

Figura 1

MF nr:	Specificita	Linia	VH
1337	TT	IGVH1-08	EVQLVETGAEVKKPGASVKVSCASDYIFTKYDINWVRQAPGGLEWMGWSANTGNTGYAQKFQGRVTMTTRDTSINTAYMELSSLTSGDTAVYFCARSSLFKTETAPYYHFALDVWGQGTITVTVSS
3125	HER3	IGVH3-30	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGSSGWPSYSNWGFDYWGQGTITVTVSS
3176	HER3	IGVH3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDWWYPYYWGFDYWGQGTITVTVSS
3178	HER3	IGVH1-2	QVQLVQSGAEVKKPGASVKVSCASGYTFTGYMHWVRQAPGGLEWMGWINPNSSGGTNYAQKFQGRVTMTTRDTSISTAYMELSRLSDDTAVYYCARDHGSRHFWSYWGFDYWGQGTITVTVSS
4863	HER3	IGVH7-4-1	EVQLVQSGSELKKPGASVKVSCASGYTSIRYALNWVRQAPGGLEWLGWINTNTGNPTYARGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARDTYDSTGYLWFDYWGQGTITVTVSS
3370	EGFR	IGVH1-18	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYGISWVRQAPGGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAKDRHWHWLLDAFDYWGQGTITVTVSS
3755	EGFR	IGVH7-4-1	QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGINANTGDPITYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGQGTITVTVSS
4280	EGFR	IGVH1-24	QVQLVQSGAEVKKPGASVKVSGYTLTELSMHWVRQAPGKGLEWMGGFDPEYKGTFFAQNFQGRVTMTEDTADTAYMELSSLRSEDVAVYYCATEGYYETTTYYYNLFDSWGQGTITVTVSS
4289	EGFR	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCKTSGYTFTDYAMTWVRQAPGGLEWMGWITTNTGDPITYAPGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARVYHWIRGFEFWGQGTITVTVSS
5777	LGR4	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFTNYVMNWVRQAPGGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARWELLDYWGQGTITVTVSS
5781	LGR4	IGVH3-23	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSVISGSGGTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGAGELDYWGQGTITVTVSS
5790	LGR5	IGVH4-39	QVQLQESGPGLVKPKSETLSLTCTVSGGSFSSSSSYWGWRQPPGKGLEWIGSFYYSGNTYYNPSLKSRTVISSEDTSKNQFSLKLSSVTAADTAVYYCARQTYSSSSWDGVLYYFDYWGQGTITVTVS S
5803	LGR5	IGVH4-59	QVQLQESGPGLVKPKSETLSLTCTVSNGSISTYYWSWIRQPPGKGLEWIGYVYVTGRTKYNPSLKSRTVISVDTSKNQFSLNLSSVTAADTAVYYCARGGIVVVAARDYYYMDVWGKGTITVTVSS
5805	LGR5	IGVH5-51	EVQLVQSGAEVKKPGESLKIACKGSGFSFTSHWIGWVRQAPGRGLEWMGVIYPGDSDTRYSPSFQGGVTVSADKSINTAYLQWNSLKASDTAIYYCARPNSGSPRYFEFFWGRGTLVTVSS
5808	LGR5	IGVH4-39	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSSSYWGWRQPPGKGLEWIGSFYYSGNTYYNPSLKSRTVISVDTSKNQFSLKLSSVTAADTAVYYCARQEYYYGSGSPSYFDYWGQGTITVTVSS
5809	LGR5	IGVH5-51	EVQLVQSGAEVKKPGESLKISCKGSGDSFISHWIAWVRQMPGKGLEWMGVIYPGDSDTRYSPSFQGGVTVISADKSITTAYLQWSSLKASDTAMYYCARHEWELLGPFYWGQGTITVTVSS
5814	LGR5	IGVH1-69	EVQLVQSGAEVKKPGSSVKVSCASGGTSTNDIAISWVRQTPGGGLEWMGSIIPILDTTDHAQKFQGRVTITADKSTNTAYMELNSLRSDDTAVYYCAREHIAARQDYFDYWGQGTITVTVSS
5816	LGR5	IGVH7-4-1	EVQLVQSGSKLKKPGASVKVSCASGYTFTSYTMNWVRQAPGGLEWMGWINTDTGDPITYAQGFTGRFVFSLDTSVSTAYLQINSLKAEDTAVYYCARGDCDSTSCYRYSYGYEDYWGQGTITVTV SS
5817	LGR5	IGVH1-69	QVQLVQSGAEVKKPGSSSVKVSCKVSGGTFRSYAISWVRQAPGGLEWMGGIIPIFDTRNYAQILQGRVTITADLSTSTAYMELNSLRSEDTAIYYCARGSDEGDWFDWPGQGTITVTVSS
5818	LGR5	IGVH1-69	EVQLVQSGTEVRKPGSSSVKVSCKASGGTFSNYAISWVRQAPGGLEWMGSIIPILGTTDHAQKFQDRVTITADKSNTTYMELSSLRSDDTAVYYCAREYIAARLDYFDSWGQGTITVTVSS
5832	RNF43	IGVH3-13	EVQLVESGGGLVQPGGSLRLSCVVSIGFTFSYYDMHWVRQVTGKGLEWVSAIGTAGATYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCARDRGYSYDAYYFDWFGQGTITVTVSS
5836	RNF43	IGVH4-39	QVQLQESGPGLVKPKSETLSLTCTVSGGSISSSNYWGWRQPPGKGLEWIGNIYYRGYTYNPSLKSRTVISVDTSKKQFSLTLSSVTAADTAMYYCAREGSDYGDYVGAFDIWDQGTMTVTVSS
5839	RNF43	IGVH3-13	EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYYDMHWVRQVTGKGLEWVSTIGATGDTYYSDSVKGRFTISRQNAKNSLYLQINSLRAGDTAVYYCVRDRGYIGYDSYYFDNWGQGTITVTVSS
5850	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFTTRYPMNWVRQAPGGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARERTNIFYDAFDIWGQGTMTVTVSS
5853	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFNSYAMDWVRQAPGGLEWMGWINTNTGNPTYAQFTGRFVFSLDTSVSTAYLEISSLKAEDTAVYYCARERHGYFEAFDIWGQGTITVTVSS
5855	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFTKYVMNWVRQAPGGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQVSSSLRAEDTALYYCARESNWNNDYFDYWGQGTITVTVSS
5862	ZNRF3	IGVH5-51	QVQLVQSGTEVKKPGESLKISCKGSGYSFTTYWIGWVRQMPGKGLEWMGIIPGDSDTRYSPSFQGGVTVISADKSISTAYLQLSLKAASDTAMYYCARRGLSMVRLSAFDVWGQGTITVTVSS
5882	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFTTRYAMNWVRQAPGGLEWMGWINTKTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARDRGSYDAFDIWGQGTMTVTVSS
5884	ZNRF3	IGVH7-4-1	EVQLVQSGSELKKPGASVKVSCASGYTFTKYAMNWVRQVPGGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVRTAYLQISSLKAEDTAVYYCARKGGSYYDWFDWPGQGTITVTVSS
5887	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFTTRYAMNWVRQAPGGLEWMGWINTNTGKPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARDKGYNNWYMGAFDIWGQGTITVTVSS
5888	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGGSMKVSCASGYTFTTRYAMNWLQAPGGLEWMGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYCARRSGSYDYFDYWGQGTITVTVSS

MF nr:	Specificit	Linia	FR	CDR1	FR2	CDR2	FR3	CDR3	FR4
133	T	IGVH1-08	EVQLVETGAEVKKPGASVKVSCASDYIFT	KYDIN	WVRQAPGQGLEWMG	WMSANTGNTGYAQKFQG	RVTMTRDTSINTAYMELSSLTSGDTAVYFCAR	SSLFKTETAPYYHFALDV	WGQGTTLTVTVSS
312	HER3	IGVH3-30	QVQLVESGGGVVQPGRLRLSCAASGFTFS	SYGMH	WVRQAPGKGLEWVA	VISYDGSNKYYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	GSSGWPSYSNWGFYD	WGQGTTLTVTVSS
317	HER3	IGVH3-23	EVQLLESGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WVRQAPGKGLEWVS	AISGSGGSTYYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR	DWWYPPYYWGFYD	WGQGTTLTVTVSS
317	HER3	IGVH1-2	QVQLVQSGAEVKKPGASVKVSCASGYTFT	GYMH	WVRQAPGQGLEWMG	WINPNSGGTNYAQKFQG	RVTMTRDTSISTAYMELSLRLSDDTAVYYCAR	DHGSRHFWYWGFYD	WGQGTTLTVTVSS
486	HER3	IGVH7-4-1	EVQLVQSGSELKKPGASVKVSCASGYTSI	RYALN	WVRQAPGQGLEWLG	WINTNTGNPTYARGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	DTYDSTGYLWFDY	WGQGTTLTVTVSS
337	EGFR	IGVH1-18	QVQLVQSGAEVKKPGASVKVSCASGYTFT	SYGIS	WVRQAPGQGLEWMG	WISAYNGNTNYAQKLQG	RVTMTTDTSTSTAYMELSLRLSDDTAVYYCAK	DRHWHWWLDAFDY	WGQGTTLTVTVSS
375	EGFR	IGVH7-4-1	QVQLVQSGSELKKPGASVKISCKASGYDFT	NYAMN	WVRQAPGHGLEWMG	WINANTGDPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDSAVYYCTR	ERFLEWLHFDY	WGQGTTLTVTVSS
428	EGFR	IGVH1-24	QVQLVQSGAEVKKPGASVKVSCVSGYTTLT	ELSMH	WVRQAPGKGLEWMG	GFDPEYEGKTFFAQNFQG	RVTMTEDTSADTAYMELSSLRSEDATAVYYCAT	EGYYETTTYYYNLFDS	WGQGTTLTVTVSS
428	EGFR	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCKTSGYTFT	DYAMT	WVRQAPGQGLEWMG	WITNTGDPTYAPGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	VYHWIRGFEE	WGQGTTLTVTVSS
577	LGR4	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFT	NYVMN	WVRQAPGQGLEWMG	WINTNTGNPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	WELLDY	WGQGTTLTVTVSS
578	LGR4	IGVH3-23	EVQLVESGGGLVQPGGSLRLSCAASGFTFS	SYAMS	WVRQAPGKGLEWVS	VISGSGGSTYYADSVKG	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK	GAGELDY	WGQGTTLTVTVSS
579	LGR5	IGVH4-39	QVQLQESGPGLVKPSSETLSLTCTVSGGSFS	SSSSYW	WIRQPPGKGLEWIG	SFYYSGNTYYNPSLKS	RVTISEDTSKNQFSLKLSSVTAADTAVYYCAR	QTYSSSWDGVLYYFDY	WGQGTTLTVTVSS
580	LGR5	IGVH4-59	QVQLQESGPGLVKPSSETLSLTCTVSNGSIS	TYYSW	WIRQPPGKGLEWIG	YVYYTGRTKYNPSLKS	RVTISVDTSKNQFSLNLSSVTAADTAVYYCAR	GGIVVVPAARDYYYMDV	WGKGTTLTVTVSS
580	LGR5	IGVH5-51	EVQLVQSGAEVKKPGESLKIACKGSGFSFT	SHWIG	WVRQKPGRGLEWMG	VIYPGSDTRYSPSFQG	QVTVSADKSINTAYLQWNSLKAASDTAIYYCAR	PNSGSPRYFEF	WGRGTTLTVTVSS
580	LGR5	IGVH4-39	QVQLQESGPGLVKPSSETLSLTCTVSGGSIS	SSSYW	WIRQPPGKGLEWIG	SFYYSGNTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	QEYYYSGSGSPSYFDY	WGQGTTLTVTVSS
580	LGR5	IGVH5-51	EVQLVQSGAEVKKPGESLKISCKGSGDSFI	SHWIA	WVRQMPGKGLEWMG	IVYPGSDTRYSPSFQG	QVTISADKSITAYLQWSSLKASDTAMYYCAR	HEWELLGPFDY	WGQGTTLTVTVSS
581	LGR5	IGVH1-69	EVQLVQSGAEVKKPGSSVKVSCASGGTST	NDAIS	WVRQTPGQGLEWMG	SIIPILDTTDHAQKFQG	RVTITADKSTNTAYMELNSLRSDDTAVYYCAR	EHIAARQDYFDY	WGQGTTLTVTVSS
581	LGR5	IGVH7-4-1	EVQLVQSGSKLKKPGASVKVSCASGYTFT	SYTMN	WVRQAPGQGLEWMG	WINTDTGDPTYAQGFTG	RFVFSLDTSVSTAFQLQINSLKAEDTAVYYCAR	GDGCDSTSCYRYSYGYEDY	WGQGTTLTVTVSS
581	LGR5	IGVH1-69	QVQLVQSGAEVKKPGSSVKVSCVSGGTFR	SYAIS	WVRQAPGQGLEWMG	GIIPIDFDRNYAQILQG	RVTITADLSTSTAYMELNSLRSEDATAIYYCAR	GSDEGDWFDP	WGQGTTLTVTVSS
581	LGR5	IGVH1-69	EVQLVQSGTEVRKPGSSVKVSCASGGTFS	NYAIS	WVRQAPGQGLEWMG	SIIPILGTTDHAQKFQD	RVTITADKSSNTTYMELSSLRSDDTAVYYCAR	EYIAARLDYFDS	WGQGTTLTVTVSS
583	RNF43	IGVH3-13	EVQLVESGGGLVQPGGSLRLSCVVSIGFTFS	YYDMH	WVRQVTGKGLEWVS	AIGTAGATYYPGSVKG	RFTISRDN SKNTLYLQMNSLRAGDTAVYYCAR	DRGYSYDAYYFDF	WGQGTTLTVTVSS
583	RNF43	IGVH4-39	QVQLQESGPGLVKPSSETLSLTCTVSGGSIS	SSNYW	WIRQPPGKGLEWIG	NIYYRGYTYNPSLKS	RVTISVDTSKKQFSLTLSSVTAADTAMYYCAR	EGSDYGDYVGAFDI	WDQGTMTVTVSS
583	RNF43	IGVH3-13	EVQLVQSGGGLVQPGGSLRLSCAASGFTFS	YYDMH	WVRQVTGKGLEWVS	TIGATGDTYYSDSVKG	RFTISRQNAKNSLYLQINSLRAGDTAVYYCVR	DRGYIGYDSYFDN	WGQGTTLTVTVSS
585	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFT	RYPMN	WVRQAPGQGLEWMG	WINTNTGNPTYAQGFTG	RFVFSLDTSVSTAFQLQISSLKAEDTAVYYCAR	ERTNFYDAFDI	WGQGTMTVTVSS
585	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFN	SYAMD	WVRQAPGQGLEWMG	WINTNTGNPTYAQAFGTG	RFVFSLDTSVSTAYLEISSLKAEDTAVYYCAR	ERHGYFEAFDI	WGQGTTLTVTVSS
585	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFT	KYVMN	WVRQAPGQGLEWMG	WINTNTGNPTYAQGFTG	RFVFSLDTSVSTAYLQVSSLRAEDTALYYCAR	ESNWNYYDYFDY	WGQGTTLTVTVSS
586	ZNRF3	IGVH5-51	QVQLVQSGTEVKKPGESLKISCKGSGYSFT	TYWIG	WVRQMPGKGLEWMG	I IYPGSDTRYSPSFQG	QVTISADKSISTAYLQLSSLKASDTAMYYCAR	RGLSMVRLSAFDV	WGQGTTLTVTVSS
588	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFT	RYAMN	WVRQAPGQGLEWMG	WINTKTGNPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	DRGSYYDAFDI	WGQGTMTVTVSS
588	ZNRF3	IGVH7-4-1	EVQLVQSGSELKKPGASVKVSCASGYTFT	KYAMN	WVRQVPQGQLEWMG	WINTNTGNPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	KGGSYYDWFDP	WGQGTTLTVTVSS
588	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGASVKVSCASGYTFT	RYAMN	WVRQAPGQGLEWMG	WINTNTGKPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	DKGYNWNMYGAFDI	WGQGTTLTVTVSS
588	ZNRF3	IGVH7-4-1	QVQLVQSGSELKKPGGSMKVSCASGYTFT	RYAMN	WLRQAPGQGLEWMG	WINTNTGNPTYAQGFTG	RFVFSLDTSVSTAYLQISSLKAEDTAVYYCAR	RSGSYYDYFDY	WGQGTTLTVTVSS

