

Supplementary Table 1. Validation of array CGH findings by FISH for the seven FFPE archival osteosarcoma samples. For each sample, signals were enumerated by counting spots in 100 non-overlapped, intact interphase nuclei per tumor tissue section.

Probe (gene)	Sample	Population of cells enumerated as containing indicated number of signals				
		1	2	polysomy	>5, <10	>10
E2F3	OS-T1	8	24	68	0	0
	OS-T2	15	50	35	0	0
	OS-T3	3	10	57	30	0
	OS-T7	0	0	18	36	46
	OS-E1	5	3	12	20	60
	OS-E2	3	5	24	38	30
	OS-E3	20	45	35	0	0
RUNX2	OS-T1	5	35	60	0	0
	OS-T2	5	10	35	40	10
	OS-T3	1	9	55	35	0
	OS-T7	0	8	46	38	8
	OS-E1	5	2	28	25	40
	OS-E2	5	10	20	40	20
	OS-E3	5	10	20	26	33
PIM1	OS-T1	10	45	45	0	0
	OS-T2	15	15	70	0	0
	OS-T3	5	15	55	25	0
	OS-T7	10	55	35	0	0
	OS-E1	3	10	47	25	15
	OS-E2	8	10	59	18	5
	OS-E3	15	20	65	0	0
FBXO9	OS-T1	5	37	58	0	0
	OS-T2	10	20	70	0	0
	OS-T3	10	20	60	10	0
	OS-T7	5	50	45	0	0
	OS-E1	5	10	35	35	15
	OS-E2	15	8	50	22	5
	OS-E3	10	30	60	0	0

Polysomy: 3-5 copies of balanced target gene and CEP 6 signals

Amplification cut-off: 10%

N.B. Conclusions were based on CEP 6 signal enumeration, which was performed as described in Materials and Methods.

Supplementary Table 2. Enumeration of segmental duplications on chromosome 6. Segmental duplications were quantified according to length of at least 5 kbp or at least 10 kbp and then arranged by cytoband. Clusters of segmental duplications 10 kbp or larger surround the region of gain ~6p21–12 common in osteosarcoma. From the aCGH analysis of 15 osteosarcoma patient samples, frequencies of partial or complete gain and/or amplification in the cohort are indicated for each cytoband. The mouse chromosomes homologous to the human chromosome 6p cytobands are listed.

Cytoband	Number of segmental duplications with given length		Cluster label and base pair length	Frequency of Partial or Complete Gain and/or Amplification (% of 15 samples)	Mouse Chromosome demonstrating homology
	Minimum length 5kb	Minimum length 10kb			
6p25.3	191	64	A (288kb)	53.33	13
6p25.2	45	0		53.33	13
6p25.1	184	0		53.33	13
6p24.3	171	0		53.33	13
6p24.2	0	0		46.67	13
6p24.1	5	0		53.33	13
6p23	17	0		53.33	13
6p22.3	148	0	B (256kb)	60.00	13
6p22.2	137	0		66.67	13
6p22.1	246	35		66.67	17
6p21.33	95	0	C (36kb)	73.33	17
6p21.32	19	14		66.67	17
6p21.31	3	0		80.00	17
6p21.2	90	0		93.33	17
6p21.1	200	0		93.33	17
6p12.3	421	1		86.67	17, 1
6p12.2	237	0		73.33	1
6p12.1	252	0	D (587kb)	73.33	1,9
6p11.2	375	63		66.67	1
6p11.1	166	20	E (609kb)	53.33	1
<i>CENTROMERE</i>					
6q11.1	21	1			
6q11.2	0	0			
6q12	185	3			
6q13	746	0			

