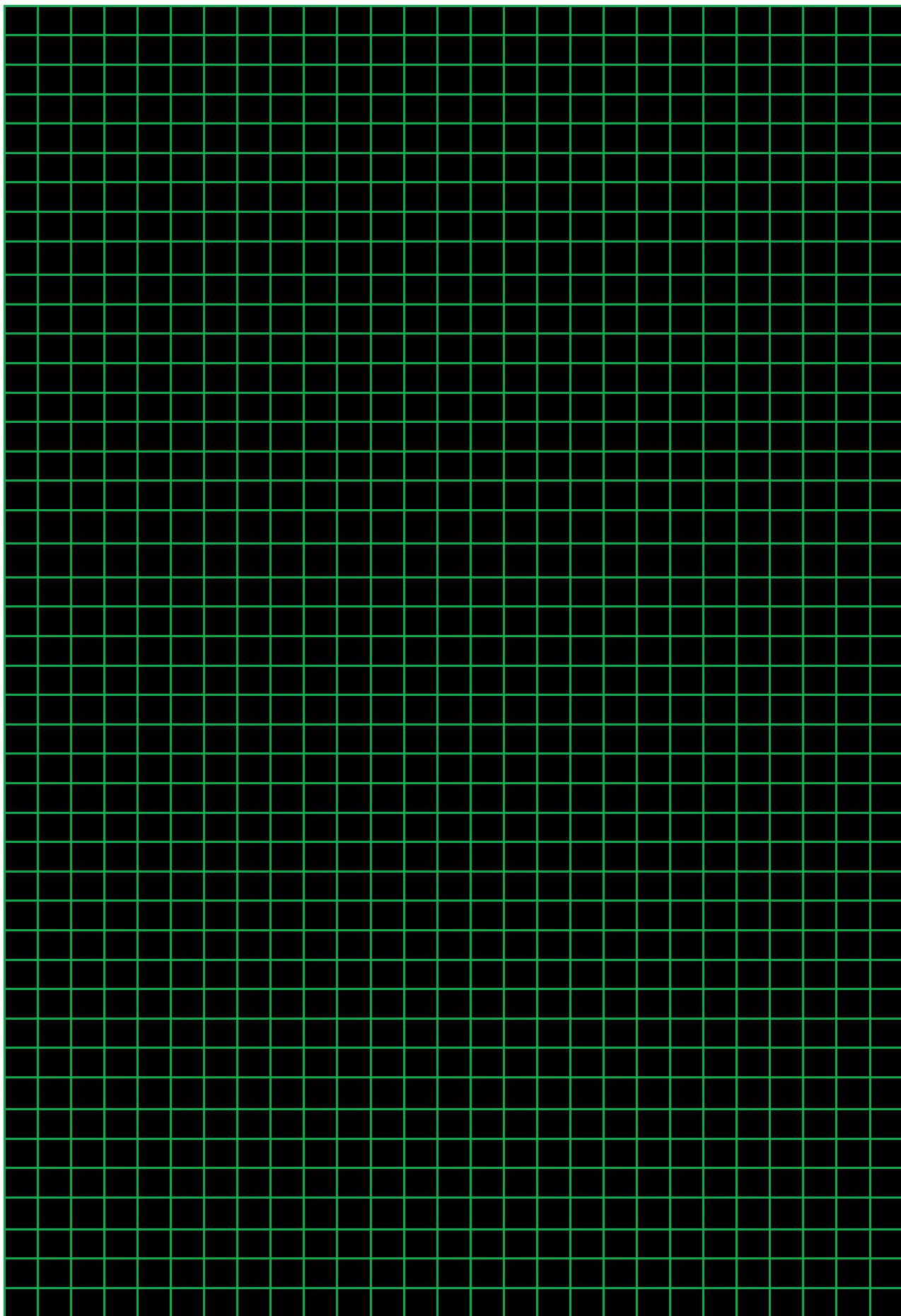


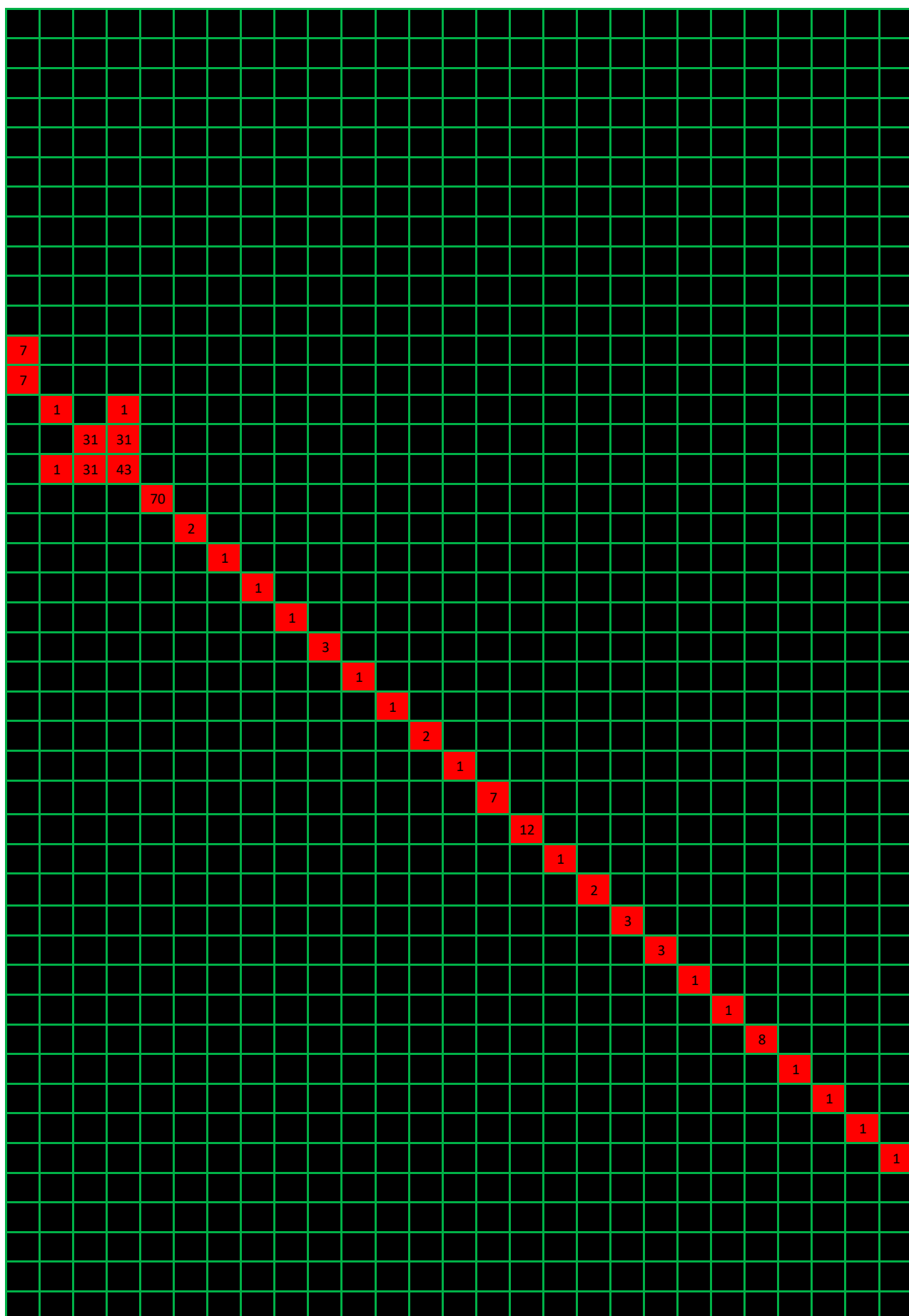


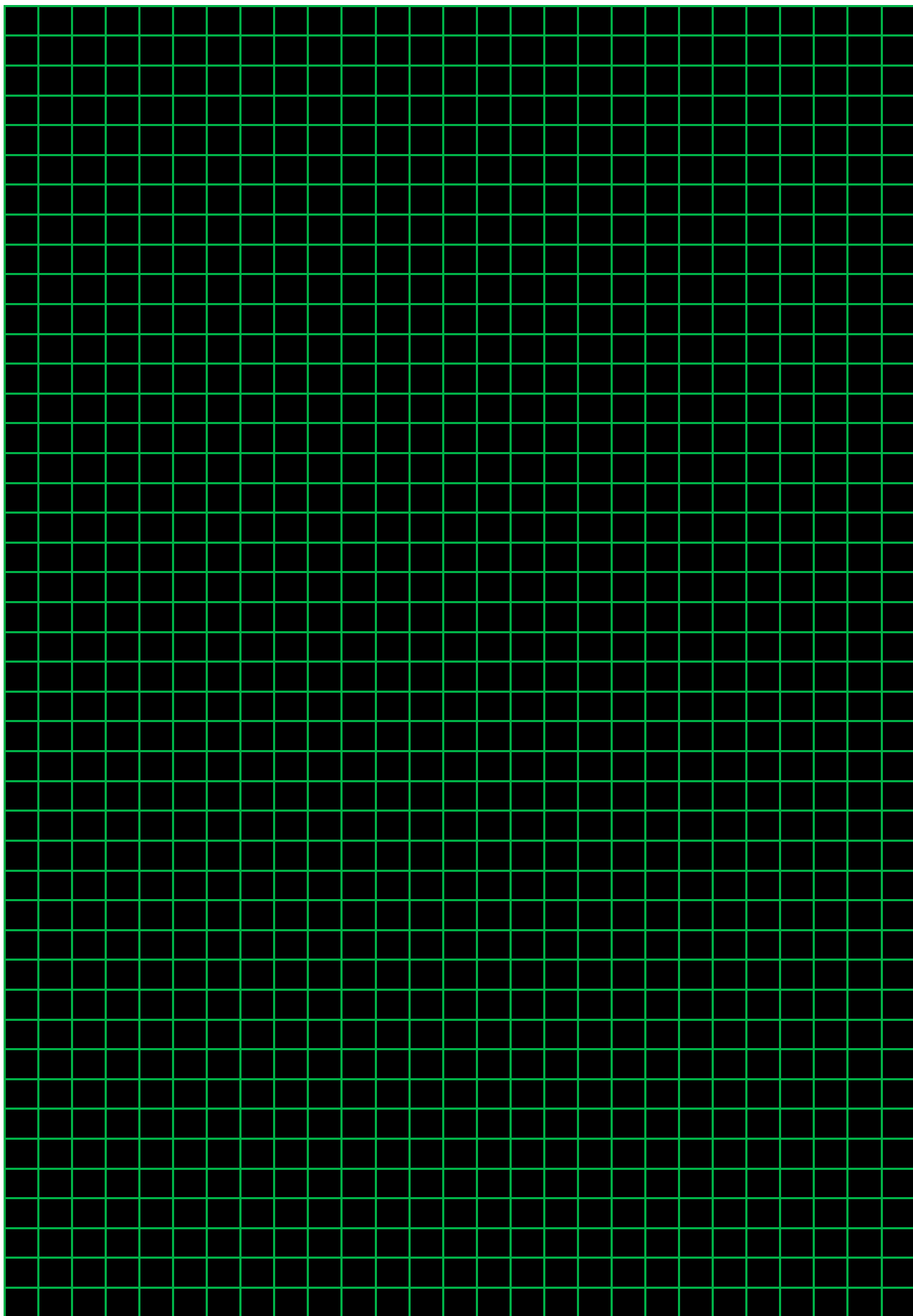