Figura 2**MF1337:**

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MF3755:

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MF3178:

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MF5790:

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MF5816:

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MF3125:

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MF3176:

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MF4863:

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MF3370:

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MF4280:

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MF4289:

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MF5777:

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MF5781:

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MF5805:

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MF5809:

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MF5818:

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 caccgtctccagt

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MF5836:

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 cgtctccagt

MF5853:

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 cgtctccagt

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cgtctccagt

MF5862:

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ggtcacctctccagt

MF5882:

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tccttggacacctctgtcagcacggcatatctgcagatcagcagcctaaaggctgaggacactgccgtgt
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cgtctccagt

MF5884:

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cgtctccagt

MF5887:

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cacgggtcacctctccagt

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attattgtgagagacggagtgaggagctactacgactactttgactactggggccagggaacctggtcac
cgtctccagt

Figura 3

Secvența de aminoacizi (A.A.) a lanțului ușor comun

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGDFTLTISLQ
 PEDFATYYCQSYSTPPTFGQGTKVEIK
 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKA
 DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Secvența adnotată: VL:

gacatccagatgacccagtcctccatcctccctgtctgcatctgtaggagacagagtcacc
 D I Q M T Q S P S S L S A S V G D R V T
 atcacttgccgggcaagtcagagcattagcagctacttaaattggtatcagcagaaacca
 I T C R A S Q S I S S Y L N W Y Q Q K P
 gggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtcccatca
 G K A P K L L I Y A A S S L Q S G V P S
 aggttcagtgccagtggtatctgggacagatttcactctcaccatcagcagtcctgcaacct
 R F S G S G S G T D F T L T I S S L Q P
 gaagattttgcaacttactactgtcaacagagttacagtaccctccaacggttcggccaa
 E D F A T Y Y C Q Q S Y S T P P T F G Q
 gggaccaaggtggagatcaaa
 G T K V E I K

CL:

cgaactgtggctgcaccatctgtcttcatcttcccgccatctgatgagcagttgaaatct
 R T V A A P S V F I F P P S D E Q L K S
 ggaactgcctctgttggtgtgcctgctgaataacttctatcccagagaggccaaagtacag
 G T A S V V C L L N N F Y P R E A K V Q
 tggaaggtggataacgccctccaatcgggtaactcccaggagagtggtcacagagcaggac
 W K V D N A L Q S G N S Q E S V T E Q D
 agcaaggacagcacctacagcctcagcagcaccctgacgctgagcaaagcagactacgag
 S K D S T Y S L S S T L T L S K A D Y E
 aaacacaaagtctacgcctgcgaagtcacccatcagggcctgagctcgcccgtcacaaag
 K H K V Y A C E V T H Q G L S S P V T K
 agcttcaacaggggagagtggttag
 S F N R G E C -

Figura 4

VH: dependent de MF (țintă): Figuri 1 și 2. CH1:

```
gctagcaccaagggcccatcggtcttccccctggcaccctcctccaagagcacctctggg
A S T K G P S V F P L A P S S K S T S G
ggcacagcgggccctgggctgcctggtcaaggactacttccccgaaccggtgacggtgtcg
G T A A L G C L V K D Y F P E P V T V S
tggaactcaggcgccctgaccagcggtgcacaccttcccggtgtcctacagtcctca
W N S G A L T S G V H T F P A V L Q S S
ggactctactccctcagcagcgctgacggtgccctccagcagcttgggcacccagacc
G L Y S L S S V V T V P S S S L G T Q T
tacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagagagtt
Y I C N V N H K P S N T K V D K R V
```

Legătură:

```
gagcccaaattctgtgacaaaactcacacatgcccaccgtgcca
E P K S C D K T H T C P P C P
```

CH2:

```
gcacctgaactcctggggggaccggtcagtccttcttccccccaaaaccaaggacacc
A P E L L G G P S V F L F P P K P K D T
ctcatgatctcccgaccctgaggtcacatgctggtggtggacgtgagccacgaagac
L M I S R T P E V T C V V V D V S H E D
cctgaggtcaagttcaactggtacgtggacggcggtggaggtgcataatgccaagacaaag
P E V K F N W Y V D G V E V H N A K T K
ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgctcctcaccgtcctgcac
P R E E Q Y N S T Y R V V S V L T V L H
caggactgggtgaatggcaaggagtacaagtgaaggtctccaacaaagccctcccagcc
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P I E K T I S K A K
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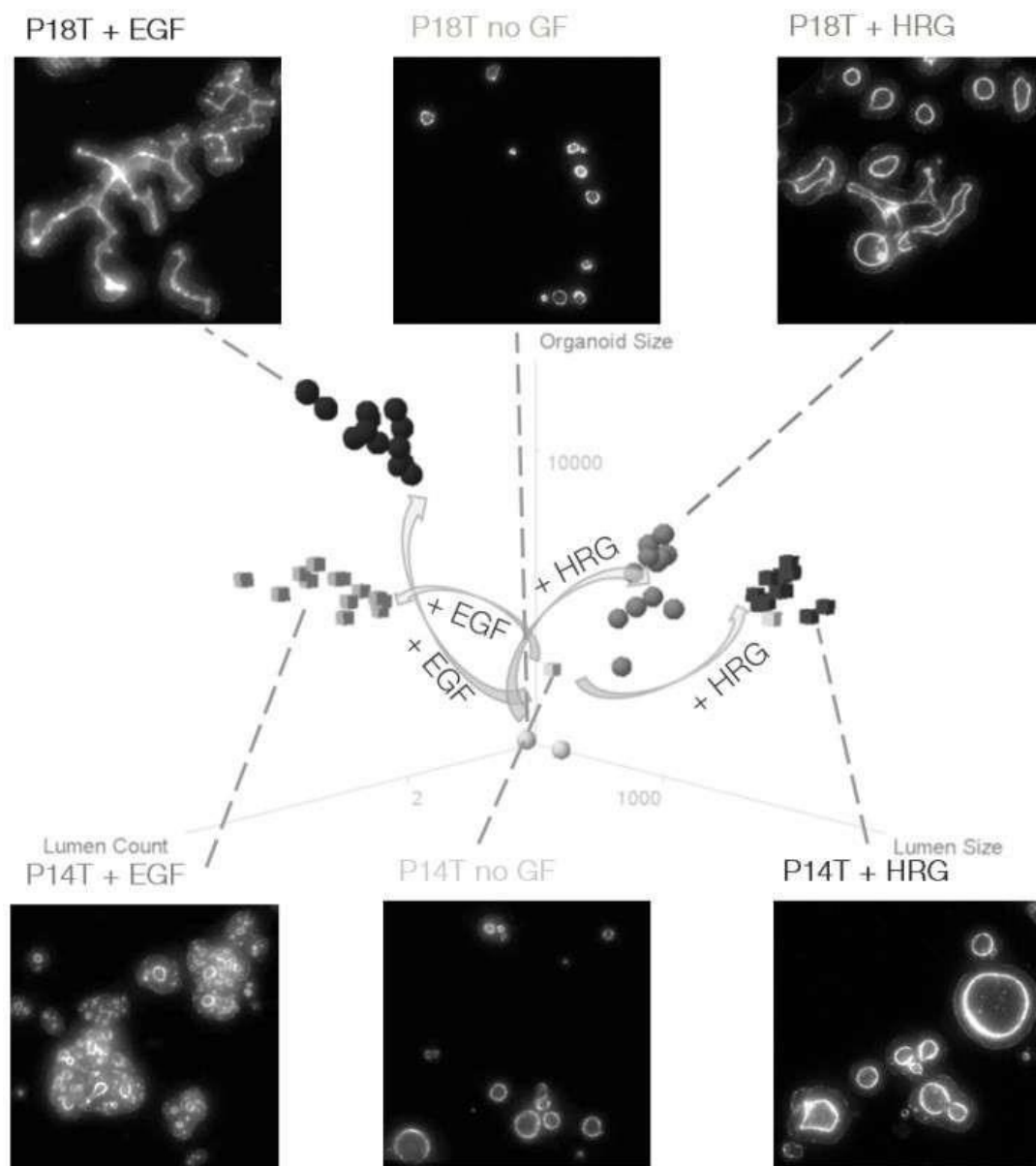
CH3: KK al DEKK

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N Q V S L K C L V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccggtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcaccgtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -
```

CH3: DE al DEKK

gggcagccccgagaaccacaggtgtacaccgaccccccatcccgggaggagatgaccaag
G Q P R E P Q V Y T D P P S R E E M T K
aaccaggtcagcctgacctgcgaggtcaaaggcttctatcccagcgacatcgccgtggag
N Q V S L T C E V K G F Y P S D I A V E
tgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactcc
W E S N G Q P E N N Y K T T P P V L D S
gacggctccttcttctctatagcaagctcacccgtggacaagagcaggtggcagcagggg
D G S F F L Y S K L T V D K S R W Q Q G
aacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagc
N V F S C S V M H E A L H N H Y T Q K S
ctctccctgtctccgggttga
L S L S P G -

Figura 5



Organoid size = dimensiune organoid

Lumen count = număr lumene

Lumen size = dimensiune lumen

Figura 6

Ser în ziua:

0

35

Diluție serică:

100x

100x

1000x

Șoarece

L19

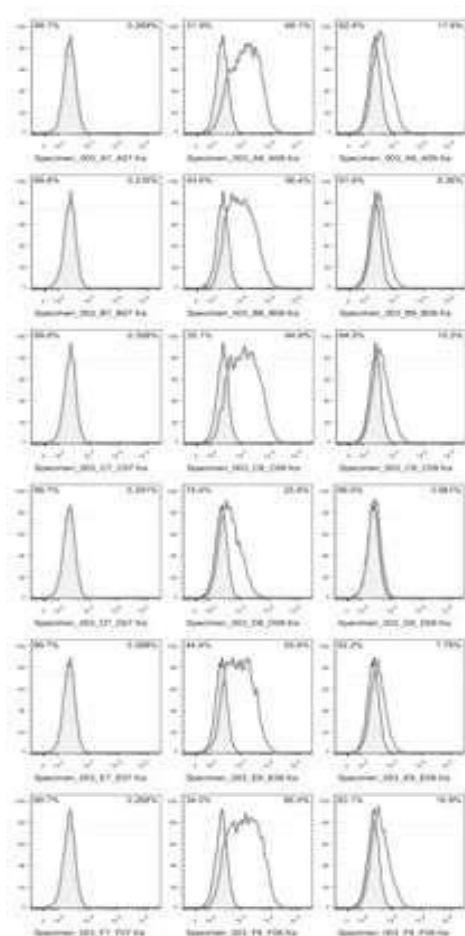
L20

L21

L22

L23

L24



Control

Anti-Myc

n.c.