6q14.1	702	0
6q14.2	92	0
6q14.3	503	0
6q15	336	1
6q16.1	372	0
6q16.2	108	0
6q16.3	478	0
6q21	587	0
6q22.1	292	0
6q22.2	150	0
6q22.31	400	0
6q22.32	83	0
6q22.33	162	0
6q23.1	54	0
6q23.2	150	4
6q23.3	51	0
6q24.1	243	0
6q24.2	33	0
6q24.3	36	0
6q25.1	56	0
6q25.2	0	0
6q25.3	206	0
6q26	159	1
6q27	140	62

Supplementary Table 3. Copy number transition locations and associated copy number change on chromosome 6 for 15 osteosarcoma samples according to aCGH. Areas of gain or loss are indicated for regions of copy number transition. Blue shading indicates chromosome 6p and unshaded regions represent chromosome 6q.

Sample	Copy number transition locations on chromosome 6		Copy Number Change
	Copy number transition start	Copy number transition end	
OS-T1	0	58,788,747	CN Gain
OS-T1	62,040,890	170,899,992	CN Gain
OS-T2	0	11,622,225	CN Gain
OS-T2	11,622,225	11,860,263	Amplification
OS-T2	11,860,263	13,026,087	CN Gain
OS-T2	13,026,087	13,755,152	Amplification
OS-T2	13,755,152	29,776,341	CN Gain
OS-T2	29,776,341	30,306,161	CN Loss
OS-T2	30,306,161	39,097,151	CN Gain
OS-T2	39,097,151	41,520,015	CN Loss
OS-T2	41,520,015	44,837,825	CN Gain
OS-T2	44,837,825	47,053,426	Amplification
OS-T2	47,053,426	47,120,506	CN Gain
OS-T2	47,120,506	53,837,523	CN Loss
OS-T2	53,837,523	55,001,643	Amplification
OS-T2	55,001,643	56,276,281	CN Loss
OS-T2	56,276,281	56,667,629	CN Gain
OS-T2	56,667,629	58,788,747	CN Loss
OS-T2	62,040,890	63,734,002	CN Gain
OS-T2	63,734,002	144,306,447	CN Loss
OS-T2	144,306,447	146,203,354	CN Gain
OS-T2	146,203,354	147,236,210	CN Loss
OS-T2	147,236,210	153,111,065	CN Gain
OS-T2	157,542,782	162,460,411	CN Gain
OS-T2	162,460,411	165,668,437	CN Loss
OS-T2	165,668,437	170,899,992	CN Gain
OS-T3	0	152,714	CN Gain
OS-T3	152,714	327,686	CN Loss
OS-T3	327,686	11,701,142	CN Gain
OS-T3	11,701,142	12,988,149	Amplification
OS-T3	12,988,149	43,947,864	CN Gain
OS-T3	43,947,864	56,558,245	CN Loss
OS-T3	56,558,245	58,788,747	CN Gain
OS-T3	62,040,890	73,969,590	CN Loss
OS-T3	73,969,590	74,671,647	CN Gain
OS-T3	74,671,647	96,139,522	CN Loss
OS-T3	96,139,522	96,960,954	CN Gain
OS-T3	96,960,954	100,251,782	CN Loss
OS-T3	100,251,782	102,376,397	CN Gain
OS-T3	102,376,397	102,486,334	CN Loss
OS-T3	102,486,334	103,456,115	CN Gain
OS-T3	103,456,115	111,346,556	CN Loss
OS-T3	111,346,556	112,337,368	CN Gain
OS-T3	112,337,368	113,703,146	Amplification
OS-T3	113,703,146	116,868,566	CN Gain
OS-T3	116,868,566	118,492,574	CN Loss
OS-T3	118,492,574	129,885,385	CN Gain
OS-T3	129,885,385	133,196,167	Amplification
OS-T3	133,196,167	134,577,723	CN Gain
OS-T3	134,577,723	138,338,065	Amplification