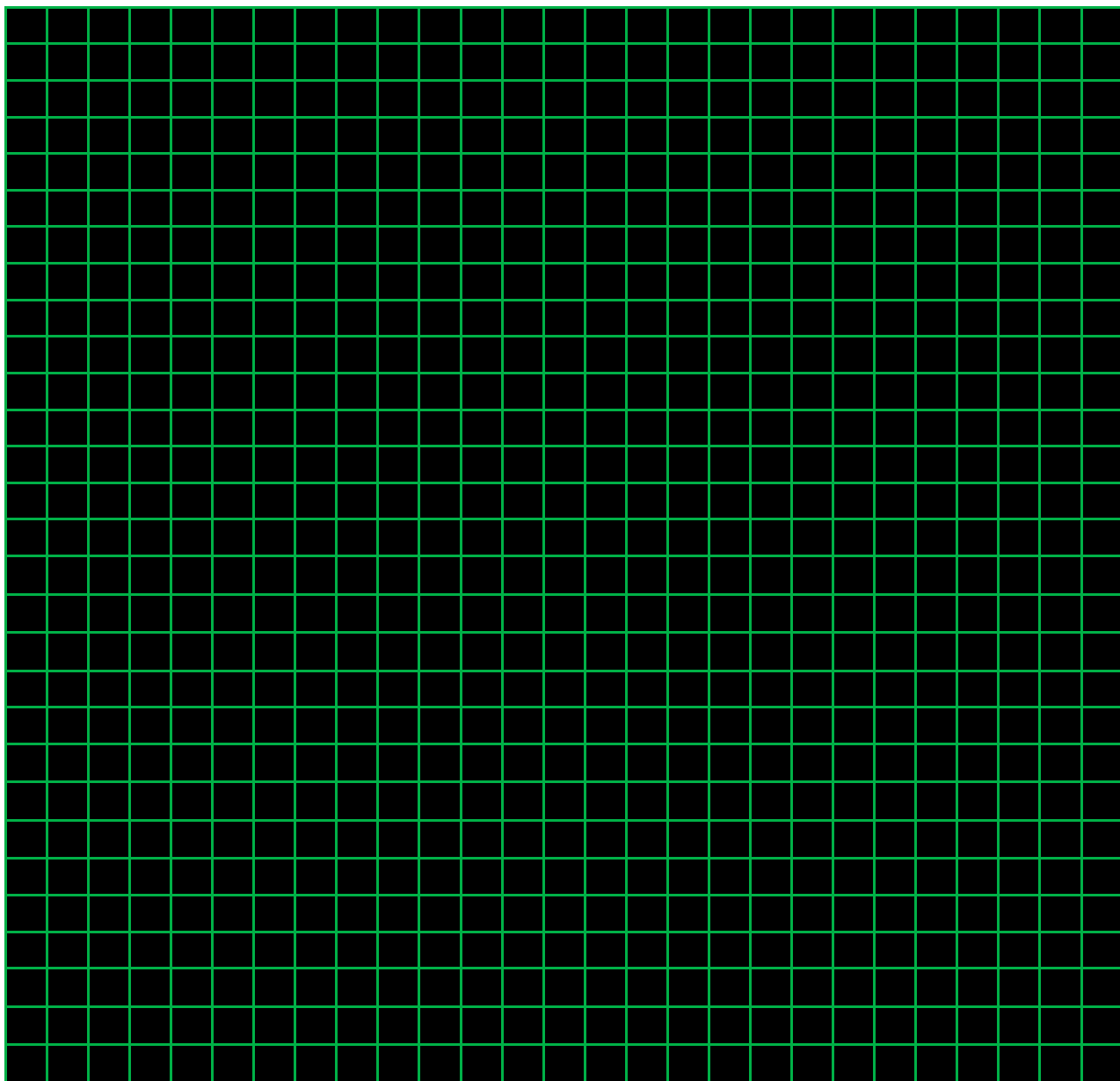


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