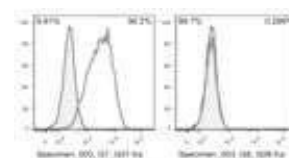


Figura 7

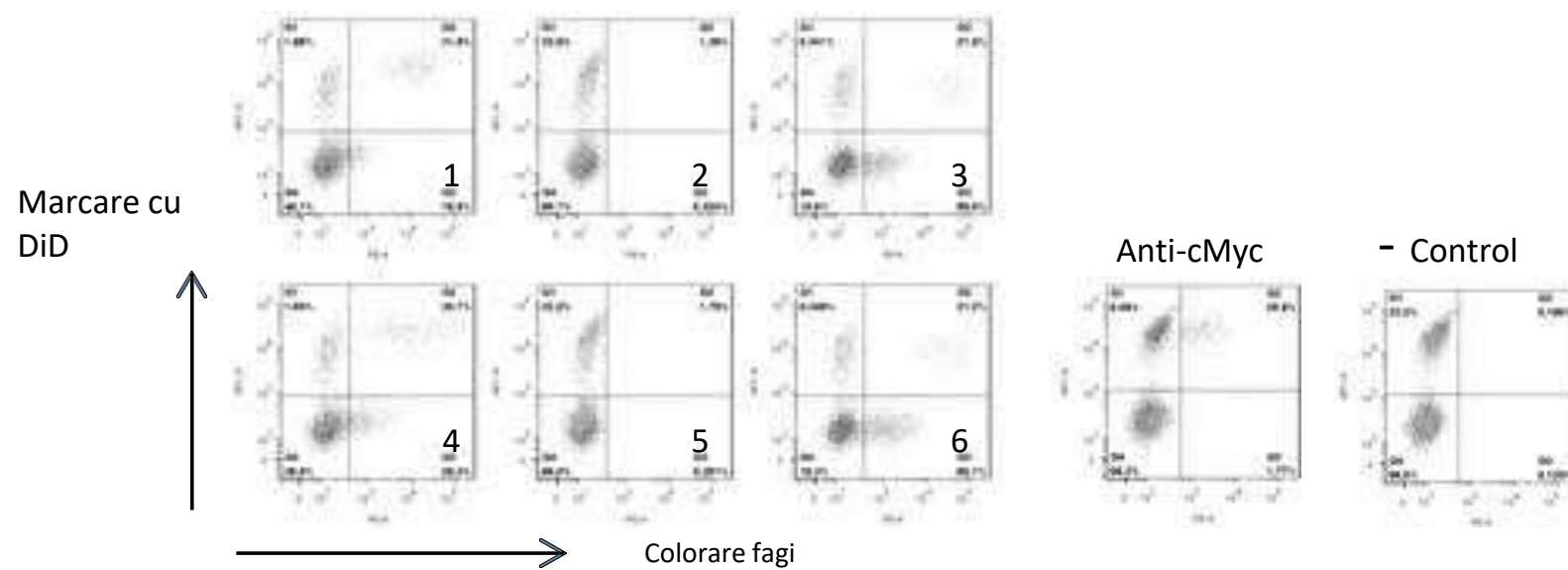


Figura 8

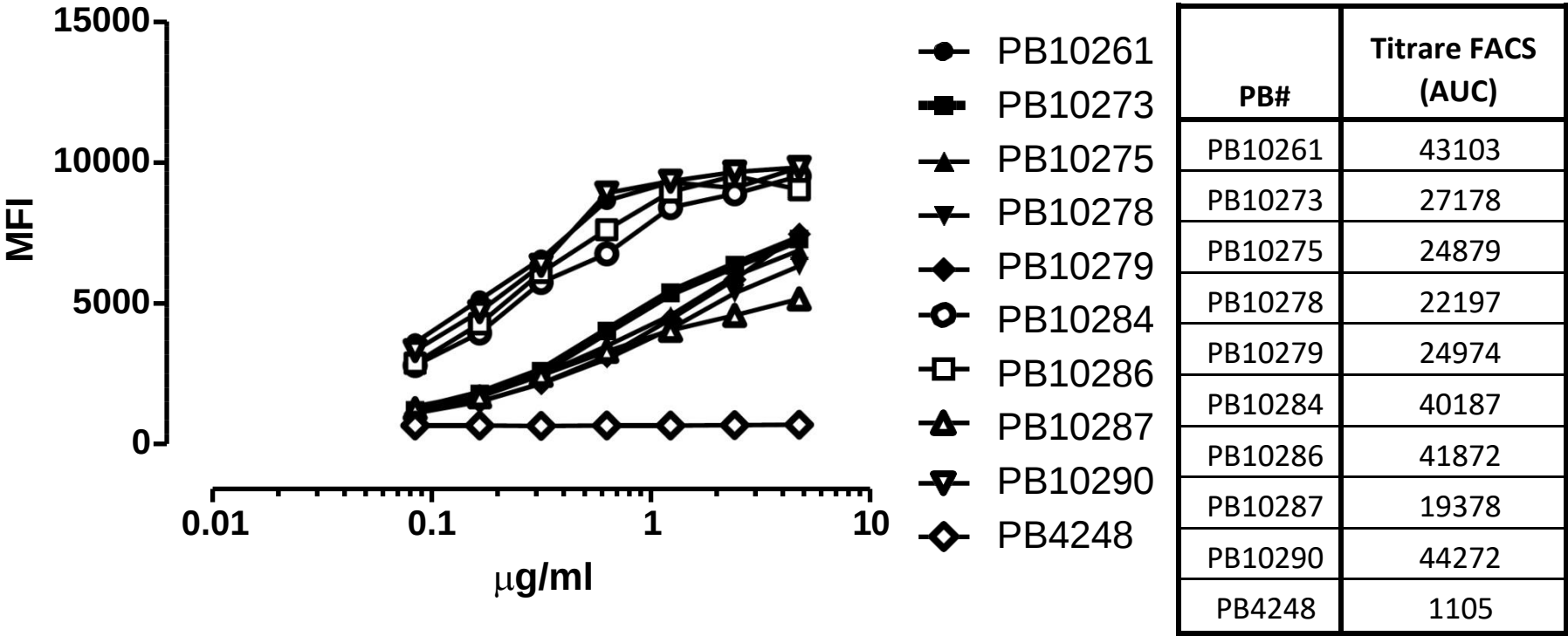


Figura 9

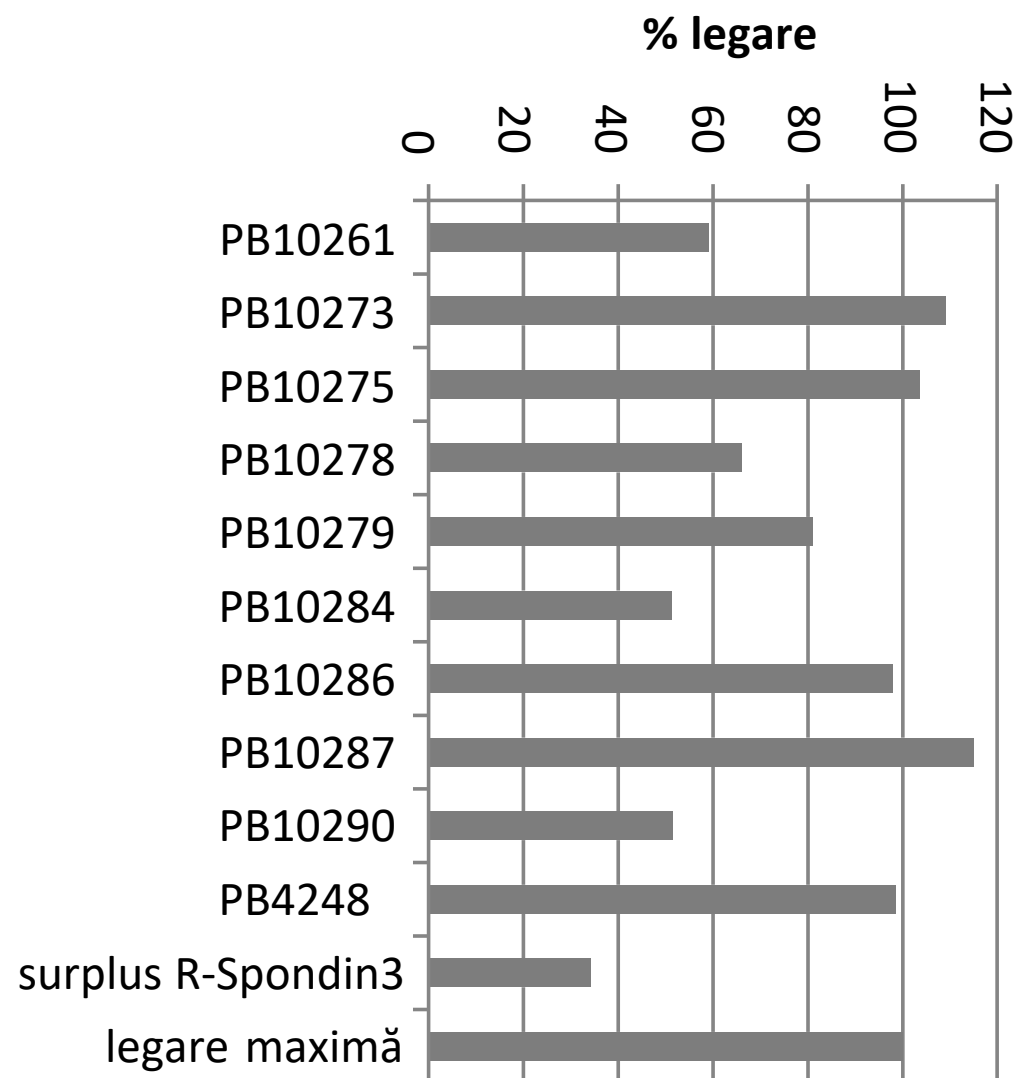
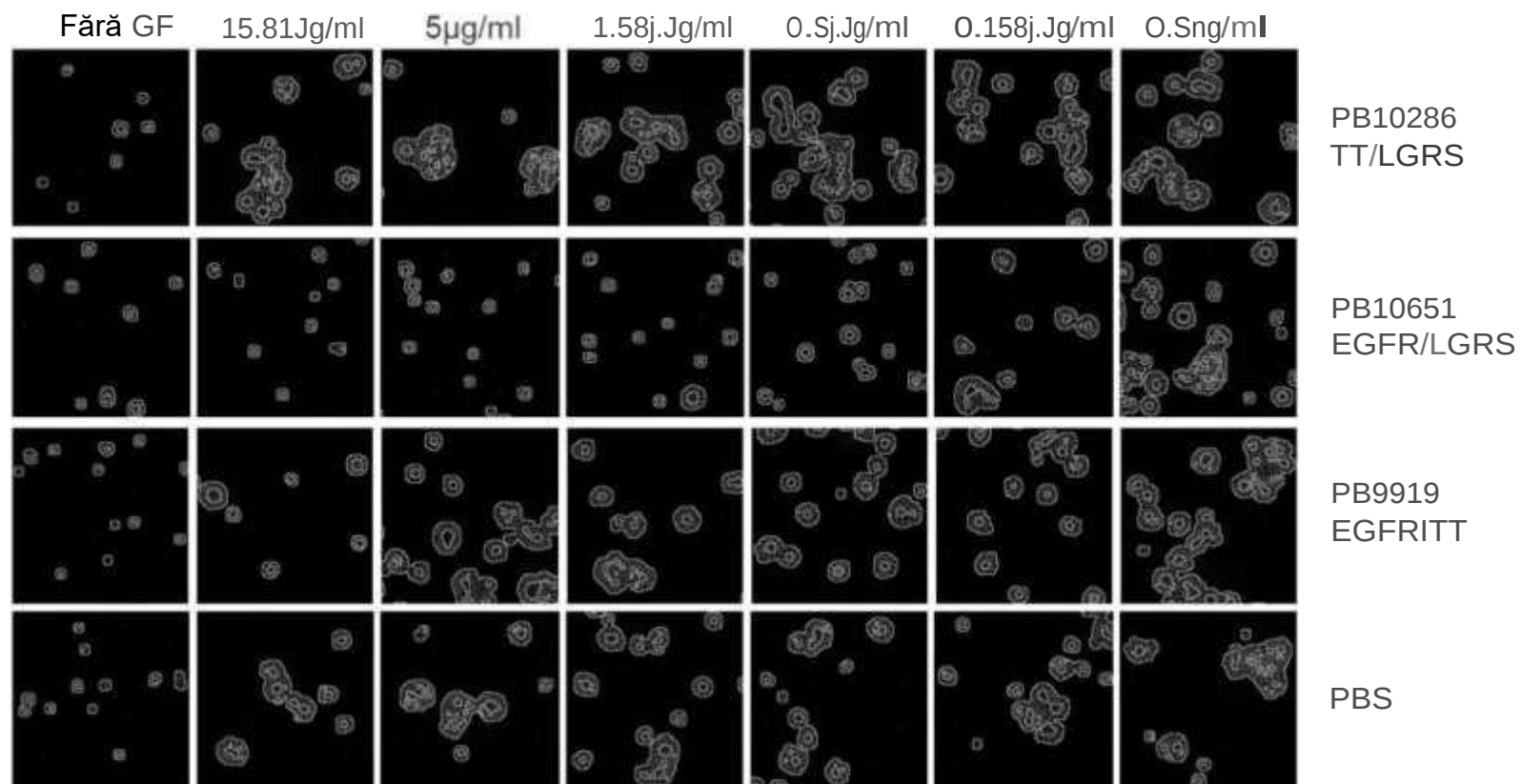


Figura 10



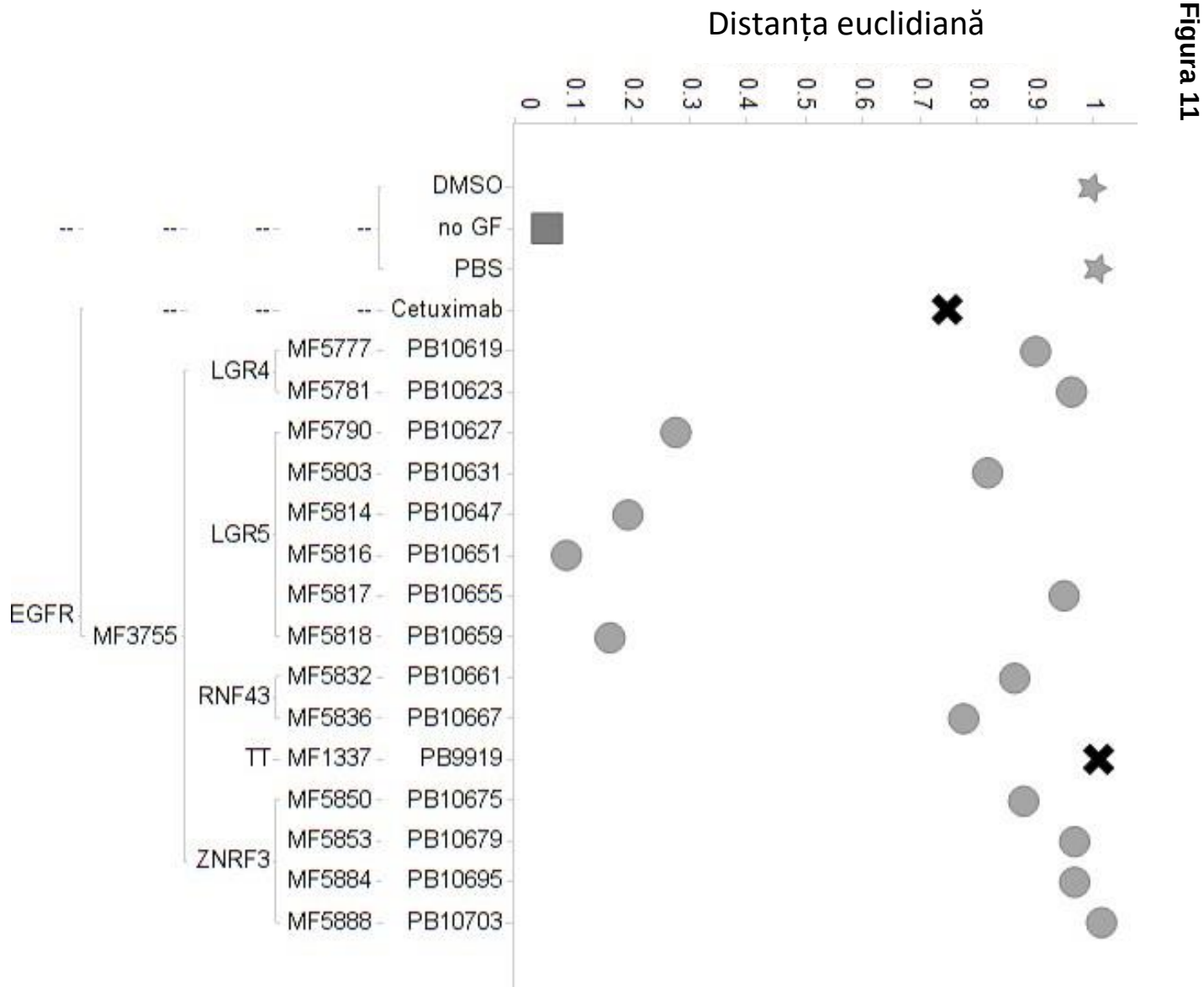
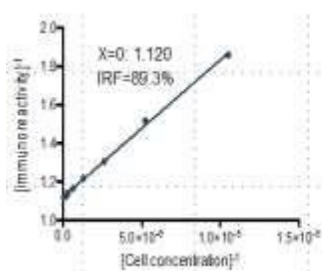


Figura 12

A



B

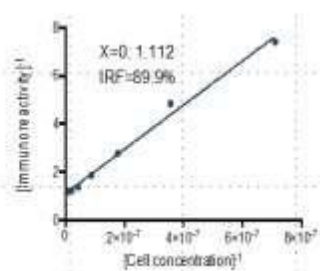
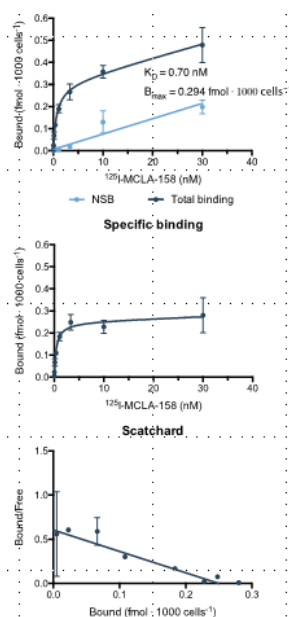
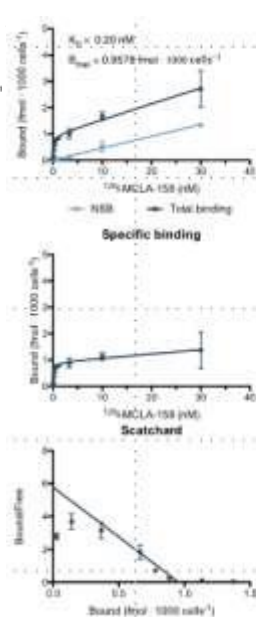