OS-T3	138,338,065	144,479,790	CN Gain
OS-T3	144,479,790	145,116,479	Amplification
OS-T3	145,116,479	147,504,385	CN Loss
OS-T3	147,504,385	147,950,912	Amplification
OS-T3	152,128,180	154,833,149	CN Loss
OS-T3	154,833,149	160,831,256	CN Gain
OS-T3	160,831,256	160,917,521	Amplification
OS-T3	160,917,521	161,311,701	CN Loss
OS-T3	161,311,701	161,618,903	Amplification
OS-T3	161,618,903	161,883,059	CN Gain
OS-T3	161,883,059	170,678,071	CN Loss
OS-T3	170,678,071	170,811,770	Amplification
OS-T3	170,811,770	170,899,992	CN Loss
OS-T4	0	32,539,336	CN Gain
OS-T4	32,539,336	32,786,995	CN Loss
OS-T4	32,786,995	54,823,633	CN Gain
OS-T4	54,823,633	54,944,045	Amplification
OS-T4	54,944,045	57,310,732	CN Gain
OS-T4	57,310,732	58,788,747	CN Loss
OS-T4	62,040,890	170,899,992	CN Loss
OS-T5	0	38,636,597	CN Loss
OS-T5	38,636,597	38,768,161	CN Gain
OS-T5	38,768,161	42,856,300	CN Loss
OS-T5	42,856,300	56,339,040	CN Gain
OS-T5	56,339,040	57,310,732	CN Loss
OS-T5	57,310,732	58,142,725	CN Gain
OS-T5	58,142,725	58,788,747	CN Loss
OS-T5	62,040,890	63,006,917	CN Gain
OS-T5	63,006,917	108,746,625	CN Loss
OS-T5	108,746,625	108,931,803	Homozygous Copy Loss
OS-T5	108,931,803	170,899,992	CN Loss
OS-T6	0	37,423,792	CN Loss
OS-T6	37,423,792	42,244,459	CN Gain
OS-T6	42,244,459	44,865,136	CN Loss
OS-T6	44,865,136	49,949,400	Amplification
OS-T6	49,949,400	51,337,510	CN Gain
OS-T6	51,337,510	58,788,747	CN Loss
OS-T6	62,040,890	74,591,912	CN Loss
OS-T6	74,591,912	75,923,593	Homozygous Copy Loss
OS-T6	75,923,593	82,266,195	CN Loss
OS-T6	82,266,195	82,532,187	CN Gain
OS-T6	82,532,187	169,593,858	CN Loss
OS-T6	169,593,858	169,988,076	Homozygous Copy Loss
OS-T6	169,988,076	170,899,992	CN Loss
OS-T7	0	189,701	Homozygous Copy Loss
OS-T7	189,701	327,686	CN Loss
OS-T7	327,686	20,146,787	Homozygous Copy Loss
OS-T7	20,146,787	20,648,847	Amplification
OS-T7	20,648,847	21,513,978	CN Gain
OS-T7	21,513,978	22,257,067	Amplification
OS-T7	22,257,067	23,475,466	CN Gain
OS-T7	23,475,466	29,141,497	Amplification
OS-T7	29,141,497	29,541,638	CN Gain
OS-T7	29,541,638	31,008,596	Amplification
OS-T7	31,008,596	33,277,199	CN Gain
OS-T7	33,277,199	33,398,225	CN Loss
OS-T7	33,398,225	33,617,227	CN Gain