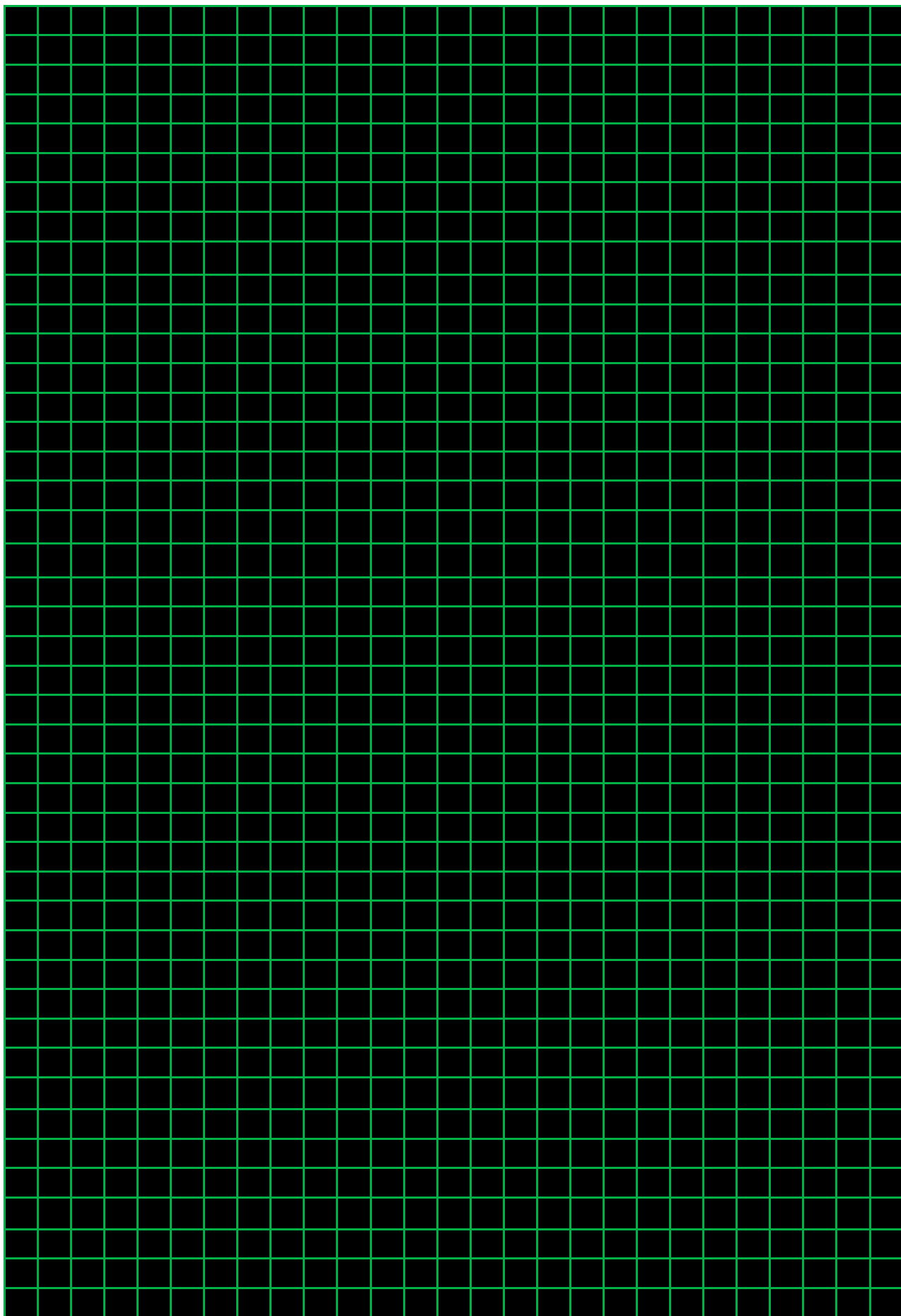


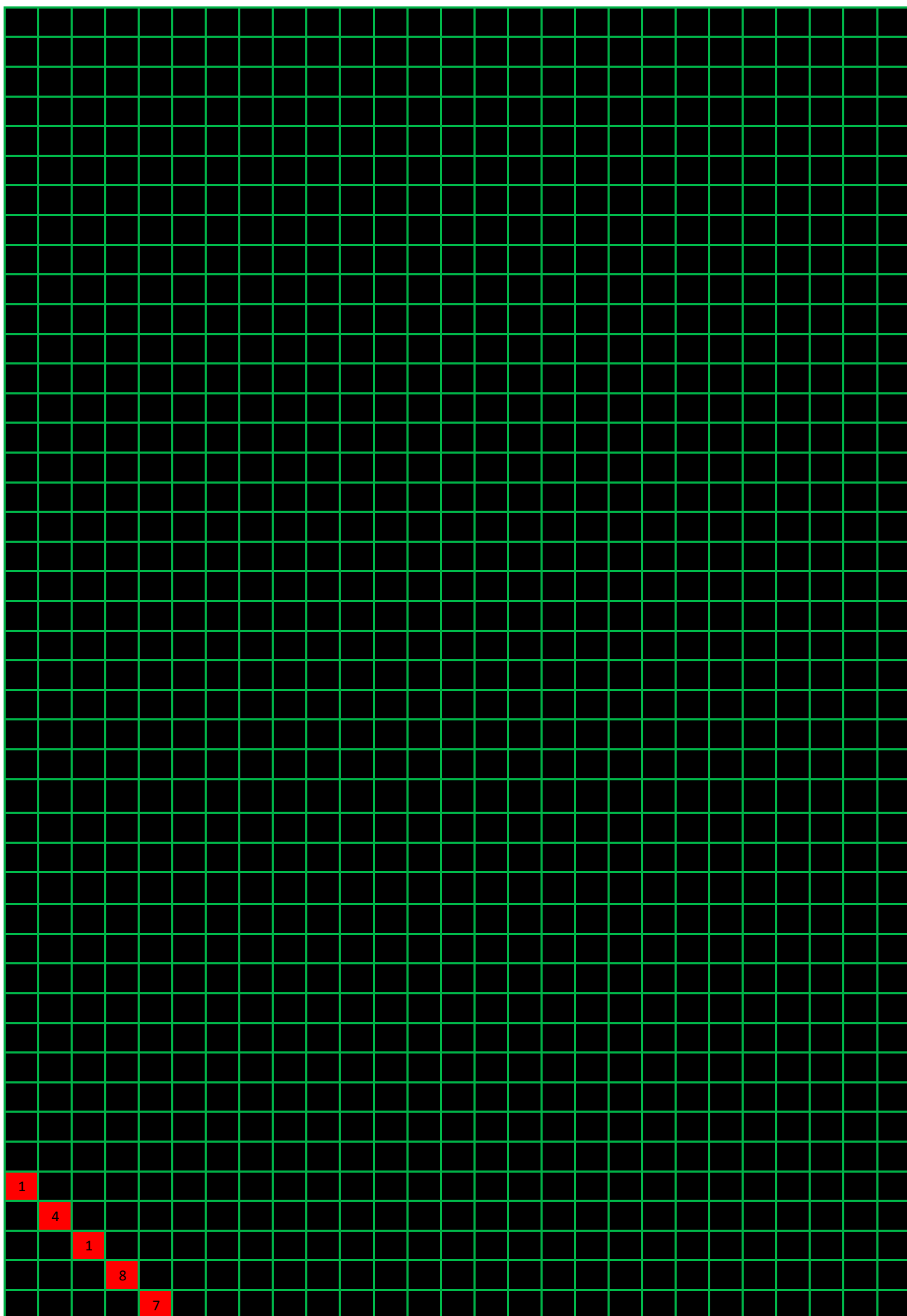


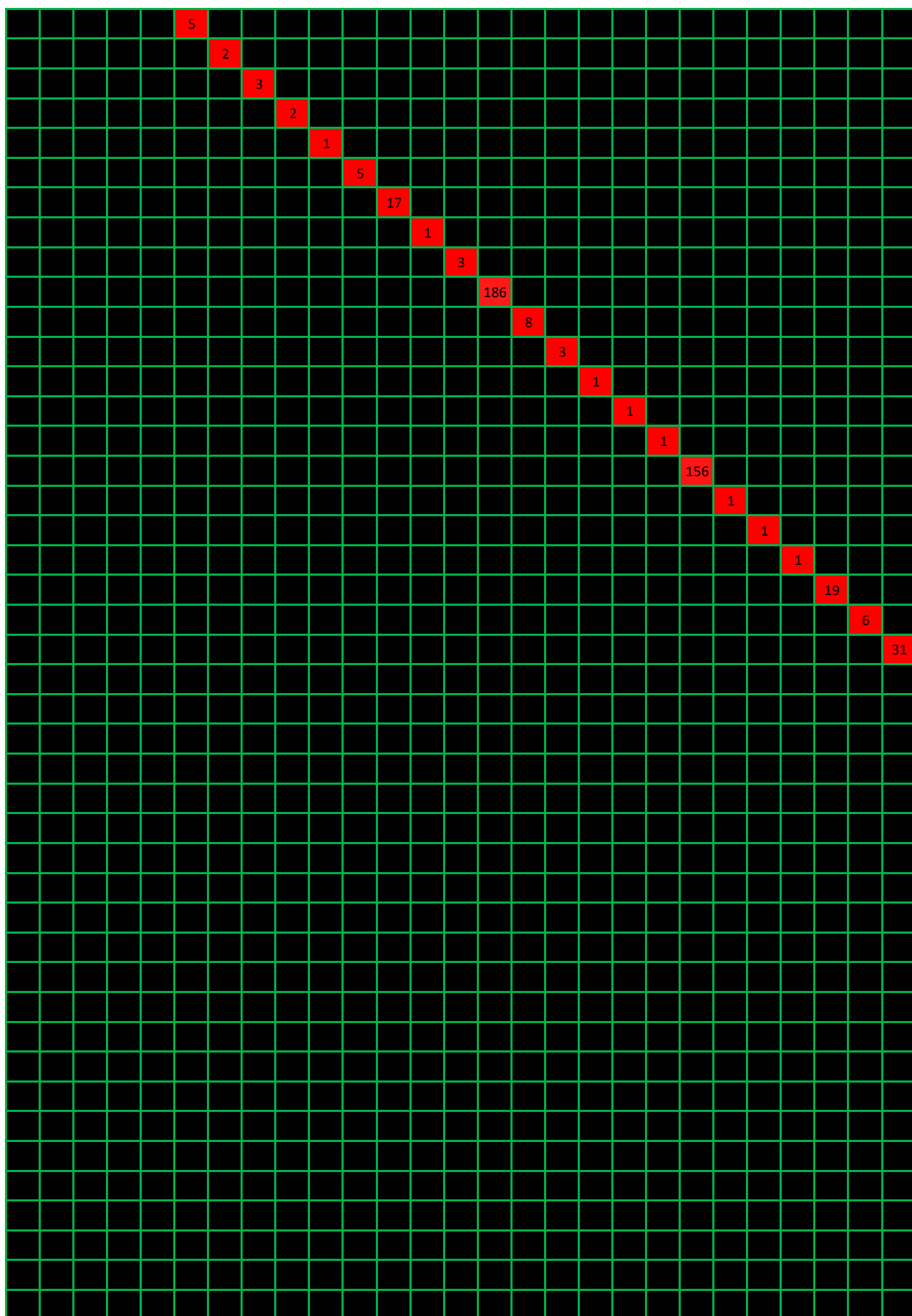
