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

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.

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	Frequency of Partial or Complete Gain and/or Amplification (% of 15 samples)	Mouse Chromosome demonstrating homology
	Minimum length 5kb	Minimum length 10kb	Saco pair longin		
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		60.00	13
6p22.2	137	0		66.67	13
6p22.1	246	35	B (256kb)	66.67	17
6p21.33	95	0		73.33	17
6p21.32	19	14	C (36kb)	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		73.33	1,9
6p11.2	375	63	D (587kb)	66.67	1
6p11.1	166	20	E (609kb)	53.33	1
CENTROMER	ΡE				
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 location	ns on chromosome 6	
·	Copy number transition start	Copy number transition end	Copy Number Change
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
0S-12	144,306,447	146,203,354	CN Gain
0S-12	146,203,354	147,236,210	CN Loss
0S-12	147,236,210	153,111,065	CN Gain
0S-12	157,542,782	162,460,411	CN Gain
0S-12	162,460,411	165,668,437	CN Loss
05-12	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 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3 OS-T3	138,338,065 144,479,790 145,116,479 147,504,385 152,128,180 154,833,149 160,831,256 160,917,521 161,311,701 161,618,903 161,883,059 170,678,071 170,811,770	144,479,790 145,116,479 147,504,385 147,950,912 154,833,149 160,831,256 160,917,521 161,311,701 161,618,903 161,883,059 170,678,071 170,811,770 170,899,992	CN Gain Amplification CN Loss Amplification CN Loss CN Gain Amplification CN Loss Amplification CN Loss Amplification CN Loss
OS-T4 OS-T4 OS-T4 OS-T4 OS-T4 OS-T4 OS-T4	0 32,539,336 32,786,995 54,823,633 54,944,045 57,310,732 62,040,890	32,539,336 32,786,995 54,823,633 54,944,045 57,310,732 58,788,747 170,899,992	CN Gain CN Loss CN Gain Amplification CN Gain CN Loss CN Loss
OS-T5 OS-T5 OS-T5 OS-T5 OS-T5 OS-T5 OS-T5 OS-T5 OS-T5 OS-T5	0 38,636,597 38,768,161 42,856,300 56,339,040 57,310,732 58,142,725 62,040,890 63,006,917 108,746,625 108,931,803	38,636,597 38,768,161 42,856,300 56,339,040 57,310,732 58,142,725 58,788,747 63,006,917 108,746,625 108,931,803 170,899,992	CN Loss CN Gain CN Loss CN Gain CN Loss CN Gain CN Loss CN Gain CN Loss Homozygous Copy Loss CN Loss
OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6 OS-T6	$\begin{array}{c} 0\\ 37,423,792\\ 42,244,459\\ 44,865,136\\ 49,949,400\\ 51,337,510\\ 62,040,890\\ 74,591,912\\ 75,923,593\\ 82,266,195\\ 82,532,187\\ 169,593,858\\ 169,988,076\end{array}$	37,423,792 42,244,459 44,865,136 49,949,400 51,337,510 58,788,747 74,591,912 75,923,593 82,266,195 82,532,187 169,593,858 169,988,076 170,899,992	CN Loss CN Gain CN Loss Amplification CN Gain CN Loss CN Loss CN Loss CN Loss CN Loss CN Gain CN Loss Homozygous Copy Loss CN Loss CN Loss
OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7 OS-T7	0 189,701 327,686 20,146,787 20,648,847 21,513,978 22,257,067 23,475,466 29,141,497 29,541,638 31,008,596 33,277,199 33,398,225	189,701 327,686 20,146,787 20,648,847 21,513,978 22,257,067 23,475,466 29,141,497 29,541,638 31,008,596 33,277,199 33,398,225 33,617,227	Homozygous Copy Loss CN Loss Homozygous Copy Loss Amplification CN Gain Amplification CN Gain Amplification CN Gain Amplification CN Gain CN Gain CN Loss 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
0S-T7	35 293 444	36 283 819	Amplification
05-T7	36 283 819	37 709 462	CN Loss
05-T7	37 709 462	/1 000 301	Amplification
05-17 05 T7	41 000 201		CN Gain
03-17	41,777,371	42,015,744	Amplification
05-17	42,015,744	40,721,457	Amplification
05-17	46,721,457	49,715,179	
05-17	49,715,179	52,954,066	Amplification
05-17	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
05-T8	26,727,200	29 124 576	CN Gain
	20,247,070	20 508 321	CNLOSS
	29,124,370	52 526 065	CN Gain
	29,500,521	52,520,005	Amplification
	52,520,005	53,010,923	
05-18	53,018,925	58,788,747	CN Gain
05-18	62,040,890	124,871,922	CN LOSS
05-18	124,871,922	138,604,858	CN Gain
05-18	141,356,365	142,361,196	CN Loss
OS-18	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
0S-T9	111,794,439	170.899.992	CN Loss
0017			
0S-T10	0	29 956 857	CN Loss
05-T10	29 956 857	30,066,168	CN Gain
05-110 05 T10	20,066,169	25,000,100	CNLOSS
03-110	30,000,108	35,940,900	Amplification
05-110	30,740,700	30,477,804	CN Coin
05-110	36,497,864	30,843,127	
05-110	30,843,127	37,709,462	Amplification
US-110	37,709,462	38,188,441	
US-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
OC T10	57 038 052	58 788 747	CN Gain

OS-T10	62,040,890	63,900,027	Amplification
OS-T10	63.900.027	66.310.880	CN Loss
0S-T10	66.310.880	68,692,340	CN Gain
0S-T10	68 692 340	71 055 544	CNLoss
0S-T10	71 055 544	71 181 602	CN Gain
05-T10	71 181 602	73 358 634	CNLOSS
05-T10	73 358 634	76,750,004	CN Gain
OS-110	75,330,034	90.041.221	
03-110	70,479,040	00,041,331	
03-110 05 T10	09,041,331	90,082,243	
05-110	90,062,245	99,138,116	CN LOSS
0S-110	99,138,116	99,702,878	Homozygous Copy Loss
0S-110	99,702,878	100,538,401	CN Gain
OS-110	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
0S-T10	142.058.368	142,903,376	CN Gain
0S-T10	142 903 376	143 727 594	CNLoss
05-T10	143 727 594	145 464 908	CN Gain
05-T10	145 464 908	153 701 160	CNLoss
05-110 05 T10	152 701 160	157 421 562	Amplification
03-110 OS T10	153,791,109	167,421,505	CN Coin
03-110	157,421,505	161,536,109	
03-110	161,000,109	163,373,793	
05-110	163,375,793	164,649,824	
05-110	164,649,824	170,899,992	
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
05-T12	41 230 683	57 538 110	
05-T12	57 538 110	58 722 020	CN Gain
OS-112	62 040 800	75 594 960	CN Gain
03-112 05 T12	75 594 940	170,800,000	
05-112	75,384,860	170,899,992	
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
0S-T13	50,444,497	58,722,020	CN Gain
0S-T13	62,040,890	101.051.500	CN Loss
0S-T13	101 051 500	140 639 758	CN Gain
OS-T13	140,639,758	170,899,992	CN Loss
OC T14	0		
05-114		30,606,525	
05-114	36,606,525	52,391,487	
US-114	52,391,487	58,722,020	UN LOSS
05-114	62,040,890	170,899,992	UN 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
CENTROMERE		
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
Х	154.91	59.5	95.41	1020	1373	3617	6.58	23.35
Υ	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
Х	0.28	9.16E-05	14.39	17.14
Υ	0.05	1.57E-05	1.44	2.39