OS-T7	33,617,227	34,516,439	CN Loss
OS-T7	34,516,439	34,832,392	CN Gain
OS-T7	34,832,392	35,293,444	CN Loss
OS-T7	35,293,444	36,283,819	Amplification
OS-T7	36,283,819	37,709,462	CN Loss
OS-T7	37,709,462	41,999,391	Amplification
OS-T7	41,999,391	42,615,744	CN Gain
OS-T7	42,615,744	46,721,457	Amplification
OS-T7	46,721,457	49,715,179	CN Gain
OS-T7	49,715,179	52,954,066	Amplification
OS-T7	52,954,066	57,310,732	CN Gain
OS-T7	57,310,732	58,212,034	CN Loss
OS-T7	58,212,034	58,788,747	CN Gain
OS-T7	62,040,890	70,683,594	CN Loss
OS-T7	70,683,594	72,705,166	Homozygous Copy Loss
OS-T7	72,705,166	89,935,258	CN Loss
OS-T7	89,935,258	92,366,541	CN Gain
OS-T7	92,366,541	98,679,921	CN Loss
OS-T7	98,679,921	117,615,498	Homozygous Copy Loss
OS-T7	117,615,498	170,899,992	CN Loss
OS-T8	0	26,127,208	CN Gain
OS-T8	26,127,208	26,247,695	CN Loss
OS-T8	26,247,695	29,124,576	CN Gain
OS-T8	29,124,576	29,508,321	CN Loss
OS-T8	29,508,321	52,526,065	CN Gain
OS-T8	52,526,065	53,618,925	Amplification
OS-T8	53,618,925	58,788,747	CN Gain
OS-T8	62,040,890	124,871,922	CN Loss
OS-T8	124,871,922	138,604,858	CN Gain
OS-T8	141,356,365	142,361,196	CN Loss
OS-T8	158,545,194	159,401,000	Amplification
OS-T8	159,401,000	160,298,910	CN Gain
OS-T8	160,298,910	163,194,893	Amplification
OS-T8	163,194,893	165,167,959	CN Gain
OS-T8	165,167,959	165,580,597	Amplification
OS-T8	165,580,597	170,899,992	CN Loss
OS-T9	0	670,563	Homozygous Copy Loss
OS-T9	670,563	23,580,255	CN Loss
OS-T9	23,580,255	58,788,747	CN Gain
OS-T9	62,040,890	72,413,422	CN Gain
OS-T9	72,413,422	111,501,835	CN Loss
OS-T9	111,501,835	111,794,439	CN Gain
OS-T9	111,794,439	170,899,992	CN Loss
OS-T10	0	29,956,857	CN Loss
OS-T10	29,956,857	30,066,168	CN Gain
OS-T10	30,066,168	35,940,960	CN Loss
OS-T10	35,940,960	36,497,864	Amplification
OS-T10	36,497,864	36,843,127	CN Gain
OS-T10	36,843,127	37,709,462	Amplification
OS-T10	37,709,462	38,188,441	CN Gain
OS-T10	38,188,441	38,768,161	Amplification
OS-T10	38,768,161	39,599,619	CN Gain
OS-T10	39,599,619	46,657,126	Amplification
OS-T10	46,657,126	49,620,310	CN Gain
OS-T10	49,620,310	50,021,645	Amplification
OS-T10	50,021,645	51,533,541	CN Gain
OS-T10	51,533,541	57,038,952	CN Loss
OS-T10	57,038,952	58,788,747	CN Gain