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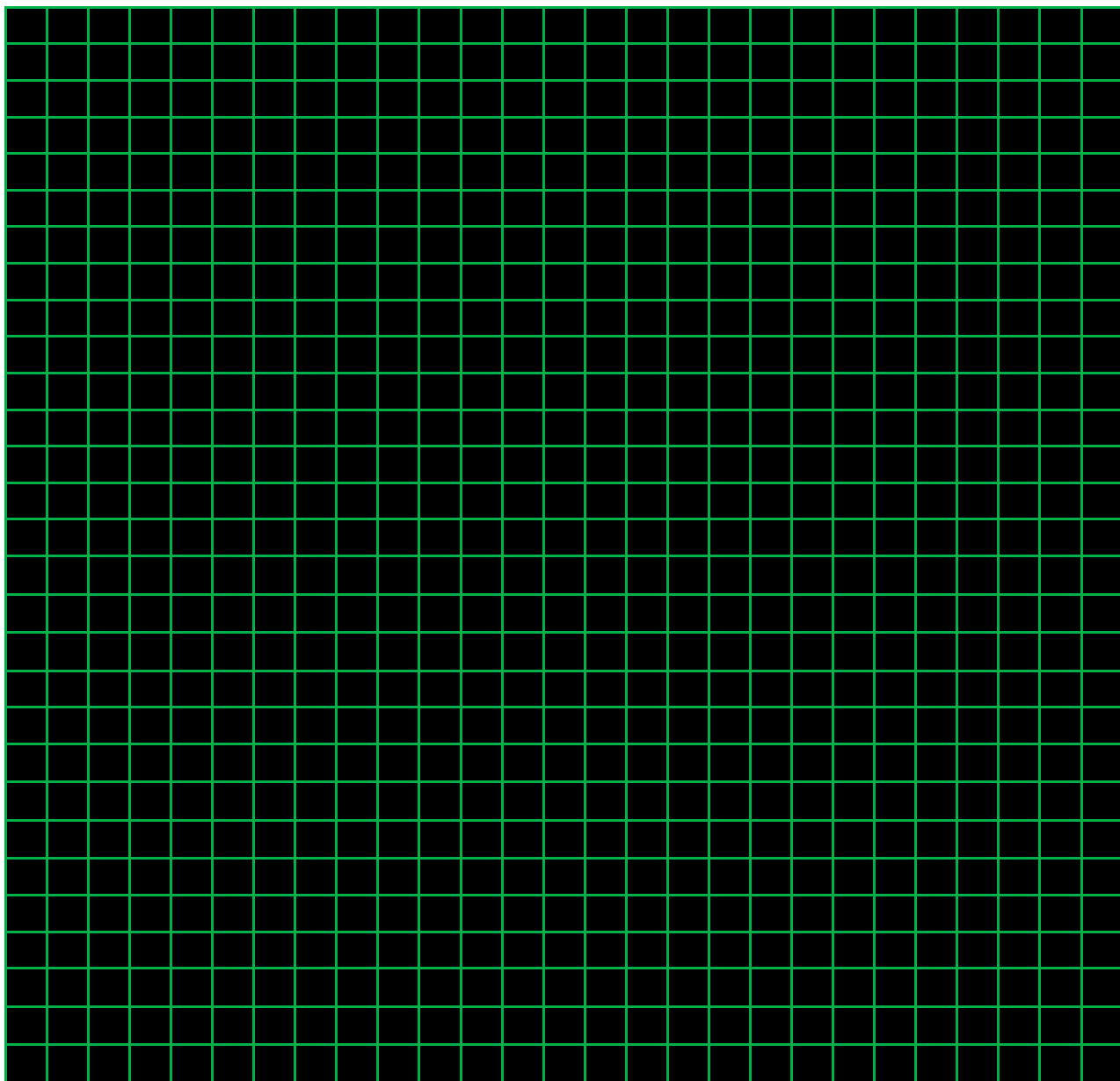
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