Figura 13

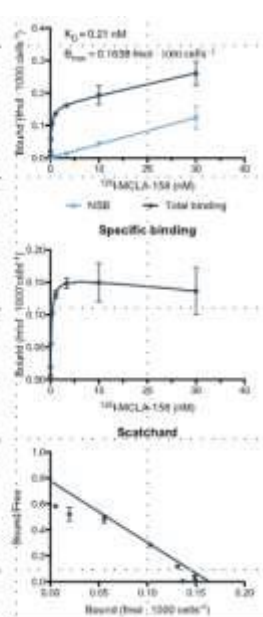
A



B



C



Immunoreactivity = imunoreactivitate

Cell concentration = concentrație celulară

Bound = legat

Specific binding = legare specifică, Total binding = legare totală

Figura 14

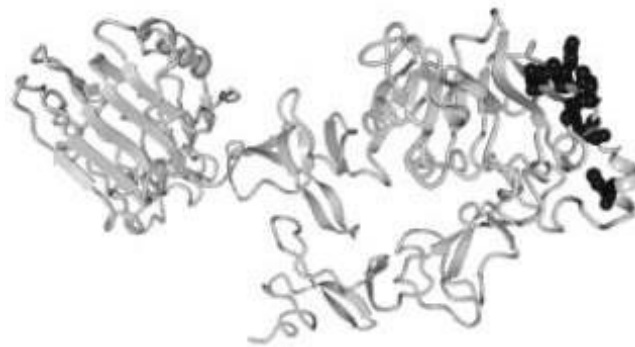


Figura 15

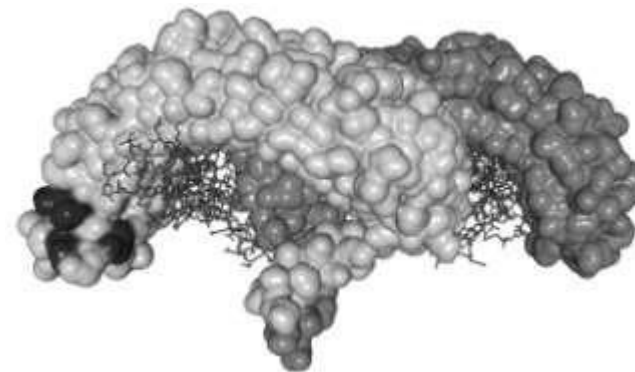


Figura 16

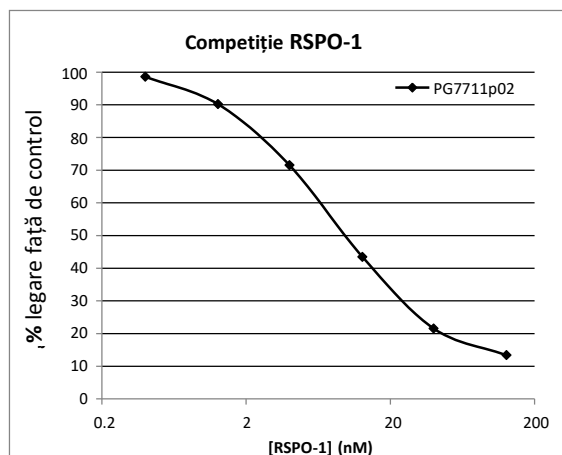


Figura 17

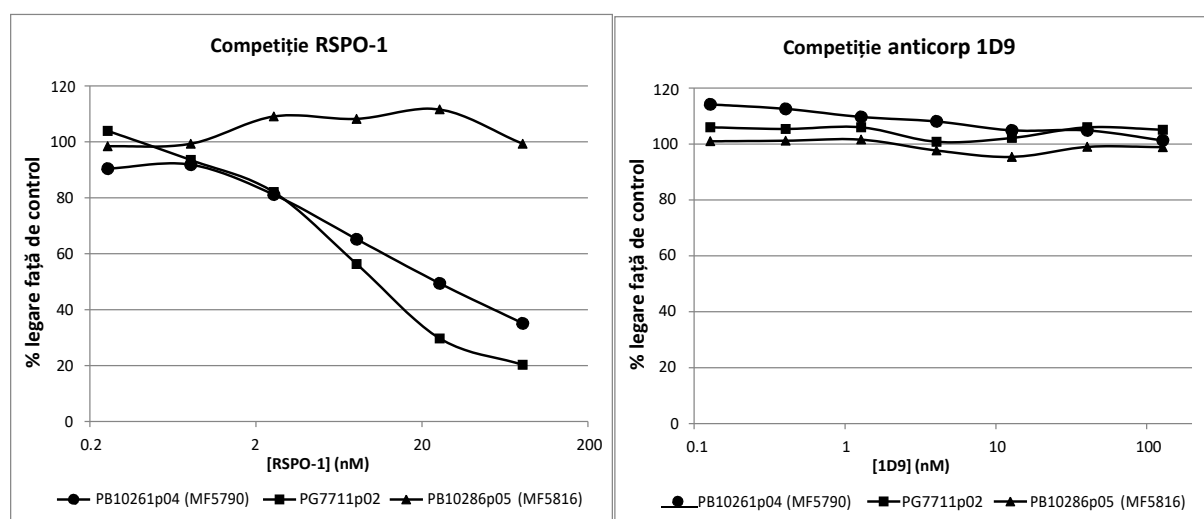


Figura 18

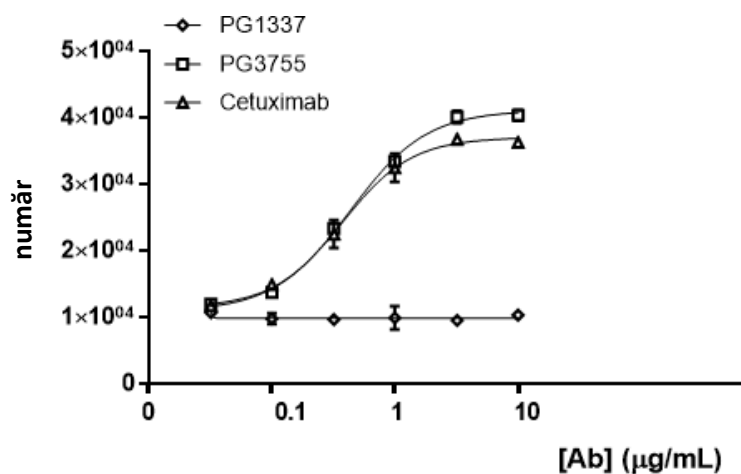


Figura 19

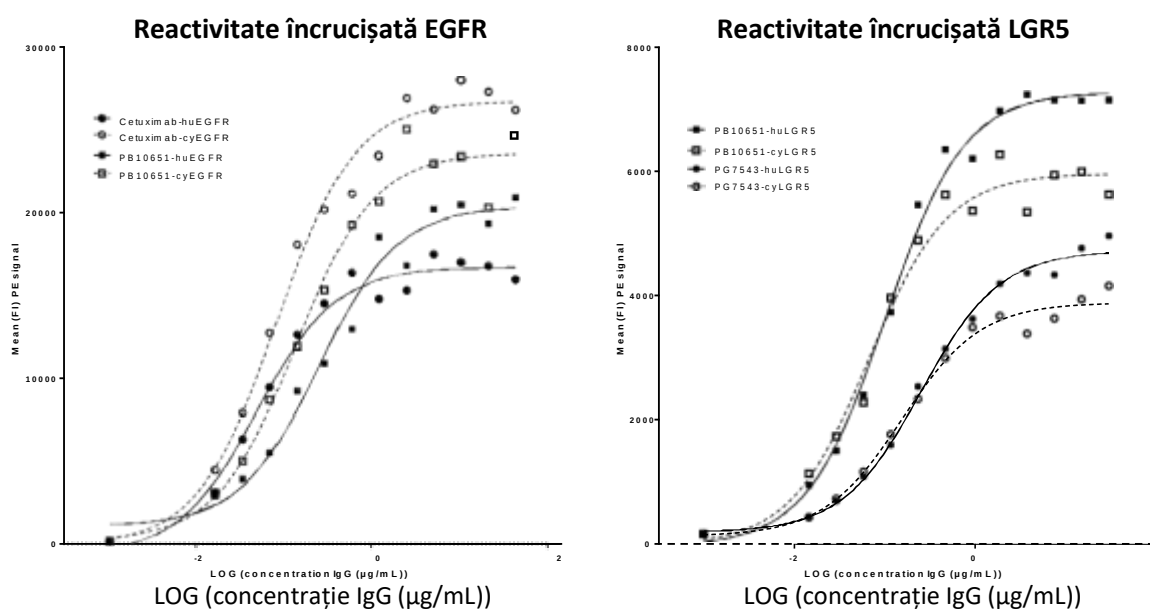
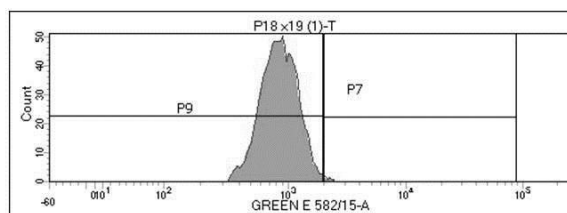