OS-T10	62,040,890	63,900,027	Amplification
OS-T10	63,900,027	66,310,880	CN Loss
OS-T10	66,310,880	68,692,340	CN Gain
OS-T10	68,692,340	71,055,544	CN Loss
OS-T10	71,055,544	71,181,602	CN Gain
OS-T10	71,181,602	73,358,634	CN Loss
OS-T10	73,358,634	76,479,046	CN Gain
OS-T10	76,479,046	89,041,331	CN Loss
OS-T10	89,041,331	90,062,245	CN Gain
OS-T10	90,062,245	99,138,116	CN Loss
OS-T10	99,138,116	99,702,878	Homozygous Copy Loss
OS-T10	99,702,878	100,538,401	CN Gain
OS-T10	100,538,401	100,975,961	CN Loss
OS-T10	100,975,961	101,604,606	CN Gain
OS-T10	101,604,606	103,971,881	CN Loss
OS-T10	103,971,881	104,624,363	CN Gain
OS-T10	104,624,363	114,279,559	CN Loss
OS-T10	114,279,559	114,582,556	CN Gain
OS-T10	114,582,556	136,172,136	CN Loss
OS-T10	136,172,136	138,531,571	CN Gain
OS-T10	138,531,571	139,054,268	Amplification
OS-T10	139,054,268	139,361,804	CN Gain
OS-T10	139,361,804	139,757,281	Amplification
OS-T10	139,757,281	142,058,368	CN Loss
OS-T10	142,058,368	142,903,376	CN Gain
OS-T10	142,903,376	143,727,594	CN Loss
OS-T10	143,727,594	145,464,908	CN Gain
OS-T10	145,464,908	153,791,169	CN Loss
OS-T10	153,791,169	157,421,563	Amplification
OS-T10	157,421,563	161,538,169	CN Gain
OS-T10	161,538,169	163,375,793	CN Loss
OS-T10	163,375,793	164,649,824	CN Gain
OS-T10	164,649,824	170,899,992	CN Loss
OS-T11	0	4,755,971	CN Gain
OS-T11	4,755,971	17,394,157	CN Loss
OS-T11	43,144,968	46,232,914	CN Gain
OS-T11	46,232,914	58,722,020	CN Loss
OS-T11	62,040,890	170,899,992	CN Loss
OS-T12	0	41,230,683	CN Gain
OS-T12	41,230,683	57,538,119	Amplification
OS-T12	57,538,119	58,722,020	CN Gain
OS-T12	62,040,890	75,584,860	CN Gain
OS-T12	75,584,860	170,899,992	CN Loss
OS-T13	0	7,970,549	CN Gain
OS-T13	7,970,549	12,250,953	CN Loss
OS-T13	12,250,953	35,347,224	CN Gain
OS-T13	35,347,224	50,444,497	Amplification
OS-T13	50,444,497	58,722,020	CN Gain
OS-T13	62,040,890	101,051,500	CN Loss
OS-T13	101,051,500	140,639,758	CN Gain
OS-T13	140,639,758	170,899,992	CN Loss
OS-T14	0	36,606,525	CN Loss
OS-T14	36,606,525	52,391,487	CN Gain
OS-T14	52,391,487	58,722,020	CN Loss
OS-T14	62,040,890	170,899,992	CN Loss
OS-T15	0	7,218,405	CN Loss

OS-T15	7,218,405	28,526,879	CN Gain
OS-T15	28,526,879	29,716,795	CN Loss
OS-T15	29,716,795	38,903,308	CN Gain
OS-T15	38,903,308	58,722,020	CN Loss
OS-T15	62,040,890	170,899,992	CN Loss

Supplementary Table 4. Chromosome 6p21 has one of the highest numbers of copy number transitions when taking cytoband size into account. Copy number transitions in multiple populations of tumours, including both gains and losses, were tallied for cytobands on human chromosome 6. The shaded row highlights cytoband 6p21 as having the highest number of copy number transitions in chromosome 6. Data was retrieved from the Progenetix CGH Database (see Materials and Methods).

Cytoband on Chromosome 6	Cytoband size (Mbp)	Number of copy number transitions
p25	7	37
p24	6.5	85
p23	2	133
p22	14.4	273
p21	15.3	721
p12	12	218
p11	3.3	72
<i>CENTROMERE</i>		
q11	3	21
q12	6.5	327
q13	5.9	181
q14	11.6	222
q15	4.6	176
q16	12.7	349
q21	9.1	383
q22	16.5	484
q23	8.7	315
q24	10	351
q25	11.8	249
q26	3.5	111
q27	6.5	28

Supplementary Table 5. Genomic rearrangements in chromosome 6p are more frequent than in the majority of other chromosomal p regions. Genomic rearrangements for multiple tumour populations were quantified for each chromosome as well as each arm of same. The top ten ranked chromosomes are indicated for total number of rearrangements (shaded in blue) and for the ratio of rearrangements in the p arm of each chromosome to the total size of the genome (shaded in pink). The latter ratio is corrected to accurately take into account the size of the chromosomes. Chromosome 6 is in the top ten for total number of rearrangements and the 6p arm is in the top ten for ratio of p rearrangements to the total genome size. Data was retrieved from the UCSC Genome Browser and the Progenetix CGH Database (see Materials and Methods).