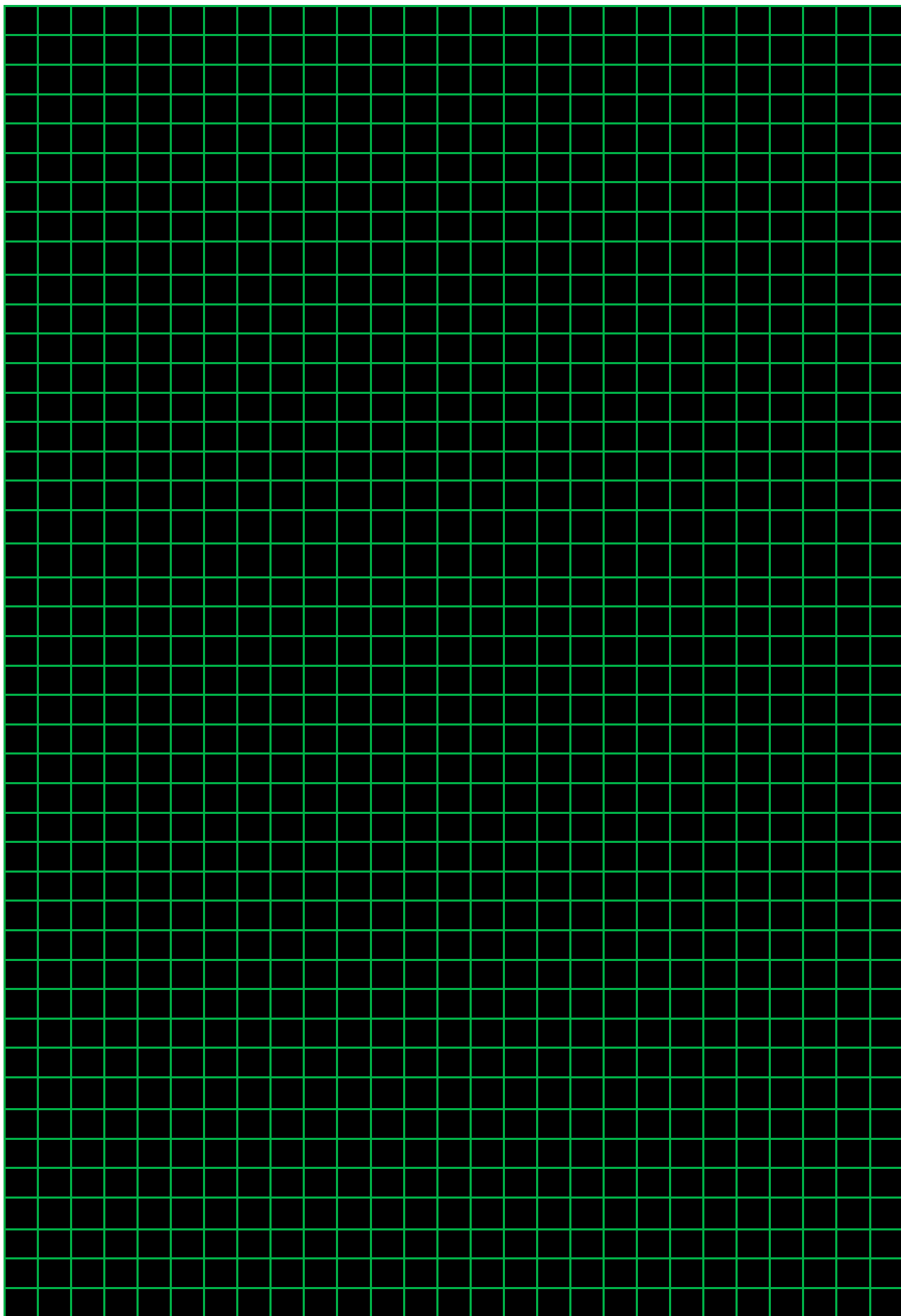
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