

Online suppl. Table 2: Frequencies of copy-number gains and amplifications of receptor tyrosine kinases and representative growth-related genes on chromosome 7 in clusters A and B.

Name of Gene	Copy-number gain			Amplification			
	Cluster A	Cluster B	p value	Cluster A	Cluster B	p value	
	(n = 51)	(n = 55)		(n = 51)	(n = 55)		
AATK	8	13	0.3388	1	0	0.4811	
ALK	6	4	0.516	0	0	1	
AXL	15	3	0.0014	1	0	0.4811	
CSF1R	10	12	0.8148	0	1	1	
DDR1	20	19	0.6887	3	3	1	
DDR2	16	19	0.8368	2	0	0.2291	
FGFR1	13	12	0.8193	2	1	0.6074	
FGFR2	5	12	0.1155	0	1	1	
FGFR3	21	17	0.314	8	4	0.2249	
FGFR4	17	8	0.0381	3	1	0.3495	
FLT1(VEGFR1)	25	19	0.168	5	1	0.1033	
FLT3	16	23	0.3158	3	0	0.1079	
FLT4 (VEGFR3)	19	14	0.2131	1	0	0.4811	
IGF1R	16	6	0.0154	2	0	0.2291	
INSR	3	2	0.6699	0	0	1	
INSRR	N/A	N/A	N/A	N/A	N/A	N/A	
KDR (VEGFR2)	4	2	0.4248	1	0	0.811	
KIT	6	3	0.3075	1	0	0.4811	
LMTK2	29	15	0.003	7	0	0.0048	
LMTK3	N/A	N/A	N/A	N/A	N/A	N/A	
LTK	N/A	N/A	N/A	N/A	N/A	N/A	
MERTK	14	12	0.6519	0	1	1	
MET	18	11	0.0861	0	1	1	
MST1R	17	7	0.0191	1	0	0.4811	
MUSK	13	9	0.3382	0	0	1	
NTRK1	13	17	0.6667	1	1	1	
NTRK2	9	7	0.5901	0	0	1	
NTRK3	14	4	0.0086	0	0	1	
PDGFRA	4	3	0.7086	0	0	1	
PDGFRB	7	8	1	0	0	1	
PTK7	22	21	0.6932	13	10	0.48	
RET	19	19	0.8405	2	7	0.1636	
ROR1	5	6	1	0	0	1	
ROR2	7	3	0.1905	0	0	1	
ROS1	10	2	0.0129	0	0	1	
RYK	9	3	0.0661	0	0	1	
STYK1	29	20	0.0508	8	3	0.114	
TEK	3	3	1	0	0	1	
TIE1	13	22	0.1484	5	2	0.2575	
TYRO3	17	15	0.5313	1	1	1	
EPHA1	6	7	1	0	0	1	
EPHA2	16	14	0.5248	0	0	1	
EPHA3	14	4	0.0086	0	0	1	
EPHA4	9	5	0.2544	0	0	1	
EPHA5	3	8	0.2052	0	0	1	
EPHA6	6	5	0.755	0	0	1	
EPHA7	3	2	0.6699	0	0	1	
EPHA8	6	12	0.2018	2	0	0.2291	
EPHA10	26	29	1	11	14	0.6554	
EPHB1	9	5	0.2544	0	0	1	
EPHB2	21	24	0.8457	2	1	0.6074	
EPHB3	24	15	0.0444	8	2	0.0464	
EPHB4	28	20	0.0786	14	5	0.0212	
EPHB6	32	27	0.1755	14	7	0.0867	
EGFR	20	7	0.0033	6	1	0.0537	
ERBB2	28	32	0.8449	7	13	0.2219	
ERBB3	17	8	0.0381	7	3	0.1905	
ERBB4	6	1	0.0537	0	0	1	
Growth-related genes on chromosome 7 except RTKs	RALA	18	9	0.0283	2	0	0.2291
	PTPN12	16	9	0.1079	4	0	0.0503
	MAFK	34	25	0.0328	23	15	0.0693
	ARHGEF5	17	15	0.5313	5	3	0.4772
	BRAF	11	9	0.6206	1	0	0.4811
	CAV1	12	8	0.3213	1	0	0.4811
	GLI3	25	11	0.0021	1	0	0.4811
	HOXA1	29	32	1	4	3	0.7086
	RABL5	21	13	0.063	4	3	0.7086
	RBM28	22	21	0.6932	8	7	0.7826
	CUL1	31	20	0.0192	11	3	0.0203
	IGF2BP3	25	19	0.168	3	2	0.6699
	RELB	25	17	0.0741	3	0	0.1079
	SEMA3E	19	7	0.006	1	0	0.4811

p values <0.05 are shown in bold. N/A: not assessable.