Chromosome	Length of Chromosome (Mbp)	Length of p arm (Mbp)	Length of q arm (Mbp)	Number of rearrangements in p arm	Number of rearrangements in q arm	Total number rearrangements	Ratio of p rearrangements to chromosome length	Ratio of total rearrangements to chromosome length
1	247.25	124.3	122.95	3660	3893	7618	14.80	30.81
2	242.95	93.3	149.65	1483	2248	4084	6.10	16.81
3	199.5	91.7	107.8	2996	2555	5926	15.02	29.70
4	191.27	50.7	140.57	1446	2642	4791	7.56	25.05
5	180.86	47.7	133.16	1911	2681	4965	10.57	27.45
6	170.9	60.5	110.4	1975	3095	5477	11.56	32.05
7	158.82	59.1	99.72	1570	2214	5031	9.89	31.68
8	146.27	45.2	101.07	2743	3718	7003	18.75	47.88
9	140.27	51.8	88.47	2316	2271	5240	16.51	37.36
10	135.27	40.3	94.97	1041	1684	3462	7.70	25.59
11	134.45	52.9	81.55	1252	3154	4903	9.31	36.47
12	132.35	35.4	96.95	1487	2423	4337	11.24	32.77
13	114.14	16	98.14	43	3638	4454	0.38	39.02
14	106.37	15.6	90.77	27	2196	2869	0.25	26.97
15	100.34	17	83.34	41	2038	2510	0.41	25.01
16	88.83	38.2	50.63	1365	1696	3764	15.37	42.37
17	78.77	22.1	56.67	2157	2496	5682	27.38	72.13
18	76.12	16.1	60.02	996	2124	4051	13.08	53.22
19	63.81	28.5	35.31	674	861	2828	10.56	44.32
20	62.44	27.1	35.34	735	1729	3559	11.77	57.00
21	46.94	12.3	34.64	28	1489	2497	0.60	53.20
22	49.69	11.8	37.89	48	937	1708	0.97	34.37
X	154.91	59.5	95.41	1020	1373	3617	6.58	23.35
Y	57.77	11.3	46.47	27	67	560	0.47	9.69

Chromosome	Ratio of p rearrangements to total number of rearrangements in chromosome	Ratio of p rearrangements to size of whole genome	Ratio of q rearrangements to q length	Ratio of p rearrangements to p length
1	0.48	1.56E-04	31.66	29.44
2	0.36	1.18E-04	15.02	15.89
3	0.51	1.64E-04	23.70	32.67
4	0.30	9.80E-05	18.79	28.52
5	0.38	1.25E-04	20.13	40.06
6	0.36	1.17E-04	28.03	32.64
7	0.31	1.01E-04	22.20	26.57
8	0.39	1.27E-04	36.79	60.69
9	0.44	1.43E-04	25.67	44.71
10	0.30	9.76E-05	17.73	25.83
11	0.26	8.29E-05	38.68	23.67
12	0.34	1.11E-04	24.99	42.01
13	0.01	3.13E-06	37.07	2.69
14	0.01	3.06E-06	24.19	1.73
15	0.02	5.30E-06	24.45	2.41
16	0.36	1.18E-04	33.50	35.73
17	0.38	1.23E-04	44.04	97.60
18	0.25	7.98E-05	35.39	61.86
19	0.24	7.74E-05	24.38	23.65
20	0.21	6.70E-05	48.92	27.12
21	0.01	3.64E-06	42.98	2.28
22	0.03	9.12E-06	24.73	4.07
X	0.28	9.16E-05	14.39	17.14
Y	0.05	1.57E-05	1.44	2.39