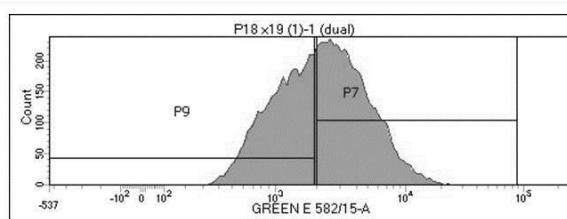
Figura 20

TT - TT



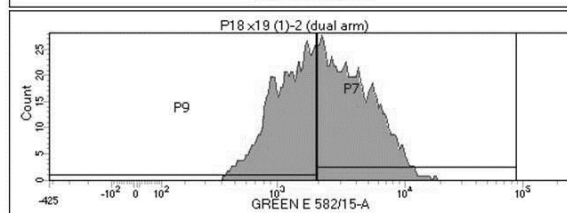
0.8% positive

MF5816 - MF5816



53.6% positive

MF5814 - MF5814



52.7% positive

Figura 21

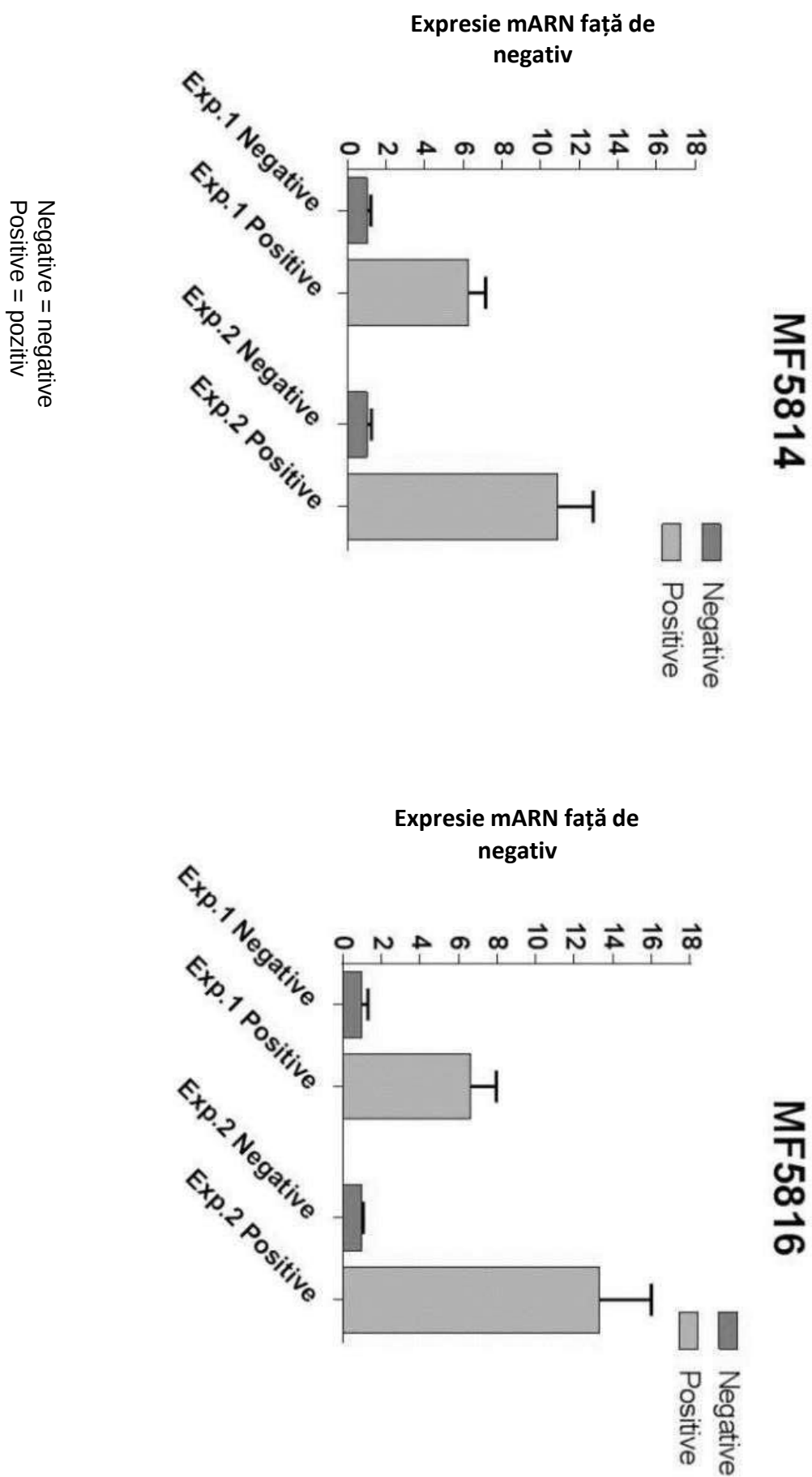


Figura 22

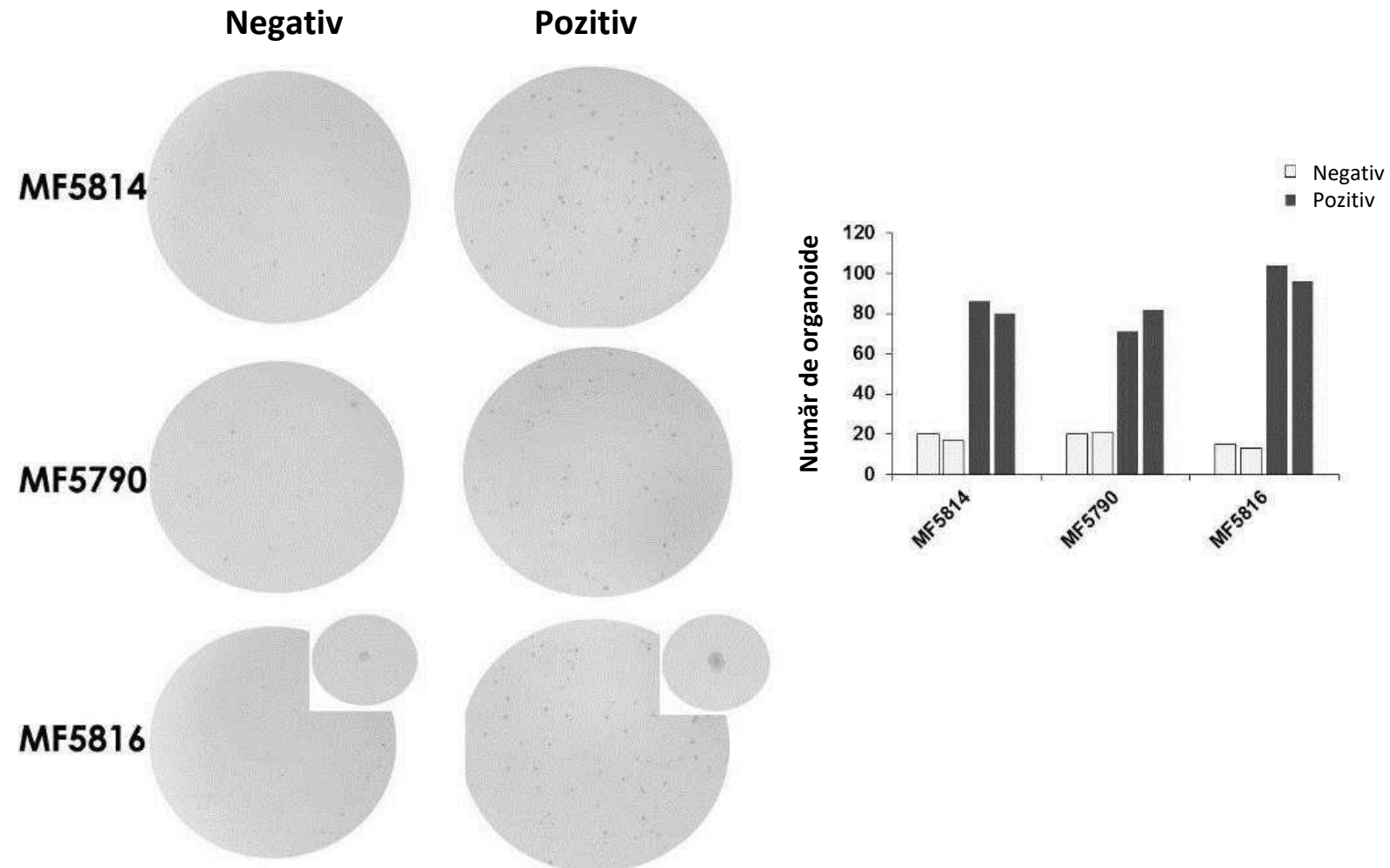


Figura 23

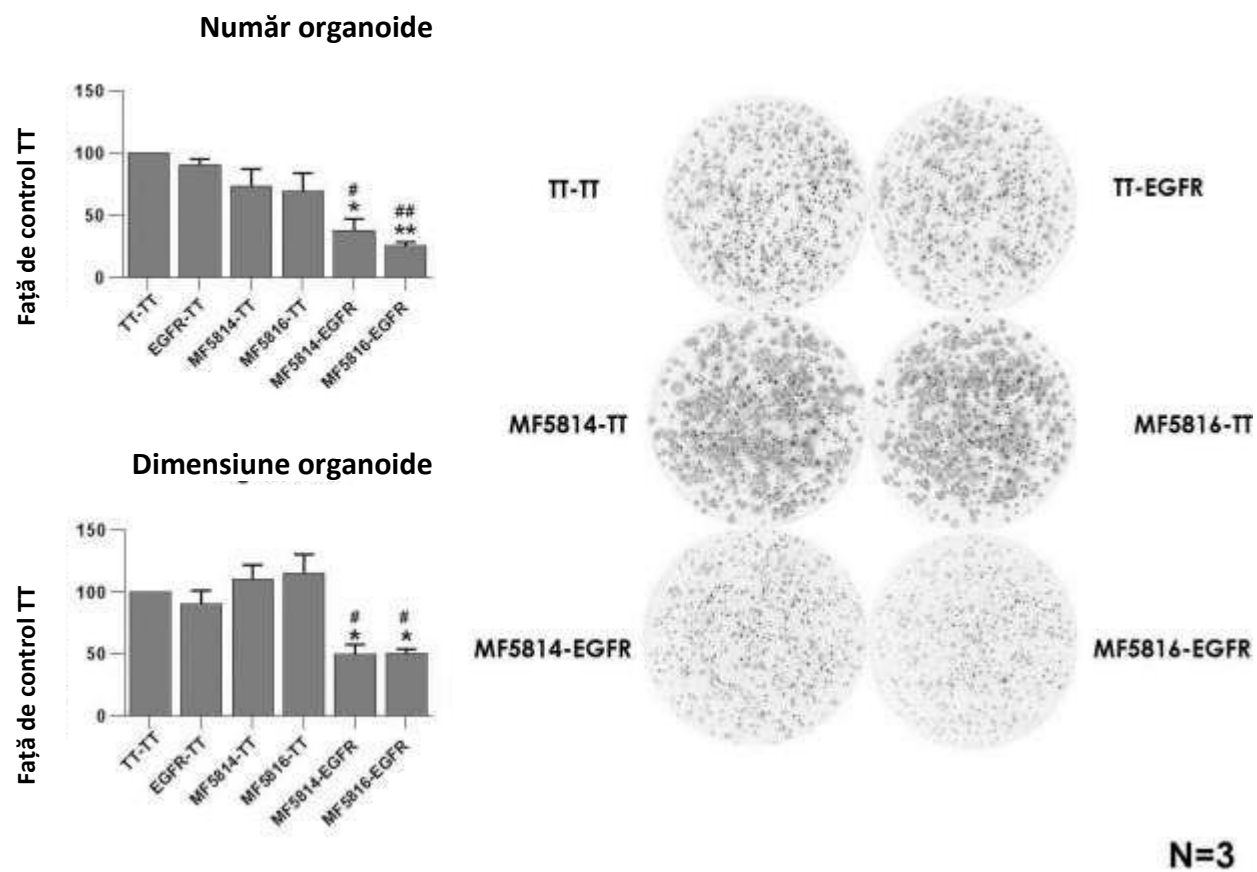


Figura 24

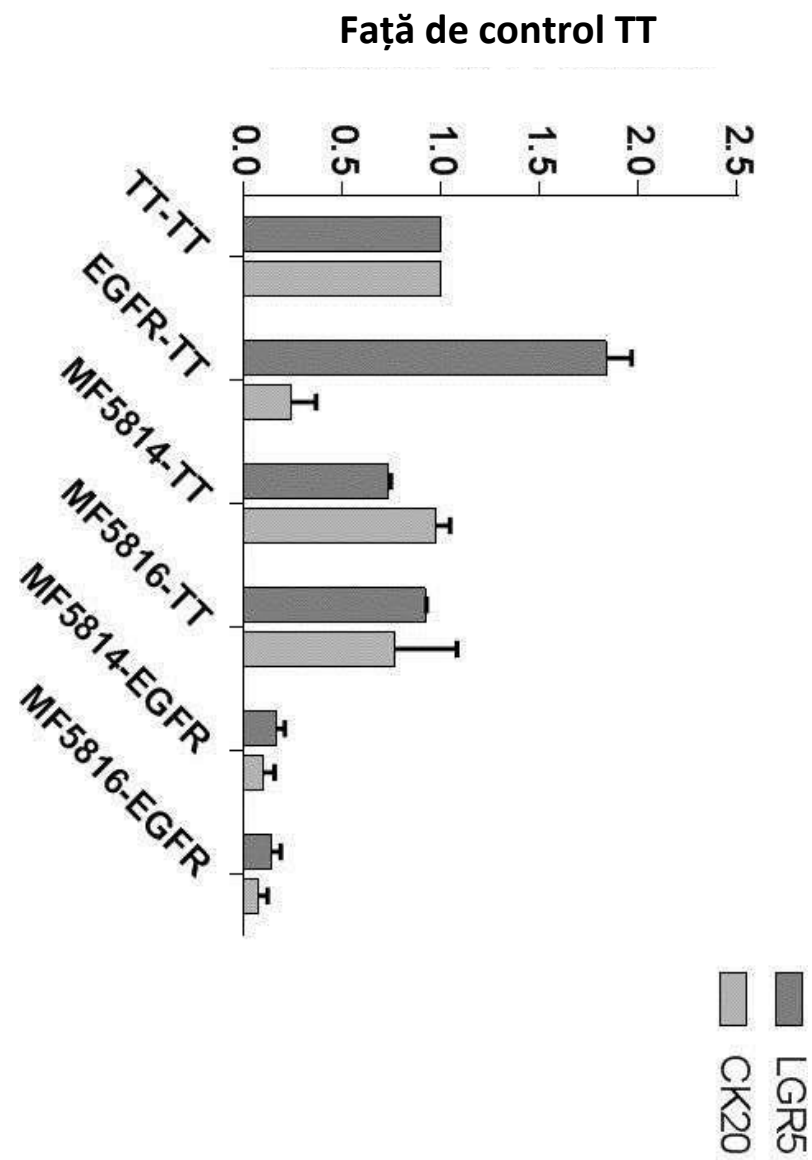


Figura 25

Figura 25A

Supercluster 1 (MF5814 și MF5818)

accessions	Size	---FW1---	CDR1-	---FW2---	---CDR2---	---FW3---	---CDR3---	---FW4---
VH1-69 J00256-AEHJ2		QVQLVQSGAEVKKPGSSVKVSCASGGTFS	SYAIS	MVRCAPGGGLEWVG	GIPIFGTANVAQKFOG	RVTITADKSTSTAYMELSSLRSEDAVYYCAR	XXXXXXXXXXXX	WGRGTLVTVSS
080514A_ABMP08_B10	10	N	N..N		S...L.VDH	N.V.....	EHIAARLDYFDY	..DL.....
080514A_ABMP08_B12	10	ST	ND	T	S...L.TDH	N.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_B08	8	R..DSV	N		S...L.TDH.Q	G.....	ERIAARQDYFDY	..Q.....
080514A_ABMP08_A11	7		N		S...L.TDH	R.SN.T	ELIAARLDYFDS	..Q.....
080514A_ABMP08_B04	7		N		S...L.TDH	SN.T	ELIAARLDYFDS	..Q.....
080514A_ABMP08_E05	7	S..K	N		S...L.TDH.N	LSN.T	ELIAARLDYFDS	..Q.....
080514A_ABMP08_E07	7	V	N		S...L.TDH	N.S.....	ELIAARQDYFDY	..Q.....
080514A_ABMP08_C03	6		N		S...L.TDH	R.SN.T	ELIAARLDYFDS	..Q.....
120514B_ABMP15_A12	5	ST	ND	T	S...L.TDH	N.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_F02	4	S..K	N		S...L.TDH.N	LSN.T	ELIAARLDYFDS	..Q.....
080514A_ABMP08_A05	3		N		S...L.TDH	N.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_B02	3	ST	ND	T	S...L.TDH	R.N.....K	EHIAARQDYFDY	..Q.....
080514A_ABMP08_D03	3	L	N		S...L.TDH.N	SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_E02	3	L	N		S...L.TDH.N	SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_E04	3	R..DSV	N		S...L.TDH.Q	G.....	ERIAARQDYFDY	..Q.....
080514A_ABMP08_C05	2		N		S...L.TDH	KS.S.MDL	EHIAARQDYFDY	..Q.....
120514B_ABMP15_B08	2		N		S...L.TDH	SN.T	ERIAARLDYFDS	..Q.....
120514B_ABMP15_E07	2	ST	ND	T	S...L.TDH	N.T.....	EHIAARLDYFDY	..Q.....
080514A_ABMP08_A03	1	N	N..N		S...L.VDH	N.V.....	EHIAARLDYFDY	..DL.....
080514A_ABMP08_A04	1		N		S...L.TDH.N	SN.T..IG.K	ERIAARLDYFDS	..Q.....
080514A_ABMP08_A06	1	N	N..N		S...L.VDH	SN.V.....	EHIAARLDYFDS	..I.....
080514A_ABMP08_A07	1	CSM..S.L.A..R..DSV	N		S...L.TDH.Q	G.....	ERIAARQDYFDY	..Q.....
080514A_ABMP08_A09	1	CSM	N		S...L.TDH	R.SN.T	ELIAARLDYFDS	..Q.....
080514A_ABMP08_A12	1	T	N		S...L.TDH	N.S.....	ERIAARQDYFDS	..Q.....
080514A_ABMP08_B06	1	ST	ND	T	S...L.TDH.N	SN.T..IG.K	ERIAARLDYFDS	..Q.....
080514A_ABMP08_B07	1	ST	ND	T	S...L.TDH	R.N.....	ELIAARLDYFDS	..Q.....
080514A_ABMP08_C04	1	T	N		S...L.TDH.N	R.AN.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_C08	1	N	N		S...L.TDH	I.T.....	ERIAARQDYFDF	..Q.....
080514A_ABMP08_C09	1		N		S...L.TDH	G..SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_C12	1	A..ST	ND	T	S...L.TDH	N.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_D06	1	ST	ND	T	S...L.VDH	N.V.....	EHIAARLDYFDY	..DL.....
080514A_ABMP08_D08	1	ST	N	T	S...L.TDHI	N.....	EHIAARQDYFDY	..Q.....
080514A_ABMP08_D09	1		N		S...L.TDH	SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_D10	1		N		S...L.TDH	SN.T	ERIAARLDYFDY	..Q.....
080514A_ABMP08_E01	1		N		S...L.TDH	KS.S.MDL	EHIAARQDYFDY	..Q.....
080514A_ABMP08_E03	1		N		S...L.DN		EHIAARQDYFDY	..Q.....
080514A_ABMP08_E09	1	S.L	ND	T	S...L.TDH	R.N.....K	EHIAARQDYFDY	..Q.....
080514A_ABMP08_E10	1	ST	ND	T	S...L.TDH	R.N.....K	EHIAARQDYFDY	..Q.....
080514A_ABMP08_F08	1	L	N		S...L.TDH.N	SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_F10	1	M..ST	ND	T	S...L.TDH	R.N.....K	EHIAARQDYFDY	..Q.....
080514A_ABMP08_G06	1	N	N..N		S...L.VDH	N.V.....	EHIAARLDYFDY	..DL.....
080514A_ABMP08_G10	1		N		S...L.TDH	E..N.S.....	ERIAARQDYFDS	..Q.....
080514A_ABMP08_H07	1	S.L.A	N		S...L.TDH	SN.T	ERIAARLDYFDS	..Q.....
080514A_ABMP08_H08	1	N	N..N		S...L.VDH	N.V.....	EHIAARLDYFDY	..DL.....
120514B_ABMP15_A01	1	L	N		S...L.DH	KS.S.MDL	EHIAARQDYFDY	..Q.....
120514B_ABMP15_A05	1		N		S...L.TDH	N.V.....	EHIAARLDYFDY	..DL.....
120514B_ABMP15_A08	1		N		S...L.TDH	SN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_A09	1		N		S...L.TDH	SN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_B03	1	R..	N		S...L.TDH	LSN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_B10	1		N		S...L.TDH	SNIT	EHIAARLDYFDS	..Q.....
120514B_ABMP15_C03	1	S..K	N		S...L.TDH.N	N.T.....	EHIAARLDYFDY	..Q.....
120514B_ABMP15_C12	1	T	N	T	S...L.TDH	SN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_D09	1	ST	N		S...L.TDH	SN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_E01	1	S.L	N		S...L.TDHYE	SN.T	ELIAARLDYFDS	..Q.....
120514B_ABMP15_E02	1		N		S...L.TDH	E..N.S.....	EHIAARQDYFDS	..Q.....
120514B_ABMP15_E04	1		N		S...L.TDH	R.N.....	EHIAARQDYFDY	..Q.....
120514B_ABMP15_E06	1	ST	ND	T	S...L.TDH	E..N.S.....	EHIAARQDYFDS	..Q.....
120514B_ABMP15_E12	1		N		S...L.TDH	E..N.S.....	EHIAARQDYFDS	..Q.....
120514B_ABMP15_F04	1		N		S...L.TDH	SK.T	ELIAARLDYFDS	..Q.....
120514B_ABMP15_F07	1		N		S...L.TDH	R.N.....	EHIAARQDYFDY	..Q.....
120514B_ABMP15_F10	1		N	T	S...L.TDH	SN.T	EHIAARLDYFDS	..Q.....
120514B_ABMP15_G01	1		N		S...L.TDH	G.....	EHIAARQDYFDY	..Q.....
120514B_ABMP15_H01	1	R..DSV	N		S...L.TDH.Q	G.....	EHIAARQDYFDY	..Q.....