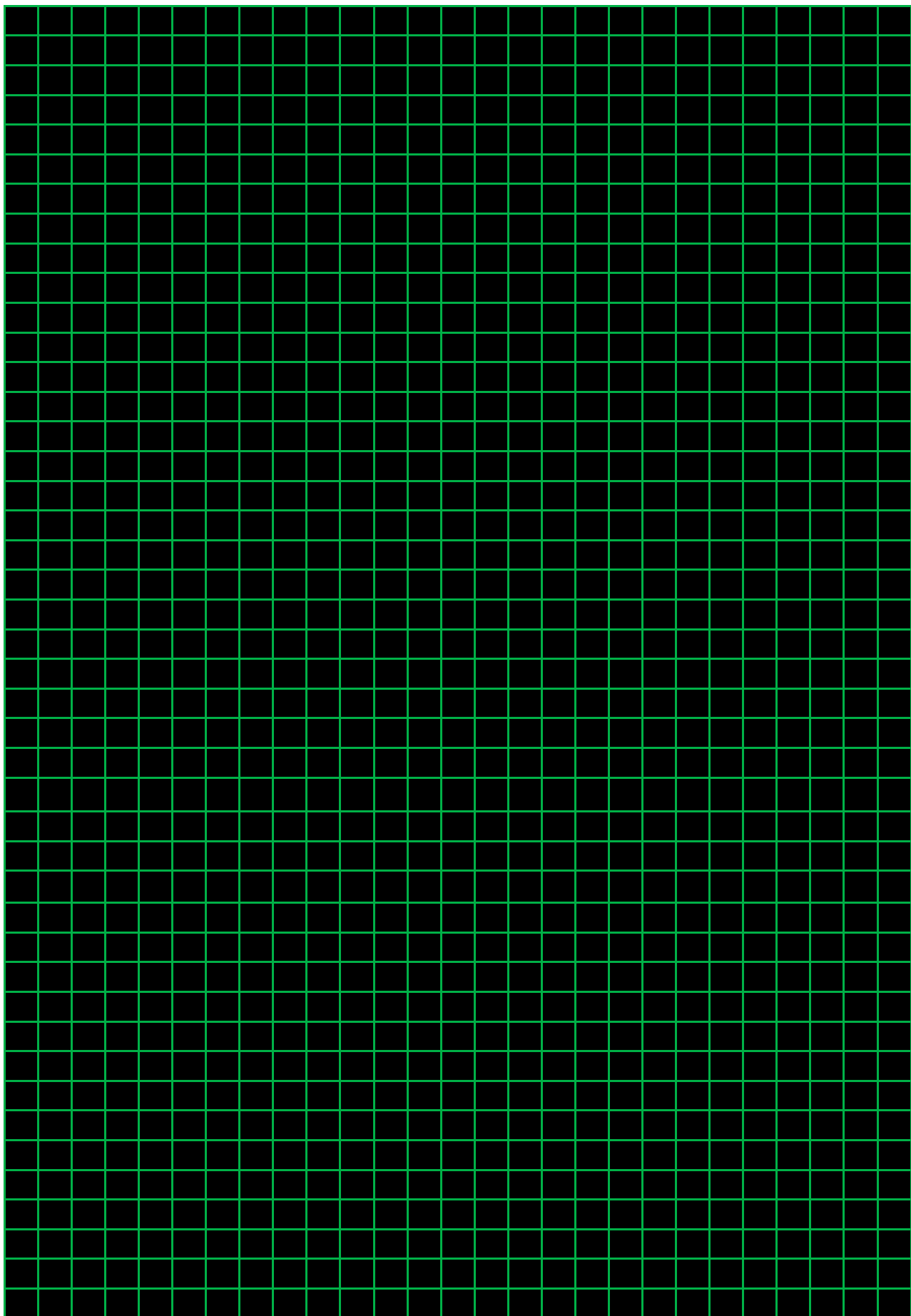


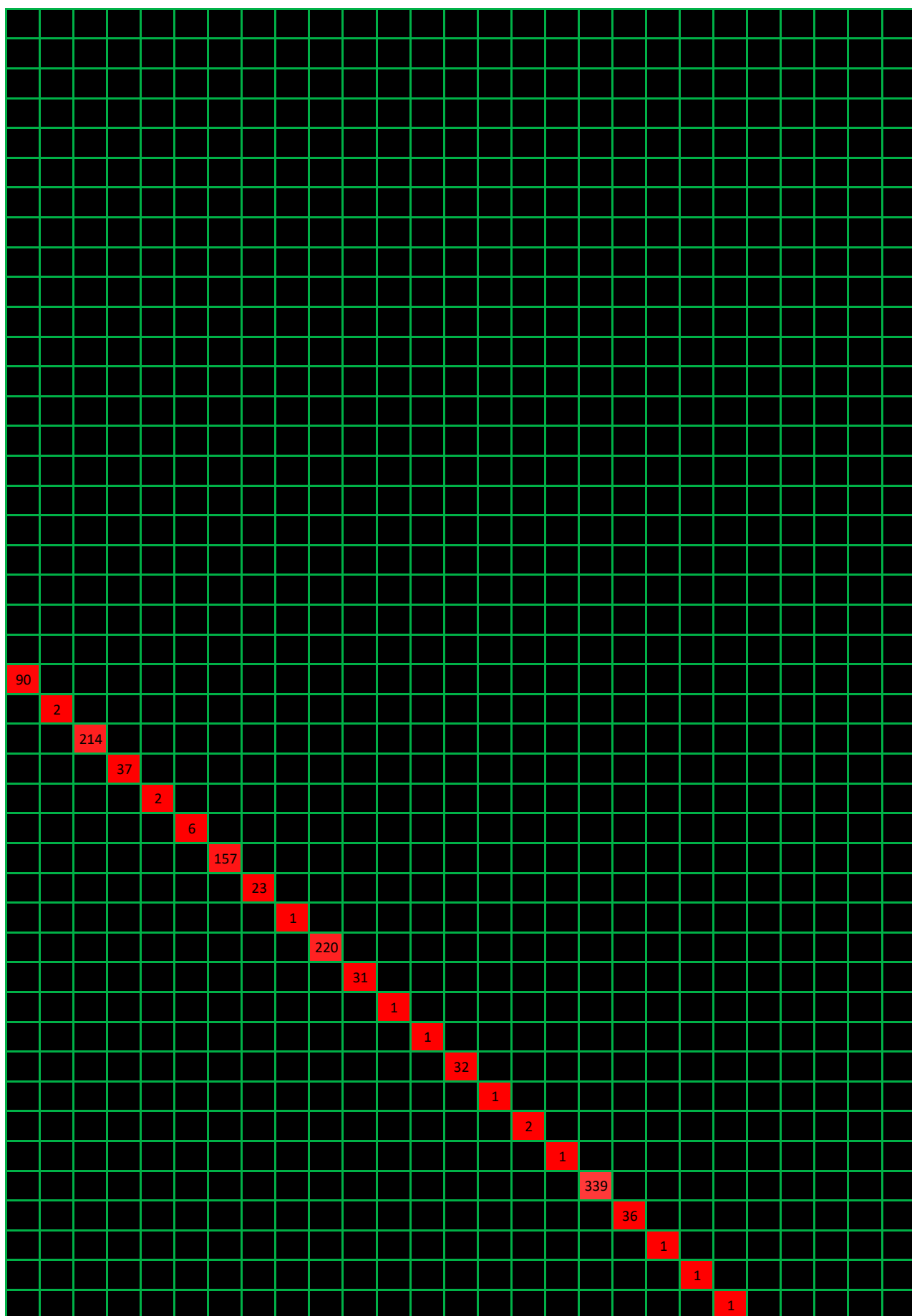












A 20x20 grid with a black background and green grid lines. A diagonal sequence of red squares is located in the top right corner, containing the numbers 1, 1, 6, 230, and 1 from top-left to bottom-right.

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