POSITIVE: K, H, R

Figura 25B

Supercluster 8 (MF5790)

```

==== 008 ====
accessions      Size      -----FW1-----      -CDR1--      -----FW2-----      -----CDR2-----      -----FW3-----      -----CDR3-----      -----FW4-----
VH4-39|J00256-AEHJ6      26      |QLQLQESGPGGLVKPSHTLSLTCTVSGGSIS|      |SSSYTWG|      |WIRQPPGKGLEWIG|      |SIYVSGSTYYNPSLKS|      |RVTISVDTSKNQESLKLSSVTAA DTAVVYCAR|      |XXXXXXXXXXXXXXXXXX|      |WGQGITVTVSS|
070514A_ABMP06_A10      1      |.V.....|      |..S..|      |.....|      |.E...N.....|      |.....E.....|      |QTYSSSWDGVLYYFDY|      |.....L.....|
090514B_ABMP13_C04      1      |.V.....|      |..S..|      |.....|      |.E...N.....|      |.....E.....|      |QTYSSSWDGVLYYFDY|      |.....L.....|
090514B_ABMP13_D06      1      |.V.....|      |..S..|      |.....|      |.E...N.....|      |.....E.....|      |QTYSSSWDGVLYYFDY|      |.....L.....|

POSITIVE: K, H, R
NEGATIVE: D, E
AMIDIC: N, Q
ALIPHATIC: A, G, L, I, P, V
AROMATIC: F, W, Y
SULFUR: C, M
HYDROXILIC: S, T

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Figura 25C

Supercluster 10 (MF5816)

accessions	Size	FW1	CDR1	FW2	CDR2	FW3	CDR3	FW4
VH7-4-1 J00256-AEHJ6		QVQLVQSGSELKPGASVKVSKASGYTF	SVAMN	NVROAPGQGLEWMG	WINTNIGNPTVAQGFTG	REVEFLDTSVSTAYLQISSLKAEDTAVYVCAR	XXXXXXXXXXXXXXXXXXXX	WGQGITVTIVSS
080514A_ABMP08_F04	4	E.....K.....	..T..		..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_A02	2	E.....	..T..		..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_B05	2	E.....	..T..		..Q.....	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_D02	2	E.....T.....	..T..		..D.....D..	T.....N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_A08	1	GCSM....S..				N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_B01	1	E.....				N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_B11	1	E.....				N.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_D05	1				..Y..D..	NN.....	GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_E11	1		..T..		..D..D..D..		GDCDSTSCRYRSGYEDY	L.....
080514A_ABMP08_G04	1		..T..		..D..D..D..	T.....N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_A06	1	E.....	N..L..			S.....	GDCDSTDCRYRSGYEDY	L.....
120514B_ABMP15_B09	1	E.....K.....	..T..	R.....	D..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_C02	1	E.....K.....	..T..		D..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_C04	1	E.....	..T..		D..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_C07	1	E.....			..K..D..	NN.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_D03	1	E.....	N..H..		D.....	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_E05	1	E.....K..E.....	..T..		D.....	N.....E.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_F02	1				D..D..D..	N.....	GDCDSTSCRYRSGYEDY	L.....
120514B_ABMP15_F09	1				D..D..D..	N.....	GDCDSTNCRYRSGYEDY	L.....
120514B_ABMP15_H04	1	T.....	..T..		D.....	T.....N.....	GDCDSTSCRYRSGYEDY	L.....

POSITIVE: K, H, R

NEGATIVE: D, E

AMIDIC: N, Q

ALIPHATIC: A, G, L, I, P, V

AROMATIC: F, W, Y

SULFUR: C, M

HYDROXILIC: S, T

Figura 26
Figura 26A

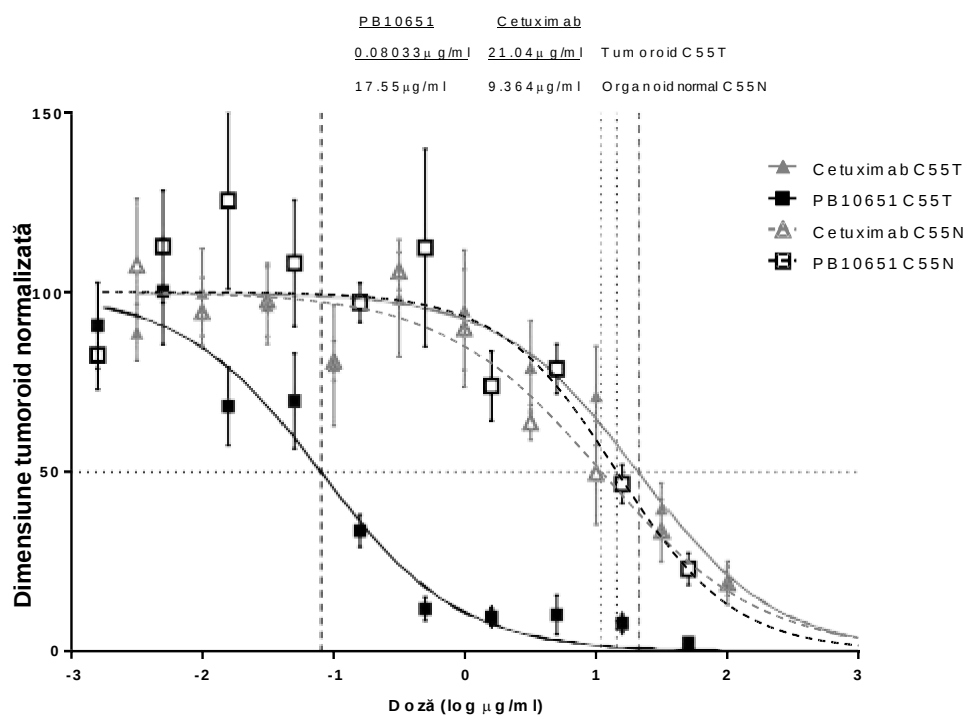


Figura 26B

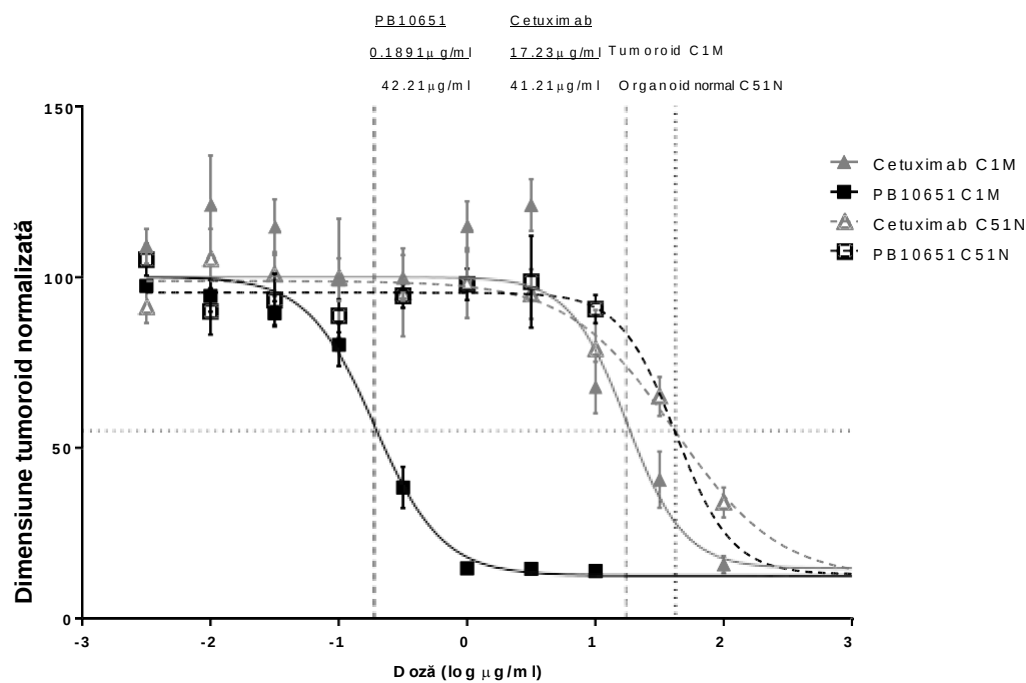


Figura 26C

IC50 (µg/ml)				
Tip organoid	Nume	Cetuximab	PB10651	Raport
Normal	C7N	13.43	19.05	0.7
Normal	C51N	52	67.45	0.8
Normal	C71N	1.37	3.09	0.4
Normal	C57N	1.08	4.52	0.2
Normal	C55N	11.17	14.86	0.8
Tumoroid	C55T	19.63	0.08	245
Tumoroid	C57T	22.75	1.25	18.2
Tumoroid	C0M	10.12	0.39	25.9
Tumoroid	C1M	24.21	0.25	96.8
Tumoroid	C65M	18.92	0.99	19.1
Tumoroid	P18T	5.17	0.25	20.7

Figura 27

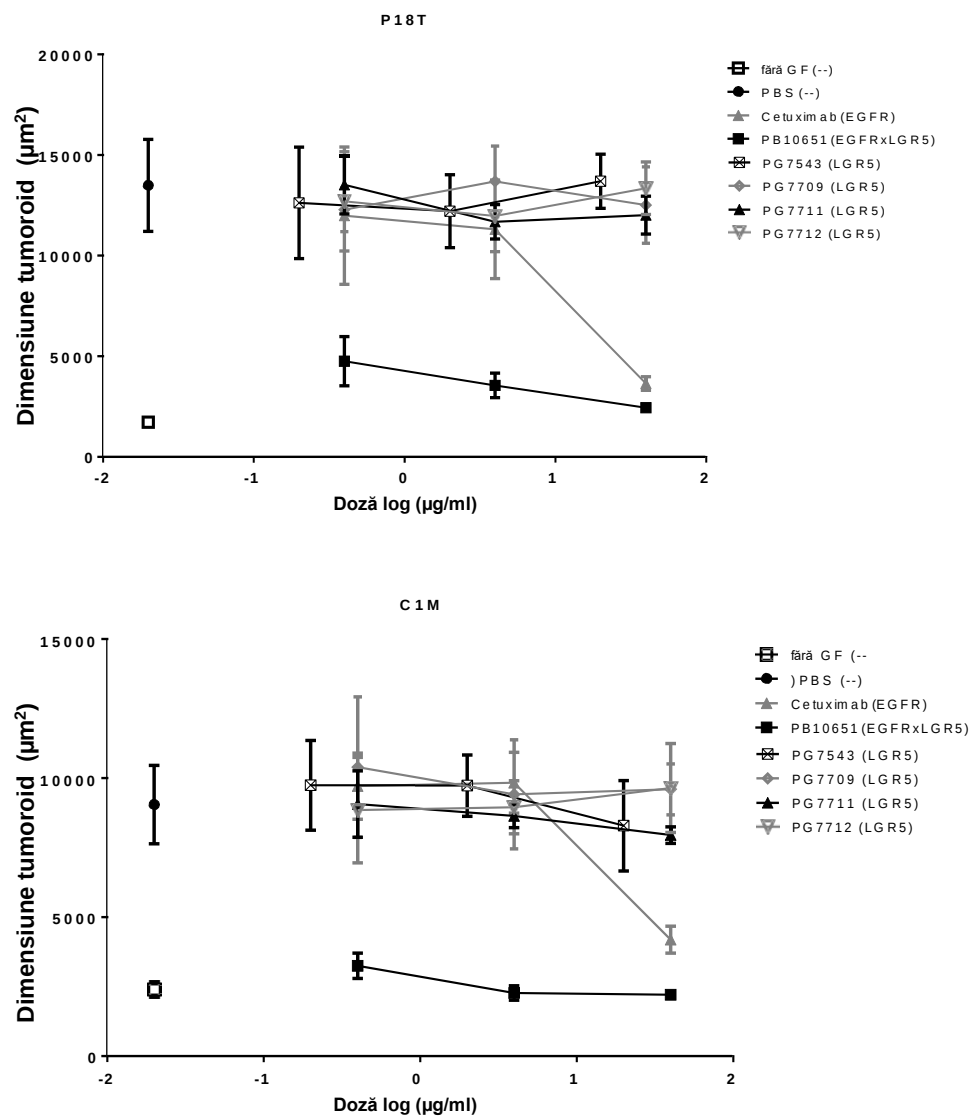


Figura 28
Figura 28A

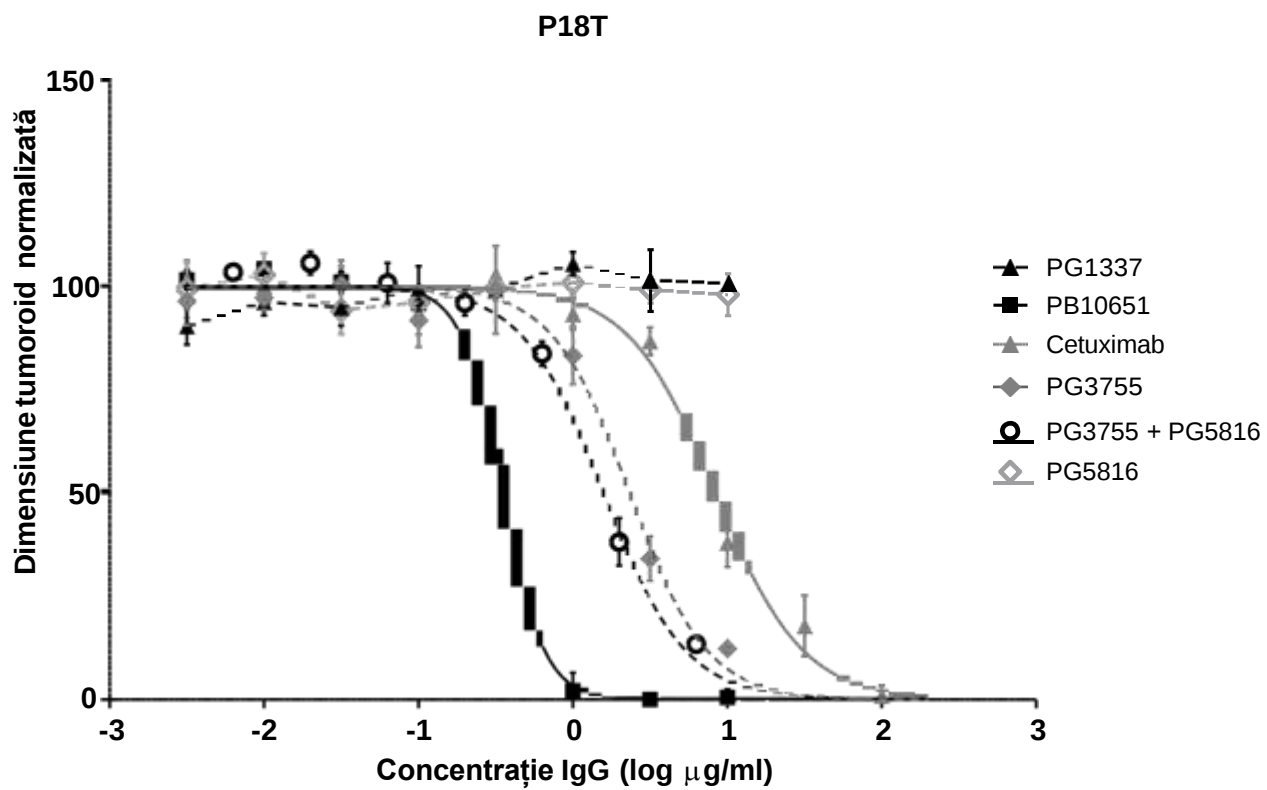
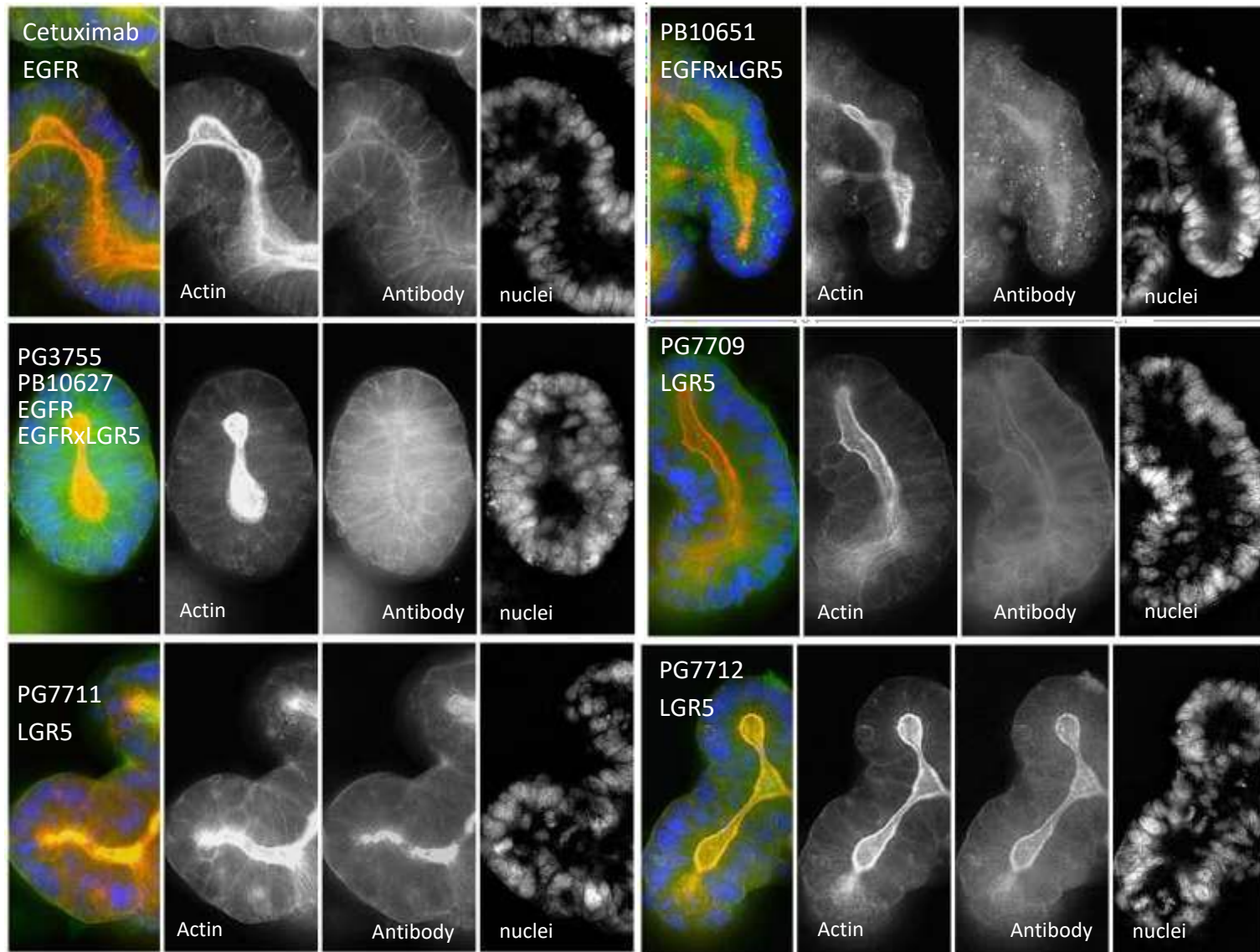


Figura 28B

Tabel IC ₅₀ (µg/ml)		Tumoare primară			Metastază			Normal				
		P18T	C55T	C57T	C65M	C1M	C0M	C51N	C7N	C71N	C55N	C57N
		IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀	IC ₅₀
EGFR	Cetuximab	8.39	28.51	15.63	15.70	17.10	3.35	26.36	16.11	3.14	2.18	4.80
EGFRxLGR5	PB10651	0.35	0.11	1.20	3.57	0.19	0.14	53.83	17.51	4.77	6.03	8.24
EGFR + LGR5	PG3755 +PG5816	1.59	7.87	16.94	8.89	2.58	1.36	2.17	2.39	0.32	0.47	1.32

Figura 29



Antibody =
anticorp

Nuclei = nuclei

Actin = actină

Figure 30
Figura 30

Nuclei = nuclei

Actin = actină

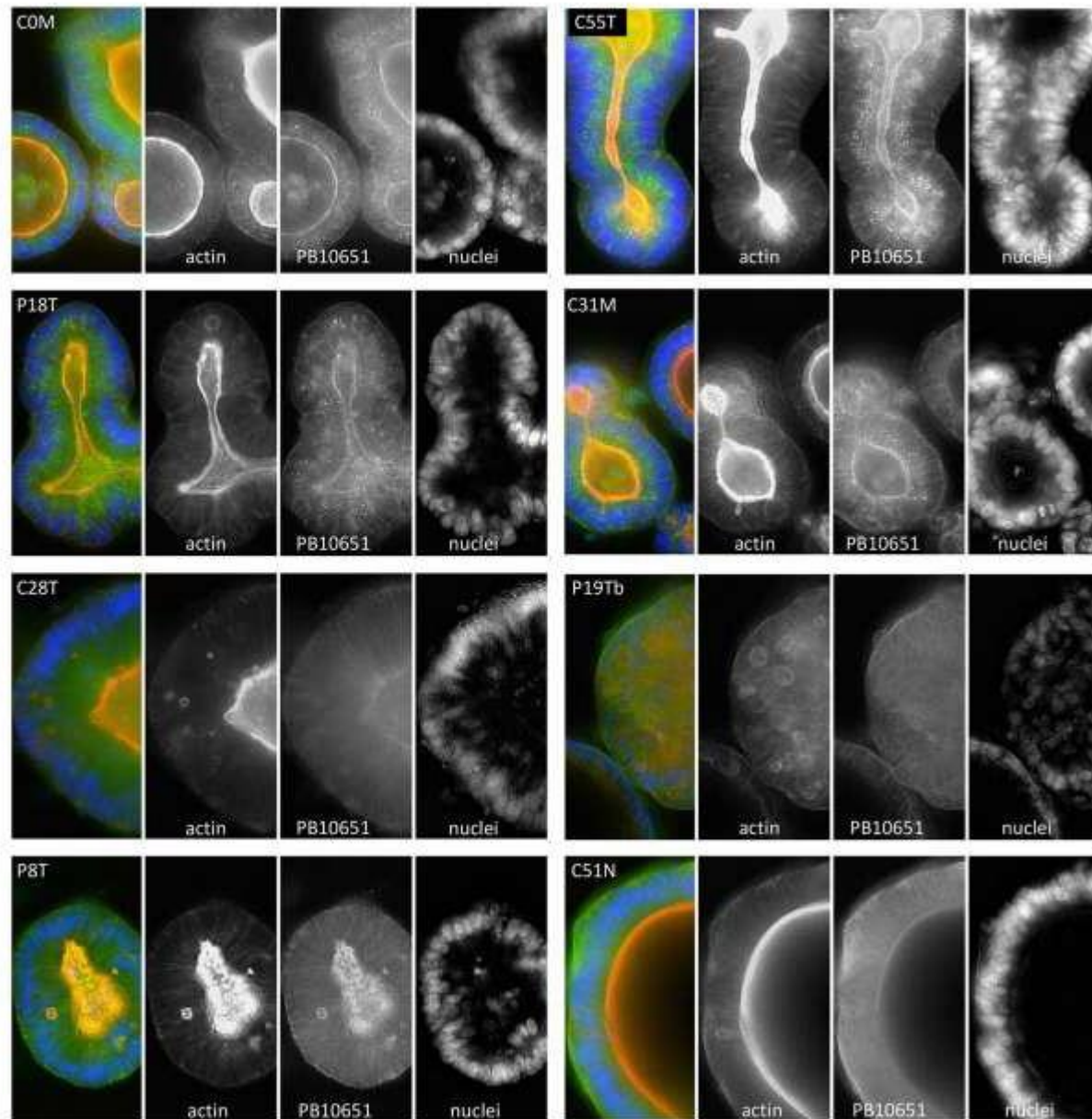


Figura 31

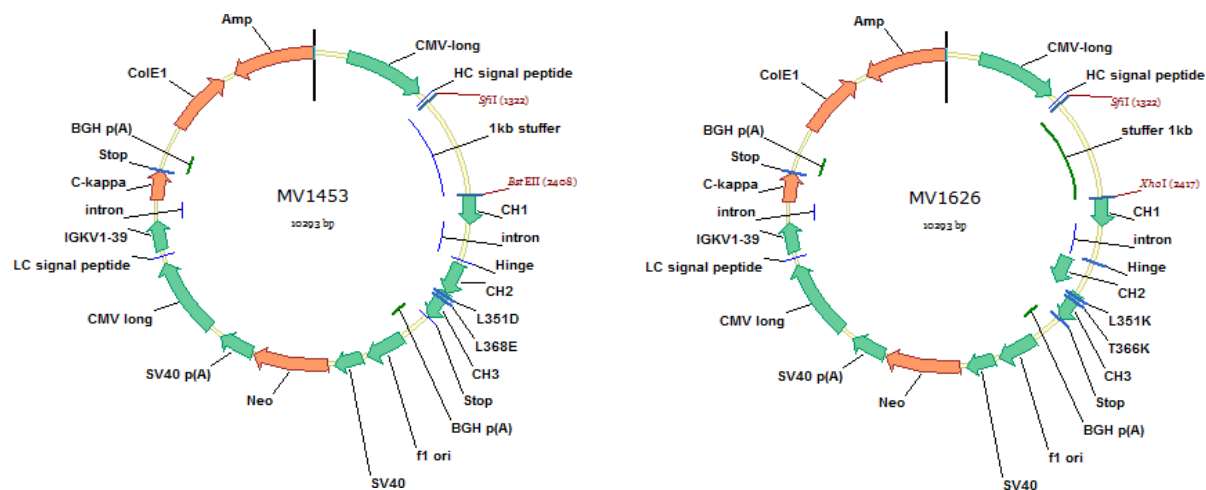
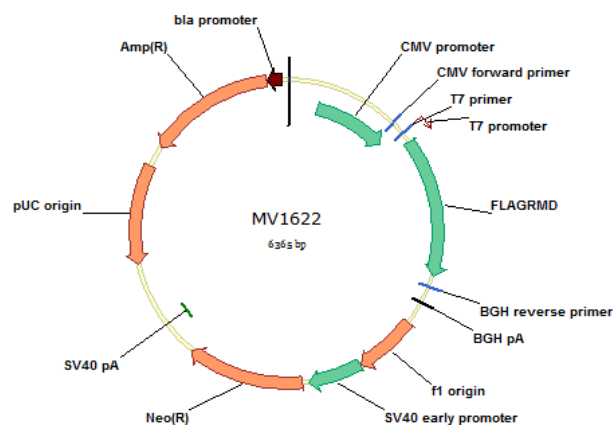


Figura 32



Signal peptide = peptida semnal
 Stuffer = secvență de umplutură
 Intron = intron
 Hinge = legătură
 CMV long = lungime CMV
 Promoter = promotor
 Forward primer = primer sens
 Revers primer = primer antisens
 Origin = origine
 Early promoter = promotor timpuriu

Figura 33

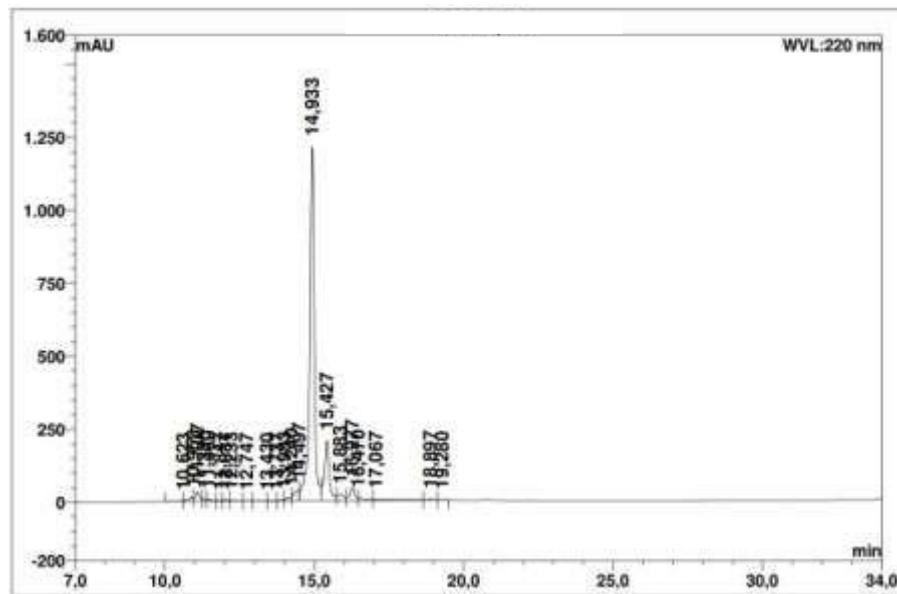
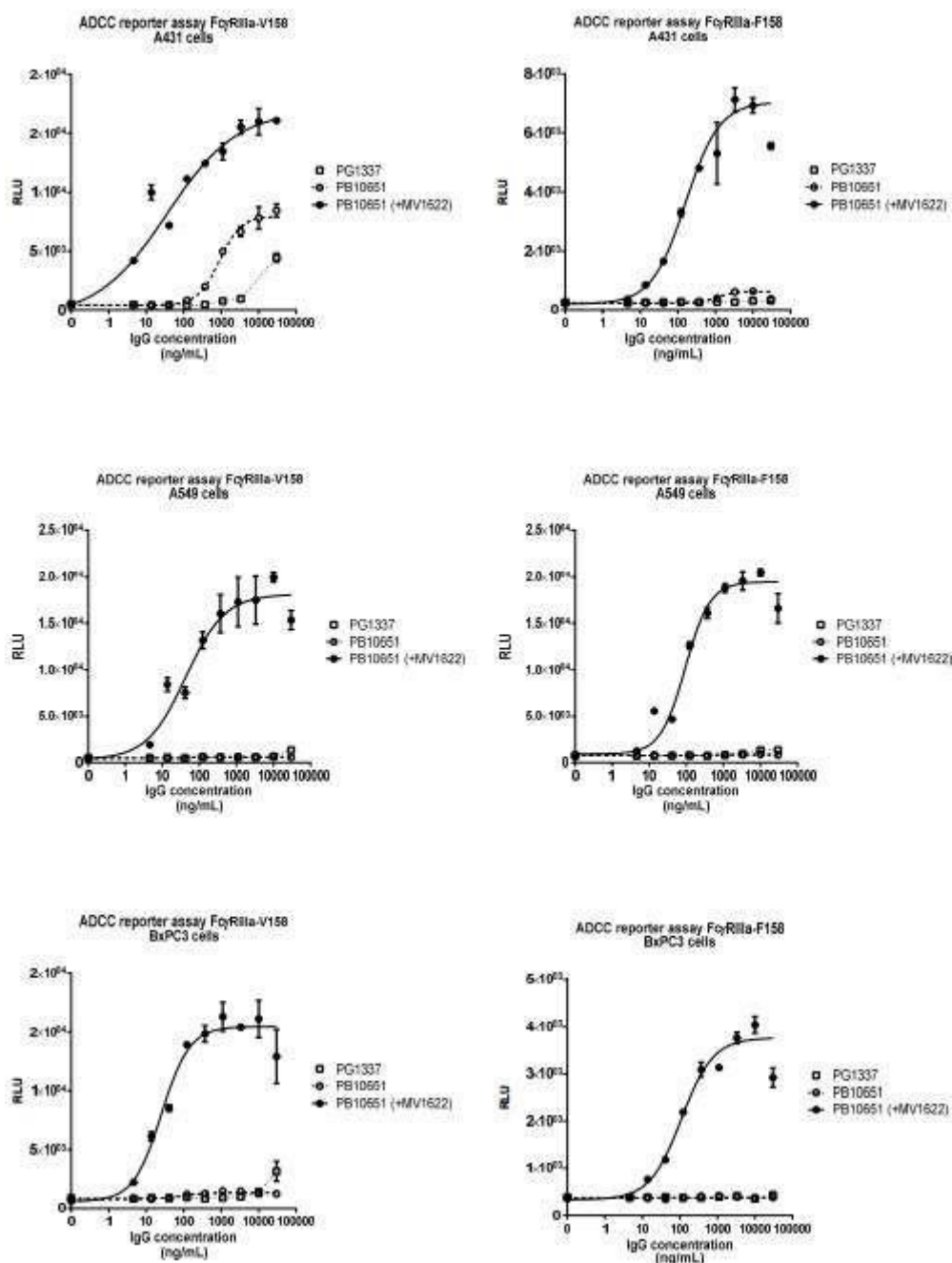


Figura 34



ADCC reporter assay = Test reporter ADCC

Cells = celule

Concentration = concentrație

Figura 35

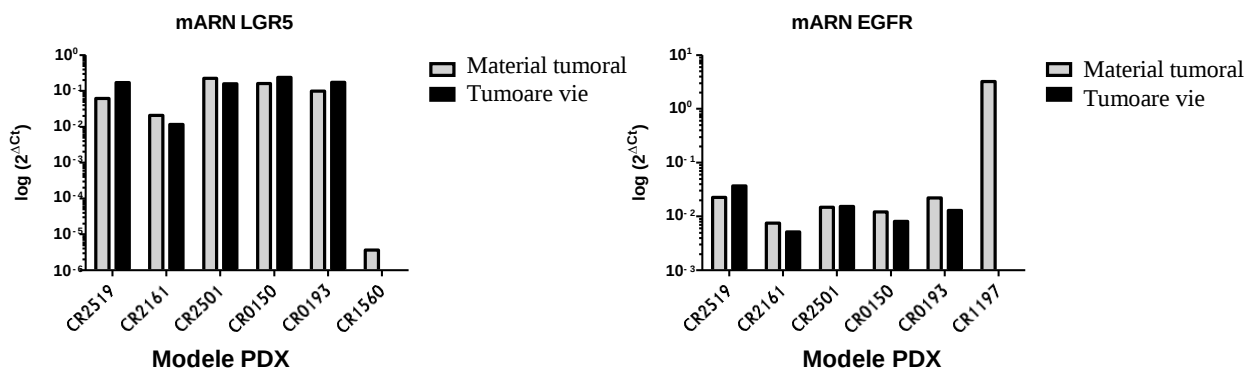


Figura 36

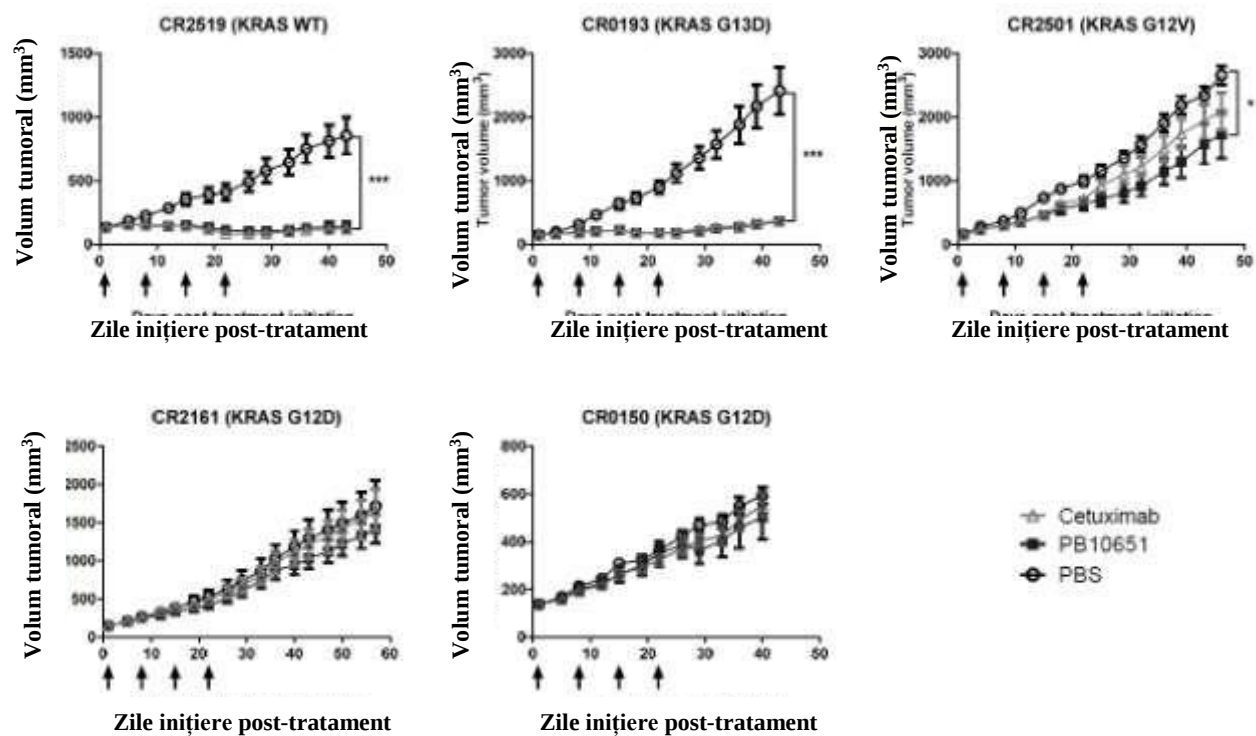


Figura 37

48h după adăugarea anticorpilor

TT-TT

EGFR-TT

Cetuximab

PB10651

Ki67

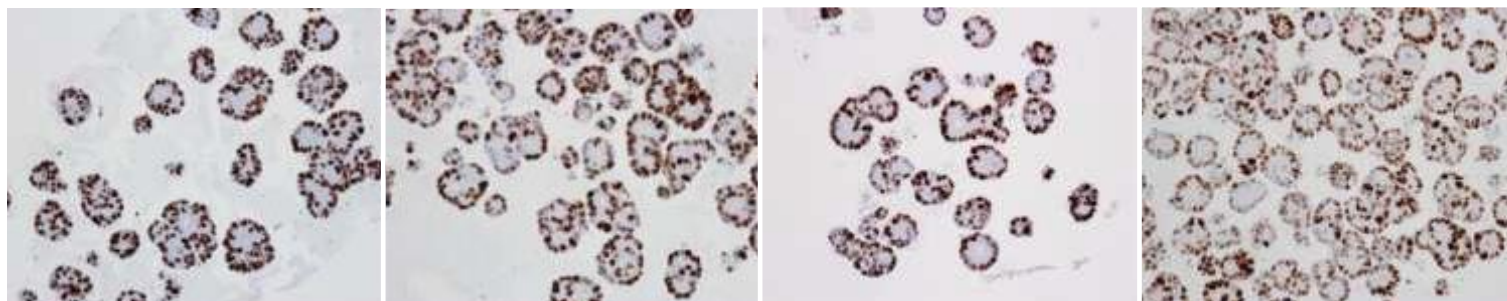
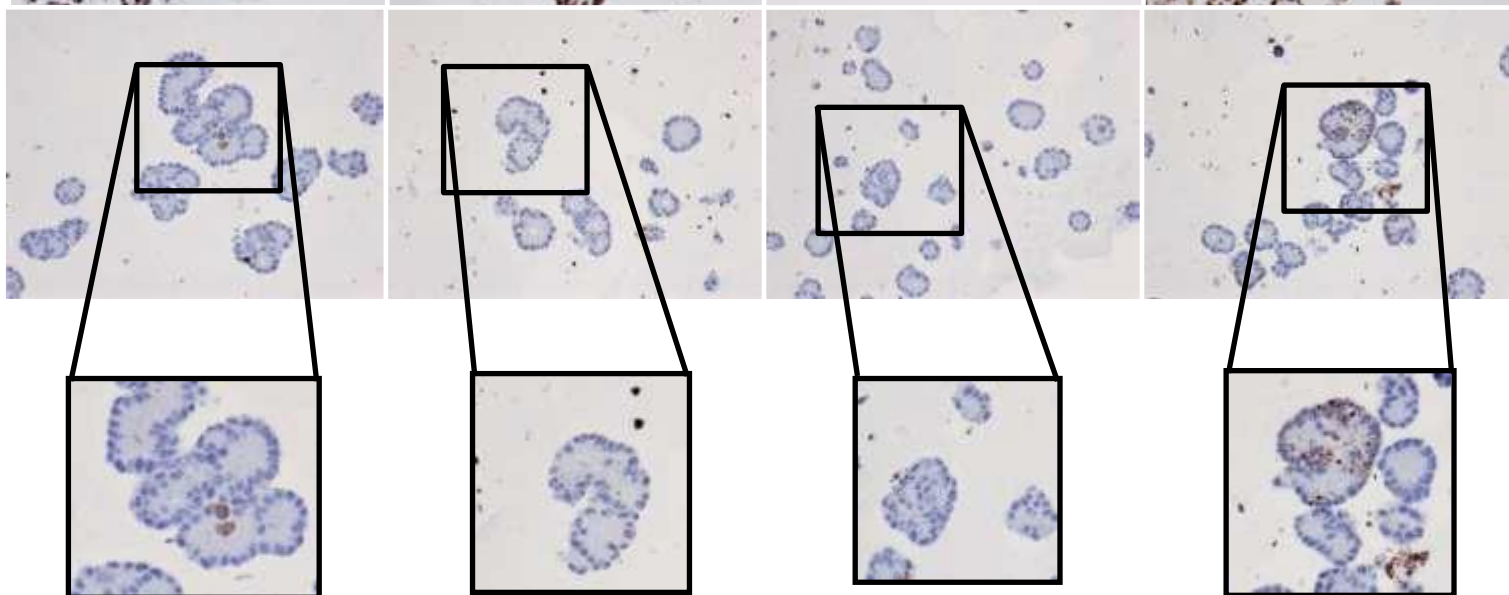
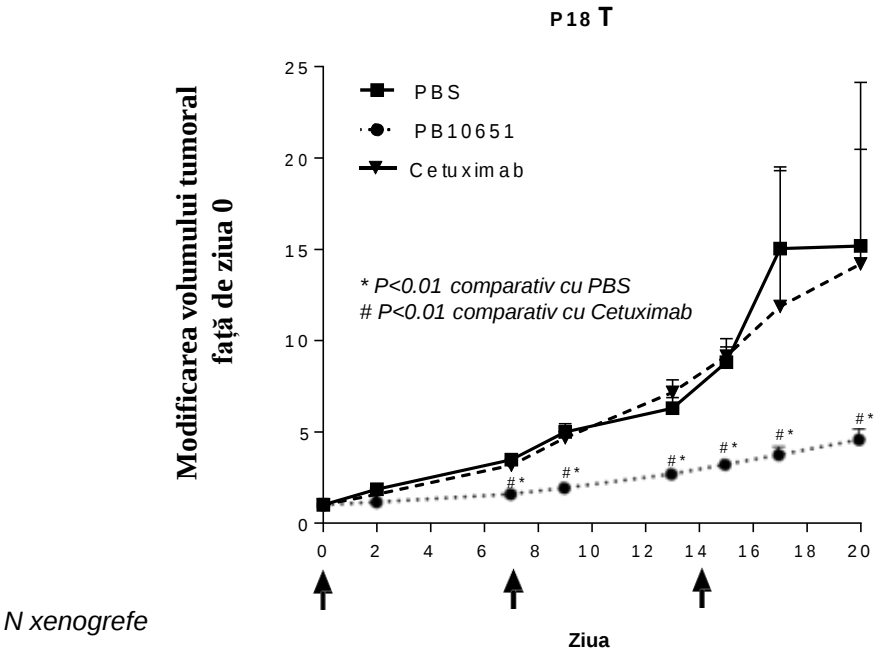
Caspaza-3
clivată

Figura 38
Figura 38A

Volum tumoral mediu în ziua 0

	Ziua 0
PBS	46.9
PB10651	47.3
CET	44.3



Ziua	0	2	7	9	13	15	17	20
PBS	29	29	29	28	25	25	6	3
PB10651	33	33	33	33	33	33	22	22
CET	29	29	29	29	26	26	6	4

Figura 39

SEQ ID NO:1

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDL
 SMNNISQLLPNPLPSLRFLEELRLAGNALTYIPKGAFTGLYSLKVLMLQNNQLRHVPTEALQNLRLSLQSLRLD
 ANHISYVPPSCFSGHSLRHLWLDDNALTEIPVQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHN
 NRIHSLGKKCFDGLHSLETLDLNYYNNLDEFPTAIRTLNLKELGFHSNNIRSPEKAFVGNPSLITIHFYDNPIQ
 FVGRSAFQHLPELRTLTLNGASQITEFPDLTGANLESRTLTLGAQISSLPQTVCNQLPNLQVLDLSYNLLEDLP
 SFSVCQKLQKIDLRHNEIYEIKVDTFQQLLSLRSLNLAWNIAIHPNAFSTLPSLIKLDLSSNLLSSFPITGLHG
 LTHLKLGTGNHALQSLISSENFPELKVIEMPYAYQCCAFGVCENAYKISNQWNKGDNSSMDDLHKKDAGMFQ
 AQDERDLEDFLDFEEDLKALHSVQCSPSPGPFKPCHELLDGWLIRIGVWTIAVLALTCNALVTSTVFRSPLYI
 SPIKLLIGVIAAVNMLTGVSSAVLAGVDAFTFGSFARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALERG
 FSVKYSAKFETKAPFSSLKVIILLCALLALTMAAVPLLGGSKYGASPLCLPLPFGEPSTMGYMVALILLNSLCFL
 MMTIAYTKLYCNLDKGDLENIWDCSMVKHIALLLFTNCILNCPVAFLSFSSLINLTFISPEVIKIFILLVVVPLPA
 CLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSINSDDVEKQCDSTQALVTFTSSITYDLPPSSVPSP
 AYPVTESCHLSSVAFVPCL

Secvența adnotată No1:

Mdtsrlgvllslpvlqlat

peptida semnal

GgssprsgvllrgcpthchcepdgrmllrvdcSDLGLSELPSNLSVFTSY regiune N

Ldlsmnnisqllpnplpslrflee	LRR1
Lrlagnaltyipkgaftglyslkv	LRR2
Lmlqnnqlrhvp tealqnlrslqs	LRR3
Lrldanhisyvppscfsglhslrh	LRR4
Lwlddnalteipvqafsrslsalqa	LRR5
mtlalnkihipdyafgnlsslvv	LRR6
Lhlhnnrihslgkkcf dglhsletl	LRR7
Dlnynnldefptairtlsln	LRR8
Lkelgfhsnnirsipekafvgnpslit	LRR9
Ihfydnpiqfvgrsafqhlpelrt	LRR10
Ltlngasqitefpdltgtanles	LRR11
Ltlgtgaqisslpqtv cnqlpnlqv	LRR12
Ldlsynlledlpsfsvcqlqk	LRR13
Idlrhneiyeikvdtfqllslr	LRR14
Slnlawnkiaiihpnafstlpslik	LRR15
Ldlssnllssfpitglhglthlk	LRR16
Ltgnhalqslissenfpelkvem	LRR17

pyayqccafgvcenayk isnqwnkgdnssmddlhkkdagmfqaqderd

Ledflldfeedlkalhsvqcspspgpfkpcelhldgwlr

regiune CRL

igvwtiavlaltcnalvtstvf

TM1estimat

rsplyispi

klligviaavnmltgvsavlagvda

TM2estimat

ftfgsfarhgawwengvgchv

igflsifasessvfltlaler

TM3estimat

gfsvkysakfetakpfss

lkviillcallaltmaavpllggsk

TM4estimat

ygasplclplpfgepstn

gymvalillnslcflmmtiaytkly

TM5estimat

cnldkgdleniwdcsmvk

hialllftncilncpvafslfssl

TM6estimat

inltfispevi

kfillvvvplpaclnpllyilfnp

TM7estimat

hfkedlvslrkqtyvwtrskhpslmsinsddvekqscdstqalvtft

sssitydlppssvpaspaypvteschlssvafvpcl parte C-terminală

Figura 40

Seq ID no: 2

MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTLQGTGFEDHFLS
 LQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIP
 LENLQIIRGNMYYENSIALAVLSNYDANKTGLKELPMRNLQEILHGAVRF
 SNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHGSCQKCDPSCPNGSCW
 GAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDECLV
 CRKFRDEATCKDTCPPMLLYNPPTYQMDVNPEGKYSFGATCVKKCPRNYV
 VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLS
 INATNIKHFKNCTSIISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKE
 ITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGGFSLAVVSLNITSLGL
 RSLKEISDGDVLIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCK
 ATGQVCHALCSPEGCGWPEPRDCVSCRNVSRGRECVDKCNLLEGEPRFV
 ENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVM
 GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCTNGPKIPSIATGM
 VGALLLLLVLVALGIGLFMRRRHIVRKRTLRLRLQERELVEPLTPSGEAPN
 QALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREA
 TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLD
 YVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAARNVLVKTPQH
 VKITDFGLAKLLGAEKEYHAEGGKVPIKWMALLESILHRIYTHQSDVWSY
 GVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKC
 WMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRA
 LMDEEDMDVDVDADEYLIPOQGGFFSSPSTSRTPLSSLSATSNNSTVACI
 DRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVPKR
 PAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNVTQPTCVNST
 FDSPAHWAKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAEYLRV
 APQSSEFIGA

Secvența adnotată nr: 2

MRPSGTAGAALLALLAALCPASRA **peptida semnal**

LEEKKVCQGTSNKLTLQGTGFEDHFLS
 LQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIP
 LENLQIIRGNMYYENSIALAVLSNYDANKTGLKELPMRNLQEILHGAVRF
 SNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHGSCQKCDPSCPNGSCW
 GAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRESDECLV
 CRKFRDEATCKDTCPPMLLYNPPTYQMDVNPEGKYSFGATCVKKCPRNYV
 VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLS
 INATNIKHFKNCTSIISGDLHILPVAFRGDSFTHTPPLDPQELDILKTVKE
 ITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGGFSLAVVSLNITSLGL
 RSLKEISDGDVLIISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSCK
 ATGQVCHALCSPEGCGWPEPRDCVSCRNVSRGRECVDKCNLLEGEPRFV
 ENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCPAGVM
 GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCTNGPKIPSIAT
domeniul extracelular

GMVGALLLLLVLVALGI **domeniul transmembranar estimat**

GLFMRRRHIVRKRTLRLRLQERELVEPLTPSGEAPN

QALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVAIKELREA
TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLD
YVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAARNVLVKTPQH
VKITDFGLAKLLGAEKEYHAEGGKVPIKWMALESILHRIYTHQSDVWSY
GVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKC
WMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRA
LMDEEDMDDVVDADAYLIPQQGFFSSPSTSRTPLLSSLSATSNNSTVACI
DRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVPKR
PAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNTVQPTCVNST
FDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGIFKGSTAENAAYLRV
APQSSEFIGA

Tirozin kinază intracelulară și parte C-terminală